

Kinship, Sex, and Biological Relatedness. The contribution of archaeogenetics to the understanding of social and biological relations

15. Mitteldeutscher Archäologentag
vom 6. bis 8. Oktober 2022 in Halle (Saale)

Herausgeber Harald Meller, Johannes Krause,
Wolfgang Haak und Roberto Risch

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Johannes Krause,
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Kinship, Sex, and Biological Relatedness – The contribution of archaeogenetics to the understanding of social relations

Roberto Risch, Wolfgang Haak, Johannes Krause, and Harald Meller

Wer gehört zur Verwandtschaft und wer nicht? Viele Menschen würden diese Frage instinktiv mit der Nennung näherer Familienmitglieder, z. B. Eltern, Geschwister, Großeltern und Kinder beantworten. Doch dieses Verständnis von Verwandtschaft, das in der Regel biologische Verbindungen umfasst, ist nur eine Sichtweise und trifft weder auf alle Gesellschaften noch auf alle Zeiträume in der Geschichte der Menschheit zu.

Mithilfe hochauflösender Sequenzierungsmethoden ist die moderne Humangenetik seit einigen Jahren in der Lage, biologische Verwandtschaftsverhältnisse (auch Blutsverwandtschaft) bis zum 10. Grad nachzuvollziehen. Hierauf basierend konnte die Archäogenetik Methoden und Verfahren entwickeln, die es bei guter DNA-Erhaltung erlauben, genetische Beziehungen zwischen Menschen zu bestimmen, die in der Vergangenheit gelebt haben. Diese biologischen Verbindungen setzen sexuelle wie soziale Beziehungen zwischen Menschen voraus, die von soziologischem und historischem Interesse sind. Eine Gleichsetzung von biologischer und sozialer Verwandtschaft oder eine Rückführung der einen auf die andere ist jedoch nur bedingt möglich und begrenzt somit die Aussagemöglichkeit rein biologischer Verwandtschaftsstudien.

Der 15. Mitteldeutsche Archäologentag hat sich den archäologischen und naturwissenschaftlichen Möglichkeiten der Bewertung verwandtschaftlicher Beziehungen in ur- und frühgeschichtlichen Zeitperioden gewidmet. Hierbei galt es, einen kritischen Fokus auf die rasch voranschreitende naturwissenschaftliche Entwicklung der Archäogenetik und die steigende Zahl von archäogenetischen Studien zu biologischer Verwandtschaft in der Menschheitsgeschichte zu legen. Ziel der Tagung war es, die theoretischen und methodischen Grundlagen dieses relativ jungen Forschungsbereiches, welcher Genetik, Ethnologie, physische Anthropologie und Archäologie verbindet, zu diskutieren bzw. zu klären. Bei der Tagung stand deshalb im Vordergrund, die Vielfalt unterschiedlicher Ansätze vor allem in Bezug auf das Verständnis von Verwandtschaft sichtbar zu machen und die Diskussion zwischen den Disziplinen zu fördern. Diese Pluralität an Begrifflichkeiten und Interpretationen ist auch im vorliegenden Tagungsband nicht eingeschränkt oder vereinheitlicht worden und spiegelt so die Breite der ethnologischen, genetischen, archäologischen und historischen Forschungsansätze und Beiträge wider. Ein Anspruch auf Vollständigkeit wie im Sinne eines Lehrbuchs kann schon deshalb nicht erhoben werden, da sich das noch junge Fachgebiet immer noch dynamisch weiterentwickelt. Ziel der Tagung war es auch, an unterschiedlichen Fallbeispielen die heuristischen Möglichkeiten dieser Diskussion und die Übertragbarkeit verschiedener Ansätze zu überprüfen (Abb. 1). Letztendlich führen vor allem diejenigen Studien zu einer Antwort, die bisher nicht sichtbare Bereiche zwischenmenschlicher Beziehungen und Organisation durch die Analyse alter DNA zugänglich machen.

Who is part of the family and who is not? Many people would instinctively reply by naming close family members, such as their parents, siblings, grandparents, and children. This notion of family, however, which usually comprises biological connections, is only one way of looking at it, and it holds true neither in all societies nor in all periods of human history.

For a few years, modern human genetics has been able to determine biological family relationships (also called consanguinity) up to the 10th degree, using high-resolution sequencing methods. On this basis, archaeogeneticists have developed methods and procedures that allow them to determine genetic relations between humans who lived in the past, provided that their DNA is well preserved. These biological connections assume sexual and social relations between humans that are of sociological and historical interest. Treating biological and social kinship equivalently, or tracing one back to the other, is, however, only possible up to a point; insights based on purely biological kinship studies are therefore limited.

The 15th Archaeological Conference of Central Germany was dedicated to the archaeological and natural-scientific possibilities of evaluating family relations in pre- and protohistoric times. The goal was to cast a critical focus on a quickly advancing natural-scientific development of archaeogenetics and on the increasing number of archaeogenetic studies of biological kinship in human history. The aim of the conference was to discuss and clarify the theoretical and methodological fundamentals of this relatively young field of research, which combines genetics, social anthropology, physical anthropology, and archaeology. Uncovering the diversity of various approaches primarily in regard to the understanding of kinship and promoting the discussion between disciplines and approaches were therefore at the centre of attention. This plurality of concepts and interpretations has not been restricted or standardised in the present conference volume, reflecting the wide range of socio-cultural, genetic, archaeological, and historical research approaches and contributions. No claim to be exhaustive in the sense of a textbook can be made if for no other reason than because this field of research, which is still young, has not ceased to evolve dynamically. Another aim of the conference was to examine the heuristic possibilities of this debate and the transferability of various approaches using various case studies (Fig. 1). Ultimately, the studies that make previously invisible areas of interpersonal relationships and organisation accessible through the analysis of ancient DNA will lead to the most promising results.

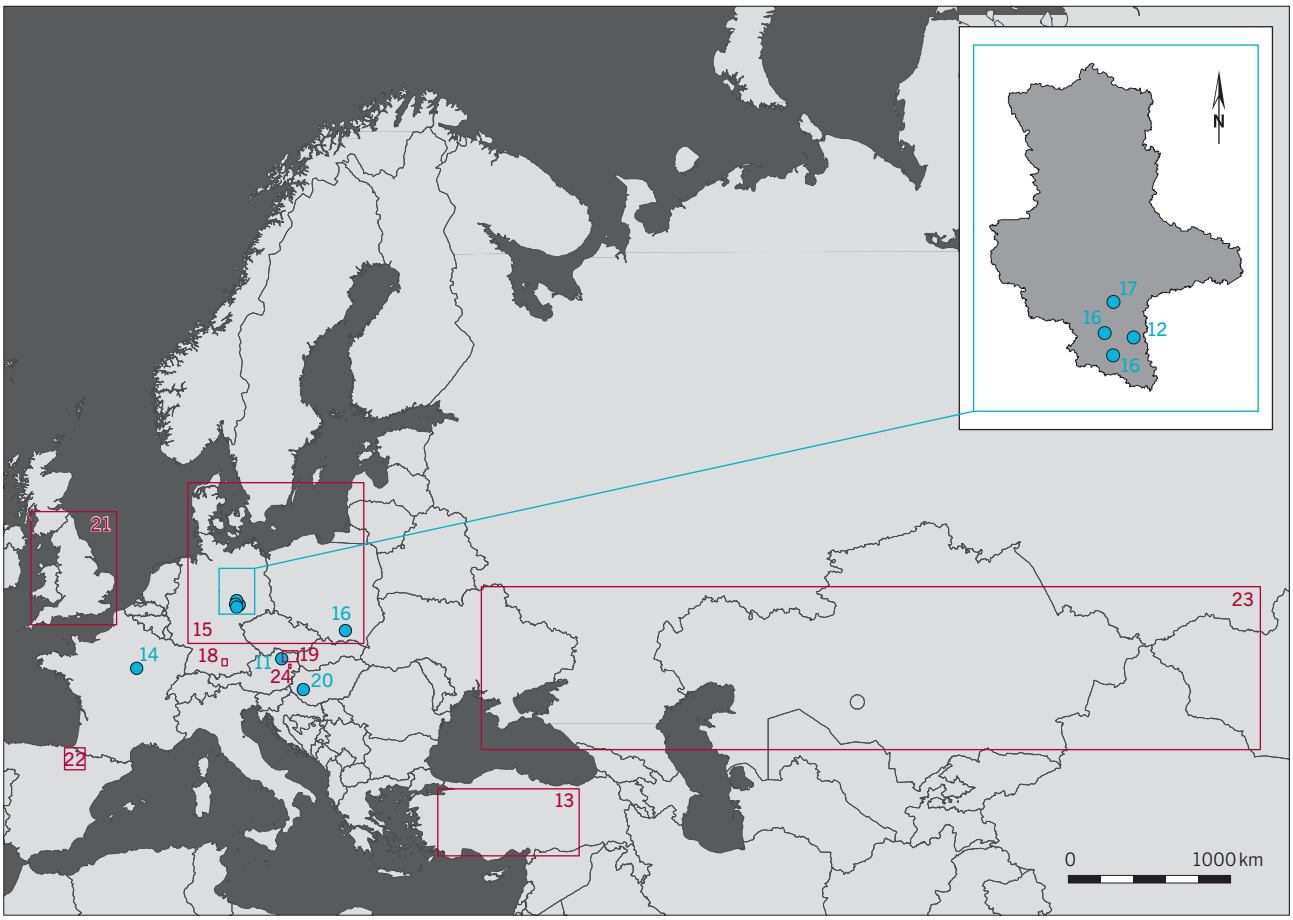


Abb. 1 Karte der in diesem Band behandelten Regionen (rot) und Orte (blau). Die Nummerierung entspricht der Reihenfolge der Beiträge im Band.

Fig. 1 *Map showing the regions (red) and sites (blue) discussed in this volume. The numbering corresponds to the order of contributions in this volume.*

11 Neugebauer-Maresch et al.; 12 Orschiedt et al.; 13 Somel et al.; 14 Rivollat et al.; 15 Johannsen; 16 Haak et al.; 17 Penske et al.; 18 Mittnik et al.; 19 Rebay-Salisbury et al.; 20 Kiss et al.; 21 Brück; 22 Papac et al.; 23 Gass; 24 Daim et al. (nicht kartiert/not mapped: 1 Thelen; 2 Alber; 3 Frieman; 4 Pohl; 5 Scally; 6 Alt; 7 Günther; 8 Ringbauer; 9 Popli et al.; 10 Friedrich et al.).

Der Beitrag der Archäogenetik in der Verwandtschaftsdiskussion

Die erste Herausforderung, der sich die Archäogenetik bei dem Verständnis zwischenmenschlicher Beziehungen anhand biologischer Nähe stellt, ist die Definition von Verwandtschaft und deren Bedeutung, etwa in Bezug auf soziale und sexuelle Ungleichheit, Arbeitsteilung oder Machtgefüge in vergangenen Gesellschaften. Während die Archäologie quellenbedingt bisher kaum in der Lage war, sichere Aussagen zu dieser Thematik zu leisten, wird der herkömmliche Verwandtschaftsbegriff in der heutigen Ethnologie kritisch hinterfragt. Ein wichtiger Teil der etablierten Verwandtschaftsstudien hat sich dabei als ein Konstrukt des westlichen, kolonialen Verständnisses von nicht-europäischen Gesellschaften herausgestellt, bei dem monogame, heteronormative und binäre Beziehungen auf alle anderen menschlichen Lebensformen projiziert worden sind (Schneider 1984; s. Beitrag Thelen in diesem Band). Hinzu kommt, dass in vielen Gesellschaften kein Verständnis oder nur eine flexible Vorstellung von Verwandtschaft existiert; etwas, was selbst in Europa bis ins frühe Mittelalter der Fall war (s. Beitrag Pohl in diesem Band). Auch neuere interdisziplinäre Untersuchungen zeigen, wie eigenartig und sonderbar das moderne, abendländische Ver-

The contribution of archaeogenetics in the kinship debate

The first challenge archaeogenetics faces in the understanding of interpersonal relations on the basis of biological proximity is the definition of kinship and its meaning, for example, regarding social and sexual inequality, division of labour, or power structures in societies of the past. Whereas archaeology has so far hardly been able to give sound insights into this topic due to the archaeological sources, the conventional concept of kinship is being critically questioned in today's socio-cultural anthropology. An important part of the established kinship studies has proven to be a construct of the western colonial perceptions of non-European societies whereby monogamous, heteronormative, and binary relations were projected onto all other forms of human life (Schneider 1984; cf. Thelen in this volume). Furthermore, many societies have either no notion or only a flexible notion of kinship, which was even the case in Europe up until the early Middle Ages (cf. Pohl in this volume). Recent interdisciplinary investigations also show how very peculiar the modern western understanding of kinship is among human societies and how significant it was for the formation of capitalism (Henrich 2020). The kind of perspective that was

ständnis von Verwandtschaft unter den menschlichen Gesellschaften ist und welche Bedeutung es für die Entstehung des Kapitalismus hatte (Henrich 2020). Eine solche Sichtweise, wie sie vor allem an westlichen Universitäten in den letzten Jahrhunderten tradiert wurde, verschließt oder verzerrt jegliches Verständnis der engeren sozialen Beziehungen anderer Gesellschaften. Welche Rolle sozialer Verwandtschaft allerdings in der Urgeschichte zukam oder ob der Begriff dort überhaupt anwendbar ist, muss bestenfalls unsicher bleiben, da uns diese Gesellschaften keine Texte, Zeichen oder bildliche Darstellungen, sondern nur archäologische Quellen wie Grabfunde, Siedlungen oder Horte hinterlassen haben. Diese eignen sich nur in den seltensten Fällen für die Rekonstruktion immaterieller sozialer Beziehungen.

Die Art und Weise, wie die biologische und soziale Reproduktion von Gesellschaften verstanden und untersucht werden sollte, wird somit in den Sozialwissenschaften derzeit neu überdacht. Zwei grundsätzlich unterschiedliche Perspektiven und Ansätze werden hierbei sichtbar. Auf der einen Seite findet eine Erweiterung des Verwandtschaftsbegriffes weit über familiäre oder hausbezogene Beziehungen statt: Freundschaft (s. Beitrag Thelen in diesem Band), Affiliationen (s. Beitrag Frieman in diesem Band), soziale Zugehörigkeit (s. Beitrag Alber in diesem Band) oder soziale Verbindungen allgemein sind zu Synonymen von Verwandtschaft geworden (Carsten 2000; Johnson/Paul 2016). Konzepte wie *kinning*, *doing kinship* oder *kin-making* sind eingeführt worden, um die soziale, aktive Komponente im Flechten und Auflösen von Verwandtschaftsbeziehungen zu unterstreichen (Howell 2006; s. Beitrag Frieman in diesem Band). Solche Praktiken entstehen durch die Pflege von Anderen, das Teilen von Essen, die gemeinsame Einnahme von Drogen, Adoption und Verstoß, kurzum das generelle Nicht- und/oder Zusammenleben/erfahren etc. (s. Beitrag Thelen in diesem Band). Damit werden auch Bereiche wie Festmahle *(feasting)* und Fürsorge, die seit längerem in der Archäologie diskutiert werden, Teil der Verwandtschaftsbeziehungen. In Anlehnung an P. Descola (2005, 489–528) wird außerdem die herkömmliche Dichotomie zwischen Kultur und Natur infrage gestellt, womit eine Verwandtschaft zu Tieren, Pflanzen, Steinen oder Erde denkbar wird, z. B. wenn diese in Gräbern zusammen mit Menschen beigesetzt sind (s. Beiträge Frieman und Brück in diesem Band). Aus dieser Perspektive könnten auch alle anderen Grabgegenstände als potenzielle Verwandte anstelle von passiven Beigaben angesprochen werden, was zweifellos neue Deutungsmöglichkeiten und Narrative in der Archäologie eröffnet. In jedem Falle schiebt diese Begriffserweiterung – absichtlich – die Bedeutung der Verwandtschaft hinsichtlich der biologischen sowie sozial-ökonomischen Reproduktion der Gruppe in den Hintergrund. Andererseits kann aber auch anhand ethnografischer Beispiele argumentiert werden, dass Kinder aufgrund ihrer »verspäteten Personwerdung« nicht unbedingt einen Platz in den Bestattungsritualen oder in der Verwandtschaft einnehmen müssen (Lancy 2014; Cveček/Schwall 2022). Diese Erweiterung und der Wandel der Begrifflichkeiten, um neuen Einzelbeobachtungen gerecht zu werden, können auch zu dem Schluss von »kinship as such has little analytical value« führen (s. Beitrag Thelen in diesem Band).

passed on mainly at western universities during previous centuries precludes or distorts any understanding of the closer social relations of other societies. However, the role of social kinship in prehistory – even whether the concept can be used there at all – has to remain uncertain at best because no texts, signs, or pictures remain of those societies but only archaeological sources, such as graves, settlements, and hoards, which are rarely suitable for the reconstruction of immaterial social relations.

The way in which the biological and social reproduction of societies should be understood and investigated is therefore being reassessed in the social sciences. Here, two fundamentally different perspectives and approaches become visible. On the one hand, an expansion of the concept of kinship far beyond relations within the family or the lived-in house is taking place: Friendship (cf. Thelen in this volume), affiliations (cf. Frieman in this volume), social belonging (cf. Alber in this volume), and social relatedness in general have become synonyms of kinship (Carsten 2000; Johnson/Paul 2016). Concepts such as kinning, doing kinship, and kin-making have been introduced to emphasise the social, active components when family relations are being established or dissolved (Howell 2006; cf. Frieman in this volume). Such practices arise from caring for others, sharing food, joint/communal consumption of drugs, adopting and expelling – in short, the general living/experiencing with or without one another, etc. (cf. Thelen in this volume). As a result, activities such as feasting and care-giving that have been the topic of discussion in archaeology for a while also become part of family relations. Following P. Descola (2005, 489–528), the traditional dichotomy between culture and nature is also questioned, and this makes kinship with animals, plants, rocks, and soil feasible – for example, when they are buried in graves together with humans (cf. Frieman and Brück in this volume). From this perspective, all other burial objects could be addressed as potential relatives instead of passive grave furnishings, which undoubtedly opens up new possibilities of interpretation and narratives in archaeology. In any case, this conceptual expansion intentionally moves the significance of kinship with regards to the biological and socio-economic reproduction of the group to the background. Using socio-cultural examples, one could, on the other hand, argue that children do not necessarily have to hold a place in the burial rituals or as part of the kin due to their »delayed personhood« (Lancy 2014; Cveček/Schwall 2022). This expansion, and the change in concepts necessary in order to accommodate new individual observations, may lead to the conclusion that »kinship as such has little analytical value« (cf. Thelen in this volume).

Nevertheless, the political control of biological reproduction and sexual relations that kinship presupposes remains a crucial aspect for the historical understanding of power, the distribution of property, and political forms in general (Foucault 1976). The connection between family, private property, and the state as argued by Karl Marx and Friedrich Engels (Engels 1884; Goody 1990) is without question rooted in the conflicts and knowledge of the 19th century; however, this connection seems to turn out to be an important factor in the formation of the occidental world (Henrich 2020). What kind of human relations have led to the prevalence of hereditary privileges and property – and ultimately to the

Die politische Kontrolle der biologischen Reproduktion und der sexuellen Beziehungen, die sie voraussetzt, bleibt jedoch ein entscheidender Aspekt für das historische Verständnis von Macht, Besitzverhältnissen und politischen Formen allgemein (Foucault 1976). Die von Karl Marx und Friedrich Engels argumentierte Verbindung zwischen Familie, Privateigentum und Staat (Engels 1884; Goody 1990) ist ohne Zweifel in den Konflikten und dem Wissen des 19. Jhs. verankert, scheint sich aber in der Herausbildung der abendländischen Welt durchaus als ein bedeutender Faktor herauszustellen (Henrich 2020). Welche Art von menschlichen Beziehungen zur Durchsetzung vererblicher Privilegien und Besitz und – letztendlich – zur Entstehung von Staaten in der Urgeschichte geführt haben, bleibt weiterhin eine entscheidende Frage der Archäologie und Ethnologie.

Im Gegensatz zur inhaltlichen und begrifflichen Erweiterung wird auf der anderen Seite der Debatte versucht, Verwandtschaft auf konkrete soziale Praktiken zu begrenzen wie »Elternschaft« oder »Mutterschaft«. Im ersten Fall wird der Fokus auf die vielfältigen sozialen Aspekte der Zeugung, Pflege, Erziehung und Beziehungen allgemein zwischen Eltern – wie auch immer definiert – und deren Kinder gerichtet (s. Beitrag Alber in diesem Band). Noch spezifischer wird die enge körperliche und emotionale Verbindung zwischen Müttern und Kindern mit dem Begriff »Mutterschaft« gefasst (s. Beitrag Rebay-Salisbury et al. in diesem Band). Zeugung, Schwangerschaft, Stillen und Pflege von Kindern sind ein grundlegender Teil der biologischen und sozialen Reproduktion von Gesellschaften, deren Bedeutung sich im archäologischen Kontext, wie z. B. durch räumliche Nähe oder gemeinsame Gräber, darstellen kann. Keines der beiden Konzepte lässt sich jedoch auf Blutsverwandtschaft reduzieren, da die Adoption von Kindern oder das Aufziehen fremder Kinder in vielen Gesellschaften von Bedeutung ist (z. B. Beitrag Alber in diesem Band).

Weitgehend unabhängig von dieser Diskussion um den Begriff Verwandtschaft und seiner Bedeutung hat in den letzten Jahren die Bestimmung der biologischen oder genetischen Beziehung in ur- und frühgeschichtlichen Gemeinschaften exponentiell zugenommen. Dank unterschiedlicher statistischer Methoden und trotz oft lückenhafter archäogenetischer Daten ist es möglich, die biologische Nähe zwischen zwei Individuen in Verwandtschaftsgraden abzuschätzen und unter Zuhilfenahme von kontextueller Information als Stammbaum darzustellen (z. B. Beiträge Günther, Mittnik et al., Ringbauer und Popli et al. in diesem Band). Wie bei modernen genetischen Daten beruht das Prinzip der Verwandtschaftsanalyse auf dem zu erwartenden Anteil an Erbmaterial, welches zwei eng verwandte Individuen teilen (z. B. 50 % bei erstgradiger Verwandtschaft), und was selbst bei geringfügiger Datenabdeckung oft noch gelingt. Diesem theoretisch erwartbaren Wert sind jedoch natürliche Grenzen gesetzt, da sich zum einen mit jedem Grad der Entfernung die Menge des geteilten Erbgutes weiter halbiert und sich zum anderen durch die zufällige Rekombination nicht einheitlich auf die Nachkommen verteilt. Tatsächlich ist ab etwa dem 10. Grad wahrscheinlicher, dass sich zwei biologisch verwandte Individuen kein Erbmaterial teilen, welches auf zwei gemeinsame Vorfahren zurückzuführen ist.

formation of states in prehistory – continues to remain a crucial question in archaeology and socio-cultural anthropology.

In contrast to the expansion in content and concepts, the other side of the debate attempts to limit kinship to specific social practices, such as »parenting« and »motherhood.« Parenting focuses on the manifold social aspects of conceiving, caring, upbringing, and relations in general between parents, however they may be defined, and their children (cf. Alber in this volume). The close physical and emotional connection between mothers and children is more specifically defined with the concept of »motherhood« (cf. Rebay-Salisbury et al. in this volume). Conception, pregnancy, breastfeeding, and caring for children are a fundamental part of the biological and social reproduction of societies, whose significance can show in archaeological contexts, for example, by spatial proximity or sharing a grave. Neither of the two concepts, however, can be reduced to biological relations because the adoption of children and the raising of other people's children are important in many societies (e.g., cf. Alber in this volume).

Largely unrelated to this discussion of the concept of kinship and its significance, the number of cases in which biological or genetic relatedness in pre- and protohistoric communities has been determined has increased exponentially in recent years. Due to various statistical methods and despite often incomplete archaeogenetic data, the biological distance between two individuals can be estimated in degrees of relatedness that can be visualised in the form of a ›family‹ tree with the aid of contextual information (e.g., cf. Günther, Mittnik et al., Ringbauer, and Popli et al. in this volume). Analogous to modern genetic data, this principle of kinship analysis is based on the theoretically expected percentage of genetic material shared by two individuals (e.g., 50 % in the case of 1st-degree relatives), which is possible despite limited data. This theoretically expectable value, however, has natural limits: on the one hand, the shared genome is halved with every additional degree, and, on the other hand, it is not distributed evenly among the offspring due to random recombination. In fact, from approximately the 10th degree onwards the probability increases that two biologically related individuals with two ancestors in common do not share any genetic material.

But a reduction of kinship – however it is defined – to genetic, genealogical, and social ancestry has far-reaching consequences for the way in which we understand the organisation of communities (cf. Scally in this volume). Beyond the primary relation of a mother with her offspring, all kinship practices are social constructs[1]. For this reason, kinship not only expresses the biological ties between individuals but is also a complex symbolic representation of certain social relations. Whereas close genetic ancestry can be staged, ignored, or simply be unknown/withheld – as, for example,

1 Here just a couple of direct quotes from anthropologists: »A kinship system does not consist in the objective ties of descent and consanguinity between individuals. It exists only in human consciousness; it is an arbitrary system of representations, not the spontaneous development of a real situation« (Lévi-Strauss 1963, 50). »Die Zurückführung der Verwandtschaft auf die biotischen Tatbestände (Rassismus, ›Stimme des Blutes‹) ist Fiktion« (Müller 1983, 165).

Eine Reduktion von Verwandtschaft, wie auch immer man diese definiert, auf genetische, genealogische und soziale Herkunft/Nachkommenschaft hat jedoch weitreichende Folgen für die Art und Weise, wie wir die Organisation von Gemeinschaften verstehen (s. Beitrag Scally in diesem Band). Über die primäre Beziehung einer Mutter zu ihrem Nachwuchs hinaus sind alle verwandtschaftlichen Praktiken als soziale Konstruktionen zu verstehen[1]. Aus diesem Grund drückt Verwandtschaft nicht nur die biologischen Bindungen zwischen Individuen aus, sondern ist eine komplexe symbolische Darstellung bestimmter sozialer Beziehungen. Während die nahe genetische Abstammung vorgetäuscht, ignoriert oder unbewusst sein/verschwiegen werden kann, wie z. B. im Falle von Vaterschaften, ermöglichen/bezwecken in die Vergangenheit gerichtete genealogische (!) Abstammungslinien eine identitäre Denkweise gegenüber dem »Anderen«, die auch auf ideologische Konstrukte wie Rasse, Volk, Kultur oder Nation übertragen werden kann. Solche Strategien naturalisieren und legitimieren wiederum soziale Ungleichheiten, Ausbeutung, Genozide, Kriege etc. (Alber/Thelen 2022). Nicht nur sind direkte genetische Abstammungen über einen Zeitraum von mehr als 300 Jahren aus oben genannten Gründen schlichtweg nicht nachweisbar (Reich 2018), vor diesem politischen Hintergrund sind auch genealogische Abstammungen fachlich irrevelant.

Während die Verbindung zwischen Verwandtschaft und biologischer Abstammung ungewiss und historisch ist, setzt die Reproduktion menschlicher Gesellschaften ungleichgeschlechtliche Interaktion voraus.

Die Genetik kann einen direkten Einblick in den natürlichen oder primären Mechanismus der biologischen Fortpflanzung geben: Abstammung und Blutsverwandtschaft. Sexuelle Beziehungen zwischen Menschen lassen sich jedoch weder auf den Akt der reinen biologischen Fortpflanzung noch auf Verwandtschaftsstrukturen reduzieren. Sie sind so vielfältig wie alle anderen zwischenmenschlichen Praktiken, die von Leidenschaft, Emotionen und Fantasie gesteuert werden, können aber gleichzeitig auch sozialen Regeln unterstehen. Die Kontrolle über die Sexualität ist ein entscheidendes Element in der Ausübung von Macht über Sexualdispositive, die versuchen, die Möglichkeiten von sexuellen Beziehungen z. B. durch Tabus, Moral, Recht und Gewalt zu begrenzen, zu regeln oder zu fördern (Foucault 1976). Während die Fortpflanzung vom Geschlechtsakt bestimmt wird, können gewisse Machtgefüge die Fortpflanzung sowie auch sexuelle Beziehungen insoweit beeinflussen, dass hierdurch Verwandtschafts- und Heiratsregeln gesteuert werden, um z. B. die Reproduktion bestimmter wirtschaftlicher, politischer und demografischer Gegebenheiten zu sichern. Inwieweit »Sex am Kreuzpunkt von ›Körper‹ und ›Bevölkerung‹ zur zentralen Zielscheibe von Macht« (Foucault 1983, 142) nicht nur in der westlichen Gesellschaft, sondern auch in vor-

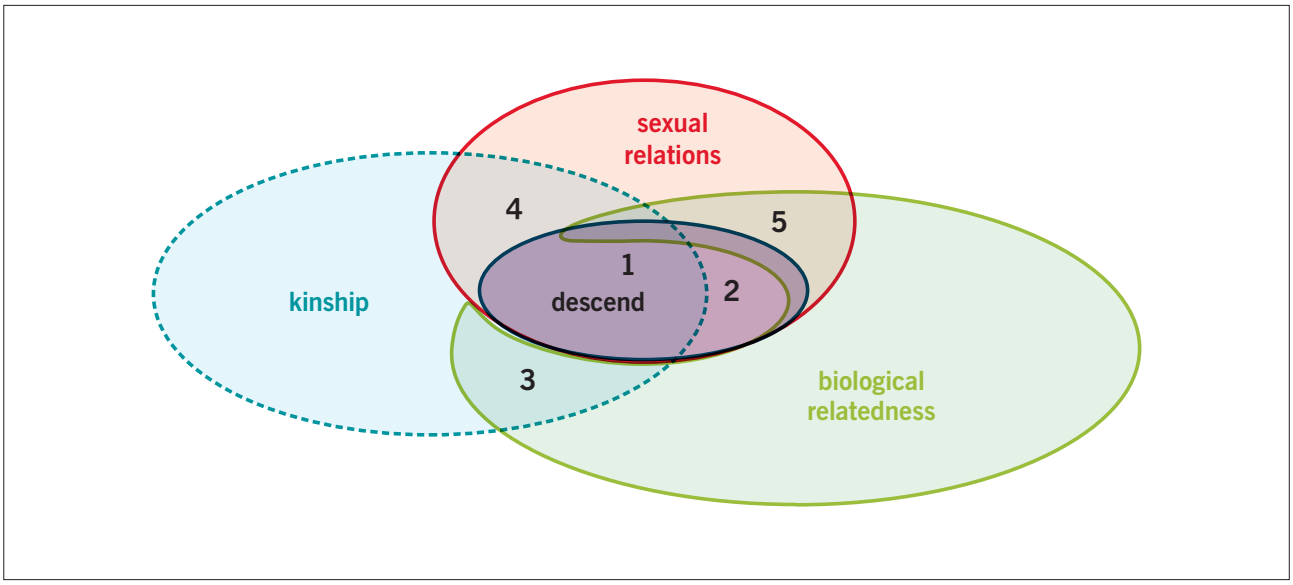
in the case of fatherhood – genealogical (!) lineages directed into the past provide/presume an identitary way of thinking towards the »other« that can also be applied to ideological constructs, such as race, people, culture, and nation. Such strategies, on the other hand, naturalise and legitimise social inequalities, exploitation, genocides, wars, etc. (Alber/Thelen 2022). For the reasons mentioned above, verifying direct genetic ancestries over a period of more than 300 years is not only simply impossible (Reich 2018); genetic ancestries are also scholarly irrelevant in light of this political background.

While the link between kinship and biological descent is uncertain and historical, the reproduction of human societies requires heterosexual interaction.

Genetic information provides direct insight into the natural or primary mechanism of biological reproduction: descent and consanguinity. Sexual relations between humans, however, can be reduced to neither the act of pure biological reproduction nor kinship structures. They are as diverse as all other interpersonal practices that are driven by passion, emotions, and fantasy, but they can, at the same time, be subject to social rules. The control of sexuality is a crucial element in the execution of power via dispositifs of sexuality; they try to limit, regulate, or promote the possibilities of sexual relations – for example, using taboos, morals, laws, and violence (Foucault 1976). Whereas procreation is determined by sexual intercourse, certain power structures can influence procreation and sexual relations to the extent that they control kinship and marriage rules, for example, to ensure the reproduction of certain economic, political, and demographic conditions. To what extent, »at the juncture of the ›body‹ and the ›population‹, sex became a crucial target of a power« (Foucault 1978, 147) therefore remains a historically central question not only in western society but also in prehistoric societies and early states. The nature of social rules also implies that, in principle, they can be broken. For the first time, archaeogenetics is in fact able to provide insights into the social and political regulation of sexuality and procreation.

The interconnectedness of sex, conception, descent, and kinship highlights the existing junctions between these events and relations that are of considerable social relevance, even if deciphering these relations turns out to be epistemologically complex (Fig. 2). The capacity of genetics to determine biological degrees of relatedness and communities of common descent is doubtlessly an expansion of the potential insights archaeology, physical anthropology, and socio-cultural anthropology may provide; at the same time, it is an invitation to better understand the relationship between the sexual, social, and biological relations in societies – without assuming that they are universal principles and without excluding them from social research as ›unnerving‹ aspects of social life.

1 Hier nur zwei wörtliche Zitate aus der Anthropologie: »A kinship system does not consist in the objective ties of descent and consanguinity between individuals. It exists only in human consciousness; it is an arbitrary system of representations, not the spontaneous development of a real situation« (Lévi-Strauss 1963, 50); »Die Zurückführung der Verwandtschaft auf die biotischen Tatbestände (Rassismus, ›Stimme des Blutes‹) ist Fiktion« (Müller 1983, 165).



geschichtlichen Gesellschaften und frühen Staaten wurde, bleibt daher weiterhin eine historisch zentrale Frage. Ebenfalls liegt es in der Natur sozialer Regeln, dass man sie prinzipiell durchbrechen kann. Die Archäogenetik ist durchaus in der Lage, – erstmals – einen Einblick in die soziale und politische Regelung von Sexualität und Fortpflanzung zu geben.

Die Vernetzung von Sex, Zeugung, Abstammung und Verwandtschaft verdeutlicht, dass Schnittstellen zwischen diesen Ereignissen und Beziehungen existieren, die von bedeutender sozialer Relevanz sind, auch wenn sich die Entschlüsselung dieser Beziehungen erkenntnistheoretisch als komplex herausstellt (Abb. 2). Das Potenzial der Genetik, biologische Verwandtschaftsgrade und Abstammungsgemeinschaften zu erfassen, stellt ohne Zweifel eine Erweiterung der Erkenntnismöglichkeiten von Archäologie, Anthropologie und Ethnologie dar, aber gleichsam auch eine Aufforderung, das Verhältnis zwischen den sexuellen, sozialen und biologischen Beziehungen in Gesellschaften historisch besser zu verstehen, statt sie als universelle Prinzipien vorauszusetzen oder als ›beunruhigende‹ Aspekte gesellschaftlichen Lebens aus der Sozialforschung auszuschließen.

Abb. 2 Die vielfältigen und wechselseitigen Bezüge zwischen sexuellen Beziehungen, Verwandtschaft, biologischer Nähe und Abstammung. Schnittfläche 1: Die biologische Reproduktion von Gemeinschaften setzt ungleichgeschlechtliche Beziehungen voraus und wird durch die in der jeweiligen Gesellschaft verankerten sozialen Normen gesteuert. Sie bestimmt die biologische Nähe der nächsten Generation; Schnittfläche 2: Sex und Fortpflanzung finden außerhalb der Verwandtschaft statt; Schnittfläche 3: Verwandtschaft und biologische Nähe sind auch unabhängig von sexuellen Beziehungen und Abstammung verbunden; Schnittfläche 4: Nicht alle sexuellen Beziehungen innerhalb von Verwandtschaft führen zu Nachkommen oder biologischer Nähe; Schnittfläche 5: Biologisch Nahestehende können sexuelle Beziehungen und Abstammung innerhalb oder außerhalb der Verwandtschaft haben (»Inzest«). Letztendlich können auch alle drei Bereiche (Genealogie, Sex und Verwandtschaft) unabhängig voneinander agieren. Die Größe der Schnittflächen repräsentiert nicht die Bedeutung der Beziehungen in unterschiedlichen Gesellschaften, sondern dient nur der visuellen Darstellung unterschiedlicher Verbindungen.

Fig. 2 *The manifold and mutual connections between sexual relations, kinship, biological distance, and descent.*
Section 1: The biological reproduction of communities requires heterosexual relations and is controlled by the social norms anchored in the respective society. It determines the next generation's biological distance; Section 2: Sex and procreation take place outside the kin; Section 3: Kinship and biological distance are also connected independently of sexual relations and descent; Section 4: Not all sexual relations between related persons lead to offspring or biological proximity; Section 5: Biologically closely related individuals can have sexual relations and descent within or outside their kin (»incest«). Ultimately, all three areas (biological relatedness, sex, and kinship) can also act independently of each other. The size of the sections does not represent the importance of the relations in various societies but only serves as a visual illustration of different connections.

Soziale und biologische Beziehungen im archäologischen und genetischen Befund

Die weitere Herausforderung, mit welcher prähistorische Verwandtschaftsanalysen konfrontiert sind, ist die Deutung archäologischer Befunde als Resultate sozialer Organisationsformen. Sexualität und Verwandtschaft (biologischer wie sozialer Art) sind immateriell und somit archäologisch als solche weder direkt noch eindeutig fassbar, außer sie werden symbolisch dargestellt bzw. abgebildet. Neben schriftlichen und bildlichen Nachweisen werden vor allem Bestattungspraktiken als Hinweise von Verwandtschaftsbeziehungen verstanden, z. B. durch die Lage der Toten zueinander oder ihre Ausstattung. Allerdings ist dieses Vorgehen eine Abkür-

Social and biological relations in the archaeological context and their genetic evidence

A further challenge prehistoric kinship analyses face is the interpretation of archaeological contexts as the results of social forms of organisation. Sexuality and (biological and social) kinship are immaterial and therefore archaeologically neither directly nor unambiguously tangible unless they are symbolically represented or depicted. Other than written and pictorial evidence, burial practices in particular serve as indications of family relations, e.g., by the position of the dead to each other, or by their grave goods. Yet, this procedure is a shortcut that overlooks the fundamental difference between both symbolic worlds. Funerary practices are undoubtedly

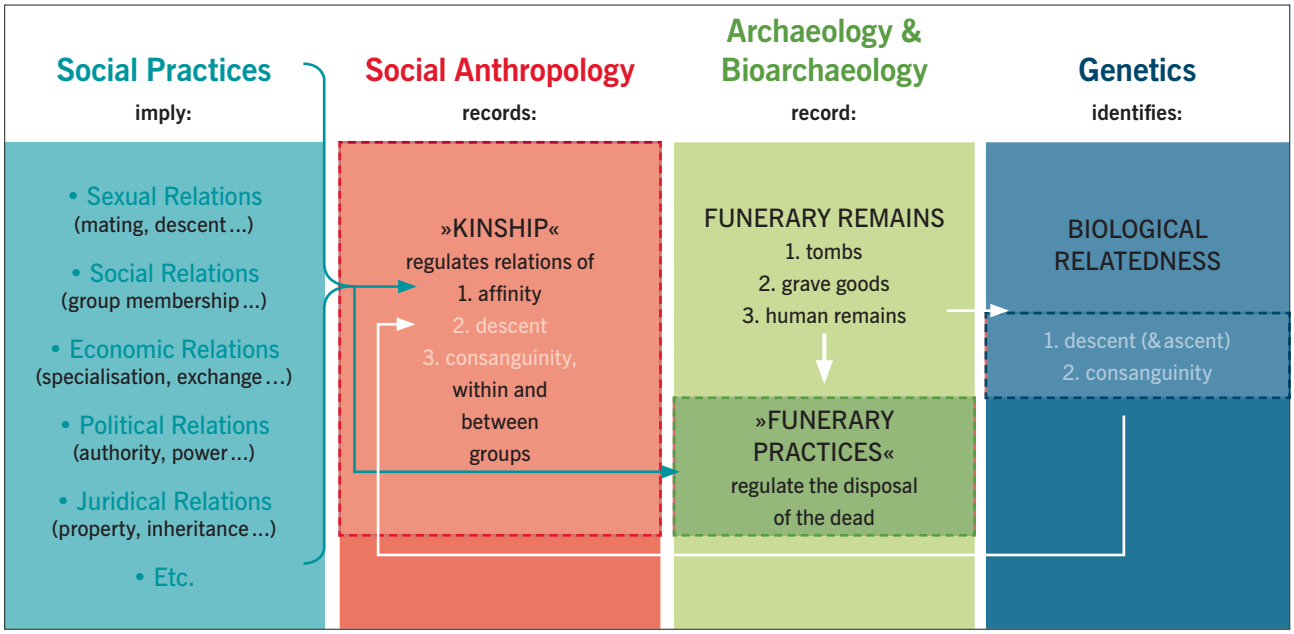


Abb. 3 Die Bereiche sozialer Praktiken und ihre Beziehung zum heuristischen Potenzial. Anthropologie, Archäologie und Genetik beleuchten jeweils unterschiedliche Ausdrucksmöglichkeiten von sozialen Beziehungen und Materialität.

Fig. 3 *The realms of social practices and their relation to the heuristic potential. Anthropology, archaeology, and genetics each highlight different expressions of social relations and materiality.*

zung, die den grundlegenden Unterschied zwischen beiden symbolischen Welten unbeachtet lässt. Bestattungspraktiken sind zweifellos das materielle Ergebnis einer Kombination aus Überzeugungen, Regeln und vermutlich auch Begriffen, die verwendet wurden, um sich toter Mitglieder der eigenen oder anderer Gemeinschaften zu entledigen. Aufgrund der Vielfalt von Bestattungsformen bieten diese Praktiken eine öffentliche Darstellung, um biologische und sexuelle, aber auch soziale, wirtschaftliche, politische, ideologische oder andere Beziehungen auszudrücken, aufzuerlegen oder zu negieren (Abb. 3). Nichts erlaubt es uns jedoch davon auszugehen, dass Bestattungspraktiken Affinitäts- oder Verwandtschaftsbeziehungen dialektisch oder indirekt widerspiegeln. Auch wenn beide symbolischen Systeme zur sozialen Reproduktion der Gemeinschaft beitragen, sind die Verbindungen zwischen ihnen alles andere als offensichtlich. Die Archäologie hat vor allem eine Reihe von Prämissen sowie statistische und Rückschlussverfahren entwickelt, um im Grabkontext erfasste Objekte bezüglich ihrer Unterschiede und Asymmetrien zwischen den Geschlechtern, Altersgruppen oder gesellschaftlichen Schichten zu deuten (z. B. Binford 1971; Chapman et al. 1981; Lull 2000). Dennoch sind wirtschaftliche Ungleichheit oder Unterschiede im Wohlstand womöglich nur eine der sozialen Beziehungen, die durch Verwandtschaftsstrukturen gelenkt werden, aber auch völlig unabhängig davon sein konnten. Unsere eigene Gesellschaft stellt ein gutes Beispiel dar, um die lose Verbindung zwischen Verwandtschaft und Bestattungspraktiken zu verdeutlichen: Während Verwandtschaft hauptsächlich eine rechtliche und wirtschaftliche Funktion erfüllt, bei der Eigentum durch Heirat und legal anerkannte Abstammung fortbesteht, spielen Unterschiede im Wohlstand in den üblichen Beisetzungs- und Einäscherungspraktiken meist keine Rolle.

Die physisch unsichtbaren und sozial willkürlichen Verbindungen zwischen Bestattungspraktiken und Verwandtschaft geben den genetischen Informationen der Bestattungen einen zusätzlichen heuristischen Wert. Da die biologischen Verbindungen eine Verwandtschaftskompo-

the material outcome of a combination of beliefs and rules, but probably also of terms used to dispose of deceased members of one's own or other communities. Due to the variability of burial forms, these practices offer a public portrayal that may express, impose, or negate biological and sexual as well as social, economic, political, ideological, or other relations (Fig. 3). However, nothing allows us to assume that burial practices mirror dialectically or reflect indirectly relations of affinity or kinship. Though both symbolic systems contribute to the social reproduction of the community, the connections between them are far from obvious. Archaeology has mainly developed a set of premises and inferential and statistical procedures to interpret objects recorded in the funerary contexts in terms of differences and asymmetries between sexes, age groups, or social classes (e.g., Binford 1971; Chapman et al. 1981; Lull 2000). Nevertheless, economic inequality or wealth differences may only be one of the social relations that could be regulated through kinship structures but could also be completely unrelated to it. Our own society provides a good example of how to portray the loose connection between kinship and funerary practices: whereas kinship mainly fulfils a juridical and economical function perpetuating property through marriage and legally recognised descent, distinctions in wealth remain largely ignored in common inhumation and incineration practices.

The physically invisible and socially arbitrary links between burial practices and kinship add an additional heuristic value to the genetic information of the burials. Since the biological ties can be a component of kinship, they also become a source of information regarding the socio-economic

nente sein können, werden sie auch zu einer Informationsquelle bezüglich der sozioökonomischen und ideologischen Beziehungen, die in ihnen im Rahmen des Bestattungskontextes und letztlich auch der Verwandtschaft dargestellt werden. Genauso wie die Sozialanthropologie seit mehr als einem Jahrhundert nach signifikanten Korrelationen zwischen Verwandtschaft und allen möglichen sozialen Praktiken sucht, um die Bedeutung von Verwandtschaft zu erfassen, können Archäologie und Genetik nur signifikanten Verbindungen zwischen Blutsverwandtschaft und anderen sozialen Praktiken nachspüren, die im Bestattungsbefund erkennbar sind (Abb. 3). Weder theoretische axiomatische noch soziale Regeln wurden bisher identifiziert, um vorherzusehen, welche Korrelationen in einem bestimmten archäologischen Kontext, einem Gräberfeld oder einer Region zu erwarten oder relevant sind. Folglich ist die interdisziplinäre Forschung zwischen Genetik, Anthropologie und Archäologie nicht auf das Testen von Hypothesen in deduktiven Ansätzen beschränkt, sondern kann intuitiv und systematisch nach möglichen Verbindungen zwischen der großen Vielfalt von Bestattungspraktiken und der begrenzten Bandbreite von genetisch möglichen Beziehungen von Abstammung und Blutsverwandtschaft suchen.

Grabbefunde sind das materielle Ergebnis von sozialen Beziehungen und Überzeugungen, die sich in den Bestattungspraktiken vergangener Gesellschaften darstellen. Sie bieten nicht so sehr ein bruchstückhaftes Bild der Vergangenheit, sondern geben Einblick in die performativen und rituellen Praktiken von sozialen Gruppen unterschiedlicher Größe, die offensichtlich mit sozialen Vorstellungen über das Leben und den Tod in Zusammenhang stehen. Welche Personen und Objekte wo und wie bestattet wurden, ergibt sich aus konkreten Entscheidungen, die in der Vergangenheit getroffen wurden, und unterliegt nicht dem Zufall oder dem Erhaltungszustand und der archäologischen Bergung. Während eine sozialanthropologische Sichtweise versucht sein könnte, den Grabbefund für ein repräsentatives, wenn auch unvollständiges Abbild der gesamten Gesellschaft zu halten, ist er in Wahrheit eine bewusste und bedeutungsvolle Auswahl von Individuen, Produkten, Materialien, Orten und Zeiträumen, die dazu dienen, soziale, wirtschaftliche und politische Beziehungen zu erklären, zu pflegen oder zu transformieren. Wer auf eine bestimmte Weise bestattet wurde und wer nicht, ist damit Ausdruck gesellschaftlicher Auswahl und Absicht.

Viele der in diesem Band vorgelegten Untersuchungen legen die Bedeutung genetischer Informationen offen, wenn es darum geht zu ermitteln, ob die Kriterien bei der Festlegung von Bestattungspraktiken auf Variablen wie dem genetischen/osteologischen Geschlecht, einem gemeinsamen Schicksal (z. B. Krankheiten) oder anderen kongenialen Besonderheiten usw. beruhten. Bereits im Jungpaläolithikum waren die Bestatteten nicht zufällig ausgewählt, wie die gravettienzeitliche Zwillingsbestattung von Krems-Wachtberg (Österreich) veranschaulicht (s. Beitrag Neugebauer-Maresch et al. in diesem Band). Unter den jung Verstorbenen im eisenzeitlichen Navarra (Spanien) wurden Zwillinge sowie Kinder mit Down- oder Edwards-Syndrom eindeutig für die Durchführung bestimmter intramuraler Bestattungspraktiken ausgewählt (s. Beitrag Papac et al. in diesem Band).

and ideological relations portrayed in them in the funerary context and, eventually, in kinship. In the same way as social anthropology has searched for over a century for significant correlations between kinship and any possible social practice in order to understand the meaning of kinship, archaeology and genetics can only look for significant links between consanguinity and other social practices appearing in the funerary record (Fig. 3). No theoretical axiomatic or social rules have so far been identified to foresee which correlations should be expected or are relevant in any specific archaeological context, cemetery, or region. In consequence, interdisciplinary research between genetics, anthropology, and archaeology is not confined to testing hypotheses in deductive approaches, but can search intuitively and systematically for possible links between the large variety of burial practices and the limited range of genetically viable relations of descent and consanguinity.

Funerary records are the material manifestation of social relations and beliefs portrayed in the burial practices of past societies. Rather than a fragmented view of the past, they provide insight into performative and ritual practices of social groups of variable size, apparently bound to social conceptions concerning life and death. Which persons and objects were interred where, and how, is the result of specific decisions taken in the past, rather than a more or less random result of material preservation and archaeological recovery. While a social anthropological perspective might be tempted to think that the funerary record is a representative but incomplete image of the whole living society, in reality it is an intentional and meaningful selection of individuals, materials, places, and temporalities used to assert, maintain, or transform social, economic, and political relations. In consequence, whoever is buried in a certain way and whoever is not expresses a social selection and an intentionality.

Many of the studies included in this volume reveal the relevance of genetic information to identify whether the criteria to define funerary practices were based on variables, such as genetic/osteological sex, a common fate such as diseases, or other congenic particularities, etc. Already in the Upper Palaeolithic, buried individuals were not randomly selected, as the Gravettian twin burial grave of Krems-Wachtberg, Austria, illustrates (cf. Neugebauer-Maresch et al. in this volume). Among those who died young during the Early Iron Age of Navarra, twins as well as children with Down and Edwards syndrome were clearly chosen for the performance of particular intramural burial practices (cf. Papac et al. in this volume). A higher prevalence of adult male than female individuals and children in burial spaces seems to be a recurrent observation in European prehistory[2], although the opposite situation has been observed, for example, in the intramural burials of Neolithic Mesopotamia and Anatolia (cf. Somel et al. in this volume) or in Early Bronze Age El Argar, south-east Iberia (Villalba-Mouco et al. 2022), where adult women are more frequent. Whether these age and sex biases reflect an uneven demographic profile due, for example, to violent encounters, or to a higher mobility of parts of the population during certain periods of their life, or to privileged access to underground burial practices by certain members, are complex but crucial questions. Some of these biases can be explained in part by integrating other archaeo-

Ein häufigeres Vorkommen erwachsener männlicher als weiblicher Individuen und Kinder in den Bestattungsplätzen scheint in der europäischen Urgeschichte eine wiederkehrende Beobachtung zu sein[2], obwohl die gegensätzliche Situation beispielsweise bei den intramuralen Bestattungen im neolithischen Mesopotamien und Anatolien bekannt ist (s. Beitrag Somel et al. in diesem Band) oder im frühbronzezeitlichen El Argar im südöstlichen Iberien (Villalba-Mouco et al. 2022), wo erwachsene Frauen überwiegen. Ob diese alters- und geschlechtsbedingten Tendenzen ein ungleichmäßiges demografisches Profil aufgrund von zum Beispiel gewaltsamen Begegnungen, einer höheren Mobilität von Teilen der Bevölkerung während bestimmter Lebensabschnitte oder privilegiertem Zugang zu Erdbestattungspraktiken für bestimmte Mitglieder widerspiegelt, ist eine komplexe, aber wichtige Frage. Einige dieser Tendenzen lassen sich zum Teil mithilfe von anderen archäologischen, genetischen und anthropologischen Nachweisen erklären, wie zum Beispiel Hinweisen auf Traumata, Unterschieden in der Ernährung oder den Grabbeigaben und isotopischen Mobilitätsindikatoren usw. Darüber hinaus können die Abstammungsstruktur und das Sterbealterprofil über mehrere Generationen Informationen über die Nutzungsdauer des Fundortes liefern, wie es für das mittelneolithische Gräberfeld von Gurgy »les Noisats« in Nordfrankreich der Fall ist (s. Beitrag Rivollat et al. in diesem Band).

Genetische Rekonstruktionen biologischer Stammbäume können auch als direkter Nachweis für den Bevölkerungsanteil dienen, der aus den Bestattungsbefunden nicht ersichtlich ist. Die Unvollständigkeit demografischer Profile ist eine wiederkehrende Eigenschaft prähistorischer Nekropolen und muss immer bedacht werden, zumal sie nie bewiesen oder quantifiziert werden kann. Fehlende Erwachsene in den rekonstruierten Stammbäumen aus archäogenetischen Untersuchungen können einen unteren Schätzwert der von den Erdbestattungsriten ausgeschlossenen Bevölkerung liefern, wenn Bestattungsplätze vollständig oder annähernd vollständig gegraben wurden. In der Siedlung der Aunjetitzer Kultur in Schiepzig, Saalekreis (Deutschland), zum Beispiel wurden mindestens 58 % der Gruppe nicht bestattet (s. Beitrag Penske et al. in diesem Band). In anderen Fällen, wie dem bronzezeitlichen Großbritannien oder Iberien, muss der Anteil bedeutend höher gewesen sein, wenn man die recht begrenzte Anzahl bekannter Gräber dort bedenkt. Angesichts der umfangreichen Grabungsflächen dürfen diese ›unsichtbaren‹ Bestatteten nicht als Folge archäologischer oder taphonomischer Fragmentierung verstanden werden, sondern sollten uns vielmehr zu der Überlegung führen, wie der menschliche Körper und seine vielfältigen Merkmale in unterschiedlichen Gesellschaften dazu genutzt wurden, soziale, sexuelle und politische Beziehungen auszudrücken, aufzuerlegen oder aufzulösen. Es ist möglich (jedoch nicht offensichtlich), dass solche Beziehungen zum *kin-making* gehörten.

2 Fowler et al. 2021; vgl. Rivollat et al. 2023; Haak et al. 2015; Beitrag Kiss et al. in diesem Band.

logical, genetic, and anthropological lines of evidence, such as signs of traumata, differences in diet or grave goods, and isotopic indicators of mobility, etc. Moreover, the structure of pedigree and age-at-death profile over generations can provide information on the duration of site use, as was explored in the case of the Middle Neolithic cemetery of Gurgy »les Noisats« in northern France (cf. Rivollat et al. in this volume).

Genetic reconstructions of biological pedigrees can also provide indirect evidence of the proportion of the population that is not evident in the funerary record. Incomplete demographic profiles are a recurrent feature of prehistoric necropolises that always have to be considered but can never be substantiated or quantified. Missing adults in the reconstructed pedigrees of archaeogenetic studies can provide a minimum estimate of the population excluded from inhumation burial rites in cases where complete or near complete burial spaces have been excavated. For example, in the Únětice settlement of Schiepzig, Saalekreis district (Germany), at least 58 % of the group was not buried (cf. Penske et al. in this volume). In other cases, such as Bronze Age Britain or Iberia, the proportion must have been substantially higher, considering the rather limited number of known burials at these sites. In view of the extensively excavated surfaces, these ›invisible‹ bodies cannot be seen as the result of archaeological or taphonomic fragmentation but should rather lead us to consider how the human body and its multiple attributes were used in different societies to express, impose, or resolve social, sexual, and political relations. It is possible (but not obvious) that such relations were part of kin-making.

The archaeogenetic studies included in the present volume also confirm the methodological importance of analysing complete burial grounds and of DNA preservation, an issue where the idea of fragmentation, data loss, and thus lack of resolution is indeed pertinent. A c. 33 % increase (from 15 to 21) of ancient genomes of the 41 individuals buried at the Early Bronze Age site of Haunstetten-Postillionstraße, Augsburg, expands the biologically related community members from seven to 14 (cf. Mittnik et al. in this volume). The extended dataset provides a much clearer view of social relations portrayed in this cemetery over at least three generations, and it confirms the initial hypothesis regarding female community or village exogamy (Knipper et al. 2017; Mittnik et al. 2019). This example also reveals the difficulty of making anthropological inferences for unrelated individuals (cf. Thelen in this volume), when a large number of the tombs could not be analysed genetically. Our understanding of the entangled biological, sexual, and social relations will definitely depend on what could be defined as ›whole-community‹-based archaeogenetic approaches.

2 Fowler et al. 2021; cf. Rivollat et al. 2023; Haak et al. 2015; cf. Kiss et al. in this volume.

Die in diesem Band vorgelegten archäogenetischen Untersuchungen bestätigen außerdem die methodologische Bedeutung der Analyse vollständiger Gräberfelder und der Konservierung von DNA – ein Thema, bei dem der Gedanke der Fragmentierung, des Datenverlustes und damit der mangelnden Auflösung durchaus angebracht ist. Eine Zunahme von ca. 33 % (von 15 auf 21) alter Genome der 41 am frühbronzezeitlichen Fundort von Haunstetten-Postillionstraße, Augsburg (Deutschland), Bestatteten erhöht die Anzahl der biologisch verwandten Mitglieder der Gemeinschaft von sieben auf 14 (s. Beitrag Mittnik et al. in diesem Band). Der erweiterte Datensatz liefert ein viel klareres Bild der sozialen Beziehungen, die in diesem Gräberfeld über mindestens drei Generationen nachvollziehbar sind, und bestätigt die Anfangshypothese bezüglich der weiblichen Exogamie der Gemeinschaft oder des Dorfes (Knipper et al. 2017; Mittnik et al. 2019). Dieses Beispiel enthüllt zudem, wie schwierig es ist, anthropologische Schlüsse bei unverwandten Individuen zu ziehen (s. Beitrag Thelen in diesem Band), wenn eine große Anzahl der Gräber genetisch nicht analysiert werden konnte. Unser Verständnis der verwobenen biologischen, sexuellen und sozialen Beziehungen wird zweifellos von dem abhängen, was als gesamtgemeinschaftliche archäogenetische Studien bezeichnet werden könnte.

Vorläufige Ergebnisse und Ausblick

Inzest oder die Vermeidung desselben ist ein Aspekt, der lange Zeit als der Kern von Verwandtschaftsbeziehungen verstanden wurde (Levi-Strauss 1949), in der neueren Anthropologie jedoch – wie schon erläutert – eher in den Hintergrund gestellt wird (Carsten 2000), allerdings genetisch gut nachweisbar ist. Mittels *runs of homozygosity* (ROH) im Genom eines Individuums kann die biologische Nähe seiner Eltern bestimmt werden. Dabei handelt es sich um Abschnitte, in denen beide elterlichen Chromosomen identisch sind, also als homozygot bezeichnet werden und die auf einen kürzlichen gemeinsamen Vorfahren der Eltern zurückzuführen sind. Umso länger und häufiger diese Abschnitte im Genom sind, umso näher sind beide Eltern miteinander verwandt (Ceballos et al. 2018). Bisherige Arbeiten wie die hier vorgelegten Studien bestätigen, dass Abstammung zwischen Geschwistern oder Cousins ersten und zweiten Grades eine Ausnahme in der Vor- und Frühgeschichte waren (Ringbauer et al. 2021)[3]. Die Vermeidung von Inzucht durch Praktiken der Exogamie, d. h. Außenheirat, wird in vielen Fällen auch durch die Vielfalt an mitochondrialen Haplogruppen widergespiegelt, die nur von Müttern an ihre Kinder vererbt werden und somit auf die biologische Nähe bzw. Distanz zwischen zwei Frauen hindeutet (z. B. Sjögren et al. 2020). In der mittelneolithischen Gemeinschaft von Gurgy, Dép. Yonne (Frankreich), wurde nur in einem Fall dieselbe mtDNA weiter als eine Generation vererbt (s. Beitrag Rivollat et al. in diesem Band). Dies setzt einerseits ein weites Netzwerk von sozialen

3 Ein erwachsener Sohn einer sexuellen Beziehung ersten Grades ist in dem bekannten Megalithgrab von Newgrange, County Meath (Irland), identifiziert und aufgrund seines monumentalen Bestattungsplatzes als ein früher Hinweis auf dynastische Eliten gedeutet worden (Cassidy et al. 2020).

Preliminary results and outlook

For a long time, incest – or avoiding it – had been seen as the gist of family relations (Lévi-Strauss 1949). As mentioned above, it has, however, rather moved into the background in later anthropology (Carsten 2000), although it is genetically clearly verifiable. By using runs of homozygosity (ROH) in an individual's genome, the biological distance of parents can be determined. ROH are sections in which both parental chromosomes are identical, also called homozygotic, and which derive from a recent ancestor both parents have in common. The longer and more often these sections occur in the genome, the closer the parents are related to each other (Ceballos et al. 2018). Previous investigations, such as the studies presented here, confirm that descent between siblings or 1st- and 2nd-degree cousins was an exception in pre- and protohistory (Ringbauer et al. 2021)[3]. Using practices of exogamy, i.e., marrying outside the community, in order to avoid incest is in many cases reflected by the diversity of mitochondrial haplogroups, which are only passed on from mothers to their children, indicating the biological proximity or distance between two women (e.g., Sjögren et al. 2020). In the Middle Neolithic community of Gurgy, Dép. Yonne (France), there was only one case in which the same mtDNA was passed on further than one generation (cf. Rivollat et al. in this volume). This requires not only a broad network of social connections between communities but also that persons were socially defined or that it was known with whom a member of the community was not to have sexual relations (offspring). Archaeology and the social sciences in general will therefore have to take a good look at complex topics that have only been discussed speculatively up until now, such as the enforcement of social norms and taboos in past societies.

In later Eurasian prehistory, these regulations seem to have been based, above all, on the practice of female exogamy between communities/settlements and virilocality, irrespective of whether their members were farmers, livestock breeders, or nomads, but also seemingly irrespective of the political organisation and social inequality of those societies. The first whole-community archaeogenetic studies of Neolithic cemeteries and megaliths of the 5th and 4th millennia BC in western Europe show that, in contrast to men, adult women rarely have parents or ancestors in their burial places. At the same time, their mtDNA haplogroups cannot be traced any further than their children's generation. Whereas the mtDNA haplogroups inherited from the mother differ substantially in the respective cemeteries, Y haplogroups inherited from the father are very homogeneous (Fowler et al. 2021; Rivollat et al. 2023; Rivollat et al. in this volume). This genetic pattern can be explained by women moving to a different community once they have reached adulthood, and at least some of their children growing up there. Evidence of this practice is also provided by stable isotope analyses of human remains (e.g., Rivollat et al. 2023; cf. Mittnik et al. in this volume). Very similar sex- and age-specific patterns also exist for the late

3 An adult son of a first-degree incestuous union has been identified in the well-known megalithic tomb of Newgrange, County Meath (Ireland), and has been interpreted as an early indication of dynastic elites due to the monumental burial place (Cassidy et al. 2020).

Verbindungen zwischen Gemeinschaften voraus, andererseits eine soziale Festlegung bzw. Kenntnis der Personen, mit welchen ein Mitglied der Gemeinschaft keine sexuellen Beziehungen (Nachkommen) haben sollte. Somit werden sich die Archäologie und die Sozialwissenschaften allgemein mit komplexen Themen auseinandersetzen müssen, wie der Durchsetzung sozialer Normen oder Tabus in vergangenen Gesellschaften, die bisher nur spekulativ diskutiert werden konnten.

In der jüngeren Vorgeschichte Eurasiens scheinen diese Regelungen vor allem auf der Praxis der weiblichen Exogamie zwischen Gemeinschaften/Siedlungen und Virilokalität beruht zu haben, unabhängig ob es sich um Ackerbauern, Viehzüchter oder Nomaden handelte und scheinbar auch unabhängig von der politischen Organisation und sozialer Ungleichheit der Gesellschaften. Die ersten gesamtgemeinschaftlichen archäogenetischen Studien von neolithischen Gräberfeldern und Megalithen Westeuropas des 5. und 4. Jts. v. Chr. zeigen, dass erwachsene Frauen im Gegensatz zu Männern nur selten Eltern oder Vorfahren in denselben Bestattungsorten haben und gleichzeitig ihre mtDNA-Haplogruppe nicht weiter als bis zur Generation ihrer Kinder verfolgbar ist. Während die weiblich vererblichen mtDNA-Haplogruppen in den jeweiligen Gräberfeldern sehr unterschiedlich sind, fallen die männlich vererbten Y-Haplogruppen sehr homogen aus (Fowler et al. 2021; Rivollat et al. 2023; s. Beitrag Rivollat et al. in diesem Band). Dieses genetische Muster lässt sich darauf zurückführen, dass Frauen bei Erreichen des Erwachsenenalters in eine andere Gemeinschaft übersiedelten, wo zumindest ein Teil ihrer Kinder aufwuchs – eine Praxis, die auch anhand von Analysen stabiler Isotopen bei Menschenresten bestätigt wird (z. B. Rivollat et al. 2023; s. Beitrag Mittnick et al. in diesem Band). Sehr ähnliche geschlechts- und altersspezifische Muster finden sich auch im späten Neolithikum des östlichen Mitteleuropas (Mittnik et al. 2019; Schroeder et al. 2019), wie in den ersten Gesellschaften mit einer hohen genetischen ›Steppenkomponente‹, die aus dem östlichen Europa zu Beginn des 3. Jts. v. Chr. in Mitteleuropa eintrafen (Haak et al. 2015; Papac et al. 2021) und sich über die nächsten Jahrhunderte über weite Teile Westeuropas mit den lokalen neolithischen und kupferzeitlichen Bevölkerungen vermischten (Olalde et al. 2018; Villalba-Mouco et al. 2021). Folglich scheint der erste große Migrationsprozess Europas nach der Verbreitung des Ackerbaus und von Viehzüchtergesellschaften aus dem Vorderen Orient zu Beginn des Neolithikums keinen grundlegenden Wandel in den virilokalen Bestattungs- und Abstammungsregeln bedeutet zu haben. Auch die derzeit verfügbaren schriftlichen und archäogenetischen Informationen zu den nomadischen Gesellschaften Eurasiens deuten auf patrilokale und -lineare Beziehungen hin (s. Beitrag Gass in diesem Band). Selbst Gesellschaften, die im 2. Jt. v. Chr. noch engen Kontakt mit und Abstammung von Jäger-Sammler-Gesellschaften Nordosteuropas aufweisen, scheinen biologische Vielfalt über eine hohe Mobilität erwachsener Frauen erreicht zu haben (Chyleński et al. 2023).

Gewissermaßen unerwartet ist auch die Beständigkeit dieses Bestattungs- und Abstammungsverhaltens in der Bronzezeit, als zu Beginn des 2. Jts. v. Chr. die ersten früh- oder protostaatlichen Organisationsformen mit erheblicher sozi-

Neolithic in the eastern part of Central Europe (Mittnik et al. 2019; Schroeder et al. 2019), such as in the first societies with a high genetic ›steppe component‹ arriving from eastern Europe at the beginning of the 3rd millennium BC (Haak et al. 2015; Papac et al. 2021) and then mixing with the local Neolithic and Chalcolithic populations in wide areas of western Europe over the following centuries (Olalde et al. 2018; Villalba-Mouco et al. 2021). The first large European migration process after the spread of farming and livestock-breeding societies from the Middle East at the beginning of the Neolithic therefore does not seem to have brought a fundamental change in the virilocal burial and ancestry rules. The currently available written and archaeogenetic information on the nomadic societies in Eurasia also indicate patrilocal and patrilinear relations (cf. Gass in this volume). Even societies that were still in close contact with northeastern European hunter-gatherer societies in the 2nd millennium BC and that descended from them seem to have reached biodiversity by means of adult women's high mobility (Chyleński et al. 2023).

To a certain extent unexpectedly, this burial and ancestry behaviour remained consistent in the Bronze Age when, at the beginning of the 2nd millennium BC, the first early or proto-state forms of organisation with considerable social distinction and the fundamental division of labour emerged in Europe (Risch/Meller 2015). The archaeological indications of centrally controlled class societies with hereditary property rules, controlling vast areas possibly in a military fashion, become apparent particularly in the Argaric culture in the southeast of the Iberian Peninsula and in the Únětice culture in Central Europe (Lull et al. 2011; Meller 2017; Risch et al. 2021). In the Argaric culture, the presence of women without any local ancestors but with a large mitochondrial diversity has been observed among the intramural burials in the palatial settlement of La Almolya, Murcia (Spain), including one of the so far richest known princely graves of El Argar (Villalba-Mouco et al. 2022). For the Únětice culture, the first evidence of this organisation of burial rituals and female mobility is now also available for a domestic community in Schiepzig; in this case, however, we are more likely looking at a lower-rung social tier (cf. Penske et al. in this volume). Other Early Bronze Age burial places do not fundamentally deviate from this pattern[4].

The number of investigated burial places is still far too insufficient to speak of a general patrilocal and patrilinear social structure in Europe beginning with the early Neolithic. Additional whole-community archaeogenetic studies will be necessary to gain better insight into the chronological and spatial differences in both the burial rituals and the social and sexual relations deduced from them. Likewise, more attention needs to be paid to the few cases of adult women with ancestors in their own burial community (cf. Penske et al. in this volume), as well as to the reasons for the aforementioned surplus of women or men in certain burial places. The seeming simplicity with which normative burial rituals characteristic of the Corded Ware, Únětice, and Argaric cultures can be interpreted often gives the much more varied burial practices observed in other areas a more ›peripheral‹ posi-

4 E.g., Mittnik et al. 2019; Zegarac et al. 2021; Papac et al. 2021; cf. Rebay-Salisbury et al. and Kiss et al. in this volume.

aler Differenzierung und grundlegender Arbeitsteilung in Europa entstanden (Risch/Meller 2015). Die archäologischen Hinweise auf zentral gesteuerte Klassengesellschaften mit vererblichen Besitzregeln, die weite Gebiete möglicherweise militärisch beherrschten, zeigen sich vor allem in dem El Argar-Phänomen im Südosten der Iberischen Halbinsel und in der Aunjetitzer Kultur in Mitteleuropa (Lull et al. 2011; Meller 2017; Risch et al. 2021). Im ersten Fall ist die Anwesenheit von Frauen ohne lokale Vorfahren mit einer großen mitochondrialen Vielfalt unter den intramuralen Bestattungen der palastartigen Siedlung von La Almolya, Murcia (Spanien), beobachtet worden, unter anderem auch bei einem der reichsten der bisher bekannten El Argar-Fürstengräber (Villalba-Mouco et al. 2022). Auch für die Aunjetitzer Kultur liegen jetzt erste Nachweise dieser Organisation von Bestattungssitten und weiblicher Mobilität für eine Hausgemeinschaft aus Schiepzig vor, wobei es sich in diesem Falle eher um eine der unteren sozialen Klassen handelt (s. Beitrag Penske et al. in diesem Band). Auch andere frühbronzezeitliche Bestattungsplätze weichen nicht grundsätzlich von diesem Muster ab[4].

Bei weitem reicht die Zahl von untersuchten Bestattungsplätzen nicht aus, um von einer allgemeinen patrilokalen und patrilinearen Gesellschaftsstruktur in Europa ab dem frühen Neolithikum zu sprechen. Weitere gesamtgemeinschaftliche archäogenetische Studien werden nötig sein, um einen besseren Einblick in die zeitlichen und räumlichen Unterschiede sowohl der Grabrituale als auch der davon abgeleiteten sozialen und sexuellen Beziehungen zu bekommen. Ebenso gilt es, jenen wenigen Fällen von erwachsenen Frauen, die durchaus Vorfahren in der eigenen Grabgemeinschaft haben (s. Beitrag Penske et al. in diesem Band), größere Aufmerksamkeit zu widmen, ebenso wie den Gründen des schon erwähnten Frauen- oder Männerüberschusses an bestimmten Bestattungsplätzen. Die scheinbare Einfachheit, mit der sich normative Bestattungsrituale, wie sie für die Schnurkeramik-, Aunjetitzer oder El Argar-Kultur kennzeichnend sind, interpretieren lassen, stellt oft die weit vielfältigeren Bestattungspraktiken, die in anderen Gebieten zu beobachten sind, in eine ›periphere‹ Stellung (Soriano et al. 2021; s. Beitrag Brück in diesem Band). Und selbst Gesellschaften mit virilokalen Bestattungsriten und den erwähnten genetischen Kriterien für weibliche Exogamie sollten in der späten Vorgeschichte keinesfalls als Ausdruck patriarchalischer Macht- und Familienstrukturen verstanden werden. Allein die wirtschaftliche und politische Vielfalt von Gesellschaften, in denen weibliche Exogamie zwischen Siedlungen – auch ethnografisch – vorkommt, schließt eine deterministische Rückführung von Machtstellungen auf Mobilitätspraktiken aus. Frauen mit einer hohen Mobilität können von ihrem Geburtsort weg-, aber auch wieder zurückgezogen sein, was ihre gelegentliche Anwesenheit an den Bestattungsplätzen ihrer Vorfahren erklären würde. Damit kommt ihnen eine sichtbare Rolle in der Errichtung und Erhaltung von zwischengemeinschaftlichen Verbindungen und überregionalen Netzwerken zu. Vielleicht erklärt sich somit letztendlich auch die Entstehung und

4 Z. B. Mittnik et al. 2019; Žegarac et al. 2021; Papac et al. 2021; s. Beiträge Rebay-Salisbury et al. und Kiss et al. in diesem Band.

tion (Soriano et al. 2021; cf. Brück in this volume). But even societies with virilocal burial rites and the genetic criteria for female exogamy in later prehistory should under no circumstances be seen as an expression of patriarchal power and family structures. The economic and political diversity of societies in which female exogamy occurs between settlements – also described by socio-cultural anthropology – excludes a deterministic link between powerful positions and practices of mobility. Women with a high degree of mobility might have moved away from but also back to their birthplace, which would explain their occasional presence in the burial places of their ancestors. This gives them a visible role in establishing and maintaining intercommunal connections and transregional networks. Maybe this high degree of female mobility ultimately also explains the emergence and spread of archaeological cultures: a concept whose meaning specialists have been arguing about for more than 100 years and which is inferred, above all, from formally regulated artefact production, particularly from pottery tradition and burial rituals (e.g., cf. Daim et al. in this volume). The associated control and transmission of knowledge are undoubtedly a power potential that may be expressed in certain extraordinarily rich women's graves following strictly standardised burial rituals of the early Bronze Age (Lull et al. 2021; Villalba-Mouco et al. 2022; cf. Mittnik et al. in this volume).

Just as interesting is the research on the biological distance among hunter-gatherer societies of the Palaeolithic and Mesolithic period; but, so far, hardly any archaeogenetic results are available. At least in the Early Holocene societies of the pre-pottery Neolithic in Anatolia (cf. Somel et al. in this volume), and possibly also in Central Germany, these relations do not seem to have played a role in the portrayal of burial rituals. The female shaman from the well-known Bad Dürrenberg grave, Saalekreis district (Germany), was only distantly related (in the $4^{th}/5^{th}$-degree) to the child buried with her (cf. Orschiedt et al. in this volume). In other cemeteries, the identification of young individuals without biological ancestors may also be seen as a result of child adoption (Fowler et al. 2021; cf. Rebay-Salisbury et al. in this volume).

The contributions presented in this volume show that archaeogenetic studies may be of great significance for completely different issues that are decisive for understanding the past but have, until now, not been the focus of the discussion on the importance of genetic approaches. The following areas shall be emphasised:

1) The rising number of genomic data should enable reliable insights into the size of social groups and, consequently, into the palaeodemography based on the genetic diversity of a group. For the necropolis of Gurgy, for example, the ROH values (see above) allowed researchers to calculate that the community buried here over seven generations was associated with a group of around 1835 persons (cf. Rivollat et al. in this volume). In the case of the Iron Age child burials from Navarra the biologically determined frequency of trisomy in humans was used to model the size of the community. The population of 625–1000 persons calculated in this way is around five times larger than the usually estimated numbers for prehistoric settlements that spread over an area of 0.75 ha (cf. Papac et al. in this volume).

Verbreitung von archäologischen Kulturen – einem Begriff, über dessen Bedeutung seit über 100 Jahren im Fach gestritten wird und der vor allem von förmlich streng geregelter Artefaktherstellung, insbesondere von Keramik- und Bestattungssitten abgeleitet wird (z. B. Beitrag Daim et al. in diesem Band) – als eine Folge hoher Mobilität der Frauen. Die damit einhergehende Kontrolle und Vermittlung von Wissen stellt ohne Zweifel ein Machtpotenzial dar, das möglicherweise in bestimmten, außerordentlich reichen Frauengräbern mit streng normierten Bestattungsritualen der frühen Bronzezeit zum Ausdruck kommt (Lull et al. 2021; Villalba-Mouco et al. 2022; s. Beitrag Mittnick et al. in diesem Band).

Ebenso interessant stellt sich auch die Erforschung der biologischen Nähe bei Jäger- und Sammler-Gesellschaften des Paläolithikums und Mesolithikums dar, über die noch praktisch keine archäogenetischen Ergebnisse vorliegen. Zumindest in den frühholozänen Gesellschaften des präkeramischen Neolithikums von Anatolien (s. Beitrag Somel et al. in diesem Band) und möglicherweise auch in Mitteldeutschland scheinen diese Beziehungen keine Rolle in der Darstellung von Bestattungsritualen gespielt zu haben. Die Schamanin aus dem bekannten Grab von Bad Dürrenberg, Saalekreis (Deutschlnad), war nur entfernt – im 4. Grad – mit dem bei ihr bestatteten Kind verwandt (s. Beitrag Orschiedt et al. in diesem Band). Auch in anderen Gräberfeldern kann die Identifizierung von jungen Individuen ohne biologische Vorfahren als Folge von Kinderadoption verstanden werden (Fowler et al. 2021; s. Beitrag Rebay-Salisbury et al. in diesem Band).

Die in diesem Band vorgelegten Beiträge zeigen, dass archäogenetische Studien noch für andere Problemstellungen von großer Bedeutung sein können, die entscheidend für das Verständnis der Vergangenheit sind, aber bisher nicht im Fokus der Diskussion zur Bedeutung genetischer Ansätze standen. Folgende Bereiche können hervorgehoben werden:

1) Bei steigenden Zahlen von genetischen Sequenzen sollte es möglich sein, verlässliche Aussagen zur Größe von gesellschaftlichen Verbänden und folglich zur Paläodemografie anhand der genetischen Vielfalt einer Gruppe zu treffen. So konnte in der Nekropole von Gurgy anhand der ROH-Werte (s. o.) errechnet werden, dass die hier über sieben Generationen bestattete Gemeinschaft mit einer Gruppe von etwa 1835 Personen verbunden war (s. Beitrag Rivollat et al. in diesem Band). Bei den eisenzeitlichen Kinderbestattungen aus Navarra wurde die biologisch bestimmte Häufigkeit von Trisomiefällen bei Menschen verwendet, um die Größe der Gemeinschaft zu modellieren. Die so errechnete Bevölkerung von 625–1000 Personen liegt etwa fünfmal über den üblicherweise geschätzten Einwohnerzahlen vorgeschichtlicher Siedlungen von 0,75 ha Fläche (s. Beitrag Papac et al. in diesem Band).
2) Auch über die Größe von Hausgemeinschaften können – z. B. bei intramuralen Grabsitten – Aussagen getroffen werden. Die Bestattung von Individuen, die nicht alle im 1. oder 2. Grad miteinander verwandt sind, innerhalb desselben Gebäudes und Wohnhorizontes führt zu dem Schluss, dass die eisenzeitlichen Häuser nicht von Kernfamilien, wie oft angenommen, sondern von erweiterten Gemeinschaften mit zwei oder mehr Elternpaaren bewohnt wurden (s. Beitrag Papac et al. in diesem Band).

2) Statements can also be made on the size of domestic communities, e.g., in the case of intramural burial customs. The burial of individuals who are not all 1st- and 2nd-degree relatives in the same building and living horizon leads to the conclusion that the Iron Age houses were not inhabited by nuclear families as often assumed but by extended communities with two or more parental couples (cf. Papac et al. in this volume).

3) Compared to radiocarbon dating, the determination of the settlement duration of a place or layer has become much more precise and reliable by combining archaeogenetic data and the anthropological age determination of the individuals. The determination of biological connections between individuals of different generations allows us to infer continuous use for 80–120 years, as was the case, for example, with both the Neolithic cemetery of Gurgy, and the graves associated with House 4 in the settlement of Schiepzig (cf. Rivollat et al., Penske et al., and Kiss et al. in this volume). On the one hand, these archaeogenetic data challenge conventional radiocarbon dating; but on the other hand, in their combined form they offer opportunities for a much finer chronology of burial places and settlement moments than has been possible in archaeology so far (cf. Friedrich et al. in this volume).

4) Another contribution of archaeogenetics concerns the interpretation of burned or otherwise destroyed layers of multiphase settlements. Up until now, the destruction and reconstruction of settlements could rarely be interpreted as a consequence of violence – such as conquests or plundering – as a chance accident, or as a simple building operation when applying purely archaeological criteria. The evidence of biological connections between intramurally buried individuals of different settlement horizons, however, provides confirmation of the continuity of the settlement community, which makes at least its violent displacement by new groups appear unlikely (Villalba-Mouco et al. 2022; cf. Papac et al. in this volume).

The contributions presented in this volume prove how crucial the genetic data – when combined with archaeology and socio-cultural anthropology – are for the interpretation of past societies and for questioning conventional models. Given the short time in which this fundamental change has taken place, above all regarding the problems and the perspectives, we may expect that additional fields of research will emerge over the next few years that will either benefit from or be disputed by the genetic data. This potential should not be perceived as a challenge to historical research and the social sciences in general, but it should lead to an increased interdisciplinary discussion of concepts and of the epistemological frame of archaeogenetics. We hope that the 15th Archaeological Conference of Central Germany (Fig. 4) and its proceedings will contribute to this cooperation and to the rejuvenation of our disciplines.



Abb. 4 Roberto Risch, Niels N. Johannsen, Johannes Krause, Holger Dietl, Joscha Gretzinger, Harald Ringbauer, Stephan Schiffels, Harald Meller, Ronny Friedrich, Sandra Penske, Mario Küßner, Jens Blöcher, Luka Papac, Torsten Günther, Aylwyn Scally, Rodrigo Barquera, Wolfgang Haak, Cosimo Posth, Volker Heyd, Eirini Skourtanioti, Mehmet Somel, Maïté Rivollat, Vanessa Villalba-Mouco, Chris Fowler, Katharina Rebay-Salisbury, Alissa Mittnik, Eleftheria Orfanou, Joanna Brück, Lara Cassidy, Christine Neugebauer-Maresch, Sabine Reinhold, Catherine Frieman, Falko Daim (nicht auf dem Bild/not in the picture: Erdmute Alber, Eduardo Amorim, Susanne Friederich, Mirosław Furmanek, Ayshin Galichi, Anton Gass, Zuzana Hofmanová, Walter Pohl, Divyaratan Popli, Tatjana Thelen).

3) Die Bestimmung der Siedlungsdauer eines Ortes oder einer Schicht ist im Vergleich zur Radiokarbondatierung durch die Kombination archäogenetischer Daten und anthropologischer Altersbestimmung der Individuen weit genauer und verlässlicher geworden. Die Bestimmung biologischer Verbindungen zwischen Individuen unterschiedlicher Generationen lässt – zum Beispiel beim neolithischen Gräberfeld von Gurgy oder bei den zu Haus 4 gehörenden Gräbern der Siedlung Schiepzig – auf eine kontinuierliche Besiedlung von 80–120 Jahren rückschließen (s. Beiträge Rivollat et al., Penske et al. und Kiss et al. in diesem Band). Diese archäogenetischen Daten stellen einerseits eine Herausforderung von herkömmlichen ^{14}C-Datierungen dar, bieten aber andererseits in kombinierter Form Möglichkeiten einer weit feineren Chronologie von Bestattungsplätzen und Siedlungsmomenten, als es bisher in der Archäologie möglich war (s. Beitrag Friedrich et al. in diesem Band).
4) Ein weiterer Beitrag der Archäogenetik betrifft das Verständnis von Brand- oder Zerstörungsschichten in mehrphasigen Siedlungen. Anhand rein archäologischer Kriterien ist es bisher nur selten gelungen, die Zerstörung und den Wiederaufbau von Siedlungen als Folge von Gewalt wie z. B. Eroberung oder Plünderung, als zufällige Unfälle oder als reine Baumaßnahme zu deuten. Der Nachweis von biologischen Verbindungen zwischen intramural bestatteten Individuen unterschiedlicher Siedlungshorizonte ermöglicht es hingegen, eine Kontinuität der Siedlungsgemeinschaft zu bestätigen, womit zumindest ihre gewaltvolle Verdrängung durch neue Gruppen unwahrscheinlich erscheint (Villalba-Mouco et al. 2022; s. Beitrag Papac et al. in diesem Band).

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Die hier vorgelegten Beiträge zeigen, wie entscheidend sich die genetischen Daten in Kombination mit Archäologie und Ethnologie für die Interpretation vergangener Gesellschaften und für die Infragestellung herkömmlicher Modelle erweisen. Angesichts der kurzen Zeit, in der dieser grundlegende Wandel vor allem in den Fragestellungen und Perspektiven stattgefunden hat, ist zu erwarten, dass sich in den nächsten Jahren noch weitere Forschungsbereiche ergeben, die von genetischen Daten profitieren oder infrage gestellt werden. Dieses Potenzial sollte von der Geschichtsforschung und den Sozialwissenschaften allgemein nicht als Herausforderung empfunden werden, sondern zu einer verstärkten interdisziplinären Diskussion von Begrifflichkeiten und dem erkenntnistheoretischen Rahmen der Archäogenetik führen. Wir hoffen, dass der 15. Mitteldeutsche Archäologentag (Abb. 4) und der daraus hervorgegangene Tagungsband einen Beitrag zu dieser Zusammenarbeit und Erneuerung unserer Disziplinen leistet.

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INTERDISZIPLINÄRE ÜBERLEGUNGEN

INTERDISCIPLINARY REFLECTIONS

Kinship: Old problems and new prospects in the conversation between archaeology and social anthropology

Tatjana Thelen

Zusammenfassung

Verwandtschaft: Alte Probleme und neue Perspektiven im Dialog zwischen Archäologie und Sozialanthropologie

Die Zusammenarbeit zwischen der Sozialanthropologie und den archäologischen Wissenschaften hat eine lange und produktive Geschichte. Neuere Forschungen in beiden Disziplinen haben Ideen über die Bedeutung von Blutsverwandtschaft in der Strukturierung menschlicher Gesellschaften hinterfragt und so die Möglichkeit für ein neues Kapitel in diesem Austausch eröffnet. Dieser Beitrag zeichnet nach, wie das Konzept von Verwandtschaft – verstanden als biologische Abstammung – zentral im interdisziplinären Dialog wurde, bevor es Gegenstand fundamentaler Kritik in der Anthropologie wurde. Das Transponieren europäischer Selbstbeschreibung auf anderweitige Gesellschaften und in die Vergangenheit wurde innerhalb der Disziplin zunehmend hinterfragt. Neuere Konzepte sehen Verwandtschaft als fließend und prozessual, auf Sorgepraktiken basierend und stellen die Unterscheidung zwischen biologisch und sozial selbst infrage. Mit der Entlarvung der Blutsverwandtschaft als europäischem Kultursymbol, stellte sich die Frage, ob das Verständnis von biologischer Verwandtschaft jemals bedeutend für die soziale Wirklichkeit irgendwo war. In Verbindung mit neuen Ergebnissen aus Biomolekularstudien lassen sich daher nun Zweifel an der Bedeutung von gemeinsamen Genen für die Geschichte der menschlichen Gesellschaft äußern. Um der Forschung eine neue Richtung zu geben, müssen wir die Trennung von biologischer und sozialer Verwandtschaft aufgeben.

Summary

Collaboration between social anthropology and archaeological sciences has a long and productive history. More recent research in both fields has challenged ideas about the significance of consanguinity in structuring human societies, opening the possibility for a new chapter in this conversation. This contribution traces how the concept of kinship – understood as biological descent – became central to the interdisciplinary dialogue before facing deep criticism in anthropology. Transpositions of European self-descriptions onto societies elsewhere and in the past have been increasingly challenged within the discipline. Newer concepts see kinship as fluid and processual, based on care practices, and question the very distinction between the biological and the social. With consanguinity largely exposed as a European cultural symbol, the question arose as to whether this understanding of biological kinship has ever been significant for social reality anywhere at all. In combination with new results of biomolecular studies, we can now cast doubt on the significance of shared genes for the history of human society. To shift the focus of research in new directions we need to give up the separation of biological and social kinship.

1 Introduction

The long history of collaboration between social anthropology and archaeological sciences demonstrates that invitations to publish across disciplinary boundaries can be a productive and mutually beneficial strategy for theoretical development. However, the transfer of ideas, concepts, and theories consistently proved more complicated than has appeared at first glance. One challenge for anthropology in interdisciplinary settings, and specifically when working together with natural, genetic, or cognitive sciences, is the different epistemological starting points. Usually, anthropologists are asked to deliver answers to »residual« questions, those aspects that seemingly »hard« facts cannot explain and are therefore seen as »cultural«. Moreover, the concepts borrowed have often already lost currency in their discipline of origin. Both these problems are found in the interdisciplinary research on kinship – a once prominent concept in anthropology that the discipline now generally sees as problematic. Nevertheless, the introduction of new techniques in biomolecular analysis seems to have brought the two disciplines closer again and now might be an appropriate time for a new phase of collaboration. However, this would necessitate revisiting fundamental questions of epistemology and the conceptual history in both fields to avoid what now seem to be dead-ends in interpretation. Therefore, the first section of this contribution traces the foundations of the interdisciplinary dialogue in which kinship, understood as descent, became a central feature of research and served as a foil for a biological interpretation of human organisation. The second section recounts the rise of more fluent and processual understandings of kinship in anthro-

pology since the 1970s. These can serve – as argued in the conclusion – as instruments to interpret the recent datasets from the distant past of humanity and thus open a new chapter in the collaboration between social anthropology and archaeology.

2 Foundations

For a long time, and increasingly with the Enlightenment and the onset of colonisation, European knowledge production has rested in large part on transferring concepts of self-description to the past or other regions of the world in inverted form (Fardon 1990; Strathern 2020). This is exactly what happened as the idea of descent constituting kinship became more important with the rise of sciences from the 17th century onwards. Within the emerging disciplinary distribution of labour, anthropology became associated with what M.-R. Trouillot calls the »savage slot« and was assigned the task of describing »exotic« forms of kinship. As it is precisely this circular exchange that constituted the basis for claims of scientific knowledge about the history of human societies in which kinship became a central tenet, it is worthwhile examining the career of the concept in social anthropology and its interchange with archaeology.

Kinship becoming such a central concept rested on two major assumptions that have both been surprisingly stable in much public and academic discourse until the present day. The first is that kinship based on heterosexual reproduction is universally important in human societies. Hence, various techniques have been developed to »prove« and display genetic or genealogical closeness as kinship (Thelen/Lammer 2021). The second assumption is more specific and asserts a decreasing significance of kinship ties in Europe, which supports delegating kinship to the historical past.

The idea of shared blood and its forms of display influenced how early anthropologists – along with missionaries, colonial officers, and other local actors – began to collect manifold systems of kinship worldwide. To document kinship as descent, already at an early stage researchers developed standardised instruments. These were largely based on the equally new ways of presenting genealogies in which the former stress on sibling groups and the representational imagery of trees with extensive political commentary gave way to simplified diagrams that »accurately« recorded relations of marriage and procreation (Hohkamp 2023; Müller-Wille/Rheinberger 2004). A key exponent of this invention of kinship was L. H. Morgan (Trautmann 1987). His famous distinction between »descriptive« and »classificatory« kinship (Morgan 1870) was instrumental in solidifying the separation between »biological« and »social« kinship. The terminology contrasted a European understanding of kinship that was based on heterosexual reproduction and thus traced descent bilaterally – from both father and mother – with systems that grouped supposedly different categories of relatives under a common term[1]. Morgan came up with this differentiation based on his interpretation of the archaeological and ethnographic evidence available at that time. He arranged kinship terms from different regions of the world side-by-side in three large tables, implying that each referred to essentially the same thing. Another factor that lent scientific credibility to kinship as descent was the »genealogical method« developed by W. H. R. Rivers (1910) and used by anthropologists well into the 20th century (Bouquet 1996). Anthropologists would ask for the terms used for various genealogical positions and visualise relationships accordingly. In short, the documented, so-called, »primitive« forms of kinship were seen fundamentally as cultural expressions of biological relations. In a kind of gold-rush, anthropology »discovered« more and more terminologies of descent and alliance. What they brought home, however, were less »scientific facts« than their own European obsessions (Strathern 2006; Živković 2022).

This understanding was neither neutral nor without hierarchy, because European researchers clearly saw their own viewpoint as the factually »correct« model. Thus, it not only reinforced the divide between nature and culture in European thinking, but it was also mapped as a temporal and spatial difference between »self« and »other«. The supposedly neutral collection of different ways to name and understand kinship translated into »bigger« questions of political and economic reproduction beyond families and households. According to the evolutionary theories at the time, the bewildering diversity of kinship was taken as an expression of different stages of human development. Some terminologies were interpreted as supporting theories about the existence of specific pre-historical hierarchies, such as matriarchal or patriarchal orderings. For instance, classificatory systems were famously understood to suggest promiscuity and a lack of certainty about fatherhood. Following the European preoccupation with paternity and patrilineality, the co-evolution of kinship and political systems was interpreted in light of a desire to secure biological fatherhood. Most influential in this trajectory seems to have been F. Engels's essay on *The Origin of the Family, Private Property and the State* (1884). While Engels relied on the anthropological knowledge of the time – most notably Morgan's – he offered an opposite interpretation of developmental stages. Instead of seeing a »civilising impact« of private property, he mourned a decline in female power, as men would gradually introduce inheritance to their (biological) children and concentrate political power through patrilineages. In short, the European obsession with fatherhood thus became aligned with and naturalised as economic and political progress. This early evolutionary model linking property, kinship, and power continues to influence many current interpretations of more recent genetic data.

The concept, new at the time, of a »relation« supported these temporal and spatial narratives even more fundamentally than the emerging practices of documentation and categorisation. Since the 17th century, finding a relation became

1 The latter might, for example, label any female relative of the previous generation with the same term as the »mother«.

increasingly of value in, and of, itself in the emerging scientific communities (Strathern 2020). Even today, it constitutes a scientific virtue and contributes to prestige to the point where scientists excuse, or at least regret, not finding a relationship. Thus, for example, a study of the shift to patrilineality in early Bronze Age Iberia, V. Villalba-Mouco et al. (2022), laments that no usable DNA could be found to prove a genetic link. The same study also places much emphasis on the links that can be established – even those as distant as the 7th degree of relatedness. This represents approximately the degree of kinship used for the marriage prohibitions in place until the Late Middle Ages in Europe. These prohibitions supported the power of the Catholic Church, because no one could really know all their possible kin to that degree: essentially any couple could be related and thus every marriage could potentially be incestuous. This leads to the question of whether finding such a genetic relationship has any meaning in early human history beyond academic discourse. If we were interest in social organisation, it might be more interesting to ask questions about the high mobility (visible among young persons of both sexes) and the high number of genetically unrelated individuals present in the settlement, both of wich the authors play down: »[...] the burials at La Almoloya seem to emphasize the closest biological ties if we disregard the number of unrelated individuals buried there« (Villalba-Mouco et al. 2022, 3). In accordance with the developmental narrative and although buried men have no adult male genetic relatives at the site, patrilinearity seems to accompany increasing complex and unequal social organisation. However, the valuable items buried with them and the sudden abandonment of the settlement could also suggest that it might have been limited to a small group of elite individuals only to be abandoned again–thus, not suggesting a kind of linear development in one direction. From their finding that adult females had no adult genetic relatives within the settlement, the authors even go so far as to infer a regular and reciprocal Levi-Straussian »exchange of women«. The idea that these females might have had partners of children else where is absent; instead the authors fall back on a norm of male control of female reproductive capacity. Such interpretations show how complicated interdisciplinary dialogue can be become. The next section, therefore, outlines some anthropological critiques of kinship that could be useful to formulate new questions and theories about human history.

3 Challenges

As already indicated, understanding consanguine kinship as a universal pattern of human organisation – and also as one that is in decline in Europe – has significant problems. The critique of the racial underpinnings, inadequate understanding of European history, and failure to recognise the diversity of practices to establish kinship can be used to overcome the social-biological divide in the search for new conceptual tools and interpretations.

As described above, adopting an evolutionary perspective allowed Western observers to dissociate themselves from internal and external others. For minority populations or people elsewhere kinship seemed to be the essential mechanism, that Europeans would overcome through modernity. This move rendered their own concept of biological kinship a non-cultural uncontested truth. Through placing kinship in the position of anteriority – the quintessential other to modernity – researchers could also remain silent about any European political interests inherent in that assumption (TallBear 2013). Even today and despite geneticists having invested much work in disassociating their research from older »racial science«, anthropologists have shown that many technologies are based on earlier statistical groupings of populations and therefore reify racial categories[2]. Specifically, if individual samples are taken as representatives of discrete groups or populations, such as »African« or »European«, apparently »hard« scientific measurements of genetic similarity will retain traces of ideas about kinship formed in 19th-century anthropology around ethnic groups being constituted by shared language, culture, territory and blood (Braun/Hammonds 2012). This also effectively obscures the importance of other forms of relatedness, as well as the potential unimportance of genetic ties for human society. The above-cited interpretation of Bronze Age patrilineages as relatedness resembles very much the kinship charts that anthropologists have long used (and criticised). Like racehorse pedigrees, such charts display certain links and hide others in producing winners (Cassidy 2009), thus these displays not only establish those relationships the scientist sees but also erase or »dis-work« others (Bird-David 2019). Selecting some connections to display, while concealing others, constructs kinship by making bonds appear natural, universal, and ontological antecedents to »culture« (Thelen/Lammer 2021).

In addition, historical research has long challenged the second central assumption, that kinship was always an important category until the advent of modernity in Europe. On the contrary, the terminology of friendship and kinship was used for a long time, largely interchangeably. Kinship designated all kinds of persons living in a household who could be related by descent or marriage – but also by felt closeness (Teuscher 2013, 100). It is only since the 17th century that kinship became singled out, with friendship (and civil society) seen as contrasting and even mutually exclusive types of relations (Strathern 2020). In the course of these developments, kinship was increasingly reduced, becoming limited to what was now seen as private family relations. More importantly, the stress on kinship as biological descent not only contradicted linguistic usage but also everyday practice. In contrast to the tale of the decline of kinship due to modernisation, it became more and more important politically and economically. Political positions became increasingly inheritable and endogamous marriage helped the accumulation of wealth. A good example is marriage between cousins, which became ever-more widespread

2 Nash 2004; Featherstone et al. 2006; Lee 2017; Jabloner 2019; M'charek et al. 2020; Tyler 2021.

among peasant and urban populations in Europe and North America from the 17th century until the middle of the 20th century (Sabean et al. 2007; McKinnon 2023). In sum, modern capitalism and the new bourgeois political order were based on kinship rather than on its decline. Nevertheless, the tale of the decline of kinship was and is persuasive in many scientific and public discourses. Enlightenment ideals are thus taken as a historical reality, with a form of social organisation based on kinship projected onto the »traditional« past. In consequence, as shown above, scientists still often work with the (implicitly) evolutionary hypothesis that »pre-modern« or »pre-state« societies were regulated by ties of kinship (Thelen/Alber 2018; Alber et al. 2023). This understanding hampers the interpretation of a more diverse past in which political and economic organisation might be differently linked to forms of belonging.

In parallel to historical research, anthropological research has increasingly criticised the European vision of »biological« or genetic kinship as foundational to all human organisation. First, the assumption that kinship norms would easily translate into practice was challenged with the empirical turn towards on-site fieldwork at the turn of the 20th century. Focussing on rules and terminologies not only obscured historical transformations but also negated differences between norms and practices. Then, from the 1970s onwards, consanguinity as a structuring element was even more fundamentally called into question (Needham 1971; Schneider 1972). This critique culminated in the insight that Europeans had exported their cultural imagery about »blood« ties to the rest of the world. Largely exposed as being a European cultural symbol, the question arose as to whether kinship in the sense of consanguinity had been significant for social reality anywhere at all.

This critique also questioned the idea that contemporary hunter-gatherer societies could serve as a foil to interpret the more distant human past and unmasked the relegation of certain forms of social organisation to a timeless ahistorical void as yet another aspect of the tale of European progress and supremacy (Fabian 1983; Chakrabarty 2000). But even if research on contemporary hunter-gatherer societies might present useful evidence, recent studies suggest that their social organisation seldom takes place along genetic kinship lines. Individual men and women often travel long distances, and the composition of small groups seems to be »remarkably cosmopolitan« (Graeber/Wengrow 2021, 122). If they gather as larger residential groups, these are not made up of a tight-knit network of genetically related individuals. Instead, only about 10 % of the existing relations represent shared genes.

The critique brought social anthropological research on kinship almost entirely to a halt until a new wave of research largely inverted the European folk wisdom of »blood is thicker than water«. In the mid-1990s to the early 2000s, a series of studies demonstrated that kinship does not produce care but rather that practices of care establish kinship relations. These studies emphasised that – in Europe and elsewhere – kinship is not assigned once at conception or birth, but in practice must be constantly attested to. These arguments are supported by research in societies in which many or even most children do not grow up with their genetic parents (see also Alber in this volume). To underline the fluid and processual nature of kinship, authors have introduced expressions such as »doing kinship« or »kinning« (Howell 2006). In sum, kinship is always »assisted«, not just when it is created through reproductive technologies, and always needs diverse »signs of relatedness« to be established, and to remain important it must be constantly affirmed (Goldfarb 2016).

More fundamentally, this research has started to question the very separation between biological and social kinship. While earlier research in archaeology and anthropology had recognised the importance of cultural differences in understanding and living kinship, this second move to unmask the separation between social and biological kinship as a cultural artifact has proven harder to digest. In their studies of establishing kinship through care, both J. Carsten's work on Langkawi, Malaysia (1997), and M. Weismantel's in Ecuador (1995) have demonstrated the importance of sharing food in establishing kinship. In these contexts, food served as an addition to the idea of sharing blood. In much of the literature, such understandings and practices would be called »social« kinship. However, these authors are actually referring to biological processes believed to make people bodily similar and therefore kin. While somewhat counterintuitive to the well-established separation, these ideas are not so far from studies that research bodily similarity established through sharing a close environment. For example, toxicologists have suggested that humans become more similar to each other through the shared toxic substances within them and in their immediate environment. Such processes can be understood as establishing (chemical) kinship, as J. Lamoreaux (2020) argues. For this interpretation to become more persuasive, shared toxic substances would need to be legitimised and institutionalised as indicators for kinship (Thelen/Lammer 2021). While this might seem a far cry from established wisdom, we only need to remember how much work was invested in earlier instruments of proving kinship (McKinnon 2021). For example, in the Late Middle Ages when the monk Peter Damian first developed the system of counting generations, which is still used today in much of the sciences, it appeared absurd to his contemporaries (Teuscher 2023). This shows the likeliness of kinship understandings to change even if they seem very natural and therefore unchangeable. To be clear, there is no doubt that findings of genetic closeness in archaeological research might be interesting (for example, for medical or migration research) but we should be cautious in attributing an undeniable meaning to them for human organisation *per se*.

With the focus on actually existing relations, a last challenge has receded from sight; genetic links that do *not* result in closeness. Arguably it is always hardest to see what could have been but did not materialise, particularly as finding a relationship is seen as desirable in the European scientific tradition (Strathern 2020). However, any analysis that does not account for all the genetically related people who decided to leave settlements like La Almoyola risks imposing anachronistic ideas on the past.

4 Is there a future for interdisciplinary dialogue on kinship?

All of this conceptual criticism begs the question of whether the term kinship still has enough analytical value to serve as a central concept in interdisciplinary dialogue. Surely, kinship can still be understood as the idea of a special bond of belonging that can be constituted through diverse (bodily, emotional, ritual, legal) practices. Empirically, it can be useful to see how specific rights and obligations can be linked to kinship and serve as principles of organisation that define identities and hierarchies (Thelen 2021). However, given the wide scope of different ideas that might underlie such conceptions and practices of belonging, kinship as such has little analytical value. Therefore, one move has been to try to replace kinship with a better term, most notably relatedness, as introduced by Carsten (1997). However, while this has drawn (again) attention to the diversity of cultural understandings of what makes people close, studies have still overwhelmingly stayed in the realm of what always has been understood as kinship and not expanded beyond private households and families. It thus would make much more sense to ask, how care is negotiated and establishes belonging, if we wish to move beyond European naturalised preconceptions of social organisation (Thelen 2015).

Social anthropology and archaeological sciences look back on a long and productive history of shared interest in kinship. However, recent research questions the projection of European ideas into other times and places. With new ethnographic studies and biomolecular data having challenged the idea that heterosexual descent is always meaningful, we can ask such new questions about social organisation. If an adult woman's skeleton is buried with a child's and they are not genetically related, this might now be interpreted as a suggestion that care practice rather than heterosexual reproduction is the central feature in establishing belonging. Moreover, since the former temporality ascribed to kinship as always already there before other ways of human connecting and therefore almost »naturally« serving as a grid for political organisation has discouraged research that asks about its making, we might ask new question about how it is actually made to count or not (Alber et al. 2023).

Finally, some humans with high degree of genetic closeness might have lived together in small groups in the past. But maybe the group was small because other genetically similar persons had left and joined other groups or lived and died alone for various reasons, and either of these might be interesting to explore. In addition to the choice of avoiding or being excluded from contact, questions of hierarchy or care between genetically dissimilar humans are also interesting. We can also take the aforementioned toxicological findings of bodily similarity seriously and ask what kind of substances other than genes made (and makes) people stick together (or not). The move not to take genetic closeness as self-explanatory enables us to ask a whole lot of other questions that could direct research into new areas and improve our understanding of human history. Resisting the temptation to fill gaps of knowledge with what seems logical in hindsight allows us to open a new chapter in the conversation between archaeological sciences and social anthropology and, what is more, would offer a new understanding of the diversity in patterns of human organisation.

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Multiple Relations: Towards an Anthropology of Parenting

Erdmute Alber

Zusammenfassung

Multiple Beziehungen: Auf dem Weg zu einer Anthropologie der Elternschaft

Trotz der großen Bedeutung von Eltern-Kind-Beziehungen in der Verwandtschaft ist Elternschaft in der Anthropologie der Verwandtschaft ein bislang untertheoretisiertes Thema. Der Beitrag skizziert eine Anthropologie der Elternschaft, die diese Zentralität anerkennt. Ihre Theorie wird zunächst anhand eines Fallbeispiels entwickelt, im Anschluss werden Debatten aufgezeigt, die für eine Anthropologie von Elternschaft wichtig sind. Hierbei werden die problematische Gegenüberstellung von biologisch versus *sozial in der Geschichte der Sozialanthropologie verortet und im Anschluss Debatten skizziert, die für eine Anthropologie von Elternschaft wichtig sind. Diese wird schließlich als relationales Konzept definiert, das durch multiple Beziehungen emergiert.*

Summary

Despite the importance of parent-child relationships in kinship, parenthood is an under-theorized topic in kinship anthropology. The paper outlines an anthropology of parenting that recognizes this centrality. Its theory is first developed on the basis of a case study, followed by debates that are important for an anthropology of parenthood. The problematic juxtaposition of biological versus *social is located in the history of social anthropology and debates that are important for an anthropology of parenthood are then outlined. This is finally defined as a relational concept that emerges through multiple relationships.*

Introduction

In September of 2022, I spoke with a young man from the Republic of Benin whom I will call Issaka. He was trained as a social geographer in Germany and works for an internationally financed environmental project. Three years ago, he married Yamila, a young woman from his home region in northern Benin, who is trained as a primary school teacher. The family is seeking to establish a middle-class life in northern Benin and by October 2022 were expecting their second child. I have known Issaka since he was a child, so we are close enough to talk about personal affairs and emotions.

Reflecting on his personal situation, Issaka told me how happy it makes him that he and his wife agree about his rural home region's established (and apparently centuries-old) practice of sending some children away for foster care[1]. He explained that, especially among couples seeking to live an urban professional life, the value of this practice was no longer self-evident. Many parents today want to bring up their biological children (his term) themselves, according to a European »nuclear family« model they consider superior to the practices Issaka and his wife grew up with.

Issaka explained that when he got married, he had not yet been sure how Yamila would react if he asked her to give one of their children to other parents. When he talked about her, he cited their agreement that children could also be raised by others as evidence that he had chosen the right woman to marry.

We also discussed the new house that he was spending every centime he had on completing. This building in the style favoured by members of the new middle classes was being built on land they had purchased in the city neighbourhood, where every urban academic aspired to build and live.

Issaka was hoping to move the whole family there before October, when his second child was due, if it was at all possible. In my own view, the house was quite far from being in a state to move into: the floors and walls were still bare cement, there was no electricity or running water, and only two of the five rooms even had windows. However, among the reasons given by Issaka as to why he had to leave his rented apartment as soon as possible were the birth rituals for his second child. Those of the first child had been held in the household of his foster parents, where he had lived while attending secondary school, and he was eager to maintain those rituals for the second under his own roof. According to local beliefs, rituals require a place of land that is the property of the person who performs them, so living in a rented apartment he would not be allowed to carry them out.

For all these reasons, Issaka told me, he was delighted that his wife shared his eagerness to take full possession of their own place. He had feared that she might feel uncomfortable moving into what could better be described as a

1 See, among others, Martin 2013; Alber 2018.

construction site than a home. But she too wanted to move as soon as possible. Their shared desire to establish their own home was, not least, in order to become more independent from their kin, especially their parents.

This conversation with Issaka is related to parenting in four meaningful ways. Most importantly, it demonstrates the importance of parenting in his reflections on his current living situation and starting his new family. Parenting is relevant to all aspects of family life, including building a family home, organising rituals, reflecting on how and where to raise the children, and, last but not least, a peaceful conjugal life.

Second, Issaka reflected on parenting as a field of insecurity and possible conflict between spouses but one that is at the same time essential to a healthy marriage. This insecurity derives from the profound changes taking place in parental practices and a corresponding diversity of norms and ideas that, as Issaka observed, are not always shared between spouses. These relate to questions about how children should be raised, under whose roof they should grow up, and who has the right and duty to educate them. Our conversation also drew attention to the materialities and ritual aspects of parenting, such as the house and birth rituals.

Although Issaka and Yamila come from similar family backgrounds – both were born in remote villages and raised in urban households where they could attend school; however, these situational similarities were not enough to guarantee a shared understanding on parenting. Issaka's happiness about his wife's opinions demonstrated how this was not at all self-evident. In a rapidly changing society like Benin, norms and ideas about childhood and proper parenting, including changing needs and requirements for education, as well as divergent generational experiences and expectations, constitute a heterogenous and sometimes contested field of ideas. Among the causes of these changes are influences from Europe and the Global North spread in the media. These favour, among other things, the model of a nuclear family with exclusive responsibility for raising children. Spouses often disagree, even when they share similar family backgrounds. This causes a sense of insecurity that troubled Issaka and, as I know from other conversations, troubles many of his contemporaries in Benin.

Third, Issaka related parenting to many other themes, such as a young middle-class family's upward social mobility, relations with his parents' generation, and building a house. Apparently, parenting is key to understanding many other aspects of the changing societal field.

Finally, Issaka does not see biological or birth parents as the only or most appropriate persons to fulfil the tasks of parenting according to the Euro-North American ideal of the nuclear family – which is also the ideal implied in national family law in Benin (African Charter 1999; République du Bénin 2002). Instead, he holds to the norms that he grew up with: it can be desirable for children to be raised by someone other than their birth parents. Part of the reason for his insecurity was not having known whether his wife, who shared his experience of having grown up as a foster child, still felt that parenting by foster parents was easy and normal. It would really be a pleasure for Issaka, he told me, to give some of his children to persons to whom he felt attached and indebted. The reverse was also true: even though he was still living in a small apartment, he had already taken in one foster child, a nephew from his village who was studying in town.

As this conversation with Issaka demonstrates, the ideal that children should be raised by their birth parents in a nuclear family is not even self-evident to emerging middle-class families in northern Benin who aspire to a lifestyle that includes many elements of the Euro-North American conjugal or nuclear model.

Biological and social kinship

The conversation with Issaka shows that practices and reflections on appropriate parenting in a middle-class setting in the Republic of Benin at the beginning of the 21st century do not easily match the widespread Euro-North American understanding of parenting as a social practice that is grounded in biological ties. However, this distinction between biological and social kinship should also not be understood as a timeless analytical category but as an assumption dating to the 19th-century foundation of the modern discipline of social anthropology. In particular, L. H. Morgan sought to »carve out certain aspects of human behaviour, isolating them for study«, as T. Trautmann's (1987, 4) account of the process of the »invention of kinship« as an object of anthropological research puts it. To make kinship an object of inquiry – and thus a universal human category – it was necessary to produce evidence by inventing methods of describing, comparing, measuring, and classifying complex social relationships all over the world. This process was accompanied by the establishment of a distinction between »modern« societies and the proper field of the new discipline of anthropology, the so-called »primitive societies«.

Morgan himself contributed to this important boundary-making between »modern« and »primitive« societies with his famous distinction between classificatory kinship systems, attributed to primitive societies and grounded in social classification, and descriptive kinship systems, which he saw as following biological distinctions (Morgan 1870). In the latter, kinship was seen to be founded on clear genealogical or biological relationships based on sexual activities, and to be researched with the genealogical method and its objectifying visual representation (Bouquet 1996). These relationships were seen to be translated into various meanings and practices through social activity. Kinship as a field of anthropological inquiry thus concerned social practices that were based on indubitable biological processes of sexuality and procreation. This meant studying topics like rules and prohibitions concerning marriage partners, kinship terminologies and their classification, and the rules and regulations of property, inheritance, and succession.

In this sense, kinship in itself was not only constituted by an epistemological nature/culture divide, but also as constituting and substantiating this divide through anthropological knowledge production. It was only decades later that anthropologists and others started to reflect critically on the history of the idea that kinship was a universal category

shared by all societies over the world and how it could even be understood as an imaginary means to make anthropological methods seem objective (Thelen/Alber 2018).

Of course, anthropology was not the only discipline where this process of inventing and establishing kinship took place: it was embedded in and related to specific epistemological processes during the 19th century. M. Hohkamp (2023) has called this period the »century of kinship« during which both natural sciences and the newly emerging humanities were fascinated by sexuality and procreation, genealogy, breeding, and the development of new methods to describe and objectify these processes.

This nature-culture divide – based on the idea of an objective »nature« or biology, but also researching heterogenous and culture-specific practices of kinship with positivist and objectifying methods – characterised the anthropology of kinship until the second half of the 20th century, when it was re-evaluated and became understood as foundational for western or Euro-North American ideas about kinship. Here, especially, the notion that »nature« or »biology« was stable and the clear basis of social relatedness was itself destabilised (Strathern 1992).

Again, this destabilisation was embedded in knowledge processes that were not restricted to anthropology alone. Among these were the development of, and anthropological reflection on, so-called »artificial reproductive technologies« like surrogate motherhood, which destabilised the idea of a »natural« unity of conception, pregnancy, and birth (Franklin/Ragoné 1998; Ragoné 2006). Who should be seen as the biological mother – the donor of the egg, or the woman who carried the pregnancy? What could be seen as nature if the beginning of human life was produced and possibly designed in the laboratory? And how could kinship be conceptualised on the basis of an idea about nature if same-sex parenting was allowed by, and established in, modern family law (Weston 1997)?

Besides challenging the biology/society and nature/culture divides, these approaches of researching kinship or more specifically, parenting, were no longer realised in societies outside the West: they brought anthropological kinship research ›back‹ to Euro-North America and closed the former spatial divide as well. This move was possible not only because kinship as a universal category had been destabilised, but also because it had been argued that while the biology/culture, or biology/society divide was not essential for distinguishing the West from the rest, it had been deeply impressed on the North American understanding of kinship (Schneider 1968).

In parallel to this destabilisation of the biology/society divide by looking at kinship and reproductive technologies in Euro-North American societies, another strand of kinship literature destabilised the idea of true biological kinship by looking at societies outside the West. Again, parenting was key.

Studies of motherhood and breastfeeding, for instance, argued that the former is often less grounded in the mother having given birth to a child than having given milk to it (Thorley 2014). If nursing seems to be more important in constituting the bond between mother and child in some societies, which should we understand as biological?

Research on foster parenting in Africa (Notermans 2004), Latin America (Weismantel 1995), or Oceania (Brady 1976; Modell 1998) has demonstrated, among other things, the importance of sharing time, food, beds, and homes to the constitution of parenthood and its acknowledgement by society. In a detailed case study in Ecuador, M. Weismantel (1995) observed that if a grandmother took care of a grandchild for an extended period they came to be seen as mother and child by not only each other but also others, who started to address her as the mother of the child based on the fact that she and the child had shared the same food over time and thus become bodily similar.

In fact, the bodily process of sharing food and bed eventually started to overwrite the now-partially fading bodily experience of giving birth and providing closeness and food that had previously established the parental relation between the birth mother and the child. Following anthropologist J. Carsten's metaphor of the »thickening« and »thinning« of kinship (Carsten 2013), here, the parental relationship with the grandmother »thickened« even as the parental relationship with the mother »thinned«, with both being imagined as physical, bodily processes that were, if you will, similarly grounded in biological substances.

Another anthropological critique that questioned the notion of a stable »biology« and a related but clearly separated practice of social relatedness started with the idea that the biological basis of fatherhood is itself a process of knowing: if not all of society is aware of the relationship between sexuality and fatherhood, what is fatherhood based on? M. Strathern (2011) took up this line of argument by looking at it in the context of artificial reproductive technologies. She argued that parenting is constituted by a fundamental asymmetry where the child is a fact in itself, a given, a phenomenon, while the parent, as the other part of the relation that constitutes parenting, is always a construct, a product of processes of knowing and stabilising knowledge that can never be completely stable.

In short, the assumption of a nature/culture, or biology/society divide in the understanding of kinship has been challenged from different perspectives of anthropological research in both the West and the Rest with increasing awareness that this divide is not universal, but rather is a foundational element of Euro-North American epistemologies of kinship.

Parenting

Parenting in its multiple forms stands at the centre of these debates: breastfeeding and the notion of shared milk, the conception of a child through a sexual or through artificial processes of uniting eggs and sperm, and living together and sharing food, all constitute parent-child relationships. All these activities relate the »parent« (whoever that may be) and the »child« (again, whoever *that* may be) to the larger society. They are restricted neither to the private realm nor to the period of childhood but take place over the whole life course.

What, then, is parenting? The examples I have presented – giving birth or food, performing rituals and having the

right to raise a particular child – are quite heterogenous, and position parents in different times and roles towards not only their children but also the state and larger society.

I define parenting as a relational concept, which encompasses multiplicities of gendered moralities, actions, care activities, knowledge transmissions and feelings between parents and children in specific historical moments and over parents and children's life courses. These contribute to the making of future, of individuals as well as of the society. It is through these multiplicities that the inter-generational relations are emerging. The categories of »parent« and »child« are, of course, not restricted to birth parents and birth children. These are themselves largely shaped by changing societal understandings of who is a parent and who a child. Parent-child relationships are often seen as symmetric, as for instance expressed in the idea of an inter-generational contract that places emphasis on balance and equalness over time. However, I would argue that these are principally asymmetrical, because due to temporal and societal change, the way in which children would one day parent with their own children might be largely different from how their parents acted as such.

In using the term »parenting« here, I follow a recent trend in social anthropology of emphasising the processual and relational character of concepts: here, more concretely, practices of parenting constitute what is understood as »parenthood«. Following H. Haukanes and T. Thelen (2010, 11), parenthood can, in short, be understood as the »socially constructed notions linked to the status of being a parent«. Parenting, in contrast, is a more dynamic concept and refers to »actual practices of parents with regard to their children« (Haukanes/Thelen 2010, 11), which – here I add to Haukanes and Thelen's definition – produce what is then understood as parenthood.

In any case, neither parenthood nor parenting has received much theoretical attention in anthropological debates. This is surprising, considering their centrality to kinship, which again demonstrates how the concrete practices that make, shape and result in alliance and descent – like practices of parenting – long remained less theorised in debates that treated kinship as constituted by alliance and descent. E. Goody's (1982) book on *parenthood and social reproduction* is one of the very few that have made this point for the field of reproduction and argues that parenthood can be understood as the most concrete activity of organising reproduction over time.

In fact, the first anthropological publications specifically on parenting or parenthood only date to the late 1970s. In the next section, I shall very briefly mention five fields of interest and their contribution to theorising parenting.

Five fields of interest in parenting

First, in the second half of the 20th century, feminist and gender studies investigated and challenged the gendered division of labour and fixed gender roles. Due to their specific interests, however, their treatment of parenthood largely reduced it to motherhood. In *Birth in Four Cultures*, B. Jordan (1978) challenged facile assumptions that assumed that the moment of birth was more »natural« in non-European societies' and about the specific ways women were supported in different states. Another important publication on motherhood was S. Hay's (1996) monograph, *The Cultural Contradictions of Motherhood*, which discusses the contradiction of intense, loving motherhood in a highly competitive North American society that asks women to realise themselves through professional advancement. Feminist studies also helped to critique the private/public divide, to reveal the political dimension of apparently private activities such as motherhood, and of course, most importantly, to stress the gendered aspects of parenthood.

Second, anthropological and (still more) sociological studies of the gendered dimension of care and global care chains (Ehrenreich/Hochschild 2003) have helped to reveal the often-transnational dimensions of childcare along with the gendered and unequal distribution and valorisation of care work. These brought attention to the consequences of attributing domestic labour to women (while often rendering it invisible) and paid labour to men (Colen 1995; Parrenas 2000; Ehrenreich/Hochschild 2003).

At the same time, through their reflections on the transfer of the work of domestic care from kin to paid workers, studies on care and parenting have brought a new level of attention to the co-production of kinship and institutional care in settings like kindergartens and organised childcare centres (Ellmer 2020). On the one hand, they opened a perspective on how parenting is only realised in the private context, but also connects households to institutions and the societal context. On the other hand, they opened a window to grasp forms of inclusion and exclusion and of possibilities and impossibilities: in fact, they again brought up the political dimension of parenting. Finally, such studies revealed the role of work in parenting – work that could be commodified, or seen as kinship and a moral obligation (Drotbohm/Alber 2015), while also demonstrating the affective and emotional side of care (here, parental care).

A third field of interest in parenthood and parental activities can be seen in the rising interest in childhood in anthropological and sociological debates since the last decade of the 20th century[2]. However, as Haukanes and Thelen (2010) have convincingly argued, they remained mainly focussed on children and childhood and often overlooked how children's rights, spaces and agencies, all of which have been intensively discussed in the so-called new childhood studies, could not be separated from parents' rights and duties and how these were situated in specific societal times and places.

Haukanes and Thelen (2010) further argued that ideas about good parenting have been overshadowed by notions of proper childhood, which they see as travelling globally in the late 20th century. One good example of this can be seen

2 James/Prout 1990; Caputo 1995; De Boek/Honwana 2005; Boyden 2006; Christensen/James 2008.

in how Issaka feared that his wife might have adopted the European idea that children should grow up with their birth parents. Debates on childhood also revealed the legal dimension of parenting. Of course, protecting children's rights requires a legal framework that obliges parents to protect their children, but this also implies the need to define who is the legal parent.

Fourth, studies of child fostering in Africa[3] and Oceania (Modell 1998; Collard 2004) have challenged Euro-North American assumptions that children are usually raised by their birth parents. I have already mentioned Goody's (1982) pioneering work on child fostering in Ghana, which substantially contributed to theorising parenthood. Her key argument is that the multiple parental roles there are key for societal reproduction. Goody defines five roles of parenting: the processes of bearing and begetting, status entitlement, further nurturing, teaching, and sponsoring children. Importantly, she argues that these tasks of parenthood can be distributed among several persons rather than being limited to the birth parents alone.

This perspective was followed and complemented by a literature on adoption and the transnational circulation of children, which demonstrated that processes of transferring parental belonging were deeply related and reproduced global political and economic inequalities. Moreover, they were linked with legal and political transformations (Bowie 2004; Howell 2006; Yngvesson 2007).

Fifth, an important strand of literature raises the topic of parenting in the context of artificial reproductive technologies that create constellations of new roles, like surrogate mothers or sperm donors, which complicate categories such as mother or father. These debates have contributed, as already mentioned, to denaturalising both motherhood and fatherhood. Later literature on »rainbow families« and queer parenting has not only deconstructed the idea of parenting as an activity organised in »normative« nuclear families with clear gender roles, but also raised awareness of questions about legally and practically defining a parent and their related rights (Greenhalgh 1995; Franklin/Ragoné 1998; Strathern 2005).

Building on Goody and Haukanes and Thelen's critiques of the concepts of parenting that are often too closely linked to discussions around childhood and child welfare, I suggest that parenting should be defined as a dynamic – and, of course, gendered – processual activity that is related to, but also constitutes, parents and children through actions of exchange, care, property transmissions and law. As such, parenting gives rise to processes that shape children's individual and (especially) societal futures. It is therefore not a dyadic relationship but a process of relating that co-constitutes parents, children, and society through the institutions involved, over time and with changing roles and meanings. This process does not end when children become adults: it continues over the life course and binds together multiple generations.

Parenting is a key activity in building new generations, making it an engine of societal change. It is therefore inherently embedded in political processes of changing societal formations. At the same time, it has the potential to reproduce or overturn social, economic and gender inequalities and is, of course, deeply shaped by legal processes.

Two temporal dimensions of parenting have not yet been adequately conceptualised. First, the inter-generational dimension cannot be reduced to a dyadic relationship between parents and their children, but often involves the grandparents as well. Second, parenting encompasses activities over the life course and cannot be limited to the period of childhood. Moreover, parenting cannot be reduced to the realm of kinship and the household. It relates institutions, households and the state in multiple ways and is key to almost all processes of belonging, including civic, religious and class belonging, but especially to stabilising and transforming gendered belonging over time.

Conclusion

I started with Issaka's reflections on his new family, and his plans for a new middle-class household that will be very different from the rural peasant household of peasants into which he was born.

That conversation touched on many of the dimensions of parenting I defined. It began as one about future-building and how Issaka imagined his family developing. Then, parenting as gendered activity came up, but not, as one might expect, because Issaka and his wife divided parental labour strictly along gender lines. It only emerged indirectly later in the conversation that Issaka, as the male head of the household, must earn money to provide for his family (including any foster children), organising physical accommodations, and materially maintain the household while his wife will have the main responsibility for everyday cleaning, feeding, dressing and supervising the children. But these highly gendered activities of parenting were less prominent in the conversation than Issaka's fear that his wife would want to follow norms closer to the idea of the nuclear family.

Parenting appeared alongside future-building and gendered labour and norms as a contested space that, as I have shown, mirrored societal frictions and transformations like the controversial shift towards the global travelling image of the nuclear family. In addition, parenting mirrors the rising inequality in Beninese society, in which middle-class urban children are educated differently from rural ones. Here, as I have argued, questions of belonging are also concerned.

Actions and activities of parenting, even those as seemingly private as those of Issaka and his wife, are contributing to the contested political arena of changing family forms and children's rights in Benin and are related to processes of class building and class differentiation. In sum, parenting relates Issaka, his wife, and their children (and those they will have in the future) to the political arena where important societal changes are made, the transmis-

3 Goody 1982; Bledsoe 1990; Lallemand 1983; Alber et al. 2013.

sion of property is organised, and future generations are shaped.

Since parenting is about belonging, not only in the sense of kinship, but to a religion, ethnicity and class, the question of where the birth rituals of the children should take place also influenced how far the children, as well as Issaka himself, would be seen as belonging to his foster parents. Negotiating whether the second child's birth ritual should be held in the house of Issaka's foster parents or his own demonstrated the importance of intergenerational entanglements. The involvement of both Issaka and his parents demonstrates how parenting relates several generations over time and how it does not end when children become adults. Like other parents, Issaka's foster father remains very present in his reflections on his future. Parenting is not limited to a short, specific, and closed phase of life, but includes multiple processes extending over one's whole lifespan that constantly relate to other activities.

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Kin and connection: Bodies and relations in archaeology and ancient genetics

Catherine J. Frieman

Zusammenfassung

Verwandtschaft und Verbindung: Körper und Beziehungen in der Archäologie und der Archäogenetik

In Verbindung mit einer präziseren absoluten Datierung haben biomolekulare Daten (d. h. alte DNA, stabile Isotope) die Praxis der Archäologie, die Fragen, die Archäologen stellen, und die Interpretationsmöglichkeiten auf der Skala des Lebens eines Individuums grundlegend verändert. Immer erschwinglichere und präzisere prähistorische biomolekulare Analysen stellen traditionelle archäologische Interpretationen in Frage, die sich aus materiellen Kulturstudien und Landschaftsuntersuchungen ergeben. Zu den neuen Wegen, die dieser Forschungsansatz eröffnet, gehört ein aufkommendes Interesse an Verwandtschaft und Beziehung sowohl bei Archäologen als auch bei Genetikern. In diesem Artikel werde ich die Spannungen zwischen genetischen Daten über Verwandtschaft und sozialen Narrativen über Verwandtschaftsbeziehungen untersuchen, um Wege aufzuzeigen, wie wir unsere Unterschiede produktiv überbrücken können.

Summary

In conjunction with more precise absolute dating, biomolecular data (i.e., ancient DNA, stable isotopes) have fundamentally changed the practice of archaeology, the questions archaeologists ask, and the possibilities for interpretation on the scale of an individual's lifetime. Increasingly affordable and precise ancient biomolecular analyses are challenging traditional archaeological interpretations emergent from material culture studies and landscape investigation. Among the new avenues opened by this new research approach is an emerging interest in kinship and relation among both archaeologists and geneticists. In this paper, I will explore the tensions between genetic data concerning relatedness and social stories of kin connection in order to suggest avenues through which we might productively bridge our differences.

1 Introduction

Identifying kin, those people to whom we are related and with whom we are in relation, occurs at the junction between social interpretation and biomolecular science (Brück/Frieman 2021), making this an exciting node in such interdisciplinary collaborations. With the advent of new and increasingly accessible biomolecular methods, archaeologists and historians have been challenged to rework old narratives and discover new ones that speak to newly revealed biological patterns. Here, I explore how kinship – both social relations and biological relatedness – might form a sort of interpretative middle ground better to integrate biomolecular and social data into archaeological narratives about the past. I build outwards from the inherent tension between the fluid world of social kin-making and the biomolecular data increasingly used to categorise past people and their relationships in order to outline paths for future research and collaboration.

2 Kinship past and present

Kinship is one of the major foci of social anthropology as it is traditionally understood as comprising a major shared element of all known human societies – our own included. Anthropologists have spent the last century mapping patterns of relation – between individuals, created through marriage or other forms of affiliation, and with other-than-human entities, such as spirits, animals and places (Sahlins 2013). This is important to understand because kin-making is a key part of how humans structure their relations with each other, with their wider community and with the non-human world. Kin relations are constituted by shared values and shared experience, as well as by shared cultural or biological lineage (Abel/Frieman 2023).

Many of the original and still foundational works on kinship emphasised society-wide models, often linked to political and economic practices, rather than individual experiences (e. g., Leach 1951; Fox 1967; Lévi-Strauss 1969). These models generalise from highly variable lived ways of relating and universalise ways of being that might look wildly different from different ›on the ground‹ perspectives. In recent decades, attention to kinship has not waned, but it has shifted from these normative structures to more complex and contingent approaches (Carsten 2004; Nash 2004; Nash 2005). The question now is not so much about identifying universal underlying structures of kinship within a given cultural group as it is about seeking to understand who kin are or might be, how they are made, and what roles they might play by dint of their kinship (Sahlins 2013).

That is, present research is more interested in kin as a dynamic verb rather than a static noun.

Contemporary anthropologies of kinship – led in large part by feminist and queer scholars – emphasise that relations between people, communities, and generations (not to mention between people and other-than-humans) are fluid, contingent, and resist categorisation[1]. They shift over an individual's life course, can be altered and manipulated as politics and personal relations demand, and are ultimately flexible enough that even strict kin categories can be expanded to absorb outsiders and create visible relations between otherwise unknown lineages. Moreover, Indigenous and First Nations scholars emphasise the extent to which kinship extends outwards to the other-than-human world, encompassing people, places, plants, and animals into mutually beneficial webs of relation and obligation[2]. Genetic data would seem to pose a challenge to this fluid and complex world of relations, as genes are widely understood as objective and evidence for immutable pre-existing patterns of relation. However, biological patterns too are understood through the lens of culture and connection, with genetic data being regularly reconstituted to conform to social conceptions of relation rather than the other way around (Abel 2021a).

2.1 Gene-ealogies and archaeologies of kinship

Archaeologists and evolutionary biologists have had access to ancient DNA data of various qualities and quantities for decades, but only with the recent development of Next-Generation Sequencing (NGS) and its successors has aDNA data become widely accessible. With increasing quantities of high-quality genetic data from a variety of people, places, periods, and archaeological cultures the relevance of these data to archaeological research has increased; and new sorts of archaeological questions have emerged. Following J. Brück and C. J. Frieman (2021), a strong interest in lineage unites much of the aDNA research produced since the advent of NGS. They divide aDNA lineage research into two broad categories based on methodological approach: research into vertical patterns of relatedness, that is, between ancient and modern populations, and research into horizontal patterns of relatedness, that is, between populations or individuals in the past. This latter approach holds considerable interest for archaeologists, as it has potential to illuminate aspects of relations that would have been knowable and experienced by past people in the course of their own lives. Recent work by C. Fowler and colleagues (2022) on biologically related individuals within a Neolithic megalithic tomb is exemplary of the fine-grained detail and new data-driven insights this sort of research can offer, even to the most heavily investigated of prehistoric practices. The genetic genealogies developed within this and other research projects clearly gives us insight into aspects of social practice, including how biological relatedness played a role in funerary rites, gendered aspects of lineage creation, and elements of reproductive choice and affiliation (Armit et al. 2023).

Nevertheless, we must approach these genetic genealogies with care. The genetic genealogy – or gene-ealogy (sensu Abel/Frieman 2023) – is one form of mapping social and genetic data together. Within the framework of kin-as-verb discussed above, to understand kinship diagrams and genealogies as technologies or kin-making tools as much as ones for kin-mapping (Nash 2008; Wolf-Meyer 2020; Abel/Frieman 2023). They do not reveal innate relations, but create kin ties between individuals, materialising a momentary or perceived relationship and reifying it temporally, as well as restricting our understanding of who can be kin, and how they become kin. Genealogies have a deep history in European culture, where they have been used as tools to create distinctions between individuals, families, ethnic groups (and later races), as well as to manifest affinities (including with deities or supernatural entities) when politically, economically or socially expedient[3]. As such, even when combined with genetic data, gene-alogies are neither objective nor without social interpretation. Indeed, sociological research finds that it is rare for contemporary people to have straightforwardly genetic-deterministic approaches to their DNA results. Instead, genetic data are assimilated selectively into identity narratives; their objectivity is questioned and assessed in relation to other forms of ancestral knowledge (Nelson 2008; Panofsky/Donovan 2019; Abel 2021). If there is to be a meaningful archaeology of kinship that exists in dialogue with, but not driven by, genetic data, this approach will play a central role.

Despite the close links between anthropology and archaeology, and the central position of kinship within the former, until recently there was little robust analysis of kinship among archaeologists. In line with broader anthropological critiques (e.g., Schneider 1984), later twentieth-century archaeologists W. L. Allen and J. B. Richardson (1971) argued that archaeological data were not suited to kinship analysis. They argued that, as kinship articulates largely on the small-scale of interpersonal relationships with culturally contingent forms and conceptions, the fragmentation and temporal breadth of archaeological materials, not to mention the typical lack of living traditions or interlocutors, made searching for past kinship structures a futile endeavour. Despite the turn to social archaeology in the 1980s, kinship (then, out of fashion in anthropology as well), never quite gained archaeological attention beyond osteological approaches to biodistance (Stojanowski/Schillaci 2006; Johnson/Paul 2016). It is these bioarchaeological models of ›kinship‹ – actually biological relatedness – that have particularly influenced the emerging field of palaeogenomics (Ensor et al. 2017).

The development of a distinct social archaeology of kin and relations is still in progress, and the newness of field means that there are not established methods for discuss-

1 McKinnon/Cannell 2013; Goldfarb/Schuster 2016; Haraway 2016; Clarke/Haraway 2018.

2 Kimmerer 2013; Andrade 2014; Todd 2017; Neale/Kelly 2020.

3 Klapisch-Zuber 2000; Thornton 2003; Martínez 2008; Guy 2018; de Miramon/van der Lugt 2019.

ing kinship – especially complex and fluid kin-making practices – in archaeology. Nevertheless, we see a rapidly growing cluster of research in this area, spurred by biomolecular developments, but branching off into several distinct and diverse directions. American anthropological archaeologist B. Ensor (2011; 2013), for example, builds from a foundation of twentieth-century kinship studies to identify descent patterns and kin relations cross-culturally. Although he agrees that social considerations are central to the organisation of kinship (Ensor 2017), nevertheless he expects generalizable patterns to be present. He identifies several archaeological domains, which he argues should give insight into lineage rules (that is, marriage patterns, residence patterns, etc.), among them the form and layout of domestic structures and settlements, and uses this model to delineate patterns of descent in diverse archaeological contexts from Europe and the Americas (Ensor 2013; Ensor 2016; Ensor 2021).

B. Mills, another American archaeologist who works primarily in the pre-colonial America south-west, takes an alternative approach, although still one that values generalisable and quantitative data. She and her colleagues (Mills et al. 2016; Mills 2018; Mills/Peeples 2019) model the movement of migrants through a social network analysis of the spread of innovative ceramic techniques and decorative schema. They understand the spread of these innovative techniques to follow the movements of skilled potters who, they argue, were largely women who travelled as marriage partners to distant communities. Their skills made them sought-after spouses and the residue of connectivity visible in the manufacture and decoration of pottery allows us insight into patterns of affiliation and descent.

By contrast, across several articles and a monograph, Brück and her colleagues[4] build a more fluid and social model of kinship, arguing that (among other things) we can follow patterns of affiliation and social kin-making in the movement of objects and materials, including fragmented human remains. Her work creates space for queer relations and relations with other-than-humans in our archaeological kinship discourse, a factor R. Crellin and O. Harris (2020) emphasise as key to formulating a sophisticated and comprehensive understanding of past people's kin-worlds. Similarly, R. Johnston (2020) looks at prehistoric practices that did ›kinwork‹, that is, the making and breaking of kin relations, from constructing and maintaining field systems and monumental earthworks to the deposition of metalwork in rivers. These sorts of activities materialise intangible kinning practices between people, places, and generations past and future.

2.2 Landscapes of inheritance in Roman Cornwall

In my own work in Cornwall in the south-west of Britain, my colleagues and I have argued that patterns of kinship and affiliation contribute to the formation of occupation patterns in the Roman-period landscape (Lewis/Frieman 2018; Frieman/Lewis 2021; Frieman et al. 2022). Here, from about the 1st century BC, we see a marked shift to settlement structured around small (c. 1 HA) enclosures from a landscape of open settlements and the occasional enclosed hill top or promontory site to one characterised by thousands of circular enclosed settlements (Cripps 2006). The majority are farmsteads with round and oval houses within, though some were evidently industrial or agricultural structures (Lawson-Jones/Kirkham 2010), with the majority being constructed in the Roman period. Some seem to have been occupied continuously for centuries (Quinnell 2004), while others saw only brief phases of occupation or perhaps even intentional abandonment after only a generation or two (Cole/Nowakowski 2021). Aside from these embanked sites and some newly identified open settlements (Young 2012; Jones 2019), there is no further evidence of settlement hierarchy; and villages or central places do not emerge until the later 1st millennium AD.

The embanked sites themselves are sometimes considered elite settlements, and some show clear evidence of elaborate entryways, multiple encircling rings of ditches and banks, and other monumental constructions (Lewis/Frieman 2018). Yet, despite these outer-works, they are almost uniformly small in size and contained just a few round or oval structures (Fig. 1). We have argued that they probably functioned much like fortified manor farms and were occupied by extended family groups. Following this model, we can see, in those sites occupied for generations or even centuries, patterns of protected, familial inheritance that saw the rights to occupy the embanked farm site (and likely also to control pasturage or other agricultural lands) passed down through an established lineage.

At the same time that these enclosed sites were settled, the Roman military was actively engaged in mining activities around the Cornish peninsula (Borlase 2020). Multiple military installations are known, some more long-lived than others, that testify to the local presence of occupying Roman forces (Fox et al. 1972; Smart 2014; Nicholas/Hartgroves 2018), yet little in the way of Roman material is present within the embanked settlements (Thomas 2016). Moreover, few of the settlements were located in visually imposing locales, or placed to control major routeways, suggesting that the power of the lineages who occupied them derived neither from contacts amongst the Roman army nor from control of the flow of goods in and out of Cornwall. Instead, we suggest that the powerful kin groups who occupied these sites were likely engaged in more complex and local status competition centred on access to prime grazing land that articulated through kinning practices, including marriages, adoptions, and other more ephemeral forms of affiliation (Frieman et al. 2022). Certainly, the pattern of land tenure and inheritance was stable enough to withstand the Roman occupation and outlast the Roman Empire, although Christianisation seems

4 Brück 2019; Brück 2021; Booth et al. 2021; Brück/Frieman 2021.

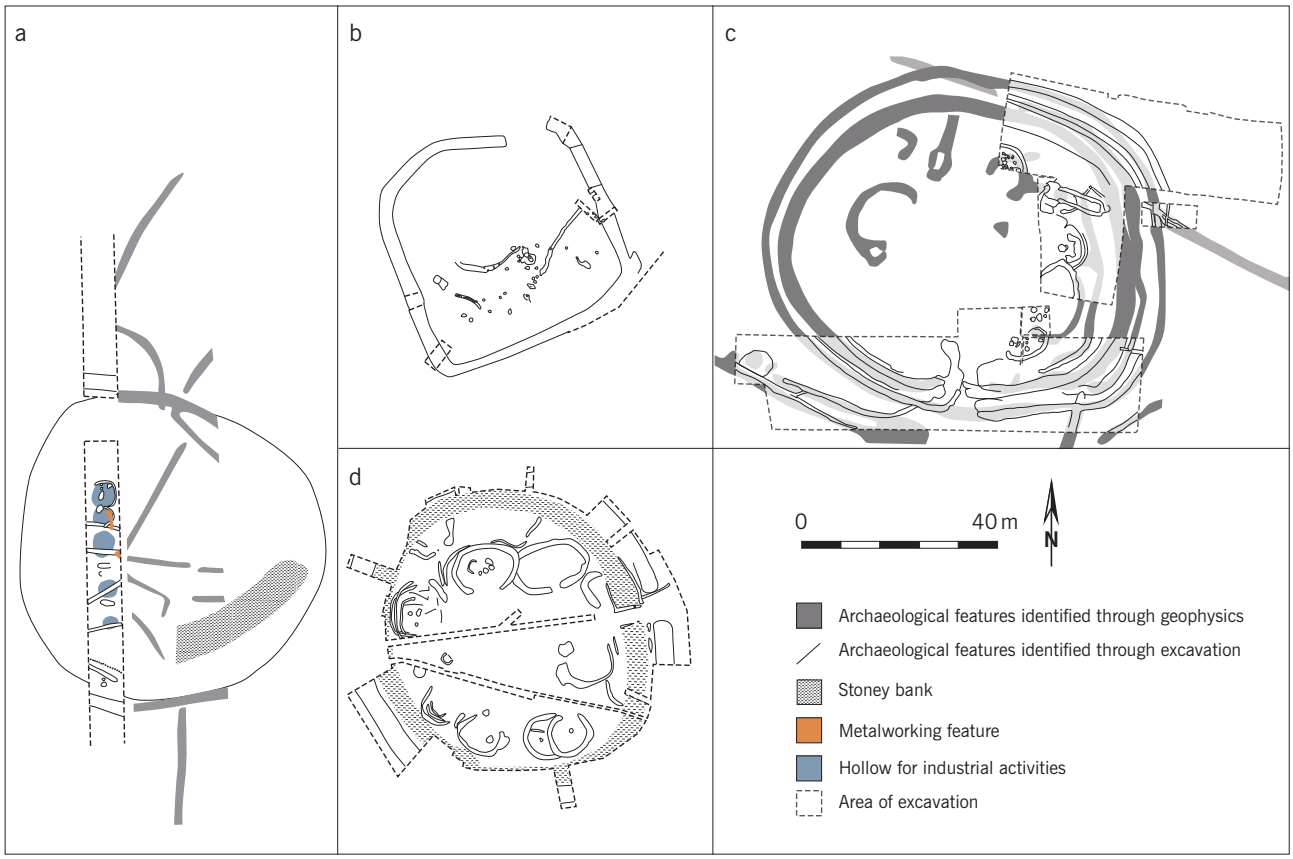


Fig. 1a–d Ground-plans of four Cornish embanked enclosures. a Little Quoit Farm, St Columb Major; b Porthleven; c Penhale Round; d Trethurgy.

Abb. 1a–d *Grundrisse von vier eingedämmten Einfriedungen in Cornwall. a Little Quoit Farm, St. Columb Major; b Porthleven; c Penhale; d Trethurgy.*

to have led to a fundamental rupture and social and geographical reorganisation (Rose/Preston-Jones 1995).

3 Messy data, messy conclusions

As we have seen, at present, there is no clear archaeology of kinship, but we are, I believe, also seeing a number of emerging ways of thinking about kin and kin-making in archaeology. This is, of course, where funerary data and genetic research become so valuable, but also so perilous. Funerary sites have attracted archaeological attention since before the formal discipline emerged, and many of our earliest methodological insights derive from the excavation of burial contexts (Schnapp 1996). There are myriad sources of information about past people and their social structure in funerary contexts. The body itself (if present and able to be analysed) offers insight about diet, health, habitual practices, and biological descent (Sofaer 2006). The grave morphology and any structural components tell us about technological and social process, including funerary rites; and grave goods, those artefacts accompanying the deceased, have been interpreted in myriad ways as markers of identity, status, or social role (Cooper et al. 2022). Further, the presence of other human remains or burial sites offers insights into patterns of occupation, funerary practice, and perhaps also kinship (Garwood 2012).

Yet funerary sites are imperfect mirrors of living society. Burials are, following M. Parker Pearson's (1999, 3) well known aphorism, for the living not the dead. We can understand funerary rites as emotionally charged events that center around the transition of a person from the living community to a state of death, but these are also often performances with actors, props, staging, and powerful political and social undercurrents (Price 2010; Hull 2014). Thus, we must take care in assuming a given grave assemblage represents any essential thing about the deceased themselves in life, rather than being elements of their accoutrement in the complex rituals designed to mark their death, transition them out of lived relationships, and rearticulate social and political ties in their absence. Moreover, the grave assemblage as revealed by archaeology is itself the product of complex and ongoing taphonomic processes – biological, geological and social – that shape aspects of preservation and association and affect our ability to interpret and understand both the human remains and the funerary practices that led to their deposition (Duday 2009; Knüsel/Schotsmans 2021).

Archaeological data are irreparably fragmented to a scale that is truly unknowable. When reconstructing social practices, including patterns of relation, from the archaeological record, we must be attentive to its incompleteness. To that end, I have developed a model of funerary uncertainty (Frieman in press). This model draws inspiration from the well-known palaeopathological model of the osteological

Aspects of uncertainty	Contingencies
Survival non-uniformity	Various taphonomic processes differentially affect the survival of human remains, leaving us with a patchy and uneven dataset that may be biased in preservation or entirely randomly preserved.
Selective deposition	Only a segment of any population – and sometimes quite a small one – was interred in archaeologically visible ways; so, by using funerary data as a key source for modelling past identities and social practices, we are drawing normative conclusions from social outliers.
Social heterogeneity in rites	The funerary record is all that remains of a variety of tangible and intangible social practices that form part of funerary rites. These may or may not engage with aspects of the decedent's identity. Funerary sites are carefully assembled in these rites, highly variable, and temporally flattened, since considerable time may elapse between a person's bodily and social deaths.

Tab. 1 The archaeothanatological paradox.

Tab. 1 *Das archäothanatologische Paradoxon.*

paradox that gives structure to the complexities of inferring patterns of health and well-being among living people from incomplete assemblages of those already dead (Wood et al. 1992). I suggest that, in order to begin making sense of the past living world via the funerary record, the »archaeothanatological paradox« requires us to take into account the complex ways the archaeological record diverges (often in unpredictable and even unknowable ways) from the world of the living (Tab. 1).

Fragmentation is not itself inimical to interpretation, but it requires us to allow for greater uncertainty in our models and to admit to the holes in our data. As we all too often lack interlocutors to explain complex cultural formations and patterns of relation only partially visible through archaeology, we build our inferences through the analysis of incomplete, overlapping and all too often contradictory bodies of data and material (Chapman/Wylie 2016). That our field is underdetermined is often cast as a weakness (Turner 2007). However, following archaeologist J. Gero (2007), the ambiguity of our data and the lack of certitude in the models we draw from it are far better reflections of the complex and messy pattern of human relations, cultural contingency, and contested meanings than any one singular narrative could offer (cf. Currie 2018; Currie 2021). Indeed, even computational biologists can see that sometimes multiple differing scenarios are equally good fits for the available data (Maier et al. 2023).

To conclude, and with all these levels of uncertainty in mind, I propose a tangible, if imperfect, model of kinship that incorporates elements visible archaeologically: ethnic-

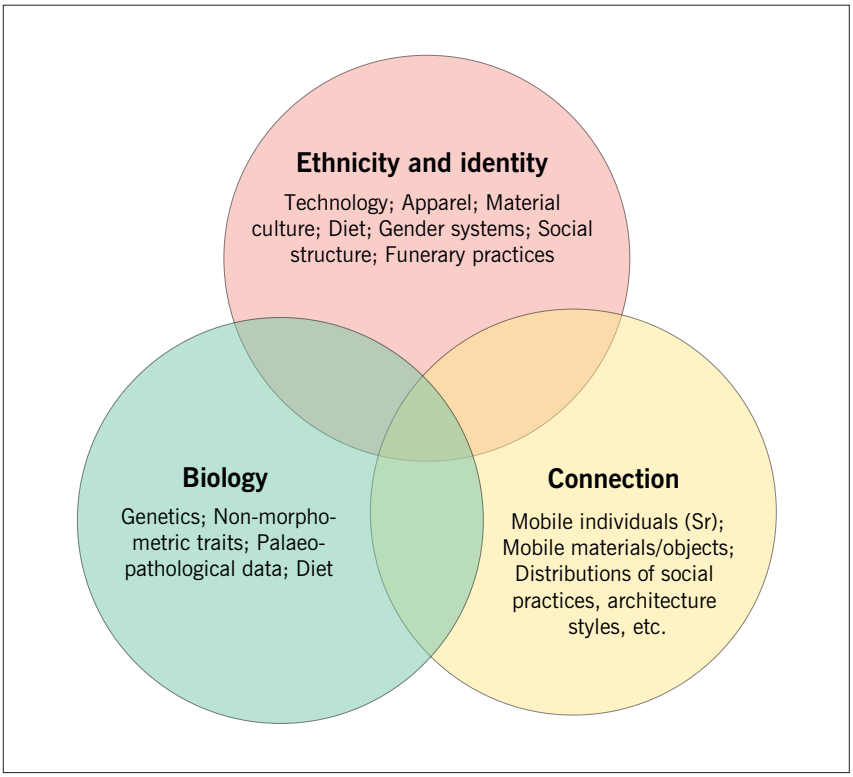


Fig. 2 A preliminary model of kinship visible archaeologically.

Abb. 2 *Ein vorläufiges Modell der archäologisch sichtbaren Verwandtschaft.*

ity/identity (technology, apparel, material culture, diet, funerary practices, etc.); connection (mobile individuals, raw materials, and things; distributions of materials, styles, etc.); and biological relatedness (genetics, non-morphometric traits, palaeopathology, etc.; Fig. 2). Ancient DNA gives us insight into one hoop of this diagram, social archaeology into another, and other archaeo-scientific and biomolecular methods into the third. In this way, the social narratives of kinwork and kin-craft, of queer kin and other-than-humans enrich the biological data, just as these biomolecular methods push us archaeologists to return to well-known sites and data to ask new questions.

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Source of Figures

1 author; a redrawn after Lawson-Jones/Kirkham 2010, Fig. 3–4; b simplified and redrawn after Jones/Kirkham 2021, Fig 6.11; c simplified and redrawn after Nowakowski/Johns 2015, Fig. 7.2; d simplified and redrawn after Quinnell 2004, Fig. 5
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What can archaeogenetics contribute to historical research on kinship and relatedness? A medievalist's view

Walter Pohl

Zusammenfassung

Welchen Beitrag kann die Archäogenetik zur historischen Verwandtschaftsforschung leisten? Die Sicht eines Mediävisten

Das Gebiet der Archäogenetik hat spektakuläre Fortschritte bei der Rekonstruktion der biologischen Verwandtschaft zwischen den Mitgliedern einer Bestattungsgemeinschaft vollzogen, die nun in umfangreichen Stammbäumen visualisiert werden kann. Die historische Interpretation dieser genetischen Ergebnisse ist jedoch alles andere als eindeutig. So wie die genetische ›Abstammung‹ (ancestry) nicht einfach die ethnische Identität widerspiegelt, sollten wir nicht davon augehen, dass solche Stammbäume einen direkten Zugang zur sozialen »Verwandtschaft« ermöglichen. Dieser Beitrag fasst kurz die anthropologischen Debatten über Verwandtschaft (ist Kinship überhaupt ein sinnvoller Begriff?) sowie neuere Forschungen über Verwandtschaft in der mittelalterlichen Geschichte zusammen und was sie für die Interpretation genetischer Daten bedeuten. Wir können mit diesem Material jedenfalls nicht ohne eine klare Unterscheidung zwischen biologischer und sozialer Verwandtschaft arbeiten und müssen alle verfügbaren Spuren verfolgen, um zu beurteilen, inwieweit sie sich möglicherweise überschnitten haben. Dies ist eine der Aufgaben des ERC Synergy Grant-Projekts HistoGenes, das sich mit der Bevölkerungsgeschichte Ostmitteleuropas vom 5. bis 9. Jh. befasst. Von einem solchen interdisziplinären Unterfangen können wir in vielen Bereichen neue Hinweise erwarten: auf reproduktive Gemeinschaften und Strategien; den Status und die Positionen von Frauen; die Bedingungen für die Vermischung (admixture); Änderung oder Bewahrung der ›ancestry‹; die sozialen Rollen und Statusunterschiede; die soziale Organisation von Bestattungsgemeinschaften; die Auswirkungen von Krankheiten; die Chronologie, den Anfang und das Ende der Gräberfelder; die Demografie der Fundplätze; die Beziehungen zwischen gleichzeitigen oder aufeinanderfolgenden Fundstellen; die Auswirkungen von Migrationen und Mobilität; sowie weitere Aspekte.

Summary

The field of archaeogenetics has made spectacular progress in the reconstruction of biological relatedness among the members of a burial community, which can now be visualised in extensive pedigrees. However, the historical interpretation of these genetic results is far from straightforward. Just as genetic ›ancestry‹ does not simply reflect ethnic identity, we should not take it for granted that such pedigrees give direct access to social ›kinship‹. This chapter briefly summarises anthropological debates about kinship (is that a meaningful term at all?) and recent research about relatedness in medieval history, and what they mean for the interpretation of genetic data. I argue that we cannot deal with that material without a clear distinction between biological and social relatedness, and have to follow all traces available to assess to what extent they may have overlapped. This is one of the tasks of the ERC Synergy Grant project HistoGenes, which addresses the population history of Eastern Central Europe from the 5th to the 9th century. In such an interdisciplinary venture, we can hope to find new clues about reproductive unions and strategies; the status and positions of women; conditions for admixture; changes or maintenance of ancestries; social roles and status differences; the social organisation of burial communities; the impact of diseases; the chronology, the beginning and the end of cemeteries; the demography of the sites; relations between contemporaneous or successive sites; the impact of migrations and mobility; as well as other aspects.

Debates about relatedness

The historical interpretation of genetic data is far from straightforward, as is the study of kinship[1]. It had long seemed self-evident that ›kinship‹ was based on biological relatedness, and that clearly-delineated kin groups were the primary form in which societies were organised, at least until the more complex, functional groupings of modern soci-

1 I use the term kinship here both for past perceptions and for modern scholarly concepts of relatedness, and for a critique of ideological overtones in both discourses. I hope it becomes clear that we need to avoid using the term for genetic reconstruction of biological relatedness. For the problems of historical interpretation of genetic evidence, see Geary/Veeramah 2016; Bösl 2017; Geary 2020; Meier/Patzold 2021; Samida 2021; Pohl forthcoming.

ety limited their influence. Indeed, we find an elaborate terminology of kinship in many texts and languages of the past, and we can assume that it mattered. If we now have the means to trace biological relatedness in the genome, scholars, and even more so the general public, might be tempted to see this as a confirmation of ideas of ›natural‹ kinship in our written sources. The same has already occurred with genetic ancestry, which has been taken to represent the biological basis for ethnic groups or nations (Geary 2020; Pohl forthcoming). However, we should not take the biological definitions of ethnicity and kinship in ancient and medieval texts for granted. Historical research on early medieval ethnicity has shown that, in many cases, it was more the idea of common blood and origin than actual shared ancestry that united an ethnic group (Geary 2002; Pohl 2013).

What the sociologist Rogers Brubaker has called ›groupism‹ (Brubaker 2004) – the habit of taking coherent ethnic groups for granted as social units – is also common in the study of kinship. But can we take coherent kin groups for granted in the Early Middle Ages? What the texts talk about when they use the language of kinship are not necessarily biological kindreds. The rhetoric of relatedness is often used to strengthen social bonds between biologically unrelated (or only loosely related) people by emphasizing their ›natural‹ character, whereas not all biological relations may be socially recognised or even become apparent. Noble kindreds are well-attested in the texts, but it is far from clear who belonged to them and who did not – just as in the ethnic groups of the period.

This leads to several problems in the historical interpretation of kinship. First, biological relatedness and social kinship surely overlap in certain cases, but they do not coincide. Therefore, we cannot automatically conclude from first- or second-degree relationships derived from the genomes that the individuals concerned were part of a family, and non-related individuals were not. Many social anthropologists have long realised this fact. According to M. Sahlins in his influential book ›What kinship is ... and is not‹ (Sahlins 2013), at the root of kin relations between humans is not the objective fact of birth, because »sexual intercourse is not prior to the social relations between persons, marriage etc. [...] What is reproduced in the birth is a system of kinship relations and categories in which the child is given a specific position and a positional value« (Sahlins 2013, 63; 65). Therefore, biological relatedness does not determine social relations, but is at least as much formed by social agency and cultural codes. As the anthropological examples that Sahlins adduces clearly show, »the different cultural discourses of procreation are highly variable as concerns the substantive relations of parents and their offspring« (Sahlins 2013, 86). We should therefore distinguish between, on the one hand, the biological links between individuals that genetic sequencing can demonstrate with great probability (although the precision diminishes beyond the third degree, and with weak signals in ancient DNA); and on the other hand, the social significance of kinship relations.

However, this distinction has been challenged because it is derived from the binary opposition between *physis* and *nomos*, nature and law/convention, fundamental in Western ontology since classical Greek philosophy. Kinship is understood quite differently in many other societies. Sahlins hinted at the problem with the Western binary model that kinship belonged to the realm of nature, whereas other social relations were constructed (Sahlins 2013, 14). His solution clearly was to focus on the variability of kinship patterns and discourses, and avoid overall models that would essentialise kinship systems.

We have to acknowledge that ideas and concepts of kinship differed considerably between societies in the past as in the present (Parkin/Stone 2014). What we should avoid, first of all, is grouping all ›traditional‹ societies (until recently the realm of ethnology) and juxtaposing them to ›modernity‹, as J. Goody has forcefully argued (Goody 1983, 3). We therefore have to historicise the terms and concepts we use, whether it is ›kinship‹, ›family‹, ›kindred‹, ›clan‹ or others – they did not mean the same in different societies. We cannot take it for granted that these concepts provided an almost immutable foundation to the development of past societies, but have to be attentive to the different ways in which they were conceived and constructed.

The basic facts of biological relatedness may be immutable, but they are surrounded by a wide area of kinship practices: fertility rates; incest taboos; marriage bans; polygyny/polyandry; regulations for abortion; uneven conditions for the survival of mothers and children; the social roles of mothers/fathers and of female/male children; relations between mother/father and child; patrilinearity/matrilinearity; the extent of adoption and ritual brotherhood; chastity requirements; inheritance rules; and the entire structuring of family relations. All of these factors result from cultural codes and social practices, and reflect back on the practices of reproduction. Therefore, they also also had an impact on the structure of biological pedigrees, which we can now reconstruct on the basis of genomic data (cf. Popli et al. in this volume). In most societies, human reproduction was one of the most highly-codified areas of life, being essential for the survival of the community, for conflict management and for individual satisfaction. In many cultural contexts, kinship could also be closely linked to transcendental spheres of inter-personality, as Sahlins has argued: He defines kinship as »mutuality of being« – »kinsfolk are persons who participate intrinsically in each other's existence« (Sahlins 2013, 9).

This wide range of issues, along with the concept of kinship, has become a fruitful area of historical research[2]. Whereas older historical scholarship has mainly followed prosopographic and genealogical approaches and has taken the existence of consistent families and clans for granted, recent research has tracked the changes and variations in concepts and practices based on relatedness. It has also shown that not only the shape, but also the importance of kinship ties differed, not only between various societies,

2 For an excellent overview for the Early Middle Ages: Hummer 2018. For medieval and early modern studies, see also Goody 1983; Murray 1983; Charles-Edwards 1993; Spieß 1996; Bouchard 2001; Mitterauer 2003; Sabean et al. 2007; Lubich 2008; Ubl 2008; Jussen 2009; Patzold/Ubl 2014.

but also within them. Kinship was also always a source of contention and conflict in which stake-holders not only pursued contrasting interests, but also could rely on differing concepts (cf. Thelen in this volume). For instance, the rather extensive incest ban up to the sixth or seventh degree that the Church prescribed in the Middle Ages met with a lot of resistance from the rulers or aristocrats concerned, but was quite regularly enforced (Ubl 2008). On the other hand, papal attempts in the 8th and 9th centuries to stigmatise or forbid marriages with women from other peoples *(alienigenae)*, based on Old-Testament precedent, had little impact in the longer term (Pohl 2007).

Is kinship an appropriate term for the wide range of meanings that the concepts and practices of relatedness can assume? Several scholars have recently argued that in fact kinship did not exist, or that the term should at least be avoided. In 1984, the social anthropologist D. M. Schneider argued that many societies around the globe did not have a concept of ›kinship‹, and that it was a modern Western creation (Schneider 1984). The ›lineage model‹ of a society constituted by male lineages proposed by H. L. Morgan in the 19th century, which had long been influential in ethnology, has largely been abandoned in the later 20th century; as A. Kuper stated: »There do not appear to be any societies in which vital political or economic activities are organised by a repetitive series of descent groups« (Kuper 2004, 93). In a more subjective sense, H. Hummer showed that the concept of kinship did not exist in the Middle Ages because »it was never an abstraction by which people of the time conceptualised their social life. There was no term ›kinship‹ that bound together the cluster of sociological phenomena that we now associate with the concept: marriage, alliance, incest, descent, terminology, procreative myths, parenthood, and so forth« (Hummer 2018, 4). The same could of course be said for terms such as society, state, economy, ethnicity, identity, culture, development and many more, without which it would be hard to interpret the past. What is important is to criticise and deconstruct these terms, and not take them for granted, ›smuggling‹ unwarranted assumptions from the present into the past. Yet, as M. Godelier has reminded us, we should then reconstruct our concepts, adapting their meaning to the evidence from the time and place under scrutiny (Godelier 2011). If we understand kinship not as a clearly-circumscribed group structure, but as a social process in which »kinship is constructed through human action or agency« (Stone 2004, 252), the concept (like that of ethnicity) may still serve to understand ways in which relatedness mattered in past societies. This requires maintaining a critical view of our own disciplines and the ways in which they have shaped their terms and models according to Eurocentric concerns (Hummer 2018, 7). Wherever available, the voices from the past can guide us in translating their concerns into modern concepts.

In the last ten to twenty years, scholars in the Humanities have made considerable efforts to liberate the study of kinship from its overwhelming biological paradigm. That also meant overcoming the way in which research on its forms fell too readily into the dichotomy of biological, that is, ›real‹, vs. spiritual/metaphorical or ›artificial‹ kinship (Hummer 2018, 84–94). As Hummer has aptly observed, in many cases a perceptive disclaimer in the introduction was followed by a rather traditional binary approach employed in the analysis. More radical models are now gaining ground (Hummer 2018, 102–111), in line with efforts to overcome white/Western epistemologies and to turn to indigenous truths. In a highly influential article, the Brazilian anthropologist E. Viveiros de Castro has turned to the way in which the Amazonian populations he studied would conceive kinship (Viveiros de Castro 2008). In their society, Viveiros de Castro argued, ›affinity‹, that is, human bonds in general, was taken to be a natural fact because it concerned all close relationships, whereas ›consanguinity‹, biological relatedness, was ›constructed‹, an outcome of certain social practices. M. Strathern (1988) has concluded from her research in Melanesia that a vital link within the community was constituted by feeding, eating, sharing, caring, or remembering, which in many societies is perceived as a participation in other bodies, whether of the living or of the dead. Kinship is thus not perceived in the Western sense as relatedness between individuals, but as based on ›dividuality‹ and ›transpersonal praxis‹ (Sahlins 2013, 19–53; cf. Alber in this volume).

These are fascinating and challenging perspectives, but they also create some problems. In the studies where these concepts were proposed on the basis of highly perceptive observation and cultural translation, they have opened new horizons. Yet as a new general paradigm intended to replace the old dichotomies, they risk liberating research on relatedness from one simplifying binary by embracing another: the contrast between Western modernity and its divisive individuality and rationality on one side, and more natural and inclusive and ›dividual‹ indigenous epistemologies – the world we have lost, or rather, destroyed. This debate is beyond the scope of this paper, and is reflected in more depth in other contributions to this volume (see the contributions of Alber, Thelen, and also Alt in this volume). It is, however, relevant for assessing the epistemological significance of the genomic evidence for our understanding of relatedness. In archaeogenetics, we invariably deal with the genome of a single human being in its biological relations to other human beings. And in archaeology, we recover the remains of distinct human bodies, which in the period were usually buried in separate graves. Native epistemologies may well have given these bodies and burials different meanings, but in most cases we can only speculate about them.

What did being related mean in early medieval Europe?

Medieval kinship is often connected with images of royal dynasties and noble families who form the basis of the state, but also tend to subvert it in the interest of their kin group. They boast of long patrilinear pedigrees and a consolidated and well-circumscribed family structure. However, scholars have long recognised that kinship in the early medieval West was hardly agnatic and patrilineal. K. Schmid (1957) and G. Duby (1981) argued that until c. 1000 AD cognatic kinship prevailed, when the ›feudal transformation‹ led to a more agnatic system and a flowering of patrilineal aristocratic lineages. That was an important step forward; but eventually, it

turned out that things are more complicated. C. Bouchard (2007) has noted a spread of patrilineage in the Carolingian period, while cognatic kin also remained important after the 11th century (Goetz 2014). The idea that distinct aristocratic kin groups were a basic feature in the Later Middle Ages has also been challenged in recent research (Bouchard 2001; Sabean/Teuscher 2007; Jussen 2009). S. Teuscher (2011) argued that the interest in bolstering one's position by a noble lineage evolved in parallel with the early modern state, only reaching its first peak in the 15th century.

Kinship certainly is rather elusive in the early medieval West (e.g. Murray 1983). As Hummer (2018, 1) has observed, »as soon as one begins to trace out a kin group, the trail just as quickly fades«. To give an example: One of the few consistently-attested early dynasties in the Early Middle Ages were the Agilolfings, the family of the 8th-century Bavarian dukes, whose prerogative to rule Bavaria was even affirmed in the Bavarian law code (Pohl 2016). Yet generations of scholars have debated who they were and where they came from, and became entangled in following seemingly contradictory traces to Suebi, Warni, Burgundians, Longobards and Franks (e.g. Jarnut 1986; Deutinger 2014). Earlier Bavarian dukes are not called Agilolfings in the texts, but we know that one of their daughters, Theodelinda, was married to the appropriately-named Longobard king Agilulf. For the last Bavarian duke Tassilo III, dethroned by Charlemagne in 788, his Carolingian mother may have been politically more relevant than his Agilolfing lineage (which is never emphasised). Therefore, if we address early medieval kinship, we should not depart from circumscribed kin groups, kindreds, families, or dynasties, but from the forms of relatedness and their relevance. This can hardly be expressed in neat patrilineages, whose nodes and connecting lines may have had rather varied significance.

Important changes in the concepts and practices of relatedness seem to have happened during Christianisation and the transformation of the Roman World, which the anthropologist J. Goody (1983) has put in focus. The prerogatives of the *pater familias* faded out to some degree, and the pagan ancestor cult was abandoned. The task of guarding the memory of the dead gradually passed to ecclesiastical institutions, who received pious donations to pray for the deceased and keep their memory alive. Burial was moved to Church grounds, and funerary ritual was gradually Christianised, which led to the (if gradual) disappearance of grave good habits and of cremation practices (Paxton 1996). Christian norms were also introduced to curb many Roman ways of constituting a family or ›*gens*‹, a clan. Taking concubines was condemned, which at least in theory reduced the options for reproduction to the legal marriage (we know that the Merovingians did not take this rule particularly seriously). Clerics, monks and nuns had to follow strict chastity, which was also recommended to lay-people except for the purpose of procreation. Divorce, for instance in cases when the wife could not give birth to children, was prohibited. It took some time until marriage became a sacrament, and the Church thus achieved full control over it. Overall, this reduction of options for reproduction must have contributed to the demographic decline that we see during this period.

Adoption, a rather current Roman practice, was also reduced and partly replaced by godparenthood (Jussen 1991). Marriage between close kin was progressively prohibited, not only between first cousins (an option in many societies), but up to the 6th and 7th degree (Ubl 2008). Widows were advised not to remarry, and certainly not within their kindred. Arguably, much of this weakened the cohesion within kin groups, and opened them up to more distant relations. Goody argued that these measures first of all were intended to strengthen ties within the Christian community at the expense of the kin groups, and to redirect much property, for which there was no close heir, to the Church (Goody 1983, 194–216). Critics have doubted whether we can assume an ecclesiastic ›grand strategy‹ to that end. There may be valid arguments against some of Goody's assertions. Yet P. Brown (2012) has clearly demonstrated that in the 5th/6th century, clerical authors developed a consistent theological argument to encourage property donations to the Church; and I. Wood (2018) has reconstructed a massive process of land transfer to ecclesiastical institutions in 6th to 8th-century Gaul, which may have amounted to about one third of the total landed property. Early medieval churchmen were perfectly capable of judging the social impact of the measures they advocated or introduced. We should not regard their actions as simply guided by material interests, though; more likely, most of them acted in a genuine belief in furthering the only salvific creed.

In what ways, then, did relatedness become significant in early medieval Europe? Here, I can just briefly sketch a few contexts where we can trace some of its meanings. The first are royal/ducal dynasties and noble lineages. In older scholarship, they were mostly regarded as well-structured Germanic male lineages, but there is little evidence that they were (Pohl 2016). There are sufficient attestations showing that a noble ancestry (*stirps*, *progenies*, *genealogia* or similar) mattered. Strikingly, though, there was little interest in how it was actually shaped. We have a 16-generation genealogy of the Ostrogothic Amals from 6th-century Italy, but it was most likely compiled by the Roman official Cassiodorus, who used it to convince the senate that their Gothic kings had a lineage as noble as the senatorial *gentes*, families. But in general, king lists were more relevant. The Merovingians did not publicise their pedigree, and even their dynastic name is first mentioned a century and a half after King Clovis united the kingdom in c. 500 AD (Wood 2003). To establish Charlemagne's pedigree, one of his courtiers asked the Longobard scholar Paul the Deacon, who inserted it in his Chronicle of the Bishops of Metz. In his version, the first ancestor was the saintly bishop Arnulf of Metz, whose son had married the daughter of the mayor of the palace, Pippin I. Thus, the Carolingian genealogy that became standard in the course of the 9th century merged a male descent from a saint and a female one from the man who had first acquired the function of mayor of the palace for the family.

This remarkable lack of interest in a precise patrilineage on the European continent in the sixth to eighth centuries is in contrast to many other contemporary societies. Genealogies are well-attested in Britain and Ireland in the period, where they were styled after Old-Testament pedigrees (Hummer 2018, 273–279), and they seem to have played a role in

Scandinavia. Aristocratic inscriptions from Tang-period China (7th/8th centuries) praise the dynasty and its ancestors in ways unknown from early medieval Europe (Tackett 2014). Even more striking is the contrast to the early Islamic period, which produced massive genealogical handbooks, for instance by al-Zubayrī (9th century) or al-Hamdānī (10th century). The individual genealogies were either traced back to the family of the prophet and established the superiority of the Qurayshīs, or to the mythical founder of the tribe; the tribal genealogies were then extended backwards to the ancestors of the North- and South-Arabians, so that theoretically every Arab could be placed in a genealogical connection to every other Arab (Szombathy 2003; Mahoney 2016). The Islamic example with its all-inclusive patrilineages is very useful for assessing what early medieval continental Europe did not produce. Although patrilineages mattered, continental European ruling and aristocratic houses had quite some leeway in manoeuvring around them. Merovingian kings were quite flexible in deciding which of their sons, usually from several partners, was legitimate; to delegitimise one of them, it was sufficient to publicly cut their long hair (Wood 2003). In Longobard Italy, several newcomers to the throne derived their legitimacy from marrying women descended from more prestigious dynasties. And in many post-Roman kingdoms, strong queens succeeded in maintaining their grip on power, often as legal guardians of their sons – for instance, Amalasuintha in Ostrogothic Italy, Brunhild (who was a Visigoth) in the Frankish kingdom and Theodelinda (whose father was a Frank from Bavaria) in Longobard Italy. Lateral kin surely also mattered in more modest families. There were only some obstacles to a wide range of lateral connections. For instance, many Roman and barbarian law codes forbade marriages between Romans and ›barbarians‹, which was not always effective (at least in royal houses) but must have had an impact (Pohl forthcoming a).

We know much less from written sources about early medieval Eastern and Northern Europe, where Christianity had never arrived or was eventually marginalised after the end of Roman rule. There are some bits of information about women and marriages in the Eastern European steppe realms. Both Attila, king of the Huns, and the early khagans of the Avars had numerous sons by several wives to whom they were simultaneously betrothed in some way (Pohl 2018, 368 f.). Once it was documented that the Avar khagan took along several of his wives on a long military expedition, where they enjoyed themselves in the hot baths of a captured city. An Avar high priest who had intercourse with one of the khagan's wives had to flee to the Byzantines to escape a death penalty. In the late Avar realm, the position of the *katun*, the (principal) wife of the khagan, must have become quite prominent. A Latin poem depicts the scene when the Avars had to submit to a Frankish army in 796, when both the khagan and the katun appeared and were told that ›their reigns‹ *(regna)* had ended. This strong role of the khagan's consort corresponds to 8th-century Old Turkic inscriptions and to Chinese sources about eastern central Asia where khagan and katun also acted in unison and had a shared rule (Pohl 2022). Written sources say little about the relations of more modest people; for that, we have to rely on archaeological, and now also on genetic evidence.

There is, of course, the chance to form hypotheses about the role of kinship among Huns or Avars from ancient and modern evidence about steppe societies[3]. Most authors assume a strong patrilinear clan structure and mobile units that roughly correspond to ›family‹ groups. These groups would then constitute overarching tribes, which in turn could form nomadic states or ›commonwealths‹ in which tribes were arranged in a hierarchical order (Kradin 2005). However, D. Sneath (2007), working on the basis of Mongol material, has challenged this model, and has argued for horizontal aristocratic power networks instead. That does not mean that we should abandon clans and tribes as possible structural elements in the organisation of European steppe empires of the Early Middle Ages; but we cannot take them for granted either.

What can the genetic study of relatedness contribute to historical knowledge about kinship?

This is not the place to describe the swift development of new bio-informatic methods to trace relatedness, which has taken place over the last few years (cf. Krause 2019; Geary 2020; Fowler et al. 2022). It is important to distinguish, however, between this relatively new approach and the older line of research on what geneticists generally call ›ancestry‹ (Mathieson/Scally 2020). This was the approach chosen in the early days of archaeogenetics, when only the non-combining parts of the genome were sequenced. Y-chromosomes could trace the male line, while mitochondrial (mt-)DNA indicated the female line. Both parts of the genome mutate only very rarely, so it was possible to extrapolate past genetic similarities from modern DNA and conceptualise differences as ›haplotypes‹. In the general public's view, this gave rise to the illusion that every modern individual carries in their genome the basically undiluted heritage of past populations. Today's individuals could still be Romans, Goths or Vikings, at least to some extent – these ancient peoples could be ›our‹ ancestors.

However, this image of ancestry was rather limited, for the direct male and female lines account for only a small percentage of the total ancestors, and the non-combining parts form a miniscule part of the genome. The two great breakthroughs since the 2000s were the opportunity to sequence whole genomes, and to analyse ancient DNA taken from skeletons. What this powerful new evidence revealed was not so much descendance but admixture. Already in the Iron Age, the population of Europe, which was the result of an admixture between several (mainly three) distinct groups of the population, had become genetically rather homogene-

3 Krader 1955; Taşbaş 2019; Pohl 2018, 198–209; see also the overview by Z. Rácz in the supplementary material, in Gnecchi-Ruscone et al. 2023.

ous, save for a few minor exceptions (Patterson et al. 2012; Krause 2019). With new methos of fine-grained analysis, however, genomic studies could move from prehistory to historical periods (Schiffels et al. 2016). Geneticists could continue to identify the components that had shaped the genomes of particular individuals of the past. They still speak of types of ›ancestry‹, for which they use proxies of other, already analysed population groups to which particular individuals or populations could be related.

For historians, the genetic use of ›ancestry‹ may be confusing (Eisenmann et al. 2018), because it does not refer to actual ancestors, just to populations with genetic similarities, which could point to common origins, later scenarios of admixture, geographical proximity, or admixture with genetically similar groups. This should not be confused with actual relatedness (Nash 2007). The risk is that claims for distinctive genetic ›ancestry‹ can be used for ideological constructs of national continuity and biological determinism (Burmeister 2021). Within a biologically-related descent group (a lin-eage of related individuals), the genetic ›ancestry‹ can differ considerably, and can also completely change within a few generations. One reproductive union of partners with different ancestry reduces the statistical average of each of these two ancestries in the children to 50 %, and if admixture continues, in the following generations to 25, 12.5 and 6.25 %. For instance, if Avar men of Eastern Asian ancestry and their descendants (as described by Gnecchi-Ruscone et al. 2022) would have continued to marry European women, their Eastern Asian ancestry could have almost completely disappeared within four generations.

Methods to ascertain actual biological relatedness on the basis of genetic data were developed more recently. A high degree of genetic similarity between two individuals can safely be ascribed to first- and second-degree relatedness, and further degrees can be made plausible with a decreasing degree of precision. Parent-child and sibling relationships can also be distinguished from each other. On the basis of these methods, and if a sufficient number of related individuals has been found, pedigrees that show the exact position of each of these closely-related individuals can be reconstructed. This method carries great potential for the analysis of the communities whose members were inhumated in cemeteries that have been completely excavated. A further approach complements the analysis of ancestry and of genetic relatedness: IBD (Identity-By-Descent) scans groups of individual genomes for identical sections, which do not prove direct descent but some kind of closer or more distant relationship, depending on the length of the shared section, possibly also through a common relative. Such relations can also be detected between analysed sites, and be visualised as regional or supra-regional networks.

The ERC Synergy Grant project HistoGenes, a collaborative project including archaeologists, geneticists, historians and anthropologists in Vienna, Leipzig, Budapest, New York and other institutions (including the State Office for Heritage Management and Archaeology Saxony-Anhalt – State Museum of Prehistory in Halle [Saale]), is currently using all these methods on an unprecedented scale of over 6000 genomes from Eastern Central Europe in the 5th to 9th centuries (Pohl et al. 2021). This allows sampling entire cemeteries, which is the best way to make sense of pedigrees and relatedness in the communities buried there (Gnecchi-Ruscone et al. 2023). At the time of writing of this article, it is too early to mention specific results, which will be published in forthcoming articles (Gnecchi-Ruscone et al. 2023; Wang et al. forthcoming). This will include the largest burial site so far to be completely analysed at Mödling in Austria (Wang et al. forthcoming). However, some observations based on the new methods can already be outlined here (cf. Daim et al. in this volume).

In the HistoGenes project, we are exploring under what conditions the analysis of genetic relatedness can unfold its full potential[4]. First, the biological pedigree cannot be used as a proxy for social kinship (Brück 2021). Second, as already stated, only entire cemeteries allow valid statements about the whole range of relatedness, and quantitative analyses of a number of issues. Large cemeteries (preferably over 100 burials) are more interesting in this respect, because statistical results can be more robust. Higher coverage yields better results. Third, this is a multi-disciplinary venture, because the pedigree alone can only provide some insights. It not only needs geneticists but also, crucially, archaeologists with access to the full range of information on the excavation. Anthropologists have to control the skeletal material, and, very importantly, provide reliable assessments of the age-at-death. This, not least, supports the construction of the pedigree, helps to establish a better chronology, and allows distinctions between age cohorts to be made. Further scientific methods that contribute are Sr, C, N and possibly O isotope analysis, hinting at mobility, changes or differences in nutrition. ^{14}C-dating is not always easy for the period under scrutiny in the project due to the fluctuations in the calibration curve, but offers an independent way to test the dating. Further scientific methods can be used on the finds where appropriate.

It is a complex workflow to which historians can and should also contribute. They will only rarely find directly relevant information about a particular early medieval site in the written record, although there are exceptions, for instance the Austrian site of Mautern (Favianis), Krems-Land district, which is being sequenced in HistoGenes, and is described in some detail in the Vita Severini recounting the activities of St Severinus in the second half of the 5th century (Pohl/Diesenberger 2001). In many other cases, historians can provide some chronological framework and historical context that are important for the interpretation of the cemetery. Specific practices of relatedness can also be compared to written evidence. To give just two examples: In some places, for instance at the Longobard-period cemetery of Szólád, Somogy County (Hungary; mid-6th century), we are missing a number of mothers whose position we can reconstruct in the pedigree (Amorim et al. 2018). One possi-

4 For the critique of archaeogenetic research that does not take archaeological and historical results into consideration, see Feuchter/Samida 2016; Pohl forthcoming.

bility to explain their absence may be found in 7th-century Longobard law, which suggests that widows were expected to return to their former families if they had no other adult male who could take them under his legal guardianship, *mundium* (Rothari 199, in Azzara/Gasparri 1992; Pohl-Resl 1993). A second example are levirate unions, again of widows who marry another male member of their family after the death of their husband. This is an arrangement repeatedly attested in Chinese sources for the Xiongnu and other steppe peoples, and could explain the cases in which women in Avar-period cemeteries also had children with their husband's brother or their stepson (Gnecchi-Ruscone 2023; Wabnitz/Liccardo forthcoming). Historians can help to design the research questions to be addressed and find historically plausible ways to interpret the evidence. In fact, the entire team should work together from the conception of the project to its publications. This is what the HistoGenes project is exploring as a best-practice model.

The close collaboration of the disciplines then allows the project team to look for hints to what degree social kinship may have corresponded to the outline of the pedigree established on the basis of the genetic evidence. In many of the cemeteries from the late 6th to the 8th century studied so far in HistoGenes, the majority of members of the community were biologically related. It should also be noted that genetically, man and wife are not related, although both have first-degree relations to their children. Wives without children in the sample count as unrelated in the pedigree, while socially they would be regarded as part of the family in their lifetime. Where we have genetic evidence for relatedness, we can assume close social relations, for instance in the case of multiple inhumations in a grave, especially of adults with children. If these were indeed parent and child, we can hypothesise that biological and social relations coincided. To a degree, that can also be inferred from burial groups constituted of closely related individuals. Grave good evidence can also point to cultural commonalities among biologically-related individuals, for instance, analogous markers of status or the use of atypical jewellery, inhumation practices or other shared cultural features within biological kindred (cf. Daim et al. in this volume).

Multiple partnerships raise the question whether these were acknowledged unions or not. Were men who had children with two or more women polygamists, serial monogamists or adulterers? And what about women with multiple reproductive unions? If their partners were closely related to each other (as mentioned above), was that a case of levirate, that is, a practice current in many societies to keep widows within the clan? The anthropological data about age-at-death may give important clues here. What we do not know, however, is whether a reproductive union was a legal marriage, an acceptable but not legally binding relationship, or whether a child had originated from a secret encounter. We cannot trace partnership if no children are buried on the site, for instance, because no children were born or the daughters married into another community. What we can note in some cases is that social links in burial or cultural features existed between biologically unrelated persons, for instance, if a woman was buried with a child that was genetically unrelated to her. The better we connect the genetic data to other types of evidence, the more information there is to gain about gender roles and the circumstances of female lives.

A crucial observation from the study of genetic pedigrees in their cultural and social context is that biological relations do not simply shape social kinship, whether to a greater or lesser degree, but depend on social practices. In that sense, the new genomic evidence supports recent approaches in social anthropology. As Sahlins has argued, every birth is the result of reproductive practices that are to a large extent guided by social norms – marriage alliances or bans, arranged or forced marriages, incest taboos, male license, and the whole set of the ›elementary structures of kinship‹, as C. Lévi-Strauss (1969) has called them (Sahlins 2013). One could also add all the strategies employed to bypass those norms and bans, often in secrecy. The elaborate genetic pedigrees produced in the HistoGenes project also illuminate the incidence of social norms (Gnecchi-Ruscone et al. 2023; Wang et al. forthcoming). They may attest to strict patrilinearity or bilateral connections, to the age when mothers first give birth, or to avoidance of consanguineous unions and to the habit of looking for reproductive partners outside the community[5]. In one cemetery, female partners were chosen almost exclusively from among women of similar ancestry. This means that what we would regard as genetic ancestry was maintained by a preferential reproductive pattern social norm over several generations. In all these senses, biological relatedness may be the result of deliberate kinship practices.

The historical evidence for early medieval perceptions and practices of kinship can help to avoid a further mistake: We should not try to arrange the pedigrees that bioinformatic methods can reconstruct within a burial community until they fit a model of clear-cut lineages or clans. What we do see in the first results is that in many burial communities, most members were in some way related to each other, and can be integrated into complex pedigrees. In the Avar period, the genetic evidence also points towards exogamy and patrilinearity. However, larger pedigrees cannot always be disentangled into distinct lineages or clans. Rather, they are connected by multiple reproductive unions, by sisters marrying into two lineages, by exceptional cases of matrilinearity, by individuals with second- or third-degree relationship with more than one male lineage, by IBD-connections between sections of the pedigree and by other overlaps. This blurred picture corresponds to the archaeological evidence, which rarely displays clear boundaries between groups of graves even if these are mostly structured by relatedness. Rather than straightening out the uncertainty in the pedigrees to arrive at clear-cut kindreds, we should take the overlaps as indications that it may not always have been clear to which clan an individual belonged (cf. Pálsson 2002).

What we can learn from recent debates about relatedness and affinity in social anthropology is that beyond the ex-

5 This would correspond to bans on marriages within a patrilinear clan of up to six generations in Turkic and Chinese society: Taşbaş 2019, 251; Holmgren 1991, 77. I would like to thank Sandra Wabnitz for advice in this matter.

planations of the evidence that seem plausible to a scientifically-trained mind, a greater variety of interpretations may be possible. This is particularly important in the illiterate societies that dominated much of Eastern and Northern Europe in the ancient and early medieval periods, where our written evidence is patchy. In the case of early medieval steppe peoples, we can extend the options for understanding their cultural codes by relying on more or less contemporary inscriptions of the ancient Turks and Bulgars, and by taking modern anthropological observations into account (Kradin 2005). However, we will not be able to reach an in-depth understanding of lived human relations among the people whose burials we have studied, which is comparable to the insights proposed by social anthropologists on the basis of their observations and ›thick descriptions‹ (Geertz 1973) of living communities. We should not be tempted to fill gaps by borrowing from the anthropology of contemporary steppe populations and generalising our reconstructions of social relations as an adequate model for ›the‹ peoples of the steppe.

On the whole, the evidence and approaches from social anthropology can be inspiring, and in some cases allow the formation of hypotheses that can then be tested against the multi-disciplinary evidence we have assembled. On the other hand, the reconstruction of genetic relations may also serve as a reminder that the hermeneutics of transpersonal relations and the indigenous epistemologies, which explain them, are not the only possible approach to past relatedness. Even in periods with a rich written record, such as the Late Middle Ages, historians can say much less about the ›mutuality of being‹ than anthropologists can find out about recent or contemporary Amazonia or Melanesia. These sophisticated models are not easily transferable to early medieval Europe.

For our field of study, we need a clear and operable distinction between the biological relatedness established on the basis of genetic data, and the social/cultural relatedness we can infer from archaeological and historical evidence. The pedigrees may already be scientific constructions, but there is little room for doubt whether or not a child was born from his/her genetic parents. Only on the basis of this distinction can we then assess in which cases the two concepts of relatedness may have corresponded or not, and detect ways in which they were entangled. Written evidence can allow tracing the social meaning that certain scenarios encountered in a burial community may have had (Halsall 1995; Halsall 1998). It should be noted that this process of interpretation of the multiple genetic, archaeological, anthropological and isotopic evidence is not a confrontation between ›hard‹ scientific data and ›soft‹ cultural hermeneutics in which only the scientific results can serve as proof. Both the bioinformatic analysis of genetic or isotopic data and the methodologies used by the historical disciplines are methods that assess probabilities, whether with or without the use of statistical tools and algorithms. If archaeological or historical dating on the one hand and the chronology of the pedigree or ^{14}C data on the other hand contradict each other, this does not necessarily mean in every case that it is the archaeological or historical chronology that is wrong. These discussions require intensive interdisciplinary collaboration and some familiarity with the methods of the other disciplines.

Used in this way, the genetic results and the complementary methods offered by other disciplines can clarify many issues raised by the sites and the periods under scrutiny: reproductive unions and strategies; conditions for admixture; changes or maintenance of ancestries; the status and positions of women; social roles and status differences; the social organisation of burial communities; the impact of diseases; the chronology, the beginning and the end of cemeteries; the demography of the sites; relations between contemporaneous or successive sites; the impact of migrations and mobility; and others. The reconstruction of biological pedigrees provides important clues to many of these issues, but it needs to be contextualised with all the other approaches that can tell us more about the distant past, with an awareness of current methodological debates.

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Roots of misunderstanding

Aylwyn Scally

Zusammenfassung

Wurzeln des Missverständnisses

Ich erörtere den interdisziplinären Dialog zwischen Genetik und Geschichte, der sich auf das Gebiet der Paläogenomik konzentriert. Hierbei betrachte ich einige der Faktoren, die zur Fehlkommunikation zwischen diesen Bereichen beitragen, und wie Forscher auf die damit verbundenen Herausforderungen reagieren können, einschließlich der Unterschiede in der Veröffentlichungspraxis, der DNA-Genealogie-Industrie und dem allgemeinen Verständnis von Abstammung.

Summary

I discuss the interdisciplinary dialogue between genetics and history, centred on the field of paleogenomics. I consider some of the factors contributing to miscommunication between these fields and how researchers can respond to the challenges they pose, including differences in publication practices, the DNA genealogy industry, and the public understanding of ancestry.

Introduction[1]

Genomes carry information about the ancestry and demography of past individuals, and are thus a source of historical evidence. In principle, this evidence is now more accessible than ever before, thanks to the development of whole-genome sequencing. However, due to a combination of demographic and methodological factors, most analyses of present-day genetic data are informative about events on a timescale of thousands rather than hundreds of years, and so until recently there has been a relative absence of genetic information on historical timescales (as opposed to prehistoric or earlier periods). There are exceptions, such as methods focusing on very rare genetic variants, which are more likely to have arisen recently (Schiffels et al. 2016), but such studies by their nature require large numbers of samples. And in many cases, there have been considerable demographic and environmental changes, including large-scale migration within and from outside the region studied, particularly during and since the medieval period. Thus, while ancestral geographic correlations do remain in present-day genetic data (Novembre et al. 2008; Leslie et al. 2015), various factors make it harder to use such data to discern subtle past effects or relationships.

The ability to sequence ancient and historical DNA has altered this picture dramatically, producing a growing number of samples which record the genetic ancestry and relatedness of past individuals from different locations and walks of life. Importantly (and barring one or two exceptions, such as King et al. 2014), it is not the ancestries themselves that are of interest so much as their association with contextual factors. Combined with additional sources of archaeological and written evidence, the potential for multidisciplinary studies is enormous, particularly on regional and local scales rather than the continental scale of many initial ancient DNA studies (Hui et al. 2023). Indeed, such interdisciplinarity is essential, for as with any evidence, genetic data alone provide a partial view, affected by biases and gaps that depend on context and time. Relating them to questions of historical or archaeological interest requires conjecture and interpretation, which change as further evidence, genetic or otherwise, becomes available.

As was the case with other new technologies in the past, the power and potential of ancient DNA has seen it rapidly established as an important archaeological tool. And as archaeologists become proficient in its methods, so too historians of the early medieval period, who make frequent use of archaeological evidence, are engaging with genetic data. Equally, as geneticists develop methods focused on historical timescales and data, research collaborations spanning genetics, archaeology and history are growing in number.

However, such interactions face several obstacles. Prior to the advent of ancient DNA, some of the frustrations experienced by archaeologists were captured, only half jokingly, in the remark that when geneticists presented their findings, they reported things that either were already known or were obviously wrong. Few researchers are as familiar as they should be with the relevant literature of other fields, but sometimes even the self-awareness of this is lacking. There remains a tendency for geneticists, particularly when communicating research to the public, to reach for outdated historical narratives and cherry-picked examples. On the other

1 Acknowledgements: John Robb, Lara Cassidy and Pontus Skoglund for useful discussions and comments.

hand, frustrations can also get entrenched and become an obstacle in themselves. Were we to formulate some guidelines for interdisciplinary research, one of them might be that if something seems ›obviously wrong‹, the misunderstanding might well be yours!

A frequent misunderstanding arises from the differences in how models are perceived and constructed. In genetics, particularly population genetics, models are deliberately abstracted and simplified as a means to interpret data quantitatively. The truth, whatever it may be, is understood to be more complex than could be represented in a useful model. Moreover, sometimes a paper may use simple models not because the authors are oblivious to the complexities of the problem but because the size of initial datasets, or novel methods, do not yet support inference under more complex models. Simple models are useful, often because insight comes from comparing how they respond to data, rather than from inferring the specific values of their parameters. Genetic population models, for example, are typically parameterised by a single ›population size‹ parameter, which ostensibly represents the number of individuals in the population, but when inferred from real data is also influenced by, and thus potentially informative about, other factors such as kinship, population structure and natural selection. Similarly, the common ancestry of multiple populations may be modeled by a simple tree, as if their separation originated in a series of clean and instantaneous splits; but inference under such a model can be a way to reveal the underlying complexities of gradual separation and cross-population gene flow. Some archaeologists are familiar with such approaches, but to others they can come across as naïve or even deliberate reductionism, and it is not uncommon to find exasperated criticism of genetic analyses along these lines.

These and other issues, differences in technical language and jargon, or the ways in which research questions are posed and addressed, are typical of the challenges in any interdisciplinary exchange. But there are also particular factors that exacerbate the problems of dialogue between these fields. Here I will touch on two of them: differences in scholarly publication practices, and the impact of commercial DNA ancestry testing.

Publication practices

The first ancient human whole genome sequence, from a Neanderthal individual who lived more than 38 000 years ago, was published in 2010 (Green et al. 2010) and was a landmark scientific achievement. Since then, the rapidly increasing number of ancient sequences and their transformative potential for understanding human prehistory have continued to attract public and media interest. Studies of ancient DNA and other developments in the new field of paleogenomics have appeared frequently in journals such as *Nature* and *Science*. Such attention may be receding as the field matures, but high-profile publication remains a realistic goal for many practitioners, particularly when presenting data from previously unstudied regions or time periods, or applying it to a long-standing question for the first time.

This experience has shaped the expectations and publishing practices of the field, in ways which contribute to miscommunication with other researchers, particularly non-scientists. Many features of high-profile journal publication have long been recognised as problematic: compressed papers, which serve primarily as an abstract for a lengthy and technical supplement; limits on the numbers of references and figures; and above all, the pressure to present research and its conclusions as groundbreaking, which is further heightened when communicating results to the press and media. Sometimes the fanfare associated with publication gives the impression, particularly outside the field, that the authors intend this to be a definitive and even final statement on the subject, when in fact it is merely a first examination. And, unfortunately, it is often what is said in the media rather than in the paper itself (the tone of which may be far more circumspect) that colleagues react to. Concerns about public misunderstanding make this fraught, particularly in the context of misrepresentation by racists, ethno-nationalists and pseudoscientists.

It is important to note that many paleogenomic studies are co-authored by both geneticists and archaeologists, and increasingly also by historians. One might imagine this would mitigate many of the problems of cross-disciplinary communication. Unfortunately, in practice it can lead to further problems, particularly where data suggest a new hypothesis or seem to favour one over another. Sometimes such collaborations are lopsided, with archaeologists regarded merely as a source of samples, or geneticists as quantitative support for an existing position. Even where, within a collaboration, there is mutual understanding of cross-disciplinary methods and aims, communicating its findings to a diverse audience is a different challenge. Papers often end up combining genetic content, which may be technical and indecipherable by non-experts, with a fully-formed archaeological or historical synthesis. The intention may be to help readers understand the implications of genetic analyses in historical or archaeological terms; but the result is often to present an argument whose basis and assumptions are impenetrable to its intended audience, yet which nevertheless purports to favour, with the authority of science, one side of a contentious debate over another.

Differences in publishing timescales, and the fact that paleogenomics is a new and rapidly changing field, also foster miscommunication. For historians, it is not uncommon to engage with arguments published decades previously if they remain current and still shape viewpoints or teaching on a topic. By contrast, the genetic approaches of two decades ago are very often obsolete. Genomic data from mitochondrial DNA and chromosome Y, for example, are still informative and useful in some contexts, but the simplistic interpretations they once supported are often not. It can come as a surprise to geneticists when a contemporary critique of approaches in genetics cites and debates such publications. But while they may be ignored by geneticists now, outside the field they appear as part of its relatively recent literature. Furthermore, some older publications are cited frequently by pseudo-scientists and pseudo-historians, thereby sustaining their influence on popular understanding and forcing historians to deal with this legacy of earlier contributions. The long half-life this gives to misleading ideas is not sufficiently appreciated within genetics.

The DNA ancestry industry

Ancestry occupies a complex and often ambiguous place in society and culture, but also a very prominent one. Popular enthusiasm for genetic genealogy has fuelled the enormous growth of the consumer DNA-testing industry over the last decade, with tens of millions of customers worldwide (Regalado 2019). The reports these companies provide to their customers, identifying distant cousins or assigning percentages of ancestry in various geographical and cultural categories, are now a significant part of how many people think about ancestry.

There are important differences between genetic ancestry, which describes the inheritance of DNA itself, and genealogical ancestry, represented by an individual's family tree or pedigree (Mathieson/Scally 2020), but methods based on genetic data necessarily rely on genetic ancestry as a marker of genealogical ancestry. Thus, when consumer genetics companies identify cousin relationships between participants, this is based on long stretches of identical genome sequence representing recent shared ancestry, and when they report percentages of ancestry, these are based on genetic similarity to groups of participants in their databases.

One can certainly question how well such reports are understood by customers. Arguably, the larger companies are relatively open about the methodologies used and interpretations given. But the marketing of these services is another matter. Advertisements vary in tone, from the frivolous, with ancestry as something relatively inconsequential and fun – the way many people view horoscopes, say – to the more serious, implying a deeper and more significant relationship between genomes and human traits. Customers are invited to plan holidays and diets, choose sports teams and construct aspects of their identity based on ancestry. Above all, they are exhorted to discover their roots.

The reception of these messages varies for different audiences, and they are targeted accordingly. For example, in societies or communities impacted by the legacy of colonialism or transatlantic slavery, the marketing reflects the fact that connections between ancestry, genetics and identity can be a highly consequential matter (Abel/Schroeder 2020). But in each case the messages play into and reinforce enduring misconceptions about ancestry. In the 21st century we may no longer aspire to trace our genealogies, like medieval princes, to mythological figures such as Noah and Adam, but the appetite for stories of personal descent from kings and emperors, or from Vikings, Celts and other historical peoples, remains undiminished. In this way, the popular concept of ancestry combines two notions which, in reality, are somewhat in opposition: the notion of origins and roots, and the uniqueness of an individual's identity.

There is of course a sense, or more accurately a time interval, in which everyone's ancestry is indeed unique. No two people have exactly the same pedigree, unless they are full siblings[2]. Differences in recent ancestry are thus literally familiar; one person may have an Irish grandparent, say, while another may have Italian ancestors a few generations further back. Intuitively, this ancestry is projected to older timescales, the first person claiming descent from the Celts perhaps, and the other from the Romans. But the intuition is misleading. The arithmetic of genealogical ancestry, in which the number of ancestors roughly doubles every generation back in time, means that inevitably there is a point in time when the number of ancestors, for any individual today, exceeds the total population alive at that time. This is the *genetic isopoint* (although as defined it is a feature of genealogical rather than genetic ancestry), and prior to it, all our pedigrees coincide.

Models of demography and global gene flow place the isopoint for present-day humans surprisingly recently, perhaps only a few thousand years ago (Rohde et al. 2004). In other words, for the vast majority of the human past, genealogical ancestry is a shared story rather than something which differentiates people. Moreover, on regional rather than global scales, pedigrees merge even more recently; for example, within Europe this occurs only seven or eight centuries ago, meaning that everyone with European ancestry is descended genealogically from Charlemagne, the Vikings, the Romans and so on. More importantly perhaps, simplistic claims about the present-day coherence of ancient or ›indigenous‹ European ancestries, which beset the popular reception of historical scholarship on the early medieval period, are undermined. For while indigeneity is applicable in regions and societies impacted by colonisation in the last few centuries, it is far less so in relation to events much further in the past. These observations are further reinforced by evidence from ancient and historical DNA, suggesting that gene flow and migration have been ubiquitous and, in some cases, very substantial in many parts of the world (Olalde et al. 2018; Skoglund/Mathieson 2018). Thus, genetic evidence is not primarily about the genetic origins of present-day nations, nor typically about the lineages of royal families and warrior clans.

Among geneticists there is concern that the marketing and presentation of consumer genetics services contributes to public misconceptions. However most take it as obvious that these services have little relevance to current research and thinking in human genetics. They are unaware of the extent to which it has come to represent their field, not only in the public mind, but also for many researchers in other disciplines, including history, anthropology and the social sciences. Critiques of human genetics from these fields frequently reference problems or misrepresentations associated with DNA ancestry tests and their reception (Hakenbeck 2019; Abel 2022).

One consequence is that an obsession with ancestry, categorisation and the simplistic representation of human diversity is projected back onto genetics as a field. And of course, geneticists do make use of categories and group labels, for example as descriptors of data (many of which come in turn from governmental or public health collection practices), or to facilitate statistical inference and modelling (Birney et al. 2021). Very rarely, or never, do such categories map straightforwardly onto the complex structure of human

2 And even siblings, if they are not twins, differ in genetic ancestry due to variation in the inheritance of chromosomal segments from their parents.

genetic diversity, and the simplistic ideas of human evolution and diversity in which they do are long outdated. But the terminology of a method often outlasts its use, and once disseminated into other contexts, can rejuvenate the old ideas from which it derives. Terms like admixture, population and ancestry, whose meanings carry different implications and broader associations outside genetics, are now part of the public conversation about human genetic diversity, thanks in part to their use by the DNA ancestry industry.

Conclusion

It can be expected that many of the difficulties discussed here will recede as the field of paleogenomics matures, as researchers are trained in its methods and become more familiar with the literature of multiple fields, and as studies move from high-profile journals to focus on more detailed, regional or local cohorts. Indeed, for the dialogue between genetics and archaeology, where quantitative and scientific methods are well established, much of this is already well underway, with research moving from population-level concerns to those of kinship and social relations. For historians it will require a greater appreciation and understanding of quantitative modelling and inference-based approaches to evidence, and the ways in which they are discussed and presented.

But, as the issues around DNA ancestry testing demonstrate, a substantial part of the dialogue between these fields is mediated through their public engagement (or lack thereof) and the impact it has on the reception of scholarship on historical and archaeological questions. For geneticists in particular there are several implications. It requires a better appreciation of the fact that, while ideas of biological race and arguments based on them may no longer be explicit in the language and theory of population genetics, they remain very much present in public discourse worldwide. This in turn requires them to think more carefully about – and change if necessary – the terminology used, not only in outreach but also in research itself, from which figures and results are frequently drawn and misrepresented (Carlson/Harris 2020). Above all, it necessitates a more concerted effort to anticipate and counter misconceptions about human genetics and ancestry, and to challenge the misrepresentations from which they stem.

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METHODEN

METHODS



Morphological kinship analysis in prehistoric burials: Theories, models, and applications

Kurt W. Alt

Zusammenfassung

Morphologische Verwandtschaftsanalyse in prähistorischen Bestattungen: Theorien, Modelle und Anwendungen

Fragen nach den sozialen Strukturen und den biologischen Verwandtschaftsverhältnissen in früheren Bevölkerungen beschäftigen Archäologie und Anthropologie seit den 1960er Jahren. Vor Etablierung der Archäogenetik bildete die morphologische Verwandtschaftsanalyse an prähistorischen Bestattungen eine praktikable Alternative, wobei primär Skelettvarianten im Schädel-, Kiefer- und Zahnbereich untersucht wurden. Eine Grenze der morphologischen Verwandtschaftsanalyse liegt in ihrer Eigenschaft als Ähnlichkeitsanalyse, d. h., sie kann phänotypisch ähnliche Individuen selektieren, aber in der Regel keine genealogische Nähe aufzeigen. Zudem bilden Familien keine genetisch klar abgegrenzten Einheiten, sondern überlappen vielmehr miteinander. Daher galt das Bilden von Gruppen genetisch ähnlicher Individuen lediglich als Hilfsmittel zur Visualisierung wesentlich komplexerer verwandtschaftlicher Strukturen. Die genetische Abstammung aller Individuen eines Fundplatzes zu rekonstruieren bildet sicherlich eine Ausnahme. Dies hat seinen Grund darin, dass auch eingeheiratete Familienmitglieder oder Individuen, welche in einem sozialen Abhängigkeitsverhältnis zur genetischen Familie stehen, häufig dem sozialen Verband zugerechnet werden, aber genetisch nicht eingeordnet werden können.

Summary

The study of biological relationships determined using skeletal remains in both archaeology and anthropology began in the late 1960s. Knowledge of genetic relationships between individuals provides the most important basis for reconstructing social structures in past populations. Prior to the development of paleogenetic kinship analysis, morphological kinship formed an important component of biological skeletal studies, primarily examining skeletal variants of skulls, jaws, and teeth. A limitation of morphological relationship analysis is that it is based on similarity, i. e., it can select phenotypically similar individuals but generally cannot reveal genealogical affinity. Moreover, families do not form genetically distinct units, but rather overlap with each other. Therefore, forming groups of genetically similar individuals was merely considered a tool to visualise much more complex kinship structures. The genetic descent of all individuals at a particular site is an exception. Here, married family members or individuals who form part of a socially dependent relationship to the genetic family are also included in the social group.

Theories and models of social structures in prehistoric communities

In archaeology, knowledge of kinship and family structures is considered to be essential in order to gain insights into the social structures of prehistoric and protohistoric communities. Approaches in archaeological research to address the social organisation of ancient communities and their socio-historical background go back to the 1970s (Binford/Binford 1968; Saxe 1970; Tainter 1978) and boomed in the 1980s[1]. Fundamental approaches regarding how to handle methodically the term *social structure* were discussed, as were important aspects for the implementation of sociological concepts in archaeology. Researchers noticed that the structure of comparable socio-economic communities follows similar, universal patterns. They were also of the opinion, however, that prehistoric and ethnographic findings may only be compared and used to draw mutual conclusions indirectly and under certain conditions. From an ethno-sociological viewpoint, the family, as the smallest social kinship group in a tribal community, plays a leading role within these societies (Fischer 1983). In order better to identify social structures in earlier populations, K. W. Alt/W. Vach (2004) compiled the theories, models, and approaches that provide insights on the one hand into the biological relationships between individuals within groups, and on the other hand between groups of individuals.

Methodical approaches regarding prehistoric kinship or social relations are based on the biohistorical sources themselves, on the transfer of cultural-historical development models of social organisation, and on general sociological criteria. Some participants in the discussion of methodologies quickly came to the conclusion that methods other than the initially favoured quantitative ones would be required in the

1 Steuer 1982; Renfrew 1984; Jørgensen 1987; van de Velde 1990; Müller 1994.

future to visualise social structures. Accordingly, attempts can first be found in the ethnoarchaeological approaches of the Anglo-American *Processual Archaeology* (Binford 1972; Saxe 1970) and its derivatives, *Postprocessual* and *Contextual Archaeology* (Hodder 1987). More attention was required, however, for socio-scientific and quantitative statistically-oriented procedures. This discussion eventually concluded that future questions on the structure of prehistoric social order could only be answered using an active interdisciplinary working approach. These questions focused on intrafamilial and interfamilial relationships, on the importance and function of social structures, on the causes of social stratification, on the determinants of social organisation, and on the reasons and conditions for mobility, migration, and segregation. Theory-driven studies on social structures in larger, demographically tangible protohistoric populations have discussed important aspects of socio-historical research objectives (Steuer 1982; Jørgensen 1987). They state that every society or social community has its own inner structure, which is based on various relationships between individuals and groups and is also characterised by vertical stratification, horizontal division, and changeability (Steuer 1982, 19).

According to general definitions, the meaning of the term ›kinship‹ is too ambiguous to use it freely in prehistoric research. The Encyclopaedia Britannica lists as one meaning: »System of social organization between people who are or are held to be biologically related or who are given the status of relatives by marriage, adoption, or other ritual«[2]. This includes both biological and social kinship, whereas archaeology and anthropology mainly focus on the genetic context (Alt/Vach 2004). In order to differentiate the biological content of the word ›related‹ from human sociological, ethnological, and historical categories, the discriminating differences in the context of the evaluation and interpretation of the sources need to be explained first. In modern society, ›kinship‹ and ›kinship systems‹ have experienced a loss or change of meaning and function, which we shall not discuss here in detail (Jakoby 2008; Hettlage 1998). In contrast to the term ›family‹, which in today's western society normally means the nuclear family (parents/children), it is harder to differentiate the term ›kin‹ because kin can be related in various ways (Plakaus 1984). In modern and traditional societies, only some family relations are biological (Bargatzky 1985). Culturally normative social factors, such as birth and rules of marriage and residence, played an important role in the past. They decisively influenced people's way of thinking, their social life, actions, and ultimately the structure of their social relations. Other factors, such as sex/gender, age, marital status, and lineage, additionally influenced the family relations and increased the individual's dependence and commitment. They also had an impact on economic, legal, political, social, religious, and ritual norms and behaviour, which, however, cannot be directly inferred from material remains and findings (Alt/Vach 2004).

Prehistoric burial – in cemeteries, tumuli, multiple inhumations, collective graves, mass graves, and the like – show highly variable burial patterns across chronological phases. These patterns can be interpreted as biological kinship but also as a multitude of other kinds of group affiliation. From an ethnological viewpoint, such groups are to be seen as solidary subsistence communities or residential units (Butzer 1987). The term ›residential unit‹ comprises the extended or joint family and includes both the genealogical relatedness as well as spouses and unmarried relatives. It may even include genetically unrelated but socially affiliated individuals. The term ›kinship‹ as an idiom for social relations can extend further than a purely biological relationship (Bargatzky 1985). Genealogically, kinship is determined by denotative and classificatory terms. In this system, collateral kin are group members that are not directly (linearly) related to each other. Patrilineal and matrilineal kin can be consanguine or affinal. We will not discuss other terms characterising family relations (lineage, clan, tribe) here in detail (Hillmann 2007; Alt/Vach 2004).

Ethnosociologically, two principles primarily determine how people live together in groups: affinity and descent. Whereas affinity encompasses the relationships between persons through marriage, descent means relationships characterised by a shared lineage. According to T. Bargatzky (1985, 48 ff.), culturally defined principles of affinity and descent can also include individuals beyond the parent-child-sibling-relationship. Marriage can therefore establish a sociocultural parenthood where biological lineage only plays a subordinate role. Ethnographically, the proposition of the universal occurrence of the nuclear family is not tenable (Bargatzky 1985). The tasks of the nuclear family as a functional unit regarding sex, reproduction, and the responsibility of bringing up children (Murdock 1949) is therefore not an inevitable and generally accepted social concept. Whereas Goodenough (1970, 19) defines the nuclear family as one »woman and her dependent children plus whoever else they are joined to through marriage or consanguinity in a minimal functioning group«, Bargatzky (1985) rejects all attempts at a universal definition due to the number and variety of exceptions. K. N. Schneider (1984) criticises the ›paradigm of kinship‹ and thinks that the ›claimed universality of kinship‹ is shaped by Eurocentrism, often leading to misinterpretation. Biological ties always create solidary relationships according to the axioms that underlie kinship. Schneider (1984) paraphrases this as »blood is thicker than water«, but these axioms are understood as specifically western European cultural phenomena (Welter 1987). These statements illustrate the complexity of social systems of relationships, which are thus difficult to categorise.

What do such statements mean in regard to the reconstruction of prehistoric living conditions, particularly in social terms? A legal principle in today's German civil code describes the role of the father/sire of a child (BGB Section 1592 No. 1) and is based on Roman civil law. This rule legally determines the father, whose identity in contrast to the mother's, is not unquestionable: »*pater est, quem nuptiae demonstrant*«. In other words, the child's father is the one who is married to the mother. As a result of the manifold nature of interpersonal relationships – one example in

2 https://www.britannica.com/summary/kinship (15.05.2023).

the present being the patchwork family – previous kin classifications derived from ethnology are now interpreted more cautiously. In cross-cultural comparison, research has to free itself methodically from value-laden connotations attached to culture-bound terms (marriage, family, kinship) in order to be able to use them ethically (Fischer 1983). On the premise of permissible archaeological-ethnological parallels, prehistoric burial communities always need to be considered also to comprise group members who lived in this community due to social assignment and were therefore buried in the same location used by this solidary community as a cemetery (unmarried family members, servants and farm hands, retinue, ›slaves‹, prisoners of war).

With regard to the meaning and the role of the kinship concept, the family group as a joint economic entity, or production community, constituted an important social factor until well into the Middle Ages (Steuer 1982; Lynch 1986). Kinship systems seem to have been the primary but not the only forces determining and driving the social order during the early period of human history. According to F. W. Sixel (1971), prehistoric and protohistoric sociocultural systems can therefore only be revealed by a kinship-based approach. The establishment of ›pre-state societies‹ as political systems, replacing previous societal structures, began during the Bronze Age at the latest (Pearson 1984; Risch 2018), even if stable political structures still did not prevail in some parts of the world where the legitimisation of power is secured by social elites and dynastic principles (Pfullmann 1997). Since the advent of ancient written sources, statements on the significance and position of the family and on kinship categories in antiquity and the Early Middle Ages have been available (Steuer 1982; Martin/Zoepffel 1989). At least for the elites, they are worded as norms. For non-literate cultures on the other hand, we can only consult ethnological comparisons (parallel phenomena). Working out family structures in burial grounds generates previously neglected information that makes an approximation of the social structure of earlier populations seem possible when considering demographic and archaeological findings, as well as including cultural anthropological and socio-scientific insights.

For some time, archaeology has been aiming at a comprehensive scientific reconstruction of former living conditions including social structures[3]. Of course, an analysis of social structures requires that they are archaeologically tangible. The most important types of sources regarding this question are collective burial places, the grave good customs, and specific funerary patterns. Intentional burials require a social code of conduct, which was established during the Late Pleistocene at the latest and allowed group burials that have first been verified for the Upper Palaeolithic (Stiner 2017; Bader 1978; Klíma 1987). A larger variety of funerary practices can be found as early as the Mesolithic period (Albrethsen/Brinch Petersen 1977; Brinch Petersen 1988; Orschiedt 2015). The transition to the producing economic system during the Neolithic lastingly changed the population structure. How fast this process turned a mostly egalitarian society into a stratified one has, however, been controversially discussed (Hodder 1984; Renfrew 1984; van de Velde 1990). As an obvious side-effect of metallurgy, the ›upper class‹ gained power and influence during the Bronze Age, which entailed comprehensive societal changes (Mays 1987). Due to access to geological deposits and the increasing technical specialisation, a social stratum emerged whose standard of living was reflected in the increased effort that was put into its members' burials. The early mediaeval cemeteries with row graves have been thoroughly examined with regard to social structure that manifested in varying grave furnishings (Arnold 1980; Steuer 1982; Pader 1982).

Archaeological attempts to understand how prehistoric cultures work as social systems are of great significance (Milisauskas/Kruk 1984; van de Velde 1990). However, without involving anthropological methods that go beyond purely paleo-demographic analyses they prove to be full of gaps and have little meaning. The qualitative and quantitative approaches used to analyse burial grounds are subject to criticism both in principle and of method. Qualitative approaches are criticised because the status reflected in the grave goods and the status achieved during life are directly associated. This is because legal and social status are treated as equal, and because the grave furnishings are assigned to historically verified social strata that are applied to non-literate eras. Alternative quantitative approaches are based on the premise that there is a direct relationship between the effort put into the burial of an individual and their social standing (Härke 1992, 24). On this basis, R. Christlein (1966) also tried to subdivide cemeteries socially according to the number and quality of grave goods. Other authors regard the social dimensions of the burial ritual under ethnological aspects (Saxe 1970) because the details of the burial depend on the tradition and attitude toward death and the hereafter (Cipoletti 1989). The models were criticised regarding both the approach and the underlying premisses (Ucko 1969). On socio-anthropological grounds, E. J. Pader (1982) argued against equating the status as reflected in the grave goods with wealth because social systems are dynamic and complex. E. Leach (1979) regarded this grave-good status less as an indicator of the social status of the dead and more an indicator of the status of the survivors. M. Kunst (1978) tried to combine paleo-demographic and archaeological data to distinguish social groups. This also barely revealed valid insights into the social structure of prehistoric communities. The situation was similar regarding family relationships and such attempts were rarely successful (Allen/Richardson 1971; Zhong-Pei 1985). The problem was therefore largely moved from archaeology to anthropology, with the aim of approaching the reconstruction of families and the clarification of potential individual kinship.

Population and genetic kinship analyses in anthropology – the era of epigenetic variants

The clarification of genetic and social relationships in the biological reconstruction of prehistoric populations was a

3 Renfrew 1984; Hodder 1987; Fischer 1987; Eggert 2012.

desideratum of prehistoric research until well into the second half of the 20th century. In biological anthropology, population studies and kinship analyses are disputed independently from archaeology. Historically, the natural sciences already cooperated closely with archaeology during the 19th century. From an archaeological viewpoint, however, they practically only served as auxiliary sciences until well into the second half of the 20th century. For this reason, and contrary to now, they were long considered as neither indispensable nor an integral part of archaeology (Alt 2010). Because anthropology was entangled in the Nazis' racial ideology, a restructuring of both personnel and methodology was necessary after World War II (Seidler/Rett 1982). The discipline's reorientation towards prehistoric anthropology (bioarchaeology) was ground-breaking. Its most important task was the reconstruction of population-biological structures and the analysis of the dynamics of the underlying processes (Wahl 1985). Another milestone was the subsequent quick adoption of methodological advances in the life sciences, biotechnology, and other research disciplines, which led to a focus on innovative laboratory methods (e.g., aDNA, trace-element and isotope analyses). In the course of two decades, these methods at least partially supplemented or superseded the predominantly descriptive anthropological methods (Grupe et al. 2015).

The general multitude of bioarchaeological research objectives regarding the source material will not be discussed in detail here. Rather, we will, and without exception, address anthropological efforts to discover and analyse phenotypically detectable differences between various populations (interpopulation analyses, population history), and potential family contexts regarding kinship between individuals within local populations (infrapopulation analyses, family analysis). Minor skeletal variants on skeletons and skulls are occasionally referenced in ancient medical scripts and by early modern anatomists, embryologists, and anthropologists (Blumenbach 1776; Russel 1900; Schultz 1954). In population studies, these skeletal variants showed familial similarities in their occurrence within groups (Shepherd 1893) and between different groups (Laughlin/Jørgensen 1956). Their significance regarding their application to humans (Berry/Berry 1967) was only justified by the research done on mice strains (Grüneberg 1952).

Systematic approaches to analyse population and kinship structures as part of the biological reconstruction of prehistoric and protohistoric populations emerged as early as the 1950s (Acsádi/Nemeskéri 1956; Laughlin 1957; Nemeskéri 1960). They were the starting signal for fundamental pioneering studies on the identification of those trait systems that can be used to clarify the relations within and between populations. Before research on ancient DNA (aDNA) was established in the 1990s, family relationships between skeletal individuals were assumed in anthropology primarily based on morphognostic, metric, morphometric, epigenetic, and sometimes pathologic abnormalities (see below). Ultimately, the study of anatomical skeletal variants prevailed. These are also called quasi-continuous, discontinuous, discrete, non-metric, or epigenetic traits. The nature of these traits called for an interdisciplinary approach taking into account specialist knowledge in embryology, anatomy, population genetics, and statistics, among others (Neiss 1964; Keats 1978; Hauser/De Stefano 1989; Czarnetzki 2000). To assess the usefulness and the value of these traits, additional parameters, such as genetics, were to be considered (Sjøvold 1984). »Epigenetic variants are an expression of the genes affecting development«, according to one summary of the traits' role (Berry/Berry 1967). Only in the recent past have computer models of the origin of variation during the evolution of anatomical variants been available (Salazar-Ciudad/Jernvall 2010).

H. Ullrich (1962) was the first to attempt to reconstruct the family structures of individuals from an Early Bronze Age cemetery. He kept developing this new branch of research and demonstrated various applications on skeletal material. It was this pioneering work that initiated the reconstruction of family relations in anthropology. As the methodological starting point of his efforts, he transferred the polysymptomatic similarity comparison successfully used in morphological DNA paternity testing (Szilvássy 1976) to skeletal remains (Ullrich 1969; Ullrich 1969a). Applying it to skeletal material should be regarded as innovative, even though the similarities regarding skeletal traits, as is the case with soft tissue traits, were known in principle (see above). On an experimental level, R. J. Berry (Berry 1963; Berry 1967; Berry 1968) and A. C. Berry/R. J. Berry (1967) had already studied the basics of non-metric skeletal variants on mice strains and transferred them to humans (Berry 1974; Berry 1975). Methodological issues in H. Ullrich's studies resulted from the selection and number of the traits used and from the lack of necessary control studies on samples with known biological kinship. The initially excessive expectation that families could in fact be distinguished and family trees could be reconstructed was heavily criticised because this was far beyond what such analyses were capable of (Bach/Dušek 1971; Czarnetzki 1973; Sjøvold 1976). The soft tissue traits most often used for human genetic paternity testing (physiognomical characteristics, friction ridges, etc.) could not be recorded on the skeleton, and the morphological traits' heritability was unknown, in contrast to that of the serological and pathological ones. Realistically, morphological kinship analyses are therefore only phenotypical similarity comparisons (Knussmann 1988).

Due to the aforementioned criticism of the selection of traits for morphological kinship analysis, epigenetic traits (rare anatomical skeletal variants) were subsequently preferred and intensely studied in the 1970s and 1980s. A. Czarnetzki (1971; 1972; 1972a), T. Sjøvold (1973; 1976), N. Ossenberg (1976), and W. Kellock/P. Parsons (1970), among others, demonstrated the significance of this trait system for population comparisons. Later, studies on family relations within local populations became another main focus thanks to the presentation of conclusive results from series with known kinship[4]. F. W. Rösing (1984) and

4 Sjøvold 1976; Sjøvold 1984; Rösing 1986; Rösing 1990; Kaufmann 1986.

R. Reinhard/F. W. Rösing (1985) suggested how to select and apply anatomical variants methodically; G. Hauser/G. F. De Stefano (1989) published an internationally acclaimed atlas on the trait complex, which, however, is limited to the skull; and most recently Czarnetzki (2000) comprehensively contributed to the research history and the significance of epigenetic traits. Mainly German-speaking anthropologists under Czarnetzki's leadership had set up in 1983 a commission in Basel that started to work out precise definitions of anatomical variants on behalf of the *Arbeitsgemeinschaft Paläoanthropologie und prähistorische Anthropologie* (Working Group Palaeoanthropology and Prehistoric Anthropology) within the *Deutsche Gesellschaft für Anthropologie* (German Association for Anthropology). Ultimately, however, it was unable to complete this task successfully.

Parallel to the development of the epigenetic traits, serological traits were tested for their use in population studies (Farkas et al. 1971; Piepenbrink 1986). R. R. Sokal (1986), Sokal et al. (1987), and Hanihara et al. (1983) examined the spatial-genetic structure of the blood-group frequencies *via* ›spatial autocorrelation analysis‹ in cemeteries. A. Salamon/I. Lengyel (1980) combined serological and immunological traits. As a similarity comparison, photo stereotomy was used for medical imaging (Riscutia et al. 1973). The biological identification of historical personalities proved to be successful (Schmidt 1974; Jungwirth/Winkler 1979; Grupe 1984) because here additional source material could often be referred to. However, the illegitimate relatives who were frequently found in the family vaults, but who did not exist according to historical sources, posed a problem (von Moers-Messmer 1983). Exhumations and reburials also often led to confusion (Ehrhardt/Czarnetzki 1982). Except in historical cases where written sources and portraits could be consulted, all the aforementioned methods and procedures were only partially convincing because they either were exclusively based on too few traits or provided too few conclusive results to verify genetic kinship. For this reason, the anatomical variants ultimately prevailed as a group of traits.

Since the 1980s, the literature has contained references to biologically determined relationships between skeletal individuals from prehistoric funerary complexes[5] and historical burials (Ehrhardt 1959; Suzuki et al. 1967; Winkler/Prohazka 1984). Normally, however, these were merely hypothetical assumptions that were rarely substantiated (Gejvall 1960). The similarities in the traits were often so striking that single traits sufficed as the basis for such assumptions. Examples of how to use epigenetic traits for similarity analyses were presented by S. Ulrich-Bochsler (1977) for individual comparisons; by J. Jungwirth/E. M. Winkler (1979) for identifying historical burials; by numerous authors for multiple inhumations, collective graves, and mass graves[6]; and by B. Hollack (1986), K. Wiltschke-Schrotta (1988), J. Desideri (2001), and others for burials from cemeteries. Unknown initial populations with a small sample size, as well as datasets reduced by the state of preservation, remained the restricting parameters. Because little was known of the genetics of anatomical skeletal variants, and because the required studies of the heritability of epigenetic traits still mostly did not exist, the application of these traits in kinship analysis remained controversial. The demands were focussed on the skeletal series of known kinship, in order to record as many indicative traits as possible and to find rare traits, on the application of heritability analyses, and on the statistical validation of the results (Rösing 1986).

Dental characteristics for population history and kinship analysis

Teeth are considered very useful indicators with which to characterise biological and cultural processes. Consequently, studying the teeth of our fossil and (pre)historic human ancestors has a long tradition (Nichol 1989; Alt 1997; Alt et al. 1997). There are two reasons for their significance as biohistorical sources: First, a large variability of traits allows statements to be made about population-biological relevance; second, traits typical of individuals or families may provide important insights regarding identity or biological relationships. Parallel to the studies on epigenetic traits in Europe, C. Turner's team in Tempe, Arizona, began looking at population studies across continents in the 1970s[7]. Non-metric, phenotypical dental traits served as their source material (Lukacs 1987; Irish 1997; Scott/Irish 2013). The accordingly established trait system (ASUDAS, Arizona State University Dental Anthropology System) comprises a selection of population-specific dental traits (diastema mediale, shovel-shaped incisors, tuberculum intermedium, and others) that can be used to show the geographical and ethnic variability of population groups in Africa, Asia, and Europe (Irish/Scott 2015; Hanihara 2013). These investigations were primarily aimed at the permanent dentition but can now be applied also to milk teeth (Paul/Stojanowski 2017). Younger generations of dental anthropologists successfully continue working with dental traits[8] with an increasing focus on their heritability (Stojanowski et al. 2019; Paul et al. 2021).

The application of the epigenetic skeletal variants ultimately failed because their heritability could not be verified due to the lack of samples with known genealogy, which are required to test their heritability. To unravel the biological relationships between individuals from prehistoric populations, we therefore decided to search for traits with available information on their heritability. The teeth and the surrounding bone structures provided such a group of traits. In contrast to the working group of Turner, who conducted extensive comparative population studies, but in close cooperation with archaeologists, we have favoured infrapopulation analyses in local burial complexes (multiple inhumations, collective graves, tumuli, burial grounds) in order to

5 Corrucini et al. 1982; Schröter 1985; Hollack 1986; Saunders 1989; Rösing 1990.
6 Breitinger 1980; Stuchlikova et al. 1985; Wahl/König 1987; Wahl/Höhn 1988.
7 Turner 1970; Turner 1979; Scott 1973; Turner 1979; Scott/Turner 1988; Turner et al. 1991.
8 Rathmann et al. 2017; Rathmann/Reyes-Centeno 2020; Rathmann et al. 2022; Gellis/Foley 2021; López-Onaindia et al. 2022; Solari et al. 2022.

uncover family relationships. We formulated the methodology and theory in numerous preliminary papers, developed it further in practice, and finally published it as my habilitation dissertation (Alt 1997). Dental and oral traits fulfil the critics' demands for a morphological kinship analysis on skeletal material in the best way possible[9]. The advantages of dental traits over epigenetic traits on the skull and the skeleton are manifold. Reasons for using this group of traits were criteria such as the usually better preservation of the jaws and teeth compared to the rest of the skeleton, the easy recording of dental traits, and, above all, the possibility of verifying the heritability of dental traits with data from living populations.

Dentistry has been used to investigate the heredity of dental and oral traits since the 20th century, including twin and family studies[10]. Similar to numerous morphological characteristics, the anatomical traits of teeth (e.g., size, shape, number) vary within populations quasi-continuously[11], which is formally referred to as phenotypical variability (Schulze 1987; Alt 1997; Turner et al. 1991). By verifying the heritability of the variability, its genetic percentage can be estimated. The tendency to develop a trait can then be divided into genetic and non-genetic components (Falconer 1984). Traits with a quasi-continuous normal distribution are phenotypically marked by a quantitatively graded expression. A threshold model of the expression of the traits can be brought in line with a multifactorial heredity of qualitative character states (present/absent)[12]. Using the threshold model, the percentage of the total variance can be calculated from the frequency of occurrence in a series of related individuals of known age and sex; this percentage is due to the additive effects of the genes and is called *inheritability* (Sjøvold 1984; Lane 1977).

When recording trait variants with threshold character in population studies, it is paramount to include both whether traits are present or absent and, if necessary, what other expressions these traits might have. The affected teeth may be ontogenetically present but have not developed normally, which means they represent teeth with micro-symptoms (also called micro-variants)[13]. When it comes to anomalies affecting the number of teeth, they are often visual, as a reduced tooth size down to peg shape. Within potential families, the group members may show entirely different variants of the trait: unilateral or bilateral absence, and size reduction or peg shape of the affected teeth.

When interpreting dental traits from inter-population and intra-population genetic studies on skeletal material, important biological mechanisms (e.g., genetic drift, isolation, founder effect) need to be taken into account to avoid false conclusions. To assess microevolutive processes, the number of persons in a population per generation is not decisive but rather the distinctly smaller number of the individuals involved in reproduction. Within small groups, such as those in remote mountainous regions or on islands, or in the case of social isolation, the frequencies of individual genes that belong to the gene pool can be changed drastically in a short space of time, either by random events or by specific behavioural patterns (Alt et al. 2013).

Basic principle of morphological intrapopulation studies using dental characteristics to discover genetic familial kinship

Morphological kinship analyses look for similarities in the visible characteristics or the appearance of individuals. The selection of relevant traits follows criteria such as a high degree of heritability, a low frequency within the population, an indicative trait expression, an extensive independence of age and sex, and a small intercorrelation of traits. Knowledge about the heritability of the included traits is the crucial criterion. The methodological principles described in the following mostly relate to dental traits (Alt 1997). Despite the far greater possibilities of genetic kinship analyses *via* aDNA studies, dental traits are still used for interpopulation and infrapopulation studies in morphological kinship analyses (see above). In fact, their potential use has even increased. Dental traits are suitable for both comparisons of fossil remains and cross-continental interpopulation studies as part of population history (Rathmann et al. 2017; Rathmann/Reyes-Centeno 2020). Apart from morphological variants of the crowns and roots of teeth, structural traits of the dental tissue (enamel/dentine), and, for example, descriptive characteristics, such as the number of teeth and anomalies in their position, can occasionally be used to determine biological kinship or similarities between groups – provided that knowledge of their genetic heredity is available (Schulze 1987; Alt 1997).

Analysing prehistoric kinship via morphological kinship analyses is fundamentally based on the ability to infer genetic relationships between individuals from the increased occurrence of rare, genetically determined traits on their skeletal remains. Not only is the more frequent occurrence of rare variants crucial, but also joint occurrence in the same individuals is of importance. The increased occurrence of several traits in the same individuals may indicate a nuclear family consisting of a father, a mother, and children, as well as other related persons (e.g., grandparents) if the accompanying archaeological and anthropological data support this (e.g., age, sex, joint burial). Several tried-and-tested procedures developed for this purpose can be used statistically to validate the findings. The significance of a trait variant as an indicator of genetic relationships between two or more individuals results from the magnitude of the frequency differences between the examined individuals and a reference population. The total local population may serve as a reference for a subgroup. With reliable knowledge about the heritability of the trait, the value of this indicator increases. Substantive knowledge about their formal genetics is available for most of the

9 Alt/Vach 1991; Alt/Vach 1992; Alt/Vach 1995; Alt et al. 1993.
10 Lewin 1928; Ritter 1937; Hughes et al. 2014; Townsend et al. 2015.
11 Stewart/Prescott 1976; Nakata 1985; Lee/Goose 1982; Townsend et al. 1994.
12 Sofaer 1970; Sofaer et al. 1972; Schulze 1987; Hauser/De Stefano 1989.
13 Sofaer 1970; Schulze 1987; Alt 1989; Hauser/De Stefano 1989.

dental traits used for morphological kinship analyses. In addition, twin and family studies in living populations exist for some of them. Recent investigations demonstrate that the trait frequencies of many of the variants have not changed considerably over long periods of time until today. To characterise the significance of odontological traits for morphological kinship analyses, we refer to the value of the traits.

After the traits have been recorded in a database, a large matrix forms the starting point of the kinship analysis. Each row of the matrix corresponds to an individual, each column to a trait. The main task is to choose blocks of rows and columns whose individuals show as many of the selected traits as possible, including all individuals or subgroups with several traits (Tab. 1). A number of mathematical-statistical methods are, in principle, suitable to find similarities in the traits (distance/cluster analysis); however, they are unsuitable for the present research objective. There are three strategies to infer clues to biologically related individuals or groups from a data matrix: Approach 1 aims at comparing trait frequencies; approach 2 examines the similarities by pairs; and approach 3 searches for conspicuous partial blocks in the data matrix. All three approaches need to fulfil certain preconditions and require their own statistical methods (Alt 1997, 205 ff.). The content-related validation of identified »conspicuousness« is additionally supported by anthropological information. Demographic data on the age and sex of the individuals are indispensable biological parameters for morphological kinship analysis (Fig. 1). Individual peculiarities beyond odontological traits (e.g., hereditary pathologies) that are shared by several individuals may constitute additional important indicators when interpreting discovered ›family‹ structures.

Beyond the statistical evaluation of discovered structures, various applications of morphological kinship analysis to prehistoric and protohistoric burial complexes have shown that a comprehensive reconstruction of social structures, especially in close cooperation with archaeology, yields results that justify the time invested. Additional archaeological information that can support evidence of kinship relationships between individuals include, among others: Information on a burial site's fine chronology and absolute dates; information on individual grave goods or associated objects, and the archaeological sex of the buried person or how their age influenced the selection of grave goods; convincing evidence regarding the spatial distribution of the graves in rows and groups (areas) within a burial ground; an indication of a potential generation of founders; and archaeological arguments for dynamic processes within a settlement[14].

Dental characteristics for population comparison and kinship analyses

The anthropological similarity analysis of the individuals from a burial complex provides insights on various levels. It facilitates, on the one hand, the structural distinction of populations or groups regarding their homogeneous or heterogeneous ethnic composition and, on the other hand, the comparison between groups. In this way, dynamic processes regulating population developments can be traced at a microevolutive level (mobility and migration). At the same time, similarity analysis lets us discern the kinship relationships of the buried persons, reconstruct potential family groups, and compile genealogies in certain cases (Herrmann et al. 1990, 326). Recognising genetic family relations during infrapopulation analyses is based on the assumption that skeletal traits occur with a certain frequency depending on the homogeneity of a group and that related individuals are more similar regarding rare morphological traits. This naturally requires knowledge about the frequency of the investigated traits in suitable reference populations.

Numerous publications on highly diverse burial complexes result from my working group's applications of the odontogenic system of traits for kinship analysis, internally called FU-DTS (Freiburg University Dental Trait System) and was developed with W. Vach[15]. With regard to the research objectives mentioned above, the examined series extends from the Palaeolithic to the Middle Ages. These studies were mostly interdisciplinary – realised in close cooperation between archaeology and anthropology. Despite the competition from the already established US American trait system called ASUDAS (Turner et al. 1991) and from the epigenetic traits favoured mainly in Europe (Czarnetzki 2000), the broader dental assemblage of traits for infrapopulation analyses, which are used to discover intra-group kinship relations, has gained international acceptance[16]. The difference between the trait complexes FU-DTS and ASUDAS is primarily quantitative because FU-DTS includes more individual traits. Both have seen an increased number of publications in recent years[17].

Direct comparison of genetic and morphologic kinship analyses in the same skeletal samples

After the establishment of aDNA analyses in bioarchaeology, dental traits were occasionally tested together with genetic markers on the same skeletal samples[18]. Initially, palaeogenetic research objectives primarily aimed at population-genetic studies on the colonisation of the continents and on population history (e.g., Haak et al. 2015). Kinship analysis in the sense of infrapopulation analyses of local

14 Alt/Vach 1991; Alt/Vach 1992; Alt/Vach 1994; Alt/Vach 1995; Vach/Alt 1993; Alt/Vach 1995.
15 Alt et al. 1992; Alt et al. 1995; Alt et al. 1996; Alt et al. 1997; Alt et al. 2003; Alt et al. 2005; Alt et al. 2013; Alt et al. 2015; Alt et al. 2019; Jørgensen et al. 1997; Alt/Vach 2001; Alt/Vach 2004; Kutterer/Alt 2007; Müller et al. 2008.
16 Spence 1996; Eades 1997; Eades 2003; Desideri 2001; Desideri 2007; Stojanowski/Schillaci 2006; Pilloud/Larsen 2011; Paul et al. 2013; Paul/Stowanowski 2015.
17 Johnson/Paul 2016; Sciulli/Cook 2016; Rathmann et al. 2017; Rathmann/Reyes-Centeno 2020; Stojanowski/Hubbard 2017; Stojanowski et al. 2019; Irish et al. 2020; Paul et al. 2021; Gellis/Foley 2021; López-Onaindia et al. 2022.
18 Shinoda et al. 1998; Corrucini et al. 2002; Adachi et al. 2003; Ricaut et al. 2010; Tan et al. 2014; Hubbard et al. 2015.

I: all individuals (n = 208)
T: Set of traits

		Freq. within	Freq. out of	Maximal number	Relative freq.
		F	*F*		(%)
t_1:	lingual marginal ridge 42 41 31 32	3	0	120	2.5
t_2:	accessory ridge 15 25	7	1	44	18.2
t_3:	over developed cusps dist. -ling. 17 27	5	2	106	6.6
t_4:	number of cusps ≥ 5 47 37	6	2	125	6.4
t_5:	shovel-shaped incisors (strong mongolide form) 12 22	7	2	77	11.7
t_6:	accessory cusplets of the mesial marginal ridge 16 26	4	1	66	7.5
t_7:	abnormal size of roots *molars*	2	1	179	1.7

F: Individual with at least two traits of ***T***

	t_1	t_2	t_3	t_4	t_5	t_6	t_7	Age anthr.	Sex anthr./arch.	Chronology
30	? ? ? ?	−−	−−	−−	++	++	−−	20–30	f/f	I.1–I.2
55	? ? ? ?	+−	−−	−−	++	−−	−−	7–14	m/?	I.2
72	− ? ? −	? ?	+?	++	? ?	? ?	−−	50–60	f?/?	(I.3–II.3)
123	−−−−	? ?	+?	?+	−−	−−	−−	40–50	f/f	I.3
175	−−−−	? ?	? ?	−?	++	−−	++	30–40	f?/?	I.2
177	?−−−	?−	+−	−−	++	−−	−−	30–40	f?/?	I.2
221	−−−−	++	−−	?−	−−	++	−−	15–20	?/f	(II.2)
242	−−−−	++	−−	++	−−	−−	−−	15–20	?/m	II.1–II.3
97	−−++	? ?	? ?	? ?	++	++	−−	7–14	?/f	II.1
101	? ? ? ?	+?	++	? ?	? ?	? ?	++	20–30	f?/f	I.3
167	? ? ? ?	?+	++	++	? ?	−−	−−	20–30	f/?	(I.2–I.3)
198	++++	+?	−−	+−	++	? ?	−−	15–20	?/f	I.1–I.2
59	−−++	+?	−−	++	+?	++	−−	7–14	?/?	I.2

$P_1(T) = 0.0000009163$ $G_1(T) \approx 0.02$

Table 31.1: Result from analysing all individuals

Tab. 1 Example data set of an odontological kinship study within the early medieval burial site of Eichstetten, Breisgau-Hochschwarzwald district (Germany) (land parcel: Wannenberg). »To formalise the research process, we define for each set of traits *T* a number *P(T)* reflecting the probability of finding the observed coincidences if the traits are allocated randomly to the individuals. The smaller *P(T)*, the less we can explain the finding by random variation. More precisely, we consider a statistic *S* summing up the number of traits in *T* shown by each individual with at least two traits in *T*. Then *P(T)* is defined as the probability of observing at least the observed value of *S*, given the missing pattern of the individuals, the frequency of each trait and independence of the traits« (Alt/Vach 1995, 104 f.). Details of the computation of *P(T)* are given in (Vach/Alt 1993, 289). »The search procedure always given us a result: the most suspicious set *T* of traits. However, the corresponding value *P(T)* gives us no information as to how suspicious this finding is. To evaluate the significance, we compute a further measure *G(T)*. This is defined as the probability of finding by our search procedure at least one set of traits of the same size as *T* which shows a smaller value than *P(T)*, assuming interdependence between traits. A high value of this global measure indicates the result of our search procedure can be explained by random variation, whereas low values indicate that there must be a systematic source, probably a true family. The global measure *G(T)* can be computed approximately by Monte Carlo simulation« (Alt/Vach 1995, 105). In our example from Eichstetten we found analysing all individuals a set of 7 traits with an approximate value of ≈ 0.02 for *G(T)*.

Tab. 1 *Beispieldatensatz für eine odontologische Verwandtschaftsanalyse innerhalb des frühmittelalterlichen Gräberfeldes von Eichstetten, Lkr. Breisgau-Hochschwarzwald (Deutschland) (Flurstück: Wannenberg). »Um den Forschungsprozess zu formalisieren, definieren wir für jeden Satz von Merkmalen* T *eine Zahl* P(T)*, die die Wahrscheinlichkeit widerspiegelt, die beobachteten Übereinstimmungen zu finden, wenn die Merkmale den Individuen zufällig zugeordnet werden. Je kleiner* P(T) *ist, desto weniger können wir den Befund durch zufällige Variation erklären. Genauer gesagt, betrachten wir eine Statistik S, die die Anzahl der Merkmale in* T *zusammenfasst, die jedes Individuum mit mindestens zwei Merkmalen in* T *aufweist. Dann ist* P(T) *definiert als die Wahrscheinlichkeit, mindestens den beobachteten Wert von* S *zu erhalten, wenn man die fehlenden Werte der Individuen, die Häufigkeit jedes Merkmals und die Unabhängigkeit der Merkmale berücksichtigt« (Alt/Vach 1995, 104 f.). Details zur Berechnung von* P(T) *finden sich in (Vach/Alt 1993, 289). »Das Suchverfahren liefert uns immer ein Ergebnis: die auffälligste Menge* T *von Merkmalen. Der entsprechende Wert* P(T) *gibt uns jedoch keine Auskunft darüber, wie auffällig dieser Befund ist. Um die Signifikanz zu bewerten, berechnen wir ein weiteres Maß* G(T)*. Dieses ist definiert als die Wahrscheinlichkeit, mit unserem Suchverfahren mindestens eine Merkmalsgruppe der gleichen Größe wie* T *zu finden, die einen kleineren Wert als* P(T) *aufweist, wobei eine gegenseitige Abhängigkeit der Merkmale angenommen wird. Ein hoher Wert dieses globalen Maßes zeigt an, dass das Ergebnis unseres Suchverfahrens durch zufällige Variation erklärt werden kann, während niedrige Werte darauf hinweisen, dass es eine systematische Erklärung für das Ergebnis geben muss – in unserem Fall vermutlich genetische Zusammenhänge zwischen den Individuen. Das globale Maß* G(T) *kann näherungsweise durch Monte-Carlo-Simulation berechnet werden« (Alt/Vach 1995, 105). In unserem Beispiel aus Eichstetten fanden wir bei der Analyse aller Individuen einen Satz von 7 Merkmalen mit einem ungefähren Wert von ≈ 0,02 für* G(T).

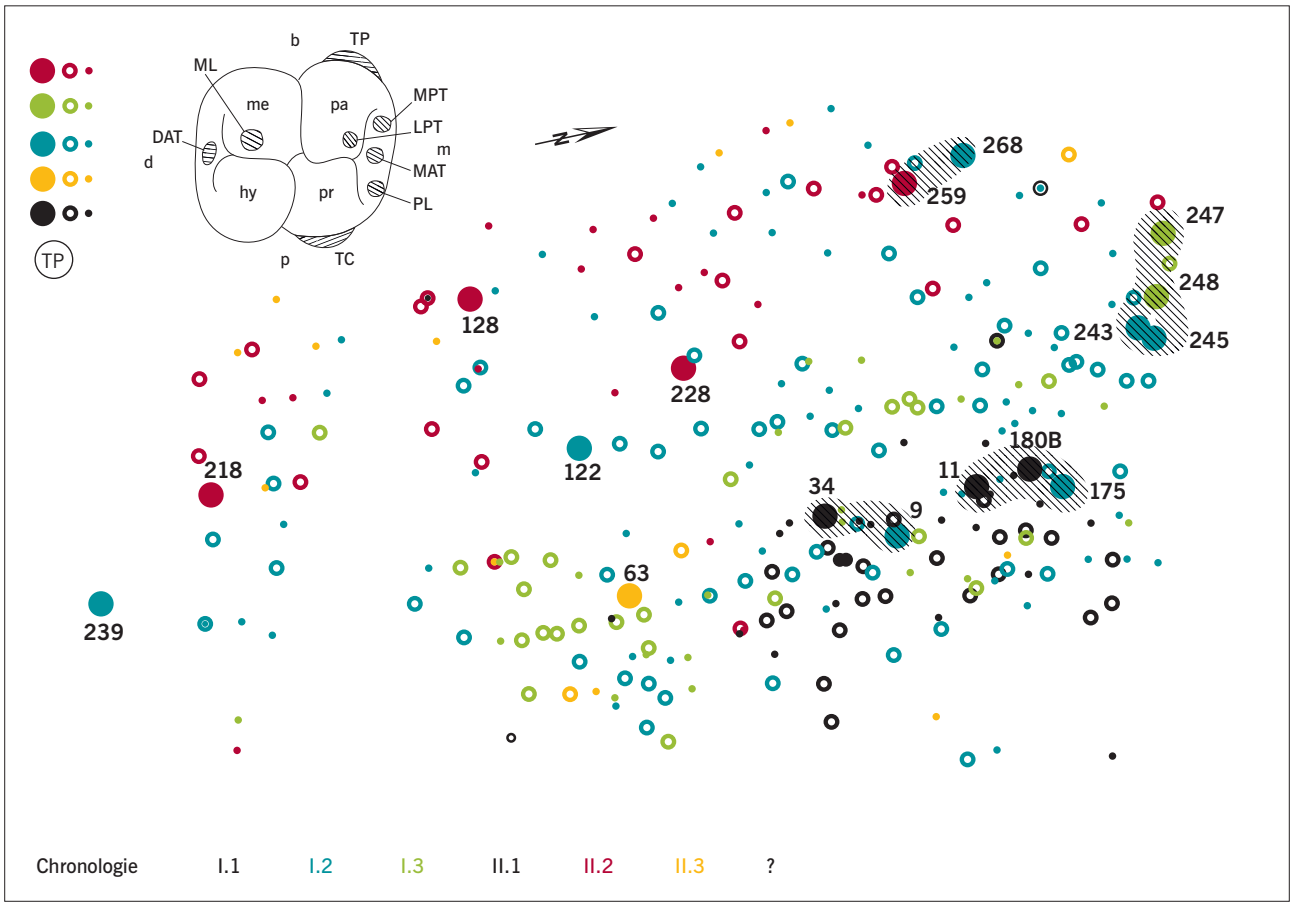


Fig. 1 Example of the spatial distribution of a trait with strikingly increased frequency in the early medieval population of Eichstetten, Breisgau-Hochschwarzwald district (Germany) (land parcel: Wannenberg). The trait, an accessory cusp on one molar, a so-called Tuberculum paramolare (TP) is observed about four times more frequently in the cemetery (8.0 %) than in the population average (2.0 %). Content-related reasons for the increased frequency can be ruled out, as the trait is relatively easy to detect. We interpret the trait's conspicuity probability of 0.0001 as evidence of ›biological‹ similarity among trait carriers. The spatial distribution of the trait supports this suggestion. The distribution of the trait remains nearly the same throughout the cemetery's occupancy period, as would be expected with population continuity. Slight fluctuations can be explained by ›missing values‹, graves that are more difficult to date, as well as by trait properties (e.g., penetrance of the trait). At the beginning of the occupation, individuals that are close or directly adjacent to each other are affected, while in later phases the trait is more dispersed across the burial ground. Graves 11, 175, and 180B form a small group to the north-west, as do graves 243, 245, 247, and 248 in the north-eastern part of the cemetery. The neighbouring graves 9 and 34 as well as 259 and 268 may also be considered spatially close. With only 17 observations and critical consideration, the relative rarity of the feature makes only the four graves in the north-west 243, 245, 247, and 248 and the nearby three graves 11, 175, and 180B stand out as ›familial‹. Despite the rarity of the trait and some spatial structure indicating some trait bearers as potentially ›biologically‹ related, we wish to infer only a conditional probability for the correctness of the assumption.

Abb. 1 *Beispiel für die räumliche Verteilung von Merkmalen mit auffällig erhöhter Häufigkeit in der frühmittelalterlichen Bevölkerung von Eichstetten, Lkr. Breisgau-Hochschwarzwald (Deutschland) (Flurstück: Wannenberg). Ein sogenanntes Tuberculum paramolare (TP) (Merkmal 192) wird im Gräberfeld etwa viermal so häufig beobachtet (8,0 %) wie im Bevölkerungsdurchschnitt (2,0 %). Inhaltliche Gründe sind für die erhöhte Häufigkeit auszuschließen, da das Merkmal relativ einfach zu erfassen ist. Die Auffälligkeitswahrscheinlichkeit des Merkmals von 0,0001 deuten wir als Hinweise auf eine ›biologische‹ Ähnlichkeit der Merkmalsträger. Die räumliche Verteilung des Merkmals unterstützt diese Vermutung. Die Verteilung des Merkmals bleibt über die ganze Belegungszeit des Friedhofs nahezu gleich, wie es bei Bevölkerungskontinuität zu vermuten ist. Leichtere Schwankungen sind durch ›missing values‹, schwerer datierbare Gräber sowie durch Merkmalseigenschaften erklärbar (z. B. Penetranz des Merkmals). Am Anfang der Belegung sind nahe bzw. direkt nebeneinander liegende Individuen betroffen, während in späteren Phasen das Merkmal stärker über das Gräberfeld streut. Die Gräber 11, 175 und 180B bilden nordwestlich ebenso eine kleine Gruppe wie die Gräber 243, 245, 247 und 248 im nordöstlichen Teil des Friedhofs. Als räumlich nahe dürfen auch noch die benachbarten Gräber 9 und 34 sowie 259 und 268 gelten. Die relative Seltenheit des Merkmals lässt bei 17 Beobachtungen und kritischer Betrachtung nur die vier Gräber in Nordwest 243, 245, 247 und 248 sowie die nahe beieinander liegenden drei Gräber 11, 175 und 180B als ›familiär‹ auffällig erscheinen. Trotz der Seltenheit des Merkmals und einer gewissen räumlichen Struktur, die einige Merkmalsträger als potentiell ›biologisch‹ verwandt ausweist, wollen wir nur eine bedingte Wahrscheinlichkeit für die Richtigkeit der Annahme herleiten.*

populations was successfully established in palaeogenetics only thanks to the possibilities of genomic studies. A few prehistoric sites, for which earlier morphological kinship analyses with the application of anatomical variants and dental traits were already available, were examined once more to determine valid data regarding sex and family relations. This allows us to compare morphologically generated results regarding family relations with the subsequent aDNA kinship analyses. The studies from my working group cited here relate to the Palaeolithic and the Neolithic. The representative case studies with a high degree of similarity between morphological and genetic kinship analysis regard the Gravettian triple burial from Dolní Věstonice, Moravia, Czech Republic (Alt et al. 1997 vs. Mittnik et al. 2016), and the Linear Pottery burial ground of Derenburg, Saxony-Anhalt, Germany (Glienke 2012; Alt et al. in press vs. Childebayeva et al. 2022). We may expect more comparisons between results from morphological kinship analyses and

genomic revisions in the coming years. Comparisons of larger burial grounds from the Early Middle Ages with corresponding data would be particularly interesting.

Conclusions

Prehistoric and protohistoric archaeology and human biology (anthropology) share roots that extend back to the 19th century (Eggert/Samida 2009). Only by establishing a prehistoric anthropology in the second half of the 20th century, however, could their successful cooperation reach a scientific profundity in terms of methods and content that accounts for their current success. The comprehensive biological reconstruction of earlier populations *via* natural scientific methods of analysis has since been one of the major tasks of physical anthropology. This includes, on the one hand, classical osteological analyses on bioarchaeological source material, still indispensable today, and, on the other hand, the laboratory methods that have only been adapted from various other disciplines with the advancement of basic research at the end of the 20th century and have consequently improved the cooperation with archaeology. These laboratory methods include bioarchaeometric procedures (palaeogenetics, isotope research), which, previously a desideratum, now facilitate the comparison between and within populations, ranging from studies on population history to kinship analyses within various burial communities.

The expansion of knowledge on the aforementioned processes has evolved from the need for the archaeological sciences and bioarchaeology to learn more about the population and colonisation history of the continents, and more about the inner structure and social structures of earlier communities and societies. Methodologically, however, from the 1960s until the 1990s only morphognostic, metric, and pathological traits were available. Expectations regarding these trait systems were initially excessive and attracted considerable criticism, particularly because the results could not be verified on skeletal material of known biological kinship. This only changed when the significance of the epigenetic traits could be developed, and the dental traits could be established as a system of traits. Information on the genetic background was already available for numerous dental traits, which facilitated, on the one hand, population comparisons internationally, mainly realised by applying the ASUDAS system, and, on the other hand, infrapopulation analyses regarding biological kinship, using the FU-DTS. The similarity comparison, i.e., inferring from morphological similarity to genetic kinship, does not provide valid data on the real composition of populations, or on differences and similarities between populations; nor do genetically verified infrapopulation analyses within burial communities or grounds. In analogy to medical risk assessment, the probabilities of occurrence facilitate more or less significant results depending on the value of the traits.

Palaeogenetics was established during the last decade of the 20th century in parallel with the morphological traits and initially aimed to answer questions of origin and descent, speciation, colonisation history, and population studies; only much later did it address genetic kinship analyses (Bösl 2017), although several spectacular individual cases were published then (Haak et al. 2008; Simón et al. 2011). These windows into the past have widened only recently (Mittnik et al. 2019; Krause/Trappe 2019), and archaeogenetics has undoubtedly increased and enriched our knowledge. The number of globally established scientists in this field, however, is limited, as are laboratory capacities, so that not every site and every research objective are currently being investigated with molecular-genetic methods. Conversely, specific applications of similarity analysis are conceivable as part of dental anthropological research objectives that do not necessarily require genetic proof.

The advances in, and popularity of, palaeogenetics and of genetic kinship analysis in this branch of research have not diminished the impact of morphological kinship analysis or made it dispensable, despite its limitations. This is demonstrated by the increase in internationally published studies on morphological similarity analyses with dental traits. As shown by successful application of both methods, morphological kinship analysis makes sense under certain conditions. This approach is suitable for preliminary studies examining family similarity as part of classical osteological basic investigations. In the case of a positive indication of similarities between individuals, these could then be validated, or not, by using palaeogenetics. Regardless of the methodology, researching our ancestors' social structures is not trivial but has limits. Numerous parameters that shaped bygone communities are set by circumstances that do not allow for the complete reconstruction of the generational sequence. In the Middle Ages, for example, married couples only lived together for about nine years on average before one of the two died, and patchwork families were therefore common. A low life expectancy, high infant mortality, and occasionally high rates of mobility and migration led to highly variable structures and dynamics within and between populations. Research *via* aDNA has long since left its teething troubles behind and has optimised the methodology by using genomics. Undoubtedly, we can ascertain that archaeogenetics has opened additional windows to our past that would otherwise be closed if only morphological procedures were available.

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Erste Methoden zum Auffinden biologischer Verwandtschaften in archäogenomischen Daten und deren Anwendung in prähistorischen Europäern

Torsten Günther

Summary

First methods for finding biological relationships in archaeogenomic data and their their application in prehistoric Europeans

Archaeogenomic research has proven to be a valuable tool for archaeological questions, initially mostly used to trace migrations of prehistoric and historic groups. Early studies largely focused on genetic similarities and dissimilarities between several ancient populations, while relationships within a group or burial site were rarely studied, partly due to a lack of suitable methodology. Tools which infer the degree of relationship used with modern DNA require high quality data but fragmentation and other post-mortem *damage to ancient DNA make the application of such tools infeasible for most archaeological samples. Most archaeogenetic research concerning kinship had long been restricted to uniparental markers (Y chromosomes and mitochondrial haplogroups), which can only* exclude *but not prove direct relationship between individuals. In 2018, we developed the software »READ« (Relationship Estimation from Ancient DNA), one of the first methods specifically designed for assessing genetic kinship in archaeogenomic datasets. My article presents the design of the method and reflects on its use over the last years.*

Zusammenfassung

Die Archäogenomik hat sich zu einem wertvollen Werkzeug für archäologische Fragestellungen entwickelt, die ursprünglich weitestgehend genutzt wurde, um Migrationen von (vor-)geschichtlichen Gruppen nachzuvollziehen. Dabei wurden hauptsächlich Vergleiche zwischen Kulturen, Gruppen und Populationen durchgeführt. Verwandtschaften innerhalb einer Gruppe wurden hingegen nicht untersucht, was zum Teil am Mangel passender Methoden lag. Methoden, die für die Verwandtschaftsermittlung mit moderner DNA verwendet werden, benötigen hochwertige Daten, was mit alter DNA durch Fragmentierung und andere post-mortem *Schäden nicht möglich wäre. Archäogenetische Studien, die sich mit biologischer Verwandtschaft beschäftigt haben, beschränkten sich lange auf uniparentale Daten (Y-Chromosomen oder mitochondriale Haplogruppen) welche nur eine direkte Verwandtschaft ausschließen, aber nicht beweisen können. Im Jahr 2018 haben wir daher das Programm »READ« (Relationship Estimation from Ancient DNA) entwickelt, eine der ersten Methoden speziell designt für die Verwandtschaftsanalyse in archäogenomischen Daten. Mein Artikel gibt einen Überblick zur Funktion der Methode und erwähnt dann erste Fallstudien, in denen »READ« verwendet wurde.*

Einleitung

Das Feld der Archäogenomik hatte im Jahr 2010 ihren großen Durchbruch mit der Entschlüsselung des Neandertaler-Genoms (Green u. a. 2010). In den folgenden Jahren wurden diese Methoden auch mehr und mehr auf DNA-Daten von modernen Menschen aus dem Holozän angewandt (Skoglund/Mathieson 2018; Liu u. a. 2021). Dabei wurden verschiedene, prähistorische Migrationsbewegungen aufgezeigt, zum Beispiel wie sich die ersten Ackerbauern während der Jungsteinzeit von Anatolien aus über ganz Europa verbreitet haben. Diese anfänglichen Studien mussten hauptsächlich mit kleinen Stichproben von etwa einer Handvoll Individuen auskommen. Das lag zum einen an den noch nicht optimierten Labormethoden zur Extraktion alter DNA. Für die Untersuchung großer Migrationsbewegungen haben allerdings bereits wenige Individuen ausreichend Information, um Schlüsse über ihre gesamte Abstammungslinie zu ziehen. In jeder Generation verdoppelt sich die Anzahl unserer Vorfahren, so dass ein einzelnes Individuum vor g Generationen 2^g Vorfahren hatte, von denen es teilweise auch DNA-Abschnitte in sich trägt (s. Beitrag Scally in diesem Band). Dementsprechend sind in der DNA einer Person nicht nur diese Person selbst, sondern auch viele ihrer genetischen Vorfahren und somit die gesamte Population repräsentiert.

Während dieses Wissenschaftsfeld bis ca. 2015 wichtige Kenntnisse zu großflächigen Bewegungen auf kontinentaler Ebene lieferte, blieben die eigentlichen Leben der Individuen, deren Sozialstrukturen und Verwandtschaftsverhältnisse verborgen (Racimo u. a. 2020). Dabei ist die Weitergabe von DNA von einer Generation zur nächsten eine der Grundlagen der Genetik und Genomik. Die DNA des Menschen ist auf 23 Chromosomenpaare (DNA-Moleküle) aufgeteilt. Kinder erhalten je eine Kopie eines Chromosoms von ihrer biologischen Mutter und ihrem biologischen Vater. Eines der Chromosomenpaare sind dabei die Geschlechtschromosomen, Individuen mit zwei X-Chromosomen sind biologisch weiblich, Individuen mit je einem X- und einem Y-Chromosom sind biologisch männlich. Zusätzlich gibt es noch mitochondriale DNA, die immer von der Mutter an ihre Kinder vererbt wird (Abb. 1). Während der Keimzellenentwicklung jeder Generation werden außerdem die beiden Chromosomen eines Paars rekombiniert, also durchmischt, wodurch jeweils eine andere Zusammenstellung der Chromosomen in die Folgegeneration weitergegeben wird.

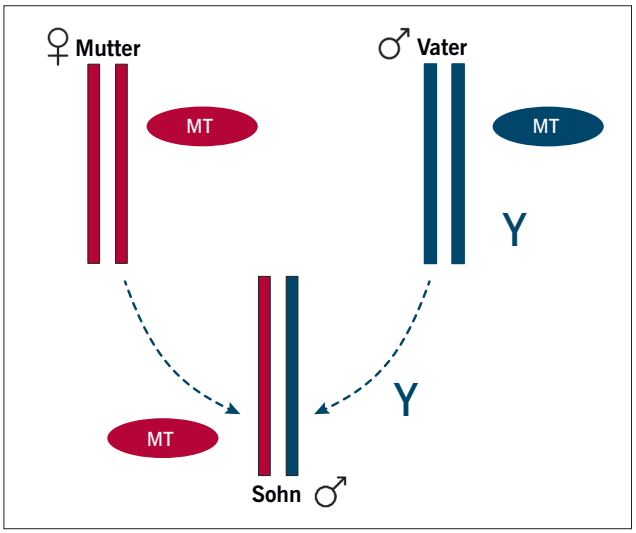


Abb. 1 Schematische Darstellung der Vererbung von Chromosomen zwischen Eltern und ihren männlichen Nachkommen. Für jedes der 22 autosomalen Chromosomenpaare erhält der Sohn je eine Kopie von Mutter und Vater. Das Y-Chromosom kommt vom Vater, die mitochondriale DNA (MT) wird von der Mutter vererbt.

Fig. 1 Schematic illustration of chromosome inheritance between parents and their male descendants. For each of the 22 autosomal chromosome pairs the son receives a copy of each the mother and the father. The Y-chromosome is derived from the father, the mitochondrial DNA (MT) is passed on by the mother.

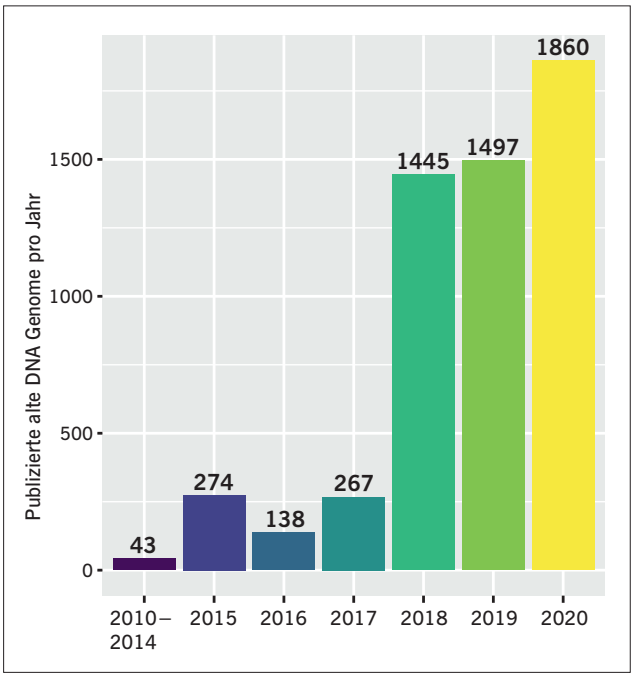


Abb. 2 Entwicklung der weltweit publizierten Genome aus der Archäogenomik bis 2020.

Fig. 2 Development of the worldwide published genomes from the field of archaeogenomics until 2020.

Eine Konsequenz dieses Prozesses ist, dass wir mit Verwandten unterschiedlichen Grades unterschiedliche Anteile unserer DNA gemeinsam haben. Verwandte 1. Grades, also Vollgeschwister und Eltern-Kinder, teilen jeweils 50 % ihrer DNA. Verwandte 2. Grades, also Halbgeschwister, Enkel-Großeltern und Tante/Onkel-Nichte/Neffe, teilen etwa 25 % ihrer DNA (Tab. 1) usw. Diese Erwartungswerte können genutzt werden, um beispielsweise in der Forensik oder der kommerziellen persönlichen Genomik Verwandte zu finden. Dazu werden Positionen im Genom benutzt, an denen zwischen einigen Individuen der Population genetische Unterschiede bekannt sind. Die Prozente aus Tabelle 1 übersetzen sich dann in den erwarteten Anteil der Positionen, die identisch zwischen zwei Verwandten sind, weil diese auf denselben Vorfahren zurückgehen. Diese Methoden für moderne DNA ließen sich allerdings nicht problemlos auf alte DNA aus der Vorgeschichte anwenden, da die Qualität der Daten deutlich schlechter ist (s. nächster Abschnitt). Deshalb beschränkte sich die Verwandtschaftsanalyse mit alter DNA hauptsächlich auf mitochondriale DNA oder Y-Chromosomen, die jeweils nur die maternale bzw. paternale Linie abbilden können. Hier kann es sogar zu zufälligen Übereinstimmungen kommen, weil ein bestimmter Typ mitochondrialer DNA oder Y-Chromosom sehr häufig in einer bestimmten Population sein kann. Deshalb kann dieser Ansatz nur bestimmte Verwandtschaften wie Vater/Sohn oder Mutter/Kind ausschließen (im Falle, dass die beobachteten Chromosomen unterschiedlich sind), aber keine Verwandtschaften beweisen.

Verwandtschaftsgrad (genetisch)	Beispiel	Erwartete prozentuale genomische Übereinstimmung
0.	Eineiiger Zwilling, Klon	100 %
1.	Vollgeschwister, Eltern-Kind	50 %
2.	Halbgeschwister, Enkel-Großeltern, Tante/Onkel-Nichte/Neffe	25 %
3.	Cousins 1. Grades	12,5 %

Tab. 1 Verwandtschaftsbeziehungen bis zum 3. Grad und deren erwartete Übereinstimmung auf Genomebene.

Tab. 1 Relationships up to the 3rd degree and their expected match at the genome level.

Die speziellen Herausforderungen alter DNA und Entwicklung von »READ«

Der Idealfall für die Untersuchung von genetischen Verwandtschaftsbeziehungen wären qualitativ hochwertige DNA-Daten aller Individuen. Das bedeutet zum Beispiel, dass wir für jede Position des Genoms den Zustand auf beiden Chromosomen kennen und auch genau wissen, welches Chromosom von welchem Elternteil stammt. Nach dem Tod eines Individuums beginnen allerdings enzymatische Prozesse, die die DNA in ihren Zellen zersetzen, weshalb die DNA aus menschlichen Überresten nur in fragmentierter Form lesbar ist. Daher wissen wir meist nicht, welche Variante auf dem paternalen oder maternalen Chromosom lag und ob wir überhaupt beide Chromosomen beobachten. Von jedem Individuum stehen die Informationen nur lückenhaft

zur Verfügung, ein daraus folgender Mangel an überlappenden DNA-Daten erschwert den Vergleich zweier Individuen.

Bis 2014/15 gab es weder die Labormethoden um genomische DNA in großen Stückzahlen zu sequenzieren (Haak u. a. 2015), noch passende Analysemethoden, um solche Daten auf biologische Verwandtschaft zu untersuchen. Beides sollte sich schlagartig ändern: allein 2015 wurden archäogenomische Daten für 274 Menschen publiziert, mehr als sechsmal so viele Individuen als bis dahin verfügbar waren (Abb. 2; Liu u. a. 2021). Gleichzeitig begann auch eine Methodenentwicklung auf bioinformatischer Seite, um alte DNA-Daten auf Verwandtschaftsbeziehungen analysieren zu können. In der Folge werde ich eine solche Methode, »READ« *(Relationship Estimation from Ancient DNA)* vorstellen, die ich ab 2015 gemeinsam mit meinem damaligen Masterstudenten José Manuel Monroy Kuhn und meinem Kollegen Mattias Jakobsson entwickelt habe (Kuhn u. a. 2018).

»READ« vergleicht Individuen in Paaren (Abb. 3), zuerst wird das Genom in Abschnitte unterteilt, die dann einzeln verglichen werden. Für jeden dieser Abschnitte wird der Anteil der Positionen berechnet, an denen die beiden Individuen den identischen DNA-Zustand tragen *(P0)*. Über alle Abschnitte hinweg kann dann ein Mittelwert berechnet werden, der etwas über die Ähnlichkeit der beiden Individuen aussagt. Allerdings wäre dieser Wert an sich noch nicht nützlich, um den Grad der Verwandtschaft abzuschätzen, da je nach Population und Populationsgröße eine unterschiedliche genetische Diversität zu erwarten ist, was sich auch in der Anzahl der genetischen Unterschiede zwischen verwandten Individuen zeigt. Entscheidend ist die Anzahl der Übereinstimmungen, die auf einen gemeinsamen Vorfahren während der letzten Generationen zurückgeht. Die Ursache der Übereinstimmung zu ermitteln, ist allerdings nicht trivial (s. Beitrag Ringbauer in diesem Band). »READ« nimmt daher an, dass die Mehrheit der Individuenpaare im analysierten Datensatz nicht nah miteinander verwandt ist, man kann also die Anzahl deren genetischer Unterschiede als Referenzwert für Nicht-Verwandte aus der gleichen Population verwenden. Dies wird zur Normalisierung der Werte genutzt und auf Basis der normalisierten Werte kann dann eine Unterscheidung in nicht-verwandt, verwandt zum 1. oder 2. Grad, oder identisch/eineiiger Zwilling getroffen werden. Die Herangehensweise von »READ« ist der Methode aus (Kennett u. a. 2017) sehr ähnlich.

»READ« wurde auf simulierten Daten, also auf Daten mit bekannten Verwandtschaftsverhältnissen getestet. Verwandtschaften bis zum 2. Grad konnten erkannt werden, selbst wenn nur etwa 10 % des Genoms für jedes Individuum bekannt waren. Generell zeigte sich, dass die Fehlerraten, also sowohl nicht erkannte als auch falsch identifizierte Verwandtschaften, stark von der Datenmenge abhingen. Je weniger Daten, umso höher waren die Fehlerraten.

Erkenntnisse aus den ersten Anwendungen von »READ«

Wie bereits erwähnt, gab es ab 2015 einen extremen Anstieg an verfügbaren genomischen Daten von prähistorischen Populationen (vgl. Abb. 2; Liu u. a. 2021). Das beinhaltete auch eine Vielzahl von Individuen aus gleichen Ausgrabungsstätten, die man direkt auf genetische Verwandtschaft untersuchen konnte. Im Rahmen der Entwicklung von »READ« wurden die 230 prähistorischen Eurasier aus (Mathieson u. a. 2015) analysiert. Die Individuen in dem Datensatz kamen aus verschiedenen Teilen Eurasiens, datierend in das Mesolithikum, Neolithikum und die Bronzezeit. »READ« bestätigte neun bereits bekannte, im 1. Grad verwandte Paare von Individuen, wie es auch in den Original-

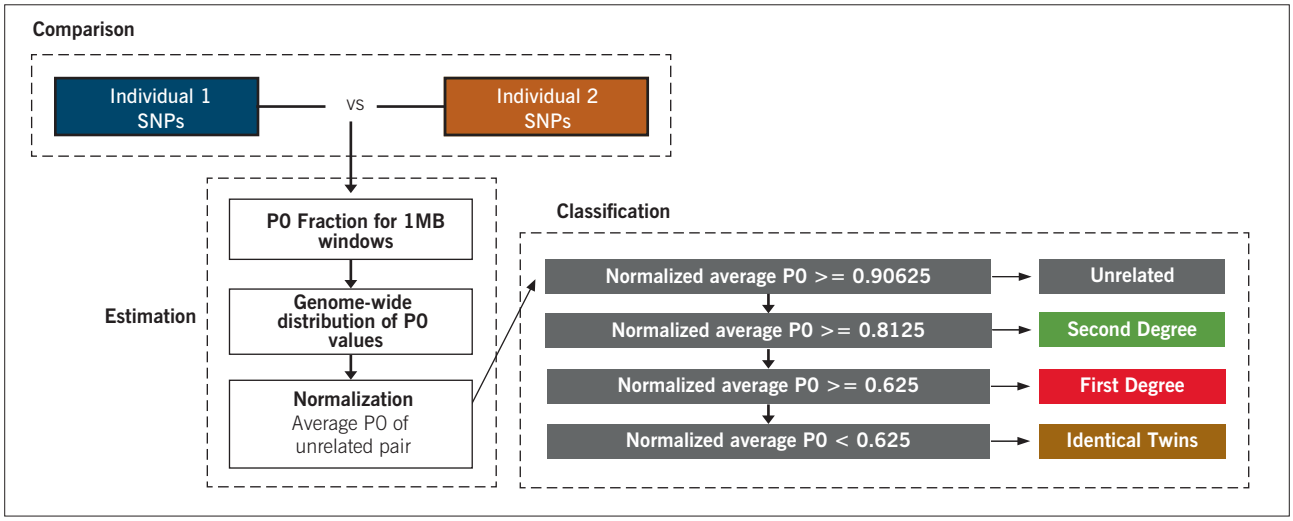


Abb. 3 Flussdiagramm zum Ablauf einer »READ«-Analyse zwischen zwei Individuen. Zuerst wird das Genom in Abschnitte von je einer Million Basen aufgeteilt und in jedem Abschnitt wird dann an überlappenden Einzelnukleotid-Polymorphismen (*Single Nucleotide Polymorphisms,* »SNPs«) der Anteil der Unterschiede ermittelt *(P0)*. Der Mittelwert über alle Abschnitte wird dann mit dem erwarteten Wert für den Vergleich zweier nicht verwandter Individuen aus der gleichen Population normalisiert. Nach der Normalisierung wird das Individuenpaar als nicht verwandt, verwandt 2. oder 1. Grades oder als identischer Zwilling klassifiziert.

Fig. 3 *Flow diagram on the process of a »READ«-analysis between two individuals. First the genome is divided into sections of each one million bases and in each section on overlapping* Single Nucleotide Polymorphisms *(»SNPs«) the percentage of differences is calculated* (P0). *The medium figure of all sections is then normalised with the expected figure for the comparison of two non-related individuals from the same population. After normalisation the pair of individuals is then classified as related, 2nd degree related or 1st degree related or as identical twins.*

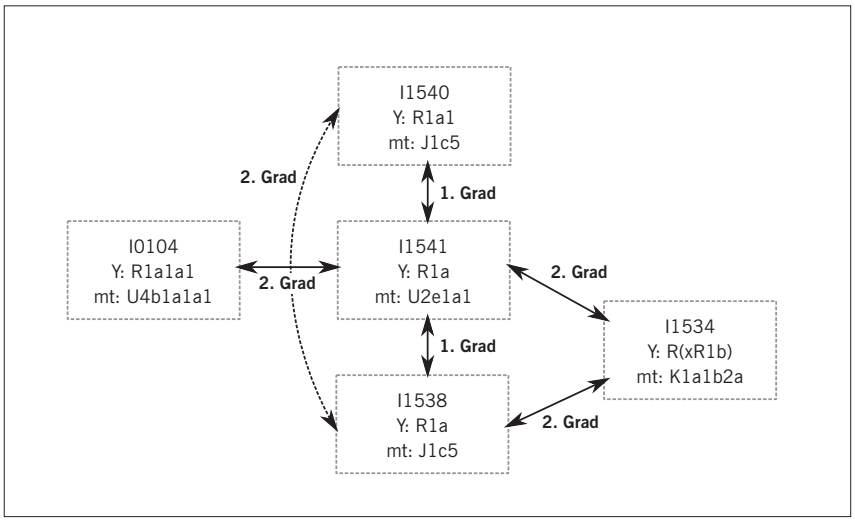


Abb. 4 Überblick über die ermittelten Verwandtschaftsbeziehungen zwischen fünf männlichen Skeletten in Esperstedt. Eine Verwandtschaftsbeziehung wurde nicht von »READ« gefunden (gestrichelte Linie). Für jedes Individuum sind auch die Haplotypen des Y-Chromosoms und des mitochondrialen Genoms angegeben. Da uns keine Informationen zum Alter zum Zeitpunkt des Todes oder direkte Radiokarbondatierungen der Individuen vorlagen, sind die Individuen nicht wie in einem Stammbaum angeordnet.

***Fig. 4** Overview of the determined relationships between five male skeletons from Esperstedt. One relationship was not found by »READ« (dotted line). For each individual the haplotypes of the Y-chromosome and of the mitochondrial genome is given. As we had no information about the age at death or direct radiocarbon dating of the individuals, they are not ordered as a family tree.*

publikationen zum Datensatz berichtet wurde (Allentoft u. a. 2015; Haak u. a. 2015; Mathieson u. a. 2015). Zusätzlich fand »READ« eine weitere Verwandtschaft 1. Grades und sechs Verwandtschaften 2. Grades. Alle als verwandt identifizierten Individuenpaare kamen jeweils von derselben Ausgrabungsstätte und hatten überlappende Radiokarbondaten (falls verfügbar).

Besonders stachen die schnurbandkeramischen Individuen aus Esperstedt heraus, die im Rahmen der Bauarbeiten zur Autobahn A 38 gefunden wurden (Leinthaler/Bogen 2006). Insgesamt lagen genomische Daten von 17 Individuen vor und es wurden sechs paarweise Verwandtschaftsbeziehungen gefunden. Fünf davon wurden um das männliche Individuum I1541 gefunden, welches offenbar mit vier weiteren männlichen Individuen verwandt war (Abb. 4). Mit dreien dieser Individuen teilte sich I1541 vermutlich auch das gleiche Y-Chromosom, was auf eine paternale Verwandtschaftslinie hinweist. I1541 wurde außerdem in einer Steinkiste etwa 700 m von den anderen Individuen begraben, was auf einen besonderen Status des Individuums hindeuten könnte (Leinthaler/Bogen 2006). Nur eine der beobachteten Verwandtschaftsbeziehungen in Esperstedt beinhaltete ein weibliches Individuum (2. Grades), was eine patrilineare Sozialstruktur für die Schnurbandkeramik in Esperstedt vermuten lässt (Haak u. a. 2008; Sjögren u. a. 2016). Bereits zu diesem frühen Zeitpunkt der Entwicklung von »READ« wurde dadurch klar, welches Potential die Verwandtschaftsanalyse hat. Gerade in Kombination mit weiteren Daten, zum Beispiel zu Art und Ort der Begrabung, Radiokarbondatierung oder Isotopenanalyse könnten diese Methoden wertvolle Erkenntnisse zur Sozialstruktur prähistorischer Gruppen aufzeigen.

Kollegen der Uppsala Universität veröffentlichten 2019 eine weitere Studie, die auch Verwandtschaftsanalyse mit anderen Datentypen kombinierte. Die Studie untersuchte megalithische Gräber mit einem speziellen Fokus auf Irland und Schweden (Sánchez-Quinto u. a. 2019). Generell gab es eine Tendenz, dass in den verschiedenen megalithischen Gräbern mehr genetisch männliche als weibliche Individuen begraben wurden[1]. Diese hatten auch gleiche oder sehr ähnliche Y-Chromosomen, was wiederum eine gewisse Patrilinearität vermuten ließ. Bemerkenswert war, dass in dem Datensatz auch Verwandtschaften zwischen verschiedenen Ausgrabungsstätten (Carrowmore und Primrose, Co. Sligo [Irland]) gefunden wurden, die etwa 2 km auseinander liegen.

Ausblick

Die Archäogenomik hat sich im letzten Jahrzehnt rapide entwickelt, weshalb mein Beitrag zu diesem Band auch einen gewissen wissenschaftshistorischen Aspekt hat. Innerhalb dieser relativ kurzen Zeit hat sich sowohl die Datenerzeugung als auch die Analysemethodik soweit entwickelt, dass Verwandtschaftsanalyse im großen Rahmen heute möglich ist und die Erstellung ganzer prähistorischer Stammbäume ermöglicht (s. andere Beiträge in diesem Band). Gleichzeitig wird die nächste Generation an Methoden für die Verwandtschaftsanalyse entwickelt, die so verfeinert sind, dass sie ermöglichen höhere Verwandtschaftsgrade als nur den 2. Grad festzustellen und die auch zur Unterscheidung zwischen Vollgeschwistern und Eltern/Kind fähig sind (s. Beiträge von Ringbauer und Popli in diesem Band; Popli u. a. 2022). Die Tagung zum 15. Mitteldeutschen Archäologentag und dieser Band zeigen, dass wir uns in einer aufregenden Entwicklung befinden. Die Archäogenomik und die Analyse biologischer Verwandtschaft sind dabei, sich zu vollwertigen Werkzeugen der Archäologie zu entwickeln durch die wir in den nächsten Jahren viele interessante Einblicke in das Leben prähistorischer Gruppen gewinnen werden (Racimo u. a. 2020).

1 Sánchez-Quinto u. a. 2019; Cassidy u. a. 2020; Fowler u. a. 2022; Elliott u. a. 2023.

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Abbildungsnachweis

1 Verf.
2 nach Liu u. a. 2021, Fig. 1
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Tab. 1 Verf.

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Detektion von langen identischen Haplotypen in alter DNA – Bestimmung von nahen und entfernten Verwandten

Harald Ringbauer

Summary

Detecting long indentical haplotypes in ancient DNA – Identifying close and distant relatives

Our new bioinformatic method called ancIBD makes it possible for the first time to find long identical DNA sequences between pairs of ancient DNA (aDNA). These so-called IBD segments (from »Identity by Descent«) must come from a common ancestor only a few generations away and are the direct genetic signals of biological relationship. Here we give an overview of the possible applications of ancIBD. For example, using IBD segments, it is possible to identify relatives up to the 6th degree – in contrast to the methods commonly used in aDNA, which only work up to the 3rd degree. Furthermore, the application of ancIBD makes it possible to measure genealogical connections between archaeological cultures within a few hundred years. We show the potential of our method by direct applications to published aDNA and find new biological connections and clusters in the West Eurasian Aeneolithic and the Bronze Age.

Zusammenfassung

Unsere neue bioinformatische Methode namens ancIBD ermöglicht es erstmals lange identische DNA-Sequenzen zwischen Paaren von alter DNA (aDNA) zu finden. Diese sogenannten IBD-Segmente (von »Identity by Descent«) müssen von gemeinsamen Vorfahren nur wenige Generationen entfernt stammen und sind die direkten genetischen Signale von biologischer Verwandtschaft. Wir geben hier eine Übersicht über die Anwendungsmöglichkeiten von ancIBD. So wird es etwa mittels IBD-Segmenten möglich, bis zum 6. Grad Verwandte nachzuweisen – im Gegensatz zu üblicherweise verwendeten Methoden in der aDNA, welche nur bis zum 3. Grad Verwandte identifizieren können. Darüber hinaus ermöglicht es die Anwendung von ancIBD, genealogische Zusammenhänge zwischen archäologischen Kulturen innerhalb weniger Jahrhunderte zu messen. Wir zeigen das Potential unserer Methode durch direkte Anwendungen auf publizierte aDNA und finden etwa neue Verbindungen und Cluster im westeurasischen Äneolithikum und in der Bronzezeit.

Dieser Artikel gibt einen Überblick über eine neue bioinformatische Methode zur Detektion langer identischer DNA-Segmente in der aDNA, also der DNA von Individuen, die vor hunderten oder tausenden Jahren gelebt haben. Die technischen Details und ersten Anwendungen beschreiben wir im Detail in einem Preprint (Ringbauer u. a. 2023). Der Fokus der vorliegenden Arbeit liegt auf einer Zusammenfassung der neuen Analyse-Möglichkeiten, die diese Methode eröffnet. Die Zielgruppe sind Leser, die an den direkten Anwendungen an aDNA interessiert sind.

Die Genome mancher Paare von Individuen teilen sich lange, beinahe identische DNA-Segmente. Diese werden oft »Identity-by-Descent« oder abgekürzt »IBD«, genannt, da sie von einem gemeinsamen Vorfahren vor nur wenigen Generationen ererbt worden sein müssen. Andernfalls wären die gemeinsamen Segmente schon zerstückelt worden, da bei jeder Generation die Genome zweier Eltern wie ein Mosaik vermischt werden. Nach nur wenigen Generationen bleiben keine langen IBD-Segmente mehr erhalten.

Daher sind lange IBD-Segmente *de facto* diagnostisch für biologische Verwandtschaften innerhalb weniger Generationen. So teilen sich nahe Verwandte eine große Anzahl von langen IBD-Segmenten (Abb. 1). Je weiter entfernt die Verwandtschaft, desto kürzer und weniger werden diese. Tatsächlich teilen sich Verwandte bis zum 6. Grad in den meisten Fällen mehrere lange IBD-Segmente, darüber hinaus werden nur einzelne oder meist gar keine IBD-Segmente geteilt – da so entfernte Verwandte sich in den meisten Fällen gar keine DNA mehr teilen. Hier meinen wir mit Grad, dass jede Verbindung zu einem Elternteil oder Kind je einen Grad addiert, während Geschwister ebenso einen Grad und Halbgeschwister zwei Grade addieren. Die genaue IBD-Segment-Verteilung ist stochastisch, da eine Rekombination zufällig entlang des Genoms passiert. Bis zum 3. Verwandtschaftsgrad treten aber klar definierte Cluster auf (vgl. Abb. 1b). Darüber hinaus kann man bis zum 6. Grad eindeutig Verwandtschaft anhand mehrerer langer IBD-Segmente nachweisen – die Cluster beginnen sich allerdings zu überlappen (vgl. Abb. 1c), oft ist für Verwandte 4–6. Grades daher keine eindeutige Bestimmung des exakten Grades möglich, und es verbleibt etwa ein Grad Unsicherheit. Das genetische Signal von IBD-Segmenten ist daher überaus spannend für Verwandtschaftsbestimmung und ebenso für demografische Analysen: Man erhält eine genetische Lupe für Verwandtschaften in der jüngeren Vergangenheit. Für moderne DNA-Daten existieren einige Methoden, diese IBD-Segmente zu bestimmen. Oft wurden diese Segmente benutzt, um mit diesem Signal wichtige demografische Parameter abzuschätzen. So wurde etwa dieses Signal verwendet, um genealogische Verbindungen aus ganz Europa über die letzten Jahrhunderte nachzuweisen und deren Intensität über diverse Zeitperioden zu ermitteln (Ralph/Coop 2013). Da geografisch weiter entfernte Gruppen immer weni-

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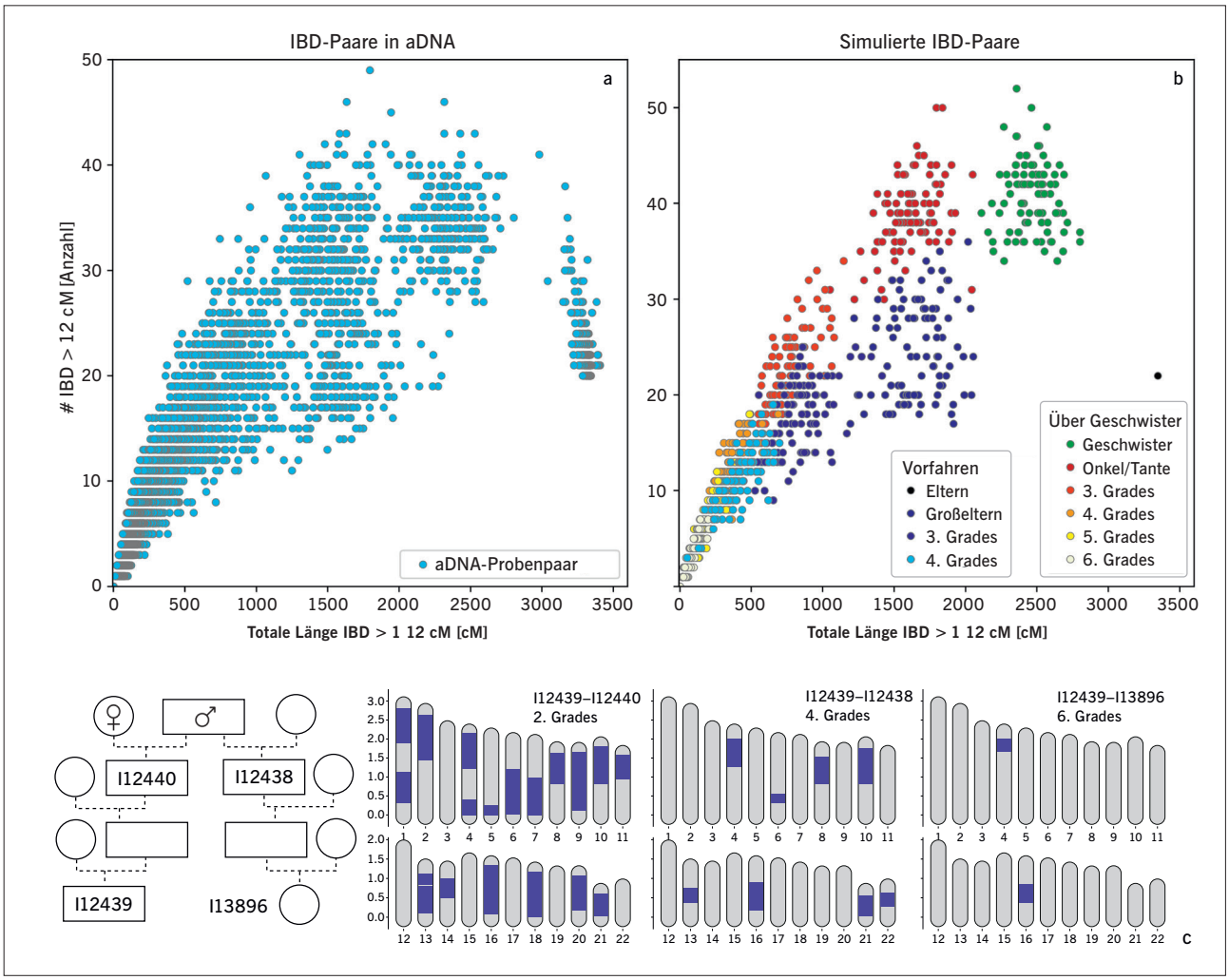


Abb. 1a–c Lange IBD-Segmente zwischen nahen Verwandten. a IBD-Segmente in einem großen aDNA-Datensatz analysiert mit ancIBD. Jeder Punkt stellt ein Paar von aDNA-Individuen dar. Es werden die Summe des Genoms und die Anzahl der langen IBD-Segmente (> 12 cM lang) dargestellt, je auf der X- und Y-Achse. Wir bemerken, dass viele Punkte 0 IBD-Segmente besitzen, aber hier nähere Verwandte der Fokus der Abbildung sind; b Simulierte IBD-Segmente zwischen verschiedenen Verwandten. Wie in a) aber wir haben die Verwandten simuliert (mit der Software PEDSIM, je 100 Replikate pro Verwandtschaftsgrad), und stellen die simulierten IBD-Segmente pro Paar dar; c Diese Abbildung stellt IBD-Segmente zwischen drei Paaren von nahen Verwandten dar. Wir zeigen Stellen im Genom (entlang der 22 Chromosome), an denen zwei Individuen IBD-Segmente besitzen (blaues Segment). Dieser Stammbaum ist Teil eines größeren rekonstruierten aDNA-Stammbaums aus Hazelton, Gloucestershire (England; Neolithikum) und wurde von C. Fowler u. a. (2022) publiziert.

Fig. 1a–c *Long IBD segments between close relatives. a IBD segments in a large aDNA dataset analyzed with ancIBD. Each point represents a pair of aDNA individuals. We plot the sum of the genome and the number of long IBD segments (> 12 cM long) on the x- and y-axes, respectively. We note that many points have 0 IBD segments, but here closer relatives are the focus of the figure; b Simulated IBD segments between different relatives. As in a) but we have simulated the distribution (using the software PEDSIM, 100 replicates per relatedness), and plot the true IBD segments; c This figure represents IBD segments between three pairs of close relatives. We show locations in the genome (along the 22 chromosomes) where two individuals have IBD segments (red segment). This family tree is part of a larger reconstructed aDNA family tree from Hazelton, Gloucestershire (England; Neolithic) and was compiled by C. Fowler et al. (2022) published.*

ger IBD-Segmente teilen, weil immer weniger gemeinsame Vorfahren vorhanden sind, sind IBD-Segmente auch ein ideales Signal um typische »Migrationsdistanzen« abzuschätzen (s. Ringbauer u. a. 2017). Da die »Hintergrundverwandtschaft« einer Population direkt mit der »effektiven« Populationsgröße zusammenhängt, wurden auch Analysemethoden entwickelt, die IBD-Segmente benutzen um Bevölkerungsgrößendynamiken über die letzten dutzenden Generationen abzuschätzen (vgl. Browning/Browning 2015).

Typische aDNA ist leider meist von weit geringerer Qualität und Sequenziertiefe als moderne DNA. Deswegen können moderne IBD-Detektionsmethoden nicht einfach direkt auf aDNA angewandt werden. So blieben bis jetzt typische aDNA-Verwandtschaftsbestimmungen nur bis zum maximal 3. Grad beschränkt, da nur durchschnittliche Statistiken über das ganze Genom gemittelt ausgenutzt werden können. Die Information von IBD-Segmenten, die oft nur einen kleinen Teil des Genoms ausmachen (vgl. Abb. 1c, zum 6. Grad Verwandte), geht darin unglücklicherweise komplett verloren.

Um das zu ändern und IBD-Segmente auch in alter DNA zu benutzen, haben wir eine neue bioinformatische Methode entwickelt, namens ancIBD, die im Detail in H. Ringbauer u. a. (2023) beschrieben ist und als Software-Paket veröffentlicht wurde. Kurz zusammengefasst gibt es zwei Schritte. Im ersten werden Lücken in der aDNA mithilfe moderner Genome gefüllt (sogenannte »Imputation«, wir benutzen die Software GLIMPSE; vgl. Rubinacci u. a. 2021). Im zweiten Schritt wenden wir dann ein von uns neu entwickeltes Hidden-Markov-

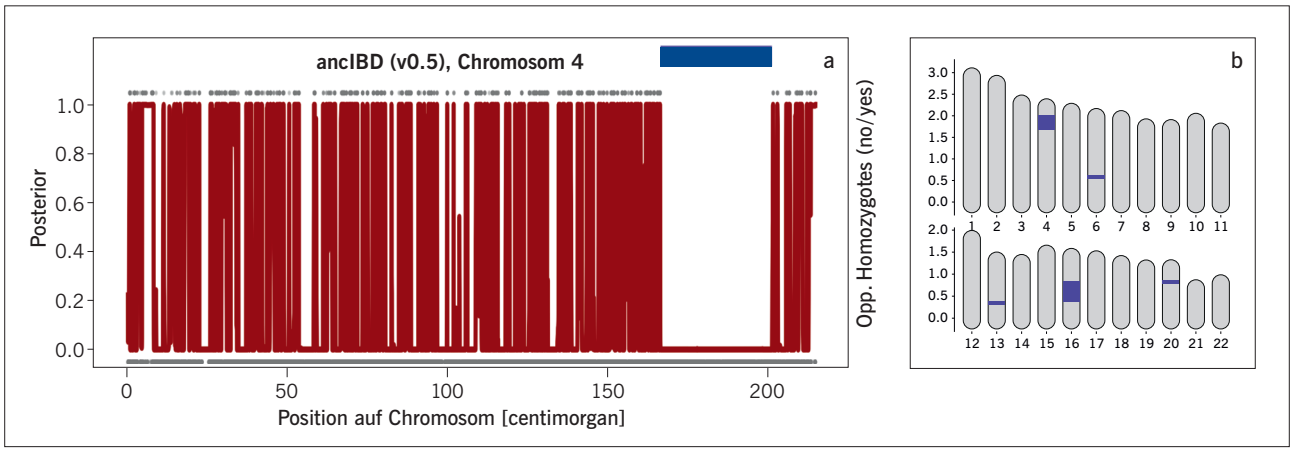


Abb. 2a–b Schematische Darstellung des Outputs von ancIBD. a Unser Algorithmus läuft entlang eines Chromosoms eines Paares von Individuen. Er findet lange genomische Sequenzen, wo beide Genome keine imputierten »Opposing Homozygotes« (graue Punkte oben) aufweisen. Basierend auf einem statistischen Posterior (rot) identifizieren wir diese Regionen als IBD-Segmente (blau); b Angewandt auf alle 22 Chromosome ergibt das alle IBD Segmente beider Individuen (blau).

Fig. 2a–b *Schematic representation of the output of ancIBD. a Our algorithm runs along a chromosome of a pair of individuals. It finds long genomic sequences where both genomes have no imputed opposing homozygotes (grey dots above). Based on a statistical posterior (red), we identify these regions as IBD segments (blue); b Applied to all 22 chromosomes, this then results in all IBD segments of both individuals (blue).*

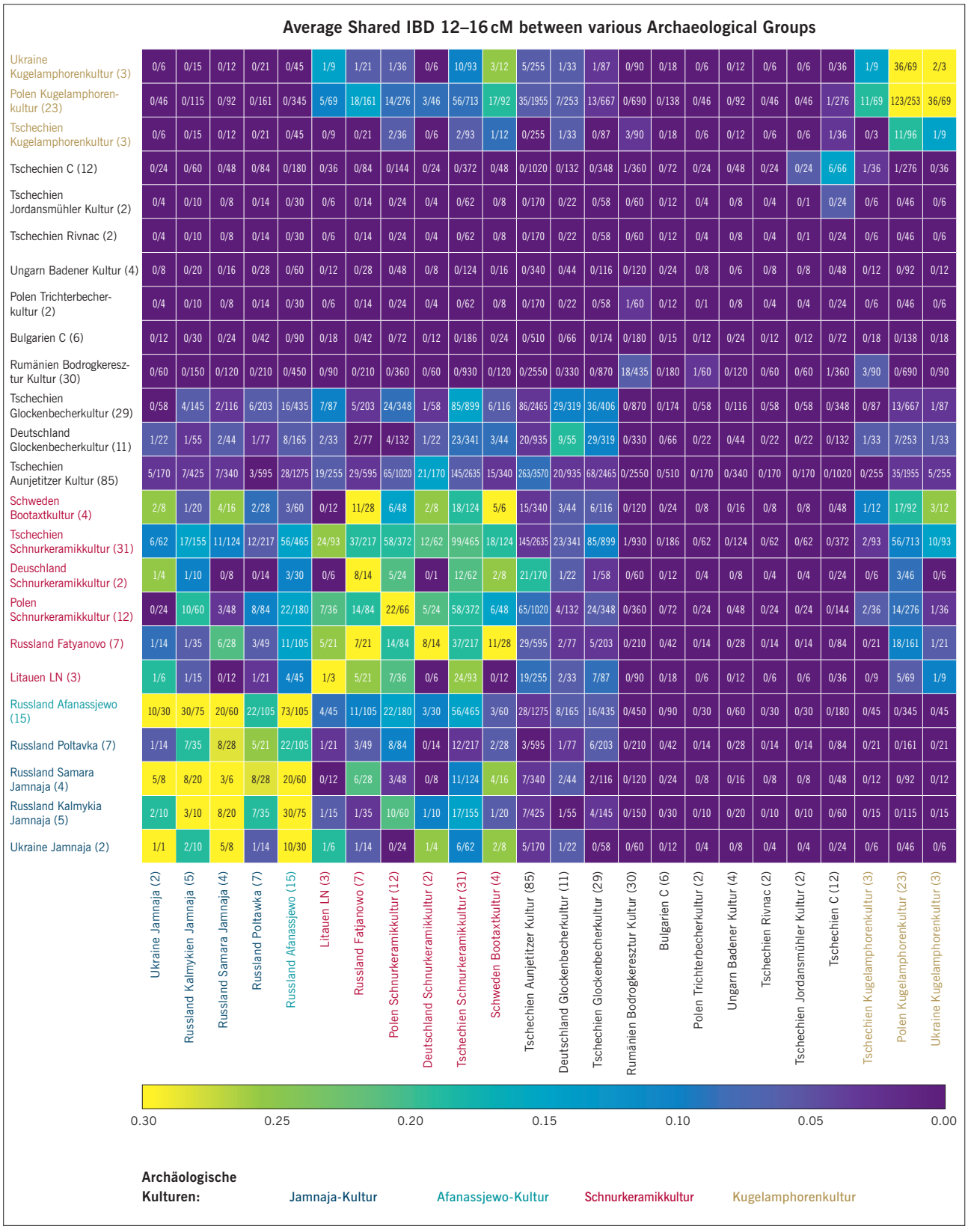
Model (HMM) an; dieses mathematische Model ist der Kern von ancIBD. Kurz zusammengefasst, suchen wir nach Stellen im Genom zweier Individuen, wo für lange Strecken keine sogenannten »Opposing Homozygotes« vorkommen, an denen die beiden Individuen je unterschiedliche Varianten homozygot (also doppelt) haben. Diese können in IBD-Segmenten nicht vorkommen, da immer zumindest ein Allel geteilt werden muss. Daher ist die Absenz von Opposing Homozygotes über lange genomische Strecken diagnostisch für IBD-Segmente (Abb. 2).

Da unsere Methode zentral auf Imputation beruht, funktioniert sie für aDNA der letzten 45 000 Jahre, mit der Ausnahme von Subsahara-Afrika wo genetische Diversität besteht die mit unserem derzeitigen Referenzpanel nur mangelhaft imputiert werden kann. Allerdings macht Imputation die Methode auch relativ datenhungrig und funktioniert daher nicht für schlecht erhaltene aDNA. Unsere Experimente haben aber gezeigt, dass etwa die Hälfte der publizierten »genomweiten« aDNA-Daten erfolgreich für IBD gescreent werden kann. Um mittlere und längere IBD-



Abb. 3a–b a Beispiel zweier Verwandter in alter DNA, die ancIBD gefunden hat, ca. 3300 v. Chr. Es handelt es sich um zwei unpublizierte Individuen, eines aus dem Kontext der Usatovokultur (Publikation in Vorbereitung; nach persönlicher Kommunikation mit D. Reich) und eines aus einem Kontext der Maikop-Kultur (Wang u. a. 2019). Mehrere lange IBD-Segmente zeigen eindeutig, dass es sich um einen biologischen nahen Verwandten – wahrscheinlich 5. Grades (4.–6. Grad möglich) – handelt. Das würde etwa zwei Individuen entsprechen, die zweite Cousins sind, also zwei gemeinsame Urgroßeltern haben; b Geographische Koordinaten der beiden Verwandten. Ein Individuum wurde im heutigen südlichen Moldawien bestattet und kann mit der Usatovo Kultur zugeordnet werden (Publikation in Vorbereitung; nach persönlicher Kommunikation mit D. Reich), das andere wurde im Nordkaukasus bestattet und kann mit der Maikop-Kultur assoziiert werden (Wang u. a. 2019). Die geographische Distanz zwischen den beiden Orten beträgt 1150 km (Luftlinie).

Fig. 3a–b *a Example of two relatives in ancient DNA c. 3300 BC found by ancIBD. They are two unpublished individuals, one from a Usatove Culture context (publication in preparation; D. Reich, personal communication) and one from a Maykop Culture context (Wang et al. 2019). Several long IBD segments clearly show that there is a biological close relative – probably 5th degree (4th–6th degree possible) – involved. This would roughly correspond to two individuals who are second cousins, i.e. where two great-grandparents are in common; b Geographic coordinates of the two relatives. One individual was buried in what is now southern Moldova and can be associated with the Usatovo culture (publication in preparation; D. Reich, personal communication), the other was buried in the North Caucasus and can be associated with the Maikop culture (Wang et al. 2019). The geographical distance between the two sites is 1150 km (linear distance).*



	Ukraine Kugelamphorenkultur (3)	Polen Kugelamphoren-kultur (23)	Tschechien Kugelamphorenkultur (3)	Tschechien C (12)	Tschechien Jordansmühler Kultur (2)	Tschechien Rivnac (2)	Ungarn Badener Kultur (4)	Polen Trichterbecher-kultur (2)	Bulgarien C (6)	Rumänien Bodrogkeresz-tur Kultur (30)	Tschechien Glockenbecherkultur (29)	Deutschland Glockenbecherkultur (11)	Tschechien Aunjetitzer Kultur (85)	Schweden Bootaxtkultur (4)	Tschechien Schnurkeramikkultur (31)	Deuschland Schnurkeramikkultur (2)	Polen Schnurkeramikkultur (12)	Russland Fatyanovo (7)	Litauen LN (3)	Russland Afanassjewo (15)	Russland Poltavka (7)	Russland Samara Jamnaja (4)	Russland Kalmykia Jamnaja (5)	Ukraine Jamnaja (2)
Ukraine Kugelamphorenkultur (3)	0/6	0/15	0/12	0/21	0/45	1/9	1/21	1/36	0/6	10/93	3/12	5/255	1/33	1/87	0/90	0/18	0/6	0/12	0/6	0/6	0/36	1/9	36/69	2/3
Polen Kugelamphoren-kultur (23)	0/46	0/115	0/92	0/161	0/345	5/69	18/161	14/276	3/46	56/713	17/92	35/1955	7/253	13/667	0/690	0/138	0/46	0/92	0/46	0/46	1/276	11/69	123/253	36/69
Tschechien Kugelamphorenkultur (3)	0/6	0/15	0/12	0/21	0/45	0/9	0/21	2/36	0/6	2/93	1/12	0/255	1/33	0/87	3/90	0/18	0/6	0/12	0/6	0/6	1/36	0/3	11/96	1/9
Tschechien C (12)	0/24	0/60	0/48	0/84	0/180	0/36	0/84	0/144	0/24	0/372	0/48	0/1020	0/132	0/348	1/360	0/72	0/24	0/48	0/24	0/24	6/66	1/36	1/276	0/36
Tschechien Jordansmühler Kultur (2)	0/4	0/10	0/8	0/14	0/30	0/6	0/14	0/24	0/4	0/62	0/8	0/170	0/22	0/58	0/60	0/12	0/4	0/8	0/4	0/1	0/24	0/6	0/46	0/6
Tschechien Rivnac (2)	0/4	0/10	0/8	0/14	0/30	0/6	0/14	0/24	0/4	0/62	0/8	0/170	0/22	0/58	0/60	0/12	0/4	0/8	0/4	0/1	0/24	0/6	0/46	0/6
Ungarn Badener Kultur (4)	0/8	0/20	0/16	0/28	0/60	0/12	0/28	0/48	0/8	0/124	0/16	0/340	0/44	0/116	0/120	0/24	0/8	0/6	0/8	0/8	0/48	0/12	0/92	0/12
Polen Trichterbecher-kultur (2)	0/4	0/10	0/8	0/14	0/30	0/6	0/14	0/24	0/4	0/62	0/8	0/170	0/22	0/58	1/60	0/12	0/1	0/8	0/4	0/4	0/24	0/6	0/46	0/6
Bulgarien C (6)	0/12	0/30	0/24	0/42	0/90	0/18	0/42	0/72	0/12	0/186	0/24	0/510	0/66	0/174	0/180	0/15	0/12	0/24	0/12	0/12	0/72	0/18	0/138	0/18
Rumänien Bodrogkeresz-tur Kultur (30)	0/60	0/150	0/120	0/210	0/450	0/90	0/210	0/360	0/60	0/930	0/120	0/2550	0/330	0/870	18/435	0/180	1/60	0/120	0/60	0/60	1/360	3/90	0/690	0/90
Tschechien Glockenbecherkultur (29)	0/58	4/145	2/116	6/203	16/435	7/87	5/203	24/348	1/58	85/899	6/116	86/2465	29/319	36/406	0/870	0/174	0/58	0/116	0/58	0/58	0/348	0/87	13/667	1/87
Deutschland Glockenbecherkultur (11)	1/22	1/55	2/44	1/77	8/165	2/33	2/77	4/132	1/22	23/341	3/44	20/935	9/55	29/319	0/330	0/66	0/22	0/44	0/22	0/22	0/132	1/33	7/253	1/33
Tschechien Aunjetitzer Kultur (85)	5/170	7/425	7/340	3/595	28/1275	19/255	29/595	65/1020	21/170	145/2635	15/340	263/3570	20/935	68/2465	0/2550	0/510	0/170	0/340	0/170	0/170	0/1020	0/255	35/1955	5/255
Schweden Bootaxtkultur (4)	2/8	1/20	4/16	2/28	3/60	0/12	11/28	6/48	2/8	18/124	5/6	15/340	3/44	6/116	0/120	0/24	0/8	0/16	0/8	0/8	0/48	1/12	17/92	3/12
Tschechien Schnurkeramikkultur (31)	6/62	17/155	11/124	12/217	56/465	24/93	37/217	58/372	12/62	99/465	18/124	145/2635	23/341	85/899	1/930	0/186	0/62	0/124	0/62	0/62	0/372	2/93	56/713	10/93
Deuschland Schnurkeramikkultur (2)	1/4	1/10	0/8	0/14	3/30	0/6	8/14	5/24	0/1	12/62	2/8	21/170	1/22	1/58	0/60	0/12	0/4	0/8	0/4	0/4	0/24	0/6	3/46	0/6
Polen Schnurkeramikkultur (12)	0/24	10/60	3/48	8/84	22/180	7/36	14/84	22/66	5/24	58/372	6/48	65/1020	4/132	24/348	0/360	0/72	0/24	0/48	0/24	0/24	0/144	2/36	14/276	1/36
Russland Fatyanovo (7)	1/14	1/35	6/28	3/49	11/105	5/21	7/21	14/84	8/14	37/217	11/28	29/595	2/77	5/203	0/210	0/42	0/14	0/28	0/14	0/14	0/84	0/21	18/161	1/21
Litauen LN (3)	1/6	1/15	0/12	1/21	4/45	1/3	5/21	7/36	0/6	24/93	0/12	19/255	2/33	7/87	0/90	0/18	0/6	0/12	0/6	0/6	0/36	0/9	5/69	1/9
Russland Afanassjewo (15)	10/30	30/75	20/60	22/105	73/105	4/45	11/105	22/180	3/30	56/465	3/60	28/1275	8/165	16/435	0/450	0/90	0/30	0/60	0/30	0/30	0/180	0/45	0/345	0/45
Russland Poltavka (7)	1/14	7/35	8/28	5/21	22/105	1/21	3/49	8/84	0/14	12/217	2/28	3/595	1/77	6/203	0/210	0/42	0/14	0/28	0/14	0/14	0/84	0/21	0/161	0/21
Russland Samara Jamnaja (4)	5/8	8/20	3/6	8/28	20/60	0/12	6/28	3/48	0/8	11/124	4/16	7/340	2/44	2/116	0/120	0/24	0/8	0/16	0/8	0/8	0/48	0/12	0/92	0/12
Russland Kalmykia Jamnaja (5)	2/10	3/10	8/20	7/35	30/75	1/15	1/35	10/60	1/10	17/155	1/20	7/425	1/55	4/145	0/150	0/30	0/10	0/20	0/10	0/10	0/60	0/15	0/115	0/15
Ukraine Jamnaja (2)	1/1	2/10	5/8	1/14	10/30	1/6	1/14	0/24	1/4	6/62	2/8	5/170	1/22	0/58	0/60	0/12	0/4	0/8	0/4	0/4	0/24	0/6	0/46	0/6

Segmente, die zumindest 12 cM lang sind, robust zu detektieren, benötigt es zumindest etwa 0,25 x durchschnittliches Coverage von Whole-Genome-Sequencing-Daten (WGS) und etwa 1 x Coverage auf 1240k oder Twist-Capture-Daten. Letztere Methode (Capture), wo gezielt aDNA von etwas mehr als einer Million Varianten angereichert wird, ist eine beliebte Technologie – der Großteil bisher produzierter alter Genome ist mittels Captures erstellt worden. Es ist eine besondere Stärke von ancIBD, auch diese Art von Daten gut verarbeiten zu können. Es sei auch gesagt, dass man ancIBD auch für schlechter erhaltene aDNA benutzen kann, der Anwender sollte sich allerdings bewusst sein, dass »False

Abb. 4 (linke Seite) Raten von langen IBD-Segmenten zwischen verschiedenen äneolithischen und bronzezeitlichen archäologischen Gruppen. Wir visualisieren Raten von IBD-Segmenten, die 12–16 cM lang sind, die wir in publizierter aDNA mittels ancIBD identifiziert haben. Jedes Quadrat stellt die Anzahl aller Paare dar, die solche IBD-Segmente aufweisen, dividiert durch alle möglichen Paare. Wenn überhaupt, hat nur ein relativ kleiner Anteil aller Paare zwischen zwei Gruppen ein langes IBD-Segment – aber diese durchschnittliche Rate, wie oft das passiert ist, ist höchst informativ. Sie ist diagnostisch für Verwandtschaften innerhalb weniger Jahrhunderte, IBD 12–16 cM müssen von gemeinsamen Vorfahren innerhalb etwa 20 Generationen stammen. Wir sehen, dass diverse Jamnajakulturen (und auch die zentralasiatische Afanassjewokultur – tausende Kilometer entfernt) einen klaren homogen Cluster bilden (beschriftet in Blau) und genauso verschiedene Schnurkeramische Kulturen, etwa die »Fatyanovo« aus Russland, »Schnurkeramik« aus verschiedenen zentralosteuropäischen Regionen und der Bootaxtkultur aus Schweden, einen weiteren Cluster bilden (beschriftet in Rot). Darüber hinaus sind zwischen den Jamnaja- und Schnurkeramik-Makro-Clustern etliche und konsistente Verbindungen ersichtlich. Interessanterweise hat die Schnurkeramikkultur zusätzlich generell starke Verbindungen zur Kugelamphorenkultur, einer Kultur aus dem Spätneolithikum, die noch keine substantielle Steppenabstammung aufweist. Da alle Schnurkeramikkulturen diese IBD-Verbindungen tragen, im klaren Gegensatz zu anderen spätneolithischen Kulturen noch ohne Steppenabstammung, impliziert dieses Signal, dass ein substantieller genetischer Beitrag der Kugelamphorenkultur »Mixture« sehr frühzeitig in der Entwicklung der Schnurkeramikkultur passiert sein muss und sich dann mit dieser Kultur ausgebreitet hat.

Fig. 4 (left page) *Rates of long IBD between different Eneolithic and Bronze Age archaeological groups. We visualize rates of IBD segments 12–16 cM long identified in published aDNA using ancIBD. Each square represents the number of all pairs that have such IBD segments; divided by all possible pairs. If anything, only a relatively small proportion of all pairs between two groups have a long IBD segment – but this average rate of how often this has happened is highly informative. It is diagnostic for kinship within a few hundred years, IBD 12–16 cM must come from a common ancestor within about 20 generations. We see that diverse Yamnaya Cultures (and also Central Asian Afanasievo Culture – thousands of kilometers away) form a clear homogeneous cluster (labeled in blue) – and also various Corded Ware cultures, e.g. »Fatyanovo« from Russia, »Corded Ware« from different Central-Eastern European regions, and »Battle Axe« from Sweden, form another cluster (labeled in red). In addition, several and consistent connections are evident between the Yamnaya and Corded Ware macro-clusters. Interestingly, Corded Ware generally has strong connections to Globular Amphora (Globular Amphora Culture), a Late Neolithic culture that still lacks substantial steppe ancestry. Since all Corded Ware cultures have these IBD connections, in clear contrast to other Late Neolithic cultures without steppe ancestry, this signal implies that substantial Globular Amphora »Mixture« must have happened very early in Corded Ware development, and then spread with that culture.*

Positives« (falsch positive IBD-Segmente) mehr werden, während die Power abfällt (manche Blöcke werden übersehen) – und zwar kontinuierlich je geringer das Coverage und je kürzer ein IBD-Segment ist. Längere Segmente sind generell einfacher zu finden als kürzere und funktionieren daher besser, auch bei weniger aDNA-Erhaltung, und je nach Fragestellungen sind auch höhere »False Positive Raten« vertretbar.

Die erste besonders spannende direkte Anwendung von ancIBD ist die Detektion von nahen Verwandten. Wir haben einen großen Datensatz von mehr als 10 000 publizierten und unpublizierten alten Genomen mit ancIBD durchleuchtet (vgl. Abb. 1a). Um nur ein aufschlussreiches Fallbeispiel herauszugreifen, haben wir nahe biologische Verwandte über mehr als 1200 km entfernt identifiziert (Abb. 3), beide stammen aus dem Äneolithikum, nördlich des Schwarzen Meeres, und sind etwas mehr als 5000 Jahre alt (basierend auf ^{14}C-Daten). Dabei handelt es sich höchstwahrscheinlich um Verwandte 5. Grades (auch 4.–6. Grad möglich), z. B. könnten es zweite Cousins (die sich zwei Urgroßeltern teilen), sein. Das zeigt eindeutig, dass zumindest ein Individuum innerhalb dieser Verwandtschaftskette mehrere hundert Kilometer zwischen Geburt und Bestattung zurückgelegt haben muss, was ein Fallbeispiel für hohe Mobilität im Äneolithikum ergibt.

Die zweite spannende Applikation sind sporadische einzelne IBD-Segmente. Ein einzelnes Paar mit einer solchen Verbindung hat noch wenig Aussagekraft, außer, dass eine biologische Verbindung in den letzten 5–50 Generationen gegeben sein muss (je länger das IBD-Segment, desto kürzer die obere Schranke). Wenn jedoch mehrere solcher Paare zwischen zwei Gruppen gegeben sind, kann man die generelle Häufigkeit solcher Verbindungen bestimmen – was, eingeteilt nach Längenkategorie, hochgradig aussagekräftig über die durchschnittliche biologische Verwandtschaft in jüngeren Zeiträumen ist. Um eine typische Anwendung zu skizzieren, haben wir wieder das westliche Eurasien im Äneolithikum und der Bronzezeit untersucht und Cluster sowie Verbindungen zwischen diversen archäologischen Kulturen identifiziert (Abb. 4; vgl. Legende).

Da das aDNA-Feld momentan rasant wächst und jedes Jahr beständig immer mehr alte Genome produziert, werden sogar noch quadratisch mehr Paare von Individuen analysierbar (in einem Datensatz der Größe n gibt es n*[n-1]/2 Paare). All diese Paare können nun mit unserer Methode ancIBD für lange IBD-Segmente gescreent werden. Damit werden rasant mehr Verwandte, auch über größere Distanzen, und Verbindungen zwischen vorgeschichtlichen Kulturen direkt messbar werden. Besonders spannend werden in naher Zukunft dann IBD-basierte demografische Analysen werden, die dann etwa Dynamiken von Populationsgrößen oder durchschnittliche individuelle Mobilität abschätzen können – auch in der Vorgeschichte. Wir hoffen daher, dass die hier vorgestellte Methode nur ein erster Schritt ist und gemeinsam mit neuen Proben und Verfahren das Fundament für eine neue Generation der aDNA-Erforschung eröffnet.

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Abbildungsnachweis

1 nach Ringbauer u. a. 2023, 15 Fig. 3
2 Verf.
3 a Verf.
b A. Swieder, LDA; Kartengrundlage: GTOPO30/SRTM mit freundl. Genehmigung des U. S. Geological Survey (USGS), der National Aeronautics and Space Administration (NASA) und der National Geospatial-Intelligence Agency (NGA), public domain; Gewässer erstellt mit Natural Earth; freie Vektor- und Raster-Kartendaten @ naturalearthdata.com
4 Verf.

Anschrift

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Estimating genetic relatedness from ancient DNA

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Zusammenfassung

Die Schätzung genetischer Verwandtschaft anhand von alter DNA

Die Analyse von genetischer Verwandtschaft prähistorischer Individuen kann einen Einblick in ihre soziale Hierarchie und Kultur ermöglichen. Dies ist auch wichtig für die nachgelagerten Genetikanalysen. Jedoch ist es schwierig, Verwandtschaft anhand alter DNA mit unterschiedlicher Herkunft wegen des niedrigen Sequenzumfangs und der Kontamination der DNA herzuleiten. Wir stellen hier KIN (Kinship INference) vor, eine Methode, die auf die Verwandtschaft eines Individuenpaares schlussfolgert, indem sie die Segmente, die identisch nach Abstammung sind und durch beide aufgewiesen werden, identifiziert. KIN kann unter der Verwendung von ≥ 0.05x Sequenzumfang akkurat Verwandte bis zum 3. Grad bestimmen und Eltern-Kind-Paare von Geschwistern differenzieren. Wir liefern zusätzliche Modelle, um DNA-Kontaminationen zu korrigieren sowie um Inzucht aufzudecken und so die Klassifikationsgenauigkeit zu verbessern.

Summary

Analyzing genetic relatedness of ancient individuals may provide a glimpse into their social hierarchy and culture, and is important for downstream genetic analyses. However, inferring relatedness from ancient DNA is a difficult problem due to low sequence coverage and DNA contamination from various sources. We present KIN (Kinship INference), a method that infers the relatedness of a pair of individuals by identifying the identical-by-descent segments that they share. KIN can accurately classify up to 3rd-degree relatives using ≥ 0.05x sequence coverage and can differentiate parent-child pairs from siblings. We provide additional models to correct for DNA contamination and detect inbreeding, improving classification accuracy.

READ (Monroy Kuhn et al. 2018) and lcMLkin (Lipatov et al. 2015) are the most commonly used software algorithms that infer relatedness with low-coverage ancient DNA data. READ is able to identify up to 2nd-degree relatives with a sequence coverage as low as 0.05x, but does not distinguish between siblings and parent-child pairs. In comparison, lcMLkin can also classify higher degrees of relatedness, while distinguishing between parent-child and siblings, but requires at least 2x sequence coverage to work efficiently (Tab. 1). There are additional challenges that these methods do not address, which affect relatedness estimates, such as DNA contamination from modern, living people and the presence of long runs of homozygosity (ROH) due to inbreeding.

Here, we present a method, KIN, which uses Hidden Markov Models (HMMs) to infer genetic relatedness between a pair of individuals. The method identifies the parts of the genomes that they share by descent and takes contamination and ROH in each individual into account (Popli et al. 2023). These shared parts of the genome are referred to as ›Identical By Descent‹ (IBD) segments. KIN consists of ten different HMMs, each modeling a different genomic distribution of IBD segments given a particular case of relatedness. We considered the following ten cases: Unrelated, 5th degree, 4th degree, 3rd degree, grandparent-grandchild, avuncular, half-siblings, parent-child, siblings, and identical. We then identify the best fitting case of relatedness for a pair of indi-

Feature	READ	lcMLkin	KIN
Coverage	≥ 0.05x	≥ 2x	≥ 0.05x
Degrees of relatedness	Up to 2nd degree	Up to 5th degree	Up to 3rd degree
Differentiation between siblings and parent-child	No	Yes	Yes
Accounts for ROH (runs of homozygosity)	No	No	Yes
Contamination Correction	No	No	Yes

Tab. 1 Comparison of READ, lcMLkin and KIN.

Tab. 1 *Vergleich von READ, lcMLkin und KIN.*

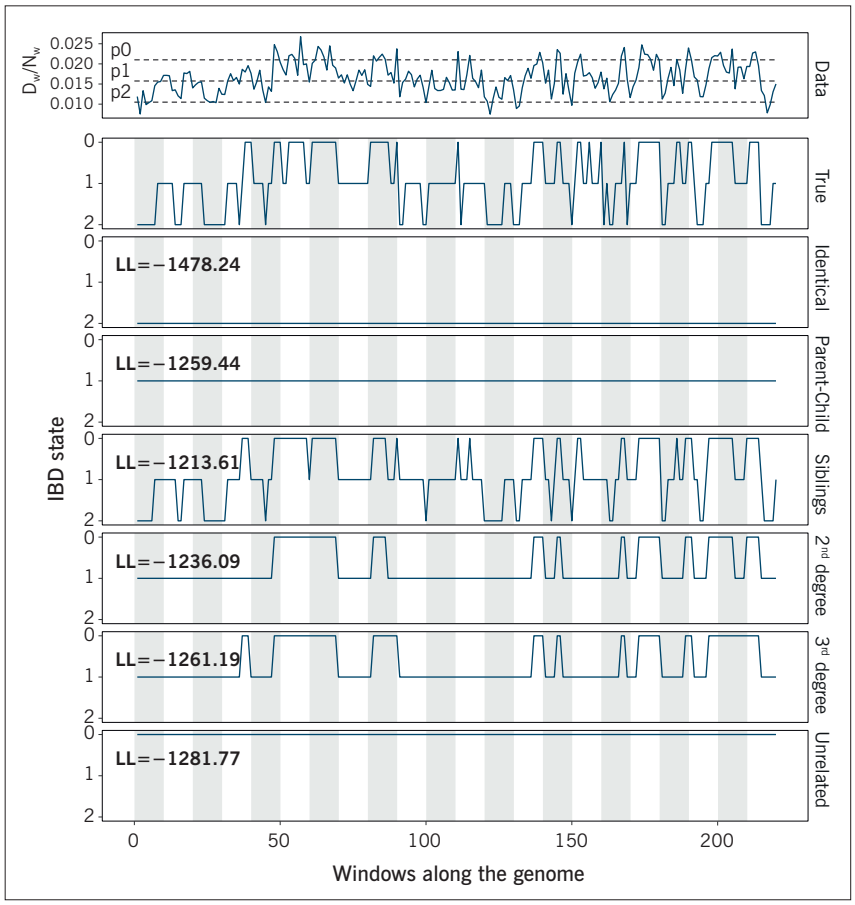


Fig. 1 Comparison of pairwise difference data and inferred IBD fragments (Identical By Descent). The top panel shows the proportion of differences in each window along the genome for a pair of simulated siblings. Dashed lines represent p_0, p_1 and p_2 estimates. The second panel shows the true IBD state for each window. The remaining panels show the IBD states predicted by particular relatedness models. The log-likelihood value for each model is shown in the upper left corner of the panel. Light and shaded backgrounds represent distinct chromosomes.

Abb. 1 *Vergleich der paarweisen unterschiedlichen Daten und daraus geschlussfolgerter IBD-Fragmente (identisch nach Abstammung). Das obere Feld zeigt die Proportion von Unterschieden für ein Paar simulierter Geschwister in jedem Fenster entlang der Genome. Gestrichelte Linien stellen p_0-, p_1- und p_2-Schätzungen dar. Das zweite Feld gibt den wahren IBD-Status für jedes Fenster wieder. Die verbleibenden Felder zeigen den IBD-Status, der durch spezifische Verwandtschaftsmodelle vorhergesagt wird. Der logarithmische Wahrscheinlichkeitswert für jedes Model wird in der oberen linken Ecke des Feldes gezeigt. Helle und schattierte Hintergründe geben eindeutige Chromosome an.*

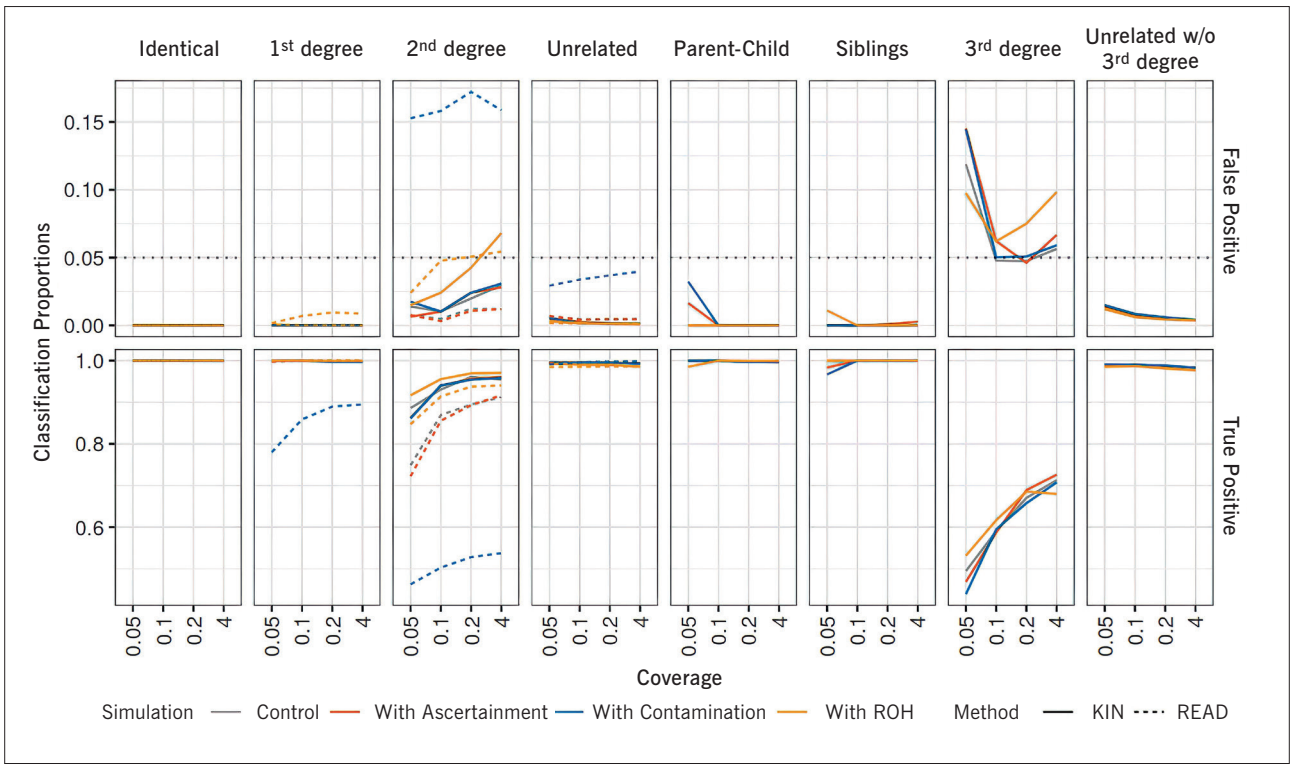


Fig. 2 Comparison of KIN with READ using simulations with different coverages and different cases of ascertainment, contamination, and ROH (runs of homozygosity). ›Unrelated‹ label here refers to KIN performance results when all Unrelated, 5th degree, 4th degree, 3rd degree pairs are labelled as Unrelated (for fair comparison with READ). ›Unrelated w/o 3rd degree‹ refers to the performance results when 3rd degree is classified separately from the unrelated individuals.

Abb. 2 *Vergleich von KIN und READ unter der Verwendung von Simulationen mit verschiedenen Erfassungsbereichen und verschiedenen Fällen von Erhebung, Kontamination und ROH (Homozygotiestrukturen). Die Bezeichnung ›Unrelated‹ beschreibt die KIN-Funktionsergebnisse, wenn alle nicht verwandt sind. Zudem werden im 5., 4. und 3. Grad Verwandte und Paare, die nicht verwandt sind (zum fairen Vergleich mit READ), aufgeführt. ›Unrelated w/o 3rd degree‹ beschreibt die Funktionsergebnisse, wenn sie separat von den nicht verwandten Individuen klassifiziert werden.*

viduals by comparing the likelihood of all the models. We noticed that KIN does not have the power to differentiate relatedness above the 3rd degree, particularly for low coverage data, so we classify these as unrelated. Similarly, we merge grandparent-grandchild, avuncular, half-siblings as 2nddegree relatives.

We evaluate the performance of KIN using simulations, and compare it to that of READ (Fig. 2). We show that both the methods perform well in control simulations (with no ROH and contamination), except in the case of 2nd-degree relatives, for which KIN has more power than READ. In simulations with contamination, we see that READ's performance is greatly affected, while KIN's performance is similar to the control. In simulations with ROH, we find that the true- and false-positive rates increase for both KIN and READ, although READ shows slightly more false positives, particularly for 2nd degree relatives with low coverage data. This effect is perhaps because ROH makes closely related individuals seem closer than they actually are. We find that both methods are not sensitive to ascertainment bias in simulations.

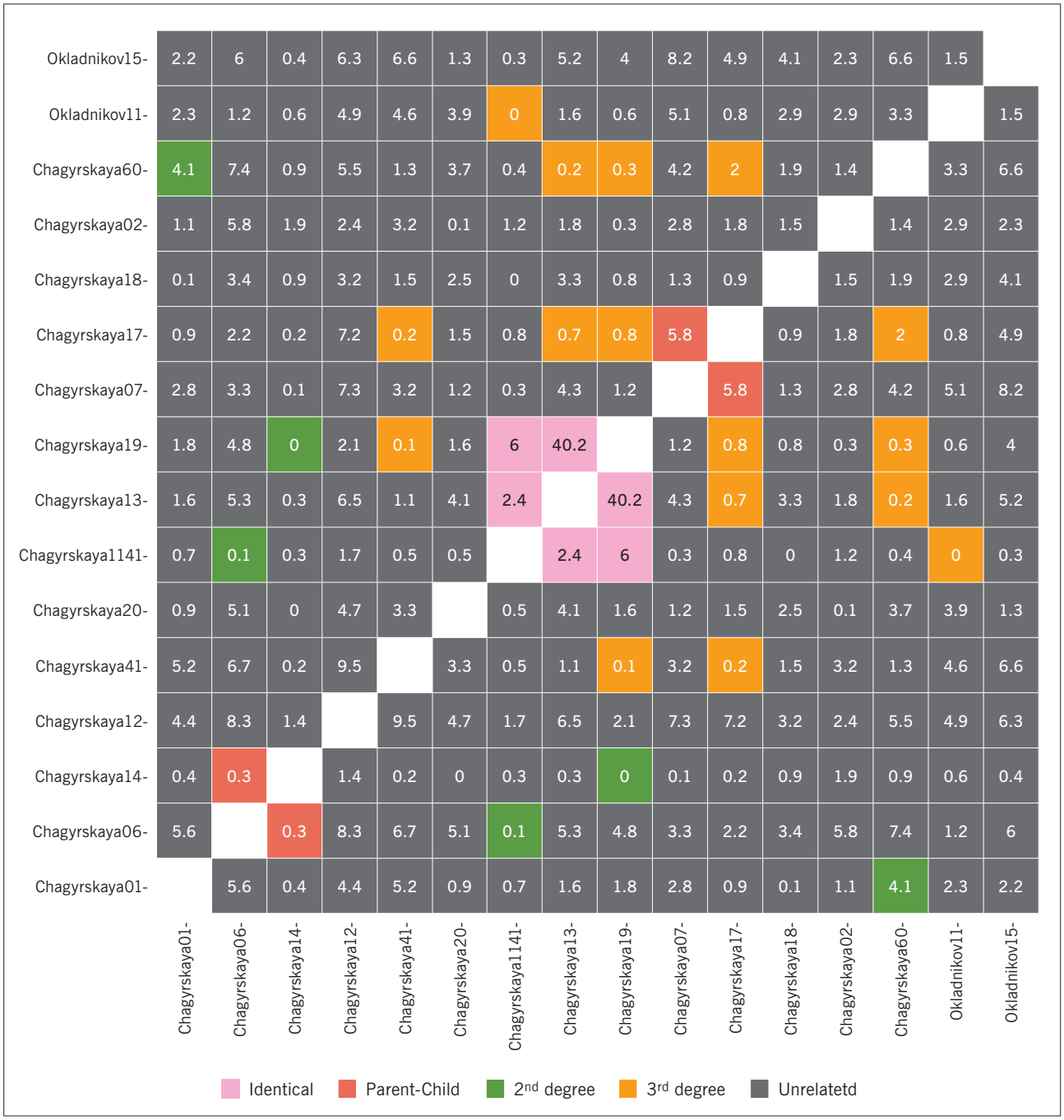


Fig. 3 Application of KIN to Neandertal remains from Chagyrskaya and Okladnikov caves, both Altai Krai (Russia). The color of a square represents the relatedness, while the number within denotes log likelihood ratio (ΔLL) between the two maximum likelihood models.

Abb. 3 *Die Anwendung von KIN an Neandertalerüberresten aus den Chagyrskaya- und Okladnikov-Höhlen, beide Region Altai (Russland). Die Farbe eines Quadrats repräsentiert die Verwandtschaft, während die Ziffer darin das logarithmische Wahrscheinlichkeitsverhältnis (ΔLL) zwischen den zwei größten Wahrscheinlichkeitsmodellen bezeichnet.*

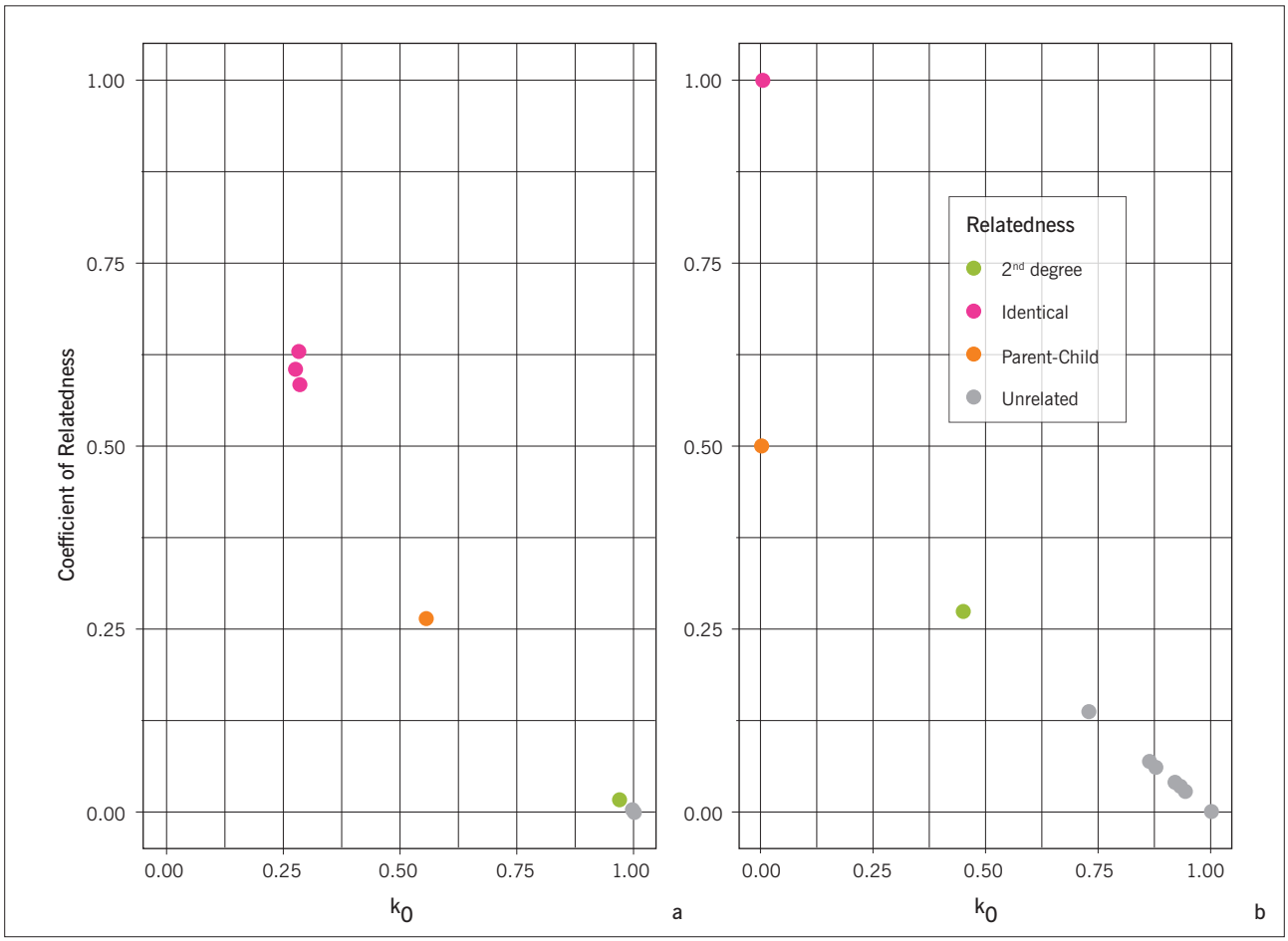


Fig. 4a–b Comparison of IBD states estimated for Chagyrskaya specimens using (a) lcMLkin and (b) KIN. Each plot shows the relatedness coefficient (calculated as k_2+k_1/2) on the y-axis plotted against k_0 (proportion of the genome with no chromosomes shared). The relatedness shown with different colors is estimated with both READ and KIN.

Abb. 4a–b *Vergleich von IBD-Zuständen, geschätzt für die Chagyrskaya-Proben unter der Verwendung von (a) lcMLkin und (b) KIN. Jeder Punkt zeigt den Verwandtschaftskoeffizienten (berechnet als k_2+k_1/2), auf der Y-Achse eingetragen gegen k_0 (Proportion der Genome ohne geteilte Chromosome). Die Verwandtschaft, die durch verschiedene Farben ausgedrückt ist, ist sowohl mit READ als auch mit KIN geschätzt.*

We apply KIN to ancient DNA data from 16 Neandertal specimens from Chagyrskaya and Okladnikov caves, Russia. This data was generated by targeted enrichment for 713 000 positions across the genome (Kolobova et al. 2020; Skov et al. 2022). The coverage ranged from 0.01x to 12.34x, and several libraries showed evidence of contamination. We find long ROH in most individuals, and are able to detect specimens that come from the same individual, as well as from three pairs of related individuals, a parent-child pair, and 2nd- and 3rd-degree relatives (Fig. 3). Our results match that of READ, except that READ does not identify the 3rd-degree relatives and does not distinguish the parent-child pair from siblings.

We next compare the relatedness coefficient (r) and the proportion of the genome in the unrelated state (k_0) obtained from KIN to those from lcMLkin for all pairs for whom the results of READ and KIN matches. We find that lcMLkin identifies four different clusters corresponding to different relatedness cases (identical, parent–child, 2nd degree and unrelated). However, the observed values for these clusters strongly deviates from expected, suggesting that the results of lcMLkin are perhaps affected by the low coverage and the presence of ROH. For example, specimens from the same individual are expected to be at $r = 1$ and $k_0 = 0$, but are observed at $r \approx 0.6$ and $k_0 \approx 0.3$ for lcMLkin (Fig. 4).

Relatedness results from KIN are in the form of a table that shows, for each pair, the most likely and second best models, along with the confidence level represented by the log likelihood ratio. This tabular format makes it easy to automatize the processing of KIN results for large datasets. We also provide a python package (KINgaroo) to make KIN input files from bam files, while optionally estimating ROH and adjusting for the contamination estimates. KINgaroo and KIN are available along with their documentation on github: <https://github.com/DivyaratanPopli/Kinship_Inference> (21.03.2023).

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1–4 D. Popli

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Calibration of ^{14}C dates using biological kinship

Ronny Friedrich, Ken Massy, and Philipp W. Stockhammer

Zusammenfassung

Die Kalibrierung von ^{14}C-Datierungen unter Verwendung von biologischer Verwandtschaft

Die Bestimmung des absoluten Alters mithilfe der ^{14}C-Datierung ist ein unverzichtbarer Bestandteil der Archäologie geworden. Als eine der wichtigsten physikalischen Datierungsmethoden wird sie ständig verbessert, sodass heutige AMS-Geräte (Beschleunigermassenspektrometer) weitaus präzisere Datierungen liefern als in der Vergangenheit. Die Präzision einer Datierung ist heute hauptsächlich durch die Kalibrierung eingeschränkt, d. h. die Übersetzung eines ^{14}C-Alters in ein Kalenderdatum. Daher kann ein höchst präzises ^{14}C-Alter wegen der Struktur der relevanten Kalibrierungskurve manchmal mehrere, weitreichende Datierungsspannbreiten hervorbringen. Dennoch können in Fällen, bei denen relative chronologische Information mit ^{14}C-Altersangaben verknüpft werden – wie etwa bei der Datierung von Individuen mit bekannten Familienverwandtschaften – diese relativchronologischen Hinweise zu präziseren Kalibrierungen und ^{14}C-Datierungen führen. In allen diesen Fällen, wo eine bayesianische Modellierung durchgeführt wird, sind die modellierten ^{14}C-Datierungen weitaus genauer als die unkontextualisierten. Eine Verkürzung der kalibrierten Datierungspannen um 40–70 % kann bei gleichzeitiger Beibehaltung ihrer Genauigkeit erreicht werden.

Summary

The determination of absolute dates with the help of ^{14}C dating has become an indispensable part of archaeology. As one of the most important physical dating methods, it is constantly being improved, so that today's modern AMS devices (Accelerator Mass Spectrometer) provide significantly more precise analytical data than in the past. The precision of a date today is mainly limited by the calibration, i.e., the translation of a ^{14}C age into a calendar date. Thus, a single highly precise ^{14}C age can sometimes yield several broad dating spans due to the structure of the relevant calibration curve. However, in cases where relative chronological information can be linked with ^{14}C ages – such as dating individuals with known family relationships – these relative chronological clues can lead to more precise calibrations and ^{14}C dates. In all cases where Bayesian modeling is performed, the modeled ^{14}C dates are significantly more constrained than the individual uncontextualised dates. A narrowing of the calibrated date ranges by 40–70 % can be achieved, while still maintaining accuracy.

Introduction

Radiocarbon dating was conceived and introduced in the 1940s as the first absolute dating technique and has revolutionised our understanding of the past when applied in archaeological research. In many other fields of research such as geochemistry, solar science and climate research, this methodology has also pushed our understanding of system earth to new limits. Since its introduction, radiocarbon dating has been continually developed. Sample preparation procedures have been developed in many laboratories to such an extent that nowadays basically all types of samples of interest for archaeologists can be analysed. The analytical techniques used for radiocarbon dating have virtually entirely moved over from the use of counting techniques to accelerator mass spectrometers (AMS), which deliver very high precision on very small sample sizes of a few grams for bone samples or milligrams for other materials. However, despite this progress, radiocarbon dating has limitations that are not related solely to analytical and laboratory aspects. The main limitation, which is inherent to radiocarbon dating, is the radiocarbon calibration.

The result of a ^{14}C analysis is a conventional radiocarbon age. Instead of providing the researchers with pure ratios of the carbon isotopes ^{14}C, ^{12}C and ^{13}C, which is essentially the outcome of the analysis, conventional radiocarbon ages are calculated and reported by all laboratories. The word »conventional« emphasizes the fact that those radiocarbon ages are calculated using certain conventions that allow us to use such dates, no matter which laboratory has produced them or when they were produced. However, some of these conventions are not fulfilled in nature so that a conventional radiocarbon age does not represent a true calendar date. In order to provide calendar dates, radiocarbon ages must be calibrated, for example using materials such as wood samples, which can be dated with alternative methods such as dendrochronology and thus yield ^{14}C ages. As early as the 1960s the first datasets were compiled of those pairs of

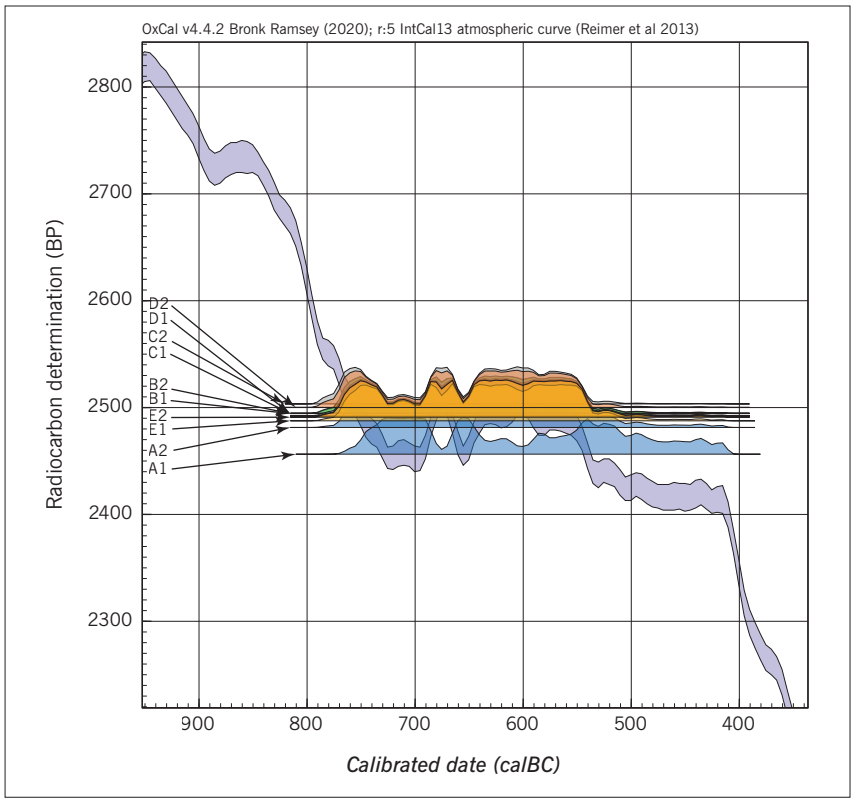


Fig. 1 A plateau-rich calibration curve (Hallstatt plateau). The calibrated ^{14}C dates of all individuals overlap to a degree where no distinction is possible. The labels on the left marked with arrows indicate the individuals as shown in Fig. 6.

Abb. 1 *Eine plateaureiche Kalibrierungskurve (Hallstattplateau). Die kalibrierten ^{14}C-Daten aller Individuen überlappen sich so weit, dass zwischen ihnen keine Unterscheidung möglich ist. Die Beschriftungen auf der linken Seite mit hinzugefügten Pfeilen bezeichnen die Individuen. Vgl. hierzu Abb. 6.*

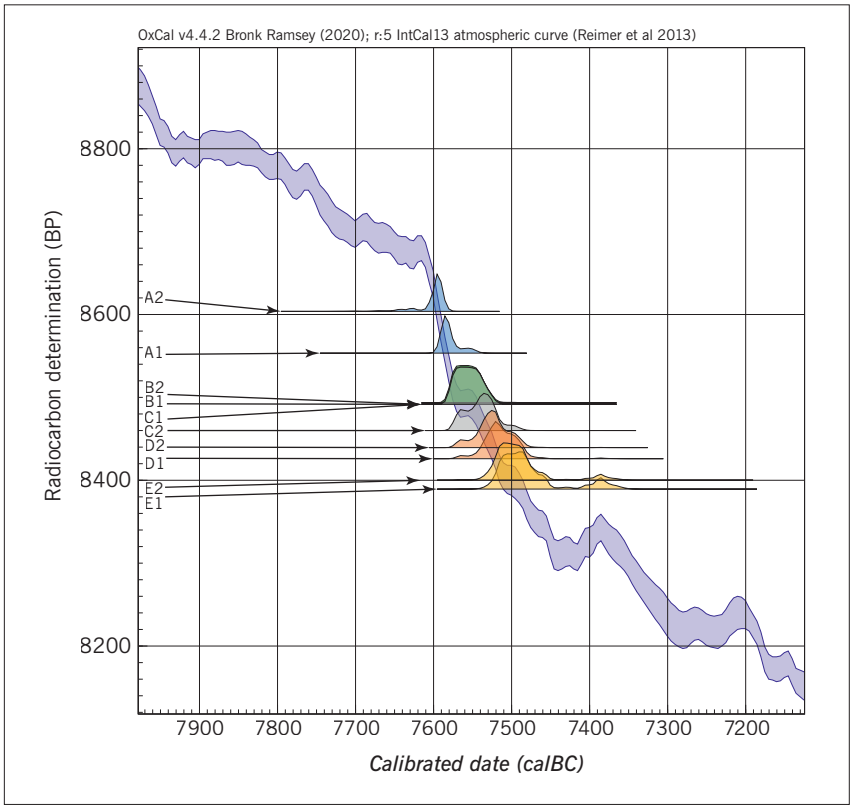


Fig. 2 A steep section of the calibration curve. The calibrated ^{14}C dates of the individuals are much narrower and overlap to a considerably lesser degree compared to a plateau-rich curve.

Abb. 2 *Ein steiler Abschnitt der Kalibrierungskurve. Die kalibrierten ^{14}C-Datierungen der Individuen liegen enger beieinander und überlappen sich weit weniger im Vergleich zu einer plateaureichen Kurve.*

known calendar dates to their conventional radiocarbon ages. Use of such large datasets allows us to assign a measured conventional radiocarbon age to a true calendar date. The most recent iteration of such a dataset applicable to samples from the whole northern hemisphere is the international calibration curve IntCal20 (Reimer et al. 2020), which covers a time period of the last 55 000 years.

The calibration curves shown in Fig. 1–4 show past changes in the ^{14}C content of the atmosphere, which are driven by many factors such as solar activity or changes in the earth's magnetic field. These variations cause the ^{14}C content of the atmosphere to fluctuate over time, which is expressed in the calibration curve as wiggles or fluctuations. A simple one-to-one relationship between a measured

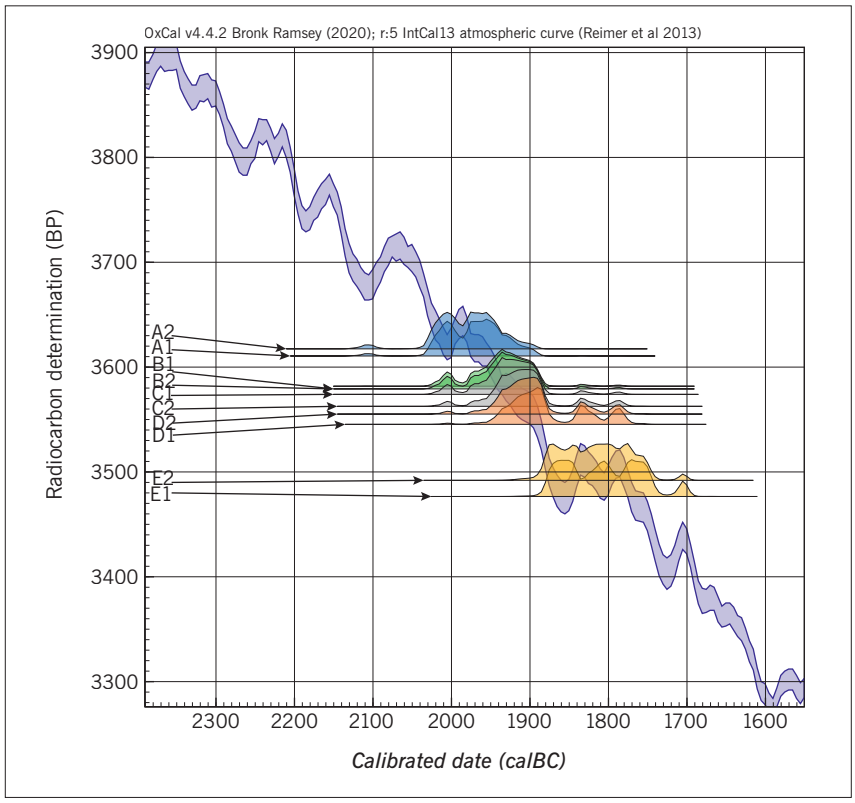


Fig. 3 A section of the calibration curve that contains some plateaus but also has steep sections. This reflects a combination of the cases with a plateau-rich or steep calibration curve. While generations 1 and 5 could be distinguished by their ^{14}C dates, the dating ranges of generations in between show considerable overlap.

Abb. 3 *Ein Abschnitt der Kalibrierungskurve, der einige Plateaus aufweist, aber auch über einen steilen Abschnitt verfügt. Dies spiegelt eine Kombination von den Fällen wider, die eine plateaureiche oder eine steile Kalibrierungskurve besitzen. Während Generation 1 und 5 anhand ihrer ^{14}C-Datierungen unterschieden werden konnten, überlappen sich die Datierungsspannen der dazwischen liegenden Generationen deutlich.*

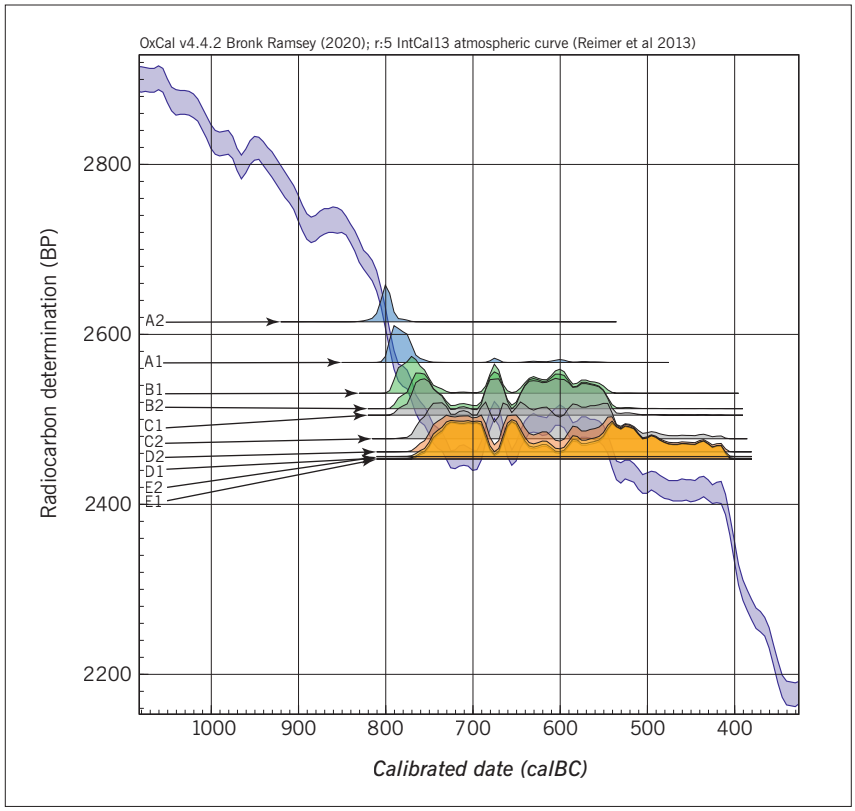


Fig. 4 A plateau-rich calibration curve (Hallstatt plateau). Compared to Fig. 1, one of the individuals (A2) is located on the steep section of the curve, right before the plateau, while all other individuals are located inside the plateau.

Abb. 4 *Eine plateaureiche Kalibrierungskurve (Hallstattplateau). Im Vergleich zu Abb. 1 ist ein Individuum (A2) auf einem steilen Abschnitt der Kurve kurz vor dem Plateau platziert, während alle anderen Individuen sich innerhalb des Plateaus befinden.*

conventional ^{14}C age to one calendar date is not given. Several calendar dates can have the same ^{14}C age. Conversely, a measured ^{14}C age typically results in multiple possible calendar dates (ranges of dates) depending on the shape of the calibration curve. A very flat section of the curve (plateau) would result in calibrated ^{14}C dates that span a very broad range (e.g., Fig. 1).

Figure 5 shows the precision of calibrated ^{14}C dates that can be achieved when calibrating conventional ^{14}C ages with an analytical precision of 20 years – a value that is achievable in laboratories today for samples spanning the past few thousand years.

Even though the measured ^{14}C age is relatively precise, the calibrated ranges can span several hundreds of years when plateaus are present in the calibration curve.

Methods and Discussion

How can we overcome this limitation and still achieve precise (and accurate) ^{14}C dates, even though the calibration curve would not provide the necessary means? In the early 1760s T. Bayes (1701–1761) formulated the Bayes' theorem, which is an approach where existing knowledge about a parameter is updated with new information from observed data. When applied to ^{14}C dating, any chronological information (of relative or absolute nature) can be combined with conventional ^{14}C ages in order to constrain better the calibrated dates. As a simple example, archaeologists may provide stratigraphic information about two subsequent burials in superposition. Even though ^{14}C dates might not be able to resolve the actual dates of the buried individuals, due to the shape of the calibration curve, the stratigraphic information shows that the individuals must have been buried one after the other. Thus, this information can be used to constrain the calibrated ages by Bayesian modeling. However, gravepit intersections are not observed very often, so that other non-stratigraphic information is needed.

The origin of the relative chronological information used for Bayesian modeling is not limited to archeological information. Today, geneticists are able to uncover family relationships in burial sites by ancient DNA analysis (e.g., Mittnik et al. 2019). These pedigrees offer a rich set of relative chronological information in the same way as stratigraphic data, albeit not in space, but by forming a »temporal stratigraphy«.

What Bayesian modeling can offer, e.g., the effects of the shape of the calibration curve when modeling, and what information is most effective in order to constrain the calibrated ^{14}C dates, has been discussed in detail in Massy et al. (2022). Here, we will give an overview about the topic and focus on the main findings of the article. While modeling of actual pedigrees is also discussed by Massy et al. (2022), here we focus specifically on the modeling of artificial pedigrees.

In order to test the applicability and effectiveness of combining pedigree information with radiocarbon dates, artificial pedigrees were constructed as shown in Fig. 6. Five generations with two individuals each were used, where the years-of-birth (YoB) and ages-at-death (AaD) are prescribed. Hence, the years-of-death (YoD) are also known.

Those prescribed pedigrees with their YoBs and AaDs (hence, YoDs) are in many ways simplified versions of the ones that archaeologists and geneticists find in nature. However, the main advantages of Bayesian modeling can be tested more clearly and transparently. The scaffold of a family tree was then assigned various sets of YoBs covering time periods in which very different shapes of the calibration curve are present – a section where a plateau-rich curve (the »Hallstatt plateau«; Fig. 1), or a steep calibration curve

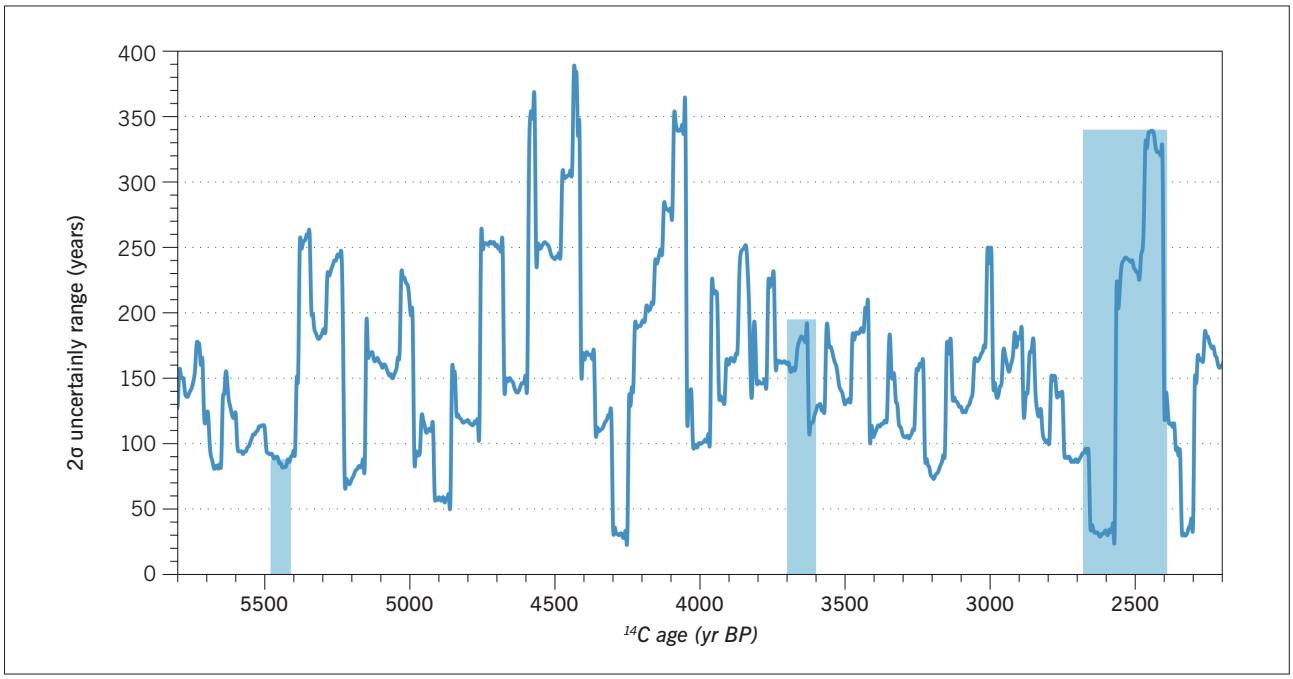


Fig. 5 Age uncertainty ranges (2σ) of calibrated ^{14}C dates depending on the measured conventional ^{14}C age (assuming 20 years of analytical precision). When a conventional ^{14}C age falls within a plateau-rich calibration curve (e.g., around 2450 or 4450 BP), the calibration delivers dates that span a very broad range. Conversely, when a steep calibration curve is present (e.g., 2300 or 4250 BP) the calibrated dates are more precise and narrower in their range. Shaded areas show the sections where the effect of Bayesian modeling was studied here.

Abb. 5 *Datierungsungenauigkeiten (2σ) von kalibrierten ^{14}C-Datierungen, abhängig von dem gemessenen konventionellen Alter (unter Annahme einer Präzision von 20 Jahren). Wenn ein konventionelles ^{14}C-Alter innerhalb eines plateaureichen Abschnitts der Kalibrationskurve fällt (z. B. um 2450 oder 4450 v. heute), dann liefert die Kalibrierung Datierungen mit einem großen Schwankungsbereich. Umgekehrt sind die kalibrierten Daten präziser und kürzer, wenn eine steile Kalibrationskurve vorliegt (z. B. 2300 oder 4250 v. heute). Eingefärbte Bereiche zeigen die in der hier vorgestellten Studie diskutierten Effekte der bayesianischen Modellierungen.*

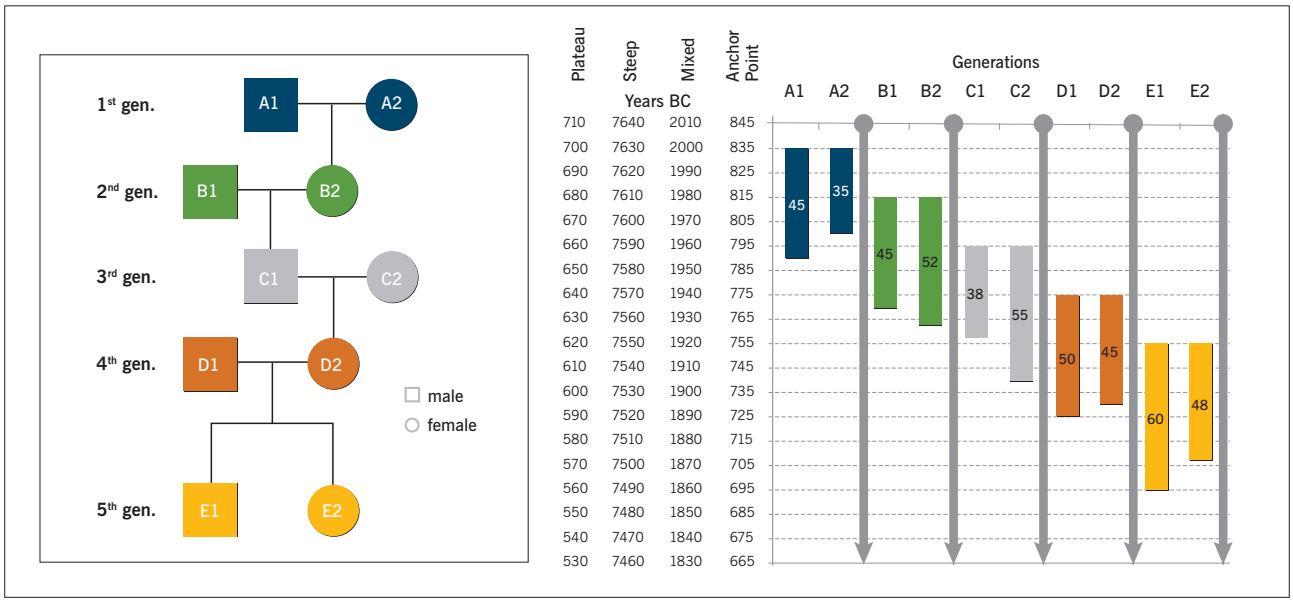


Fig. 6 Artificially constructed pedigree used for Bayesian modeling. Five generations with two individuals each were used in which the dates-of-birth (YoB) and ages-at-death (AaD) are prescribed. Several sets of YoB's are used to reflect periods with different shapes of the calibration curve.

Abb. 6 *Künstlich konstruierter Stammbaum, der für die bayesianische Modellierung benutzt wird. Es wurden fünf Generationen mit jeweils zwei Individuen verwendet, bei denen das Geburtsjahr (YoB) und das Alter zum Todeszeitpunkt (AaD) vorgegeben sind. Mehrere Reihen von Geburtsjahren (YoB's) wurden genutzt, um Zeitperioden mit verschiedenem Verlauf der Kalibrierungskurve zu berücksichtigen.*

dominates (Fig. 2), and a more mixed-feature curve (Fig. 3) that neither shows large plateaus nor very steep sections. Modeling[1] was performed with two sets of prior information:

1. Sequencing of the generations (using the OxCal command »sequence«), as given by the layout of the artificial pedigree but maintaining the individuals within a generation in no particular order (encapsulating those ^{14}C data using the OxCal command »phase«). The generations were placed in sequence with the prescribed information that individuals forming generation 2 died after those of generation 1 and so on.
2. Adding a time interval between the generations (using OxCals command »interval«) in order to constrain the fact that individuals of different generations died in a defined period of time after each other. This interval reflects the reproductive age of individuals in the past. The information can be precisely prescribed for the constructed pedigree as the difference between the mean YoDs between two generations.

The conventional ^{14}C ages that reflect the prescribed YoDs for the individuals are taken from the respective value in the calibration curve IntCal13. The results of the calibrations are shown as 2σ ranges.

In general, when using actual ^{14}C samples from archaeological contexts, the ^{14}C ages need to be corrected for the Human Bone Collagen Offset (HBCO). This takes into account that a ^{14}C age of human collagen does not allow definition of the date of YoD. Bone collagen is a mixture of collagen build-up over the course of the lifetime of an individual (Barta/Štolc 2007). More details on the effect of the HBCO correction can be found in Massy et al. (2022).

Plateau calibration curve

The Hallstatt plateau was used to investigate the benefits of combining ^{14}C ages with pedigree information. Figure 1 shows this section of the calibration curve, which mainly consists of one large plateau spanning almost 400 years.

One conventional ^{14}C age of around 2450 years BP (similar to individual A1) always results in calibrated dates ranging from approximately 800 to 400 cal BC. Resolving the dates of individuals who died during this period of time without prior information is not possible. However, using known family relationships between individuals can substantially improve the precision of the dates.

Figure 7 shows the unmodeled ages (light gray) for each individual when the pedigree information is not considered. All of these calibrated dates are basically identical and cannot be distinguished from each other. The modeled ages are displayed (in their respective colors) when family relationships are incorporated. In Fig. 7a only the sequence of the generations is considered. This sequence results in a substantial shortening of the calibrated ranges. While individual D2 (generation 4) has an unmodeled calibrated range of approximately 780–520 cal BC (260 years) the modeled range is reduced to 680–540 cal BC (140 years) – a reduction of 46 %. Adding an interval to the Bayesian model between the generations, so that the generations are

1 Using the software OxCal, see Bronk Ramsey (2009).

separated by a certain (prescribed) amount of time (Fig. 7b), can reduce the calibrated ranges even further. Looking at individual D2 again, the modeled dates now range from 625–525 cal BC (100 years). A reduction of 61 % compared to the unmodeled results. Similar improvements are seen for all the individuals in the pedigree. Besides narrowing the calibrated ranges, and thus improving the precision of the dates, the results remain accurate. The prescribed YoDs of all individuals (red triangles in Fig. 7) fall within the modeled date ranges.

Steep calibration curve

In stark contrast to the plateau-rich calibration curve, a steep gradient provides short time spans of calibrated ^{14}C dates, even when no other chronological information is considered (Fig. 2 and 8).

The range of calibrated dates are much narrower and even without modeling there is some chronological separation between the generations and lesser overlap compared to the plateau-rich setting. However, subsequent generations could not be fully resolved, even in the presence of a steep gradient within the curve.

Sequencing of the radiocarbon dates from the generations (Fig. 8a) and adding an interval between the generations (Fig. 8b) narrows the modeled calibrated dates adding more separation between the generations. Using individual D2 as an example again, Bayesian modeling narrows the unmodeled calibrated date from spanning approximately 90 years down to 45 years (when sequenced only) and down to 40 years (when adding an interval between the generations), representing a reduction in time-span of 50 % and 55 %. While adding an interval between the generations improves the precision of the calibration only slightly compared to sequencing only, the accuracy is improved considerably. The prescribed YoDs (red triangles) are located more

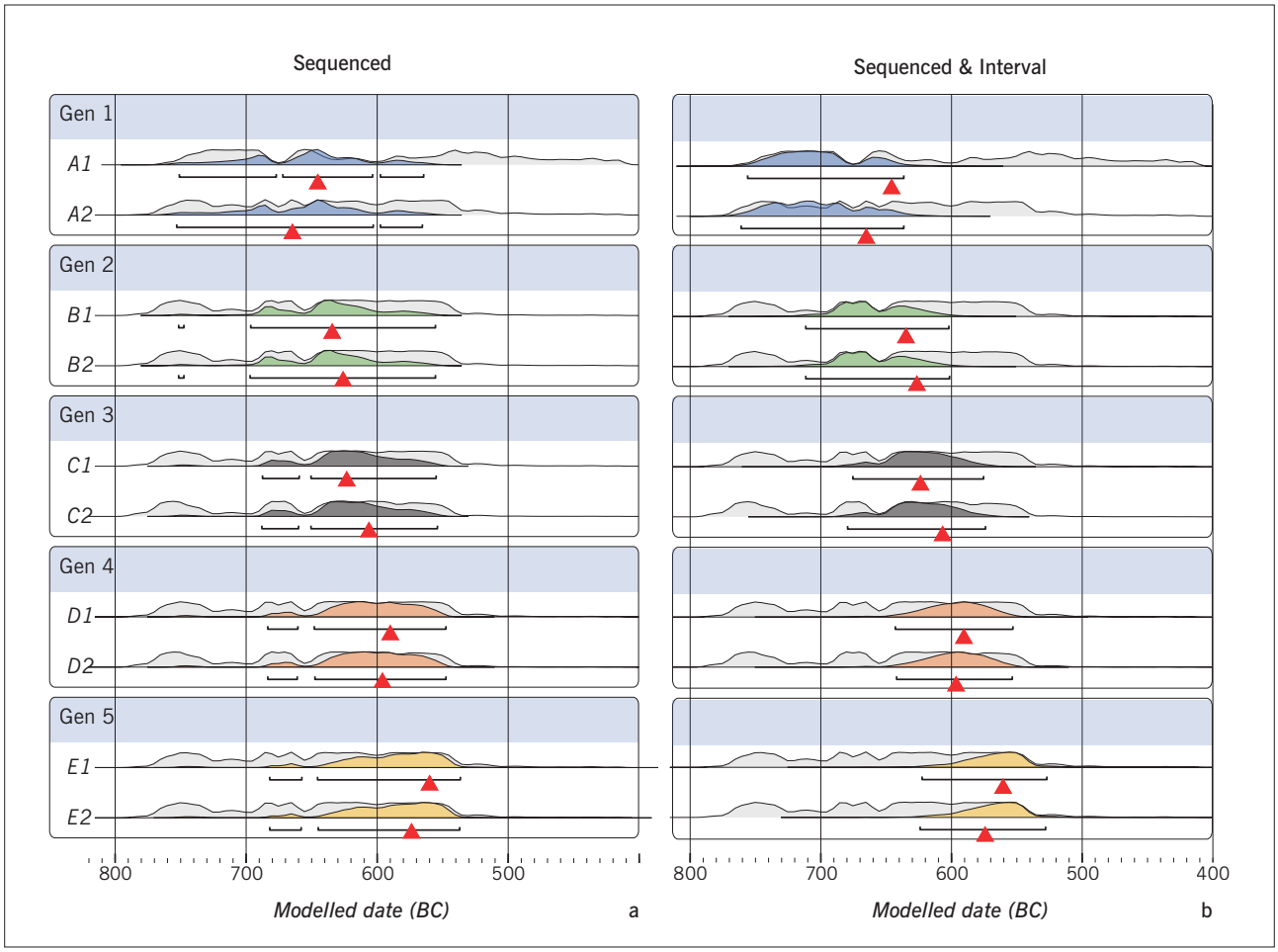


Fig. 7a–b Calibrated dates for the individuals forming the pedigree on a plateau-rich calibration curve. Unmodeled dates without considering the pedigree information are shown in light gray. All of the calibrated dates are basically identical and could not be distinguished from each other. The modeled dates are displayed in their respective colors where the family relationships are used with U-shaped brackets showing the 2σ calibrated date ranges after modeling. a Only the sequence of the generations is considered; b an interval is added between the sequenced generations, which narrows the date ranges even further.

Abb. 7a–b *Kalibrierte Datierungen der Individuen des Stammbaumes, die auf einer plateaureichen Kalibrierungskurve liegen. Nicht modellierte Datierungen, bei denen die Stammbauminformationen nicht berücksichtigt wurden, sind grau unterlegt. Alle kalibrierten Datierungen sind identisch und konnten nicht voneinander unterschieden werden. Die modellierten Datierungen sind in ihren jeweiligen Farben den benutzten Familienverwandtschaften zugeordnet und die U-förmigen Klammern zeigen die 2σ kalibrierten Datierungsbereiche nach der Modellierung. a Nur die Generationenabfolge ist berücksichtigt; b ein Zeitintervall ist zwischen den aufeinanderfolgenden Generationen eingefügt, was die Datierungsspannbreiten noch weiter verkleinert.*

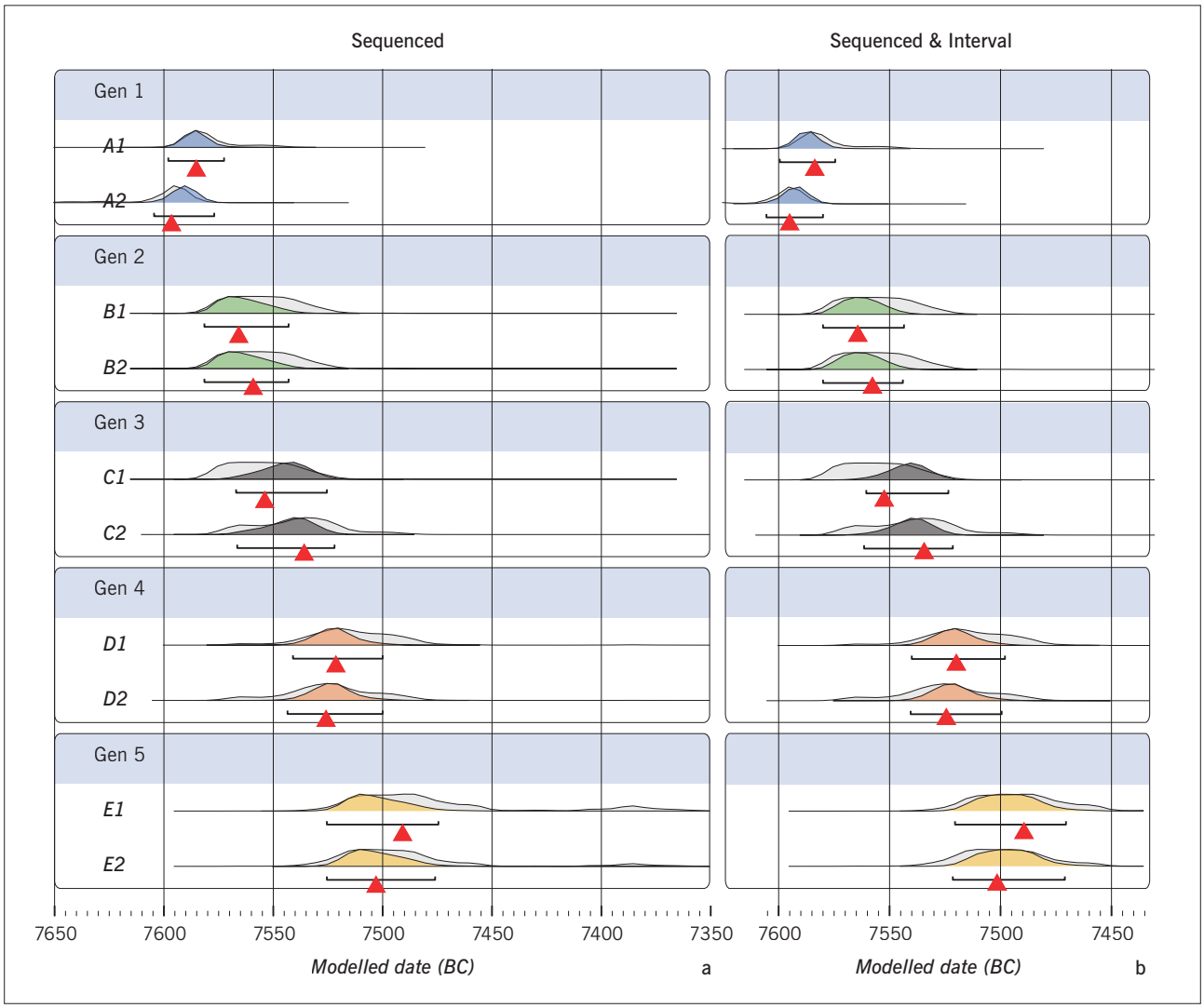


Fig. 8a–b Calibrated dates for the individuals forming the pedigree on a steep calibration curve. Unmodeled dates not considering the pedigree information are shown in light gray. Even when unmodeled, the calibrated age ranges are much narrower compared to the plateau-rich calibration curve. The modeled dates are displayed in their respective colors where the family relationships are used with U-shaped brackets showing the 2σ calibrated date ranges after modeling. a Only the sequence of the generations is considered; b an interval is added between the sequenced generations, which narrows the date ranges slightly further.

Abb. 8a–b *Kalibrierte Datierungen der Individuen des Stammbaumes, die auf einem steilen Abschnitt der Kalibrierungskurve liegen. Nicht modellierte Datierungen, bei denen die Stammbauminformationen nicht berücksichtigt wurden, sind grau unterlegt. Sogar unmodelliert sind die kalibrierten Datierungsschwankungen weit kürzer im Vergleich zu der plateaureichen Kalibrierungskurve. Die modellierten Datierungen sind in ihren jeweiligen Farben den benutzten Familienverwandtschaften zugeordnet und die U-förmigen Klammern zeigen die 2σ kalibrierten Datierungsbereiche nach der Modellierung. a Nur die Generationenabfolge ist berücksichtigt; b ein Zeitintervall ist zwischen den aufeinanderfolgenden Generationen eingefügt, was die Datierungsspannbreiten noch weiter verkleinert.*

towards the center of the calibrated ranges when compared to the sequencing-only dates.

Mixed calibration curve

The results of the tests using the mixed calibration curve with plateaus intersected by steeper sections are a combination of the plateau and steep-gradient data (Fig. 3 and 9). Unmodeled calibrated ranges are relatively broad. Individual D2 calibrates to approximately 1970–1780 cal BC (190 years), while individuals forming the first generation can be separated from the 5th generation by their ^{14}C dates; however, subsequent generations in between cannot be separated.

Combining the pedigree information with the ^{14}C data improves the precision of the calibrated ranges yet further. The improvement between sequencing the generations only and adding an interval between them is only marginal. Both setups, however, narrow the calibrated range of D2 down to 60 years – a substantial improvement of 68 %.

Anchor point example

In this example (Fig. 4 and 10), the YoD's of the artificial pedigree are moved slightly to older dates compared to the Hallstatt-plateau example. Now, the YoD of one of the individuals (A2) falls within the steep section of the calibration

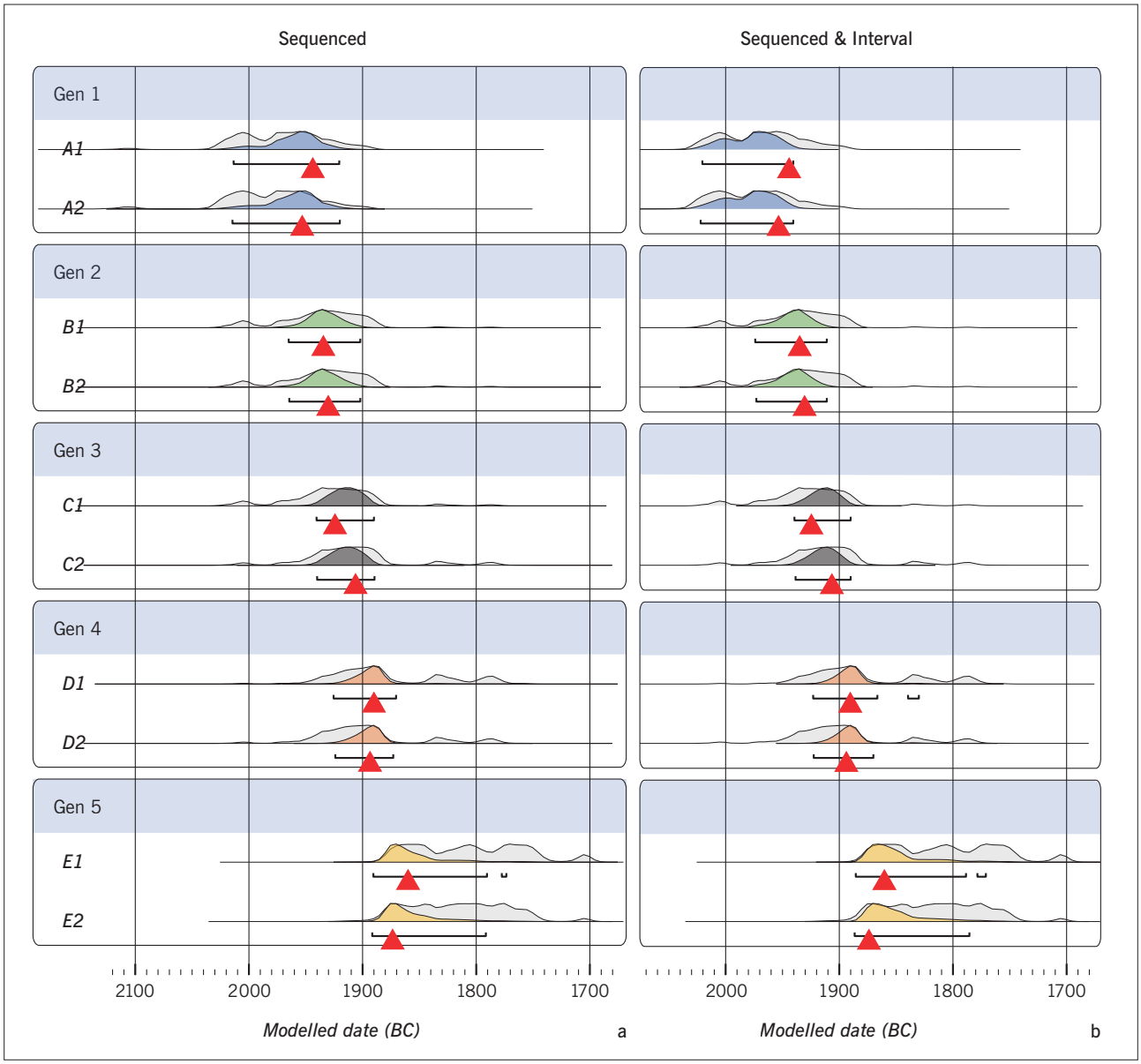


Fig. 9a–b Calibrated dates for the individuals forming the pedigree on a section of the calibration curve with some plateaus but also steep sections. Unmodeled dates not considering the pedigree information are shown in light gray. While generation 1 and 5 could be distinguished by their ^{14}C dates, subsequent generations close to each other show considerable overlap. The modeled dates are displayed in their respective colors where the family relationships are used with U-shaped brackets showing the 2σ calibrated date ranges after modeling. a Only the sequence of the generations is considered; b an interval is added between the sequenced generations, which narrows the date ranges moderately.

Abb. 9a–b *Kalibrierte Datierungen der Individuen des Stammbaumes, die auf einigen Plateaus aber auch steilen Abschnitten der Kalibrierungskurve liegen. Nicht modellierte Datierungen, bei denen die Stammbauminformationen nicht berücksichtigt wurden, sind grau unterlegt. Während die Generationen 1 und 5 durch ihre ^{14}C-Datierungen unterschieden werden konnten, liegen darauffolgende Generationen eng beieinander oder überlappen. Die modellierten Datierungen sind in ihren jeweiligen Farben den benutzten Familienverwandtschaften zugeordnet und die U-förmigen Klammern zeigen die 2σ kalibrierten Datierungsbereiche nach der Modellierung. a Nur die Generationenabfolge ist berücksichtigt; b ein Zeitintervall ist zwischen den aufeinanderfolgenden Generationen eingefügt, was die Datierungsspannbreiten noch weiter verkleinert.*

curve, immediately before the Hallstatt plateau; this forms an anchor point on the steep section of the curve.

While A2 can be calibrated to a very narrow unmodeled date range of approximately 50 years, all other individuals fall within the plateau. Their calibrated ranges span at least 200 years, or even approximately 350 years when the full range of the plateau is considered. Using individual D2 again as an example, the modeled date when generations are sequenced only is narrowed to a range spanning 210 years instead of 360 years (unmodeled), representing a reduction of 42 %. By adding an interval between the generations, the reduction is 220 years. In this setup, adding the interval pushes the calibrated dates further into the plateau, which consequently widens the calibrated ranges as opposed to narrowing them further, as in the other examples. Please see Massy et al. (2022, Fig. 18) for more information on how to constrain further the calibrated date ranges.

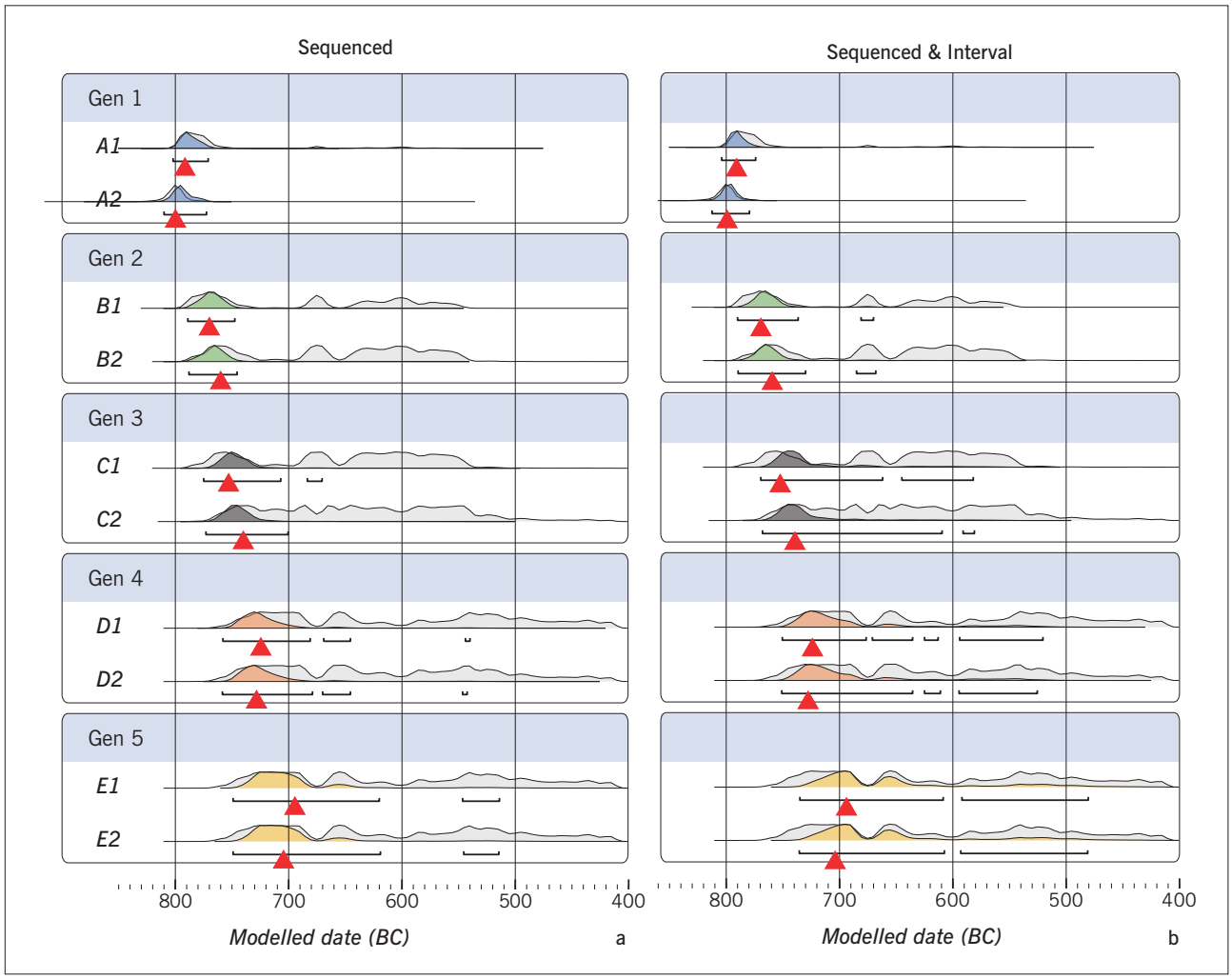


Fig. 10a–b Calibrated dates for the individuals forming the pedigree on a section of the calibration curve with a wide plateau (Hallstatt plateau). One individual (A2), however, is located on the steep section of the curve. Unmodeled dates not considering the pedigree information are shown in light gray. The modeled dates are displayed in their respective colors where the family relationships are used with U-shaped brackets showing the 2σ calibrated date ranges after modeling. a Only the sequence of the generations is considered; b an interval is added between the sequenced generations. Here, adding an interval pushed some of the ^{14}C ages further into the plateau, leading to slightly broader age ranges.

Abb. 10a–b *Kalibrierte Datierungen der Individuen des Stammbaumes, die auf einem Abschnitt der Kalibrierungskurve mit einem breiten Plateau (Hallstattplateau) liegen. Ein Individuum (A2) befindet sich auf dem steilen Abschnitt der Kurve vor dem Plateau. Nichtmodellierte Datierungen, bei denen die Stammbauminformationen nicht berücksichtigt wurden, sind grau unterlegt. Die modellierten Datierungen sind in ihren jeweiligen Farben den benutzten Familienverwandtschaften zugeordnet und die U-förmigen Klammern zeigen die 2σ kalibrierten Datierungsbereiche nach der Modellierung. a Nur die Generationenabfolge ist berücksichtigt; b ein Zeitintervall ist zwischen den aufeinanderfolgenden Generationen eingefügt, was dazu führt, dass einige ^{14}C-Alter weiter ins Plateau gerückt sind und es so zu etwas breiteren Altersschwankungen kommt.*

Conclusion

In all of the examples shown, combining ^{14}C ages with chronological information taken from pedigrees improves the precision of the calibrated ^{14}C dates. Generally, the range of calibrated dates is always narrower when modeled. An improvement of 40–70 % can be attained, depending on the shape of the calibration curve and the actual location of the ^{14}C data on the curve. Sequencing the generations alone in many cases already provides substantial improvements. Moreover, adding an interval between the generations does not always reduce the calibrated ranges in situations when the ^{14}C ages are moved into a more plateau-like section. As shown in Massy et al. (2022), even if individuals of only 2 generations can be identified, Bayesian modeling already provides more precise dates. The more generations that are included, the more the ^{14}C dates can be constrained. Generations that are bracketed by others benefit most from modeling because their dates can be constrained by the earlier and later generations. The shape of the calibration curve, however, is still restrictive. In plateau-like calibration curves the modeled ^{14}C dates still span relatively broad periods of time. In all cases, Bayesian modeling narrows the calibrated ranges and still conserves the prescribed YoDs. Thus, the precision is improved while maintaining accuracy.

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Source of Figures

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FALLSTUDIEN – STEINZEITEN

CASE STUDIES – STONE AGES

Verwandtschaft im östlichen Gravettien am Beispiel von Krems-Wachtberg

Christine Neugebauer-Maresch, Maria Teschler-Nicola, Thomas Einwögerer, Marc Händel und Ulrich Simon

Summary

Kinship in the eastern Gravettian using the example of Krems-Wachtberg

At the well-known Gravettian site Krems-Wachtberg in Lower Austria, archaeological investigations were carried out in the years 2005–2015 by the »Quaternary Archaeology« research group of the Austrian Archaeological Institute (OeAI) of the Austrian Academy of Sciences (OeAW)[1]. Already in the first year of research, a double burial of newborns was uncovered not far from a large fireplace and in the following year 2006 another infant grave was discovered in its immediate vicinity. Both graves were recovered en bloc *and brought to the Natural History Museum in Vienna, where measures were taken for securing, preserving and documenting the findings. At the same time, prerequisites and possibilities for non-destructive data collection and scientific analysis of the human skeletal remains using µCT[2] were examined. However, the properties of the surrounding loess sediment did not allow for recording of the skeletal remains in a precision required to serve as basis for a scientific evaluation, so it was decided to fully uncover and excavate the skeletal remains of the newborns from Grave 1 in 2015. Initially, the research focused on the assessment of the infant´s age at death (Grave1/Ind2 died perinatal; Grave1/Ind1 4–5 weeks later, Grave2/Ind3 died after 11–12 weeks), the determination of the genetic sex (Ind1, Ind2 and Ind3 are male), the clarification of postulated kinship (Ind1 and Ind2 were identified as monozygotic twins, Ind3 as a third-degree relative) and the affinity to Gravettian Eurasian hunter-gatherer groups. It was not only possible to substantiate the archaeological parallels between the approximately 31 000 year old burials of Krems-Wachtberg and Dolní Věstonice through molecular biological findings. Our investigations were also able to show impressively that the Gravettian burial rituals, in addition to the well-known personalized symbolic actions, also included the reopening of a grave and the change/manipulation of its layout and content.*

Zusammenfassung

An der altbekannten Gravettien-Fundstelle Krems-Wachtberg in Niederösterreich wurden in den Jahren 2005–2015 archäologische Untersuchungen durch die Forschungsgruppe »Quartärarchäologie« des Österreichischen Archäologischen Institutes (ÖAI) der Österreichischen Akademie der Wissenschaften (ÖAW) durchgeführt[1]. Bereits im ersten Forschungsjahr konnte unweit einer großen Feuerstelle eine Doppelbestattung von Neugeborenen und im Folgejahr 2006 in unmittelbarer Nähe ein weiteres Säuglingsgrab freigelegt werden. Beide Gräber wurden en bloc *geborgen und an das Naturhistorische Museum in Wien verbracht, wo Maßnahmen zur Sicherung, Konservierung und Dokumentation getroffen und die Voraussetzungen und Möglichkeiten für eine nicht-destruktive Datenerhebung und wissenschaftliche Analyse der* in situ *vorliegenden menschlichen Skelettreste mittel µCT[2] geprüft wurden. Die Eigenschaften des umgebenden Lösssediments erlaubten jedoch keine trennscharfe Erfassung der Skelettreste, die als Grundlage für eine wissenschaftliche Auswertung hätten dienen können, sodass entschieden wurde, die Skelettüberreste der Neugeborenen aus Grab 1 im Jahr 2015 vollständig freizulegen. Der Forschungsfokus lag zunächst auf der Sterbealter-Abschätzung (Grab1/Ind2 verstarb perinatal; Grab1/Ind1 4–5 Wochen später, Grab2/Ind3 verstarb nach 11–12 Wochen), der Ermittlung des genetischen Geschlechts (Ind1, Ind2 und Ind3 sind männlich), der Klärung postulierter familiärer Relationen (Ind1 und Ind2 wurden als monozygote Zwillinge identifiziert, Ind3 als Verwandter dritten Grades) sowie der Affinität zu gravettienzeitlichen eurasischen Jäger- und SammlerInnen Gruppen. Es gelang nicht nur, die archäologischen Parallelen zwischen den rund 31 000 Jahre alten Bestattungen von Krems-Wachtberg und Dolní Věstonicé durch den molekularbiologischen Befund zu untermauern. Unsere Untersuchungen konnten überdies auch eindrucksvoll zeigen, dass die Bestattungsrituale des Gravettien neben bereits bekannten personalisierten symbolischen Handlungen auch die Wiederöffnung eines Grabes und die Veränderung/Manipulation seiner Anlage und seines Inhalts umfassten.*

Fundort und archäologischer Befund

Die Stadt Krems an der Donau liegt zentral in Niederösterreich und markiert den Ausgang der Wachau, einem eng eingeschnittenen Tal, das sich von Melk auf ca. 36 km Länge bis zur Öffnung des Tullner Beckens erstreckt und im Jahr 2000 zum UNESCO-Weltkulturerbe ernannt wurde (Abb. 1). Eine Reihe von Flüssen entwässert hier in die Donau, so die Krems

1 Die Untersuchungen wurden vom österreichischen Wissenschaftsfonds FWF im Rahmen mehrerer Projekte (FWF P-17258, FWF P-19347, FWF P-21660, FWF P-23612) gefördert. Zusätzliche finanzielle Unterstützung leistete das Land Niederösterreich.

2 Diese Untersuchungen wurden an der FH OÖ Forschung & Entwicklung GmbH in Wels durchgeführt.

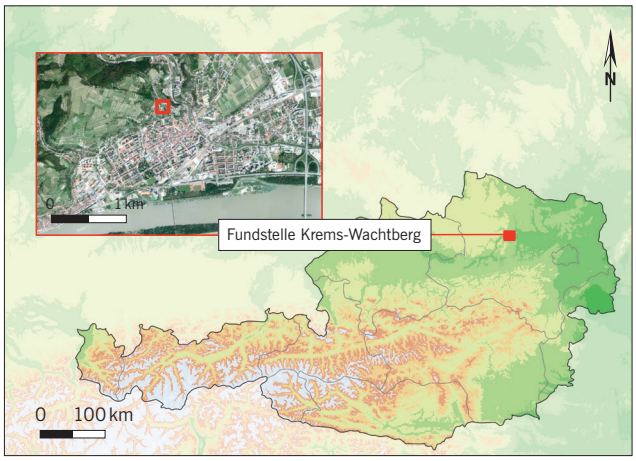


Abb. 1 Österreichkarte mit der Lage von Krems/Donau.

Fig. 1 *Map of Austria with location of Krems.*

und der Kamp von Norden und die Traisen und die Perschling von Süden. Sämtliche dieser Flusstäler weisen altsteinzeitliche Besiedlungsspuren auf.

In dem Bereich zwischen Donau und Kremsfluss liegt der Kuhberg, dessen südöstliche Abdachung als Wachtberg bezeichnet wird. Das ehemalige Wachtertor und der heute noch erhaltene Pulverturm an dieser Stelle markieren Teile der nördlichen Befestigung der Altstadt von Krems. Die hier bis zu 15 m mächtige Lössauflagerung wird durch einen tiefen Einschnitt in nord-südlicher Richtung, der Schießstattgasse, erschlossen. Der sogenannte Hundssteig, ehemals ein schmaler Hohlweg vom Wachtertor hinunter ins Kremstal, ist in der Paläolith-Literatur wohlbekannt, hatte man doch um 1900 im Zuge der Abbauarbeiten der dortigen Ziegelei eine gewaltige Menge an Fundmaterial geborgen, das dem frühen Aurignacien zugeschrieben wurde. 100 Jahre später machten hier Bauarbeiten Denkmalschutzgrabungen notwendig, die von der Prähistorischen Kommission der Österreichischen Akademie der Wissenschaften 2000–2002 durchgeführt wurden und neue Einblicke in die Stratigraphie ermöglichten (Neugebauer-Maresch 2008). Es zeigte sich, dass an diesem Hang nicht nur Fundschichten des Aurignacien, sondern auch des Gravettien vorhanden sind. Alle paläolithischen Horizonte liegen unter einem deutlich ausgeprägten und großflächig vorhandenen doppelten Ascheband, das als Rest von Steppenbränden interpretiert wird und auf ca. 30 500 cal BP datiert werden konnte (Einwögerer u. a. 2009). Es dient als wichtiger Markerhorizont, der sowohl die isolierten Grabungsflächen am Hundssteig, als auch diese mit den anderen Fundstellen am Wachtberg stratigraphisch miteinander verbindet und zudem das Ende der jungpaläolithischen Nutzung des Wachtbergs anzeigt (Händel 2017). Im Zuge der Umfeldprospektionen mittels Rammkernsondierungen wurde westlich der Schießstattgasse, ca. 100 m nördlich des Hundssteiges und benachbart zu einer 1930 von J. Bayer betreuten Grabungsstelle, ein besonders erfolgversprechendes Areal identifiziert. Diese Fundstelle ist unter dem Namen »Krems-Wachtberg« bekannt (Einwögerer 2000). 2005–2015 konnten hier Geländearbeiten durchgeführt werden, die in den ersten beiden Jahren zur Entdeckung der beiden außergewöhnlichen jungpaläolithischen Bestattungen führten. Im Verlaufe weiterer umfangreicher Denkmalschutzgrabungen und Rammkernsondierungen ließ sich ein Fundortcluster von rund 2,5 ha ermitteln, dessen paläolithischer Nutzungsschwerpunkt in das ältere Gravettien vor rund 33 000–31 000 Jahre cal BP datiert (Einwögerer u. a. 2014; Händel u. a. 2021).

Während der Feldarbeiten an der Fundstelle Krems-Wachtberg 2005–2015 konnten rund 160 m² freigelegt und umfangreich dokumentiert werden (Simon u. a. 2019). Die an dieser Stelle 8 m mächtige Lösssequenz bildet ein wichtiges Sedimentarchiv, das den Zeitraum von 40 000–20 000

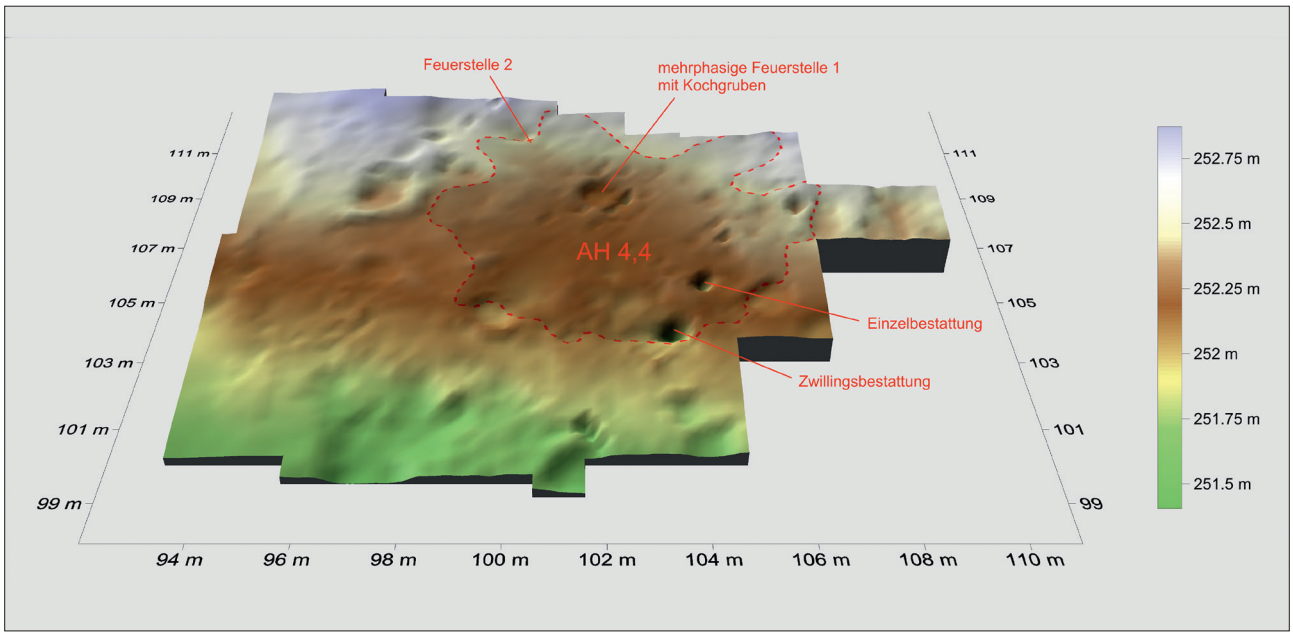


Abb. 2 Krems-Wachtberg. Oberflächenmodell des archäologischen Horizonts AH 4 mit den wichtigsten Befunden des Begehhorizonts AH 4,4/4,3.

Fig. 2 *Krems-Wachtberg. Surface model of archaeological horizon AH 4 with main anthropogenic structures of occupation horizon AH 4.4/4.3.*

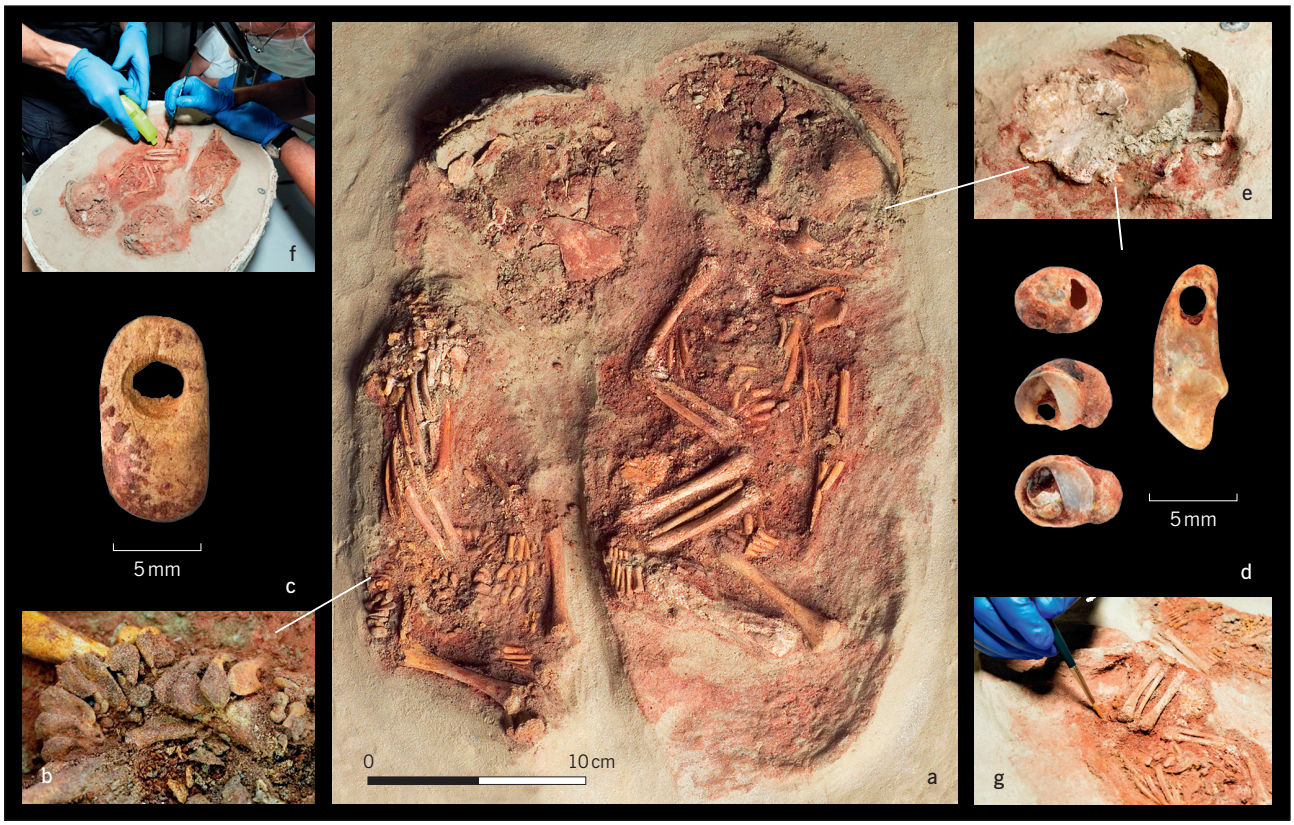


Abb. 3a–g Krems-Wachtberg, Zwillingsbestattung Grab 1. a Doppelbestattung; b Fundlage der Elfenbeinanhänger Ind1 im Detail; c Elfenbeinanhänger; d gelochter Fuchszahn und gelochte Mollusken Ind2; e Fundlage gelochter Anhänger Ind2; f Freilegung der Skelette mit deutlich erkennbarem Verlauf der Rötelstruktur insbesondere bei Ind1; g Detail Ind2 bei Freilegung im Labor.

Fig. 3a–g *Krems-Wachtberg, twin burial grave 1. a double burial; b find location of the ivory pendants Ind1 in detail; c ivory pendant; d perforated fox tooth and perforated molluscs Ind2; e find location of perforated pendants Ind2; f exposure of the skeletons with structure of red ochre in particular Ind1; g detail Ind2 during excavation in the laboratory.*

abdeckt und auf unterschiedlichste Arten beprobt und analysiert werden konnte[3].

Die bedeutsamste Fundschicht fand sich in einer Tiefe von mehr als 5 m. Dieser archäologische Horizont (AH4) wurde zum Teil noch *in situ* (AH 4,4/4,3), zum Teil bereits bewegt (4,11), angetroffen (Abb. 2). Der *in situ*-Befund lag an einer Position, an der die Hangneigung deutlich geringer war als in der Umgebung. Zentral befand sich eine große, mehrphasige Feuerstelle mit rund 1 m Durchmesser, bei der die Füllung der letzten Brandphase bereits kurz nach der Besiedlung infolge einer Destabilisierung der Oberfläche durch Solifluktion abgetragen wurde (Händel u. a. 2021). Die Gruben, die die beiden Bestattungen bargen – eine Doppelbestattung (Grab 1) und eine Einzelbestattung (Grab 2) – befanden sich nahe dem Südostrand dieses *in situ*-Befundes, rund 3 bzw. 4 m von der Feuerstelle entfernt.

Die aus Grab 1 (Abb. 3a) geborgenen Skelettüberreste, ihrer Aufdeckung entsprechend als Individuum 1 (Ind1) und Individuum 2 (Ind2) bezeichnet, fanden sich in einer ca. 36 x 28 x 20 cm (L x B x T) messenden Grube in fast 5 m Tiefe (Einwögerer u. a. 2006; Einwögerer u. a. 2008). Beide Körper waren ähnlich, in linksseitiger Hockerlage mit Kopf nach Norden und Blick nach Osten deponiert worden. Dennoch ließen sich Unterschiede in Lage und Ausstattung erkennen: Ind1 nahm mit dem Rücken der nördlichen Grubenwand anliegend einen räumlich kleineren Sektor des Grabes ein als Ind2, das ungefähr mittig in der Südhälfte der Grube platziert worden war und dessen Körperstamm sich in Rückenlage befand. Zudem fanden sich im Bereich des Beckens von Ind1 53 Elfenbeinanhänger, die aufgrund ihrer Anordnung und Position zu einer Kette aufgefädelt gewesen sein müssen (Abb. 3b–c). Bei Ind2 wurde erst im Zuge der endgültigen Freilegung im Labor ein gelochter Eisfuchszahn und drei kleine gelochte Schneckenhäuser im Halsbereich entdeckt, die wir als Bestandteile einer Kette interpretieren (Abb. 3d–e). Diese Objekte waren auf den zuvor durchgeführten CT-Scans nicht erkennbar.

Die Skelettüberreste beider Kinder waren in Rötel eingebettet, was auch zur Verfärbung von Knochen und Beigaben führte. Im Verlaufe der unter Lupenbetrachtung vorgenommenen Reinigung der Fundoberfläche wurden klare Grenzen zwischen Rötelfärbung des am Knochen angrenzenden Sediments und dem umgebenden Sediment erkannt. Diese Zone verlief in einem gleichmäßigen Abstand etwa 3 mm entlang der cranialen Reste und verlief im Bereich der postcranialen Skelettabschnitte etwa entlang der ursprüng-

3 Händel 2017; Sprafke u. a. 2020; Hambach 2010; Lomax u. a. 2014; Terhorst u. a. 2014; Groza u. a. 2019; Händel u. a. 2021.

lichen Weichteilgrenze (vgl. Abb. 3f), sodass man annehmen kann, dass roter Farbstoff in Pastenform auf die Körper aufgetragen wurde, und diese nicht nur in eine Rötelstreuung gebettet wurden. Abgedeckt wurde die Grube mittels eines Mammutschulterblattes, das eindeutig für diesen Zweck modifiziert worden war: Die Spina scapularis wurde durch mehrere Schläge sorgfältig reduziert, um eine flache Abdeckung zum Schutz der Bestattungen zu erhalten. Brandspuren am Gelenk des Knochens können nicht mit Sicherheit dem Bestattungsvorgang zugeschrieben werden. An der hangabwärts gerichteten Seite lag das Schulterblatt auf einem Elfenbeinspan auf.

Grab 2, mit der Einzelbestattung eines Säuglings, Individuum 3 (Ind3), befand sich rund 1 m nördlich von Grab 1. Der Körper war ebenfalls als Hocker mit Blickrichtung nach Osten, allerdings auf seiner rechten Seite aufliegend mit dem Kopf nach Süden bestattet worden (Abb. 4). Die Grabgrube zeichnete sich deutlich als rot gefärbtes, leicht spindelförmiges Oval von 45 x 22 cm und 15 cm Tiefe im Löss ab. In ihrer Verfüllung fand sich eine Elfenbeinnadel, die rund 2 cm über den cranialen Resten in Längsachse des Körpers positioniert war. Im Gegensatz zu den mit dem Schulterblatt abgedeckten Neugeborenen aus dem Grab 1 sind die Skelettelemente dieses Säuglings sehr schlecht erhalten. Viele Abschnitte waren nur als Verfärbung im Einbettungssediment erkennbar, lediglich einige Schaftfragmente von Langknochen und einige Teile des Craniums (etwa das Os petrosum sowie einzelne Milchzähne) sind vorhanden, weisen aber starke postmortale Erosionsspuren auf. Der Körperstamm ist ebenfalls nur in kleinsten Fragmenten repräsentiert. Die Rötelbettung ist intensiv und es fanden sich Stücke des roten Farbstoffs im Sediment; körperliche Konturen wie im Falle der beiden Neugeborenen aus Grab 1 waren nach dem Abtragen der Rötelbedeckung nicht erkennbar. Die deutlich sichtbare, spindelförmige Rötel-Sedimentgrenze könnte (in Kombination mit der vorgefundenen Nadel) auf eine nicht erhaltene Umhüllung aus einem organischen Material hindeuten. Aufgrund der generell schlechten Erhaltung der körperlichen Reste wurde von einer weiteren Freilegung abgesehen; dieses Grab ist *in situ* als Anschauungs- und Studienobjekt erhalten und wurde kürzlich an den Eigentümer, die Niederösterreichische Landessammlungen (Asparn/Zaya), übergeben.

Bioanthropologische, molekularbiologische und chemometrische Ergebnisse

Da Funde von Bestattungen perinataler Kinder aus dem Jungpaläolithikum nur in geringer Zahl dokumentiert sind (s. dazu die Ausführungen von Nava u. a. 2017), kommt den am Wachtberg in Krems im Siedlungskontext entdeckten Gräbern mit Skelettüberresten von Neugeborenen bzw. Säuglingen als Informationsquelle für Fragen der Individualentwicklung, der regionalen sowie überregionalen Beziehungen und der Rekonstruktion von thanatologischen Handlungen im Bestattungskontext eine herausragende Bedeutung zu. Daher wurde im Sommer 2015, mit Abschluss der 11. Grabungskampagne, die auch das Ende der Feldforschungen an diesem Fundplatz bedeutete, die vollständige Freilegung der Bestattung 1 (Doppelbestattung) unter Mitarbeit der ArchäologInnen und AnthropologInnen durchge-

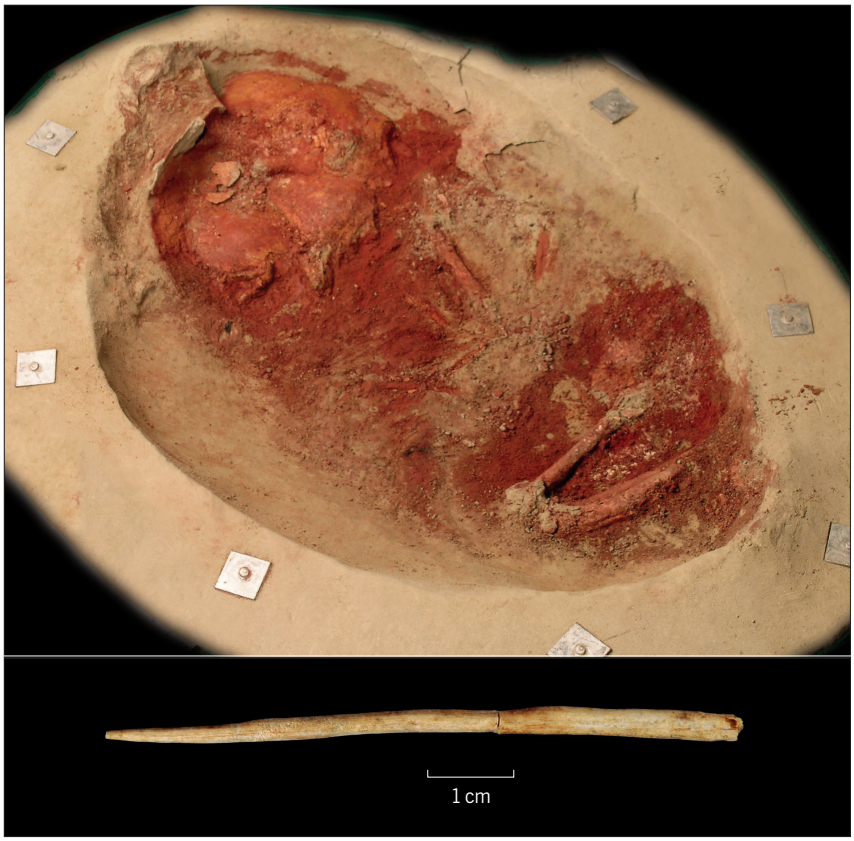


Abb. 4 Krems-Wachtberg Grab 2.

Fig. 4 *Krems-Wachtberg Grave 2.*



Abb. 5 Freilegungsarbeiten an der Krems-Wachtberg Zwillingsbestattung im Labor im NHM-Wien 2015.

Fig. 5 *Excavation of the Krems-Wachtberg twins in the laboratory at the NHM Vienna 2015.*

führt. Diese fand in einem für präparatorische Arbeiten bestgeeigneten Raum der Anthropologischen Abteilung statt, der nicht nur die sicherheitstechnischen Anforderungen erfüllte, sondern auch eine ungestörte und fokussierte Teamarbeit ermöglichte. Nach einer ausführlichen Dokumentation des *Status quo* wurde mit der vollständigen Freilegung der oberflächlich gelegenen Skelettelemente begonnen. Dabei wurden die Sedimente unter Lupenbetrachtung schichtweise entfernt und jede Lage mittels Streifenlichtscan (Breuckmann smartSCAN HE 5 Megapixel Color 3D Scanner; Abb. 5) und Oberflächenfotografie (Nikon D600) dokumentiert. Diese Vorgehensweise bildet die Grundlage für eine 3D-Rekonstruktion der Skelettüberreste sowie ihrer Lage, der Grabstruktur und der Einbringungsabfolge der Körper[4]. Die beiden Säuglinge der Doppelbestattung wurden – ungeprüft und spontan – als »Zwillinge vom Wachtberg in Krems« angesprochen. Daher wurden bereits im Verlauf der Freilegung Proben für molekularbiologische Untersuchungen entnommen, die sowohl das Geschlecht der drei Kinder wie auch ihre mögliche genetische Verwandtschaft klären sollten (Teschler-Nicola u. a. 2020).

Molekularbiologische Analyse: Im Falle der Wachtberg-Funde hatten wir gute Argumente dafür, dass endogene DNA für eine molekularbiologische Analyse zur Feststellung einer verwandtschaftlichen Nähe der Kinder aus Grab 1 ausreichend vorhanden sein würde, da eine Pilotstudie bereits mit kleinsten Probenmengen der (schlecht erhaltenen) Reste des Säuglings aus Grab 2 erfolgreich verlaufen war (Fu u. a. 2016). Daher stand zunächst der Aspekt der Verwandtschaftsbeziehung der beiden Neugeborenen im Forschungsfokus, um abzuklären, ob ein solches für die Bestattung in einem gemeinsamen Grab ausschlaggebend gewesen sein könnte. Dabei gelang es, aus den Ossa petrosa von Ind1 und Ind2 eine überraschend große Anzahl von Einzelnukleotid-Polymorphismen (SNPs) auf den Chromosomen 1–22 zu erzielen (Ind1 722 470 SNPs, Ind2 264 785 SNPs), die eine gute Voraussetzung sowohl für die Verwandtschaftsanalyse der Krems-Wachtberg Kinder wie auch den Populationsvergleich mit überregionalen Fundclustern bildete. Darüber hinaus konnte sowohl bei den beiden Neugeborenen aus Grab 1 wie auch dem Säugling aus Grab 2 das genetische Geschlecht als ›männlich‹ bestimmt werden (s. Teschler-Nicola u. a. 2020, Tab. 1).

Um die Verwandtschaft und genetische Affinität zu beurteilen, wurden populationsgenetische Analysen durchgeführt, in die die beiden Neugeborenen Ind1 und Ind2 und die bereits veröffentlichten Daten des Säuglings Ind3 vom Wachtberg sowie Individuen anderer jungpaläolithischer und mesolithischer Fundstellen einbezogen wurden. Es zeigte sich, dass Ind1 und Ind2 signifikant mehr Allele

4 GFF NÖ: Digitale Rekonstruktion anthropologischer Funde – eine Pilotstudie zur 30 000 Jahre alten Doppelbestattung von Neugeborenen am Kremser Wachtberg (Projekt-ID: FTI17-010).

mit Ind3, dem Säugling aus Grab 2 gemeinsam haben, als mit allen anderen analysierten jungpaläolithischen/mesolithischen Proben, mit Ausnahme von Dolní Věstonice 13 (s. Teschler-Nicola u. a. 2020, Abb. 3a; Suppl. 2). Dies weist auf eine enge genetische Verbindung zwischen Individuen aus den beiden zeitgleichen Fundorten hin. Daher wurden die Individuen aus Dolní Věstonice herangezogen, um den Verwandtschaftsgrad der Wachtberg-Kinder zu beurteilen (dafür wurden die SNP-Abweichungsraten innerhalb der Population für nicht verwandte Individuen berechnet; Olalde u. a. 2019): Die Ergebnisse zeigen, dass es sich bei den Säuglingen aus der Bestattung 1 um eineiige Zwillinge handelt, die ihr gesamtes Genom teilen, während Ind3 wahrscheinlich ein Verwandter dritten oder höheren Grades war, da der paarweise Test zwischen Ind2 und Ind3 einen höheren und nicht überlappenden Verwandtschaftskoeffizienten ergab als zwischen jedem Krems-Wachtberg-Individuum und dem Individuum Dolní Věstonice16 (Teschler-Nicola u. a. 2020). Die drei Krems-Wachtberg-Kinder zeichnen sich auch durch die gleichen Y-Chromosomen- und Mitochondrien-Haplogruppen aus.

Sterbealtersabschätzung: Die unterschiedliche symbolische Behandlung und Lage der Zwillinge deutet, wie erwähnt, auf eine mögliche nicht synchrone Bestattung hin, die mit einem unterschiedlichen Sterbealter erklärt werden könnte. Da es nicht möglich war, eine chronologische Abfolge der Grablegung auf stratigraphischer Grundlage eindeutig zu klären, rückte die Sterbealtersbestimmung der Kinder in den Forschungsfokus. Obwohl die postcranialen Überreste der Zwillinge auf den ersten Blick durch ihren scheinbar guten Erhaltungszustand beeindrucken (vgl. Abb. 3), war eine Altersschätzung durch Substanzverluste und Erosionen, häufig auch dem Fehlen entsprechend gut erhaltener korrespondierender Langknochen der Zwillinge erschwert. Einzige Ausnahme bildeten die Tibiae, die bei einer fast identischen Länge (Ind1 = 62,5 mm, Ind2 = 63,0 mm und einer daraus rekonstruierten ähnlichen Körpergröße von ca. 50,1 cm) ein Sterbealter zwischen dem 9. und 10. Mondmonat nahelegen. Messungen an anderen Skelettelementen zeigen Variationen ebenso wie geringe Größenunterschiede zwischen den Kindern, wie es bei Zwillingen des Öfteren zu beobachten ist (Blickstein/Kalish 2003). Ob die bei Ind1 diagnostizierte Entzündung des Periosts (Knochenhautentzündung) bei der körperlichen Entwicklung eine Rolle spielte, bleibt zu klären, da sich ein Vitamin-C-Mangel normalerweise erst mehrere Monate nach der Geburt in Form von subperiostalen Knochenneubildungen manifestiert (Ortner/Putschar 1981). Einbezogen in die Diagnose wurde auch das Os tympanicum (Kósa 1978; Weaver 1979; Schaefer u. a. 2009) bzw. der Anulus tympanicus; Aufgrund von Größe und morphologischen Details sowie der Tatsache, dass dieser Knochenring noch nicht mit der Squama temporalis verbunden war (ein Prozess, der etwa in der 35. Schwangerschaftswoche beginnt und kurz vor der Geburt abgeschlossen ist), gehen wir von einem Entwicklungsstadium kurz vor der Ossifikation aus, d. h., einer vor dem Termin erfolgten bis termingerechten Geburt (Scheuer/MacLaughlin-Black 1994; Schaefer u. a. 2009). Diese Beobachtung deckt sich mit Daten aus neueren Studien, die die Schwangerschaftsdauer bei menschlichen Zwillingen auf 35 bis 37 Wochen schätzen, während die Gestationszeit bei Einzelkindern bei etwa 40 Wochen liegt.

Da es nicht möglich war, anhand dieser Merkmalsregionen das Sterbealter präziser zu fassen, wurden auch die bei allen drei Kindern erhaltenen oberen zweiten Milchschneidezähne (i2) als aussagekräftige morphometrische und chemische Informationsträger in die Studie einbezogen (Lewis 1991; Scheuer/MacLaughlin-Black 1994; Cardoso 2007). Die Zähne der Zwillinge sind morphologisch (in Form und Größe der Dentin-Schmelz-Grenze (DEJ) praktisch ident (vgl. Teschler-Nicola u. a. 2020, Fig. 4; Suppl. Fig. 1), allerdings übertrifft Ind1 in allen Dimensionen (mesio-distale und bukko-linguale Dimensionen, Kronenhöhe, Schmelz- und Dentin-Dicke und -volumina) jene seines Zwillingsbruders. Dies weist zwar auf ein fortgeschritteneres Zahnreifungsstadium bei Ind1 hin, könnte aber auch – wie in Zwillingsstudien dokumentiert – aus einer unterschiedlichen pränatalen Versorgung oder anderen umweltbedingten Einflüssen auf die phänotypische Variation der Zähne resultieren (Townsend u. a. 2009; Kabban u. a. 2001). Eine Eingrenzung des Sterbealters versprachen wir uns daher vom Nachweis einer sogenannten Neonatallinie (NNL) im Kronenschmelz (Eli u. a. 1989; Skinner/Dupras 1993; Zanolli u. a. 2012) und der Prismenlängenbestimmung. Die NNL ist nur in Milchzähnen und den ersten bleibenden Molaren nachweisbar. Es handelt sich um eine dunkel gefärbte Linie, deren Manifestation mit Geburtsstress (Schour 1936; Smith/Avishai 2005) und der damit verbundenen Dysfunktion der Ameloblasten (schmelzbildenden Zellen im Zahn) in Verbindung gebracht wird. Diese Linie trennt den prä- und postnatal gebildeten Schmelz ebenso wie das prä- und postnatal gebildete Dentin. Ihre Ausprägung wurde an histologischen Zahnschnitten und µCT-Bildern der zweiten Milchschneidezähne verifiziert: Bei Ind3 war eine NNL deutlich zu erkennen, bei Ind1 weniger ausgeprägt, dabei sehr nahe und parallel zur Schmelzoberfläche verlaufend und bei Ind2 fehlte sie (vgl. Teschler-Nicola u. a. 2020, Fig. 4). Darüber hinaus beobachteten wir bei allen Individuen akzentuierte weitere, meist kürzere Linien im Schmelz, die bei Ind3 am stärksten ausgeprägt waren.

Trotz taphonomisch veränderter Schmelzoberfläche war es weiters möglich, auch die Prismenlängen und damit die Kronenbildungszeit (s. Birch/Dean 2014) zu bestimmen. Die Ergebnisse deuten darauf hin, dass Ind2 perinatal, d. h., um die Geburt, Ind1 4–5 Wochen nach der Geburt und Ind3 11–12 Wochen nach der Geburt verstorben war. Zwillingsschwangerschaften gelten als Hochrisikoschwangerschaften und auch die Geburt ist mit einem höheren perimortalen Mortalitätsrisiko der Kinder verbunden (Kiely 1990; Marviate/Norman 1992). Das oben erwähnte Symptom der subperiostalen Knochenneubildung an den Schienbeinen von Ind1 und die im Zahnschmelz zusätzlich zur NNL ausgebildeten Linien weisen auf schwere Stressepisoden und/oder eine unzureichende Versorgung hin, die zum frühen Tod der Perinaten beigetragen haben könnten.

Chemometrische Analyse (Barium-Calcium-Verhältnis als Still-Marker): Zur Aufdeckung der frühkindlichen Ernährungsgeschichte wurde auch ein Biomarker für das Stillen – das Barium-Calcium-Verhältnis in den Zähnen und die räumliche Verteilung von Barium (Ba) im Zahnschmelz –

herangezogen (Smith u. a. 2017). Die Methode beruht auf dem für unterschiedliche Entwicklungsperioden typischen Ba-Eintrag im Zahnschmelz: Die pränatalen Ba-Werte sind niedrig, da die Übertragung durch die Plazenta begrenzt ist, nachgeburtlich erfolgt (in den meisten Fällen) die Anreicherung durch den Verzehr der Muttermilch. D. h., das mit der Nahrung in den Zahnschmelz aufgenommene Ba/Ca-Verhältnis müsste (unter bestimmten Bedingungen) bei der Geburt ansteigen und für die Dauer des Stillens erhöht bleiben (Austin u. a. 2013). Sollten die Wachtberg-Kinder die Geburt überlebt haben und gestillt worden sein, wäre ein höherer Ba-Eintrag im Zahnschmelz nach der Manifestation der NNL zu erwarten. Verwendet wurden Dünnschnitte der zweiten Schneidezähne (i2s), an denen mit Laser-Ablation die Verteilung des $^{138}Ba/^{43}Ca$-Verhältnisses im Dentin, sowie im pränatalen und postnatalen Schmelz bestimmt wurde (Details s. Teschler-Nicola u. a. 2020, 8, »Methods«).

Im pränatal gebildeten Schmelz von Ind1 findet sich eine akzentuierte Linie. Es handelt sich dabei nicht um die NNL, sondern ein durch ein anderes »Stress-Ereignis« verursachtes Merkmal (s. Teschler-Nicola u. a. 2020, Fig. 5). Der vor dieser atypischen Linie gebildete pränatale Schmelz weist ein etwas niedrigeres $^{138}Ba/^{43}Ca$-Verhältnis auf als der nach der Stresslinie gebildete pränatale Schmelz. An der NNL steigt das $^{138}Ba/^{43}Ca$-Verhältnis deutlich an und bleibt bis zur Schmelzoberfläche erhöht. Wie bei Ind1 wird der pränatale Schmelz von Ind2 ebenfalls von einer Stresslinie durchschnitten, das $^{138}Ba/^{43}Ca$-Verhältnis vor und nach dieser Schmelzlinie ist ähnlich wie bei Ind1. Interessanterweise kann auch in der äußersten Schmelzschicht von Ind2 ein erhöhtes $^{138}Ba/^{43}Ca$-Verhältnis festgestellt werden, ähnlich wie in der post-NNL-Schmelzschicht von Ind1, obwohl bei Ind2 keine NNL identifiziert werden konnte. Ind3 zeigt keinen signifikanten Anstieg des $^{138}Ba/^{43}Ca$-Verhältnisses im post-NNL-Schmelz im Vergleich zum prä-NNL-Schmelz. Im Gegensatz dazu ist Barium in der äußeren Schicht des post-NNL-Schmelzes abgereichert (hier dürfte es sich um einen diagenetischen Effekt handeln, der über die Analyse weiterer Elementverhältnisse, etwa das $^{27}Al/^{43}Ca$-Verhältnis, abgeklärt werden konnte, (s. Teschler-Nicola u. a. 2020, Abb. 5). Interessanterweise ergibt das ermittelte $^{138}Ba/^{43}Ca$-Verhältnis bei Ind3, für das eindeutig ein Überleben von etwa 3 Monaten als gesichert gelten kann, keinen signifikanten Unterschied zwischen dem Schmelz vor und nach der NNL. Die Veränderung des $^{138}Ba/^{43}Ca$-Verhältnisses bei bzw. nach der Geburt kann jedoch aufgrund von interindividuellen Unterschieden im Ba-Gehalt der Muttermilch (Austin u. a. 2013) oder Schwierigkeiten beim Stillen variieren. Die Antwort auf die Frage nach den Ursachen des fehlenden Ba-Eintrags im Schmelz von Ind3 muss daher offenbleiben. Auffällig ist allerdings, dass der post-NNL-Schmelz von Ind3 eine rudimentäre, wenn auch gut entwickelte, postnatale Inkrementallinie zeigt, an der sich ein vermindertes $^{138}Ba/^{43}Ca$-Verhältnis im Vergleich zum pränatalen und früh-postnatalen Schmelz erkennen lässt. Diese Beobachtung deutet darauf hin, dass Ind3 während seines kurzen postnatalen Lebens weitere (möglicherweise ernährungs- oder krankheitsbedingte) Stressepisoden durchlaufen hat.

Kurz lassen sich die Ergebnisse der $^{138}Ba/^{43}Ca$-Analyse folgendermaßen zusammenfassen: Die diagenetischen Veränderungen im Schmelz wurden bei allen drei Individuen analysiert und signalisieren lediglich einen unbedeutenden Einfluss auf das biogene Barium (und Strontium). Das bedeutet, dass der Anstieg des $^{138}Ba/^{43}Ca$-Verhältnisses von Ind1 genau an der NNL als Veränderung der chemischen Information interpretiert werden kann, die dem Stillvorgang entspricht. Der Anstieg vom pränatalen Schmelz zum postnatalen Schmelz beträgt > 30 % und stimmt mit Beobachtungen zur Ernährungsumstellung beim heutigen Menschen überein (Austin u. a. 2013). Die Daten für Ind2 liefern keinen eindeutigen Hinweis auf »gestillt« oder »nicht gestillt«. Der erhöhte $^{138}Ba/^{43}Ca$-Wert im äußersten Zahnschmelz könnte eventuell als (sehr) kurzes Überlebenssignal von Ind2 gedeutet werden. Diese Schicht ist im Vergleich zu Ind1 dünn, sodass das höhere Sterbealter bei Ind1, das auch aus der Zahnschmelzmikromorphologie ablesbar ist, als gesichert gelten kann.

Diskussion und Zusammenfassung

Prä- bis perinatale Bestattungen des anatomisch modernen, paläolithischen Menschen sind nur in geringer Zahl nachgewiesen.

In der bekannten Lokalität von Dolní Věstonice sind keine Funde von prä- bis perinatalen Bestattungen überliefert[5]. Allerdings scheinen im sogenannten »Massengrab« von Předmostí, dessen Skelettreste nicht erhalten geblieben sind, wohl auch perimortal Verstorbene bzw. Säuglinge bestattet gewesen zu sein, wie den Aufzeichnungen zu entnehmen ist (Svoboda 2008).

In manchen Fällen wurden die zarten Knochen erst bei der Bearbeitung des allgemeinen osteologischen Fundmaterials als solche erkannt (z. B. Wilczyce in Polen; Irish u. a. 2008) und können deshalb – ohne hinreichenden Befund – nicht zweifelsfrei als deponierte Relikte im Sinne von Bestattungen interpretiert werden.

Als weiteres Beispiel kann hier das auf 41 349 ± 176 cal BP (indirekt aus Holzkohle) datierte und damit sehr frühe Grab aus Nazlet Khatar (Gouv. Sauhadsch, Ägypten; Grab 1) erwähnt werden: 1980 bei Grabungen entdeckt und zunächst zeitlich als jünger eingeschätzt, findet sich in dem 1981 verfassten kurzen osteologischen Bericht lediglich der Hinweis auf ein sehr schlecht erhaltenes Skelett; Sterbealter und Geschlecht waren nicht näher bestimmbar, aber unter den Knochen des erwachsenen Individuums konnten einige Rippenfragmente und Wirbel eines »Neugeborenen oder, mit größerer Wahrscheinlichkeit, eines Fötus« identifiziert werden (Vermeersch 2002, 277).

5 Das Kindergrab DV 3 aus DV I (Klíma 1995) dürfte altersmäßig zu infans I und nicht zu den prä- bis perinatalen Bestattungen gehören.

Eingebettet in einer mittelpaläolithischen Schicht der Mezmaiskaya Höhle (Rajon Apscheronsk, Russland [nördlicher Kaukasus, Krasnodar]) wurden aus einer Grube kindliche Schädelreste geborgen, die auf ein Sterbealter zwischen dem 7. Fötalmonat und dem 2. postnatalen Monat hindeuten (Golovanova u. a. 1999) und möglicherweise mit einem Steinblock abgedeckt waren. Eine Direktdatierung ergab allerdings ein jungpaläolithisches Alter von rund 30 000 Jahren (unkalibriert; Pettitt 2011, 91).

Die interessanteste und mit 27 810–27 430 cal BP ähnlich alte Parallele zu den Neugeborenen des Wachtberges stammt aus der Höhle von Santa Maria di Agnano in Ostuni (Apulien, Italien). Es handelt sich um das Grab einer ca. zwanzigjährigen Frau, die in linksseitiger Hockerlage und in Rötel gebettet begraben wurde. In ihrem Becken fanden sich Skelettüberreste eines Fötus, im Kopfbereich hunderte von durchlochten Muscheln und Canidenzähnen (Zierde einer Kopfbedeckung?) (Coppola 2008; Pettitt 2011, 185 Fig. 6,19; Nava u. a. 2017). Das Entwicklungsalter des Fötus wurde aus der Zahnschmelzentwicklung abgeleitet und ergab ein Alter zwischen 31. und 33. Schwangerschaftswoche. Da der Fötus eine korrekte Beckenlage aufwies und keine Anzeichen einer krankhaften Veränderung diagnostiziert werden konnten, weder an den mütterlichen (normalgeformtes Becken) noch an den kindlichen Resten, wurde der frühe Tod der Schwangeren – und damit auch ihres Kindes – mit Stressepisoden in Verbindung gebracht. Anzeichen dafür lieferten, den Wachtberg-Kindern vergleichbare, »Stress-Linien« im Zahnschmelz der Milchzähne (Nava u. a. 2017).

Bereits deutlich jünger, d. h. um 14 500–13 900 cal BP datieren die teilweise mit Rötel überzogenen Skelettreste (Street u. a. 2006), die 1953 gemeinsam mit Artefakten aus einer Sandgrube bei Irlich geborgen und danach in einem lokalen Museum verwahrt worden waren. Sie wurden erst im Jahr 2000 wiederentdeckt und einer wissenschaftlichen Analyse zugeführt. Die Skelettreste konnten vier Individuen, einem jungadulten Erwachsenen und drei Kindern, zugeordnet werden, darunter ein Säugling, der im Alter von 6–12 Monaten verstorben war. Es muss offenbleiben, um welche Art von Bestattung – Einzelgräber, Doppelgräber oder eine Mehrfachbestattung – es sich gehandelt haben könnte. Lediglich aus der Rötelfärbung der Skelettüberreste ist auf eine Grablegung der Körper zu schließen (Orschiedt u. a. 2017).

Sind schon perinatale Bestattungen im Paläolithikum generell nur selten dokumentiert, so sind Zwillingsbestattungen aus dieser Periode ein Novum.

In prähistorischen Fundkontexten wurden Zwillinge bislang nur indirekt erschlossen, wobei die Beweisführung entweder auf physischer Ähnlichkeit (z. B. Zahnmorphologie) oder auf Merkmalen des Bestattungskontextes ruht.

Ein (unbestätigter) Fall dieser Art könnte bei einem auf ca. 11 500 cal BP datierten Fund aus Upward Sun River (Alaska, USA) gegeben sein: eine Doppelkörperbestattung und eine Brandbestattung in Superposition. Im komplett mit Ocker bedeckten Doppelgrab fand sich Individuum 1 am Westrand der Grube in regulärer Hockposition, Individuum 2 zentral an der Grubensohle, mit seinem Oberkörper über den Beinen und den Knien dicht am Brustkorb anliegend. Individuum 1 hat die Geburt ca. fünf Wochen überlebt, Individuum 2 verstarb bereits vor der Geburt. Nach B. A. Potter u. a. (2014) könnte es sich bei Individuum 2 um eine Sekundärbestattung handeln, die bei der Grablege von Individuum 1 andernorts exhumiert wurde. Eine aDNA-Analyse zur Klärung der vermuteten Verwandtschaft konnte nicht durchgeführt werden.

Zwei weitere, allerdings deutlich jüngere Funde liegen aus Spanien vor und datieren in die Eisenzeit: An der Fundstelle von Olèrdola (Barcelona) wurde ein Doppelgrab entdeckt, in dem zwei Säuglinge (Mädchen?), die möglicherweise innerhalb der ersten Wochen (max. vier Wochen nach ihrer Geburt) verstarben, gemeinsam bestattet wurden (Crespo u. a. 2010). Die aDNA-Analyse blieb ohne Ergebnis, sodass der Zwillingsstatus zwar wahrscheinlich, aber molekularbiologisch nicht verifiziert werden konnte. Der zweite Fund stammt aus El Castejón de Bargota (Navarra) und betrifft zwei gemeinsam in einem Grab bestattete perinatale Individuen. Da ihre körperliche Entwicklung ungefähr der 40. Schwangerschaftswoche entsprach, dürften die Neugeborenen kurz nach ihrer Geburt verstorben sein (de Miguel 2009).

Bislang sind nur zwei Fälle aus archäologischen Kontexten bekannt, in denen der seltene Befund von Zwillingen aus der Anordnung der Skelettüberreste von zwei Föten bestätigt scheint: ein Fall eines erschwerten oder gestörten Geburtsverlaufes (Dystokie) aus Grab R11 von Lokomotiv (Sibirien, Russland; 8000–7000 cal BP; Lieverse u. a. 2015) und ein aus der Zeit zwischen 1600–1800 n. Chr. stammender Fall einer Zwillingsschwangerschaft bei den Arikara (Dakota, USA; Owsley/Bradtmiller 1983).

Eine aDNA-analytische Bestätigung der engen Verwandtschaft haben all diese Befunde aus verschiedenen Gründen bislang nicht erfahren.

Die vorliegende bioanthropologische Untersuchung konzentrierte sich auf die beiden Säuglingsbestattungen, die in der bekannten jungpaläolithischen Fundstelle von Krems-Wachtberg in Niederösterreich entdeckt wurden und von denen eine, das 2005 entdeckte Grab 1, den bemerkenswerten Fall einer Doppelbestattung repräsentiert, deren Verwandtschaft durch die aDNA-Analyseergebnisse abgesichert wurde: Es handelt sich um den ungewöhnlichen Fall von eineiigen Zwillingen, deren Geschlecht, ebenfalls über diesen molekularbiologischen Zugang, als männlich identifiziert werden konnte. Auch beim dritten Säugling, der in dem nahegelegenen Grab 2 bestattet worden war, handelt es sich um einen Jungen, genetisch einen nahen Verwandten der Zwillinge (vermutlich 3. oder höheren Grades). Eindrucksvoll bestätigen die Ergebnisse der aDNA- Analysen damit nicht nur das seltene Ereignis einer »Zwillingsschwangerschaft«, sondern auch, dass Gruppen von Jäger- und SammlerInnen vor 31 000 Jahren enge familiäre Einheiten bildeten und zu den räumlich nächst gelegenen Gruppen im benachbarten Mähren in einer Verwandtschafts-(Herkunfts-?)beziehung standen (Fu u. a. 2016) – was sich auch aus dem Fundmaterial und den Bestattungssitten andeutet (Rötelverwendung, Grababdeckungen mit modifizierten Mammutschulterblättern).

Basierend auf der Konstruktion des Doppelgrabes, der unterschiedlichen Platzierung und individuellen symboli-

schen Behandlung der Säuglinge, wurde auch die Hypothese formuliert, dass der perinatale Tod und die Beisetzung nicht zeitgleich erfolgt war und das lediglich mit einer abnehmbaren Sonderkonstruktion (Mammutschulterblatt und Stoßzahnfragment) bedeckte Grab vermutlich wieder geöffnet wurde. Zeugnisse eines solchen Szenarios bzw. eines »reopenings« von paläolithischen Gräbern sind rar und generell kritisch zu hinterfragen, da zuverlässige Dokumentationen oft fehlen oder nicht den modernen Standards genügen. Für unsere Fragestellung der sekundären Öffnung von paläolithischen Gräbern können wir zumeist nur Mehrfachbestattungen heranziehen. Aus den späteren Perioden wissen wir, dass Bestattungen mit Abdeckung eher Hohlräume bewahren und daher auch leichter wiedergeöffnet werden können. Unikate und sehr gut dokumentierte gravettienzeitliche Befunde stammen aus der Höhle von Cussac (Dordogne, Frankreich; Aujoulat u. a. 2004; Kacki u. a. 2020)[6]. Die hier vorhandenen sechs Individuen sind aufgrund von ^{14}C-Daten als zeitgleich mit der dortigen Höhlenkunst anzusehen. Alle sechs Individuen weisen postmortale Manipulationen an ihren körperlichen Resten auf, die zum Teil natürlich entstanden sein können, aber zumindest teilweise nur durch bewusste sekundäre Eingriffe durch den Menschen zu erklären sind. Auch sogenannte Schädeldeponierungen können dem Nachweis sekundärer Dislozierungen dienen, wenngleich sekundäre Öffnungen von Gräbern meist nicht nachgewiesen sind. Dieser Befund bleibt moderneren Grabungen vorbehalten, wie etwa jenen in 'Uyun al-Hammam (Irbid, Jordanien; ca. 12 000 cal BP), bei dem der Schädel sekundär aus Grab B entfernt und in Grab VIII beigesetzt wurde (Maher u. a. 2011). Ebenso konnte in der Rakefet-Höhle (Nordisrael; ca. 12 000 cal BP) innerhalb einer Gräbergruppe mit 29 Skeletten auf 15 m², bekannt durch Nachweise von Blumenschmuck im Bestattungsritual (Nadel u. a. 2013), ein sekundärer Eingriff eindeutig in Form der Entnahme des Schädels von Homo 28 festgestellt werden.

Im Falle der Wachtberg-Zwillinge konnten wir durch die Anwendung morphometrischer und chemometrischer Ansätze zur Schätzung des Sterbealters, einschließlich der Analyse des von Barium gelieferten Stillsignals, ein leicht abweichendes Sterbealter für die beiden Säuglinge feststellen: Während Ind2 in dem für moderne Zwillinge errechneten perinatalen Zeitfenster verstarb, überlebte Ind1 wahrscheinlich etwa 4–5 Wochen. Dies impliziert, dass die Beisetzung von Ind1 im gleichen Grab dessen Wiedereröffnung erforderte. Da die körperlichen Reste der beiden Kinder in einer ungestörten *in situ*-Lage, ohne Sedimentbedeckung, sondern lediglich von einer millimeterdünnen Schicht aus rotem Ocker überzogen, aufgefunden wurden, muss die Beisetzung von Ind1 zu einem Zeitpunkt erfolgt sein, als die Weichteile von Ind2 noch nicht vollständig abgebaut waren. Aus forensischer Sicht ist es wahrscheinlich, dass die Verwesung des Leichnams von Ind2 das Stadium »post bloat« erreicht hatte (Janaway u. a. 2009). Obwohl unklar ist, welchen Einfluss die fehlende Sedimentbedeckung und die Rötelbedeckung auf das Tempo der Verwesung der Weichteile gehabt haben könnte, ist es denkbar, dass biotische und abiotische Umweltfaktoren in einem Winter oder beginnenden Frühjahr unter den periglazialen Bedingungen vor 31 000 Jahren sowohl eine verzögerte Verwesung als auch eine Austrocknung begünstigt haben könnten. Dies kann erklären, dass bei der Wiedereröffnung des Grabes und der Einbettung von Ind1 keine erkennbaren Lageveränderungen oder Beschädigungen an den Skelettresten von Ind2 verursacht wurden. Obwohl für die Bestattungsrituale des Gravettien eine personalisierte symbolische Behandlung dokumentiert ist (Trinkaus/Buzhilova 2018), zeigt unsere Untersuchung der Säuglinge vom Wachtberg in Krems eindrucksvoll, dass die gravettienzeitlichen Bestattungsriten auch die Wiedereröffnung eines Grabes und die Veränderung/Manipulation seiner Anlage und seines Inhalts umfassen können.

6 Die Befunde wurden ausschließlich aus Fotos und 3D-Dokumentationen erstellt.

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Abbildungsnachweis

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The Shaman and the Infant: The Mesolithic Double Burial from Bad Dürrenberg, Germany

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Zusammenfassung

Die Schamanin und der Säugling: Die mesolithische Doppelbestattung aus Bad Dürrenberg, Deutschland

Die 1934 bei Bauarbeiten im Kurpark von Bad Dürrenberg, Saalekreis, entdeckte Doppelbestattung einer erwachsenen Frau und eines Säuglings gehört zu den herausragenden Grabbefunden des Mesolithikums in Mitteleuropa. Trotz der widrigen Fundumstände und der Bergung des Fundes durch Laien mit Unterstützung eines Restaurators konnte eine Vielzahl der zahlreichen Beigaben und der Skelettreste geborgen werden. Die außergewöhnliche Ausstattung der in sitzender Haltung bestatteten Frau mit einem Säugling umfasst neben Silexartefakten und Felsgesteingeräten auch Knochen- und Geweihartefakte, ein Rötelstück, zahlreiche Tierknochen einschließlich der Panzer von mindestens drei Sumpfschildkröten und teilweise durchbohrte Tierzähne. Zusammen mit einem schädelechten Rehgeweih und ursprünglich sechs zum Teil durchbohrten Eberhauern stellen diese Funde wahrscheinlich einen Kopf-/Körperschmuck dar. Das Grab wird aufgrund seiner Ausstattung als Bestattung einer Schamanin gedeutet. Verschiedene pathologische Befunde an den Frontzähnen und Anomalien der Halswirbelsäule sowie der Schädelbasis unterstützen diese Interpretation.

Nachgrabungen an der Fundstelle im Zuge der Vorbereitungen der Landesgartenschau 2024 ergaben nicht nur neue Erkenntnisse zur Deponierung und Positionierung der Körper, sondern erbrachten eine Vielzahl von Neufunden, die eindeutig dem Grab zugerechnet werden können. Neben durchbohrten Tierzähnen, Faunenresten und Steinartefakten konnte auch eine große Anzahl von menschlichen Skelettresten geborgen werden. Vor allem das nur teilweise erhaltene Skelett eines Säuglings konnte ergänzt werden. Die Entdeckung des Felsenbeines ermöglichte auch bei diesem Individuum eine genetische Analyse. Im Ergebnis zeigt sich, dass es sich um einen Jungen handelt, der nicht der Sohn der Schamanin ist, sondern im 4. oder 5. Grad mit ihr verwandt ist.

Summary

The double burial of an adult woman and an infant, discovered in 1934 during construction works at the spa gardens of Bad Dürrenberg, Saalekreis district, is regarded as one of the outstanding burial finds of the Mesolithic in Central Europe. Despite the unfavourable circumstances of the find and the recovery by lay people with the assistance of a conservator, a large number of the many grave goods and skeletal remains could be rescued. The unusual equipment of the woman with an infant, who was buried in a seated position, comprises flint artefacts and solid rock tools, but also bone and antler artefacts, a piece of red ochre, a number of animal bones including the shell of at least three terrapins and partly pierced animal teeth. Together with real deer antlers and originally six partly pierced boar's tusks these finds are probably head/body ornaments. Due to its grave goods the burial is interpreted as that of a shaman. Several pathological finds on the anterior teeth and anomalies of the cervical vertebrae and the skull base support this interpretation.

Subsequent excavations at the site as part of the preparations for the State Garden Exhibition 2024 brought not only new revelations about the deposition and positioning of the body to light, but also revealed a multitude of new finds, which could be clearly attributed to the burial. Beside of pierced animal teeth, remains of fauna, lithic artefacts and a large amount of human skeletal remains could also be recovered. But especially the only partially preserved skeleton of an infant could be added to. The discovery of the petrosal enabled a genetic analysis at this individual. The result showed that it is a boy, who is not the son of the shaman, but is 4th or 5th degree related to her.

Site and find history

The burial site from Bad Dürrenberg, Saalekreis district, was discovered when digging a trench for a water pipe in the spa gardens of Bad Dürrenberg on 4 May 1934. The burial was found in a central location in the spa gardens about 80 m east of the current edge of the slope to the Saale (Fig. 1). The grave was partially uncovered with the help of local historians and reported to the »Landesanstalt für Vorgeschichte« in Halle. The restorer, W. Henning, recovered the burial and the grave goods after some objects had already been removed from the grave by the construction work and the lay researchers involved (Bicker 1936). In addition, a two-page report and a documentation sketch were made by W. Henning in plan and section (Find spot archive, LDA Halle, ID 1955, OA Bad Dürrenberg). Beyond that, no photographs were taken, nor was it precisely recorded how exactly the skeletal remains had lain in the grave or where the individual grave goods had been located. Only a curved posture with a clearly higher skull and upper arms positioned obliquely upwards was noted, indicat-

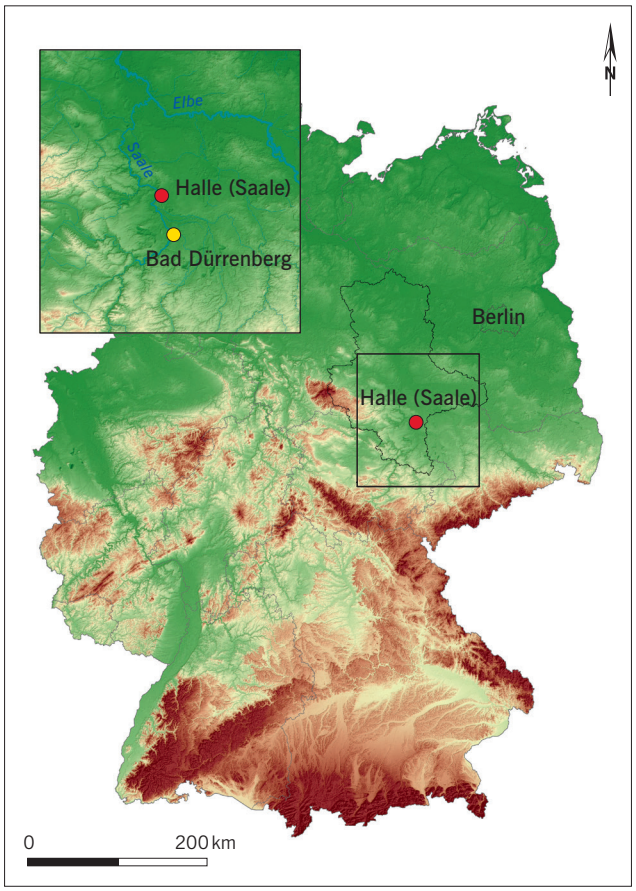


Fig. 1 Location of the Bad Dürrenberg, Saalekreis district, burial close to the Saale River.

Abb. 1 *Fundort des Grabes von Bad Dürrenberg, Saalekreis, in der Nähe des Flusses Saale.*

ing a seated position (Bicker 1936, 60). According to the documentation, the orientation of the burial pit was east-north-east–west-south-west, the skull is said to have been facing south. The burial pit was 90 x 55 cm and not very large. The soil of the lower 30 cm of the grave-pit was apparently strongly interspersed with red ochre, which is clearly visible not only on the skeletal remains but also on the objects found in the grave. During the excavation, the skeletal remains of an infant were also identified. Based on the skull fragment mentioned in the report of Henning, which lay between the thighs of the buried adult, the position of the infant was reconstructed (Bicker 1936, 60). The position of the grave goods remains largely unclear, only the stone axe below the right upper arm is explicitly mentioned in Henning's report.

Grave goods

The grave at Bad Dürrenberg contains an unusual number of grave goods for the Mesolithic period (Fig. 2). The few graves from this period in Central Germany known so far contain either no or only a few objects; these grave goods are mostly flint artefacts. Thus, not only the quantity of objects, but also their composition, is remarkable in the grave of Bad Dürrenberg[1].

One of the central objects are the antlers of a roebuck, which was about 2 years old (Fig. 3). These show a few signs of modern damage, which most likely originated during the recovery process; however, older fractures are also apparent. The older breakage pattern could be associated with a deliberate dressing of the piece. Around the base of the antlers, there are numerous traces of cuts from de-fleshing or skinning. A total of six boar tooth lamellae were discovered of which the only two pierced specimens were most likely located in the neck area of the woman in the grave. The lamellae were made from longitudinally split canines and show evidence of polishing and rounding, as well as traces of their manufacture. One piece has a total of four perforations, three at the base and one at the tip. While the base was damaged recently, the hole at the tip was made in prehistoric times. A pierced fragment of a hyoid bone from a wild boar was also found, along with six pierced incisors from wild boar, which show clear signs of wear. Further pierced animal teeth could be assigned to aurochs and bison. A total of 33 incisors and three canines were identified, half of which have pierced roots. Another 16 incisors and two canines come from red deer and do not show any perforations. Also from red deer is a metatarsal that has been split lengthwise, with signs of wear at the tip. In this spot, especially on the inner side, a strong red ochre adhesion is visible, which could match a piece of red ochre that shows signs of wear. Other bone implements are present including awl-like implements, two of which were made from metatarsal bones of red deer and three others were obtained from metatarsal and metacarpal bones from roe deer. The pieces show polishing and rounding and reveal traces of manufacture. There is also a pierced implement obtained from a heavily reworked antler base of a red deer.

In addition to bone artefacts, several flint artefacts were also found. These include two flakes, seven blades and a piece of debris. In addition, there are 29 microliths and two microlithic flakes, which were discovered after the recovery of the finds in a right humerus of a crane that had been prepared to serve as a container. In addition to these flint implements four ground stone artifacts were found in the grave at Bad Dürrenberg. Among these is a flat axe which, as mentioned above, is thought to have been deposited below the buried person's right humerus. The piece is almost completely polished and for many years had been classified as a chronological reference to the transition between Mesolithic and Neolithic (Geupel 1977), or originally even belonging to the Neolithic (Bicker 1936). Since several dated polished rock axes from the Mesolithic are now available (Fischer et al. 2009; Little et al. 2017; Gramsch 2021), this can no longer be used as an argument against an earlier Mesolithic date (see below for the absolute dating of the human and animal skeletal remains from the grave). In addition, an oval flat and a triangular stone pebble are present. The pieces show polish-

1 Bicker 1936; Geupel 1977; Teichert/Teichert 1977; Grünberg et al. 2016, 296–323; Dietl et al. in press.

Skeletal element	Lab Number	^{14}C date in BP	Calibrated years BC 1σ range	Calibrated years BC 2σ range
Homo, Femur	BLN-2130	7580 ± 80	6564–6271	6593–6246
Homo, Femur	BLN-2221	7730 ± 80	6638–6476	6768–6423
Homo, Costa	OxA-29229	5643 ± 30	4536–4409	4543–4368
Homo, Costa	OxA-3136	7930 ± 90	7032–6689	7060–6599
Homo, Fibula	OxA-31090	8012 ± 40	7050–6829	7062–6706
Capreolus, Mandibula	OxA-31091	7906 ± 37	6903–6654	7032–6647
Capreolus, Scapula	OxA-31093	8006 ± 37	7048–6830	7059–6706
Emys orb., Carpapace	OxA-31092	8335 ± 40	7480–7346	7524–7195

Tab. 1 Overview of available radiocarbon dates.

Tab. 1 *Übersicht über die verfügbaren Radiokarbondaten.*

ing, impact marks and other signs of use. Next to these is a percussion stone with clear fields of scars, polishes, and traces of red ochre.

In addition to the bone artefacts and the tooth ornaments, which originate from the main hunted fauna of the Mesolithic (wild boar, roe deer, red deer and aurochs, or bison), there are isolated bone fragments from the grave context that can be interpreted as grave goods. These include an unmodified thoracic vertebra fragment and a metacarpal bone of the roe deer. The roe deer is additionally represented by three lower jaw halves from at least two animals, an isolated incisor and three scapula fragments, also from at least two animals. Only the lower jaw halves show modifications and the fracture patterns clearly indicate that they were smashed when fresh as there are no traces of cutting. In addition, a hock bone from a beaver and a shoulder blade from a hedgehog are present, together with various small and very small bone fragments that could not be determined in more detail. One of the indeterminate fragments shows signs of cutting. Besides the already mentioned humerus of a crane, which served as a container for microliths, a tibiotarsus bone from a crane is present but does not show any modifications. A total of 120 fragments of river mussels of various species with ochre residues attached to them were also found in the tomb. In addition, 64 fragments of at least three shells of the European pond turtle comprise material from the original find in the 1930s. Traces of modification in the form of scratches and cuts on the inside of the carapaces indicate that they were cleaned of adhering soft tissue and that the dorsal vertebrae, which are fused to the inside of the carapace, were also removed. This, together with the absence of other skeletal elements and fragments of the abdominal carapace, indicates that only the carapaces were given as grave goods.

Dating

The controversial discussion about the chronology of the grave was mainly ignited by the existence and the secure grave affiliation of the polished flat axe (see Geupel 1977), which led to a first conventional ^{14}C dating in 1979. The humerus, femur and tibia of the right side of the body were taken as sample material, but only the femur was used for the two dating procedures (laboratory protocol Berlin)[2], the other two skeletal elements of the sampling have since been lost.

Table 1 summarizes the results of the various absolute dating efforts made to date. While the conventionally measured ^{14}C-dates of the Berlin laboratory appear too young in comparison with the dates from Oxford (OxA-3136, 31090–31093), and are outdated from today's point of view, the two solid dates of the human remains together with the two roe deer dates according to the sum calculation in the range of 2σ (95 % probability) result in a time horizon of 7000–6800 cal BC for the grave of Bad Dürrenberg. The grave of Bad Dürrenberg thus dates to the early Atlantic in terms of climate history.

The human skeletal remains

The human skeletal remains of the double burial were examined several times[3]. The anthropological age-at-death and sex determinations yield the remains of a 30–40 year-old woman and a 6–8 month-old infant, whose sex could not be determined as the decisive traits are not developed at this age. Ongoing investigations as part of the follow-up investigation of the site have retrieved further skeletal remains of the two individuals from the grave at Bad Dürrenberg. In addition to the completion of the skeletal remains, especially of the infant skeleton, a re-evaluation of the pathological findings noted in the past is also being undertaken. The 30–40 year-old woman was a gracile person with a body height of about 1.55 m, typical for the period. Remarkable about her skeleton is the absence of distinct muscle attachments, especially on the lower extremities, which are commonly found in hunter-gatherers. Slight signs of wear on the spine (spondylosis deformans) in the area of the lumbar and thoracic vertebrae indicate a certain physical strain in the area of the trunk.

At the base of the skull there is an anomaly at the edge of the great occipital hole (foramen magnum), in the form of a small constriction. This area, which has already been consid-

2 Thanks to Dr. J. Gresky, DAI Berlin, for researching the original dating protocols.

3 Heberer 1936; Grimm 1957; Orschiedt 1999; Porr/Alt 2006.

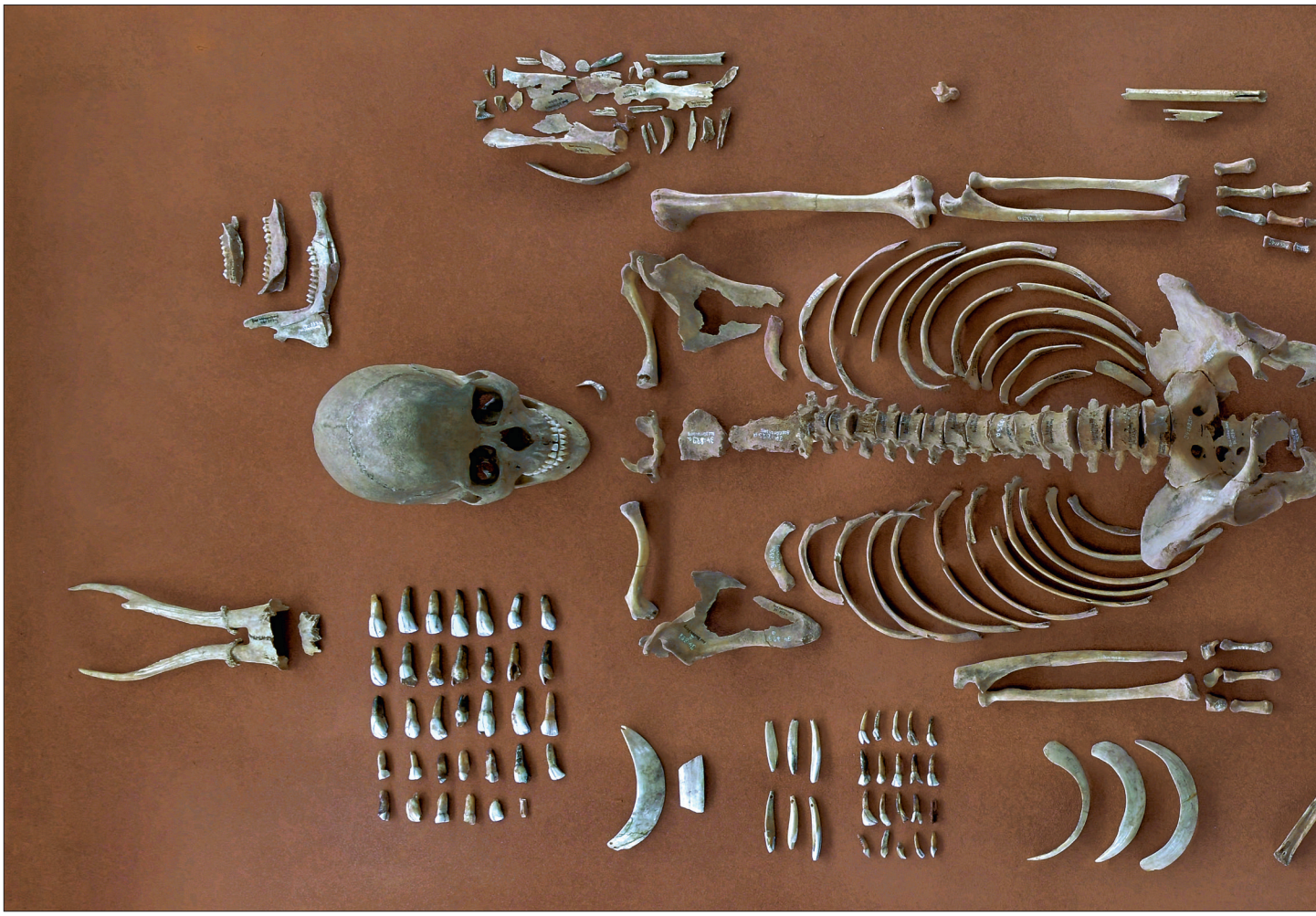


Fig. 2 Display of finds from the 1934 excavation at the State Museum of Prehistory Saxony-Anhalt.

Abb. 2 *Ausstellung der Funde von der Ausgrabung im Jahr 1934 im Landesmuseum für Vorgeschichte Sachsen-Anhalt.*

ered evidence of decapitation, is the imprint of an abnormally developed blood vessel (Orschiedt 1999, 128 f.). The first cervical vertebra is incompletely formed due to a congenital growth defect and has only reached 40 % of the arch. The rounded end of the vertebral arch corresponds to the previously observed defect at the large occipital hole (Fig. 4). In this context, the hypothesis was formulated that a pinching of the blood vessel with various sequelae appears possible with a corresponding head posture (Porr/Alt 2006). The discovery of the 2nd cervical vertebra among the finds of the re-excavation could be confirmation of this. This vertebra also shows an anomaly, which is limited to the vertebral process in the form of a protruding bone clasp. This makes a blockage of one of the blood vessels leading to the brain plausible. This can be caused intentionally by adopting a certain head posture. The consequences are unlikely to have been serious or hazardous to the person's health. However, it is conceivable that a nystagmus, i. e., an involuntary movement of the eyeballs, could be caused by the blockage of a blood vessel. This unusual feature might have been perceived as uncanny and when initiated on purpose may have reinforced or even justified her role as a shaman.

Another peculiarity is a conspicuous tooth abrasion in the area of the upper central incisors (Orschiedt 1999, 128). This abrasion, which only affects the two anterior teeth and whose specific orientation towards the palate is referred to as the LSAMAT phenomenon (Lingual Surface Attrition of the Maxillary Anterior Teeth), has so far been demonstrated several times and in different temporal and geographical contexts (Fig. 5). A cause of this specific kind of abrasion is not known, but is usually interpreted as the use of the anterior teeth as tools or as a »third hand« (Alt/Pichler 1998, 399; Porr/Alt 2006, 400–402). In this context, the fact that the nerve cavity of both teeth is opened seems unexplained. Usually, secondary dentine is formed in the nerve cavity during tooth grinding, which protects the nerve from exposure should the tooth grinding reach this area. In this case, the grinding must have occurred so quickly that the corresponding process could no longer be initiated. Bacteria could then penetrate through the exposed nerve cavity to the root of the tooth and cause inflammation. Traces of this apical process can be seen on the maxilla. What activities may have caused the opening of the nerve cavity will be the subject of future investigations.

The re-excavation of the site

In the run-up to the opening of the State Garden Show in the spa gardens of Bad Dürrenberg, originally scheduled for 2022,



extensive construction measures were planned for renovation and redesign. Against this background, the opportunity arose for a follow-up investigation of the site where the so-called »Shaman of Bad Dürrenberg« was found. A first search excavation led to the localization of the pipe trench that had originally led to the discovery of the grave in 1934. Traces of red ochre in the uppermost layer filling the trench gave a first indication of the correct location of the grave. However, an expected visible disturbance outside the pipe trench as evidence of the excavation of 1934 was missing. An alternative explanation, which suggests that the original uncovering and salvage was not carried out from above, but deliberately from within the pipe trench, thus appeared conceivable and with it the possibility of preserving the areas of the burial pit lying above the buried female and child. The excavation of the pipe trench over a length of 5 m revealed a pronounced disturbance of the soil profile in the expected location of the burial pit, which was interpreted as an indication of the intervention carried out in 1934 to recover the finds. In addition, the fill in/back material contained accumulations of red ochre along the entire length of the worked section and numerous finds with colour adhesions that corresponded to those of the known find inventory. These were concisely concentrated in the area of the disturbance recorded in the trench profiles. Besides numerous faunal and human skeletal remains and flint artefacts, the pierced animal teeth deserve special mention. The total area of the postulated burial pit on both sides of the pipe trench was recovered in the form of 2 blocks in order to process it under workshop conditions (Fig. 6).

Already during the excavation in the field, it became apparent that the upper layers of the burial pit defied a purely visual recording. By uncovering the recovered blocks, the structure of the burial pit could finally be documented. An upper part with a trough-shaped profile could be distinguished from a shaft-like lower part. In the lower part, the remains of a rectangular construction were found, the north-eastern corner of which was still preserved at a height of about 20 cm. Wooden imprints indicate a wattle-like construction with steep walls, which was lined with clay and backfilled with clay towards the wall of the burial pit (Fig. 7). Its base corresponds in shape and orientation to the »burial pit« recorded in 1934. Thus, it was not the burial pit itself that was documented at the time, but rather its chamber-like installation in which the skeletons and the grave inventory were located.

As already mentioned, besides numerous faunal and archaeological objects the new finds also contained a number of human skeletal remains. In addition to hand and foot bones and rib fragments, also vertebrae and vertebral fragments could be assigned to the adult female. The skeletal remains of the infant, which was only incompletely recovered in 1934, could be complemented substantially. However, due to the highly fragmentary preservation, this work has not yet been completed. The most important new finding with regard to







Fig. 3 (left page) Roe deer antler, perforated and unperforated teeth of aurochs/bison, red deer and wild boar.

Abb. 3 (linke Seite) *Rehgeweih, durchlochte und ungelochte Zähne von Aurochsen/Bison, Rothirsch und Wildschwein.*

Fig. 4 Anomaly of the skull base and incomplete formation of the atlas bone.

Abb. 4 *Anomalie der Schädelbasis und unvollständige Ausbildung des ersten Halswirbels.*

Fig. 5 Abrasion of the upper central incisors with open pulp chamber.

Abb. 5 *Abnutzung des oberen mittleren Schneidezahns mit offener Zahnmarkkammer.*

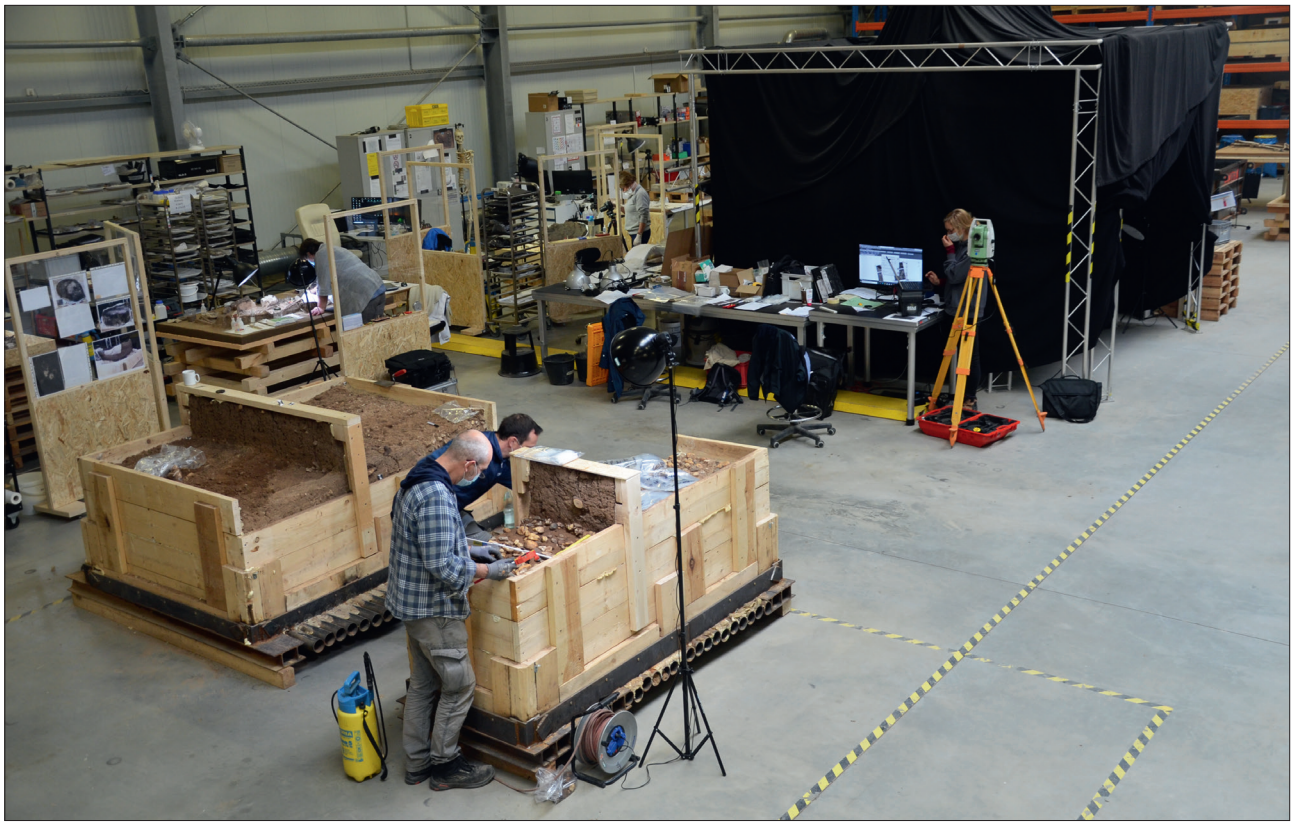


Fig. 6 The two removed blocks containing the remains of the burial pit during excavation at the State Office for Heritage Management and Archaeology Saxony-Anhalt.

Abb. 6 *Die zwei geborgenen Blöcke, die die Überreste der Grabgrube enthielten, während der Ausgrabung des Landesamtes für Denkmalpflege und Archäologie Sachsen-Anhalt.*

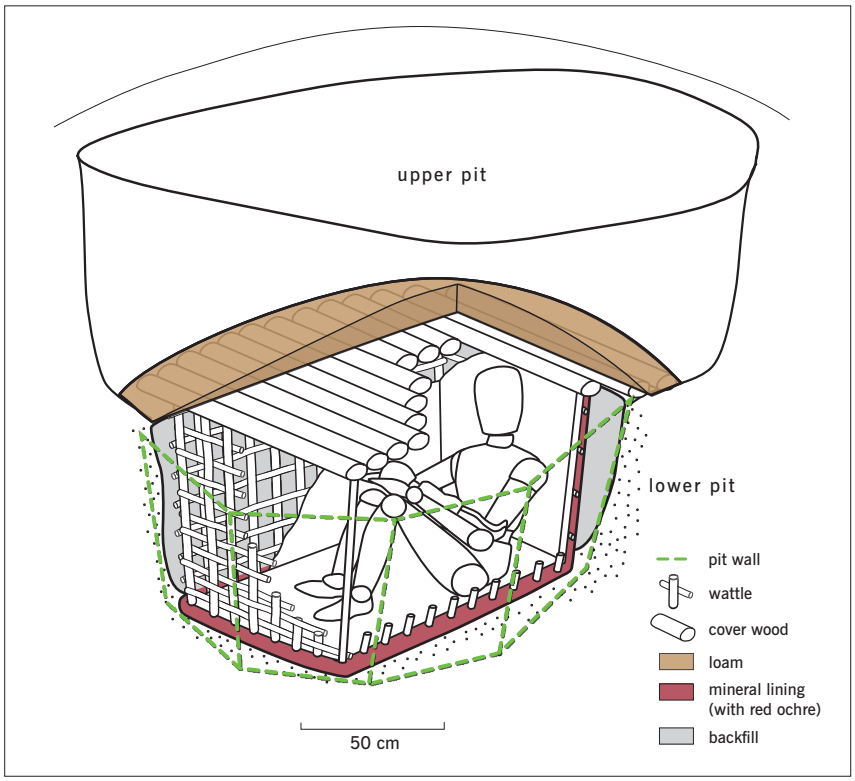


Fig. 7 The reconstruction of the burial pit, which has a basket-like structure in which the bodies of the shaman and the infant were deposited in a sitting position.

Abb. 7 *Die Rekonstruktion der Grabgrube, die eine korbähnliche Struktur hatte, in die die Körper der Schamanin und des Säuglings in sitzender Position plaziert wurden.*

the preservation of the child was certainly a pars petrosa (petrous bone), which for the first time made a genetic examination of this individual possible.

Genetic results from the genome-era

The first attempts to retrieve ancient human DNA from the burials at Bad Dürrenberg were made in 2003–2006 together with colleagues from the Department of Anthropology at the Johannes Gutenberg University of Mainz. For this purpose, one of the authors (W. H.) collected samples from the compact bone of the left femur and a tooth (33) of the adult female, as well as sample of the femur of the child. At that time, ancient DNA studies were still in their infancy and the classical PCR-based method were used. The retrieval of authentic ancient human DNA, free of modern-day contamination and thus not delivering false-positive results, was often met with skepticism, and any results had to withstand scrutiny (Willerslev/Cooper 2005). Following the strict criteria for replication and authentication of the results, several hundred base pairs of the hypervariable region of the human mitochondrial genome from the adult female could be retrieved. These results, attributing the Bad Dürrenberg individual to mitochondrial haplogroup U4, were published in 2009, alongside a number of hunter-gatherer individuals from Europe (Bramanti et al. 2009). The fact that nearly all hunter-gatherer individuals known at the time belonged to haplogroup U, which was considered on the oldest maternal lineages in Europe (Richards et al. 2000), and different from the lineages commonly found in early European farmers from the Neolithic period, lend support to the antiquity and the credibility of the results.

The revolutionary breakthroughs in Next Generation Sequencing methodologies and associated Bioinformatics emerging in 2005 also propelled ancient DNA research into unprecedented spheres, and it soon became possible to generate complete genomes from prehistoric humans (Metzker 2010). In combination with refined methods to extract DNA and avoid contamination, and the realization that the petrous portion that forms the solid bone capsule around the human hearing apparatus preserves the highest amount of endogenous human DNA (Pinhasi et al. 2015), this revolution also led to the idea to revisit the ›shaman lady‹ in order to generate genomic data. First, another piece of long bone was tested, but yielded only very limited results. In the same year, her petrous bone was sampled using a minimally invasive method by drilling from the base of the skull to preserve the fully intact skull. At this time, given the refined methods at hand, re-sampling of the infant skeleton was also considered, but deemed not justifiable, given the highly fragmentary nature of the skeletal remains. However, the bone powder from the female's petrous bone proved to be a treasure trove for ancient DNA analyses. Genetic sexing quickly confirmed her as a biological female, but this came no longer as a surprise. Fast forward a few years, the first genome-wide data from the adult female was published (Rivollat et al. 2020) and a complete genome with 13X coverage soon thereafter (Childebayeva et al. 2022).

With the availability of genome data from several thousands of modern and now also from prehistoric and historic human genomes, it is possible to reconstruct a genetic history of many regions of the world. The genomic ancestry profile of the ›shaman lady‹ falls squarely within several dozen other Mesolithic hunter-gatherer individuals from central and western Europe, a profile which is commonly coined »Western (European) Hunter-Gatherer ancestry« or »WHG« ancestry (Lazaridis et al. 2014; Fu et al. 2016; Posth et al. 2023). This ancestry emerged from south/southeastern parts

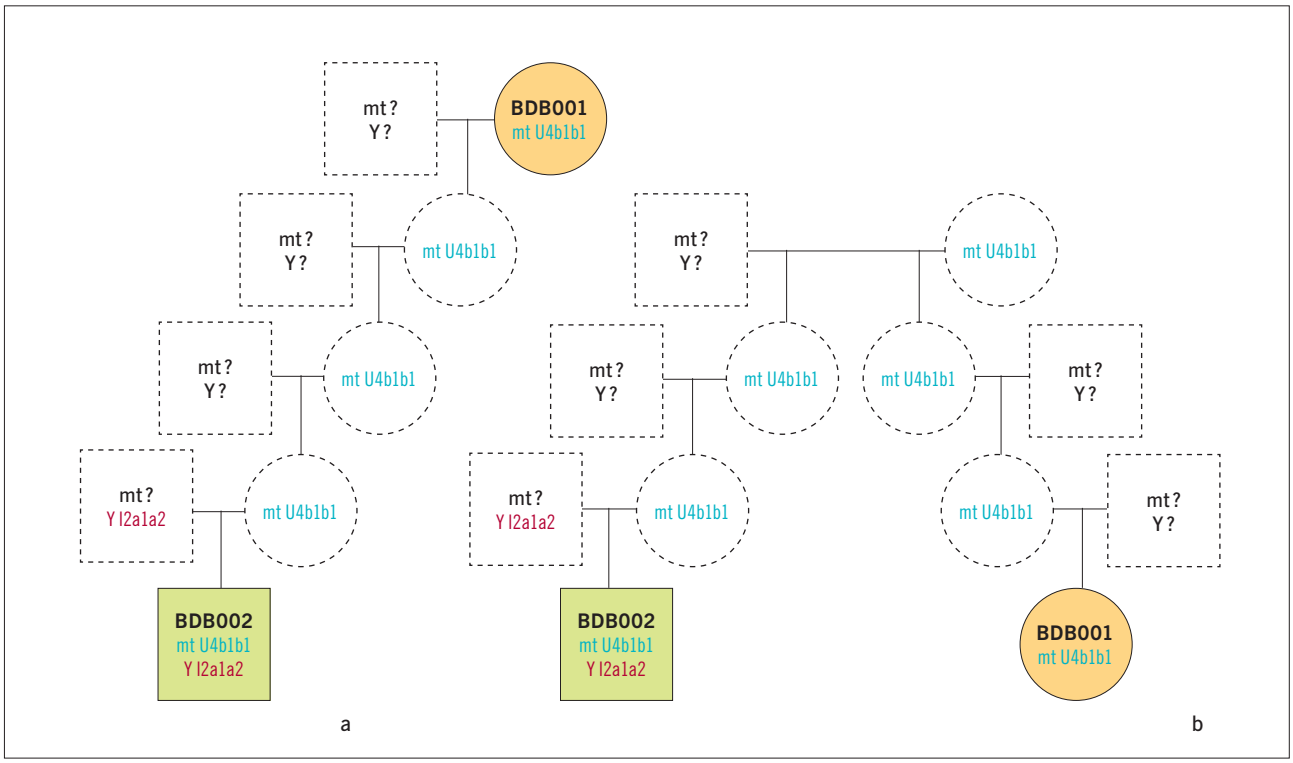


Fig. 8a–b Ilustration of two possible relationship scenarios between the adult female (BDB001) and the boy (BDB002) from Bad Dürrenberg. a 4th degree generational descent on the mother's side (5th would be another generation added); b alternative constellation of a 5th degree relationship in which both individuals could have overlapped during their lifetime. Of note, slight balancing variations in the number of generations on each side of this pedigree are also possible. Circles and squares depict genetic females and males, respectively. Blank symbols with dashed outline represent unsampled relatives; mt mitochondrial haplotype; Y Y-chromosomal haplotype.

Abb. 8a–b *Darstellung von zwei möglichen Verwandtschaftsszenarien zwischen der erwachsenen Frau (BDB001) and dem Jungen (BDB002) aus Bad Dürrenberg. a Abstammung 4. Grades mütterlicherseits (5. Grades wäre eine weitere Generation zugefügt); b alternative Konstellation einer Verwandtschaft 5. Grades in der beide Individuen zeitgleich gelebt haben. Leicht abgewandelte Alternativen in der Anzahl der Generationen auf beiden Seiten dieses Stammbaums sind auch möglich. Kreise und Quadrate stellen jeweils genetische Frauen und Männer dar. Leere Symbole mit gestrichelter Umrandung repräsentieren nicht beprobte Verwandte; mt mitochondrialer Haplotyp; Y Y-chromosomaler Haplotyp.*

of Europe during the Epipaleolithic and was soon replacing the prevailing Magdalenian-associated ancestry in post-LGM Europe to then become the predominant type of genomic ancestry during the early Holocene in western/central Europe, as the naming suggests. Eastern Europe was home to a related but distinguishable form of ancestry (Eastern European Hunter-Gatherer ancestry; EHG), and both mixed in a longitudinal region of overlap stretching from Scandinavia to the Baltics and from the Ukrainian forest steppe to the Middle Danube region. Her mitochondrial genome could also be completed, which not only confirmed the PCR-based findings from early studies, but also refined the haplotype call to lineage U4b1b1.

Having the complete genome sequence data from a person allows the exploration of any gene of interest for which the function is known or the association is established reasonably well. This also includes genes that encode the phenotypic appearance, which are not the primary interest of population geneticists given the connotations associated with skin, hair and eye colour. However, having the opportunity to know what prehistoric individuals looked like is critical in order to generate reconstruction for the purpose of museal illustration. In fact, the numerous life-like illustrations by K. Schauer form an integral part of the State Museum of Prehistory in Halle and especially the portrait of the ›shaman lady‹ has appealed to a large number of visitors since the opening of the second part of the permanent exhibition in 2004. Thus, it was important to update the portrait with the current genetic findings. Indeed, the phenotypic variants analyzed in the Bad Dürrenberg genome inform us that the shaman had a relatively dark skin complexion, dark, straight hair and blue eyes. This combination was quite common among hunter-gatherer individuals from Western Europe and the shaman lady shared this appearance with contemporaneous Mesolithic individuals from sites such as Loschbour, Mullerthal (Luxembourg), La Braña, Asturias (Spain), or Cheddar Man in Somerset (Britain)[4].

However, one of the most pressing questions that could not be answered, even with a complete genome at hand, was whether she was the mother of the infant, related to the child in any way, or perhaps not related at all. The answer to this would require genomic data from the child for direct comparison in order to look for shared portions of the genome, as would be expected in the case of closely related individuals. The sensational retrieval of the petrous bone(s) during the re-examination of the original find spot finally opened up

4 Lazaridis et al. 2014; Olalde et al. 2014; Mathieson et al. 2015; Brace et al. 2019.

this unique opportunity. And indeed, the genetic analysis of the well-preserved petrous provided the long-awaited answer. The genome-wide data from the child show that it also carries the same genetic ancestry, so undoubtedly belongs to the same time period and thus highly relevant to the burial context described above (unpublished data). Further, genetic sexing revealed that the skeletal remains of the infant belong to a boy.

Using established methods (Monroy Kuhn et al. 2018) that can detect biological relatedness in ancient DNA data reliably up to the second degree, resulted in the surprising finding that both individuals are not closely related in the first degree, i. e., they are not mother and son, or siblings. A 2nd degree relationship could also be excluded, which means that an aunt-nephew or grandmother-grandson relationship can also be ruled out.

However, since high-quality data from both individuals, and especially from the female was available, we could also employ a newly developed method[5], which scans the genome data for the presence, amount, and length of tracts in the genome that are shared by two individuals, so-called identity-by-descent (IBD) tracts. This method, optimized to deal with missing data, as is common in fragmented ancient DNA, allows the detection of biological higher degree relatedness, and with reservations, up to the 10th degree. Concerning the two Bad Dürrenberg individuals, we found that the number and length distribution of identify-by-descent tracts that are shared between the pair is equivalent to genetic relatedness of the 4th or 5th degree. This degree of relatedness could be equivalent to 4 or 5 generations apart, assuming a direct line, which would make the adult female the potential great-great-(great)-grandmother of the boy.

However, the relationship does not necessarily have to be in the direct line, which means that the pair could also be 1st cousins, once or twice removed, or 2nd cousins, or the female could be the great-grand-aunt of the boy. Given that both share the same mitochondrial haplogroup means that a direct generational relationship of 4th or 5th degree on the mother's side is indeed possible, and also limits the number of alternative constellations to relationships on the maternal side of the family.

Figure 8 illustrates two possible scenarios: a) a generational relationship, which renders it rather unlikely that the female would have known about the existence of her great-great-(great)-grandson due to the temporal gap of at least 60–80 years, and b) an alternative 5th degree constellation on the maternal side, in which both might have overlapped during their lifetime, and in which she (or any of the parental ancestors of both) might have known about her kin relation to the boy.

The petrous bone of the boy now also allows a direct ^{14}C dating of the child burial. Analyses are currently underway, applying a sensitive new method that is also minimally invasive. The date holds the potential not only to lend support to one of the two relatedness constellations, but also will further corroborate the temporal framework of the burial context.

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5 ancIBD; <https://pypi.org/project/ancIBD/> (22.03.2023); Ringbauer et al. 2023.

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Intramural burials in Neolithic Anatolia: What do they tell us about social organisation?

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Zusammenfassung

Intramurale Bestattungen im neolithischen Anatolien: Was sagen sie uns über die soziale Ordnung aus?

Ein gängiges Modell des sozialen Wandels während des Neolithikums geht davon aus, dass sich die Gesellschaften zunächst in Kernfamilien und später in Großfamilien organisieren, wobei patrilineale und patrilokale Traditionen zunehmend vorherrschen. Für dieses Modell gibt es zwar ethnografische Belege, aber nur indirekt, und eine ausführliche Bewertung wäre nur möglich, wenn man die sozialen Stukturen prähistorischer Gesellschaften im Neolithikum entschlüsseln würde. Die Messung der genetischen Verwandtschaft zwischen Gruppen räumlich geclusterter intramuraler Bestattungen (unter dem Fußboden) im neolithischen Südwestasien bietet eine einzigartige Gelegenheit, die Gültigkeit dieses Modells zu untersuchen.

Wir fassen hier die Ergebnisse von zwei neueren archäogenomischen Studien zusammen, die fünf Siedlungen umfassen. In allen drei untersuchten frühneolithischen Fundstellen (ca. 8500– 7500 v. Chr.) – Aşıklı, Boncuklu und Çayönü – umfassen Co-Bestattungscluster häufig enge genetische Verwandte. Im Gegensatz dazu handelt es sich bei den beiden spätneolithischen Fundstellen (ca. 7000–6000 v. Chr.) – Çatalhöyük und Barcın – bei den untersuchten Bestattungen meist um Jugendliche (subadult), die viel seltener miteinander verwandt sind. Die veröffentlichten Stichproben sind zwar klein, deuten aber insgesamt auf einen zeitlichen Wandel der Traditionen hin. Wir finden auch erwachsene Frauen, die häufig mit ihren genetischen Verwandten auf frühneolithischen Fundstellen bestattet wurden. Wir diskutieren die Ergebnisse im Zusammenhang mit Modellen der neolithischen sozialen Organisation und des Wandels.

Summary

A common model of social change during Neolithic transitions involves societies first organised along nuclear family lines and later organised as extended families, with an increasing prevalence of patrilineal and patrilocal traditions. Ethnographic evidence can be found in support of this model, but is indirect. An in-depth evaluation would only be possible by deciphering the social structures of prehistoric societies undergoing Neolithic transitions. Measuring genetic relatedness among groups of spatially clustered intramural burials (subfloor burials) in Neolithic Southwest Asia provides a unique opportunity to address the validity of this model.

We here summarise results from two recent archaeogenomic studies covering five settlements. In all three early Neolithic (c. 8500–7500 BC) sites investigated, Aşıklı, Boncuklu, and Çayönü, co-burial clusters frequently comprise close genetic relatives. In contrast, in the two late Neolithic sites (c. 7000–6000 BC) studied, Çatalhöyük and Barcın, burials studied are mostly subadults and these are much less frequently related. The published sample sizes are small but overall suggestive of a temporal change in traditions. We also find adult females frequently buried with their genetic kin in early Neolithic sites. We discuss the results in the context of models of Neolithic social organisation and change.

1. Introduction

The emergence of sedentary life and food production involves one of the most dramatic transformations in the history of our species. During this transformation, human beings began to engage with their social and natural environments in radically new ways, which in the long run resulted in the development of increasingly more complex social organisations with various forms of social inequality, private property, and central authority. At the very centre of this transformation was the emergence of a new social and economic unit, i.e., »the kin-related household«, which was frequently organised along patrilineal authority. In this chapter, we summarise current genomic evidence on the social organisation of early and late Neolithic societies in Anatolia and North Mesopotamia and the temporal dynamics of this transformation.

1.1. Social organisation of foragers versus food-producers: the ethnographic evidence

The shift towards a greater role of biological relatedness in social organisation in food-producing societies can be inferred from ethnographic studies of modern-day foragers and traditional agriculturalists or horticulturalists. For instance, data from various forager bands, which usually comprise

some dozens of individuals, suggest relatively fluid relations within a band, with a significant fraction of group members being biologically unrelated. Moreover, post-marital residence choices appear devoid of a clear bias towards joining the family of one gender, i. e., patrilocality or matrilocality[1]. Conversely, in traditional food-producing societies, biological family ties bear significance for social coherence and cooperation; patrilineal and patrilocal traditions are also predominant. Historical and archaeological records, as well as linguistic data, also suggest that patrilineal organisation was widespread (even if not universal) throughout the history of agricultural societies (reviewed in Marlowe 2004; Ember 2011; Bentley 2022).

Multiple lines of evidence thus suggest a change that either accompanied or followed the shift to food production, and which fundamentally reorganised relationships: relatively fluid relationships among foragers versus frequently genetic kin-based and patrilineal or patrilocal organisation in food producers. Although this is not an absolute dichotomy – e.g., matrilineal organisation can be frequently observed in traditional horticulturalist societies (Shenk et al. 2019) –, we can see a general distinction in dynamics between these two types of societies. An enticing question is how this shift in social organisation toward biologically related, kin-based household and family organisations materialised over time in sedentary, food-producing societies.

1.2. Archaeogenomic insights into prehistoric social organisation

Already a decade ago, archaeogenetic studies using mitochondrial DNA (mtDNA) and the Y-chromosome had begun to reveal the presence of biological family members in co-burials or multiple burials in Europe, providing early support for the prevalence of patrilocal traditions in Neolithic and post-Neolithic societies (Haak et al. 2008; Simon et al. 2011; Szécsényi-Nagy et al. 2015). This line of work has advanced rapidly with the advent of archaeogenomics (Racimo et al. 2020). The evidence can be deduced in various ways. One involves the direct estimation of genetic kinship levels (i. e., the degree of genetic relatedness) between individuals co-buried in the same spaces using genome-wide data. Another involves studying whether genetic relatedness between generations follows the male or the female lines. A third approach involves testing whether female or male burials within a locality show higher degrees of genetic variation, which would be consistent with female or male exogamy, respectively.

For instance, M. Sikora et al. (2017) reported genetic data from three co-burials at Upper Palaeolithic Sunghir in Siberia, in which the interred were accompanied by rich burial gifts. None of the pairs turned out to be close relatives. The lack of close relatedness among plausibly socially related individuals would be in line with the notion of genetic kinship not being central to forager social organisation, even though the sample size was too small to allow generalisation. In contrast, data from various studies on Late Neolithic and Early Bronze Age Europe[2] showed strongly patrilineal relationships among individuals buried in the same or similar contexts, with multiple generations nearly exclusively being linked via the male line. Female exogamy in Neolithic and Bronze Age Europe is also supported by the observations of non-local strontium isotope signals in females (Bentley et al. 2012; Knipper et al. 2017; Mittnik et al. 2019).

The picture of Neolithic and Bronze Age social organisation in Europe thus appears largely homogeneous, at least given current archaeogenomic and isotopic evidence. Agriculturalist groups in this continent had probably already adopted family-based and patrilocal organisations by the time of their arrival.

What then remains to be investigated genetically is how the earliest Neolithic societies in West Eurasia first underwent an organisational shift. In other words, how were the first Neolithic societies in the early Holocene Fertile Crescent, i. e., sedentary foragers, organised, and how did their organisation patterns change through the Neolithic Transition?

1.3. The question of social organisation in the Neolithic Fertile Crescent

Archaeological analyses suggest an early biological family-focused shift in social organisation during neolithisation, already by the Pre-Pottery Neolithic (PPN). K. V. Flannery (2002), mainly inspired by ethnographic studies, suggested that the earliest sedentary PPN communities may have been structured as nuclear family groups, because in communal forager societies »[f]ood storage is out in the open and shared by all occupants of the settlement [...]. There is little incentive to intensify production in such societies, since whatever is produced must be shared« (Flannery 2002, 421). K. W. Alt et al. (2013) similarly argue that »[...] open access to resources and land – had to be reduced to a circumscribed group before regular farming and herding could be successfully established. [...] [F]amilial relationships might have become influential or decisive« (Flannery 2002, 1). Flannery (2002) suggests that at some stage in the PPN, villages were organised around nuclear families living in rectangular buildings with private storage and later-arriving societies were organised around extended families. Others have further developed this model of increasing household autonomy, again suggesting that Pottery Neolithic (PN) period societies were organised as extended-families (Kuijt et al. 2011; Atakuman 2014).

Despite widespread reference to the Flannery and I. Kuijt model of household formation, empirical evidence from Neolithic societies has been sparse. Indeed, the architecturally visible »house« is probably the primary context defining the »household« in the Neolithic Fertile Crescent, but archaeologically, it has not been easy to define the nature of relations among the household members: were the co-residents genetically kin, or was household membership defined with reference to other criteria such as gender, age, or task orientation?

1 Marlowe 2004; Wilkins/Marlowe 2006; Hill et al. 2011; Bailey et al. 2014; Walker 2014; Dyble et al. 2015.

2 Szécsényi-Nagy et al. 2015; Sánchez-Quinto et al. 2019; Mittnik et al. 2019; Cassidy et al. 2020; Fowler et al. 2022; Villalba-Mouco et al. 2022.

Direct answers to these questions are not available, and arguably the most promising source of information derives from subfloor burials in the Neolithic Fertile Crescent (see below).

Hence, the last decade has seen a number of attempts to study biological kinship among subfloor burials in Neolithic south-west Asia. The earliest of such studies were analyses of dental traits and mtDNA. Studying dental traits at Levant PPNB sites, two studies by Alt and colleagues reported patterns consistent with endogamy (Alt et al. 2013) and with matrilocality (Alt et al. 2015), while a pilot analysis of mtDNA fragments from PPNB Tell Halula, north Syria did not yield any clear patterns (Fernández et al. 2008). Surprisingly, a study on the Anatolian PN site of Çatalhöyük, involving a large dataset of c. 300 adult skeletons, found no evidence of higher biological relatedness among burials within the same building compared to burials in different buildings (Pilloud/Larsen 2011; Larsen et al. 2019). The authors interpreted this pattern as evidence of a type of »social kinship« governing Çatalhöyük society, or at least Çatalhöyük burials. Another study using this dataset also reported higher dental trait variability in females than in males, implying a patrilocal residence pattern (Larsen et al. 2015). Meanwhile, in 2019, an ancient mtDNA study on 10 individuals buried across three Çatalhöyük buildings found no single individual with the same haplotype (Chylenski et al. 2019), which is also in line with the lack of biological clustering among co-burials and/or patrilocality. However, given high amounts of noise in dental analyses, the limited information provided by mtDNA, and the small number of sites studied, the issue of the organisation of Neolithic societies and the role of biological relatedness in burial choices have remained largely open.

2. Archaeogenomic insights into social organisation in Neolithic Turkey

2.1. Intramural co-burials in Neolithic Turkey

Over the last years, we have been producing genomes from Neolithic period Turkey with the goal of understanding both interregional mobility and also within-settlement traditions, including genetic kinship between co-burials. We are particularly fortunate that a considerable number of Neolithic north Mesopotamian, Central Anatolian, and west Anatolian settlements observed the tradition of intramural burial, i. e. interring some of their dead within settlements, and frequently within buildings (beneath floors), or next to buildings during a structure's use. This tradition is also found in other parts of Neolithic south-west Asia, such as the Levant and south Caucasus.

Intriguingly, intramural and subfloor burial traditions appear to have accompanied the development of permanent dwellings during the PPN period. However, these traditions varied significantly in both space and time. For instance, excavation at the Late Epipaleolithic-PPNA layers of north Mesopotamian Körtik Tepe revealed over 1000 subfloor burials (Erdal 2015), while no such dominant pattern has been found in other PPNA sites, such as at Göbeklitepe (Gresky et al. 2017). In contrast, pioneer PPNB sites, such as north Mesopotamian Çayönü, or Central Anatolian Aşıklı and Boncuklu, revealed modest frequencies of subfloor burial, suggesting that some individuals were selected for subfloor burials, while others were buried in communal buildings and graveyards; e.g., the Skull Building of Çayönü houses remains from hundreds of individuals (Özdoğan/Özdoğan 1989). Studying more than one hundred burials from north Syrian PPNB Tell Halula, Guerrero and colleagues have described a highly standardised interment tradition, placing bodies upright and in flexed form in the main entrance to the buildings (Guerrero et al. 2009). These authors have also highlighted the notable variability of burial practices among PPNB settlements in south-west Asia, such as the lack of burials outside buildings in some sites, or the lack of burial gifts in the south Levant.

Selective intramural burials are also observed in Late Neolithic Turkey, although not at all sites. In north Mesopotamian Hakemi Use, subadults and adult females are overrepresented among its c. 100 excavated intramural burials (Erdal 2013). In Central Anatolia, Çatalhöyük has frequent subfloor burials, with c. 800 excavated and including both subadults and adults of both sexes; nevertheless, the excavators believe not all burials were intramural (Larsen et al. 2015). Only infants were found in late PN Central Anatolian Köşk Höyük subfloor graves, small numbers of adults in south-west Anatolian Bademağacı, and either no burials or rare infant burials in west Anatolian sites, such as Ulucak and Çukuriçi. In north-west Anatolia, intramural burials are more frequent at some sites, where individuals were either buried in open spaces between houses (e.g., Barcın, Pendik, Bahçelievler) or in extramural graveyards at the edges of the dwelling areas (e.g., Ilıpınar, Aktopraklık, Yenikapı); rarely, infants were also found in subfloor graves at some of these sites (Düring 2011; Erdal/Takaoğlu 2021).

In addition, there appears to be a trend towards more female burials in various sites (e.g., in Aşıklı) and for a temporal increase in relative female frequencies among adult burials as estimated by osteological analyses (Fig. 1). What is also clear is that intramural burial customs varied with respect to both sex and age, both among contemporaneous villages, and over time, during the transition from sedentary hunter-gatherers to intensive farming communities.

Irrespective of this temporal variation, many Neolithic intramural burials are found in spatial clusters where they are associated with specific spaces, usually buildings. Frequently, these clusters do not represent simultaneous burials, but burials in proximate spaces across multiple decades. We term these clusters »co-burials«. Archaeologists commonly assume that these clusters comprise socially-related individuals.

Whether these intramural co-burials represent genetically related individuals has been a major question for the archaeology of the Neolithic Fertile Crescent (Hodder 2011). The observations on Çatalhöyük dental remains by Pilloud and Larsen (2011) found no evidence for genetic similarity within buildings and has consequently further fuelled the debate. We have recently started investigating this question in a systematic manner and here we will present a summary of results from two recent publications, by R. Yaka and colleagues (2021) and by N. E. Altınışık and colleagues (2022). These studies surveyed genetic kinship across five Neolithic sites: three from the Aceramic/PPN period, namely Aşıklı Höyük and Boncuklu in Central Anatolia and Çayönü in north Mesopotamia; and two from the PN period, Çatalhöyük in Central Anatolia and Barcın in west Anatolia (see map and timeline in Fig. 2).

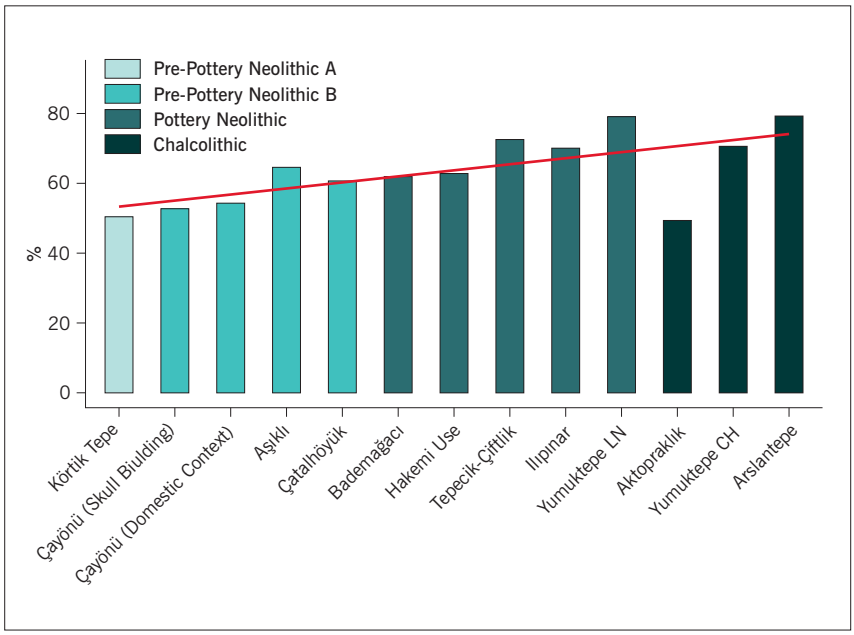


Fig. 1 The proportion of females among burials with osteologically identified sex in Neolithic sites in Turkey.

Abb. 1 *Der Anteil an weiblichen Bestattungen mit osteologisch bestimmtem Geschlecht von neolithischen Fundstellen in der Türkei.*

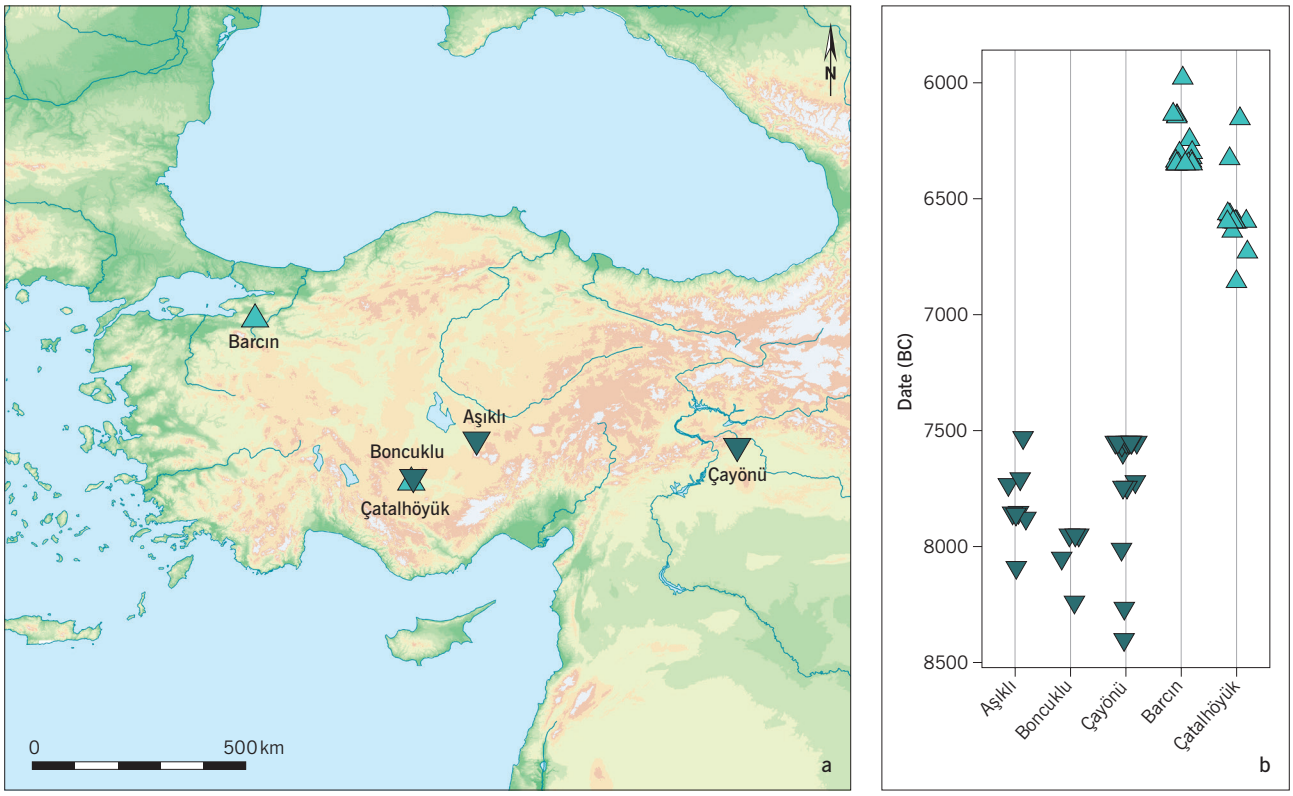


Fig. 2a–b Map and timeline of Neolithic sites analysed for genetic kinship among co-burials. Published genomes from the PPN/Aceramic period sites are shown as dark green triangles while those from the PN/Ceramic period sites are shown as turquoise triangles.

Abb. 2a–b *Karte und Zeitachse neolithischer Fundstellen, die auf genetische Verwandtschaft unter den Mehrfachbestattungen analysiert wurden. Veröffentlichte Genome von Fundstellen der vorkeramischen Periode sind als dunkelgrüne Dreiecke dargestellt, diejenigen von Fundstellen der keramischen Periode als türkise Dreiecke.*

2.2. Estimating genetic kinship degrees and consanguinity in Neolithic settlements

The two studies used a total of 64 genomes from the five Neolithic sites mentioned. Most of the genomes were of low coverage (< 0.3x). The majority (61 %) was produced by our group in Ankara; these were based on direct shotgun sequencing and whole genome capture (Kılınç et al. 2016; Yaka et al. 2021; Altınışık et al. 2022). Meanwhile, some of the Boncuklu and all of the Barcın genomes were published by other laboratories; a few of these were shotgun sequenced (Hofmanová et al. 2016) but mostly were SNP capture-generated genomes (Mathieson et al. 2015; Feldman et al. 2019).

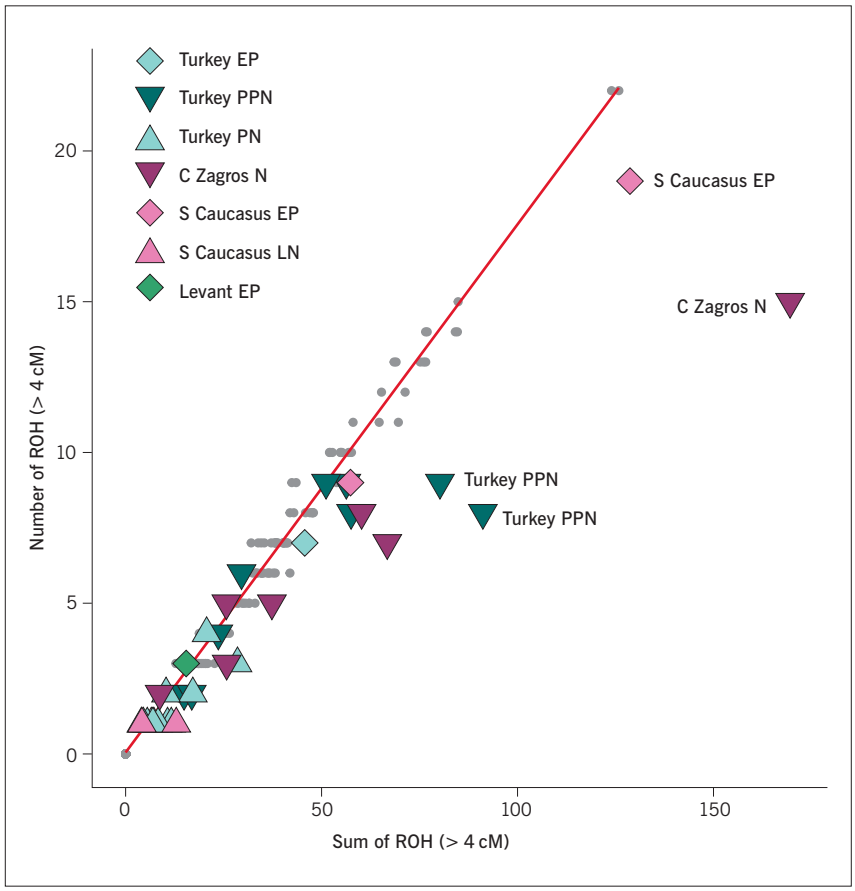


Fig. 3 Number versus sum of runs of homozygosity (ROH) in published late Pleistocene and early Holocene south-west Asian genomes. The red diagonal line was computed using short ROH values (4 to 8 cM) in present-day West and Central Eurasian individuals to represent individuals with no consanguinity, with shifts towards longer ROH, to the right, suggesting consanguinity (see Altınışık et al. 2022). A PPN individual (c. 7500–7000 BC) from Wezmeh Cave in Central Zagros (Broushaki et al. 2016) shows the strongest deviation, while two individuals from PPN Central Anatolia show only modest shifts. In none of these genomes, however, do ROH levels reach that expected for first cousin offspring.

Abb. 3 *Anzahl im Vergleich zur Summe von Homozygotiesequenzen (ROH = Runs of homozygosity) in veröffentlichen spätpleistozänen und frühholozänen südwestasiatischen Genomen. Die rote Diagonallinie wurde mit Hilfe von kurzen ROH-Werten (4 bis 8 cM) in heutigen west- und mitteleurasischen Individuen berechnet, um Individuen ohne Blutsverwandtschaft darzustellen; Verschiebungen hin zu längeren ROH-Werten nach rechts deuten auf Blutsverwandtschaft hin (siehe Altınışık et al. 2022). Ein vorkeramisches Individuum (ca. 7500–7000 v. Chr.) aus der Wezmeh Höhle in Zentral-Zagros (Broushaki et al. 2016) zeigt die stärkste Abweichung, während zwei Individuen der vorkeramischen Periode C in Anatolien nur geringe Verschiebungen zeigen. In keinem dieser Genome erreichen die ROH-Ergebnisse den Wert, den man für Nachkommen von Cousins ersten Grades erwartet.*

Estimating correct genetic kinship degrees using low-coverage genomes is a challenge, therefore we resorted to using multiple methods in parallel. These included specifically: READ, which uses the pairwise genetic distances in the sample for normalisation and direct estimation (method-of-moments) of relatedness level (Monroy Kuhn et al. 2018); lcMLkin (Lipatov et al. 2015) and ngsRelate (Hanghøj et al. 2019), which both use population allele frequency estimates and a probabilistic framework for relatedness estimation and TKGWV (Fernandes et al. 2021), which also uses population allele frequency estimates but performs direct estimation of relatedness.

These methods are theoretically also sensitive to varying levels of inbreeding in the sample. Pairs who are highly consanguineous may be inferred to be related at higher degrees than their direct relationship. Previous work has identified cases of relatively high consanguinity in Neolithic societies[3]. We have accordingly analysed the available genome sample from Neolithic Turkey using the hapROH method (Ringbauer et al. 2021), which includes 18 individuals from the aforementioned five sites with sufficient genome coverage to calculate runs of homozygosity. Some individuals from Late Pleistocene and early Holocene sites have relatively high levels of ROH due to small population sizes. Meanwhile, although modest levels of consanguinity can be observed in the sample (Fig. 3), no individual was identified with high consanguinity (e.g., first cousin mating). This contrasts with common consanguinity observed today in modern-day populations in south-west and Central Asia (Bittles/Black 2010; Ceballos et al. 2021; Ringbauer et al. 2021).

2.3. Genetic kinship in co-burials in PPN/Aceramic Neolithic sites

Our sample from Boncuklu (Baird et al. 2018), in the Central Anatolian Konya Plain, included a single cluster of burials in two proximal buildings (Yaka et al. 2021) (Fig. 4). Buildings here are small and round, with the burials dated to c. 8300–8000 BC. Published aDNA data (Kılınç et al. 2016; Feldman et al. 2019) was available in a co-burial cluster of five individuals, four adults and a perinatal baby. The adults were estimated to be related as a sibling pair and a parent-offspring pair. Surprisingly, the perinatal baby, buried in the same grave as a middle-aged adult female, was unrelated to everyone else in the sample (Yaka et al. 2021).

In Aşıklı (Özbaşaran 2011; Özbaşaran/Duru 2012), from the Cappadocia region in Central Anatolia, we encountered a similar picture (Yaka et al. 2021) (see Fig. 4). The sample included a single co-burial cluster in two proximate round buildings. This represents the early phase of Aşıklı Höyük occupation (c. 8200–7700 BC), which later continues with

3 Broushaki et al. 2016; Cassidy et al. 2020; Ceballos et al. 2021; Ringbauer et al. 2021.

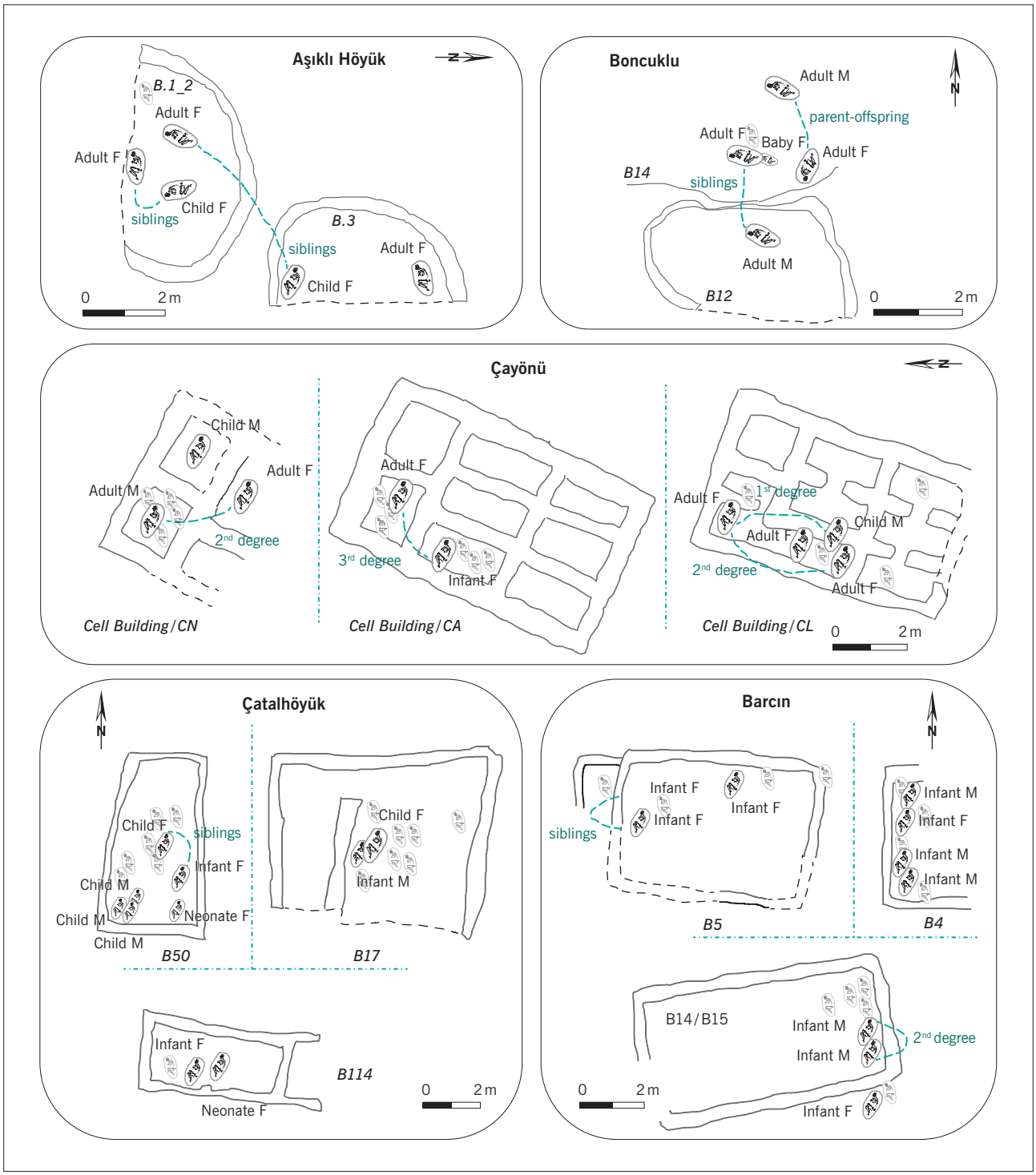


Fig. 4 Genetic kinship among intramural burials across five Neolithic sites. The figure was recreated based on related figures from Yaka et al. (2021) and Altınışık et al. (2022). Buildings and subfloor burials are represented symbolically (not to scale). Estimated close genetic relationships between individual pairs are shown as dashed lines. Flexed skeleton symbols in dark grey indicate individuals with sufficient aDNA data, which are also marked by their age and sex. Flexed skeleton symbols in light grey indicate individuals who were not sampled for aDNA, or did not yield sufficient aDNA (age or sex not shown). Building numbers are shown in italics.

Abb. 4 *Genetische Verwandtschaft bei intramuralen Bestattungen an fünf neolithischen Fundstellen. Die Abbildung wurde auf der Grundlage ähnlicher Abbildungen aus Yaka u. a. (2021) und Altınışık u. a. (2022) neu erstellt. Gebäude und Bestattungen unter dem Fußboden sind symbolisch dargestellt (nicht maßstabsgetreu). Vermutete enge genetische Beziehungen zwischen einzelnen Paaren sind als gestrichelte Linien umgesetzt. Symbole für gehockte Bestattungen in dunkelgrau bezeichnen Individuen mit ausreichenden aDNA-Daten, bei denen auch Alter und Geschlecht bestimmt sind. Symbole für gehockte Bestattungen in hellgrau zeigen Individuen an, die nicht für aDNA beprobt wurden oder nicht genügend aDNA lieferten (Alter und Gechlecht nicht angegeben). Gebäudenummern sind kursiv gesetzt.*

rectangular and larger buildings. We could obtain usable aDNA from five individuals from within the co-burial cluster. All five were females. Two pairs (4 out of 5) were estimated to be siblings (both were adult-child pairs). One of the sibling pairs was buried in neighbouring buildings (B.1_2 and B.3), and another in the same building (B.1_2). Only one

individual here, a young female buried in B.3, had no identified relatives (Yaka et al. 2021).

In north Mesopotamian Çayönü (Özdoğan/Özdoğan 1989), our sample included three co-burial clusters within separate three rectangular buildings, all from the Cell Building subphase (c. 7500–7200 BC) (Altınışık et al. 2022). Genomes with sufficient aDNA data to allow kinship estimation comprised nine individuals in total, a small subset of the total number of 29 individuals interred within the same buildings. Seven of these nine had 1st, 2nd or 3rd degree-related kin identified in the same buildings (see Fig. 4).

Notably, in all three sites adult females were found buried with relatives, including siblings and potential nephews. This is interesting because it does not align with expectations under female exogamy (see Discussion).

2.4. Genetic kinship in co-burials in PN/Ceramic Neolithic sites

Our sample from Çatalhöyük in the Central Anatolian Konya Plain (Düring/Marciniak 2005; Hodder 2007) included three co-burial clusters in separate buildings (see Fig. 4). The burials have been dated to c. 7000–6500 BC (Yaka et al. 2021). We studied ten individuals, all subadults. Interestingly, only one pair of these ten subadults were estimated to be siblings. None of the rest had identified relatives within the sample.

In Barcın, from north-west Anatolia (Gerritsen/Özbal 2019), we again had three co-burial clusters, with infants buried within, or next to, three separate buildings and which were dated to c. 6500–6000 BC (Yaka et al. 2021). Two pairs of relatives were found in two of these clusters (a sibling and a second-degree pair), while the rest of the individuals had no relatives identified.

3. Discussion

The current set of genomic data published in these two studies is admittedly small, but it already implies a number of features that may characterise the organisation of Neolithic societies in Anatolia and north Mesopotamia.

3.1. Close biological ties among co-burials in early sedentary communities

First, data from the three PPN/Aceramic sites suggest that co-burials within buildings in these early sedentary societies were frequently close biological families. As mentioned earlier, we do not know whether these burials represented individuals using the buildings during their lifetime. Testing this could be theoretically possible by studying inter-building dietary differences among contemporaneous burials (e.g., Knüsel et al. 2021), or by using other markers of shared space use, or using sedimentary DNA. However, comprehensive work in this direction is lacking and the question remains largely unanswered. For now, we can only speculate about whether the co-burials represented »households«. Assuming this to be the case, our observation would suggest an early adoption of a biological family-based organisation in sedentary societies, in the PPN/Aceramic period, before full-scale food production had started. This would be consistent with the notion of investment in a built environment being facilitated by biological family-based organisation (Flannery 2002; Kuijt et al. 2011).

3.2. Change in co-burial and/or organisation traditions over time

The second and rather unexpected finding is the apparent shift in co-burial traditions between the PPN/Aceramic and PN Ceramic sites studied. The difference becomes conspicuous when the data are summarised as the proportion of individuals buried in the same building with identified relatives (Fig. 5). Compared to the three PPN/Aceramic sites, the frequency of close relatives identified among co-buried individuals is distinctly lower in the two PN/Ceramic sites. Notably, the latter are settlements with full agriculture and animal husbandry, and with private storage within buildings (reviewed in Düring 2011).

A possible confounding factor here is age: the available aDNA data in co-burial clusters in the two PN/Ceramic sites only represented subadults, whereas the PPN/Aceramic data included both adults and subadults. In Çatalhöyük, the fact that we only studied subadults was due to significantly higher aDNA preservation in subadult burials compared to adult burials in this site – a phenomenon speculated to be related to the age-dependent treatment of corpses in this site (Yaka et al. 2021a). Because we did not have access to pre-screening data from Barcın, we do not know whether the same issue applies there. Irrespective of the cause, that the PN/Ceramic period is only represented by subadults raises the question of whether the difference between PPN and PN sites in co-burial genetic kinship patterns could in fact reflect different burial treatments between age groups. Two observations suggest otherwise. One is based on the the analysis of dental traits by M. A. Pilloud and C. S. Larsen (2011), which found limited or no clustering within buildings and which largely comprised adults (c. 150 adult remains). Another is based on the mtDNA analysis of 10 adult Çatalhöyük burials within three buildings that found no pair of maternal relatives (Chylenski et al. 2019). Hence, it appears that the observed difference between PPN and PN sites cannot be explained simply by differences in sample age composition.

Why subfloor co-burials of the PN period appear frequently to comprise unrelated individuals remains a major question. An explanation has been put forward by I. Hodder (2022), suggesting that the co-burial of unrelated individuals in Çatalhöyük could reflect traditions that evolved to consolidate community ties across biological families, possibly as a response to forces that disrupted those communal ties, influenced by the development of private storage and the potential for increasing inequality. These traditions could involve buildings inhabited by biological families burying the dead of other families (Kuijt 2002), of widespread child

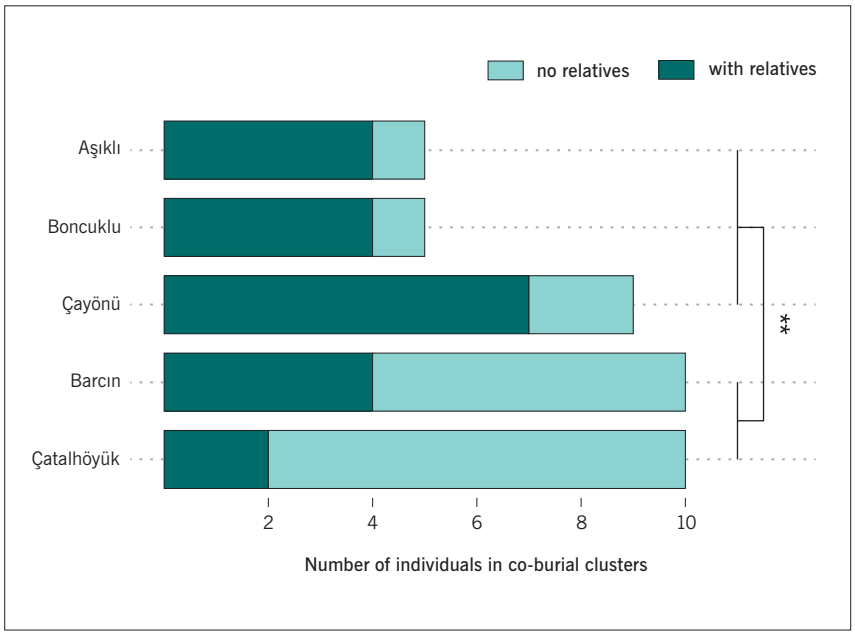


Fig. 5 Kinship frequencies among co-burial clusters in five Neolithic sites. The figure represents a summary of the data in Fig. 4, with each individual being classified as having been identified with co-buried relatives, or with no co-buried relatives identified. The difference between the three PPN and two PN sites was tested using the Fisher's exact test (p = 0.004), shown as two asterisks (**) on the figure.

Abb. 5 *Häufigkeit von Verwandtschaftsbeziehungen innerhalb von Mehrfachbestattungsgruppen an fünf neolithischen Fundstellen. Die Abbildung stellt eine Zusammenfassung der Daten in Abb. 4 dar, wobei jedes Individuum mit oder ohne mitbestatteten Verwandten identifiziert wurde. Der Unterschied zwischen den drei vorkeramischen und den zwei keramischen Fundstellen wurde mit dem exakten Test von Fisher (p = 0.004) untersucht, in der Abbildung durch zwei Sternchen (**) gekennzeichnet.*

fostering/adoption as documented in the ethnographic record[4], or of buildings being used by fluid social groups.

3.3. A model for changing gender relationships and social organisation through Neolithisation

The third observation arising from the data is the absence of evidence for female exogamy (patrilocality) in the PPN/Aceramic data. In Boncuklu and Aşıklı we have adult women buried with their possible siblings. In Çayönü, we have two adult females estimated to be 2nd degree relatives, and an adult female with an estimated great nephew. The sample size is small but the pattern is suggestive. Assuming it will be supported by future data, we can imagine three scenarios to explain this: either female exogamy was not widely practised; or a high frequency of adult females stayed with their families without having children; or female exogamy was practised, but upon death, adult women were moved back and interred with their biological family, a tradition reported in ethnographic research (Ensor et al. 2017). In either case, the available picture from these three PPN/Aceramic sites is in contrast to Neolithic Europe, which presents a clear picture of female exogamy, where adult female burials within a cemetery are found only to be related to their offspring (reviewed in Bentley 2022).

Hence, the data suggest, albeit highly tentatively, the following model: the earliest sedentary societies of the PPN/Aceramic period had adopted biological-family-based organisation without a patrilocal bias. With intensifying agricultural and food production practices, at least some societies in PN/Ceramic Anatolia responded by adopting new traditions that attempted to maintain fluidity and communal ties and compensate for the elevated stresses caused by increasing autonomy, wealth accumulation and inequality among households. How long these traditions may have continued is unclear. However, Neolithic societies in Europe of the following millennia had already become organised along highly patrilocal and patrilineal lines. Biased post-marital residence towards a single gender may have evolved to minimise property inheritance conflicts (an issue that does not concern mobile foragers). In this model, the reason why most societies adopted patrilocal (instead of matrilocal) traditions could be related to different gender roles in inter-group aggressive encounters (Ember 2011). Equally, the social and economic requirements of agricultural life may also have supported male polygamy, which could boost offspring numbers and hence labour force per household.

Further research and evidence will be needed to test this model fully. In addition, it will be important to study the same process in other societies that independently underwent the transitions to food production and sedentism.

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4 E.g., Schildkrout 1973; Silk 1987; Alber 2003; Berman 2014.

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Source of figures

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Investigating Neolithic social structures on the basis of unprecedentedly large family trees from the site Gurgy ›les Noisats‹ in France

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Zusammenfassung

Die Untersuchung von neolithischen sozialen Strukturen auf der Grundlage von großen Stammbäumen von der Fundstelle Gurgy ›les Noisats‹ in Frankreich

Die Aufklärung von Verwandtschaftsstrukturen in vergangenen Gesellschaften steht im Mittelpunkt von gruppeninternen Studien in der Archäologie und Anthropologie. Jedoch war die komplette Rekonstruktion von genetischer Verwandtschaft im archäologischen Kontext kaum realisierbar gewesen. Die Optimierung von Methoden zur Analyse alter DNA macht es nun möglich, genomweite Daten für mehrere Individuen einer einzigen Fundstelle zu erhalten. Diese Daten ermöglichen die Rekonstruktion genetischer Verwandtschaft und erlauben es Rückschlüsse auf die demografische Struktur sowie soziale Organisation prähistorischer Gesellschaften zu ziehen.

Wir stellen hier die Analyse genomweiter Daten von der mittelneolithischen Fundstelle Gurgy ›les Noisats‹, Département Yonne (Frankreich), vor. Auf der Grundlage einer umfassenden Beprobungsstrategie und der gezielten Anreicherung von 1240k SNPs (Einzelnukleotid-Polymorphismen), konnten wir Daten von 94 der insgesamt 128 Individuen gewinnen. Mit Hilfe eines Multi-Proxy-Ansatzes sowie etablierten und neuen Methoden der biologischen Verwandtschaftsbestimmung, war es uns möglich, zwei große Stammbäume zu rekonstruieren: einer, der 63 Individuen über sieben Generationen miteinander verbindet, und ein anderer, der 10 Individuen über vier Generationen verknüpft. Die kombinierten Daten deuten auf eine patrilokal und patrilineal organisierte Gesellschaft hin, welche Exogamie praktizierte. Das weitgehende Fehlen von genetischen Verwandtschaften zwischen nicht-lokalen Frauen und die Analyse der Verwandtschaft im elterlichen Hintergrund der Individuen weist auf ein breiteres regionales Netzwerk hin. Strontiumanalysen bestätigten den nicht-lokalen Ursprung von erwachsenen Frauen, zeigten aber auch nicht-lokale Merkmale der Gründer der Erstgeneration der Fundstelle. Darüber hinaus deuten die osteologischen Sterbealterschätzungen der ersten und letzten Generationen der Stammbäume auf eine viel engere zeitliche Spanne der Besiedlung der Fundstelle hin.

Diese überraschend großen Stammbäume bieten Einblicke, die über die unmittelbare genetische Verwandtschaft hinausgehen und es uns ermöglichen, die Gruppenstruktur, ihre Größe sowie Begräbnis- und Siedlungspraktiken innerhalb eines viel breiteren sozialen und kulturellen Kontextes zu untersuchen.

Summary

The elucidation of kinship structure in past societies has been at the centre of intra-group studies in archaeology and anthropology. However, the full reconstruction of genetic relatedness in archaeological contexts has rarely been feasible. With the optimization of ancient DNA (aDNA) methods, it is now possible to obtain genome-wide data for multiple individuals from a single site. This data allows the reconstruction of biological relationships and inferences on the demographic structure and social organisation of prehistoric societies.

Here, we present genome-wide data from the French Middle Neolithic site of Gurgy ›les Noisats‹, Yonne Department. On the basis of extensive sampling and the use of the 1240k SNP (Single Nucleotide Polymorphisms) capture array, we obtained data from 94 out of a total of 128 individuals. Using a multi-proxy approach, and following established and novel methods to determine biological relatedness, we were able to reconstruct two large pedigrees: one connecting 63 individuals over seven generations, and another with 10 individuals over four generations. From our combined data, we inferred a patrilocal and patrilineal system, and the practice of female exogamy. The absence of genetic affinities between non-local females and the analysis of parental background relatedness suggest a wider regional network. Strontium analyses confirmed the non-local origin of adult females, but also revealed non-local signatures in the first-generation founders of the site. Moreover, osteological age-at-death estimates from the first and last generations of the pedigrees indicated a much narrower chronological range of the occupation of the site.

These unprecedentedly large genealogies provide insights that go beyond the immediate genetic relatedness and allow us to study the group structure, its size, as well as funerary and settlement practices within a much broader social and cultural context.

Introduction

The first communities of farmers settled in the northern half of modern-day France at around 5200–5000 cal BC during the early phases of the Neolithic, expanding mainly from central Europe along the Danubian route of diffusion (Allard 2007). Following this early phase, groups then segmented into several smaller cultural entities and in smaller territorial areas, which stabilized during the Middle Neolithic; sometimes this also led to competition (Gallay 2007).

With the transition to the Middle Neolithic, the complexity of the funerary practices increased in the Paris Basin, and more specifically in the Yonne Valley. The Cerny culture (Constantin et al. 1997), partly derived from the Villeneuve-Saint-Germain culture and representing the final phase of the Linear Pottery culture (LBK), was present in the region from about 4700 cal BC and is known for its associated monumental funerary structures, the so-called *Structures de Type Passy* (STP, ~4700–4300 cal BC). Exogenous influences are, however, also visible in the archaeological record. For example, the southern Chasséen Culture is represented in the artefacts from the graveyard Monéteau ›Macherin‹, Yonne Department (France; Augereau/Chambon 2011), with different grave goods from the Mediterranean sphere being found all over the Paris Basin (Lichardus-Itten 1986; Sidéra 2010), while the Chamblandes-like rigid containers, found in several sites in the southern Paris Basin, point to cultural influences from the Alps and central France (Moinat/Chambon 2007).

Overall, archaeological cultures do not always accord with burial complexes, as different burial types or body positions have been found within the same archaeological cultural groups (Thomas 2011). The spatial boundaries between groups are also not strict, and rather are fluid. Most of the funerary sites (n = ~20) located in the Paris Basin *sensu stricto* include STP monuments (Chambon/Thomas 2010).

Although contemporary with STP sites, Gurgy ›les Noisats‹, Yonne Department (France; Rottier et al. 2005) is one of the few sites that stand out. The complete excavation of the graveyard of Gurgy ›les Noisats‹ took place between 2004 and 2007 under the direction of S. Rottier (Rottier et al. 2005; Rottier 2007). A total of 134 pits were excavated at the site, uncovering 128 individuals, which makes Gurgy currently the biggest funerary site for the Neolithic in the Paris Basin. Direct radiocarbon dates from human remains range between 5000 and 4000 cal BC, but the most intensive occupation period ranges from 4900 to 4500 cal BC, corresponding to the end of the early Neolithic and the beginning of the Middle Neolithic. A few double, but mainly single burials were uncovered, displaying a wide variety of grave types and cultural influences, including: burials in pits without construction; burials in pits with a cover; burials in rigid containers; and burials in niches (Rottier 2007). Burials in rigid containers echo those found in regions like modern-day Switzerland or the Massif Central and are associated with the Chamblandes phenomenon (Moinat/Chambon 2007). By contrast, burials in niches are common in the Paris Basin during the late LBK phase (Thevenet 2010). Grave goods, notably pottery and flint tools, are scarce and randomly distributed across the cemetery. The elements of adornment are noteworthy for their diversity (Rottier et al. 2005). Overall, there are no diagnostic artefacts that assign Gurgy to a particular Neolithic culture.

Several studies were conducted on the human remains to understand the structure of the Gurgy site[1]. The first population genetics studies explored the mitochondrial genetic diversity[2] and were completed recently by a broader genomic study of western European Neolithic farmers that also included 22 individuals from Gurgy (Rivollat et al. 2020). An integrative study combining mitochondrial data (n = 55) with archaeological data was also performed to understand the organisation of the site and to see whether any archaeological feature could be linked to specific maternal lineages (Le Roy et al. 2016). However, no correlation between mitochondrial lineages and archaeological data could be demonstrated.

The optimization of aDNA methods over the last few years has made it possible to obtain genome-wide data (i.e., nuclear and mitochondrial) and to estimate precise genetic relationships between individuals. With these new data, finer-scale local analyses are now feasible, they are increasingly finding use, and they are capable of exploring questions concerning kinship structures and site organisation. This newly gained resolution offers new elements of discussion for the investigation of social structures. Here, we present a summary of the results from our genomic study applied on an extensive sampling of the site of Gurgy ›les Noisats‹. We were able to retrieve genome-wide aDNA data for 94 individuals, allowing us to explore biological relatedness between most of the deceased, and to infer, beyond the biological structure, insights into the social organisation of this Neolithic community. The complete study and associated data are available in Rivollat et al. (2023).

Data generation and pedigree reconstruction

We attempted to sample Gurgy ›les Noisats‹ as completely as possible. Of the 128 individuals buried at this site, 110 showed skeletal preservation suitable for aDNA analysis. Petrous bones were collected whenever possible (n = 94), followed by teeth (n = 7), and other bones, such as tibia (n = 1), femur (n = 1), radius (n = 1), scapula (n = 1), phalanx (n = 1), and unspecified bones (n = 4). Samples were processed in the cleanroom facilities of the former Max Planck Institute for the Science of Human History, Jena (now Max Planck Institute for Evolutionary Anthropology, Leipzig), Germany and the Laboratory PACEA, Bordeaux University, France. Each sample was drilled, and bone and/or tooth powder was used to produce DNA extracts from which partial uracil-DNA-glycosylase (UDG) double-stranded DNA libraries with unique

1 Le Roy 2015; Le Luyer et al. 2016; Rey et al. 2017; Rey et al. 2019; Rey et al. 2021.

2 Documenting the maternally inherited lineages; Rivollat et al. 2015; Le Roy et al. 2016; Rivollat et al. 2017.

index pairs were generated. After screening of ~5 million reads by shotgun sequencing, we selected libraries with > 0.1 % endogenous human DNA (n = 105), which were hybridised in-solution to an oligo-nucleotide probe set to enrich for ~1.2 informative nuclear Single Nucleotide Polymorphism (SNP) markers (capture 1240k; Fu et al. 2014; Mathieson et al. 2015). An in-house capture for the complete mitogenome (Maricic et al. 2010; Haak et al. 2015) was applied to all samples. Genetic sex was determined for all individuals (Mittnik et al. 2016) and a capture targeting the entire mappable region of the Y-chromosome was applied to all genetically determined males (n = 57; Rohrlach et al. 2021). We were able to retrieve genome-wide aDNA data for 94 individuals, 22 of which were published previously (Rivollat et al. 2020), as well as mitogenomes from 99 individuals. Individuals who were covered at less than 20000 SNP sites, who were lacking typical patterns of DNA damage at the read ends (4 to 18 % of deamination), and/or libraries showing contamination in both nuclear and mitochondrial genomes (< 5 %; Fu et al. 2014; Korneliussen et al. 2014) were excluded from further analyses.

To determine biological relatedness for first-degree (parent-offspring and siblings) and second-degree relationships (grandparents-grandchildren, uncle/aunt-nephew/niece, and half-siblings), we combined two established methods designed for low-coverage aDNA data. We used *READ* (Monroy Kuhn et al. 2018), which calculates and averages the pairwise mismatch rate and can identify up to first- and second-degree relationships. We then used *lcMLkin* (Lipatov et al. 2015), which estimates the probability of identity-by-descent (IBD) from genotype likelihoods to differentiate between parent-offspring and siblings among first-degree relationships. We combined these estimates with contextual information, such as age-at-death, genetic sex, and uniparentally-inherited markers, to reconstruct pedigrees (Fig. 1). Lastly, we estimated genetic links between related individuals by analyzing the inferred shared IBD segments (Ringbauer et al. 2023), which helped us to confirm genetic relatedness up to the tenth degree.

In parallel with the investigation of the genomic data, we explored individual mobility *via* strontium isotope analyses ($^{87}Sr/^{86}Sr$) using a laser-ablation technique (Lazzerini et al. 2021) on 57 of the individuals. To contextualise the new genomic data, we commissioned new radiocarbon dates, in addition to the 25 dates that were already available (Rivollat et al. 2015). We used a GIS (Geographic Information System) approach, as applied previously on the mitochondrial data from Gurgy (Le Roy et al. 2016), to investigate the potential correlation between the spatial location of the individuals at the site and genomic and archaeological data. We then applied a Bayesian modelling to the radiocarbon dates using information about the generational succession from the pedigrees to explore the date ranges of the occupation time of the site.

Inferences on the social and residence patterns

We reconstructed two large pedigrees (Fig. 1). Pedigree A connects 64 individuals, 20 females and 44 males, spanning seven generations, and Pedigree B connects 12 individuals, seven females and five males, covering five generations. Among the remaining 18 individuals we identified three additional pairs of first-degree relatives. One adult male (GLN311) has two second-degree relatives in Pedigree A, while the 11 remaining individuals are not closely related to any individuals of either pedigree. The two pedigrees are clearly reflected in the spatial layout of the necropolis (Fig. 2). Pedigree A occupies the main space, while Pedigree B is located on the north-eastern side. In both pedigrees we

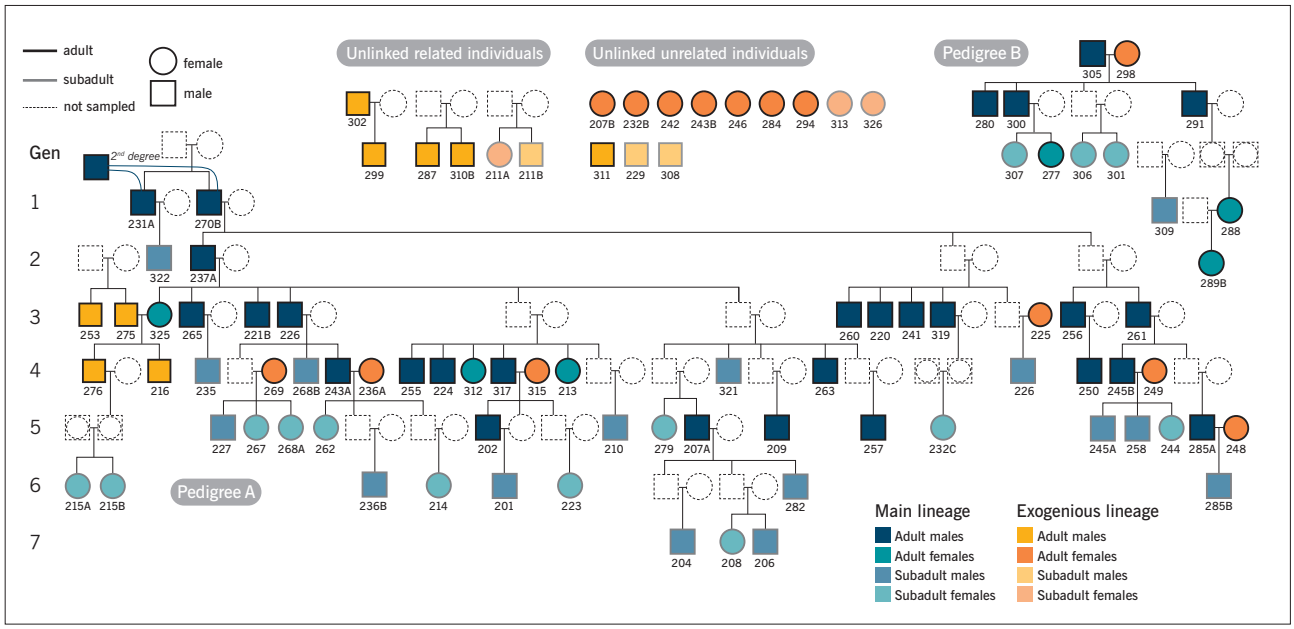


Fig. 1 Reconstructed pedigrees of the Gurgy group coloured by main or exogenous lineages, sex, and age at death.

Abb. 1 *Rekonstruierte Stammbäume der Individuen von Gurgy, farblich gekennzeichnet nach Haupt- und Nebenlinien, Geschlecht sowie Alter zum Todeszeitpunkt.*

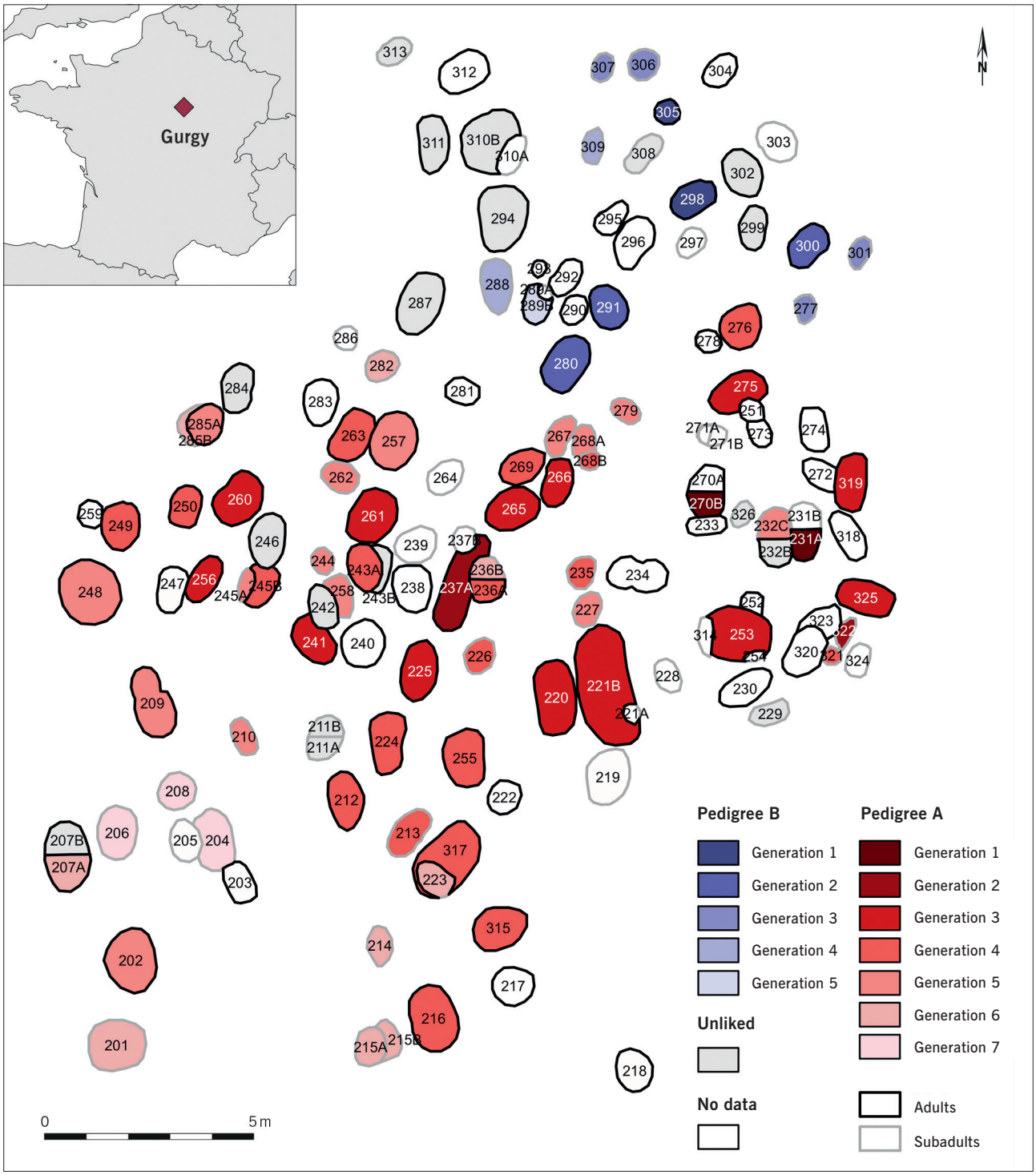


Fig. 2 Geographical location of the Gurgy ›les Noisats‹ site, Yonne Department, in present-day France (inset) and the site layout representing the spatial distribution of the pedigrees and generations.

Abb. 2 *Geografische Lage der Fundstelle Gurgy ›les Noisats‹, Département Yonne, im heutigen Frankreich (Markierung) und der Gräberfeldplan, der die räumliche Verteilung der Stammbäume und Generationen widerspiegelt.*

observed a spread from the founder generations towards the south-west, by generations through time. Spatial distances are significantly correlated with genetic distances (Mantel test: $r = 0.2$, $p < 0.001$), implying that individuals were preferentially buried near their biological family members.

The reconstructed pedigrees A and B are the first of such a large size from a prehistoric site and allow unprecedented insight into the biological structure of the group, and the social rules that might have led to the observed structure in this particular funerary community.

Patrilineality

Closer inspection of the pedigrees (Fig. 1) revealed almost exclusively that each generation is linked to the previous



Fig. 3 Gurgy ›les Noisats‹. Photograph of male individuals GLN237A and GLN221B, son and grandson, of GLN270B, Pedigree A's main ancestor, who were buried in the largest pits of the necropolis.

Abb. 3 *Gurgy ›les Noisats‹. Befundfoto der männlichen Individuen GLN237A und GLN221B, Sohn und Enkel vom Hauptvorfahr des Stammbaums A (GLN270B), welche in den größten Gruben des Gräberfelds bestattet waren.*

generation through the biological father, which connects the whole group of Gurgy ›les Noisats‹ through the paternal line. The paternal lineage is characterised by Y-chromosome haplogroup G2a2b2a1a2, which is carried by 89 % of the males in the group. The main paternal line of Pedigree A starts with individual GLN270B and his brother GLN231A. Of the three sons of GLN270B, only one, GLN237A, was buried at the site, and had a large number of children whose descendants were also buried at the site. The importance of the main paternal lineage can be traced in the subsequent generation directly following GLN270B, as the two largest graves of the site were built for his son GLN237A, as well as his grandson GLN221B (Fig. 3). We thus hypothesise that a form of social status was transmitted along the paternal line to his son and grandson.

The patrilineal system as shown by the genetic connections is also visible in some of the archaeological features (Le Roy et al. 2016). Here, the burials of fathers and their subadult male offspring are located significantly closer to each other than any other pairs of individuals, even though we observed a general trend of spatial clusters according to genetically closely related individuals (Fig. 4).

Patrilocality and female exogamy

In parallel with the patrilineal pattern, evidence suggested the practice of patrilocality within the group. Adult females buried at the site, whether they were mothers or not, had no parents buried at the site, which means that they came from

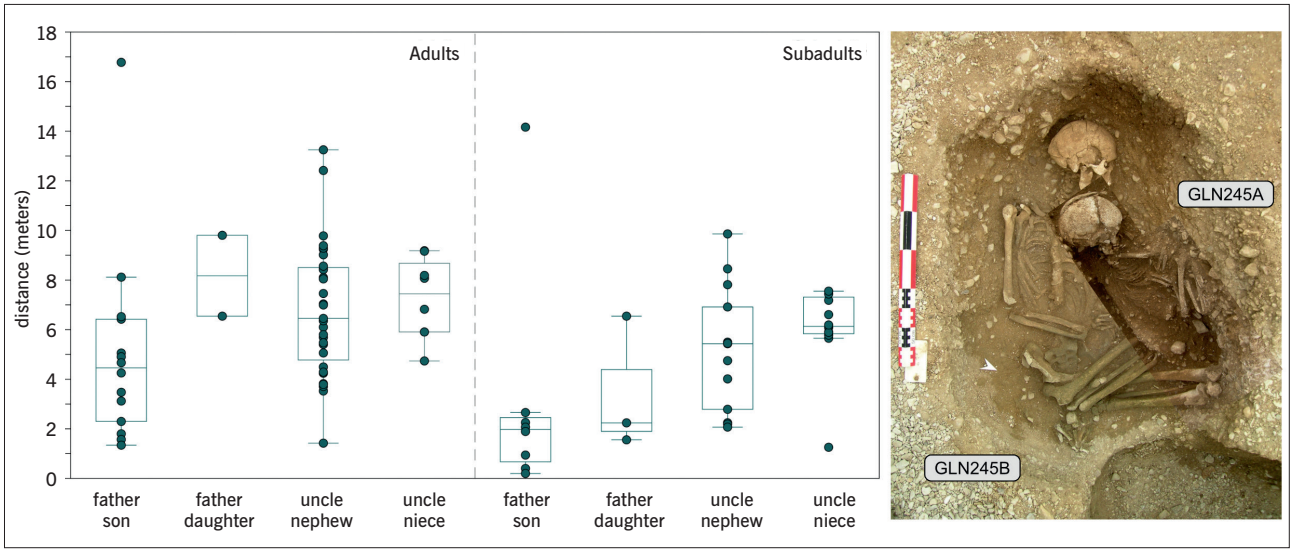


Fig. 4 Gurgy ›les Noisats‹. Spatial distances of father-offspring and uncle-nephew/niece pairs. Fathers and subadult sons are, on average, buried significantly closer to each other than any other pairs. The photograph shows the male individual GLN245B and his son GLN245A buried in the same pit.

Abb. 4 *Gurgy ›les Noisats‹. Räumliche Entfernungen von Vater-Kind- und Onkel-Neffe/Nichte-Paaren. Väter und subadulte Söhne sind im Durchschnitt weitaus näher zueinander bestattet, als alle anderen Paare. Das Foto zeigt das männliche Individuum GLN245B und dessen Sohn GLN245A, die in der gleichen Grube begraben wurden.*

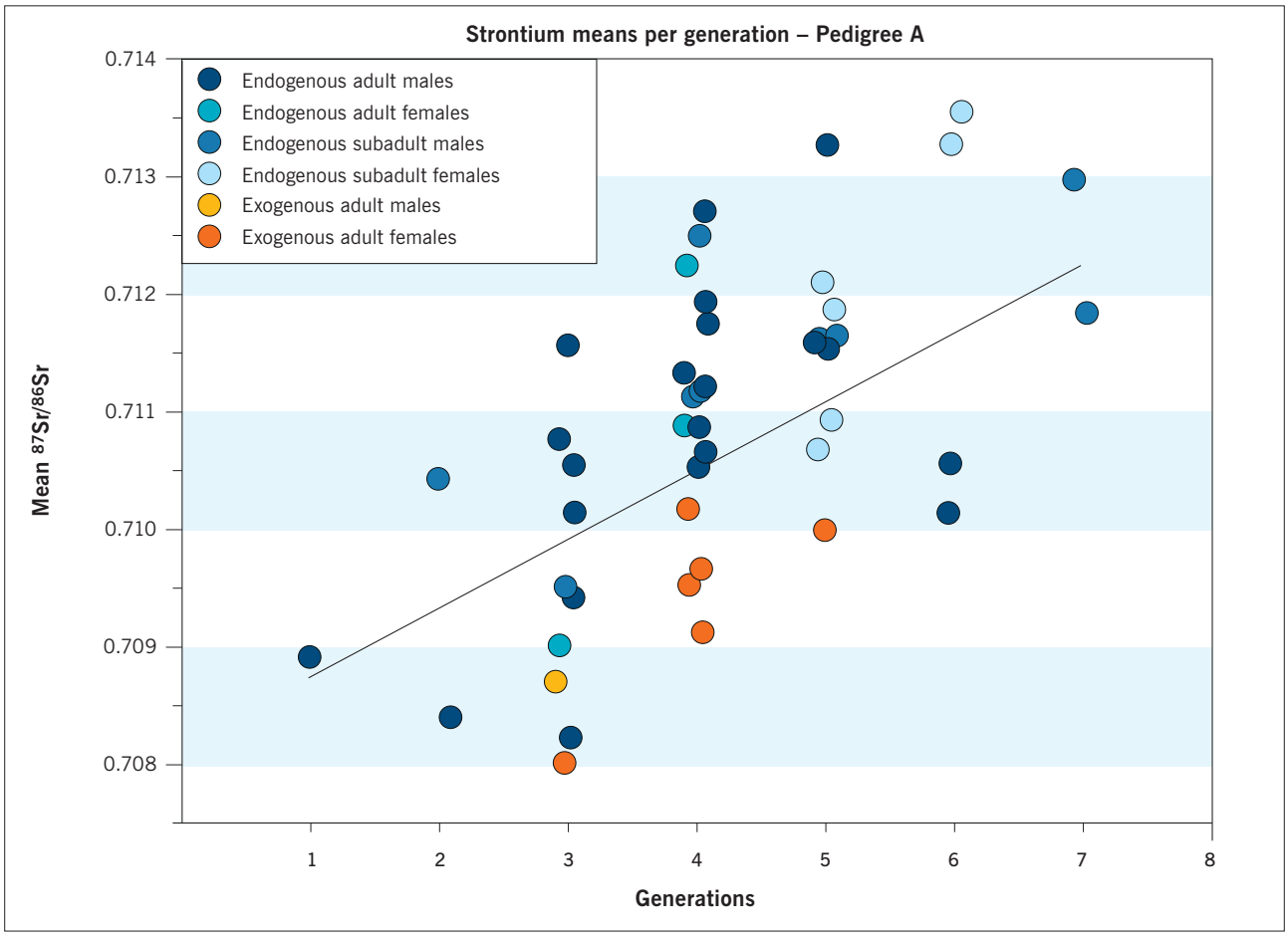


Fig. 5 Gurgy ›les Noisats‹. Mean $^{87}Sr/^{86}Sr$ ratio per age and sex cohort across generations. A significant difference between sex can be observed per generation ($p = 0.01474$).

Abb. 5 *Gurgy ›les Noisats‹. Mittleres $^{87}Sr/^{86}Sr$-Verhältnis nach Alter und Geschlechtergruppe über Generationen hinweg. Ein statistisch signifikanter Unterschied zwischen den Geschlechtern kann in jeder Generation beobachtet werden ($p = 0.01474$).*

a different lineage than those of the main pedigrees (Fig. 1). Six out of 20 of these individuals represent an exception to this rule (GLN325, GLN212, GLN213, GLN277, GLN288 and GLN289B), with only two out of these six having children buried at the site. We note that almost all female descendants from the main lineage who reached an adult age are not present at the site. Indeed, if we consider a natural sex ratio of 1.05:1 males/females at birth (Howell 1976), the ratio of 4.5:1 observed at Gurgy points to a strong imbalance in favour of males among the adult descendants. This can in part be explained by males staying within the group, i.e., suggesting practices of patrilocality akin to the patrilineal structure proposed above in conjunction with female exogamy, in which females move from their birthplace to their reproductive partner's home. Seven adult females were not connected to the pedigrees, and also were not more distantly related as shown by the IBD sharing analysis. Therefore, we speculate that these females could have been the partners of lineage males, but with whom they either did not have any offspring together, or whose common children were not buried at the site, or for whom DNA was not recovered, which would have linked these females through their children to the pedigrees.

Strontium (Sr) isotope analyses provided critical insights into individual mobility. Here, unrelated adult females and some of those with no parents at the site showed lower $^{87}Sr/^{86}Sr$ ratios than males from the same generation (Fig. 5). While the geological reference map does not allow us to infer a specific geographic origin, this finding provides further evidence that these females grew up in different places before joining the Gurgy community.

The mitochondrial diversity in Gurgy also showcases the female mobility pattern, as the mothers of each generation contributed new mtDNA lineages, but none of these mitochondrial haplogroups was transmitted further than one daughter/son generation. The exception was for the lineage daughter GLN325 who stayed with her biological family and later passed her mitochondrial haplogroup on to her offspring in the next generation.

Female connections

Based on the observed pattern of a female exogamic residential system practised by the Gurgy group, we explored the specific affinities between these females to gain an understanding of the wider network to which this community is connected. Overall, the heatmap generated from IBD sharing shows only very few connections between females

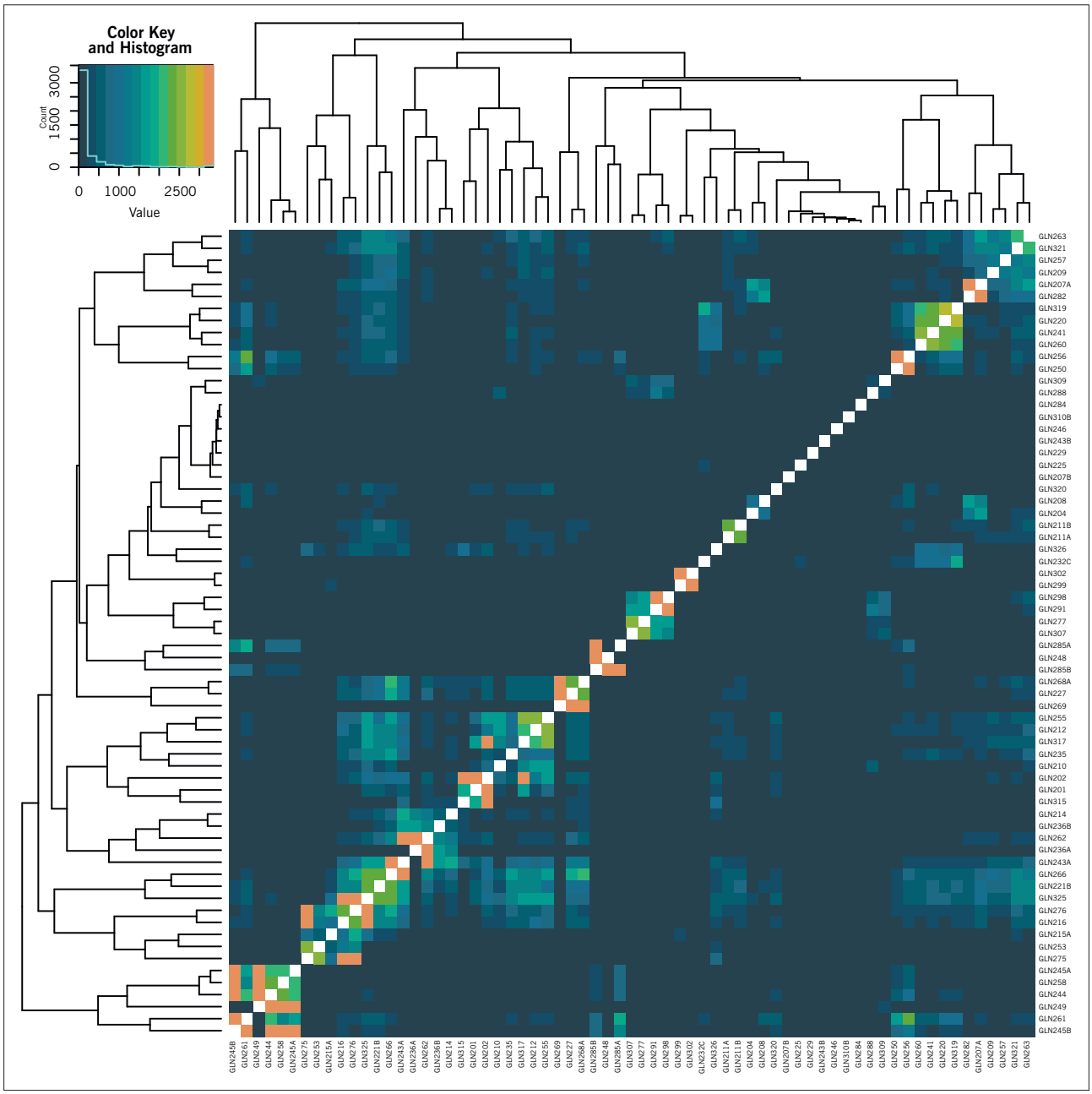


Fig. 6 Gurgy ›les Noisats‹. Heatmap showing pairwise IBD sharing between individuals with more than 500 000 SNPs (n = 72). Different clusters of lighter color reveal the extra-links between the different branches and pedigrees.

Abb. 6 *Gurgy ›les Noisats‹. Das Wärmebild zeigt die paarweise IBD-Verteilung zwischen Individuen mit mehr als 500 000 SNPs (n = 72). Verschiedene Cluster in hellerer Farbe zeigen die zusätzlichen Verknüfungen zwischen den einzelnen Verzweigungen im Stammbaum.*

(Fig. 6). We detected three pairs of females who were related in the third or fourth degree, while all other pairs were not genetically related, or too distantly related to be detected. This is consistent with the expected background diversity of the population. The analysis of runs of homozygosity (when an individual carries the same genomic segment inherited from a common ancestor via both parents) also shows no signs of inbreeding within the group (Fig. 7). Only one individual, GLN282, carries long runs of homozygosity, a pattern which suggests that he was the offspring of a second or third cousin relationship. The overall level of background relatedness corresponds to a medium-sized effective population, when compared to, for example, Early Neolithic groups from central Europe (Ringbauer et al. 2021; Childebayeva et al. 2022).

The results of the IBD sharing analysis are consistent with the inferred mating network from the exogenous connections identified through the reconstructed pedigrees, and revealed additional connections beyond the reconstructed pedigrees, which indicates links through female lines (Fig. 6). Here, we observed several pairs within the pedigrees that, according to the reconstructed pedigrees, appear to share more IBD than expected, but without questioning the robustness of this reconstruction. This includes individuals within Pedigree A, but also between Pedigrees A and B. Intriguingly, all detected links, although relatively

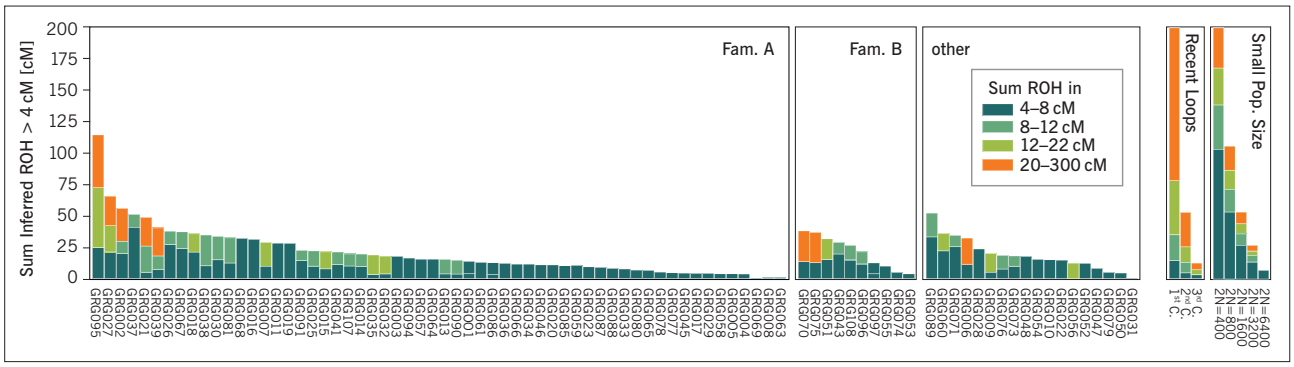


Fig. 7 Gurgy ›les Noisats‹. Runs of homozygosity. Selected individuals with more than 300 000 SNPs (n = 86) and simulated data for inbred individuals from parents related at the first- to third-degree, and for individuals from small populations with different sizes for comparison. Individual GLN282 (GRG095) shows an inbreeding signal similar to a first-cousin union, but both carried ROH are 20–22 cM long, therefore this individual is more plausibly the offspring of 2nd or 3rd cousins.

Abb. 7 *Gurgy ›les Noisats‹. Verlauf von Homozygotie. Ausgewählte Individuen mit mehr als 300 000 SNPs (n = 86) und zum Vergleich simulierte Daten für inzüchtige Individuen von Eltern, die ersten bis dritten Grades verwandt waren, sowie für Individuen aus kleineren Populationen unterschiedlicher Größe. Das Individuum GLN282 (GRG095) weist ein Inzuchtsmerkmal ähnlich dem einer Verbindung zwischen Cousin und Cousine ersten Grades auf, aber beide ROH sind 20–22 cM lang, daher ist es plausibler, dass dieses Individuum der Nachkomme von Cousin und Cousine zweiten oder dritten Grades ist.*

distant, can only be explained through the female lines. A likely explanation is a scenario in which female descendants of those females who had left the Gurgy community returned after a few generations to find a partner in Gurgy upon their return. Alternatively, incoming female partners came from the same community and were maternally related. Both cases would imply that the network of reciprocal mobility within which these movements happened was small enough to retain continuous connections (intentional or unintentional), but at the same time was also sufficiently large to integrate entirely unrelated females. In sum, this lends support to the existence of a relatively wide and fluid exchange network comprising many, potentially smaller, groups, a phenomenon which was described as ›generalised exchange‹ in ethnographic studies (Lévi-Strauss 1971). On the basis of the ROH length distribution, we estimated the effective population size of the communities contributing to the genetic diversity observed at Gurgy to have been ~1835 individuals (1631–2077 95 % CI; Ringbauer et al. 2021). The distribution of runs of homozygosity across Gurgy individuals suggests that most pairs of parents were related to each other *via* co-ancestors within the preceding 5 to 30 generations.

Occupation of the site

Beyond the kinship structure of the Gurgy group, the pedigrees also contained information about the duration of the site occupation. Individual GLN270B, the male founder of the main paternal line of Pedigree A, has a particular archaeological status as his burial is the only secondary burial of the site deposited inside the grave of the female GLN270A, from whom we could not obtain DNA data (Fig. 8). Only his long bones were placed in the pit, likely in a bundle next to the articulated skeleton of GLN270A, while the rest of his skeleton was missing. This suggests that these remains have been transferred and buried during the early phase of the site, probably because he represented, together with his brother GLN231A, the main ancestors of the pedigree, and was potentially the senior lineage male. This suggests that this grave was a founding event in the history of the necropolis, even though the relation to the female GLN270A remains unclear. GLN270A could be a close relative (mother, sister, daughter, or further connection?), or a reproductive partner. Alternatively, it could also be the burial of a random person, whose grave-pit was prepared and to whom the remains of GLN270B were added opportunistically. Irrespective of the reasons, the will to translocate the remains of this main ancestor to the site at Gurgy, even if he had potentially died a long time before the secondary burial, marks the importance of him and his lineage to the creation of this new burial place for, and by, his descendants. If GLN270A was indeed the partner in life of GLN270B, then it is also interesting to note that the translocated remains were buried with her and not his brother (GLN231A), or with his potential uncle or half-sibling, GLN320. This would further underpin the significance of this lineage, now represented through her.

The pedigrees reveal an absence of subadults amongst the first four generations in Pedigree A (5 out of 36 individuals), which is rather surprising in light of the estimated mortality patterns in archaic populations (Gage 1989; Wood et al. 2002). However, this pattern is reversed across the last three generations, with 20 out of 25 individuals being subadults. The overall trend is consistent with a scenario in which an entire group of several generations moved near to this new burial site, leaving behind their deceased offspring at a previous funerary site, but transferring the ›ancestor/founder‹ GLN270B. Additionally, the fact that many parents are missing in the last generations suggests that this process was repeated and that the group moved on to settle elsewhere, again leaving behind children who had already passed away at the time. The Sr isotope data provide a further line of evidence in support of these interpretations. Here, $^{87}Sr/^{86}Sr$ ratios are low (~0.709) for the earlier generations, and overall similar to exogenous females, which indicates a non-local origin of the founders (Fig. 5). In contrast,

Sr ratios in males continuously increased with generations, approximating the local Sr signal.

When both pedigrees are compared, overlapping ^{14}C date ranges and the 3rd–4th degree connection between GLN263 and GLN298 suggest relative contemporaneity of both. Nevertheless, despite clear evidence for seven consecutive generations in Pedigree A, the occupation time of the site was relatively short. Excluding the founding and outward migrating last generations, the duration of the site's use was likely only 3–4 generations, or 84–112 years (1 generation = 28 years; Fenner 2005). Bayesian modelling of all available radiocarbon dates allowed us to place the interval for Pedigree A to between the late 48th and the late 47th century BC.

We speculate that the use of the graveyard corresponds to the duration of dwellings. The typical duration of a longhouse of the Neolithic Linear Pottery Culture was estimated to be between 20–30 years (Modderman 1968) and up to 75–100 years when maintained (Rück 2007). Experimental archaeology suggested that the lake dwellings in the Jura of the late Neolithic period would have lasted for a period of about ten years without proper maintenance (Pétrequin et al. 2015). However, no settlement was found directly associated with the Gurgy graveyard, precluding the integration of contextual details. An alternative, or complementary, explanation for a limited occupation time could be the depletion of local soils or other natural resources, driven by non-sustainable agricultural practices that could have taken different forms; however, this is still the subject of intense debate (Boserup 1965; Pétrequin et al. 2015).



Fig. 8 Gurgy ›les Noisats‹. Photo of female individual GLN270A (no genetic results) with the reburied remains of the main male ancestor GLN270B of Pedigree A.

Abb. 8 *Gurgy ›les Noisats‹. Befundfoto des weiblichen Individuums GLN270A (keine genetischen Ergebnisse) mit den wieder bestatteten Überresten des männlichen Hauptvorfahrens GLN270B von Stammbaum A.*

Inferences beyond the site: questioning the regional network

The biological structure of the group buried at Gurgy revealed by the two main pedigrees and the unlinked individuals sheds light on some of the rules that potentially governed this community. The patrilineal, patrilocal, and female exogamic pattern we observed requires a population large enough to avoid recurrent close-related females amongst those who came to join the Gurgy group, as was also shown by the background relatedness of the analysis of runs of homozygosity. However, this network of relationships with other groups includes occasional unions with (distantly) related women from the same source group, suggesting preferential links, abiding alliances, or dependencies between some groups.

The independent lines of evidence suggest that the social system at work in the Gurgy community implies a number of external groups presumably bound by reciprocal alliances, which may have been structured by a range of features, such as population size, access to and exchanges of resources, a socio-economic network, or common linguistic and cultural affinities (e.g., shared language[s] and belief systems).

The occupation of the necropolis could be narrowed down to between the late 48th and the late 47th century BC, based on Bayesian modelling. From an archaeological perspective, the Gurgy site stands in contrast to the regional context of contemporaneous monumental sites that are associated with the Cerny Culture, and which were built for selected individuals (Chambon/Thomas 2010). Fleury-sur-Orne, Calvados Department, in Normandy is the only monumental site from the Cerny area that has been genetically investigated to date and it shows a strong social selection of individuals buried in different monuments according to different patrilineal lineages (Rivollat et al. 2022). Given the structural differences between Fleury and Gurgy, but also taking into account the STP sites from the Paris Basin, it remains difficult to draw conclusions by combining information obtained from both studies.

In the case of Gurgy, it is possible that two different communities co-existed in the same region: one that buried their dead at Gurgy and one that had used the STPs, with different funerary practices and attitudes towards social ranking. This hypothesis is reflected in the material culture, as Gurgy does not show a clear attribution to the Cerny Culture, although the site is contemporaneous and Cerny sites are located nearby. Gurgy burials show multiple influences from different cultures, some local, such as alcove burials from LBK-derived groups in the West, while others originated further away, like Chamblandes cists from the Alps, or specific shells from the Mediterranean area. However, if Gurgy was culturally isolated from the surrounding context, this would be inconsistent with the genetic evidence that shows strong links with a wider biological net-

work over several generations, or would instead imply that the network exclusively exceeded the Cerny lacuna.

Given the absence of selection of individuals on the basis of sex, age, economic or social hierarchies at the regional level in Gurgy, an alternative interpretation would be that the site represented the burial practices of the non-elite for a broader society in which the STP-buried individuals were the elite at the regional level. Under this assumption, as the Gurgy site was used by a single group, which was genetically highly related, we would expect contemporaneous graveyards of similar sizes to meet the expectations from the observed genetic diversity estimates, such as mitochondrial haplogroup diversity and runs of homozygosity. However, only three other contemporaneous graveyards without monuments are known from the area, and these are all much smaller: Monéteau ›Macherin‹ located only 3 km from Gurgy and having *Chassen* components, Vignely ›La Porte aux Bergers‹, Seine-et-Marne Department, and Chichery ›sur les Pâtureaux‹, Yonne Department, with 15, 17, and 27 buried individuals, respectively[3]. If we consider the total number of individuals buried at these sites as potential non-elite, this number (n = 187) is too low compared to the known 120 individuals buried at the monumental STP sites (Chambon 2003; Chambon/Thomas 2010; Thomas 2011). This might suggest a strong bias in the excavation strategy or the preservation of the sites.

Looking at the site level, we observe subtle elements of, if not hierarchy, then at least specific consideration of some individuals, such as the larger sizes of the graves of GLN207B's son (GLN237A) and grandson (GLN221B). However, this example is far from the ostentatious demonstration visible in the STPs, with none of the elements present in STP sites that emphasize a hierarchical structure (monuments, gender-related scenography, grave goods; Chambon/Thomas 2010) are visible at Gurgy. Admittedly, GLN207B, the main ancestor of the largest pedigree, has a very specific funerary treatment compared to all other individuals buried in Gurgy, but no other sign of power/wealth in the material culture was found. We suggest that it was important for his community/lineage to (re)bury him in the same place where his descendants will be buried for a few generations, but not at the level of supra-regional significance outside the community.

On the basis of combined evidence available at present, we favour the latter hypothesis, suggesting that the different necropolises without monuments in the Paris Basin do in fact represent the non-elite, while many others, which we would assume to have had a similar structure and/or organisation, have not yet been found. This is more in line with the genetic data showing a wide and connected network over several generations. Overall, the lack of comparative data from STP sites and non-monumental sites present in the region imposes a limitation that does not allow us to go beyond a tentative interpretation of our findings.

Conclusion

These largest pedigrees reconstructed from ancient human DNA data so far represent a major and unprecedented step forward in our understanding of the social organization of a human group from Gurgy ›les Noisats‹, and of Middle Neolithic societies of Western Europe more broadly. What remains to be determined is whether our findings are an exception among the Neolithic societies, where the observed variety of different funerary settings is striking, or whether Gurgy represents the norm of governing social structures and kinship practices during the 5th millennium BC. Therefore, our work provides an anchor for further archaeogenetic studies to reach a general consensus on the potentially diverse social organisation(s) of Neolithic societies in Europe.

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Socioeconomic organisation in the Globular Amphora network during the earliest 3rd millennium BC

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Zusammenfassung

Sozioökonomische Organisation im Netzwerk der Kugelamphorenkultur im frühesten 3. Jt. v. Chr.

In diesem Artikel werden Anhaltspunkte präsentiert und verglichen, die Aufschluss über Aspekte der sozialen und wirtschaftlichen Organisation in verschiedenen Teilen des großen geografischen Gebiets in Mittel-, Ost- und Nordeuropa geben, das das Netzwerk der Kugelamphorenkultur im frühen 3. Jt. v. Chr. umfasst. Das »Kugelamphoren-Netzwerk« bezieht sich hier auf Regionen, in denen Gemeinschaften erheblich von Elementen der Kugelamphorenkultur beeinflusst wurden, unabhängig davon, ob sie das gesamte Spektrum der materiellen Kugelamphorenkultur und ihres Ritus umfassten oder nur einige Elemente. Diese Diskussion präsentiert Beispiele verschiedener archäologischer Beweislinien, die hinsichtlich der Organisation von Gruppen aufschlussreich sein können, einschließlich Aspekten wie der Strukturierung von Gräberfeldern sowie Siedlungs- und Mobilitätsmustern. In einigen Fällen war es möglich, diese Arten von Beweisen durch aDNA-Informationen über biologische Beziehungen zwischen Individuen, die in Gräbern gefunden wurden, zu ergänzen, was eine völlig neue Ebene der detaillierten Interpretation von Verwandtschaftsstrukturen eröffnete. Wie bei den meisten bekannten Varianten menschlicher sozialer Organisation dürften Verwandtschaftsstrukturen – die in erheblichem Maße, aber nicht ausschließlich in biologischen Beziehungen verwurzelt sind – für die soziale Organisation von Kugelamphorengruppen von zentraler Bedeutung gewesen sein, die wiederum wahrscheinlich eng mit der Konfiguration wirtschaftlicher Aktivitäten, Siedlungsformen, Mobilität und Austauschmustern verknüpft war. Der Beitrag veranschaulicht die Vorteile integrierter Datensätze, die molekulare und traditionelle archäologische Beweislinien verbinden und dabei helfen, das Verständnis der Organisation und sozialen Matrix dieser und anderer prähistorischer Gemeinschaften umfassender zu verstehen.

Summary

This article presents and compares evidence informing on aspects of social and economic organisation in different parts of the large geographical area in central, eastern and northern Europe encompassing the Globular Amphora (GA) network during the earliest 3rd millennium BC. ›The GA network‹ here refers to regions in which communities were influenced significantly by GA cultural elements, whether including the full range of GA material culture and customs or only some elements. The discussion presents examples of different archaeological lines of evidence that may be informative regarding the organisation of groups, including such aspects as the structuring of cemeteries and settlement and mobility patterns. In some cases, it has been possible to supplement these types of evidence with aDNA information on biological relations between individuals found in graves and tombs, opening up an entirely new level of detailed interpretation of kinship structures. As in most known variants of human social organisation, kinship structures – to a significant extent but not exclusively rooted in biological relations – are likely to have been central to the social organisation of GA groups, which, in turn, was probably closely integrated with the configuration of economic activities, settlement forms, mobility and exchange patterns. The paper argues for the benefits of integrated datasets cross-cutting molecular and traditional archaeological lines of evidence, aiding more fully the understanding of the organisation and social matrix of these and other prehistoric communities.

Introduction

From around 3100 BC, the Globular Amphora (GA) material culture complex – often simply referred to as the Globular Amphora Culture – spread from its centre of origin in present-day Poland to encompass large parts of Central and Eastern Europe. In addition to the distinctly shaped ceramic amphora after which it was named, it also included certain flint and bone tools, stone battle axes, a range of symbolic or ornamental amber and bone artefacts, as well as specific types of burials and animal depositions. Many communities that formed part of this supra-regional complex not only shared these stylistic elements in material artefacts and structures, but presumably also a more or less similar combination of economic strategies, social organisation and ritual practices (Szmyt 2017). However, what we may refer to as the wider ›Globular Amphora network‹ also included adjacent regions in which communities were influenced significantly by GA cultural elements without adopting the full range of GA material culture and customs. Figure 1 shows the extent of the GA complex proper during the earliest 3rd millennium BC, along with an example of the latter type of region,

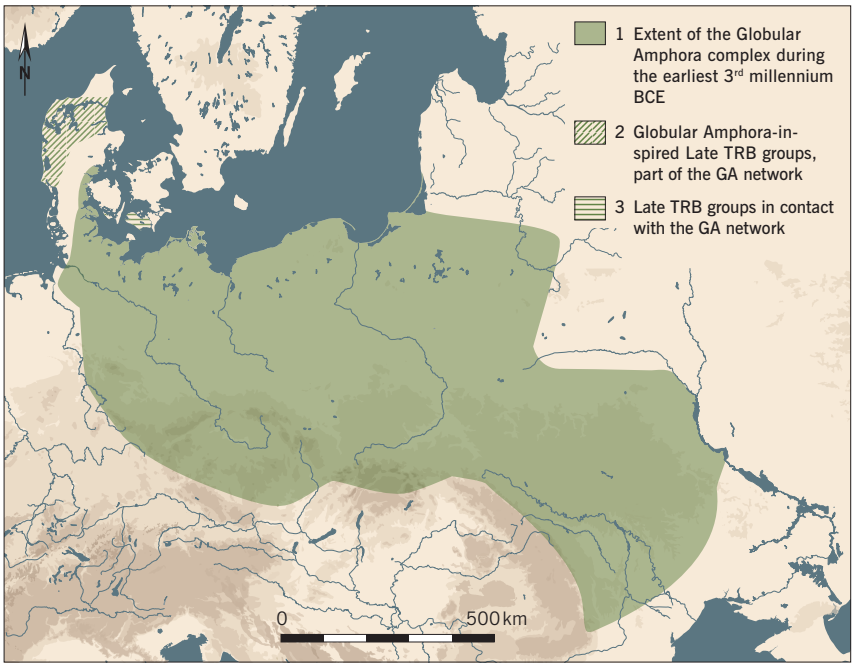


Fig. 1 Map of Europe showing the distribution during the earliest 3rd millennium BC of: 1 the Globular Amphora (GA) complex; 2 GA-inspired Late TRB groups, which were part of the GA network, northern and western Jutland Peninsula; and 3 Late TRB groups in contact with the GA network, southern Danish isles.

Abb. 1 *Karte von Europa, die die Verbreitung im frühesten 3. Jt. v. Chr. zeigt von: 1 dem Kugelamphoren (GA)-Komplex; 2 Kugelamphoren inspirierte späte Trichterbecherkultur (TRB)-Gruppen, die Teil des Kugelamphoren-Netzwerks auf der nördlichen und westlichen Halbinsel Jütland waren; 3 späte TRB-Gruppen auf den süddänischen Inseln, in Kontakt mit dem Kugelamphoren-Netzwerk.*

i.e., the Jutland Peninsula, which will be discussed further below. Moreover, even within the more narrowly defined GA complex, significant cultural variation and exceptions are found – including not only stylistic differences in material culture, but also variation on such fundamental parameters as settlement patterns, subsistence strategies and burial forms[1]. This variation makes it meaningful to consider the supra-regional phenomenon we can identify archaeologically in terms of a range of different *constellations of* GA Culture. In other words, what extended across the vast area outlined in Fig. 1 were different versions of, or in some regions, more sporadic elements of GA Culture – rather than *the* GA Culture, understood as a uniform package. Nonetheless, as we shall see below, it still makes sense to discuss certain cultural trends in the realm of socioeconomic organisation that pervaded significant parts of the GA network and in many regions set it apart from previous Neolithic developments.

The following discussion presents examples of evidence informing on aspects of socioeconomic organisation in different parts of the GA network during the earliest 3rd millennium BC. In order to address ›socioeconomic organisation‹, in the sense intended here, the discussion will proceed from two starting premises. The first premise is that kinship structures – to a significant extent (though not exclusively) rooted in biological relations – are likely to have been central to the social organisation of most prehistoric communities, as indeed they are to traditional (premodern) societies more widely (cf. Bentley 2022). The second premise is that the same social organisation was, in turn, probably closely integrated with the configuration of economic activities, settlement forms, mobility and exchange patterns (Ember 2011). If these two premises are valid for understanding the socioeconomic organisation of communities in the GA network, it follows that approaches which combine multiple lines of evidence, cross-cutting recent bioarchaeological advances and traditional archaeological data and including both regional and local scales of analysis, are more likely to succeed (cf. Johannsen et al. 2017; Racimo et al. 2020). As often in archaeology, the relevant types of data are not uniformly distributed within the GA network, thus underlining the importance of comparing across regions.

Socioeconomic organisation in the Globular Amphora complex

A classical model of GA socioeconomic organisation is shown in Fig. 2. This model was first developed as an attempt to capture and represent the overall impression of GA socioeconomic organisation that was forming on the basis of archaeological evidence concerning different aspects of GA Culture in Central Europe (Szmyt 1996; Czebreszuk/Szmyt 2011). To understand the basis for the model, we shall briefly summarise the information and interpretations underlying it. These data were partly available at the time when it was originally presented, but new finds and analyses have since then substantiated the model further.

Several lines of evidence have indicated that the subsistence economy of the GA was based mainly on animal husbandry, whereas arable agriculture played only a minor role. In addition to bone remains reflecting meat consumption in settlement contexts, the importance of animal husbandry is shown by abundant depositions of animals or animal parts in ritual contexts, e.g., joints of meat as accompanying food in human burials, and of more or less whole animals – often cattle – in ›animal burials‹, often associated with human graves. In addition to cattle, the domestic animals kept included pigs, sheep, goats and dogs (Woidich

1 Szmyt 1999; Woidich 2014; Szmyt 2017; Piličiauskas et al. 2021; cf. Müller in press.

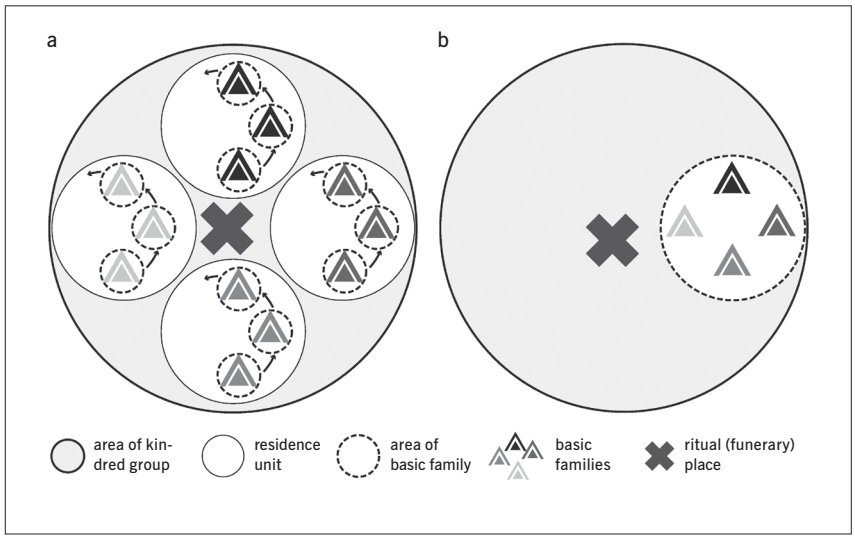


Fig. 2a–b Model of socioeconomic organisation of GAC communities in Kuyavia. a Maximal dispersion; b Minimal dispersion.

Abb. 2a–b *Modell der sozioökonomischen Organisation der Kugelamphorenkultur-Gemeinschaften in Kujawien. a maximale Streuung; b minimale Streuung.*

2014; Szmyt 2017). A limited number of stable isotope analyses (C and N) and lipid analyses on pottery, informing on the diet of GA individuals, have yielded results fully compatible with a diet predominated by meat and dairy from domestic animals (Eriksson/Howcroft 2013; Roffet-Salque et al. 2017; Schroeder et al. 2019).

The dominant form of GA settlement remains found are single homesteads and camp sites, whereas larger settlements with several, potentially contemporary houses are rare. However, there are clearly exceptions, for instance in the case of communities in Upper Silesia, which seem to have been an integrated part of the GA complex, but which nonetheless opted for living in longhouses in what appear to be classical agricultural farmsteads or larger hamlets also associated with previous Neolithic groups in the area[2]. In general, though, both economic and settlement evidence indicate that most GA groups were relatively mobile (Müller 2001; Szmyt 2002; Woidich 2014). The basic pattern of mobility appears to have involved regular, relatively short-range movements within large territories, presumably for the purpose of seeking out optimal grazing for the animals across the annual cycle. Recent isotope analyses ($^{87}Sr/^{86}Sr$ and $\delta^{18}O$) on humans and cattle have arrived at the same overall conclusion (Gerling 2015; Nowaczyk et al. 2017). Here, it is interesting to note an observation made in the western part of the GA complex, where GA sites tend to cluster differently in the landscape from both preceding and contemporaneous Neolithic (e.g., Bernburg) groups (Woidich 2014, 95–96). This observation potentially provides a further indication that the socioeconomic strategy of GA groups was somewhat distinct from that of these other Neolithic groups. Occasionally, mobility among GA communities may have involved farther-reaching movements but even though their mobility was likely configured mainly around needs and preferences associated with animal husbandry, it probably differed substantially from what we could refer to as full-blown pastoral nomadism (cf. Honeychurch/Makarewic 2016).

GA communities buried their dead in a variety of different ways, with some regional variation. The most prevalent form is inhumation burial in a stone cist, but other forms, such as simple pit graves as well as larger tombs with stone kerbs or stone pavement, also occur regularly. Inhumation burial of more or less intact bodies dominates, but in some cases bodies are disarticulated, and partially or completely cremated human remains occur. Where larger funerary areas have been excavated, fewer than 20 individuals are usually found within the same cemetery (Nowaczyk et al. 2017; Szmyt 2017).

On the basis of the archaeological information on their economic strategy and settlement and mobility patterns, as well as the organisation of their cemeteries, the basic organisational unit of GA communities appears to have been the family or extended family group. However, these small groups probably aggregated into larger groups, plausibly tied together by kinship, on one or several occasions during the year (Szmyt 2002; Szmyt 2017). These aggregations most likely occurred at or near the cemeteries, which likely constituted a stable, cultural element across generations. Here, social interaction, including not least communal ritual activities, may have functioned to reinforce the coherence and identity of a larger group, whilst simultaneously coordinating or regulating the activities and social links between the smaller social units. Feasts or symbolic consumption of wealth, such as the slaughtering and deposition of cattle and other domestic animals (Pollex 1999; Szmyt 2006), are likely to have been particularly important in this connection. In addition to exchange of partners through cross-group marriage, one of the concrete organisational aspects probably negotiated at these localities was the division or sharing of land-use between groups, which is likely to have been crucial for a socioeconomic system emphasizing mobility. Here, the cemeteries may have played a key role as durable ideological reference points in the landscape (Szmyt 2002; Schroeder et al. 2019).

2 M. Furmanek, Personal Communication. Kiel, March 17th, 2023.

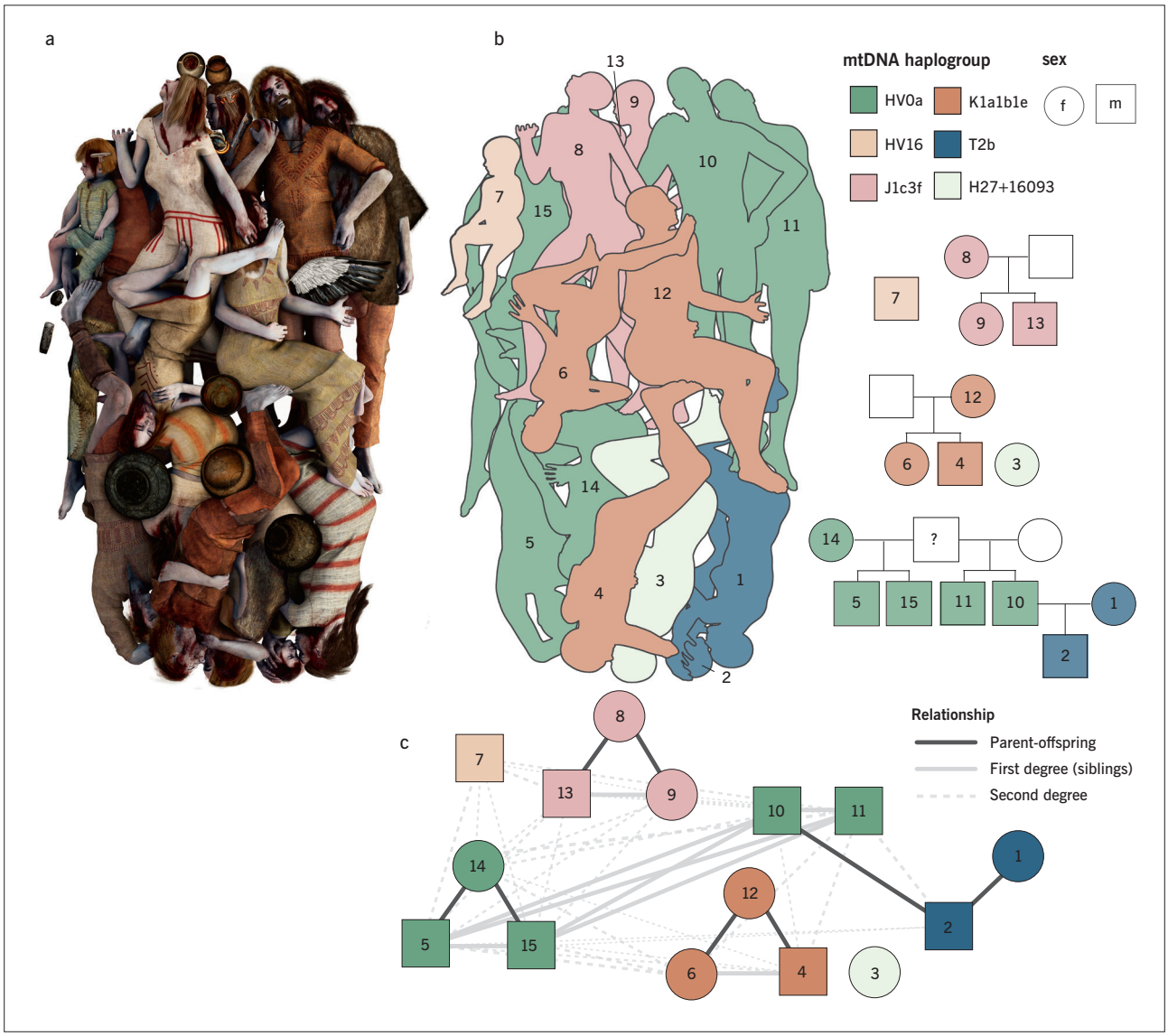


Fig. 3a–c a Artistic reconstruction of the Koszyce, Lesser Poland Voi. (Poland), mass burial based partly on phenotypic traits inferred from the ancient genomes; b schematic representation of the burial and pedigree plots showing kinship relations between the Koszyce individuals inferred from genetic data; c kinship network based on kinship coefficients inferred from IBS scores for pairs of Koszyce individuals showing first- and second-degree relationships.

Abb. 3a–c *a Künstlerische Rekonstruktion der Massenbestattung von Koszyce, Woi. Kleinpolen (Polen), teilweise basierend auf phänotypischen Merkmalen, die aus den alten Genomen abgeleitet wurden; b schematische Darstellung der Bestattungs- und Ahnentafeln, welche die aus genetischen Daten abgeleiteten Verwandtschaftsbeziehungen zwischen den Individuen aus Koszyce zeigen; c Verwandtschaftsnetzwerk basierend auf Verwandtschaftskoeffizienten, die aus IBS-Bewertungen für Paare aus Koszyce abgeleitet werden, die Beziehungen ersten und zweiten Grades aufweisen.*

Archaeogenetic evidence

The archaeological model of GA socioeconomic organisation summarised above was first developed well in advance of the breakthrough of genomic and genome-wide aDNA analyses. In this light, its compatibility with recent archaeogenetic results informing on the same topic is remarkable. In a recent study, H. Schroeder et al. (2019) were able to analyse in detail the biological relationships among 15 children, women and men, whose skeletal remains were found in a mass burial near the village of Koszyce, Lesser Poland Voi., in southern Poland in 2011 (Przybyła et al. 2013). As illustrated in Fig. 3, these individuals, who had all been killed by blows to the head, but who were then buried with GA material culture as grave goods, appear to have been members of what we might call an ›extended family‹. Almost all of them were connected via several first- and second-degree relationships, and four nuclear families were identified in the grave, three of them represented by mothers and their children. As already indicated, the Koszyce mass burial reflects a violent event that was catastrophic to the group in question, and the under-representation of the older males/fathers in the grave further suggests that they were absent when disaster struck; indeed, although entirely hypothetical, it is possible that they were the ones who buried their kin. Whatever the case, the genetic information clearly confirms the impression that the seemingly careful placing of specific individuals next to one another had not been coincidental. Closely related kin were buried next to each other: a mother was buried holding her child, and in several cases siblings were placed side by

side. The only father present in the grave was individual 10, whose partner and son were placed together opposite him in the grave. And individual 14, the oldest individual in the grave, was buried close to her two sons (individuals 5 and 15), while individual 8, a 30–35 year-old woman, was buried with her teenage daughter (individual 9) and 5 year-old son (individual 13). The parents of a young boy (individual 7), aged 2–2.5 years, were not in the grave, but he had been placed next to other individuals to whom he was closely related through various second-degree relationships. Evidently, these individuals were buried by people who knew them well and placed them in the grave according to their family relationships (Schroeder et al. 2019).

Despite the atypical and dramatic background of the Koszyce burial, the buried individuals provide valuable information on the social structure and kinship system of the community that they represent. Looking at the burial arrangement in combination with the biological data, it seems clear that in this group, genetic and reproductive relationships were also considered key social relationships. Further, as exemplified by individual 3, an adult female who is not genetically related to anyone in the grave (but placed close to individual 4, a young man), the pedigrees of females and males in the grave show a clear pattern. According to mitochondrial DNA data combined with Y chromosome (NRY) data on the seven females and eight male individuals buried, there were six female lineages represented in the grave, while all of the males appear to belong to the same lineage (Schroeder et al. 2019). This suggests that the community at Koszyce was organised along patrilineal lines of descent, aligning with previous evidence suggesting that this was a common form of social organisation among Late Neolithic communities in Central Europe, often combined with female exogamy – i.e., women joining/marrying outside their own social group and into the group of their partner (Haak et al. 2008; Knipper et al. 2017).

While the genetic analyses of the individuals from the Koszyce mass burial do not in themselves prove any specific mode of socioeconomic organisation, the results are fully compatible with the archaeologically based model of GA socioeconomic organisation presented above. In particular, it seems on the one hand that nuclear families formed a basic social unit in the community in question but, simultaneously, also that these ›basic units‹ joined each other in larger, extended family groups, plausibly for parts of the year only – as indeed suggested by the archaeological model. Interestingly, evidence from another part of the GA network points to a similar mode of organisation.

The wider Globular Amphora network: the example of the Jutland Peninsula

On the Jutland Peninsula, Denmark, a body of evidence centring around the so-called stone heap grave custom is pertinent to the present discussion of socioeconomic organisation during the earliest 3rd millennium BC. The stone heap graves, which have been found at more than 50 sites located in a zone covering the northern and western parts of the peninsula (see Fig. 1), are clear manifestations of the participation of their makers in the supra-regional GA network (Johannsen/Laursen 2010). Constructed during the period 3100–2800 BC, these graves appear to have been vehicle graves in which single individuals were interred either in a fully functional or more symbolic vehicle placed in a more or less rectangular structure and equipped with a draught team of two oxen (Fig. 4). The animals were placed with their bodies in the two associated oblong pits with their heads resting high on the adjacent surface, facing away from the quadrangular structure, as if ready to pull the vehicle behind them, before the whole structure was covered by a large heap of stones. As discussed at length elsewhere, the stone heap graves are clearly a particular regional manifestation of the custom of burying cattle, often in pairs, which was also practiced by many communities in the GA complex to the south and south-east of the peninsula (Johannsen/Laursen 2010; Johannsen/Kieldsen 2014; Johannsen et al. 2016).

Unfortunately, soil conditions in north-western Jutland have not permitted the preservation of organic remains that could provide a basis for archaeogenetic analyses of the buried individuals, as we have seen exemplified with the Koszyce grave elsewhere in the GA network. Despite this rather significant limitation, the stone heap graves do yield information that is directly relevant to our discussion here. The clear thematic focus of the stone heap graves is stressed by their alignment in small linear groups that in some places accumulated into large, linear cemeteries (Jørgensen 1977; Fabricius 1996). These followed the corridors of transport used in the area in question (Johannsen/Laursen 2010). However, what is particularly noteworthy in the present context is a clear pattern indicated by thorough typo-chronological analyses of the artefacts deposited as grave goods in these graves (Fabricius 1996, 210 ff.). Individual groups (rows) of stone heap graves seem to have accumulated, each on their own, across a longer time span, probably over generations. An illustration of this pattern is shown in Fig. 5, which shows a small group of graves at the site Øster Ristoft, western Jutland, but the same overall principle has also been identified at other sites in the north-western part of the peninsula, such as Bondesgård, Herrup and Øster Brændgård (Fabricius 1996, 214 ff.). Whether or not the cemetery at a given site encompassed a single or multiple groups of graves, each group appears to have its own history of accumulation. As noted by K. Fabricius (1996, 247), this pattern suggests that most of these groups reflect funerary activities of individual social units, possibly household or family units.

Looking into the wider landscape context of the stone heap grave custom may provide the necessary background for understanding this pattern, which seemingly emphasises small social units that in some contexts aggregated into larger units. Contemporaneous settlement evidence in the area consists of scattered occurrences of small-scale evidence for domestic activity and dwelling that appear to reflect a rather flexible way of inhabiting and moving around in the landscape (Davidsen 1978; Johannsen et al. 2016). The pollen record of this part of the Jutland Peninsula shows significant variation between sequences for different localities,

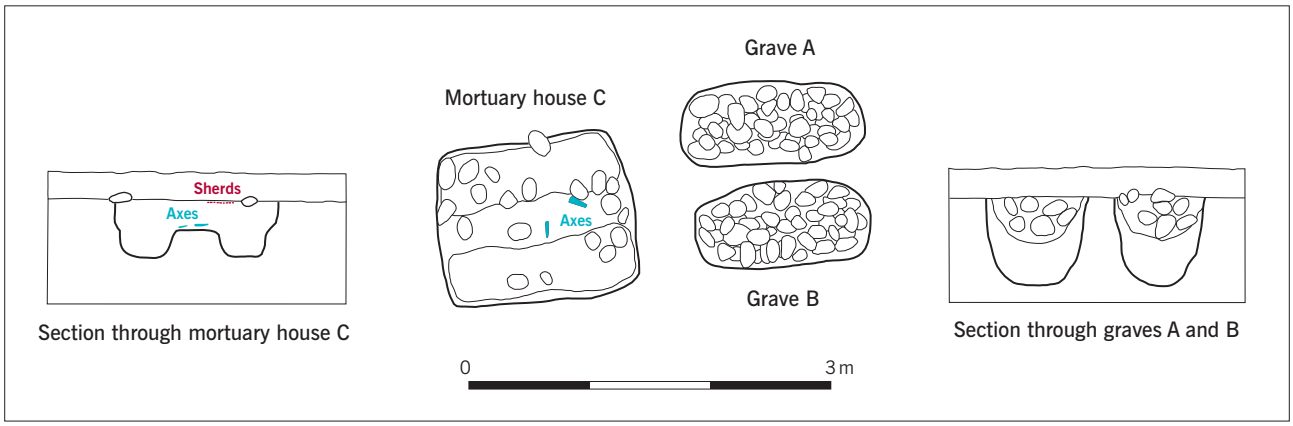


Fig. 4 Stone heap grave at Vroue Hede, northern Jutland Peninsula (Denmark), in plan and section. The finds have been plotted onto the section through the quadrangular feature C (Vroue Hede II, Structure IX).

Abb. 4 *Steinhaufengrab bei Vroue Hede, nördliche Halbinsel Jütland (Dänemark), im Grundriss und im Schnitt. Die Funde wurden auf dem Schnitt durch den viereckigen Bef. C (Vroue Hede II, Struktur IX) aufgetragen.*

but the dominant picture is a trend towards a gradual opening of the landscape with larger areas of pasture forming during this period (and continuing in the subsequent Corded Ware period) (Odgaard 1994; Andersen 1998; Hübner 2005, 702–707). Together with the settlement data, the pollen record thus points towards the predominance of a particular socioeconomic strategy, with an emphasis on animal husbandry, in northern and western Jutland during the earliest 3rd millennium BC. Furthermore, when plotted on a soil classification map, sites with stone heap graves can be shown to be located predominantly in areas with different types of sandy soil, combined with a relative vicinity to the coast/fiords and/or major river valleys (Fig. 6). While the light, nutrient-poor soils in these areas are of very low quality for traditional arable agriculture, the vegetation here is correspondingly sensitive to a sustained grazing pressure, which would quickly have promoted growing patches of open land, dominated by grasses and herbs – i.e., further grazing potential. And with good access to shore meadows, river valleys and drier parts of the inland, a pattern of settlement and mobility centred around these sites would have been particularly well-suited to provide suitable foraging environments for the animals at different times of the year (Johannsen et al. 2016).

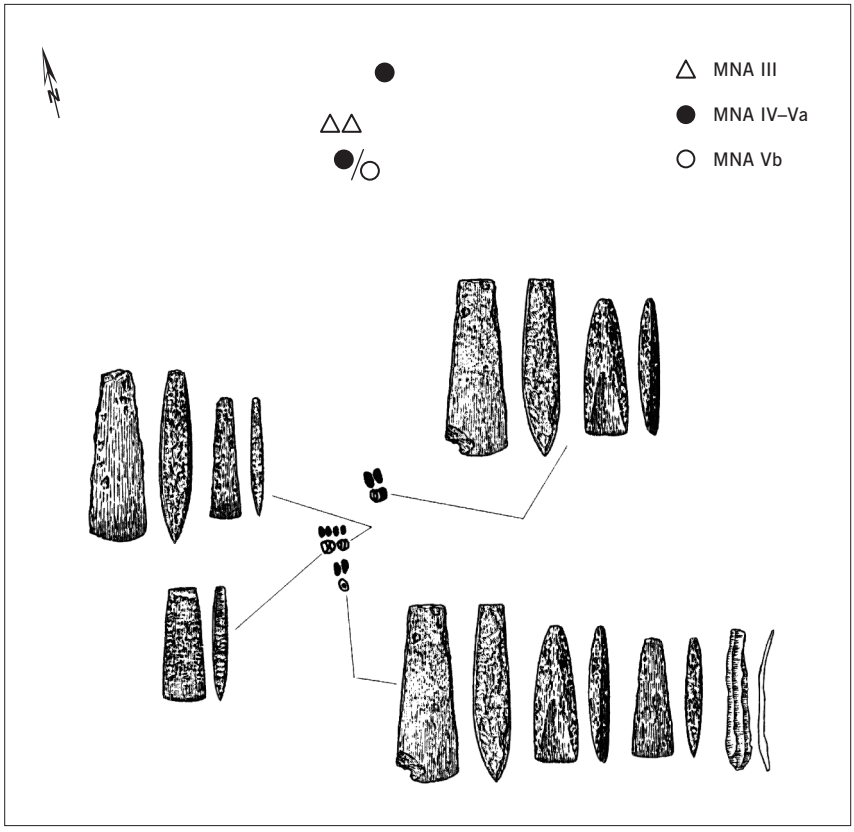


Fig. 5 Relative dating of four stone heap graves excavated at Øster Ristoft, western Jutland Peninsula (Denmark). The graves are dated typo-chronologically to three subsequent sub-periods of the regional chronology (MN = Middle Neolithic), representing an approximate time span of 200 years, c. 3000–2800 BC.

Abb. 5 *Relative Datierung von vier Steinhaufengräbern, die in Øster Ristoft, westliche Halbinsel Jütland (Dänemark), ausgegraben wurden. Die Gräber sind typochronologisch auf drei aufeinanderfolgende Unterperioden der regionalen Chronologie (MN = Mittelneolithikum) datiert, was einer ungefähren Zeitspanne von 200 Jahren entspricht, also ca. 3000–2800 v. Chr.*

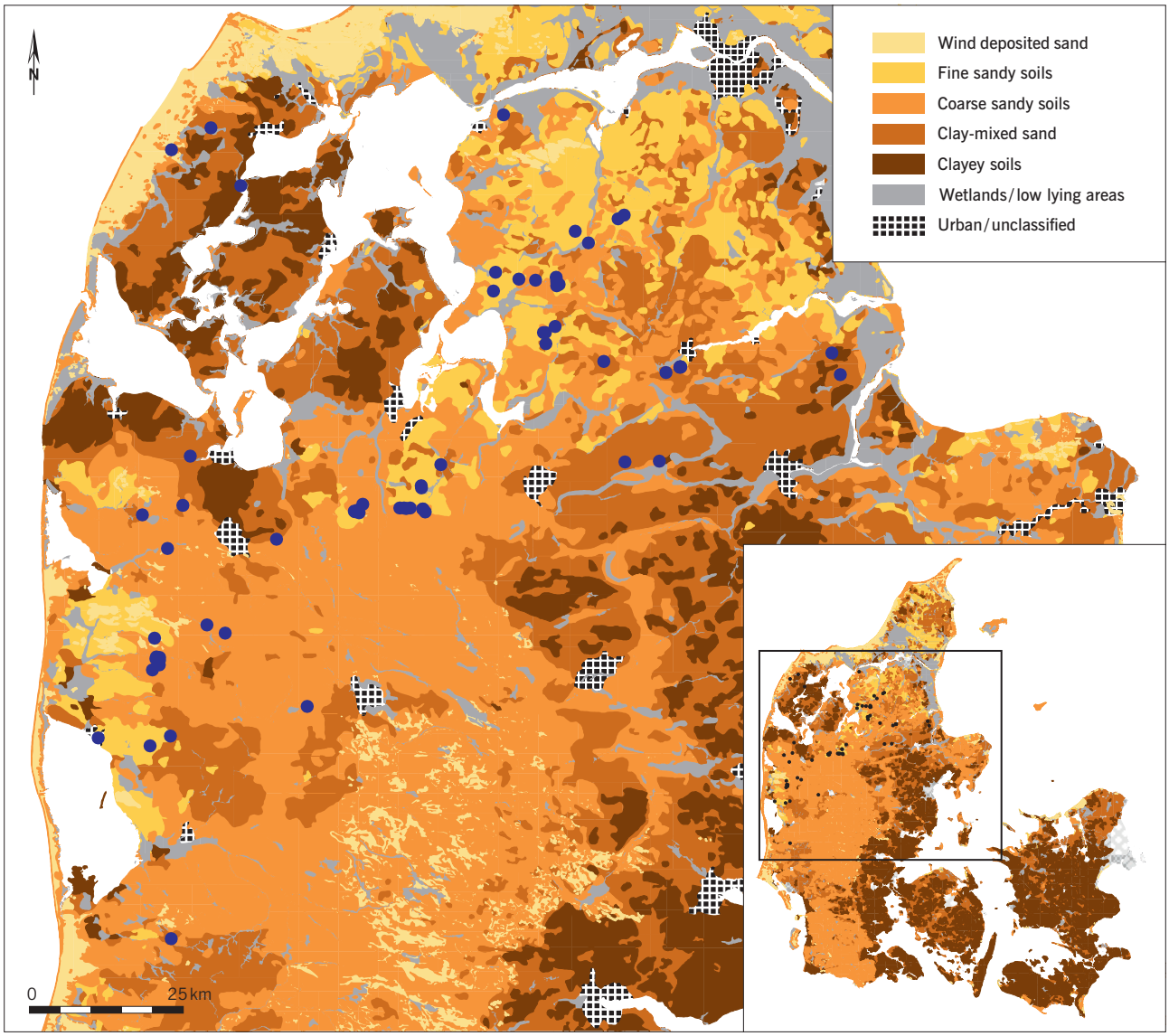


Fig. 6 Distribution of stone heap graves (blue dots) sites in relation to different soil types on the Jutland Peninsula.

Abb. 6 *Verteilung der Steinhaufengräber (blaue Punkte) in Bezug auf verschiedene Bodentypen auf der Halbinsel Jütland.*

Conclusion

As illustrated by the brief discussion above, very different lines of evidence point to rather similar conclusions regarding the socioeconomic organisation of communities in several different regions within the GA network. Even if the evidence is somewhat uneven and variable in character, it does indicate the emergence of a type of socioeconomic organisation that differed from those of previous Neolithic groups. A further observation is that combining different lines of evidence – from traditional archaeological data to recent archaeogenetic results – seems to lend support to the initial assertion of this discussion, namely that biological kinship patterns, social organisation and the economic strategies chosen by these communities were closely and functionally integrated with one another. Future work will hopefully strengthen our basis for inferring socioeconomic organisation in the GA network (and in other past societies), particularly by building up broad-spectrum regional datasets that look beyond individual sites and types of data (Johannsen et al. 2017). However, even on the basis of the present state of research, and despite the limitations of this brief treatment, looking across different lines of evidence does allow us to sketch a picture that is likely to have been more or less valid for many (but not all) of the communities that participated in the GA network.

In summary, a probable mode of life for many groups in the GA network can be described in the following way: Families, or extended families, sustained themselves mainly through animal husbandry supplemented by some other resources, wild as well as domestic, and moved within a defined (if perhaps loosely defined) territory up to several times in a year. Potentially, these groups may have split up into even smaller subunits when favourable, e.g., with some individuals staying at the base settlement and some herding animals to exploit particularly good feeding opportunities for a limited period of time. At certain times, basic social units aggregated into larger groups at ideologically

key points in the landscape, perhaps concentrating mainly near the cemeteries, where social, economic and biological exchange took place; allowing socioeconomic rules and territorial agreements to be reconfirmed or negotiated anew. The socioeconomic organisation of these communities thus appears to have combined substantial, probably cyclical, mobility with normative and physical elements of stabilisation that allowed for a predominantly pastoral land-use, while maintaining pro-social interaction between related groups inhabiting the same regional landscape. Needless to say, the picture just sketched is in part hypothetical, but hopefully the discussion above has illustrated ways towards establishing a more accurate and nuanced understanding of how life was organised among communities in the Globular Amphora network – and towards understanding prehistoric socioeconomic organisation more broadly through combinations of molecular and more traditional archaeological lines of evidence.

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Sources of figures

1 1 following Szmyt 2003, 403 Fig. 1; Woidich 2014, 90 Fig. 18 with additions; 2 following Johannsen et al. 2016, 37 Fig. 1 with additions; 3 following Woidich 2014, 90 Fig. 18

2 after Czebreszuk/Szmyt 2011, 279, Fig. 8; cf. Szmyt 1996

3 after Schroeder et al. 2019, 10708, Fig 3; reconstruction by M. Podsiadło

4 redrawn after Jørgensen 1993, 113

5 after Fabricius 1996, 221 Fig. 321

6 after Johannsen et al. 2016, 47 Fig. 9

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Multiple graves from Corded Ware sites in Eulau, Oechlitz, and Szczepanowice

Wolfgang Haak, Mirosław Furmanek, and Harald Meller

Zusammenfassung

Mehrfachbestattungen der schnurkeramischen Fundstellen Eulau, Oechlitz und Szczepanowice

Mehrfachbestattungen sind wichtige Beispiele für die Erforschung biologischer und sozialer Verwandtschaftsverhältnisse und haben schon immer Archäologen und Anthropologen veranlasst, über die Beziehungen zwischen gemeinsam bestatteten Individuen und deren Gründe zu spekulieren. Die schnurkeramischen Mehrfachbestattungen in Eulau, Burgenlandkreis, waren Bestandteil einer der ersten Studien zu biologischer Verwandtschaft mithilfe alter DNA. Seither sind sie ein sinnbildliches Beispiel für ›Kernfamilien‹ und Verwandtschaftsanalysen in vorgeschichtlichen Gesellschaften geworden. Zwischenzeitlich sind weitere schnurkeramische Mehrfachbestattungen gefunden worden, die Eulau in ihrer gesamten Bestattungspraxis sehr ähnlich sind. Zwei von diesen, die in Oechlitz, Saalekreis, in Sachsen-Anhalt und die in Szczepanowice, Woiwodschaft Kleinpolen, sind nun unter der Verwendung von neuesten Genomsequenzierungstechniken und anschließenden populationsgenetischen und biologischen Verwandtschaftsanalysen untersucht worden. Wir stellen hier zunächst einen Vergleich der drei Fundstellen vor, erfassen die Gemeinsamkeiten und Unterschiede, und erörtern anschließend die Rekonstruktion von Verwandtschaftspraktiken in den spätneolithischen schnurkeramischen Gemeinschaften in Mitteleuropa. Gemeinsame Merkmale sind die Ähnlichkeit der Lage der Bestatteten und das Vorhandensein von Anzeichen perimortaler Gewalt an allen drei Fundstellen. Dennoch gibt es feine Unterschiede, was die Architektur und den Grabtypus sowie die darin vorkommenden Grabbeigaben betrifft. Schließlich zeigt die genetische Analyse sehr enge biologische Eltern-Kind-Beziehungen zwischen Individuen in jeder der drei Bestattungen an. Allerdings fehlen zwei Mütter an zwei Fundstellen und es wurden einmal Halbgeschwister nachgewiesen.

Summary

Multiple burials are prime examples for biological relatedness and kinship studies, and have always triggered archaeologists and anthropologists to speculate about the relationships between individuals that were buried together and how this might have come about. The multiple Corded Ware-associated burials from Eulau, Burgenlandkreis district, were the subject of one of the first studies of biological relatedness through ancient DNA, and have since become an emblematic example for ›nuclear families‹ and kinship analyses in prehistoric societies. Meanwhile, other Corded Ware-associated multiple burials have been found, which are very similar in the overall funerary layout to Eulau. Two of these, Oechlitz, Saalekreis district, in Saxony-Anhalt and Szczepanowice, Lesser Poland Voivodeship, have now been studied using state-of-the-art genome sequencing techniques followed by population genetic and biological kinship analyses. Here, we present a comparison of the three sites and discuss the commonalities and differences, and the implications for the reconstruction of kinship practices in Late Neolithic Corded Ware communities in Central Europe. Common features are the striking resemblance in the layout of the bodies and the presence of signs of perimortem violence in all three sites. However, subtle differences exist with respect to the architecture and type of graves and the associated grave goods. Lastly, the genetic analyses reveal very close biological parent-offspring relationships between individuals from each burial, with two mothers missing at two sites and one case of half-siblings.

Introduction

Recent methodological advances in ancient DNA analysis and bioinformatics have made it possible to generate and co-analyse hundreds of ancient human genomes from various time periods and regions around the world. The considerable success rates of retrieving ancient human DNA also enable intra-site studies, i.e., the analysis of several or all individuals buried at the same site or from a similar burial context, i.e., entire graveyards, necropoles, or other burial communities. To date, a considerable number of aDNA-aided biological relatedness studies have been conducted, which prompted the topic of this volume and the conference held in October 2022. In this context, the multiple burials of Eulau have provided the foundation for research on intra-site demographic structures and inferences about kinship based on biological relatedness.

Multiple burials are defined as the (often simultaneous) inhumation of two or more individuals according to culturally prevailing burial rites in the same earthen grave or grave structure. This is different from collective, communal grave structures, e.g., megalithic cairns, which can include dozens or even hundreds of individuals and have been used for several decades. By contrast, mass graves, which can also include more than a handful individuals, such as the Globular Amphora site Koszyce, Lesser Poland Voivodeship (Schroeder et al. 2019), describe a single tragic event (of violent or pandemic nature) and often do not display signs of specific burial rites or care in the deposition of the deceased.

Double burials are the most common form of multiple burials. Depending on the age-at-death and anthropological sex of the co-buried individuals, these burials have often been readily interpreted by excavators. Two adult individuals of opposite sex and gender are often interpreted as couples, while two subadults would often be considered as being siblings. Likewise, the combination of a subadult and an adult would often invoke a parent-offspring relationship, which in the case of adult females and newborns is hardly questioned at all. As a consequence, it is then considered as surprising when close biological relatedness is not confirmed despite a common burial, as in the case of the 5th millennium BC grave clusters from Krusza Zamkowa, Kuyavian-Pomeranian Voivodeship, in Poland (Juras et al. 2017). The source of the existence of more complex social kinship systems beyond biological relatedness can be traced back to the early Neolithic of central Anatolia (Chyleński et al. 2019; Yaka et al. 2021; Pearson et al. 2023). Cases with more than two individuals, sometimes up to nine (e.g. Salzmünde, Saalekreis district; Alt et al. 2017) or more (Eulau; Haak et al. 2008)[1] are less common but also provide more room for interpretation and speculation. Multiple burials of three, four, or five individuals, as presented here, come with a particular appeal to the archaeologist, researcher, or museum's visitor alike, and naturally spark curiosity as to what might have caused such a particular burial situation. This fascination is further enhanced by the observed context, i.e., the way in which the bodies were oriented, often ›facing‹ each other, seemingly ›holding hands‹, or laid out in ›eternal embrace‹. Additional evidence, e.g., from paleopathologies, healed or *perimortem* injuries, sparks further interest.

As a consequence, researchers are confronted with a considerable number of immediate questions: Who are these people? How and why did they die? Did all of them die at the same time, on the same day? If not, when? What happened on that day? Are the individuals biologically related to each other? Who buried them? Or, when a non-natural cause of death is suspected, what or who killed them? Thanks to the numerous state-of-the-art methods available today, nearly all of these questions can be addressed by integrated, multidisciplinary research, and every participating discipline can contribute to answering the bigger questions of who, where, when, what, how, and why? Beyond the immediate questions, there are meta-level questions that require specialist knowledge, e.g., about the material and cultural background, economy or subsistence of the buried persons. For example, can burial rites be confirmed by genetic sexing? Other questions pertain to the observation of overarching, generalisable trends, which can only be observed when many comparable contexts are analysed.

Here, we focus on multiple burials from three sites from Central Europe, in today's Germany and Poland, which are associated with the Corded Ware cultural complex. The Corded Ware (also known as Single Grave, Battle Axe) cultural complex is an archaeological stratum on the basis of similarities in material cultural remains that are found in continental North-central, Northeast, and Eastern Europe, and dates to ~2900–2200 BC, broadly covering the Final Neolithic, Copper Age, or Early Bronze Age chronological periods of the various geographic regions[2].

The Corded Ware complex is named after characteristic pottery imprints. A distinctive feature of this period is a consistent set of artifacts in the burial context, consisting of typologically similar stone axes, amphoras and beakers that are decorated with cord impressions and ornamentation composed of cuts and stamps. During its early phase, the material culture is relatively uniform, which is often interpreted as a consequence of the relatively rapid expansion process of the new population. Over time, regional variation becomes more pronounced, which is thought to have resulted from influences of earlier, local cultural traditions, embedded in a network of relationships within which new practices and symbols circulated (Furholt 2014). The emergence of the Corded Ware cultural complex is linked to a major change in the cultural landscape of Central Europe and coincides with the collapse of previous cultural centers with their socio-economic systems.

The carriers of this culture are thought to have had a semi-pastoral subsistence and evidence of agricultural activities is less frequently recorded than in earlier Neolithic societies. Corded Ware-associated settlements, or housing complexes, are also very rare. Gimritz, Saalekreis district, and Vliněves, Central Bohemian Region, are examples of sites where settlement and burial ground are clearly linked (Friederich/Jarecki 2019). More recently, it has also been possible to identify trapezoidal houses in excavations, which are attributed to the Corded Ware cultural complex (Risch et al. 2021; Risch et al. 2022).

The Corded Ware funeral rites were a reflection of the ideological changes of the time, through which gender, individual and group identities, and social roles were expressed. This was done by varying the ways in which the dead were placed in the grave and in the composition of grave offerings. These regularities were observed throughout the 3rd millennium BC, but the way in which they were implemented was cultural, and perhaps of ethnic nature. They expressed a sense of group membership, which led to

1 E.g. Bronocice, Świętokrzyskie Voivodeship, pit 36-B1 with 17 individuals; Milisauskas et al. 2016; Cienkosz-Stepanczak et al. 2017.

2 Glob 1945; Fischer 1958; Strahm/Buchvaldek 1992; Furholt 2014; Schwarz 2015; Schwarz 2021.

the observed spatial and chronological variability. Corded Ware burials are usually recognised by the assembly of characteristic artifacts, which follows a certain pattern and has more or less standardised grave goods: drinking sets (e.g., typical cord-ornamented pottery), weaponry (e.g., battle-axes, arrowheads), ornaments (e.g., tooth pendants from dog, wolf, wild boar or deer), and food offerings. From the beginning, the orientation and positioning of the bodies in crouched position, together with type and placement of furnishings primarily emphasised gender differentiation (Bourgeois/Kroon 2017). These characteristics are more pronounced in the western part of its distribution, where they differ strikingly from neighbouring, and potentially competing, groups that are associated with the so-called Bell Beaker phenomenon. Here, Corded Ware-associated males are buried with the head toward the west, in a right-side-flexed position, facing south. Females are buried with the head toward the east, in a left-side-flexed position, facing south. By contrast, males associated with the Bell Beaker phenomenon are often buried in north-south orientation with the head toward the north, in a left-side-flexed position, facing east. Accordingly, Bell Beaker-associated females are buried in south-north orientation with the head toward the south, in a right-side-flexed position, facing east (Fischer 1956; Häusler 2008; Wentink 2020).

The Corded Ware complex, while being a readily recognisable cultural horizon in Europe's prehistory, has moved again into the spotlight through archaeogenetic studies[3]. These studies uncovered a genomic transformation in Europe that equals the one of the preceding Meso-Neolithic transition in magnitude. Corded Ware-associated individuals were shown to carry a specific type of genomic ancestry, the so-called steppe-related ancestry, which was maximised in emerging pastoralists in the Eastern European steppe and forest steppe belt, but was not found among the local Late Neolithic groups that were derived culturally and genetically from early European farmers. Corded Ware-associated individuals carried approx. 70–80 % of this steppe-related ancestry, which showed that the discontinuity and succession of cultures during the early 3rd millennium BC was driven by expanding semi-pastoralist groups from the northeastern parts of temperate Europe (Papac et al. 2021). More broadly, the arrival of genetic ancestry associated with steppe pastoralists attests to a substantial genetic transformation in Europe that started around 5000 years ago, the aftermath of which still resonates strongly in genomes of all present-day Europeans (Olalde et al. 2018; Olalde et al. 2019; Villalba-Mouco et al. 2021). By mixing with local European farmers, they formed a genetic gradient from North-East to South-West Europe and as such the basic genetic makeup of most modern-day Europeans.

In contrast to the preceding cultural assemblages of central Europe, for which collective burials were the predominant form, single graves are a distinctive feature of the Corded Ware and more generally the societies of the 3rd millennium BC (Furholt 2019). They were part of often complex funerary constructions, frequently with burial mounds (kurgans). After ~2600/2500 BC, multiple burials appear more frequently, often with two or three but rarely with more individuals. However, in contrast to collective burials, which were used over generations, these describe singular temporal entities. The Corded Ware Culture graves, whether flat or with mounds, form smaller or large cemeteries, e.g., at Profen, Burgenlandkreis district, Lauda-Königshofen, Main-Tauber-Kreis district (Ortolf 2014), Vikletice, Ústecký Region (Buchvaldek/Koutecký 1970), Vliněves (Dobeš/Limburský 2013) and Żerniki Górne, Lesser Poland Voivodeship (Kempisty/Włodarczak 2000). As a result, and despite the above-mentioned pioneering study on Eulau, surprisingly little is known about the demographic features and social organisation of the Corded Ware communities. The three multiple burials presented here thus provide a first foray into biological relatedness and kinship structures among Corded Ware groups. It should be noted that similar Corded Ware sites with multiple burials are known, e.g., from Hanau-Mittelbuchen, Main-Kinzig-Kreis district, Dittigheim, Main-Tauber-Kreis district, Gaimersheim, Kösching, both Eichstätt district, and Bergrheinfeld, Schweinfurt district (Heyd 2021), but these have not yet been subject to multi-disciplinary investigations.

Eulau

The four multiple Corded Ware-associated burials from Eulau, Saxony-Anhalt, were the subject of one of the first studies of biological relatedness through ancient DNA analysis prior to the high throughput sequencing era (Haak et al. 2008; Meyer et al. 2009). These studies highlight the integrated efforts and lines of evidence of various disciplines, including use of stable isotopes, paleopathologies, typologies of artifacts and involvement of experts from modern-day crime scene investigation. Overlapping radiocarbon dates point to a relatively precise date between 2675 and 2495 cal BC. Three of the four multiple burials from Eulau are featured in the permanent exhibition at the State Museum of Prehistory in Halle (Saale) in Germany. For detailed results on these investigations and the resulting interpretation we refer to the original studies. For the purpose of comparison in this manuscript, we will focus predominantly on burial 99 from Eulau, which contains four individuals – two adults and two subadults buried closely together – and thus provides the blueprint for the layout of the characteristic Corded Ware multiple burials. While the original genetic study was carried out with PCR-based methods, i.e., prior to the ›genomic revolution‹ in ancient DNA research, the results still hold firmly and do not raise doubts about the assignments of biological relatedness. Briefly, the two adult individuals, a female and a male are buried according to the prevailing burial rites described above (Fig. 1a). The two subadult individuals were found to be boys, who shared the mitochondrial DNA haplogroup with the adult

3 Allentoft et al. 2015; Haak et al. 2015; Saag et al. 2017; Saag et al. 2021; Papac et al. 2021.

female, while the STR (short tandem repeat) profiles of the Y-chromosome are shared with the adult male (consistent with Y-chromosome lineage R1a). The allelic profiles of the autosomal STRs further show that the boys each share alleles with both adults. Together, the combined results indicate that the burial consists of adult parents and their two sons. Paleopathological evidence for healed fractures, but also perimortem violence (blunt force trauma to skulls, arrowheads embedded in vertebra or chest), suggest an untimely death of all individuals from the four multiple burials from Eulau (Meyer et al. 2009). The close grouping of all burials points to a single violent event, e.g., a raid or an attack, that affected the entire, or large parts, of the local Corded Ware community. Further, the generally careful arrangement of the burial situation hints at in-depth knowledge about the relationship between the individuals and their cultural/spiritual background and thus suggests that some members of the community had survived the attack and buried the dead according to the funerary rites.

It is interesting to note that the two subadult sons were not oriented according to the standard practices used for Corded Ware males, but instead each was oriented toward a parent. It is possible that this was done to express the close kinship between the children and their parents, or, alternatively, that the two sons were too young, and thus possibly not yet initiated to be granted the full burial rite of adult males.

Oechlitz

The second Corded Ware-associated multiple burial is from the site Oechlitz (feature 25645), also located in Saxony-Anhalt, and not too far away from Eulau (Fröhlich/Becker 2017; Mühlenbruch 2020). The grave includes five individuals and was surrounded by a characteristic ring ditch. Radiocarbon dates range between 2558 and 2207 cal BC. According to the orientation of the skeletons, two of the adult individuals could be recognised as potential males, but are tilted towards southwest, while the other individuals are oriented 90 degree off-axis, tilted southeast (Fig. 1b). Genetic sexing and biological relatedness testing on the basis of genome-wide autosomal SNP data, mitochondrial genome and Y-chromosome SNP data revealed that all individuals are first-degree-related to each other, and represent either a parent-offspring or sibling relationship. Taking the age at death of the individuals into account, we were able to reconstruct a single unambiguous pedigree, which centers around a male adult (individual 4), who holds his youngest daughter (individual 3), while his adolescent son (individual 5) is buried behind him, and his two older daughters (individuals 1 and 2) at their feet. Both daughters would match the canonical orientation of females but are tilted southwards. Interestingly, the biological mother of the four children is missing, but we can infer that she carried mitochondrial DNA haplogroup U4a2 like her children. By contrast, the father carries U5a1a2b, and Y-lineage R1a-M417, which he also passed on to his son. R1a-M417 is by far the most common Y-chromosome lineage among Corded Ware individuals and attains a frequency of ~90 % among the males of the later classical Corded Ware period between ~2700–2400 BC. Standard pathogen screening of the shotgun genome data did not yield any significant hits that could be assigned to common bloodborne pathogens. However, similarly to the Eulau individuals, the anthropological report describes evidence for blunt end or semi-sharp trauma to the skull bones, also indicating a violent death. Again, the constellation, the ceremonial artifacts and the intentional, careful placement of the dead (e.g., individual 1 embraces individual 3) suggest that those who buried the five individuals not only knew about their cultural and spiritual background, but also about their biological relationships.

Szczepanowice

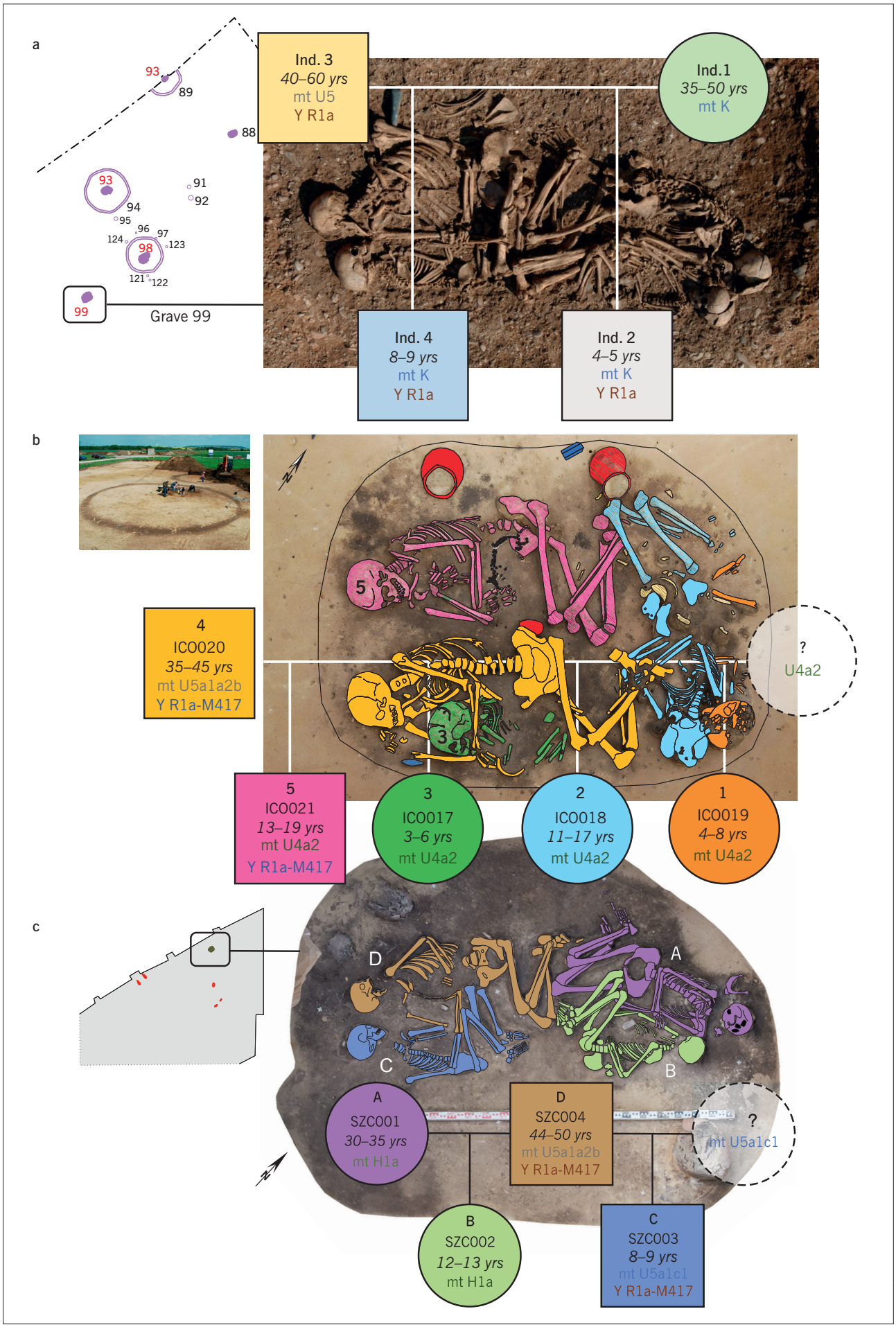
A third example is the multiple burial from the site Szczepanowice in Lesser Poland in today's Poland (Fig. 1c)[4]. This grave contains four individuals and the layout of the bodies very closely resembles grave 99 from Eulau. The catacomb grave with a depth of 180 cm has a clearly marked entrance corridor and it featured numerous grave goods that can be ascribed to the Kraków-Sandomierz group of the Corded Ware complex: six vessels (an amphora and five beakers), an axe made of serpentinite (from Lower Silesia), a flint axe, two retouched flint blades, four flint arrowheads, five flint flakes, bone artefacts (a chisel, two awls, an antler wedge, a punch, a bone tube), a copper lunula (in association with eastern European metallurgy, especially with Yamnaya), three copper earrings, oval bone beads, and a figure-eight bone pendant. Overlapping radiocarbon dates point to an absolute date between 2450 and 2300 cal BC.

We found that individuals A and B are genetically female and share the same mitochondrial haplogroup, while indi-

Fig. 1a–c (right page) Corded Ware-associated multiple burials. a Eulau, Burgenlandkreis district (Germany); b Oechlitz, Saalekreis district (Germany); c Szczepanowice, Lesser Poland Voivodeship (Poland). Filled coloured squares and circles indicate biologically male and female individuals, respectively. Open circles with dashed lines indicate inferred individuals that were missing from the graves. The estimated age at death is given in years (yrs); mt = mitochondrial haplogroup; Y = Y-chromosomal haplogroup.

Abb. 1a–c (rechte Seite) *Schnurkeramische Mehrfachbestattungen. a Eulau, Burgenlandkreis (Deutschland); b Oechlitz, Saalekreis (Deutschland); c Szczepanowice, Woiwodschaft Kleinpolen (Polen). Die ausgefüllten farbigen Quadrate und Kreise stellen jeweils biologisch männliche und weibliche Individuen dar. Offene Kreise mit gestrichelten Linien symbolisieren hergeleitete Individuen, die in den Gräbern fehlten. Das geschätzte Alter zum Zeitpunkt des Todes ist in Jahren (yrs) angegeben; mt = mitochondriale Haplogruppe; Y = Y-chromosomale Haplogruppe.*

4 For a photogrammetric model of the grave by Maksym Mackiewicz see: <https://sketchfab.com/3d-models/corded-ware-multiple-burial-szczepanowice-pl-b964d2f65fad4f33be415970eee559bc> (16.03.2023).


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Grave 99
Ind. 3
40–60 yrs
mt U5
Y R1a
Ind.1
35–50 yrs
mt K
Ind. 4
8–9 yrs
mt K
Y R1a
Ind. 2
4–5 yrs
mt K
Y R1a
b
4
IC0020
35–45 yrs
mt U5a1a2b
Y R1a-M417
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U4a2
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IC0021
13–19 yrs
mt U4a2
Y R1a-M417
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IC0017
3–6 yrs
mt U4a2
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IC0018
11–17 yrs
mt U4a2
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IC0019
4–8 yrs
mt U4a2
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D
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C
B
A
SZC001
30–35 yrs
mt H1a
D
SZC004
44–50 yrs
mt U5a1a2b
Y R1a-M417
?
mt U5a1c1
B
SZC002
12–13 yrs
mt H1a
C
SZC003
8–9 yrs
mt U5a1c1
Y R1a-M417

viduals C and D are genetically male and carry Y-haplogroup R1a-M417, which matches well with the males from the two other sites and Corded Ware-associated males more broadly. Detailed analyses of biological relatedness between individuals revealed a 1st-degree relationship between individuals A and B, B and D, C and D, and a 2nd-degree relationship between individuals B and C. Combining the results from the uniparentally inherited mitochondrial and Y-chromosome haplogroups, the genetic sex, and the age at death of the individuals, we were able to unambiguously reconstruct a pedigree as shown in Fig. 1c. The subadult female individual B is the daughter of individual A (mother, adult female) and individual D (father, adult male). The subadult individual C is the son of individual D but unrelated to individual A, the adult female. Hence, the biological mother of C is unknown and not buried at the site, making the two subadult individuals B and C half-siblings, which is consistent with the 2nd-degree relationship between the two subadults.

As for Oechlitz, standard pathogen screening of the shotgun genome data also did not yield any significant hits that could be assigned to common bloodborne pathogens. However, as described in both examples above, there is also evidence for interpersonal violence at Szczepanowice in the form of perimortem traumata. One arrowhead was found very close to the femur of a female (adult female; individual A) and was probably stuck in the body of the victim at the time of inhumation. The adult male's skull shows traces of a double trepanation, with signs of wound healing. However, he also has a fractured nose and a perimortem fracture of the femur. Both subadults have fractures of the *cervical vertebrae* which may be perimortem.

Like at the two other sites, and despite the untimely death of the individuals, the layout and the orientation of the dead indicate knowledge about the kin relations and the cultural/spiritual background.

Side-by-side comparison and discussion

When the combined evidence from the three sites is compared, we observe a number of similarities, but also differences (Tab. 1). The analysis of biological relatedness shows that all individuals are closely related to each other, with the exception of the parent pair (where present), and all three burials include individuals from two generations. From a modern-day, Western perspective, this constellation would be recognised as a core or ›nuclear‹ family, consisting of a pair of parents and their offspring. However, this only holds true for Eulau and the genetic results show that a swift assessment based on preconceived ideas could lead to a wrong perception. For example, at Oechlitz we find that the oldest female (individual 2) is not the partner of any of the two male individuals, but instead the daughter and sister, respectively. The osteological age at death estimates between 11–17 years and indicates that the proposed age would possibly lie below the reproductive age at the time, at least for having given birth to two younger children. However, this was previously impossible to verify or refute. The unambiguous constellation of a father buried with his son and three daughters, while the actual biological mother is missing from the grave, would have been only one of many possible, and perhaps not the most plausible, scenarios.

The same can be said about the burial from Szczepanowice, which at face value appears to be identical to Eulau. The integrated results instead show that the grave contains a trio of mother-father-daughter, but that the second and youngest child (a boy; individual C) is only related to the adult male, and thus the step-brother of individual B. The mother of this boy is not buried in the grave. Under the assumption that the boy was the offspring from a previous partnership, and that his mother potentially passed away during childbirth, it is interesting to note that this boy is in fact younger than his half-sister. This makes a scenario of serial monogamy in the suggested order less likely, but it is not possible to make further generalising inferences from a single observation.

Taken together, it becomes clear that a simple *a priori* assessment of multiple burials of comparable layout and form as ›nuclear families‹ cannot always be inferred, and thus is not an advisable conclusion. However, given that all children and adolescents are oriented towards a parent seems to emphasise the social (and perhaps known biological) bonds and indicates the recognition of the subadults as kin. In turn, based on the context, the subadults cannot be considered to constitute socially and economically independent entities, and this allows us to refer tentatively to ›family graves‹, but by applying the necessary caution, which involves the recognition that these ›family units‹ can take on and be expressed in different forms.

The intentional arrangement of the bodies, the evidence of perimortem violence and the absence of evidence for secondary inhumations or later disturbances suggest a single event horizon for each of the three burials. The perimortem fractures and traumata indicate acts of interpersonal violence, potentially as part of group conflicts, but it remains unclear why these individuals faced a premature death. Potential scenarios were discussed for the site of Eulau, where grave 99 is interpreted in context with three other multiple burials, which are highly likely contemporaneous and also show evidence of violence. On the basis of the demographic structure of the buried, which represents children and older adults, and typological examination of the purported murder weapons (arrowheads in chest and *lumbar vertebrae*) it was suggested that the Corded Ware community at Eulau faced a hostile attack by a competing group (of the Globular Amphora Culture or Schönfeld group), in which the young and fit fought back or fled, and eventually buried their dead according to Corded Ware burial rites and with inside knowledge about the kinship structure (Meyer et al. 2009; Ganslmeier/Literski-Henkel 2014).

Whether interpersonal violence in the form of an attack of an outside party was the primary cause of death is a central question pertaining to all individuals from all three sites. At Eulau, evidence of perimortem violence is only evident from adult individuals, while the subadults buried at Oechlitz (4 out of 5) and Szczepanowice also show evidence of perimortem violence. Was the Corded Ware period a particularly unruly time? Is this evidence for competition between groups, as suggested for Eulau, or internal strife?

Site	Eulau, Burgenlandkreis district	Oechlitz, Saalekreis district	Szczepanowice, Lesser Poland Voivodeship
Individuals	4	5	4
Simultaneous inhumation	yes	yes	yes
Orientation adults	According to burial rite	According to burial rite, tilted SW/NE, subadults off-axis	According to burial rite, tilted SW/NE
Grave type	Simple grave pit	Simple grave pit, ring ditch	Catacomb grave
Grave goods	Stone axes, bone pin, flint blades, meat offerings	Pottery, stone axes, flint blades, bone beads, dog teeth pendants, boar teeth, shell beads	Pottery, stone axes, arrowheads, flint, adzes, bone tools, lunula, bone pendants, copper rings, etc.
Perimortem violence	yes	yes	yes
Pathogens	Unknown	no	no
Biological Relatedness	yes	yes	yes
Interpretation	›Nuclear family‹	›Nuclear family‹? Biological mother is missing	›Patchwork family‹ One of the biological mothers is missing
Lineality/locality	Unknown/patrilocal based on Strontium isotope data	Likely patrilineal/unknown	Patrilineal/unknown

Tab. 1 Comparison of the main features and observation for the three multiple burial sites.

Tab. 1 *Vergleich der Hauptbefunde der drei Fundstellen mit Mehrfachbestattungen und Bemerkungen dazu.*

Alternative explanations for an overkill, that is more deaths than expected from single combat, could involve executions, which could be interpreted as *Totenfolge*, i.e., the ritual practice of voluntary or involuntary ›following into death‹. In both cases, this would mean the termination of a lineage, either by deliberate (hostile) elimination at the hands of the attackers, or by economic necessity on behalf of the resident community. In the latter case, it remains unclear whether this was an integral part of the rites and rules of the Corded Ware communities.

Whether the three burials allow generalisable inferences to be made about kinship practices and the social organisation also needs careful discussion. Evidence for patri- or matrilineality or -locality cannot be expected to be strong when made on the basis of only two generations per site. At Oechlitz, and in particular at Szczepanowice, we observe that the pedigree is linked through the paternal line, with one adult female (a mother) missing in each case. It is possible that this happened simply by chance. If a group with patrilocal and patrilineal organisation with reciprocal female exogamy is assumed, then it is also possible that the missing females were buried elsewhere, possibly following a return to their place of birth. Likewise, it is possible that both female individuals were among the survivors, or socially sanctioned to be co-buried, which would explain the apparent first-hand knowledge about the relations of the deceased. At the same time, this would mean that *Totenfolge* (in this case of the widows as in *sati*; Fisch 2005; Schneewind 2007) was not a common practice and could be rejected for the Corded Ware communities.

Further evidence in support of patrilocality comes from the analysis of stable isotope data, such as $^{87}Sr/^{86}Sr$ (Strontium), which can also inform on patterns of mobility and in turn locality. To date, Sr data is only available for the four multiple burials from Eulau (Haak et al. 2008), where it could be shown that male individuals and children present the local Sr ratio, while the female individuals (including individual 1 from grave 99) show a non-local Sr signature. Clearly, although more data is needed, this example shows that Sr and dietary isotopes form a critical part of integrated bioarchaeological studies. Additional evidence for patrilineality and patrilocality comes from other Corded Ware sites with predominantly single graves, e.g., Esperstedt, Saalekreis district, in Saxony-Anhalt. The biological relatedness of the genomic data available thus far shows that many male individuals buried at the site are related to each other in the first or second degree (Monroy Kuhn et al. 2018). However, on the basis of this and additional unpublished data, we also noticed a stark deficit in female burials, which could certainly bias our interpretation toward patrilineality, even though the absence of female burials remains unexplained.

The strongest evidence for a patrilineally organised society comes from the population genetic analyses of genome-wide data from all Corded Ware-associated individuals available thus far. As shown by L. Papac and colleagues (Papac et al. 2021) in a transect through time study in Bohemia, Czech Republic, which included 31 and 21 individuals from the early and late Corded Ware phases, respectively, the Y-chromosome lineage diversity was reduced sharply by the time of the late Corded Ware phase. This situation was continued, albeit with a different lineage in the overlapping and succeeding phase of the Bell Beaker phenomenon, before the strict reduction was broken up and replenished by the time of the Early Bronze Age starting ~2200 BC. This marked reduction in Y-chromosome lineage diversity was shown not to be a random process, as the autosomal diversity was not affected, but must have been driven by the establishment of strict social conventions that controlled kinship and mating practices.

The example of the Bohemian site Vliněves, Central Bohemian Region, in the same study also shows an initially large genetic diversity among individuals that were granted a Corded Ware burial according to the local customs. Interestingly, the most extreme cases in a gradient of genomic ancestry distribution (i.e., with and without steppe-related ancestry) are all female individuals, which shows that the expanding Corded Ware society not only included lineage females, but also integrated local non-lineage females, which argues against the model of an exclusively male-driven expansion from regions in eastern Europe. However, also here the genetic homogenisation during the following consolidation phase of the Corded Ware period hints at an increase of patrilocality and patrilineality.

In conclusion, the currently available data suggests that the communities associated with the Corded Ware cultural complex were likely organised in patrilineal and patrilocal groups with a certain extent of female exogamy, also involving the integration of local females during the initial expansion phase. The insights gained from the integrated analysis of the three multiple burials show that the Corded Ware-associated groups valued lineage, i.e., familial ties formed by biological and social bonds, as far as the situation of the funerary expression is concerned. Whether these bonds were also the foundation of the Corded Ware society of the living and thus formed an integral part of the socio-cultural profile requires further investigation, ideally by combining as many lines of evidence and as many different types of contexts as possible.

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Source of Figures

1 a photo J. Lipták, München; excavation map LDA; pedigree W. Haak
b photo A. Moser, S. Gottwald, LDA; pedigree W. Haak
c photo and map M. Furmanek; pedigree W. Haak

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FALLSTUDIEN – BRONZEZEIT

CASE STUDIES – BRONZE AGE

Life and work – A possible ›house community‹ at the Early Bronze Age settlement of Schiepzig in Central Germany

Sandra Penske, Torsten Schunke, Jörg Orschiedt, Adam B. Rohrlach, Harald Meller, Wolfgang Haak, and Roberto Risch

Zusammenfassung

Leben und arbeiten – Eine mögliche »Hausgemeinschaft« in der frühbronzezeitlichen Siedlung von Schiepzig in Mitteldeutschland

Die gemeinsame archäologische und archäogenetische Analyse von zehn Individuen, die in der frühbronzezeitlichen Siedlung von Schiepzig begraben wurden, liefert neue Einblicke in die Beziehung zwischen den typischen Langhäusern der Aunjetitzer Kultur und den Menschen, die sie errichteten und bewohnten. Genetische Verwandtschaftsanalysen ergaben einen Stammbaum, der mindestens 15 Individuen umfasst, sich über vier Generationen erstreckt, und zudem in Verbindung mit einem der Langhäuser steht. Die Integration archäologischer und anthropologischer Ergebnisse ermöglicht es uns, intensiv diskutierte Themen in der prähistorischen Archäologie anzusprechen, wie z.B. die Größe einer Gemeinschaft, die Belegungsdauer der Häuser und die Praxis der Körperbestattung im Vergleich zu anderen, weniger sichtbaren Bestattungsformen.

Summary

Combined archaeological and archaeogenetic analyses of ten individuals buried in the Early Bronze Age settlement of Schiepzig provide new insights into the relation between the typical Únětice longhouses and the communities that constructed and occupied them. Genetic relatedness analyses associated with one of the longhouses have revealed a pedigree of more than 15 individuals spanning over four generations. The integration of archaeological and anthropological evidence allowed us to address long-debated issues in prehistoric archaeology, such as community size, house duration, and the practice of inhumation burials versus other, albeit undetected, funerary practices.

Introduction

Rescue excavations in the municipality of Schiepzig, close to today's city of Halle in Central Germany, between October 2005 and March 2006 and between October and December 2007, led to the discovery of an Early Bronze Age settlement of the Únětice Culture (Schunke 2018; Damrau et al. 2019; Duchniewski et al. 2019). It was placed in an excellent topographic location, on a ~20 m high fluvial terrace south of the fertile Saale River Valley, close to salt-bearing springs. The location of the settlement is unusual because it was built on the edge of an artificially excavated ~40 m long and 30 m wide depression, which occasionally held water and became a pond-like feature during the time the settlement existed. The depression held a well-preserved archaeological level with a large amount of faunal remains and stone tools. The archaeozoological and functional analyses of these finds suggest that a substantial number of cattle were butchered and processed in this area (Morgenstern in press; Sferrazza in press; Eguíluz et al. in press). The local production of salt is indicated by *briquetage* debris and could have been related to the conservation of freshly butchered meat.

The preservation of specific activity areas is unique in the context of Únětice settlement archaeology. The study of such areas is usually hampered by the disturbance of its floor levels after millennia of ploughing. Outside the discovered working area, the post holes of different constructions, pits, and a series of burials could be recovered. On its southern side, three typical Únětice longhouses could be identified based on the setting of the post holes (Tab. 1; Fig. 1). The overlapping ground plans indicate that not all three houses could have existed at the same time but suggest at least two successive building phases. Cylindrical and truncated cone-shaped pits have been found in the vicinity of the buildings, which probably were used for storage. Two parallel lines of post holes seem to correspond to a footbridge leading from the longhouses to the working area (Fig. 1).

Seven burials were excavated in the immediate surroundings of these houses, at the southern side of the settlement (Fig. 1). The majority of graves contained no apparent grave goods, with the unusual exception of feature 16047, which contained two bronze needles (one of them transformed into an awl), one bronze awl with a bone handle, a pottery vessel, and a cattle meat offering (Moser 2017). Human remains were only preserved in four of the graves, two of which could be used for ancient DNA analysis (16047/SCI008 and 16051/SCI009; Tab. 1; Fig. 2a).

A fourth longhouse was located north of the working area, and its ground plan could be partly recovered (Tab. 1; Fig. 1). Nine burials were excavated in its surroundings, two

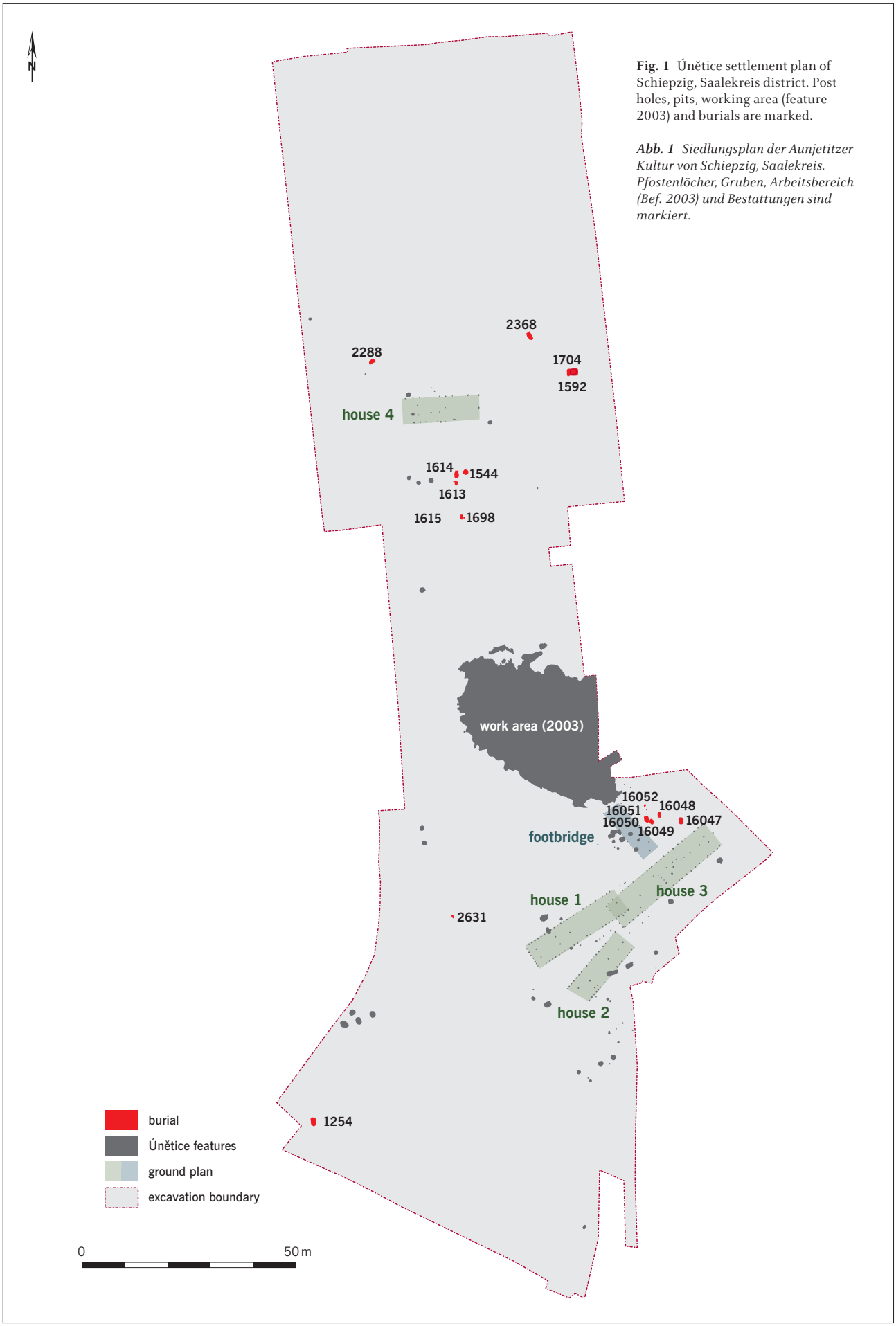


Fig. 1 Únětice settlement plan of Schiepzig, Saalekreis district. Post holes, pits, working area (feature 2003) and burials are marked.

Abb. 1 *Siedlungsplan der Aunjetitzer Kultur von Schiepzig, Saalekreis. Pfostenlöcher, Gruben, Arbeitsbereich (Bef. 2003) und Bestattungen sind markiert.*

House Nr.	Building Type (according to Schunke/Stäuble 2019; Risch et al. 2022)	Length (m)	Width (m)	Surface (m^2)	Orientation (1–360°)
SZ-01	Salzmünde (two trusses)	25.40	6.00	152	57
SZ-02	probably Salzmünde	> 17.70	5.80	> 102.70	50
SZ-03	Salzmünde (two trusses)	30.70	6.80	208.70	40
SZ-04	Salzmünde (two trusses)	> 17.60	5.90	> 103.80	87

Tab. 1 Architectural variant, size and orientation of the Únětice houses at Schiepzig, Saalekreis district.

Tab. 1 *Architektonische Varianten, Größe und Ausrichtung der Häuser der Aunjetitzer Kultur in Schiepzig, Saalekreis.*

of which contained a pot and/or a pin made out of bone or copper. Eight burials yielded remains of eleven individuals, eight of which could be used for ancient DNA analyses (SCI001–007 and 1704/SCI010) (Tab. 2; Fig. 2b).

Overall, the house plans, house sizes, and the rather poorly equipped burials correspond to what is usually known from Early Bronze Age settlements in Central Germany (Risch et al. 2022). Based on archaeological criteria and an extensive series of radiocarbon dates from the working area (Moser 2017), we suggest that the house structures, the burials, and therefore the settlement of Schiepzig existed between ~ 2150–1850 cal. BC. However, due to uncertainty margins, these dates do not allow us to confirm if the site was occupied for 300 years or a slightly shorter period.

The aim of the present study is to better understand the social organisation of early Únětice settlements with a particular focus on the community that built and lived in their characteristic longhouses. The combination and integration of genetic, archaeological, anthropological, and spatial information allows possible insights into kinship structures to be gained, to estimate the size of such communities, and to constrain the duration of the Únětice settlement at Schiepzig.

The anthropological record of the Schiepzig settlement

During the excavations in Schiepzig, in total 17 grave features of the Únětice Culture were discovered; nine were around house 4, seven around and near houses 1–3, and one additional grave was found in isolation. Four graves yielded no human remains (features 1592, 16048, 16049, 16052) and the skeletal remains from one grave (feature 2631) could not be found at the time of the investigations. Thus, 14 graves were available for anthropological evaluation (Orschiedt in press). The majority of these graves were spatially related to the houses, with seven of the graves located south (features 1544, 1613, 1614, 1615, 1698), east (features 1592, 1704), north-east (2368), and north-west (2288) of house 4, while another seven are related to houses 1–3 (features 2631, 16047, 16048, 16049, 16050, 16051, 16052; Fig. 1–2). One feature (1254) was laid out as an isolated single grave, which is over 50 m south-west of house 1, but it contained no human remains (Fig. 1). While one grave around house 4 is a double burial (feature 1613), feature 1615 is a triple burial consisting of a primary deposit of a body (1615-1) and two secondary deposits (1615-2–3; Fig. 3).

The burials are poorly, or only partially, preserved and are fragmented, which affects the certainty of identification of age, sex, and pathological changes of the individuals. The bone substance, on the other hand, is mostly well-preserved but in some cases, the investigations were complicated by erosion or calcareous sinter deposits.

In total, we found five subadult and nine adult individuals. While the child burials were not morphologically sexed for methodological reasons, the sex of all nine adult individuals could be determined (Tab. 2). However, the sex of four individuals could only be determined by a single varying criterion. Therefore, with one exception, these determinations are to be regarded as uncertain. The biological sex of one male and four female individuals could be reliably determined on a morphological basis. Genetic sex determination is therefore of great importance in the final evaluation of the burials. One burial was identified as probably male (1615, Ind. 3) and two others as likely male (1614, 16050) due to their incomplete preservation and age. Together with the genetically sexed children, we find an equal representation of genetically male and female individuals. In contrast, among the adult individuals, whose sex could be determined reliably, a surplus of females over males (5:2) can be observed.

Due to the small sample size, and the partially poor preservation, the age distribution does not give a clear picture. The under-representation of children of the infans I age group indicates that only a part of a larger population was buried here. It is striking that apart from three individuals that could only be generally determined as adults (adult-mature), only one early adult individual is present. The majority of the individuals of the adult and mature age groups (n = 8) are at least late-adult to early-mature (30–50 years) and late-mature (50–60 years).

Further investigations with the aim of assessing the disease burden of the individuals revealed no pathological features with the exception of the burial from feature 2631. In this isolated burial of a 7–8-year-old child, a congenital *coxa antetorta* was found, which had led to an internal rotation of the knees and thus to a walking disability (Jani et al. 1979; Pichler/Schunke 2019). In addition, the child had a marked enlargement of the skull and a divergence of the sagittal suture, which could indicate a hydrocephalus. This

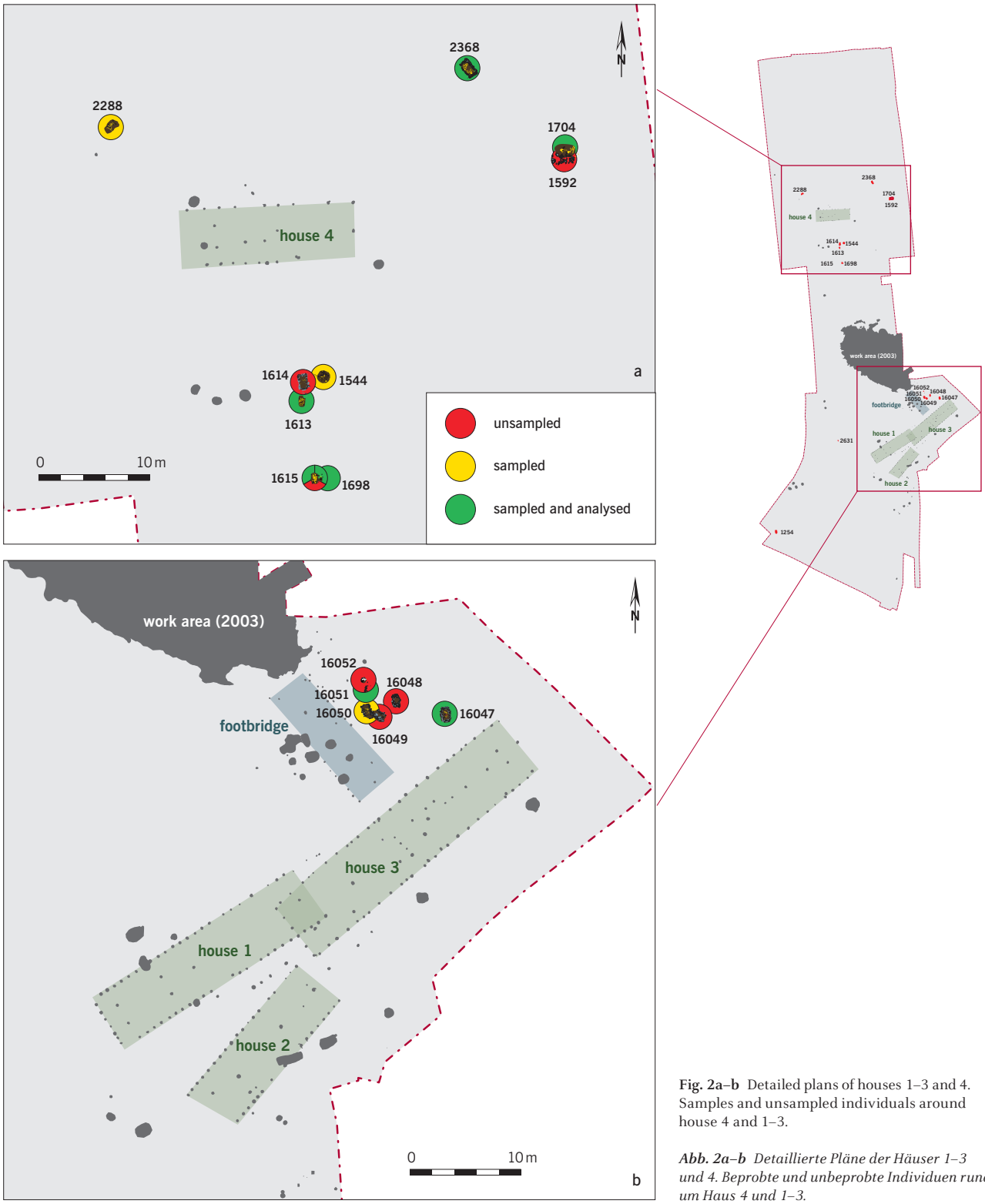


Fig. 2a–b Detailed plans of houses 1–3 and 4. Samples and unsampled individuals around house 4 and 1–3.

Abb. 2a–b *Detaillierte Pläne der Häuser 1–3 und 4. Beprobte und unbeprobte Individuen rund um Haus 4 und 1–3.*

disease can be congenital or acquired, e.g., through inflammation (Aufderheide/Rodríguez-Martín 1998, 57–58).

Pathological changes in the skeletal remains of adult individuals are commonly observed especially in the area of the masticatory apparatus and the joints, independent of the archaeological horizon. Among the adults from Schieppzig, dental pathologies were observed in six individuals (1613, Ind. 1; 1615, Ind. 1–2; 1704; 2288; 2368), of which three are cases of periodontopathy, three individuals with apical processes, and two cases of caries. Overall, the disease burden can be considered rather low. This also applies to the diseases of the spine, which are only recognisable in three older individuals of the age groups early and late maturity (40–60 years; 1615, Ind. 1; 2288; 2368) and which also show slight degenerative changes in other joint areas. In individual cases, further pathological changes indicate hormonally controlled processes, unspecific injuries and cartilage or joint damage.

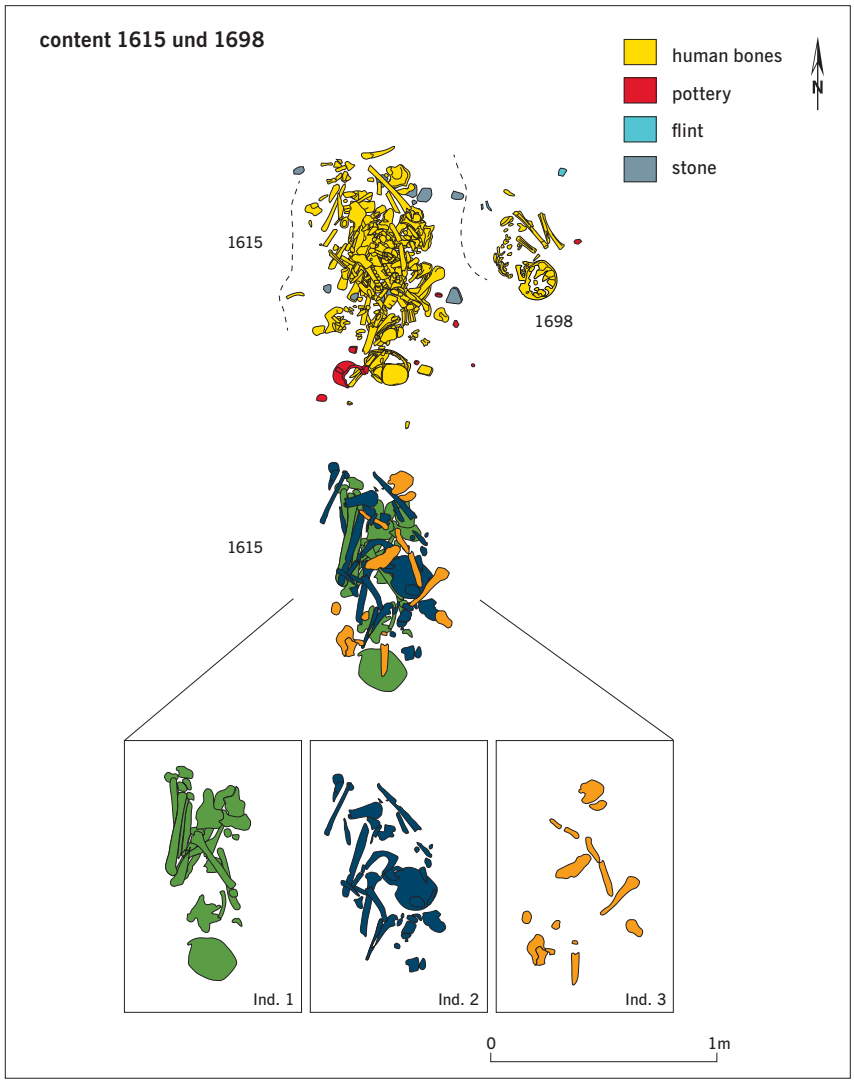


Fig. 3 Burials 1615 and 1698. Detailed plans of the remains belonging to three individuals in 1615. The lower one, Ind. 1 in primary position, and the other two, Ind. 2 and 3 in secondary position.

Abb. 3 *Bestattungen 1615 und 1698. Detaillierte Pläne der sterblichen Überreste von drei Individuen aus der Bestattung 1615. Das untere Individuum, Ind. 1 in primärer Position, und die anderen beiden, Ind. 2 und 3 in sekundärer Position.*

With regard to the stress characteristics, which can be recognised by clear expressions or changes in the attachment points of muscles and ligaments, the assessment is limited by the skeletal posture. In total, indications of greater physical stress were found in eight adult individuals (1544; 1613, Ind. 1; 1615, Ind. 1–3; 1704; 2288; 2368). A difference between the sexes is not observed. As expected, older adults in the mature (40–60 years) and late adult (30–40 years) age groups show stronger stress characteristics. An exception is the clear stress pattern of a young man aged 12–14 (1544), which suggests that subadult individuals were involved in the work process from an early age. However, apart from the fact that certain muscle groups in the area of the upper extremities, such as raising and lowering the arms and the shoulder and neck area, were heavily loaded, no detailed movement sequences can be reconstructed from these load characteristics. This also applies to the load on the lower extremities. All muscles involved here are relevant for locomotion and stabilisation. Overall, it can be seen that both the upper and lower extremities were heavily loaded in individual subjects.

The comparison of the individuals from Schiepzig with a comparative sample of 190 individuals from the Middle Elbe-Saale region (Nicklisch 2017, 80–102) shows a generally poorer preservation of the former. While the age structure is similar in terms of the ratio of adult to subadult individuals, there are differences in the distribution of sexes. While there are more males in the comparative sample, the Schiepzig individuals show a surplus of females among the adults. There are hardly any differences with regard to body height; the women and men from Schiepzig are within the range of variation of the comparative sample, but tend to be located in the lower to middle range of the variation. By contrast, the differences in dental pathology are striking: the Schiepzig series has a significantly lower frequency and intensity of caries. This also applies to the frequency of dental calculus and could be related to a lower consumption of carbohydrates in combination with better oral hygiene. Overall, the individuals from Schiepzig represent a group of people that were carrying out physically demanding work, but at the same time were apparently well nourished and also had an average-to-low disease burden.

Biological relatedness estimation

Eight out of twelve individuals of the Early Bronze Age individuals buried around and associated with house 4, as well

House	ID	Feature	Lab ID	Ind.	Morphological/ Genetic sex	Age	Age group
4	2006:1793	1544	SCI001		–/m	12–14 12.7 ± 2.2	Infans II
	n.a.	1592			No bone preservation		
	2006:1925	1613	SCI002	1	w/w	50–60	Late mature
	2006:1925	1613	SCI003	2	–/m	7 ± 2 7.3 ± 2.2/6.9 ± 2.1	Infans II
	2006:1927	1614			m??/n.a.	20–60	Adult-mature
	2006:1937	1615	SCI004	1	w/w	50–60	Late mature
	2006:1937	1615	SCI005	2	w/w	30–35	Late adult
	2006:1937	1615**		3	m?/n.a.	25–30	Early adult
	2006:2062	1698	SCI006		–/w	5 ± 1.5 5.1 ± 2.1	Infans I
	2006:2068	1704	SCI010		w/w	30–50	Late adult – early mature
	2006:2170	2368	SCI007		m/m	40–50	Early mature
1–3	n.a.	1254			No bone preservation		
	2006:2140	2288**			w/n.a.	40–50	Early mature
	2006:2238	2631*			n.a.	7–8	Infans II
	2007:43547	16047	SCI008		w?/w	35–50	Late adult – early mature
	n.a.	16048			No bone preservation		
	n.a.	16049			No bone preservation		
	2007:43574	16050**			m??/n.a.	20–35	Adult
	2007:43581	16051	SCI009		–/m	9 ± 2	Infans II
	n.a.	16052			No bone preservation		

Tab. 2 Age and sex determination of burials from Schiepzig. Age data of the children: age estimates based on teeth are given first (Ubelaker 1978), followed by age estimates based on long bone measurements (Cardoso et al. 2013). *Currently not traceable, the information given refers to published data (Pichler/Schunke 2019). **Individuals associated with feature numbers 1615-3, 16050 and 2288 were sampled at a later stage and results are unavailable at the time of publishing. n.a. = not available.

Tab. 2 *Alters- und Geschlechtsbestimmung der Bestattungen aus Schiepzig. Altersangaben der Kinder: Zuerst werden Altersschätzungen auf Basis der Zähne angegeben (Ubelaker 1978), gefolgt von Altersschätzungen auf Basis von Röhrenknochenmessungen (Cardoso et al. 2013). *Derzeit nicht nachvollziehbar, die Angaben beziehen sich auf veröffentlichte Daten (Pichler/Schunke 2019). **Individuen, die mit den Befundnummern 1615-3, 16050 und 2288 assoziiert sind, wurden zu einem späteren Zeitpunkt beprobt und die Ergebnisse waren zum Zeitpunkt der Veröffentlichung noch nicht verfügbar. n. a. = nicht verfügbar.*

as two of the six individuals buried near houses 1 to 3, were used for ancient DNA (aDNA) analyses. We were able to successfully generate high-quality genome-wide data (1240k SNP capture data, (Mathieson et al. 2015) for all ten of them (Fig. 2). To estimate possible genetic relatedness between the individuals we used READ (Monroy et al. 2018) and identity-by-descent analysis (IBD; Ringbauer et al. 2023).

House 4

We found close genetic relationships between seven out of the eight individuals associated with house 4, and based on the integration of contextual evidence (age at death, mitochondrial DNA and Y-chromosomal haplogroups) we were able to reconstruct a pedigree spanning over four generations (Fig. 4).

From the triple burial, two out of three individuals yielded aDNA results from which a parent-offspring relationship could be reconstructed. Individual 1615/SCI004 was the mother of 1615/SCI005, an individual that died around the age of 30–35 years (Fig. 3). Individual 1698/SCI006 from a single burial was found to be the granddaughter of 1615/SCI004 and the niece of 1615/SCI005. 1698/SCI006 died when she was around 5 years old. A male individual, 1544/SCI001, buried close to the aforementioned female individuals, was related in the first degree to 2368/SCI007, a second male individual, buried to the north of house 4. Both male individuals carry the same Y-chromosome (I2a2a) and mitochondrial haplogroup (T2a1a), which suggests that 1544/SCI001 and 2368/SCI007 were brothers. Results of the IBD analysis shows that the two brothers were also related in the third degree to both 1615/SCI004 and 1615/SCI005, but the quality of the genetic relationship to these individuals was different: Individual 1615/SCI004 was related to 1544/SCI001 and 2368/SCI007 in direct gen-

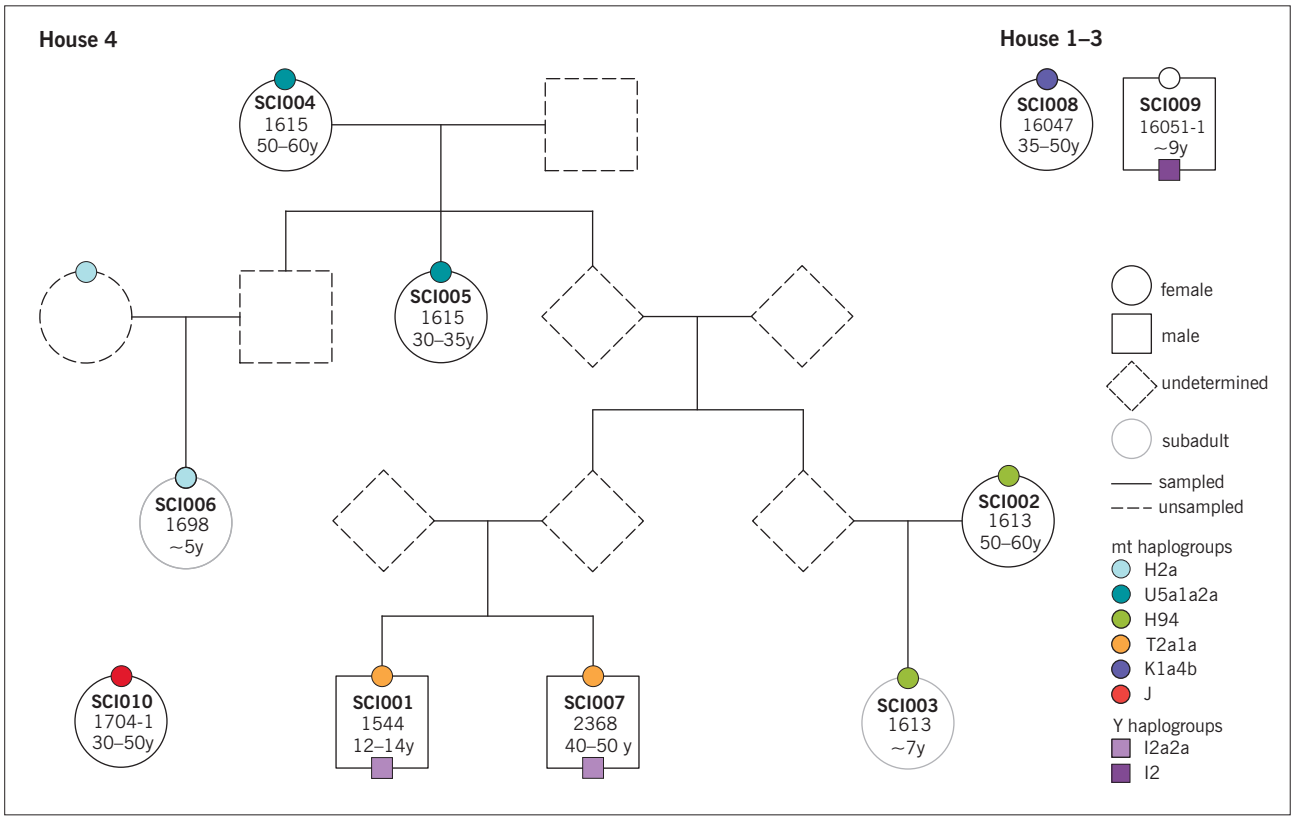


Fig. 4 Genetic relationships between individuals associated with houses 4 and 1–3. Pedigree reconstructed based on READ, IBD, mitochondrial (mt) and Y-chromosome haplogroups for individuals buried around house 4, comprising four generations. Individual 1704/SCI010 and the two individuals from around the houses 1–3 were not genetically related to individuals from the pedigree.

Abb. 4 *Genetische Beziehungen zwischen Individuen, die mit den Häusern 4 und 1–3 verbunden sind. Rekonstruierter Stammbaum basierend auf READ-, IBD-, mitochondrialen (mt) und Y-Chromosomen-Haplogruppen für Individuen, die rund um Haus 4 begraben sind und vier Generationen umfassen. Das Individuum 11704/SCI010 und die beiden Individuen aus der Umgebung der Häuser 1–3 waren genetisch nicht mit Individuen aus dem Stammbaum verwandt.*

erational line and thus the great-grandmother of the brothers, whereas 1615/SCI005 was their great-aunt (Fig. 5).

Two female individuals from a double burial, 1613/SCI002 and 1613/SCI003, shared a first-degree relationship and the same mitochondrial haplotype, while IBD analysis further indicates a parent-offspring relationship with 1613/SCI002 being the mother of 1613/SCI003. IBD analysis also shows that 1613/SCI003 was related in the third degree to other individuals from the pedigree (Fig. 5), and again in direct generational line to 1615/SCI004, whereas 1613/SCI002 was only related to her daughter and thus can be considered an exogenous female. These relationships fit into the existing pedigree with 1615/SCI004 being the great-grandmother, 1615/SCI005 the great-aunt to 1613/SCI003, and the brothers 1544/SCI001 and 2368/SCI007 their first cousins.

1613/SCI002 and the mother of 1698/SCI006 provide evidence for two exogenous females. In addition, the diamond-shaped parental unions in the 2nd and 3rd generation of the pedigree suggest one, if not two, more exogenous females. This observation is further supported by a replacement of mitochondrial haplogroups in every generation. This indicates that the generations are connected by the male line rather than the female line, resulting in possible patrilineality and patrilocality. Individual 1615/SCI005 was the only adult lineage daughter buried at the site (Fig. 4).

In addition to the individuals that can be placed into the pedigree, 1704/SCI010, a 30–50-year-old female individual, was buried at house 4 and was not related to any other individual buried at the site (Fig. 5). Although the available ^{14}C date indicates that 1704/SCI010 was contemporary with the group of biologically related individuals, this female was not buried among this group but in an isolated tomb northeast of house 4. In this case, spatial distancing of the burials seems to mirror biological distance (Fig. 6).

House 1–3

Out of seven burials only three contained skeletal remains. Two individuals were identified as male by osteological criteria, the third was an infant whose sex could not be determined. Only two individuals could be used for ancient DNA analyses and the genetic sex of the infant 16051/SCI009 could be determined as male, whereas the genetic sex of 16047/SCI008 was female and therefore differed from the anthropological determination. Both individuals, a 35–50-year-old female (16047/SCI008) and a ~9-year-old boy (16051/SCI009) were found to be neither related to each other nor genetically connected to the pedigree from house 4 or to 1704/SCI010 (Fig. 5). Like the unlinked individual 1704/SCI010, their mitochondrial and Y-chromosome haplogroups are not found among the individuals of the pedigree

and IBD analysis did not detect any genetically long-distance relationships with other individuals (Fig. 3).

Discussion and Conclusion

The results presented in this study provide critical insights into the livelihood, settlement and social structure of Early Bronze Age communities from Central Germany associated with the Únětice Culture. On the basis of the available data, we were able to reconstruct a pedigree spanning four generations involving seven individuals buried around house 4, which represents a typical Únětice longhouse. Therefore, burials around house 4 likely belonged to a closely related kin group, or a potential ›house community‹. The reconstructed pedigree indicates that at least another eight individuals are missing, and suggests a minimum group size of 15 individuals associated with the long house. This does not include potential siblings or additional children. Indeed, the large majority of burials contained adults, whereas only two children between 5–7 years of age were included in this funerary space. Considering that the mortality rate among children during the Únětice period between the ages of 0–5 years might have been as high as 47 % (Nicklisch 2017, 105), other burial grounds or rites must have existed for sub-adult individuals. The fact that the ten burials found around house 4 kept 13 individuals, seven of which belong to the pedigree, suggests that only a fraction of the group, approximately 42 %[1], was granted a burial around house 4. This situation is even more pronounced around houses 1–3, where the size (Tab. 1) and architectural complexity of these three buildings exceeds by far in capacity the number of burials. In contrast to house 4, it is also possible that these buildings were not used as housing/living complexes, but instead were used for specialised activities, such as barns for storage or stockpiling in relation to the central feature 2003. In view of the frequent location of burials at a certain distance south of the Únětice buildings (Fig. 2a), it is also possible that the burials of house 3 are located outside the limits of the Schiepzig excavation area and, consequently, have not been found yet (Fig. 2b).

One anthropologically determined adult male (1614) buried south of house 4 could not be analysed for DNA, whereas the third individual of feature 1615-3 and a female individual (2288) have not been genetically analysed yet. Moreover, two graves (1254, 1592) spatially related to house 4 did not preserve any human remains, but probably belonged to adult individuals based on the size of the wooden coffin and stone protection. Therefore, it remains unclear whether these individuals were genetically related to the other burials and would occupy missing nodes in the pedigree. It is worth noting that one of the males (1615-3) was buried together with the female individuals 1615/SCI004 and 1615/SCI005. Therefore, considering the order of deposition (Fig. 3) and age at death it is likely that feature 1615-3 is the child of 1615/SCI004, the mature female buried first within the pit, and sibling of 1615/SCI005. It is also possible that 1615-3 is the partner of 1615/SCI004 and putative father of 1615/SCI005, or alternatively he was not related to either.

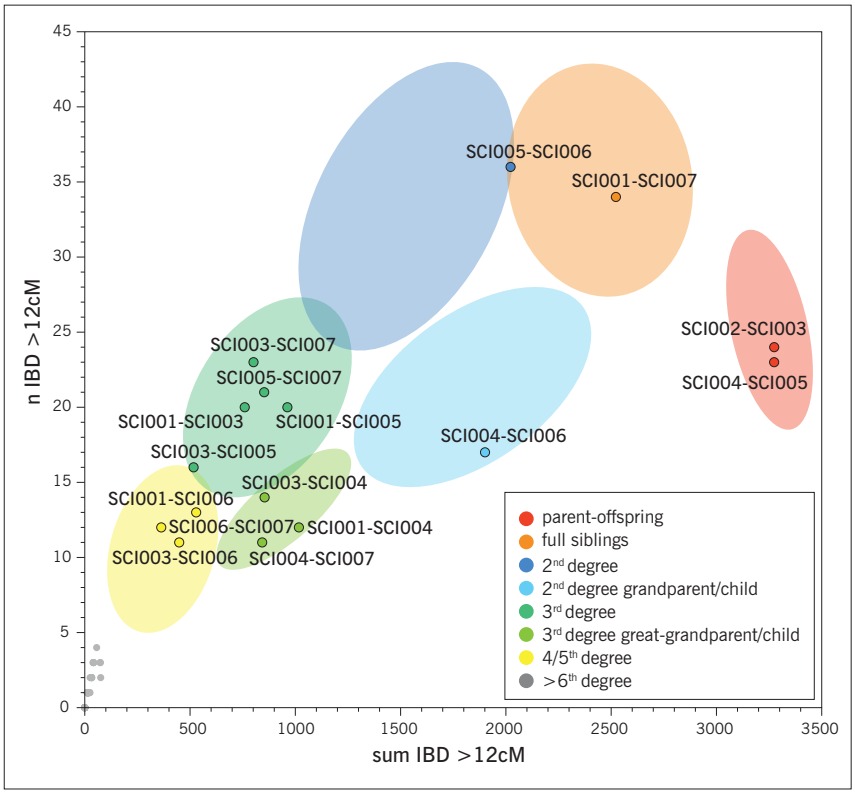


Fig. 5 Identity-by-descent (IBD) within individuals from Schiepzig. Plotting the sum versus the number of shared tracts of IBD in window sizes of > 12 cM resolves degrees of biological relatedness up to the 4–6th degree. Coloured ellipses indicate the observed range of degrees of relatedness from comparative and simulated data.

Abb. 5 *Identity-by-Descent (IBD) bei Individuen aus Schiepzig. Durch Aufzeichnen der Summe gegen die Anzahl gemeinsam genutzter IBD-Teile in Fenstergrößen von > 12 cM werden Grade der biologischen Verwandtschaft bis zum 4.–6. Grad zerlegt. Farbige Ellipsen geben den beobachteten Bereich der Verwandtschaftsgrade aus Vergleichs- und Simulationsdaten an.*

1 15 is the minimal number of individuals necessary to generate the reconstructed pedigree (Fig. 4). Applying a child mortality of 50 % we can tentatively add another nine individuals (estimated from the three attested children predicted to have been born in Schiepzig in each of the three offspring generations). From this extrapolated number of 24 individuals, seven have been identified genetically.

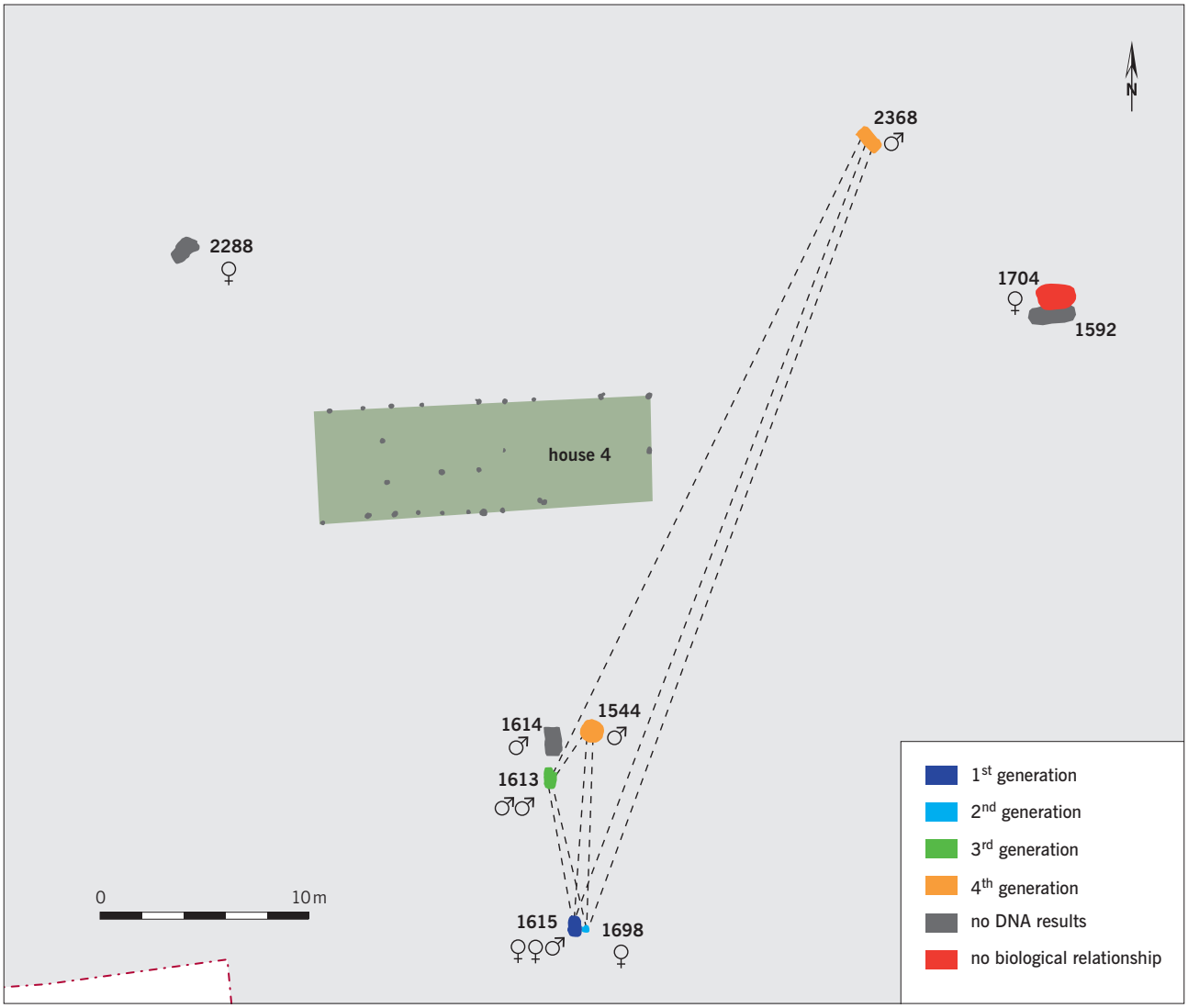


Fig. 6 Detailed plan of the individuals buried around house 4. Colours indicate the maternal mt haplogroup and dashed lines show the connection of the burials via genetic relationships.

Abb. 6 *Detaillierter Plan der um Haus 4 herum begrabenen Individuen. Die Farben zeigen die mütterliche mt-Haplogruppe an und gestrichelte Linien stellen den Zusammenhang der Bestattungen über genetische Beziehungen dar.*

The mothers of at least two generations were not related to anyone in the pedigree except their children, suggesting they came from a different house or community. That suggests the practice of female exogamy that has been observed also in other studies of the European Early Bronze Age (Mittnik et al. 2019; Žegarac Leskovar/Premrov 2021; Villalba-Mouco et al. 2022). Further, albeit subtle, support for this conclusion comes from the stable dietary isotope data. While all individuals of Schiepzig show high $\delta^{15}N$ values, indicating their direct relation with the butchering or animal processing activities at the site, the adult woman 1704/SCI010, who shows no biological relationship with other individual from Schiepzig, has markedly lower $\delta^{15}N$ and $\delta^{13}C$ values. This would imply that she consumed significantly less animal protein and suggests that she could have come from a different region or belonged to a lower social echelon. On the other hand, at least one female lineage daughter, (individual 1615/SCI005) remained in, or returned to, the settlement before she died in her 30s, providing an exception to the rule.

The spatial distribution of the seven genetically linked individuals reveals that not all members were buried in the same funerary area. While members of all four generations were buried south of house 4, the 40–50-year-old male of grave 2368/SCI007 may represent the last individual to die at the site, and was buried over 35 m north from his brother's grave 1544/SCI001, who died at much younger age (Tab. 2; Fig. 6). However, it is also possible that he passed away after the house was abandoned and was therefore not clearly spatially associated.

The interpretation concerning the few genetically analysed individuals around houses 1–3 is different and based on only very few data points, and thus does not allow firm conclusions to be drawn. The finding that individuals 16047/SCI008 and 16051/SCI009 were genetically unrelated does not preclude the existence of a ›house community‹ similar to that of house 4, particularly given that the majority of burials (potential nodes) has not been tested. Hypothetically speaking, it is possible that individuals 16047/SCI008 and

1704/SCI010 were exogenous females who formed unions with lineage males of each respective house, but who had no offspring together that would link them to a pedigree. Overall, however, non-genetic relationships also played a major role in prehistoric societies, but it remains unclear how these are reflected with regards to prevailing burial customs at Schiepzig. Furthermore, it raises questions about the nature and purpose of such social relationships, including possible dependent relationships between people. Answering such questions is, however, outside the scope of this current study.

Importantly, the pedigree not only informs us about the approximate number of people associated with a longhouse, but can also provide a temporal estimate with regards to the duration of such a building. In our case, four generations would provide a maximum upper estimate of 126 years considering a mean generation time of 29 years (Fenner 2005; Nicklisch 2017). More concretely, taking the estimated age at death of individuals and the ages of mothers into account, we estimate a combined lifespan of ~ 80–120 years from the pedigree as a proxy for the duration of house 4 at Schiepzig. This assumes that the house lasted until: 1) the oldest individual of the last generation 2368/SCI007 passed away at the age of 40–50 years; 2) that he, his mother and his grandmother were born in Schiepzig; 3) that his mother, grandmother and great-grandmother 2368/SCI007 gave birth to their children when they were between 20 and 30 years old; and 4) that the great-grandmother belonged to the founding generation of house 4, which she helped to build when she was ~ 20 years old. This »most likely scenario« can be put into context with the more speculative estimates from the archaeological record and experimental archaeology, which range from 75–100 years for longhouses of the Early Neolithic Linear Pottery Culture (Rück 2007) to lower estimates of 20–30 years (Modderman 1972), in line with Late Neolithic palafite houses (Petrequin/Petrequin 2016). Average occupation spans of c. 150 years have also been established for Scandinavian Bronze Age longhouses on the basis of radiocarbon dates (Artursson 2009). Alternatively, if we assume that the first generation contributed to the erection of the building and the last generation decided to build a new one, this would leave an intersection of two main generations that had been living in or using the house effectively. This would reduce the estimated time of occupancy substantially. The spatial separation of burial 2368/SCI007, indicates that house 4 might have been abandoned at the time of his death, which would shorten the sequence by ~ 25 years. Indeed, shorter occupancies of 50–100 years have been suggested for the settlement of Schloßvippach, Sömmerda district (Germany), based on stratigraphic indicators (Walter et al. 2019, 422). Irrespective of the true scenario, the genetic results of the Schiepzig burials provide for the first time an estimate of the life span of the Únětice longhouses based on independent evidence.

It is clear that the social structure inferred from the biological relatedness analyses of the Early Bronze Age Únětice house community found at Schiepzig cannot be applied universally to other Únětice societies, but it provides a first insight into the relations existing within communities in Early Bronze Age Central Germany. Further Únětice burial grounds will have to be analysed genetically in order to determine whether certain genetic relationships within and between houses and communities were sanctioned or allowed, which has the potential to provide a robust scaffold for extended social kin relationships.

Acknowledgements

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Source of Figures

1–3 J. Filipp, Bad Bibra
4 S. Penske
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Kinship, status, and mobility in the Bronze Age Lech Valley

Alissa Mittnik, Ken Massy, Corina Knipper, Ronny Friedrich, Johannes Krause, and Philipp W. Stockhammer

Zusammenfassung

Verwandtschaft, Status und Mobilität im bronzezeitlichen Lechtal

Während der mitteleuropäischen frühen Bronzezeit, die von zunehmender Mobilität und Austausch geprägt war, traten hierarchische Gesellschaftsstrukturen hervor. Belege hierfür finden sich in den ungleichen Bestattungszeremonien, wie das Auftreten von Fürstengräbern in der Region der Aunjetitzer Kultur. Solche vermeintlich überregionalen Eliten wurden in den archäologischen Befunden in Süddeutschland aus dieser Zeit nicht beobachtet. In dieser Region lebten viele kleine Gemeinschaften, die einzelne landwirtschaftliche Gehöfte bewirtschafteten. Die mit diesen Gehöften assoziierten Gräberfelder brachten jedoch archäologische Funde zu Tage, die die Region in ein weiterreichendes mitteleuropäisches Netzwerk einbetten. Sie legen sogar Statusunterschiede innerhalb von Haushalten nahe.

Eine ganzheitliche Herangehensweise, welche genetische, isotopische, archäologische, metallurgische und anthropologische Daten von 107 endneolithischen bis mittelbronzezeitlichen Individuen kombiniert, die in der Mikroregion des Lechtals in der Nähe von Augsburg ausgegraben wurden, erlaubt uns Einblicke in beispielloser Auflösung in die Dynamiken von sozialem Gefüge und Mobilität zu gewinnen, die den Epochenwandel vom Neolithikum zur Bronzezeit begleiteten. Wir sehen, dass diese Gemeinschaften Teil eines lange Zeit bestehenden exogamen Mobilitätsnetzwerkes waren, das weitreichende Kontakte gestärkt haben muss.

Reichtum und/oder Status innerhalb der Haushaltsgemeinschaften hingen auch mit biologischer Verwandtschaft zusammen, was die Anhäufung von wertvollen Grabbeigaben innerhalb patrilinealer Mehrgenerationsfamilien vermuten lässt. Die naturwissenschaftlichen Analysen zeigten, dass einige Frauen, die – nach den Beigaben zu schließen – in den Bauernhöfen des Lechtals ein hohes Ansehen genossen, in mindestens 350 km vom Lechtal entfernten Regionen aufwuchsen. In den Haushalten lebten zugleich Individuen von geringerem Status, die mit niemandem genetisch verwandt waren. Hier deuten sich komplexe Haushaltsstrukturen an, wie sie in ähnlicher Weise aus dem antiken Griechenland und Rom etwa 1500 Jahre später bekannt sind, und bezeugen eine lange Geschichte sozialer Ungleichheit innerhalb von Haushaltsverbänden.

Summary

During the Central European Early Bronze Age, a time of increasing mobility and connectivity, hierarchical societal structures emerged. Evidence for this proposal is based on the inequality of burial ceremonies, such as the establishment of princely graves in the regions of the Únětice Culture. Such putative supra-regional elites were not observed in the archaeological record of Southern Germany at the time, which attests to many small communities operating single farmsteads. The cemeteries associated with these farmsteads, however, reveal archaeological finds that connect the region to a wider Central European network and suggest status differences even within households.

A holistic framework combining genetic, isotopic, archaeological, metallurgical and anthropological data from 107 Final Neolithic to Middle Bronze Age individuals excavated in the microregion of the Lech Valley near Augsburg provides us with an unprecedentedly high-resolution insight into the dynamics of social interaction and mobility that accompanied these cultural transitions. We find that the communities were part of a long-standing exogamous marriage network, which would have strengthened wide-ranging contacts.

Wealth and/or status within the household community was generally correlated with biological relatedness, suggested by the accumulation of valuable grave goods within multigenerational patrilineal families. We detect the presence of unrelated, high-status women, who grew up in regions at least 350 km from the Lech Valley. Unrelated, lower-status individuals were nevertheless part of the same households, a social organization that anticipates similar complex household structures known from ancient Greece and Rome some 1500 years later and attests to a deep history of social inequality within kin groups.

Introduction

After overcoming many »teething troubles« (Hagelberg et al. 2015), the study of ancient DNA has proved instrumental in unravelling some of the most contested and long-standing major questions in European prehistory, such as the mode of the Neolithic transition (e.g. Skoglund et al. 2012; Lazaridis et al. 2014), or the human migrations at the onset of the European metal ages (e.g. Allentoft et al. 2015; Haak et al. 2015). In the latter case, the study of ancient genomes has documented the spread of a type of genetic ancestry that first emerged among early pastoral groups from Eastern Euro-

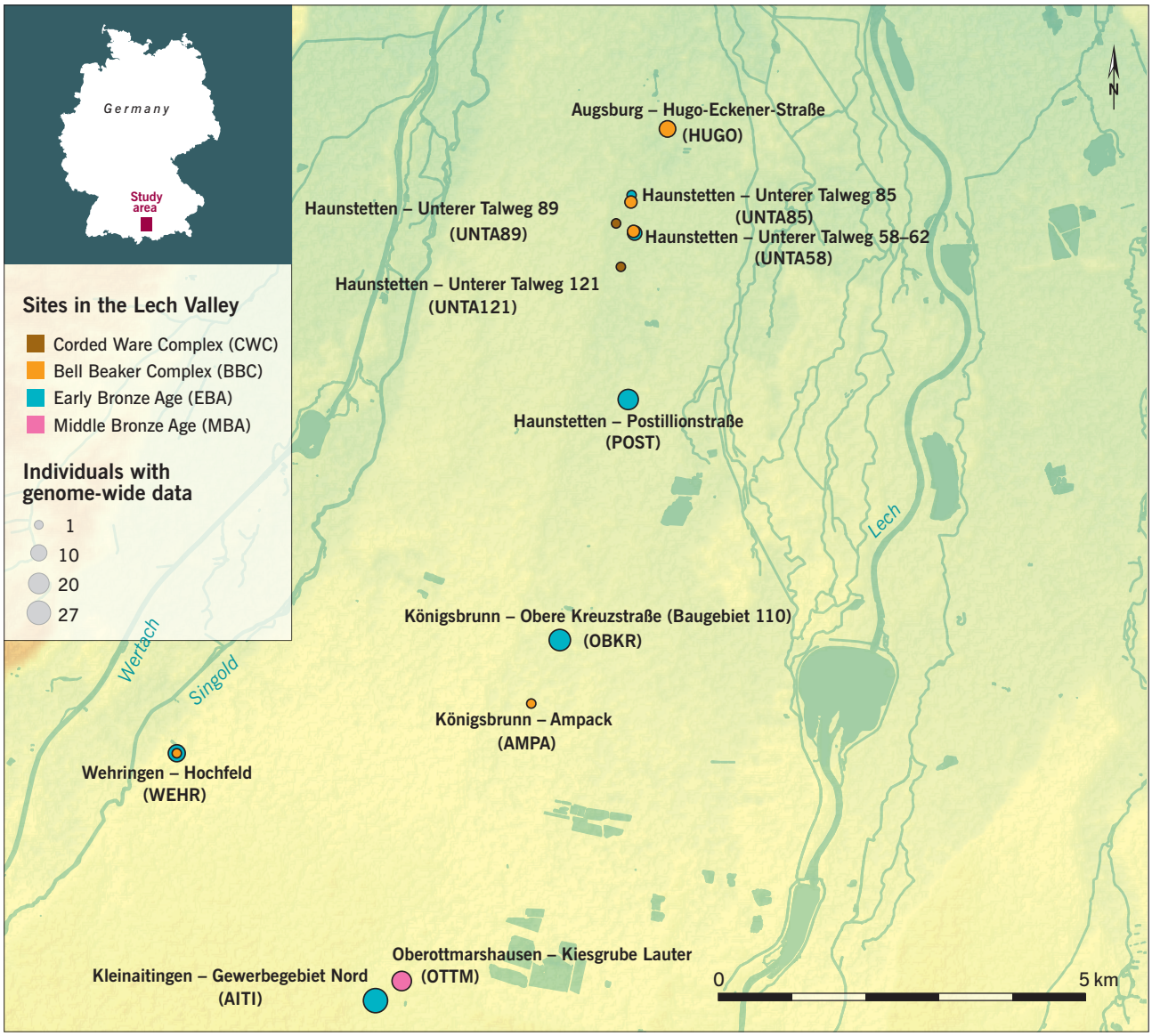


Fig. 1 The studied microregion of the Lech Valley in southern Germany and sites with genome-wide ancient DNA data. Sites are mapped and marked according to their chronological assignment and are labeled with full site name and abbreviation.

Abb. 1 *Die untersuchte Mikroregion des Lechtals in Süddeutschland und die Fundstellen mit genomweiten alten DNA-Daten. Die Fundstellen sind nach ihrer chronologischen Zugehörigkeit eingefärbt und jeweils mit dem vollen Fundstellennamen sowie Abkürzung angegeben.*

pean steppes and forest-steppes into Eastern and Central Europe in the early 3rd millennium BC, and its subsequent dispersal throughout Europe by the early 2nd millennium BC, and which was associated with newly emerging cultural complexes such as the Corded Ware and Bell Beaker cultural complexes[1]. While these findings have given some insight into the broad sequence of events during those tumultuous eras, questions remain as to how fine-scale dynamics, involving the social organization of communities and interactions of their members, affected, and were in turn affected, by the large-scale changes happening in the European record. In particular, the increase of social inequality, the unequal distribution of power and economic wealth within a society, from the European Neolithic onwards, associated with populations' growth, emerging new technologies, and increased complexities of modes of living and political systems[2], has been a major focus of archaeological inquiry. In the past, researchers have used various approaches, including analysing material culture, technology and interconnectedness, diet, gender and mobility to study social inequality. Adding the analysis of ancient DNA to the arsenal of methodologies within the archaeological sciences now provides us the opportunity to incorporate evidence of biological relatedness between individuals into a holistic approach to address aspects of kinship, family structure and inheritance in the formation of the societies of Europe's early metal ages.

1 Allentoft et al. 2015; Haak et al. 2015; Mathieson et al. 2018; Mittnik et al. 2018; Olalde et al. 2018; Olalde et al. 2019; Furtwängler et al. 2020; Papac et al. 2021; Saupe et al. 2021; Villalba-Mouco et al. 2021.

2 McGuire/Paynter 1991; Elliott 2017; Kohler et al. 2017; Müller 2017.

Background

In 2013, under the title »Times of Upheaval – Interdisciplinary investigations of social and population dynamics at the onset of the Central European Bronze Age (2500–1400 BC) in Southern Bavaria, Germany«, a project funded by the Heidelberg Academy of Sciences set out to investigate a case study of a microregion undergoing the major cultural shifts of the Final Neolithic and the Early and Middle Bronze Ages (EBA and MBA). Besides archaeological (Massy 2018), osteological and genetic analyses on the human remains excavated from several sites in the region, the research comprised a thorough reassessment of the region's chronology with a gapless series of new radiocarbon dates (Stockhammer et al. 2015a; Stockhammer et al. 2015b), the analysis of isotopes obtained from enamel for the reconstruction of individual mobility (Knipper et al. 2017) and of diet (Massy et al. 2017), as well as metal analysis to determine the origin of raw materials used for the production of the locally found artefacts.

The microregion under study is an approximately 10 x 30 km stretch of land along the Lech Valley, ca. 6 km south of the center of the modern city of Augsburg, Bavaria (Fig. 1). The fertile Loess soil made it an attractive area for agricultural settlement in the 3rd and 2nd millennium BC (Bartelheim 2010) and the amount of excavated burials suggests it was one of the most densely populated regions in Southern Germany during the EBA (Massy 2018). The archaeological record indicates the presence of a series of small unfortified hamlets, large enough to be operated by and sustain a small community of people. They were located like »pearls on a chain« along the border of the Loess terrace and often

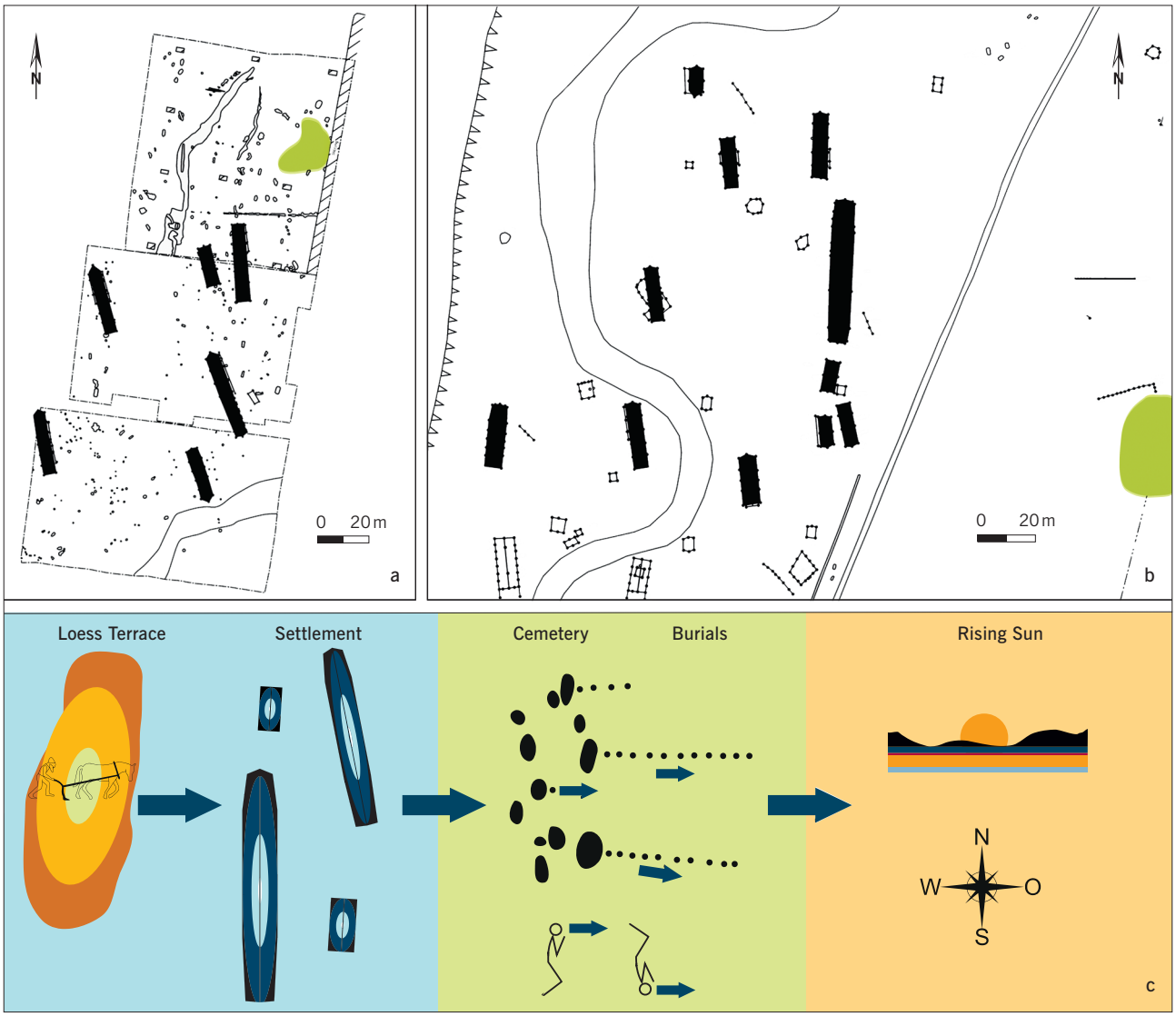


Fig. 2a–c Topographical comparisons of settlements (blue) and their accompanied burial sites to the east (green) in the Lech Valley. a Haunstetten – Unterer Talweg 111–115; b Haunstetten – Unterer Talweg 85; c Schematic representation of the area of the living with farming ground and hamlets (blue); the area of the dead with burials of both sexes facing east and post alignments in the same direction (green); the direction of the rising sun (orange).

Abb. 2a–c *Topografische Vergleiche von Siedlungen (blau) und den dazugehörigen Gräberfeldern im Osten (grün) im Lechtal. a Haunstetten – Unterer Talweg 111–115; b Haunstetten – Unterer Talweg 85; c Schematische Darstellung des Gebiets der Lebenden mit landwirtschaftlichen Flächen und Weilern (blau); der Bereich der Toten mit Bestattungen beider Geschlechter mit nach Osten gerichtetetem Blick und in dieselbe Richtung verlaufende Pfostenreihen (grün); die Richtung des Sonnenaufgangs (orange).*

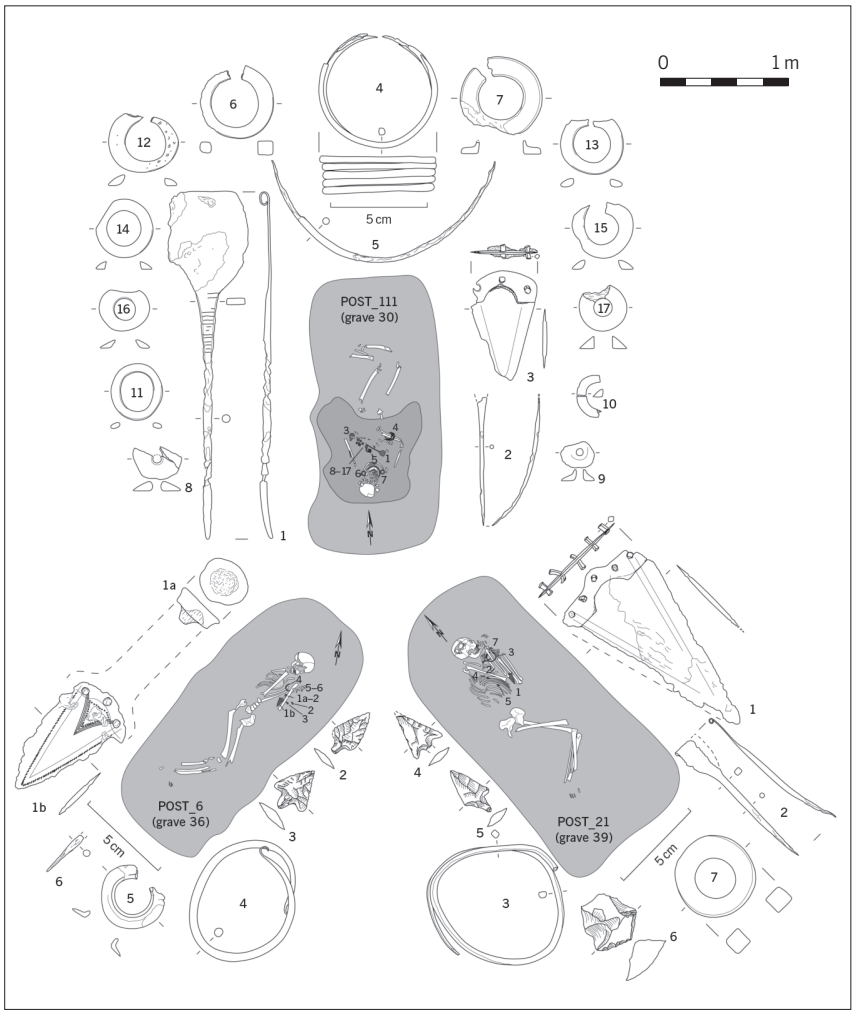


Fig. 3 Haunstetten-Postillionstraße, city of Augsburg. Burials POST_111 (female, 25–45 years), POST_6 (male, 14–16 years) and POST_21 (male, 25–35 years) with their grave goods. All three individuals are 2nd degree-related to each other, show comparable high status grave good assemblages, are buried in the southern part of the cemetery and belong to its younger phase according to the radiocarbon dates.

Abb. 3 *Haunstetten-Postillionstraße, Stadt Augsburg. Die Gräber POST_111 (weiblich, 25–45 Jahre), POST_6 (männlich, 14–16 Jahre) und POST_21 (männlich, 25–35 Jahre) mit ihren Grabbeigaben. Alle drei Individuen sind 2. Grades miteinander verwandt, weisen Grabbeigaben von vergleichsweise hohem Status auf, sind im südlichen Teil des Gräberfeldes bestattet worden und gehören den Radiokarbondatierungen zufolge in die jüngere Phase des Gräberfeldes.*

within less than 1 km distance from each other. These hamlets are often accompanied by a cemetery to the east, containing up to a few dozen graves, presumably including several generations of individuals who operated and lived at the farmstead (Fig. 2; Massy 2018). Thus, these individuals represent what we define as a »household« – a group of people living in a closed architectural space (such as a hamlet), who are connected through shared traditions and daily practices, and may include both biologically related and unrelated individuals (Louise et al. 2010).

The Lech Valley, as part of the so-called Straubing Culture of the Northern Alpine EBA, exhibits the richest burials in the region with respect to amount and quality of metal grave goods and the high proportion of burials that received grave goods. There is, however, an absence of conspicuous »princely graves« containing prestigious gold artefacts or weapons, which emerged during the EBA in many other regions of Europe (Vandkilde 1999; Vandkilde 2016), such as, for example, the contemporaneous Únětice Culture. These burials attest to an increase in trans-regional connectivity based on trade of raw materials and knowledge that accompanied the novel technology of metallurgy, and a resulting negotiation of power hierarchies that led to an emphasis on warriorhood and weapons[3].

The degree of inequality with regard to wealth and power is less evident in the Lech Valley. Agriculture as the main source of limited individual and communal wealth was proposed by M. Bartelheim to have led to »flat hierarchies« with local to micro-regional structure (Bartelheim 2002; Bartelheim 2010). Nevertheless, stratification with regard to wealth and/or status within the Lech Valley burial communities is suggested by differences in grave furnishing, ranging from very rich to no grave goods at all. Hierarchies may have resulted from kin-groups or communities participating in and controlling trans-regional networks of exchange of raw materials, objects, technologies, and ideas[4]. The importance of knowledge and influence in trans-regional networks would have also allowed traders and craftsmen to achieve power and status outside of their kin-group (Bertemes 2004; Bertemes 2010; Nessel 2012). Other aspects likely played a role in positioning individuals within social structures, such as age and gender. The importance of gender in organizing the society of the Lech Valley is suggested by the adherence to the practice of gendered burial orientation that followed widespread customs. For example, during the Corded Ware period individuals were buried facing south, males were laid crouched on their right and females on their left, and during the Bell Beaker period

3 Vandkilde 2006; Harding 2007; Stockhammer 2015; Hansen 2016.

4 Bertemes 2010; Krause 2010; Strahm 2010; Kneisel/Müller 2011.

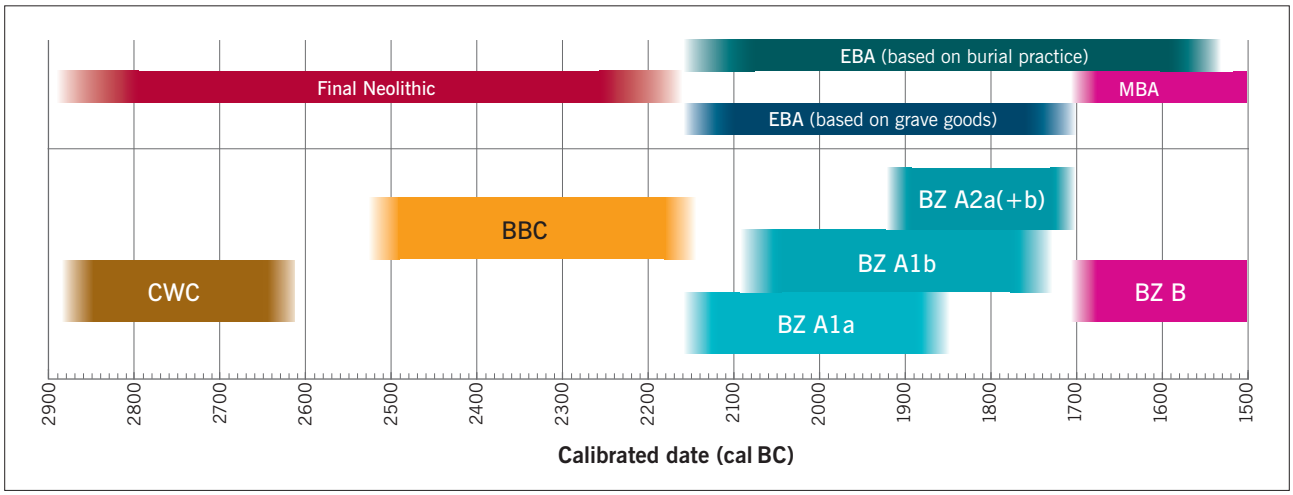


Fig. 4 Chronological sketch of radiocarbon dates from the Lech Valley and their associated cultural groups. The gap between Corded Ware (CWC) dates and Bell Beakers (BBC) is most likely due to the lack of dated individuals, rather than a real hiatus. Early Bronze Age (EBA) dates are differentiated between burials with grave goods and their relative chronological assignment and the typical crouched position (burial practices). Radiocarbon dates for the Middle Bronze Age (MBA) burials from the Lech Valley extend until ca. 1300 cal BC.

Abb. 4 *Chronologische Darstellung von Radiokarbondaten aus dem Lechtal und die damit verbundenen kulturellen Gruppen. Die Lücke zwischen den Schnurkeramikdaten (CWC) und der Glockenbecherkultur (BBC) ist höchstwahrscheinlich auf den Mangel an datierten Individuen zurückzuführen und stellen keine wirkliche Lücke dar. Die frühbronzezeitlichen Daten (EBA) werden zwischen Bestattungen mit Grabbeigaben, ihrer relativen chronologischen Zugehörigkeit und der typischen Hockerhaltung (Bestattungssitte) unterschieden. Radiokarbondaten für die mittelbronzezeitlichen Bestattungen (MBA) im Lechtal reichen bis ca. 1300 cal BC.*

and EBA facing east, males were laid crouched on their left side and females on their right. Gender differences are also observed in the furnishing of burials and in costumes, e.g., complex head-dresses were found exclusively with females, while daggers and other weapons were most commonly found with males (Fig. 3). In contrast to the Únětice Culture of Central Germany, where women were commonly poorly furnished, women in the Straubing Culture exhibited markedly richer burial goods, suggesting they played a more significant role in this society, akin to what is seen in the Únětice Culture of Bohemia (Ernée et al. 2020).

In view of the complex interaction of the different aspects under which social organization can be constructed, the integration of genetic data, which allows us to identify biological ties within burial communities, i.e. households, is crucial in providing an understanding of the size and the structure of kin-groups. This information also allows recognition of patterns of residence and inheritance, and in turn reveals the mechanisms behind the rise in social inequality that marks the onset of the Bronze Age.

Genetic data

We prepared ancient DNA libraries (Kircher et al. 2012; Dabney et al. 2013; Rohland et al. 2015) and employed shotgun-sequencing and hybridization-capture approaches for the mitochondrial DNA (Maricic et al. 2010). We did this for a panel of ca. 1.2 million single-nucleotide polymorphisms (1240K SNP set) on the nuclear genome, which are informative for genetic ancestry (Fu et al. 2013; Haak et al. 2015; Mathieson et al. 2015) and allowed us to generate genome-wide data for 138 individuals excavated in the Lech Valley, dated from the Final Neolithic to Middle Bronze Age (ca. 2900–1300 cal BC; Fig. 4; Massy 2018).

After authentication, validation and quality control, described in detail in C. Knipper et al. (2017) and A. Mittnik et al. (2019), we retained sufficient nuclear data suitable for a relatedness analysis of 101 individuals. These acquired data include two individuals from two burial sites associated with the Corded Ware Complex (CWC), dated to ca. 2750–2460 BC, 13 individuals from five Bell Beaker Complex (BBC) burial sites, dated to ca. 2480–2150 BC, 73 individuals excavated at 6 sites dated to the EBA (ca. 2150–1550 BC) and 13 individuals from a Middle Bronze Age site (ca. 1700–1300 BC; Fig. 1 and Appendix 1). In addition, we generated 133 complete, or nearly complete mitochondrial genomes, which provided information about maternally inherited lineages (Appendix 2). Following the publication of Mittnik et al. (2019), we generated genome-wide data for additional individuals. While the complete analyses of these data are still in progress, we take the opportunity to recapitulate in this paper the main observations laid out in Knipper et al. (2017) and Mittnik et al. (2019) and illustrate them with the case study of the EBA site Haunstetten-Postillionstraße, city of Augsburg (abbr. POST; Wirth 1993; Massy 2018), for which we present the preliminary results of analyses for six additional individuals, bringing the total number of individuals with working genomic data from this site to 21, of the 23 individuals sampled for DNA and the 41 individuals excavated from the site (Tab. 1).

Population trajectories in the Late Neolithic-Early Bronze Age transition

We visualize the genetic diversity seen in the ancient populations of the Lech Valley in relation to the neighboring regions, and respective sites, of Central Germany, Poland, Bohemia, Singen, and Switzerland by means of principal

Individual ID (Site ID_Feat. Nr.)	Labor Nr.	^{14}C Age	±	cal 2σ	Age in years	Data available	Covered SNPs (1240K SNP set)	Genetic Sex
POST_38	MAMS 18963	3717	23	cal BC 2197–2034	> 21	in prep.	493851	male
POST_50	MAMS 18966	3707	24	cal BC 2196–2029	30–35	Mittnik et al. 2019	815920	male
POST_12	MAMS 18956	3697	20	cal BC 2190–2028	7–11	Mittnik et al. 2019	85202	female
POST_44	MAMS 18964	3681	23	cal BC 2139–1979	30–45	Mittnik et al. 2019	909788	male
POST_24	MAMS 18959	3679	20	cal BC 2137–1980	6–10	in prep.	150449	male
POST_47	MAMS 18965	3662	24	cal BC 2134–1956	20–30	Mittnik et al. 2019	63467	male
POST_2	MAMS 18953	3648	19	cal BC 2126–1948	> 20	Mittnik et al. 2019	24140	female
POST_99	MAMS 18969	3641	25	cal BC 2130–1930	20–30	Mittnik et al. 2019	1041643	female
POST_111	MAMS 18970	3639	20	cal BC 2122–1941	(25)-45	in prep.	97296	female
POST_84	MAMS 18967	3638	24	cal BC 2126–1928	3–5	in prep.	60263	female
POST_131	MAMS 18971	3635	20	cal BC 2120–1938	6–10	Mittnik et al. 2019	49130	female
POST_140	MAMS 18973	3631	20	cal BC 2114–1926	> 25	Mittnik et al. 2019+in prep.	353742	male
POST_85	MAMS 18968	3631	24	cal BC 2120–1921	2–4	Mittnik et al. 2019	22942	male
POST_35	MAMS 18962	3621	20	cal BC 2033–1918	35–55	Mittnik et al. 2019	869649	female
POST_32	MAMS 18961	3619	20	cal BC 2032–1916	20–30	Mittnik et al. 2019	101581	female
POST_137	MAMS 18972	3613	20	cal BC 2029–1912	9–15	in prep.	229287	male
POST_16	MAMS 18957	3612	20	cal BC 2029–1911	> 25	Mittnik et al. 2019	24590	female
POST_28	MAMS 18960	3608	20	cal BC 2027–1906	17–25	Mittnik et al. 2019	503443	male
POST_21	MAMS 18958	3606	20	cal BC 2025–1903	25–35	in prep.	169497	male
POST_1	MAMS 18952	3583	28	cal BC 2024–1882	4–6	Mittnik et al. 2019	50042	female
POST_6	MAMS 18955	3574	19	cal BC 2009–1883	14–16	Mittnik et al. 2019	998686	male

Table 1 Overview of samples with genome-wide data from the EBA site of Haunstetten-Postillionstraße, city of Augsburg.

Tabelle 1 *Übersicht über die Proben mit genomweiten Daten der frühbronzezeitlichen Fundstelle Haunstetten-Postillionstraße, Stadt Augsburg.*

component analysis, thus projecting the ancient individuals on a scaffold of modern-day Western Eurasians who were characterized at ~ 600 000 SNP positions (Fig. 5). The first principal (PC1) component distinguishes European and West Asian populations, while the second principal component (PC2) serves to differentiate ancestry derived from 4th millennium BC steppe pastoralists in the upper part (in the following denoted »steppe-like ancestry«) and ancestry derived from European Middle and Late Neolithic farmers in the lower (»farmer-like ancestry«). In modern-day Europeans,

mtDNA haplogroup assignment	Y-chromosomal lineage assignment	Consistency with local isotopic signature	Number of grave good types	Relation to core pedigree	Burial features and grave goods
H1e	R1b-P312	consistent	0	no	
T1a1	R1b-P312	consistent	6	yes	burial mound, post alignment, dagger, three arrow heads, metal pin, bangle, bone disc, two cattle teeth
J1c3g	n/a (female)	consistent	0 (robbed)	no	
K1a3a	R1b-P312	consistent	0 (slightly disturbed in Roman period)	yes	post alignment
H1b1	R1a-M417	consistent	1	no	ceramic vessel
K2a5	R1	consistent	4	yes	arrow head, bangle
n/a	n/a (female)	consistent	2 (robbed)	no	large paddle headed pin, neck ring
K1a4a1	n/a (female)	inconsistent	3	no	neck ring, two lunula shaped pendants, awl
U5b2b2	n/a (female)	uncertain	6	yes	burial mound, post alignment, dagger, large and small paddle headed pins, neck ring, bone disks
X2b+226	n/a (female)	consistent	2	yes	bone disks
T2c1d+152	n/a (female)	consistent	4	yes	paddle headed pin, awl, bangle, bone disks
H41a	R1b-P312	consistent	2	yes	dagger, bone pin
X2b+226	R	consistent	1	yes	stone pendant
H41a	n/a (female)	consistent	4	yes	large paddle headed pin, two bangles, awl
T2	n/a (female)	inconsistent	4	no	two earrings, two bangles, fingerring, bone disk
T2c1d+152	R1b-P312	consistent	0 (robbed)	yes	burial mound, post alignment
T2f8a	n/a (female)	consistent	0 (robbed)	no	
K2a5	R1b-P312	consistent	0 (maybe more recent disturbance)	yes	
n/a	R1b-L52	consistent	5	yes	dagger, two arrow heads, paddle headed pin, bangle, bone disc
H2a1a	n/a (female)	consistent	2	yes	bone pin, bone disk
U5a1a1+16362	R1b-P312	consistent	5	yes	dagger, two arrow heads, bangle, bone pin, bone disc

who are descended mainly from a mixture between those two groups, the percentage of either ancestry is correlated with geography, producing an approximate north-east to south-west cline of decreasing steppe-like ancestry (Lazaridis et al. 2014; Allentoft et al. 2015; Haak et al. 2015). This »mixing of ancestry« first took place during the 3rd and 2nd millennium BC, as large-scale long-distance mobility and emerging networks of connectivity brought people of very distinct ancestries together. This resulted in a cline of large genetic diversity between the two »ancestral poles« that can even be seen within a single site, such as our case study of POST (Fig. 5). Some general geographical and cultural patterns can be recognized: The individuals of the CWC, located in Central and Eastern Europe, who are arguably culturally most

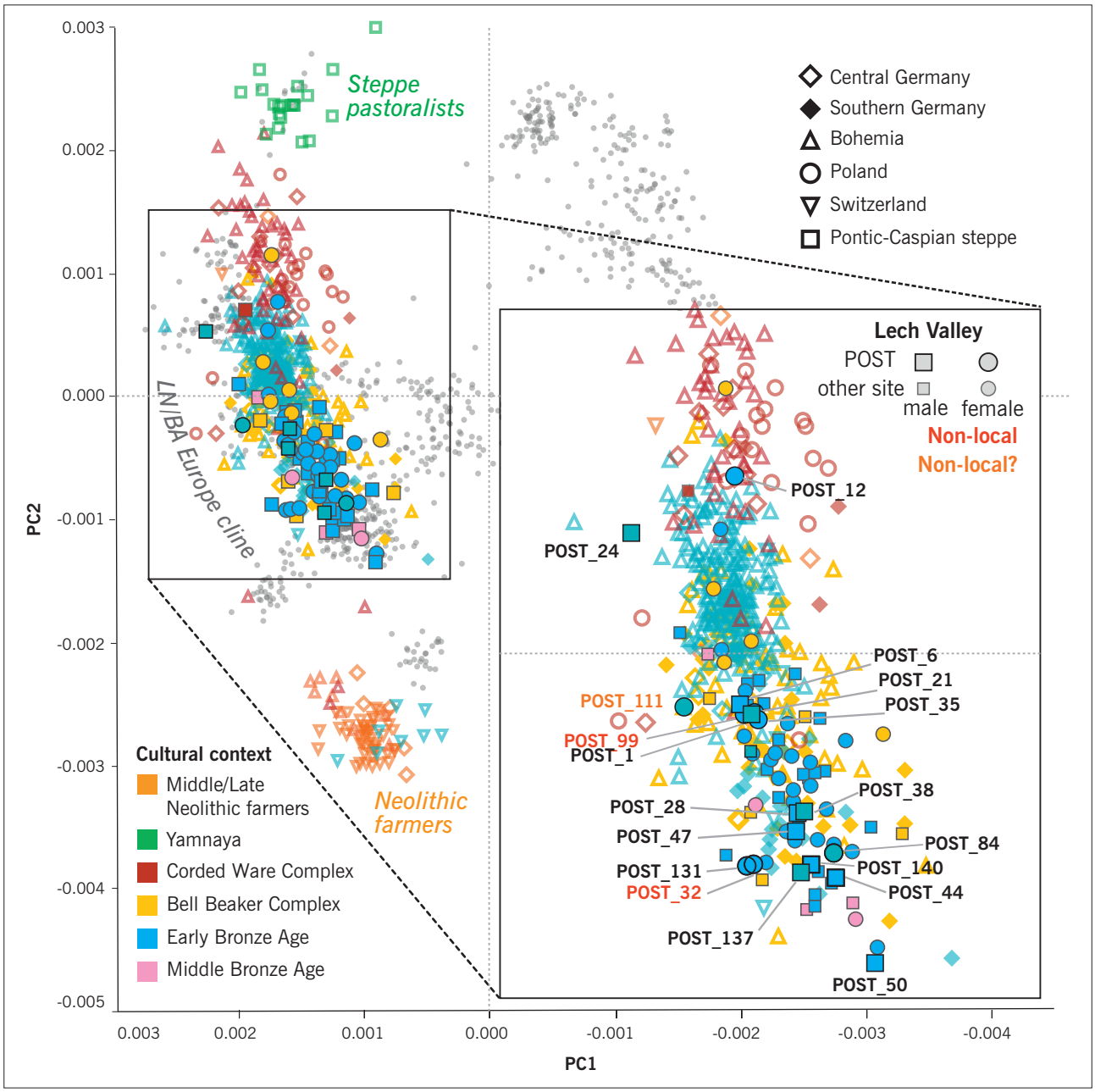


Fig. 5 Principal component analysis of the genotype data of Lech Valley and other relevant ancient individuals. The first and the second principal (PC1 and PC2) are constructed using modern-day West Eurasian individuals (grey dots). Ancient individuals are color-coded by their chronological or cultural assignment and their origin is indicated by shape. The inset in the lower right corner shows a zoom-in on the Lech Valley individuals. Males and females are represented by squares and circles, respectively. Individuals from Haunstetten-Postillionstraße (POST) are labelled and shown with larger symbols.

Abb. 5 *Analyse der Hauptbestandteile der Genotypdaten der Individuen aus dem Lechtal und anderen relevanten prähistorischen Individuen. Die erste und die zweite Hauptkomponente (PC1 und PC2) sind mit Hilfe von modernen westeurasischen Individuen konstruiert (graue Punkte). Prähistorische Individuen sind nach ihrer chronologischen oder kulturellen Zugehörigkeit farblich markiert und ihre Herkunft ist als bestimmte Umrissform angegeben. Die Einfügung in der unteren rechten Ecke zeigt vergrößert die Individuen des Lechtals. Männer werden als Quadrate und Frauen als Kreise dargestellt, Individuen von Haunstetten-Postillionstraße (POST) sind gekennzeichnet und werden mit größeren Symbolen angegeben.*

similar to the steppe pastoralists, are also overall genetically closest to them, and very distinct from the preceding Neolithic farmers of the same regions that lack any steppe-like ancestry. Individuals of the succeeding BBC, which was present from Central Europe to the Atlantic, are found again to have more farmer-like ancestry. High individual mobility together with shared cultural practices and norms in this period likely facilitated the spread of steppe-like ancestry westward and the resurgence of farmer-like ancestry in the east (Olalde et al. 2018). In the EBA, a genetic differentiation between the Únětice Culture of Central Germany and Bohemia and the Northern Alpine EBA groups emerges, with the latter overall having less steppe-like ancestry. In the Lech Valley, where a chronological continuum from the BBC to the EBA exists (Stockhammer et al. 2015a; Stockhammer et al. 2015b), genetic continuity cannot be rejected, and is even suggested by the persistence of some mitochondrial haplotypes (Knipper et al. 2017; Appendix 2).

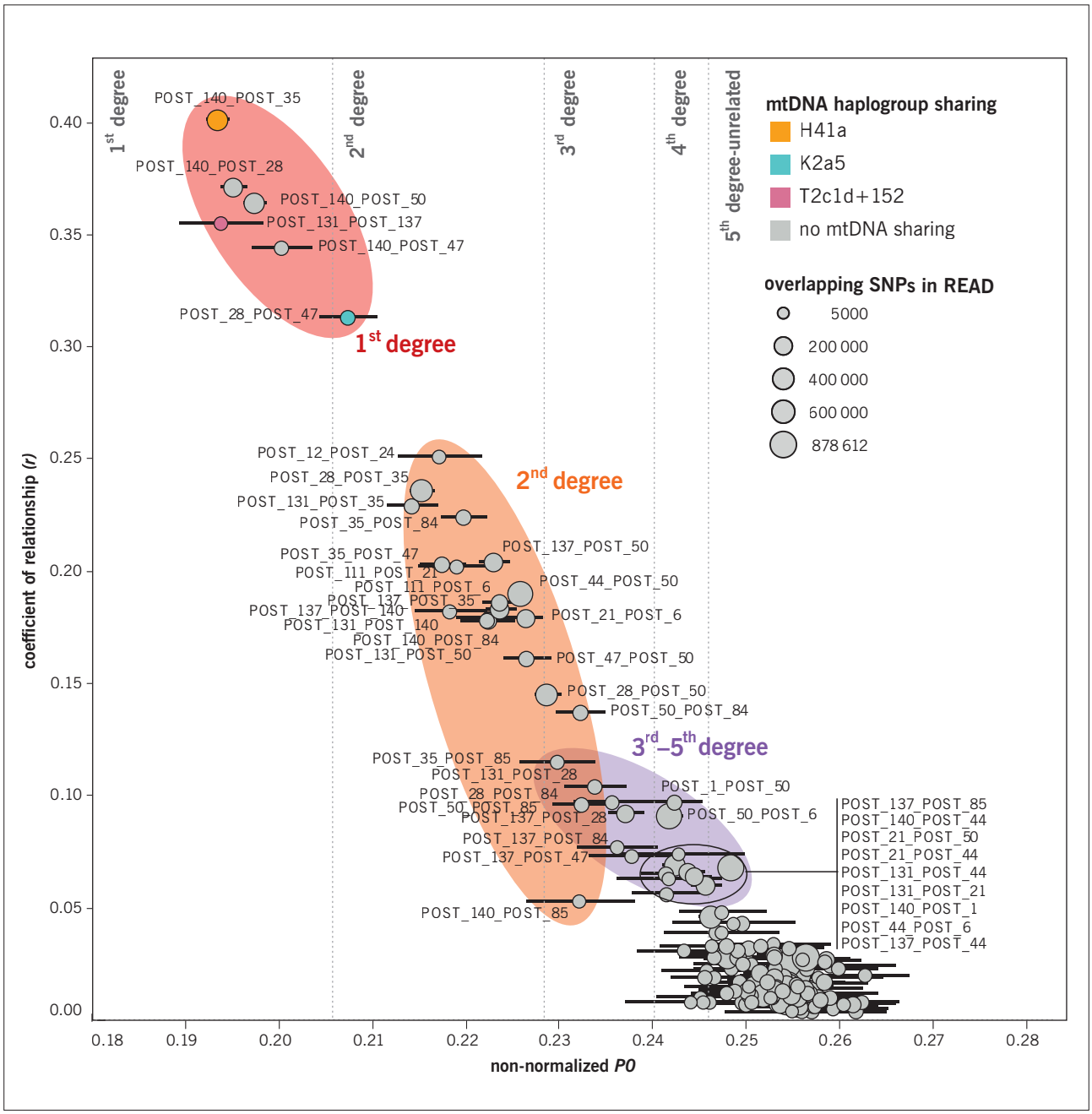


Fig. 6 Results of relatedness analysis. P0, calculated with READ is plotted against *r*, calculated with lcMLkin. Horizontal error bars represent 2 standard errors for P0. Vertical dotted lines show the cut-off for each degree of relatedness as estimated following the approach in READ, using the median P0 value for all pairs that have coverage on at least 5000 SNPs. Shaded ellipses highlight the clusters corresponding to each degree of relatedness. Due to the uncertainty in the analysis, especially in pairs that have low coverage, the assignment of the degree of relatedness can be ambiguous.

Abb. 6 *Ergebnis der Verwandtschaftsanalyse. P0, das mit READ berechnet wurde, ist gegen* r *aufgetragen und mit lcMLkin berechnet. Horizontale Fehlerbalken stellen 2 Standardfehler für P0 dar. Senkrechte gepunktete Linien zeigen den geschätzten Grenzwert für jeden Verwandtschaftsgrad, wie er nach dem Ansatz von READ unter Verwendung des mittleren P0-Wertes für alle Paare mit einer Abdeckung von mindestens 5000 SNPs geschätzt wurde. Schraffierte Ellipsen heben die Cluster hervor, die mit jedem Verwandtschaftsgrad korrespondieren. Wegen der Ungenauigkeit in der Analyse, besonders bei Paaren, die eine niedrige Deckung besitzen, kann die Zuordnung zu dem Verwandtschaftsgrad unsicher sein.*

At POST, we find that the genetic diversity of the majority of individuals matches the diversity seen across all of Southern Germany during the EBA. However, contact with other regions is suggested by the presence of two subadults, POST_12 and 24, who are genetic outliers more consistent with the genetic diversity seen in the regions of the Únětice Culture. Furthermore, the male POST_24 carries the Y-chromosomal R1a-M417 lineage, which was widespread in the CWC and was also found in EBA Bohemia (Papac et al. 2021). On the other hand, all other males for whom a Y-chromosomal lineage can be assigned belong to the R1b-P312 lineage, which is associated with the spread of the BBC.

Overall, the genetic diversity in the Lech Valley is upheld from the EBA into the MBA, although there is an increase in farmer-related ancestry over time (Mittnik et al. 2019).

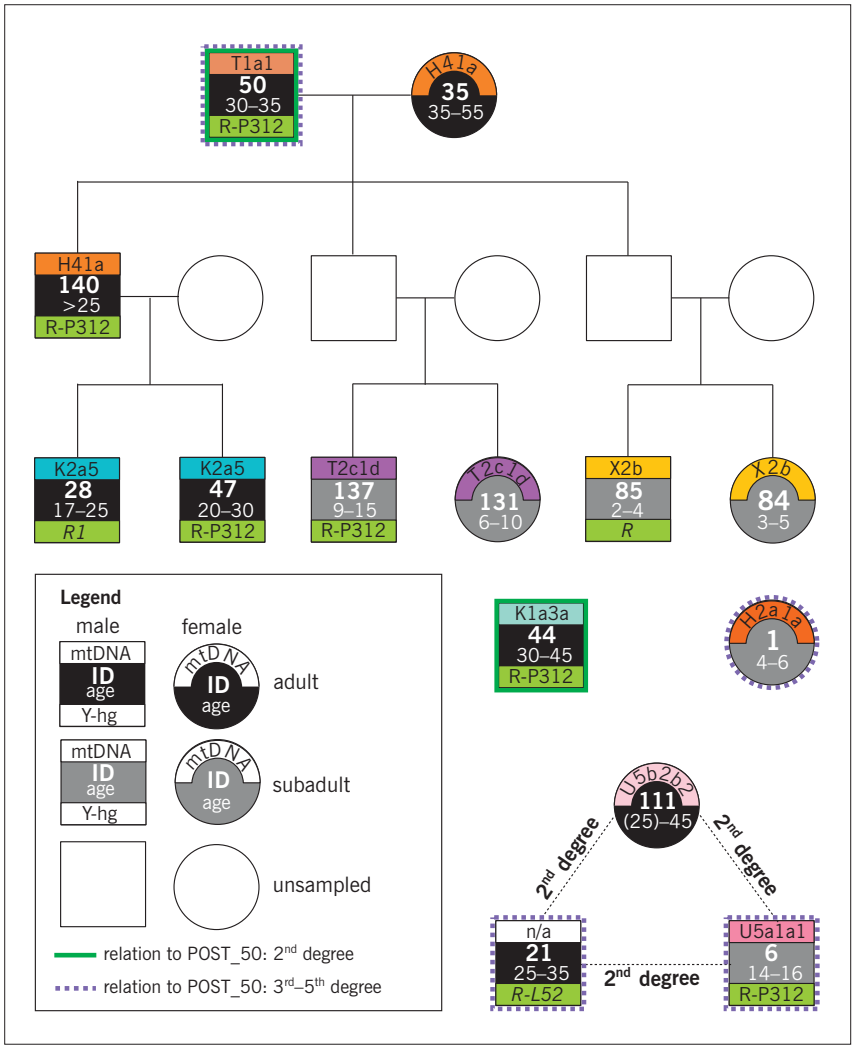


Fig. 7 Reconstructed family tree of Haunstetten-Postillionstraße (POST). In this burial site, at least three generations are connected by a paternal lineage. Black symbols denote adult individuals and grey filled symbols subadult individuals, unsampled individuals inferred in the tree are denoted by unfilled symbols. Upper and lower colored bars on each symbol represent mtDNA and Y-chromosomal haplogroups, respectively. All Y-chromosomal haplogroups in the tree are consistent with belonging to the lineage R1b-P312, and are denoted with italics where they are not fully resolved. The bottom right part of the figure shows individuals that are part of the core pedigree, but whose position in the family tree cannot be determined. Colored outlines show the degree of relatedness to POST_50.

Abb. 7 *Rekonstruierter Stammbaum von Haunstetten-Postillionstraße (POST). In diesem Gräberfeld sind mindestens drei Generationen durch eine paternale Linie miteinander verbunden. Schwarze Symbole kennzeichnen adulte Individuen und grau ausgefüllte Symbole subadulte Individuen. Nicht beprobte Individuen, die im Stammbaum angenommen werden, sind als leere Symbole angegeben. Die oberen und unteren Farbbalken in jedem Symbol stellen jeweils die mtDNA und Y-chromosomale Haplogruppen dar. Alle Y-chromosomalen Haplogruppen im Stammbaum gehören konsistent zu der Linie R1b-P312 und sind in kursiver Schrift angegeben, wenn sie noch nicht vollständig bestimmt sind. Der rechte untere Teil des Diagramms zeigt Individuen, die Teil der Kernabstammung sind, aber deren Position im Stammbaum nicht zugewiesen werden kann. Farbliche Umrandungen zeigen den Verwandtschaftsgrad zu POST_50.*

Patrilineality, female exogamy and kinship-based inequality

We calculate two different measures of relatedness with the tools READ (Monroy Kuhn et al. 2018) and *lcMLkin* (Fig. 6; Lipatov et al. 2015). *P0*, estimated with READ, quantifies the pairwise mismatch in SNP variants between two individuals and becomes higher, the more distantly two individuals are related. *lcMLkin* calculates the coefficient of relatedness *r*, the fraction of the genome common to two individuals due to direct kinship, i.e., 0.50 for parent and offspring or full siblings, 0.25 for grandparent and grandchild, etc. These estimates are possible up to the 5th degree of relatedness and are subject to some uncertainty due to the incomplete and damaged nature of ancient DNA data. Nevertheless, together with the information provided by maternal and paternal uniparentally inherited markers, the mtDNA and Y-chromosome, respectively, and the age of death of the individuals, they allow us to reconstruct family relationships.

At POST (Fig. 7) we construct a multigenerational pedigree of at least three generations, and at Wehringen-Hochfeld and Königsbrunn-Obere Kreuzstraße, both Augsburg district, of at least four generations, corresponding to a use of the farmsteads and cemeteries for about 100 years. All multigenerational lineages were strictly patrilineal. Among the pedigrees of offspring we did not find a single adult daughter, but ten adult sons, as well as subadults of both sexes. This is consistent with a society that practices female exogamy in which a daughter leaves her parental residence upon reaching a certain age for the purpose of marriage. In accordance with this, none of the adult women were related to anyone else at the same site, besides their own offspring. Close biological relationships of 1st or 2nd degree are mostly found within sites and only in one case (the potential half-sisters POST_99 and OBKR_76, who are both isotopically non-local) between sites.

The newly generated data for POST increases the number of individuals that can be securely identified as part of the main pedigree from seven to 14. The centrality of the parents POST_50 and 35 in the northern part of the cemetery, where their descendants are buried in close proximity, becomes very apparent (Fig. 8). Moreover, this highlights the social cohesion that accompanied biological relatedness within this society. It is possible that the pair represents the founders of this hamlet. The only individual that might precede them is POST_44, who was also buried in the northern part of the cemetery and is a 2nd degree relative of POST_50, i.e., his grandfather, uncle, or paternal half-brother. The placement of these individuals in the earlier generations of the pedigree is consistent with the early

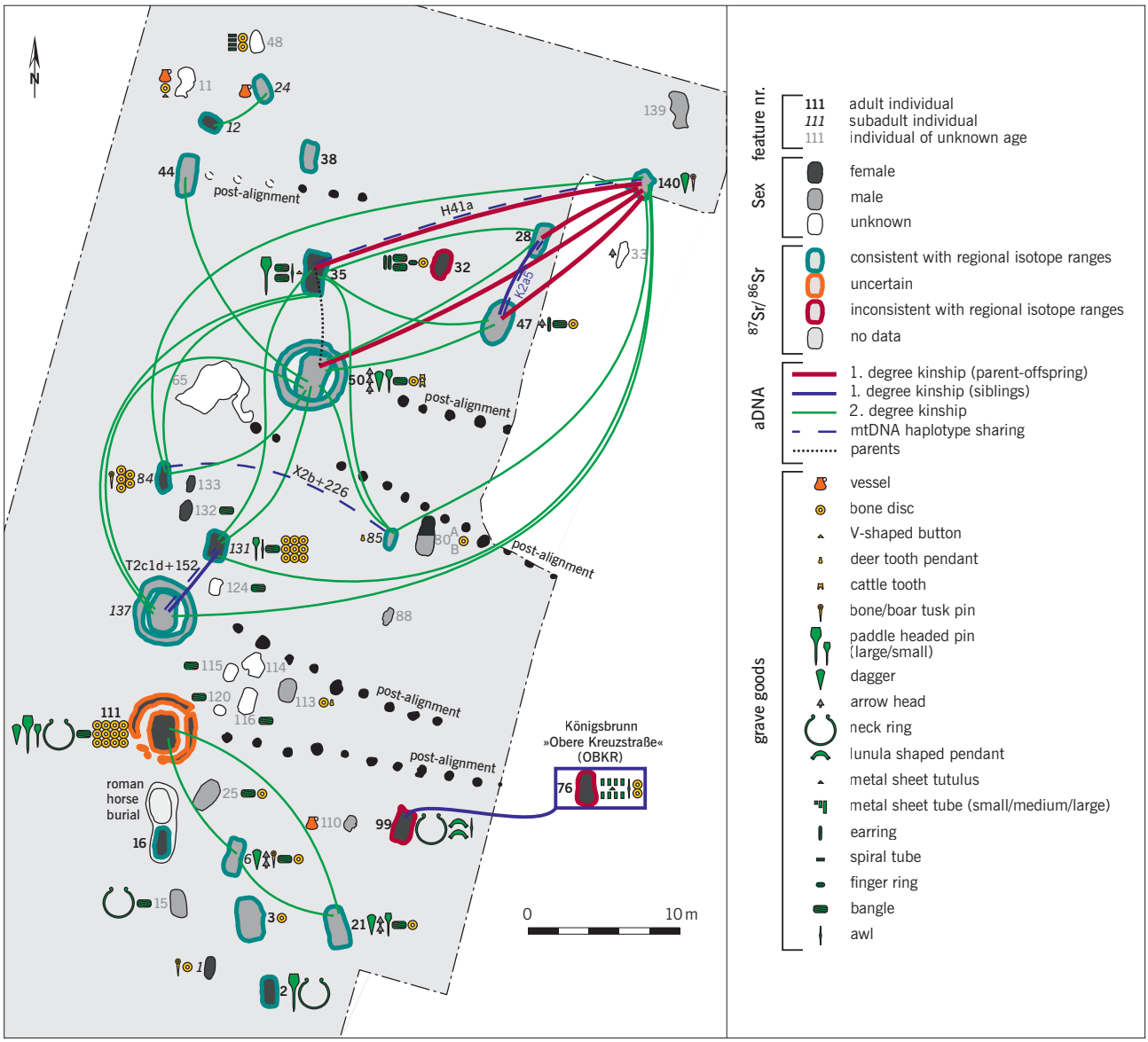
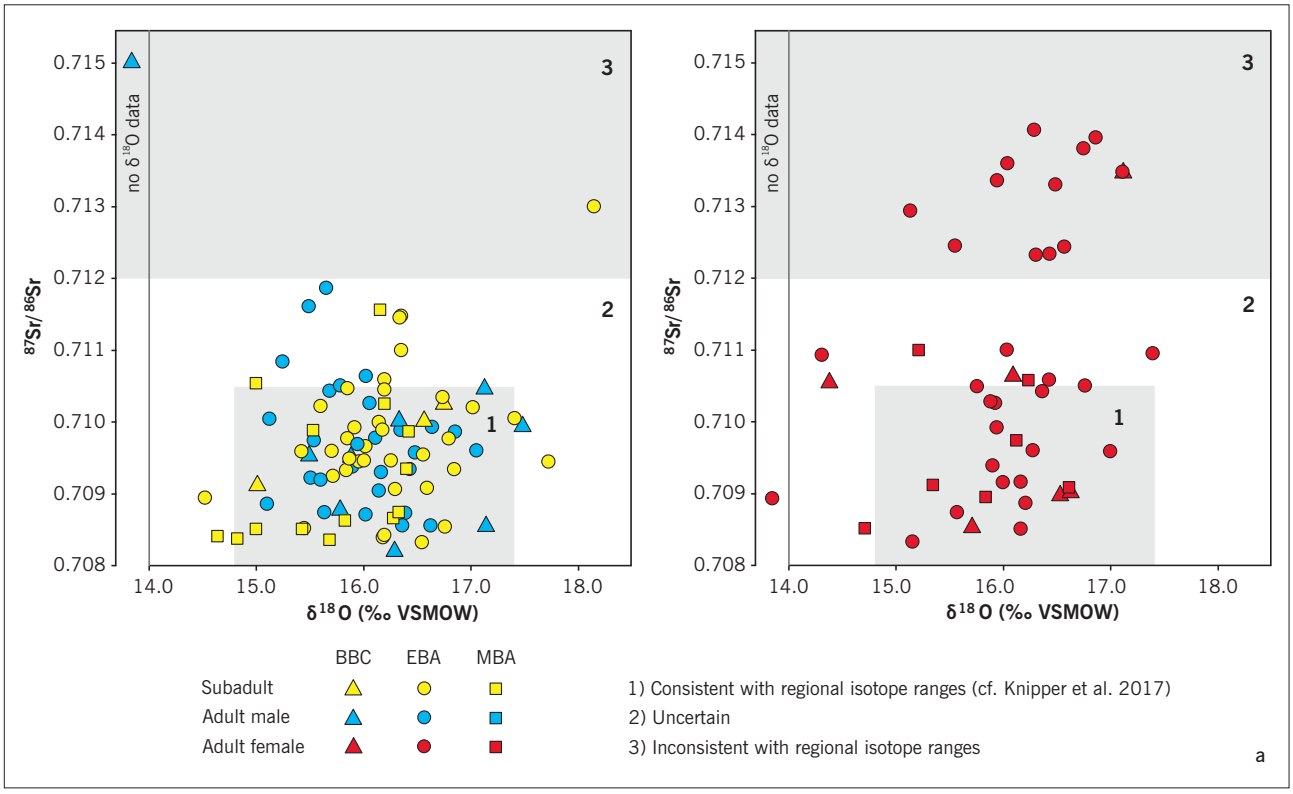


Fig. 8 Early Bronze Age burial site of Haunstetten-Postillionstraße (POST). Burials are labeled with the feature number in black for individuals that were sampled for ancient DNA and in grey for unsampled individuals. Three of the 41 graves (POST_50, 111 and 137) were covered with burial mounds. Those, and two additional ones (POST_44 and 65), were accompanied by post alignments marking them above ground as important individuals. The possible founding couple of the core pedigree, POST_50 and 35, was buried in the northern part of the cemetery with two generations of descendants buried in close proximity. All sampled individuals of the northern group with metal grave goods are biologically related to each other except the non-local female burial (POST_32). Burials belonging to a second branch of the pedigree, related to POST_50, are found in the southern part of the cemetery and are also richly furnished (POST_111, 6 and 21). Individuals POST_12 and 24 in the northern part of the cemetery are related to each other but not to the core pedigree. The second non-local individual within the cemetery (POST_99) was very well furnished and only biologically related to another non-local female (OBKR_76) from the cemetery of Königsbrunn-Obere Kreuzstraße, Augsburg district (OBKR).

Abb. 8 *Frühbronzezeitliches Gräberfeld von Haunstetten-Postillionstraße (POST). Die Gräber sind mit Befundnummern gekennzeichnet: schwarz bei Individuen, denen Proben für alte DNA entnommen wurden und grau, bei denen keine Proben entnommen wurden. Drei der 41 Gräber (POST_50, 111 und 137) waren mit Grabhügeln bedeckt. Diese und zwei weitere (POST_44 und 65) wurden zudem von Pfostenreihen begleitet, die sie obererdig als wichtige Individuen markierten. Das mögliche Gründerpaar, POST_50 und 35, war im nördlichen Bereich des Gräberfeldes bestattet, und zwei Generationen von Nachkommen waren in nächster Nähe begraben. Mit der Ausnahme des nicht-lokalen weiblichen Individuums (POST_32) sind alle ausgewählten Individuen der nördlichen Gruppe mit Grabbeigaben aus Metall biologisch miteinander verwandt. Gräber, die zum zweiten Strang des Stammbaums gehören und mit POST_50 verwandt sind, fanden sich im südlichen Teil des Gräberfeldes und sind zudem reich ausgestattet (POST_111, 6 und 21). Die Individuen POST_12 und 24 aus dem nördlichen Teil des Gräberfeldes sind miteinander, aber nicht mit der Kernabstammung verwandt. Das zweite nicht-lokale Individuum innerhalb des Gräberfeldes (POST_99) war sehr reich ausgestattet und nur mit einer anderen nicht-lokalen Frau (OBKR_76) aus dem Gräberfeld Königsbrunn-Obere Kreuzstraße, Lkr. Augsburg (OBKR), biologisch verwandt.*

radiocarbon dates (Massy 2018). We have discovered in the southern part of the cemetery a group of three individuals who are also part of the larger pedigree (Figs. 3 and 8). The possibly non-local adult female POST_111 is not directly biologically related to POST_50, but shares descendants with him in POST_6 and 21. Therefore, this group represents a side branch of the family tree to the descendants of POST_50 and 35. POST_111 could plausibly be the partner of POST_50's brother or son by a woman other than POST_35. The subadult POST_1 is also distantly related to POST_50, by the 3rd to 5th degree, but an definite placement within the pedigree is not possible.



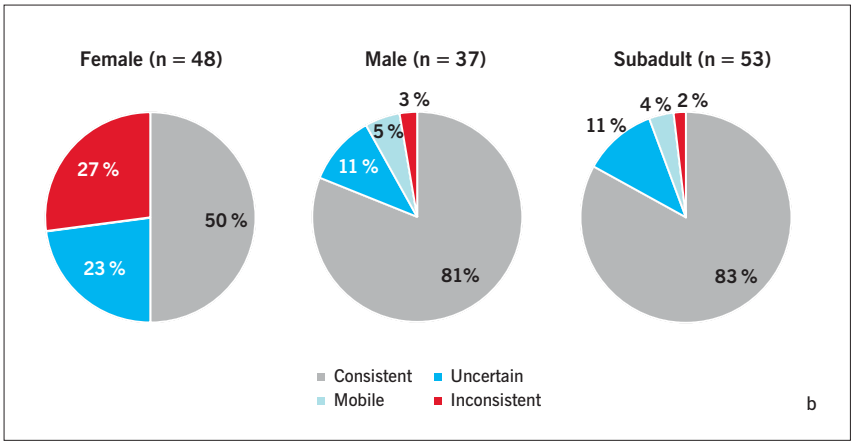


Fig. 9a–b Haunstetten-Postillionstraße. Results for stable isotope analysis in the study area. a Scatter plot of oxygen and strontium isotope ratios in tooth enamel grouped according to age, sex, and archaeological cultural association. b Consistency of strontium and oxygen isotope ratios with the baseline ranges of the study area, breakdown according to sex and age.

Abb. 9a–b *Haunstetten-Postillionstraße. Ergebnisse der stabilen Isotopenanalyse aus dem Arbeitsgebiet. a Streudiagramm von Sauerstoff- und Strontium-Isotopenverhältnissen im Zahnschmelz, gruppiert nach Alter, Geschlecht und archäologischer Kulturzugehörigkeit. b Konsistenz von Strontium- und Sauerstoff-Isotopenverhältnissen mit den Basislinienbereichen des Arbeitsgebietes, aufgeteilt nach Geschlecht und Alter.*

Markers of wealth or high status are concentrated with members of this »core pedigree«, an observation that can be generalized for the whole Lech Valley, where we see a correlation of the number of grave good types with the fraction of relatives found within the same site (Mittnik et al. 2019). Most notably, above-ground grave monuments that marked the buried as important individuals, such as burial mounds (POST_50, 111 and 137) and post alignments (POST_50, 111, 137 and 44), were only found for members of the core pedigree[5]. Similarly, daggers were only given to members of the core pedigree (POST_50, 140, 111, 6 and 21). That high-status markers are also found with subadults indicates that wealth and status were inherited by offspring from their parents and that their social status was inherited rather than acquired during their lifetime.

The burial of a woman at POST_111 is remarkable, as the individual has a burial mound, the grave site is richly furnished with items typical for high-status female burials, such as a neck ring, copper pins and perforated disks made of antler, but also contains a dagger, which is usually only reserved for high status male burials in the Straubing Culture (Fig. 3; Massy 2018). These markers could signify an outstanding role for this woman in the community.

We identified only one other related pair within the site: the children POST_12 and 24, buried in close proximity to each other on the northeastern fringe of the cemetery, are 2nd degree relatives, unconnected by biological relatedness to the core pedigree. As mentioned, these two individuals are also genetic outliers to the EBA Lech Valley population and more similar to the individuals of the Únětice Culture

5 POST_65 also has a post alignment, but could not be sampled because it did not contain any skeletal remains due to modern disturbances.

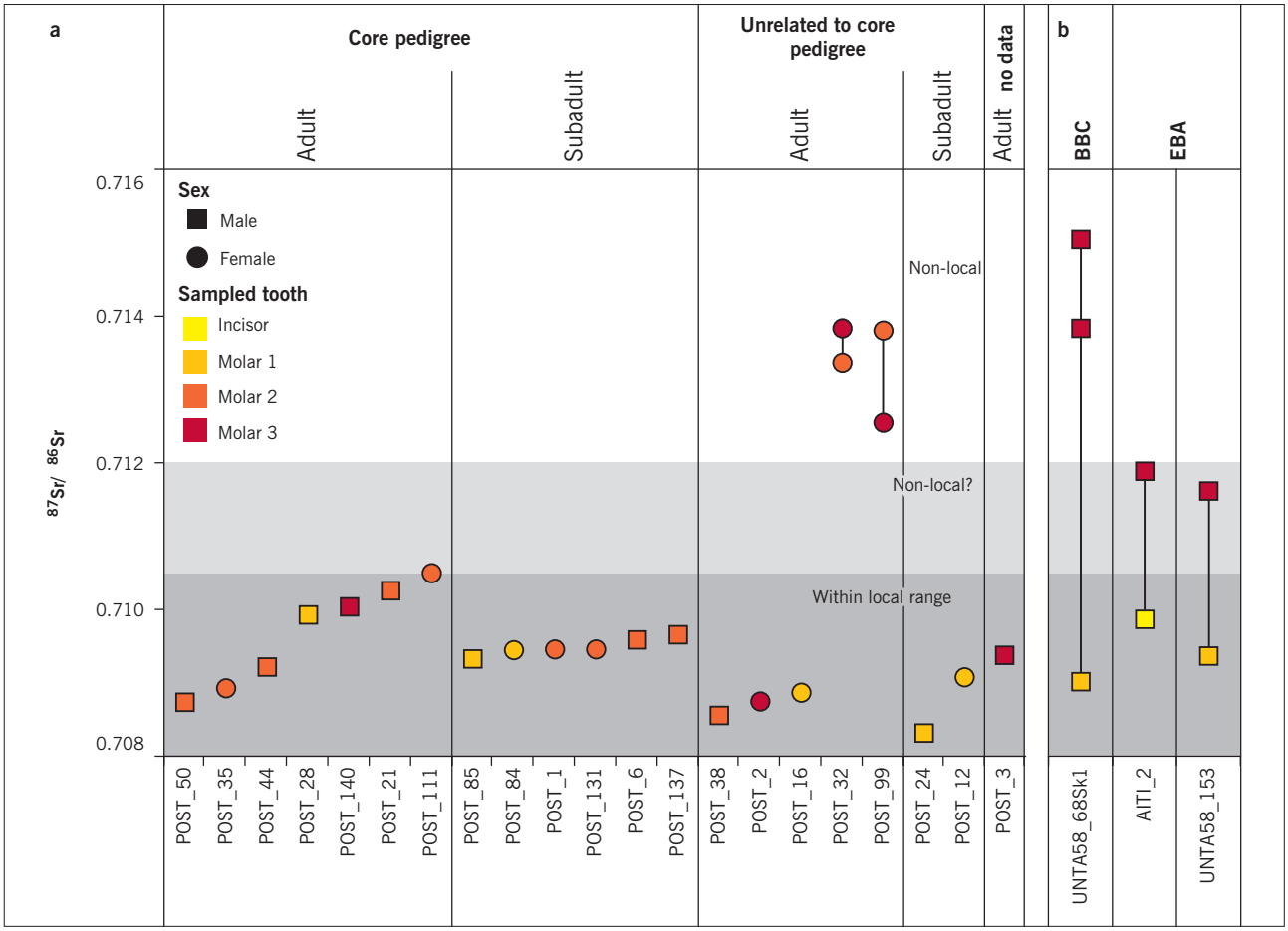


Fig. 10a–b Haunstetten-Postillionstraße (POST). Selected $^{87}Sr/^{86}Sr$ isotopic ratios measured from teeth. a Strontium isotope ratios for individuals from POST, grouping members and non-members of the core pedigree together, respectively. POST_32 and POST_99 fall within the non-local range of values for both the early-developing tooth and molar 3, which develops in late adolescence, indicating that they moved to the Lech Valley only after adolescence. b Three cases of males with notable $^{87}Sr/^{86}Sr$ value shifts between an early-developing tooth and molar 3, indicating residence outside of the local range during adolescence. BBC Bell Beaker Complex; EBA Early Bronze Age.

Abb. 10a–b *Haunstetten-Postillionstraße (POST). Ausgewählte $^{87}Sr/^{86}Sr$-Isotopenverhältnisse, gemessen im Zahn. a Strontium-Isotopenverhältnis von Individuen aus POST, wobei Mitglieder und Nichtmitglieder der Kernabstammung jeweils zusammengruppiert dargestellt sind. POST_32 und POST_99 fallen in den nicht-lokalen Bereich der Werte für sowohl den frühentwickelten Zahn als auch den Molar 3, der sich im späten Adoleszentenalter herausbildet, was darauf hindeutet, dass sie erst nach der Adoleszenz ins Lechtal gezogen sind. b Drei Fälle von Männern mit merklichen $^{87}Sr/^{86}Sr$-Werteverschiebungen zwischen dem frühentwickelten Zahn und Molar 3, was auf einen Aufenthalt außerhalb des lokalen Bereichs während des Erwachsenenalters hindeutet. BBC Glockenbecherkomplex; EBA Frühe Bronzezeit.*

(Fig. 5). Both individuals were radiocarbon dated to the earliest phase of the EBA (phase 1; Massy 2018) and are amongst the oldest burials in the cemetery. Their strontium values are consistent with the locally bioavailable strontium, and they are not accompanied by any metal grave goods[6]. We find such individuals (isotopically local, poorly furnished and biologically unrelated to the respective core pedigree) at each EBA site. This suggests the presence of lower-status individuals and even families who were differentiated from the members of the core pedigree, but like them, they made regular use of the same cemetery and thus were also residents of the local hamlet. This likely reflects social stratification in a society in which it was commonplace for individuals of different wealth and status to live together as part of complex households. We interpret this group of people as menial workers, or possibly even slaves; however, it remains uncertain whether religion, worldviews, or social institutions, such as »classes« or »castes«, contributed to the creation and maintenance of the status distinctions seen in Lech Valley farmsteads (Stockhammer/Massy 2023).

Patterns of mobility

Measurements of $^{87}Sr/^{86}Sr$ and $\delta^{18}Op$ values in dental enamel revealed stark sex- and age-based differences that are in concordance with a patrilocal society that practices female exogamy (Fig. 9a). 28 % of adult females showed isotope ratios that were clearly non-local, while 50 % were con-

6 POST_12 might have been furnished but could have been robbed in ancient times.

sistent with the local range. In contrast, only 3 % of adult males and 2 % of subadults had non-local values, while the majority (84 % and 82 %, respectively) were consistent with the local range (Fig. 9b; Mittnik et al. 2019). Notably, non-local women, like POST_32 and 99, were generally of high-status, but did not have any offspring or other relatives among the communities with which they were buried. Based on similarities of grave-items and isotope data, some individuals could have come from areas inhabited by the Únětice Culture, about 350 km away. Similar strontium isotope values in pairs of second and third molars from the same women suggest that these individuals went through residential changes during adolescence or later, after full formation of the enamel on their teeth (Fig. 10a). Therefore, their age and acquired knowledge might have situated them as influential agents of cultural transmission, more so than could be expected for younger children. Their role in the communities they were buried in is unexplained, but might be illuminated by future research revealing their relatives at other sites outside of the Lech Valley. Their grave good assemblages do, however, fit perfectly within the local grave furnishing of women of the Straubing Culture. Thus, we may assume that they were substantially integrated in the household communities of the Lech Valley, notwithstanding their foreign origin.

Three males had notable changes in the strontium ratios of their first molars, which were within the isotope range of the Lech Valley, to more radiogenic values in their third molars (Fig. 10b). This suggests that these individuals moved away from the study area during late childhood or adolescence and returned later in life. Practices, such as apprenticeship or fosterage, could account for this residence change (Stockhammer/Massy 2023).

Conclusion

The examination of family structures and social disparities is crucial to understand the social organization of ancient societies, and this includes biological factors such as genetic ancestry and relatedness[7]. Integrating archaeological, anthropological, genetic, and isotopic evidence from the EBA Lech Valley reveals that communities were organized in socially stratified, complex households in which wealth and status were likely inherited within a long-standing patrilineage that operated a farmstead. Strikingly, the patrilineal residence rule persisted during the transition from the Late Neolithic BBC to the EBA. Similar complex household forms are known historically millennia later in the *oikos* of Classic Greece and the Roman *familia*, both comprising the kin-related family and their slaves (Dixon 1992; Cox 1998). The practice of female exogamy was the norm in a society that was supra-regionally well-connected. In particular, long-distance mobility, evidenced in adult women and to a lesser extent in adolescent males, could have facilitated and reinforced the same networks that also served as the vectors for the trade of raw material and products, as well as the transfer of knowledge and culture.

7 E.g. Sanchez-Quinto et al. 2019; Schroeder et al. 2019; Fowler et al. 2022; Villalba-Mouco et al. 2022.

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Sources of figures

1 A. Mittnik; Tableau 2020.4.1, OpenStreetMap
2 K. Massy, adapted from Massy 2018, 110; Fig. 56; Pl. 143B2; 144A2
3 K. Massy, adapted from Massy 2018, pl. 33A; 34C; 36A
4 K. Massy, adapted from Stockhammer/Massy 2023, 174; Fig. 8.2
5–8 A. Mittnik
9 C. Knipper, adapted from Mittnik et al. 2019; Fig. S10; S11
10 A. Mittnik

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Appendix 1

Dating	mtDNA haplogroup assignment	Number of individuals assigned to haplogroup in period	Shared mtDNA lineage	mtDNA lineage sharing across period
CWC	V2	1		
	W3a1c	1		
BBC	H1	1		
	H15a1	1		
	H2a1	1		
	J1c	1		
	J1c1b1a	1		
	J1c2	1		
	J1c3g	1		
	K1a	2	UNTA58_68Sk2, UNTA58_67	
	K1a4a1	1	OBKR_2, OBKR_93, WEHR_1192SkA	yes
	T2b33	1		
	U4d3	1		
	U5a1a1	1		
	U5a2b3	2	HUGO_169Sk1, HUGO_169Sk2	
	U5b2a3	1		
	U5b2b3a	1		
	U5b2b4	2	HUGO_180Sk1, HUGO_180Sk2	
EBA	H	1		
	H1+152	2	AITI_35, AITI_37	
	H13a2b2a	2	WEHR_1415adult, WEHR_1415child	
	H1af	1		
	H1b1	1		
	H1ba	1		
	H1c	1		
	H1e	3	AITI_62A, AITI_62B	
	H1j2	1		
	H23	1		
	H27+16093	1	OBKR_85, OTTM_97	yes
	H2a1	1		
	H2a1a	2		
	H2a2a1	1		
	H3	1		
	H41a	2	POST_140, POST_35	
	H49	1		
	H4a1a1a	1		
	H5a4a1	1		
	H5d	1		
	H6a	1		
	H7a1	1		
	HV	1		
	HV0	1		
	I1a1	2	AITI_77A, AITI_77B	
	J1c2c2	3	AITI_36, AITI_70, AITI_72	
	J1c3	1		
	J1c3g	1		
	J1c8a	1		
	J2b1a	1		
	K1a	1		
	K1a1b1g	3	WEHR_1380, WEHR_1414, UNTA58_149	
	K1a2a	1		
EBA	K1a3	3	OBKR_80, OBKR_86	
	K1a3a	1		
	K1a4a1	3	OBKR_2, OBKR_93, WEHR_1192SkA	yes
	K1c1	1		
	K2a5	3	OBKR_67, POST_28, POST_47	
	R1a1a	1		
	T1a1	1		
	T2	1		
	T2a1b1a1b	1		
	T2c1d+152	2	POST_131, POST_137	
	T2f8a	1		
	U4a	1		
	U4a1a	4	AITI_119, AITI_120, AITI_86, AITI_87	
	U4a1b	1		
	U5a1a1+16362	1		
	U5a1i1	1		
	U5b1c2	3	UNTA58_150, UNTA58_151, UNTA58_152	
	U5b2a1a1	1		
	U5b2a2b	1		
	U5b2b2	1		
	U5b2b3a	1		
	V	3	WEHR_1474, WEHR_1564, WEHR_1586	
	V1a	1		
	V2	1		
	V7	3	OBKR_5, OBKR_6, OBKR_84	
	X2b	2	OBKR_81, OBKR_82	
	X2b+226	5	AITI_95, AITI_32, POST_85, POST_84, OTTM_151ind2	yes
MBA	H	1		
	H13a1a1	2	OTTM_151ind1, OTTM_152	
	H1e6	1		
	H27+16093	1	OBKR_85, OTTM_97	yes
	H3	1		
	H3ag	1		
	HV16	1		
	J1c3e1	1		
	J1c3g	1		
	J2b1a5	1		
	T2b21	1		
	T2b23	1		
	U5a1j	1		
	U5b1d1a	1		
	U5b3	1		
	V1b	1		
	X2b	2		
	X2b+226	1	AITI_95, AITI_32, POST_85, POST_84, OTTM_151ind2	yes

Appendix 2

Individual ID	Site name	Latitude	Longitude	LaborNr.	^{14}C Age	±	cal 2σ
HUGO_167	Augsburg – Hugo-Eckener-Straße	48.32852	10,898	MAMS 18912	3741	24	cal BC 2270–2039
HUGO_168	Augsburg – Hugo-Eckener-Straße	48.32852	10,898	MAMS 18913	3788	23	cal BC 2289–2141
HUGO_169Sk1	Augsburg – Hugo-Eckener-Straße	48.32852	10,898	MAMS 18914	3942	25	cal BC 2562–2345
HUGO_171	Augsburg – Hugo-Eckener-Straße	48.32852	10,898	MAMS 18917	3815	25	cal BC 2387–2146
HUGO_180Sk1	Augsburg – Hugo-Eckener-Straße	48.32852	10,898	MAMS 18918	3860	25	cal BC 2461–2210
HUGO_180Sk2	Augsburg – Hugo-Eckener-Straße	48.32852	10,898	MAMS 18919	3871	25	cal BC 2463–2235
HUGO_190	Augsburg – Hugo-Eckener-Straße	48.32852	10,898	MAMS 18921	3748	19	cal BC 2268–2046
POST_1	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18952	3583	28	cal BC 2024–1882
POST_12	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18956	3697	20	cal BC 2190–2028
POST_131	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18971	3635	20	cal BC 2120–1938
POST_140	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18973	3631	20	cal BC 2114–1926
POST_16	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18957	3612	20	cal BC 2029–1911
POST_2	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18953	3648	19	cal BC 2126–1948
POST_28	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18960	3608	20	cal BC 2027–1906
POST_32	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18961	3619	20	cal BC 2032–1916
POST_35	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18962	3621	20	cal BC 2033–1918
POST_44	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18964	3681	23	cal BC 2139–1979
POST_47	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18965	3662	24	cal BC 2134–1956
POST_50	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18966	3707	24	cal BC 2196–2029
POST_6	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18955	3574	19	cal BC 2009–1883
POST_85	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18968	3631	24	cal BC 2120–1921
POST_99	Haunstetten – Postillionstraße	48.29573	10,891	MAMS 18969	3641	25	cal BC 2130–1930
UNTA121_FK61	Haunstetten – Unterer Talweg 121	48.31181	10,890	MAMS 23728	4234	24	cal BC 2904–2711
UNTA58_68Sk1	Haunstetten – Unterer Talweg 58–62	48.31611	10,892				
UNTA58_68Sk2	Haunstetten – Unterer Talweg 58–62	48.31611	10,892	MAMS 18935	3910	20	cal BC 2470–2310
UNTA58_147	Haunstetten – Unterer Talweg 58–62	48.31611	10,892	MAMS 18937	3612	25	cal BC 2031–1900
UNTA58_149	Haunstetten – Unterer Talweg 58–62	48.31611	10,892	MAMS 18938	3597	24	cal BC 2023–1892
UNTA58_152	Haunstetten – Unterer Talweg 58–62	48.31611	10,892	MAMS 18942	3558	23	cal BC 2007–1779
UNTA58_153	Haunstetten – Unterer Talweg 58–62	48.31611	10,892	MAMS 18943	3553	24	cal BC 1971–1776
UNTA85_1336	Haunstetten – Unterer Talweg 85	48.31966	10,892	MAMS 18948	3893	22	cal BC 2465–2300
UNTA85_1343	Haunstetten – Unterer Talweg 85	48.31966	10,892	MAMS 18949	3819	24	cal BC 2397–2149
UNTA85_1412	Haunstetten – Unterer Talweg 85	48.31966	10,892	MAMS 18951	3602	25	cal BC 2025–1895
UNTA89_FK231	Haunstetten – Unterer Talweg 89	48.31707	10,889	MAMS 23729	4155	23	cal BC 2875–2635
AITI_119	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21594	3470	27	cal BC 1882–1696
AITI_120	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21595	3417	27	cal BC 1866–1638
AITI_2	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21562	3477	28	cal BC 1884–1698
AITI_32	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21565	3454	28	cal BC 1878–1691
AITI_33	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21566	3364	28	cal BC 1742–1562
AITI_36	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21568	3552	27	cal BC 2006–1774
AITI_37	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21569	3560	28	cal BC 2013–1777
AITI_40	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21570	3469	28	cal BC 1882–1695
AITI_43	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21571	3486	27	cal BC 1888–1701

Chronology	Age in years (anthropological determination)	Sex determined by archaeology	Sex determined by anthropology	Genetic Sex (M=Male, F=Female, U=Unknown)	SNPs of 1240K set used for relatedness analysis	SNPs of 1240K set used for population genetic analysis after quality filtering	mtDNA haplogroup assignment	Most derived reliable Y-chromosomal haplogroup assignment	Consistency with local isotopic signature
BBC	> 21	M	n/a	U	20164	n/a	U5b2b3a	n/a	consistent
BBC	> 25	F	n/a	F	933961	326173	H1	n/a (female)	uncertain
BBC	> 21	M	n/a	M	536670	62676	U5a2b3	G2-M3267	consistent
BBC	12–18	F	n/a	F	235885	19512	U5a1a1	n/a (female)	consistent
BBC	> 21	M	n/a	M	679566	77226	U5b2b4	R1b-M269, CTS623	uncertain
BBC	9–15	F	n/a	M	282333	36558	U5b2b4	F-P160	consistent
BBC	> 21	U	n/a	F	736279	97567	J1c3g	n/a (female)	inconsistent
EBA	4–6	F	U	F	47671	n/a	H2a1a	n/a (female)	consistent
EBA	7–11	U	U	F	81420	n/a	J1c3g	n/a (female)	consistent
EBA	6–10	F	U	F	46843	n/a	T2c1d+152	n/a (female)	consistent
EBA	> 25	(M)	U	M	314636	28835	H41a	R1b-P312	consistent
EBA	> 25	F	U	F	23398	n/a	T2f8a	n/a (female)	consistent
EBA	> 20	U	U	F	22955	n/a	n/a	n/a (female)	consistent
EBA	17–25	M	U	M	476398	476398	K2a5	R1b-P312	consistent
EBA	20–30	F	(F)	F	97406	n/a	T2	n/a (female)	inconsistent
EBA	35–55	F	U	F	827092	195171	H41a	n/a (female)	consistent
EBA	30–45	M	M	M	853686	853686	K1a3a	R1b-P312	consistent
EBA	20–30	M	U	M	60612	60612	K2a5	R1	consistent
EBA	30–35	M	(M)	M	770026	770026	T1a1	R1b-P312	consistent
EBA	14–16	M	U	M	933318	933318	U5a1a1+16362	R1b-P312	consistent
EBA	2–4	M	U	M	21939	n/a	X2b+226	R	consistent
EBA	20–30	F	U	F	991199	428612	K1a4a1	n/a (female)	inconsistent
CWC		M	M	M	20552	n/a	V2	n/a	consistent
BBC	> 21	M	n/a	M	555552	555552	J1c	G2a-PF3170	inconsistent
BBC	> 21	F	n/a	F	805134	182894	K1a	n/a (female)	consistent
EBA	35–55	F	n/a	F	177067	13319	H2a1	n/a (female)	inconsistent
EBA	9–15	M	n/a	M	26755	n/a	K1a1b1g	BT-M9242	consistent
EBA	7–12	F	n/a	F	72129	n/a	U5b1c2	n/a (female)	consistent
EBA	12–21	M	n/a	M	197341	197341	R1a1a	R1b-L23	uncertain
BBC	> 21	M	n/a	F	123823	n/a	H2a1	n/a (female)	consistent
BBC	> 21	F	n/a	M	794981	794981	J1c2	R1b-P312	consistent
EBA	3–5	(M)	n/a	M	299953	299953	H	R1b-CTS3575, L773, PF6434,PF6497	consistent
CWC		M	M	M	33712	n/a	W3a1c	n/a	inconsistent
EBA	13–17	M	(M)	M	534416	534416	U4a1a	R1b-P310	consistent
EBA	ca. 30	M	M	M	506947	506947	U4a1a	R1b-P312	consistent
EBA	50–60	M	M	M	745241	745241	H6a	R1b-P312	uncertain
EBA	14–25	F	(F)	F	32296	n/a	X2b+226	n/a (female)	inconsistent
EBA	5–8	M	U	M	56287	n/a	H2a2a1	F-P159	uncertain
EBA	20–23	M	M	M	20990	20990	J1c2c2	BT-M9138	consistent
EBA	5–6	F	U	F	55773	n/a	H1+152	n/a (female)	uncertain
EBA	21–45	M	M	M	200941	200941	T2a1b1a1b	R1b-L500	uncertain
EBA	ca. 30	M	M	M	853589	853589	X2b+226	R1b-P312	consistent

Individual ID	Site name	Latitude	Longitude	LaborNr.	^{14}C Age	±	cal 2σ
AITI_5	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21564	3493	28	cal BC 1892–1704
AITI_50	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21572	3505	33	cal BC 1920–1705
AITI_51Sk2	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21573	3531	34	cal BC 1946–1754
AITI_55	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21575	3504	33	cal BC 1919–1705
AITI_62A	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21576	3459	34	cal BC 1881–1691
AITI_62B	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21577	3478	33	cal BC 1889–1695
AITI_65adult	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21578	3456	34	cal BC 1881–1690
AITI_66	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21580	3489	34	cal BC 1899–1696
AITI_70	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21582	3594	37	cal BC 2116–1785
AITI_72	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21583	3508	34	cal BC 1926–1705
AITI_77A	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21584	3548	34	cal BC 2008–1769
AITI_77B	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21585	3469	35	cal BC 1885–1693
AITI_78	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21586	3474	34	cal BC 1887–1694
AITI_86	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21587	3480	34	cal BC 1891–1694
AITI_87	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21588	3433	28	cal BC 1876–1660
AITI_92	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21590	3489	28	cal BC 1889–1701
AITI_95	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21591	3422	28	cal BC 1870–1640
AITI_98	Kleinaitingen – Gewerbegebiet Nord	48.22281	10,845	MAMS 21592	3370	27	cal BC 1742–1613
AMPA_1	Königsbrunn – Ampack	48.25886	10,873	MAMS 18887	3924	23	cal BC 2476–2310
OBKR_117	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18911	3581	23	cal BC 2019–1883
OBKR_2	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18888	3599	22	cal BC 2023–1894
OBKR_47	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18894	3671	22	cal BC 2136–1977
OBKR_50	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18895	3623	23	cal BC 2112–1912
OBKR_6	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18890	3611	23	cal BC 2029–1903
OBKR_66	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18896	3609	22	cal BC 2028–1903
OBKR_67	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18897	3599	22	cal BC 2023–1894
OBKR_73	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18898	3603	23	cal BC 2024–1897
OBKR_76	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18899	3567	23	cal BC 2013–1785
OBKR_80	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18901	3664	24	cal BC 2134–1959
OBKR_81	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18902	3602	24	cal BC 2024–1896
OBKR_82	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18903	3600	24	cal BC 2023–1894
OBKR_84	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18905	3575	25	cal BC 2021–1830
OBKR_86	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18907	3615	24	cal BC 2032–1901

Chronology	Age in years (anthropological determination)	Sex determined by archaeology	Sex determined by anthropology	Genetic Sex (M=Male, F=Female, U=Unknown)	SNPs of 1240K set used for relatedness analysis	SNPs of 1240K set used for population genetic analysis after quality filtering	mtDNA haplogroup assignment	Most derived reliable Y-chromosomal haplogroup assignment	Consistency with local isotopic signature
EBA	ca. 25	F	F	F	131559	n/a	H5d	n/a (female)	consistent
EBA	2–4	(M)	(M)	M	320590	320590	J1c3	R1b-L11	consistent
EBA	21–23	U	M	M	22615	n/a	H7a1	n/a	consistent
EBA	55–65	M	M	M	38146	n/a	K1c1	n/a	uncertain
EBA	11–12	M	U	M	17758	n/a	H1e	n/a	uncertain
EBA	7–9	M	U	M	28277	n/a	H1e	n/a	consistent
EBA	21–25	F	F	F	524061	71181	H1af	n/a (female)	consistent
EBA	30–40	F	F	F	721756	176496	U5b2b3a	n/a (female)	inconsistent
EBA	20–21	M	M	M	372392	372392	J1c2c2	R1b-P312	consistent
EBA	35–40	M	M	M	701339	701339	J1c2c2	R1b-P312	consistent
EBA	3–4	F	(F)	F	255749	25350	I1a1	n/a (female)	consistent
EBA	3–4	F	(F)	F	309480	25494	I1a1	n/a (female)	consistent
EBA	30–60	U	M	M	659930	659930	H3	R1b-P312	uncertain
EBA	4–6	U	U	M	37702	n/a	U4a1a	n/a	consistent
EBA	30–40	F	F	F	220561	29564	U4a1a	n/a (female)	consistent
EBA	21–23	F	F	F	475755	84076	H5a4a1	n/a (female)	consistent
EBA	30–45	F	F	F	629248	136157	X2b+226	n/a (female)	consistent
EBA	5–7	M	(M)	M	329102	329102	H49	R1b-P312	uncertain
BBC	> 21	M	M	M	768956	87767	T2b33	n/a	consistent
EBA	21–24	U	M	M	561240	69931	U4a1b	I-CTS5650, CTS48, FI2	consistent
EBA	25–30	F	F	F	365032	31240	K1a4a1	n/a (female)	consistent
EBA	25–35	F	(M)	M	53435	n/a	J2b1a	n/a	consistent
EBA	25–30	F	F	F	683096	135818	HV0	n/a (female)	inconsistent
EBA	15–18	F	U	F	39654	n/a	V7	n/a (female)	consistent
EBA	40–60	F	F	F	355759	25529	U4a	n/a (female)	inconsistent
EBA	40–60	M	M	M	338941	37580	K2a5	R1b-P312	consistent
EBA	20–25	(F)	F	F	103942	n/a	U5b2a1a1	n/a (female)	uncertain
EBA	25–30	F	F	F	23910	n/a	K1a	n/a (female)	inconsistent
EBA	30–40	M	M	M	718030	718030	K1a3	R1b-P312	consistent
EBA	ca. 4	F	U	F	63138	n/a	X2b	n/a (female)	consistent
EBA	ca. 3	F	(F)	F	17462	n/a	X2b	n/a (female)	consistent
EBA	ca. 1–2	F	U	F	23817	n/a	V7	n/a (female)	consistent
EBA	30–40	M	M	M	463560	50295	K1a3	R1b-P312	consistent

Individual ID	Site name	Latitude	Longitude	LaborNr.	^{14}C Age	±	cal 2σ
OBKR_93	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18908	3621	23	cal BC 2111–1907
OBKR_95	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18909	3608	23	cal BC 2027–1901
OBKR_96	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18910	3567	23	cal BC 2013–1784
OBKR_9A	Königsbrunn – Obere Kreuzstraße (Baugebiet 110)	48.26656	10,879	MAMS 18891	3596	22	cal BC 2022–1892
OTTM_109	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21550	3360	37	cal BC 1743–1534
OTTM_141	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21552	3297	36	cal BC 1681–1499
OTTM_142	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21554	3309	37	cal BC 1682–1504
OTTM_151ind1	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21555	3370	38	cal BC 1749–1535
OTTM_151ind2	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21556	3288	27	cal BC 1623–1504
OTTM_152	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21557	3295	28	cal BC 1630–1505
OTTM_154	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21558	3449	72	cal BC 1949–1563
OTTM_156	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21559	3241	28	cal BC 1609–1442
OTTM_165	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21561	3349	29	cal BC 1735–1535
OTTM_81	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21542	3277	33	cal BC 1630–1459
OTTM_84	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21543	3283	32	cal BC 1636–1465
OTTM_87	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21544	3324	34	cal BC 1687–1517
OTTM_91	Oberottmarshausen – Kiesgrube Lauter	48.22519	10,850	MAMS 21545	3075	41	cal BC 1426–1230
WEHR_1192SkA	Wehringen – Hochfeld	48.25283	10,809	MAMS 18922	3810	19	cal BC 2331–2150
WEHR_1192SkB	Wehringen – Hochfeld	48.25283	10,809	MAMS 18923	3523	18	cal BC 1918–1772
WEHR_1193	Wehringen – Hochfeld	48.25283	10,809	MAMS 18924	3544	19	cal BC 1945–1777
WEHR_1414	Wehringen – Hochfeld	48.25283	10,809	MAMS 18927	3601	19	cal BC 2022–1897
WEHR_1415adult	Wehringen – Hochfeld	48.25283	10,809	MAMS 18929	3573	19	cal BC 2008–1883
WEHR_1415child	Wehringen – Hochfeld	48.25283	10,809	MAMS 18928	3596	19	cal BC 2021–1893
WEHR_1474	Wehringen – Hochfeld	48.25283	10,809	MAMS 18930	3614	19	cal BC 2029–1916
WEHR_1564	Wehringen – Hochfeld	48.25283	10,809	MAMS 18931	3594	19	cal BC 2020–1892
WEHR_1586	Wehringen – Hochfeld	48.25283	10,809	MAMS 18932	3550	19	cal BC 1951–1779

Chronology	Age in years (anthropological determination)	Sex determined by archaeology	Sex determined by anthropology	Genetic Sex (M=Male, F=Female, U=Unknown)	SNPs of 1240K set used for relatedness analysis	SNPs of 1240K set used for population genetic analysis after quality filtering	mtDNA haplogroup assignment	Most derived reliable Y-chromosomal haplogroup assignment	Consistency with local isotopic signature
EBA	18–23	F	F	F	221774	19117	K1a4a1	n/a (female)	consistent
EBA	13–15	F	(F)	F	28989	n/a	V1a	n/a (female)	consistent
EBA	30–40	F	F	F	104670	n/a	H1j2	n/a (female)	consistent
EBA	25–30	F	F	F	587323	72499	K1a2a	n/a (female)	uncertain
MBA	7–19	U	U	M	22775	n/a	X2b	n/a	consistent
MBA	30–50	U	(F)	F	39028	11728	H3ag	n/a (female)	consistent
MBA	17–21	F	F	F	285671	55652	U5b1d1a	n/a (female)	consistent
MBA	2–3	U	U	F	387779	41835	H13a1a1	n/a (female)	consistent
MBA	20–50	U	U	F	609841	220702	X2b+226	n/a (female)	uncertain
MBA	2.5–4	U	U	M	52779	n/a	H13a1a1	n/a	consistent
MBA	2.5–4	U	U	M	41091	41091	H3	CT-M5757	consistent
MBA	15–18	U	U	M	135811	135811	V1b	R/K2b2a2-P227	uncertain
MBA	20–40	U	F	F	131014	17727	H	n/a (female)	consistent
MBA	3–4	U	n/a	F	37195	n/a	T2b21	n/a (female)	consistent
MBA	30–40	U	n/a	F	171214	13913	U5b3	n/a (female)	consistent
MBA	30–50	F	U	F	376731	65045	HV16	n/a (female)	uncertain
MBA	50–70	U	U	F	63982	n/a	J1c3g	n/a (female)	consistent
BBC	> 21	M	n/a	M	936299	936299	K1a4a1	R1b-P312	consistent
EBA	> 21	F	n/a	F	249376	25647	U5b2a2b	n/a (female)	uncertain
EBA	> 21	F	n/a	F	69513	n/a	H4a1a1a	n/a (female)	inconsistent
EBA	15–18	M	n/a	U	182178	n/a	K1a1b1g	BT-M9214	consistent
EBA	> 21	F	n/a	F	878099	209150	H13a2b2a	n/a (female)	consistent
EBA	0–6	U	n/a	M	529351	529351	H13a2b2a	R1b-L151	consistent
EBA	> 21	M	n/a	M	499656	65029	V	CT-M5681	consistent
EBA	> 21	M	n/a	M	308916	35242	V	CT-M5711, M5782	consistent
EBA	> 21	F	n/a	F	952940	379408	V	n/a (female)	consistent

Tracing mother-child relations in Austrian Early Bronze Age communities through mitochondrial DNA

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Zusammenfassung

Mutter-Kind-Beziehungen in österreichischen Gemeinschaften der frühen Bronzezeit im Spiegel mitochondrialer DNA

Die Kombination aus archäologischer Kontextanalyse und antiken genetischen Daten liefert wichtige Einblicke in das soziale Gefüge der Bronzezeit, einschließlich Verwandtschaft, persönliche und emotionale Verbindungen sowie den sozialen Status von Einzelpersonen innerhalb von Gemeinschaften. In diesem Beitrag untersuchen wir Mutter-Kind- und andere Familienbeziehungen in frühbronzezeitlichen Doppel- und Mehrfachbestattungen aus Niederösterreich (ca. 2200–1600 v. Chr.). Soziale und emotionale Verbindungen können aus der Art und Weise abgeleitet werden, wie Körper zueinander in Beziehung gesetzt, nach dem Tod gehandhabt und behandelt wurden sowie aus den in den Gräbern platzierten Gegenständen, die der Nahrungsaufnahme und Pflege dienen sollten. In sechs von elf untersuchten archäologischen Kontexten wurde eine enge genetische Verwandtschaft durch mitochondriale DNA festgestellt. Frauen und Kinder, die gemeinsam begraben wurden, waren jedoch nicht unbedingt verwandt. Dies könnte darauf hindeuten, dass die Ideologie von Mutterschaft nicht ausschließlich mit biologischen Müttern in Verbindung gebracht wurde und Kinderbetreuung gemeinschaftlich organisiert war.

Summary

The combination of archaeological context analysis and ancient genetic data provides important insights into the social fabric of the Bronze Age, including kinship, personal and emotive connections, and the social status of individuals within communities. In this contribution, we investigate mother-child and other family relationships in Early Bronze Age double and multiple burials from Lower Austria (c. 2200–1600 BC). Social and emotional links may be inferred from the ways bodies were placed in relation to each other, handled and treated after death, and through objects placed in the graves intended for feeding and care. A close genetic relationship through mitochondrial DNA was found in six out of 11 investigated archaeological contexts. Women and children buried together, however, were not necessarily related. This might suggest that the ideology of mothering was not exclusively associated with biological mothers and caregiving was organised communally.

Introduction

In recent years, the interest in exploring motherhood in history and prehistory has increased, with cultural-historical or social archaeological approaches[1], as well as bio-archaeological, evolutionary, isotopic and genetic approaches to motherhood on the rise (Gowland/Halcrow 2020; Hassett 2022; Rebay-Salisbury et al. 2018). In addition to the biological framework of sexual reproduction, motherhood includes a range of cultural choices and practices that are fruitful to explore for a better understanding of motherhood in the past.

Whereas researching motherhood tackles both the biological aspect of pregnancy, parturition and breastfeeding and the ideological and social aspects of childcare embedded in the social framework (Rich 1995), mothering is a term used for the childcare practices associated with mothers. Mothers traditionally, historically, and still today predominantly perform childcare, whereas fathers, older siblings and grandparents may help or substitute at times; childcare is thus strongly associated with women's social roles (Spencer-Wood/Seifert in press).

To what extent biological relatedness underpins mother-child relations varies between cultures and has yet to be explored for Central European Bronze Age communities. Kinship in general is comprised of a web of relations through a range of social mechanisms, including descent and marriage, as well as adoption and friendship (Chapais 2008; Stone 2009). The importance of genetic relatedness to the construction of kinship is hotly debated amongst anthropologists[2], and equally important to explore archaeologically (Johnson/Paul 2016).

Cemeteries, or other archaeological contexts in which individuals are buried together in close bodily contact, are particularly well suited for an analysis of kinship. Regardless of

1 Cooper/Phelan 2017; Hackworth Petersen/Salzman-Mitchell 2012; Myers 2017; O'Reilly 2014; Romero/López 2018.

2 E.g. Carsten 2003; Sahlins 2011; 2011a; Schneider 1984; Shapiro 2018.

the cause of death, they imply relationships of kinship, familiarity or affection between the individuals. A woman buried with a child is often assumed to be the mother – be it biological or social – but infants may also be included in graves for reasons other than relatedness, e.g., similar time of death, convenience, or protection. Testing the relationship between women and children buried together may reveal if, and to what extent, social concepts of motherhood implied a genetic link and whether childcare was organised individually or communally.

Mitochondrial DNA analysis

Within the framework of the project ›The value of mothers to society: responses to motherhood and child-rearing practices in prehistoric Europe‹, we applied mtDNA analysis to 28 individuals from 11 selected Early Bronze Age (c. 2200–1600 BC) burial contexts in Lower Austria to clarify their genetic relationship. Since mtDNA is normally inherited from the mother only, it is particularly suited to investigate mother-child relationships – a mismatch rules out a maternal relationship. In addition, mtDNA is present in multiple copies per cell, which makes it more likely to produce results in small and degraded samples (Parson et al. 2018; Rott et al. 2018).

Minimising damage to the collections curated by the Anthropological Department of the Natural History Museum in Vienna was the guiding principle in our sampling strategy. Originally, we aimed at obtaining two 100–150 mg samples per individual to optimise the chances of yielding DNA suitable for analysis. From 2015–2017 we primarily targeted petrous bone, femur and teeth in individuals from Franzhausen, Unterhautzenthal and Zwingendorf. Targeting the osseous inner ear inside the petrous pyramid appears to return the highest endogenous aDNA yields (Pinhasi et al. 2015), but it is present only twice in the body, and then only when recovery of the whole body was possible.

After running the first batch of analysis, it became clear that samples from the pulp area of deciduous and permanent teeth are best suited. For the second batch of samples from Schleinbach, therefore, we selected only one tooth per individual. For those solid tissue samples (teeth and bones) that contained enough starting material, two series of analyses based on milled and drilled powder were performed. Otherwise, only one of the methods was applied. The analysis followed the protocol described in Parson et al. (2018).

In brief, the surfaces of the remains were initially mechanically treated using a Dremel tool and subsequently chemically cleaned using a 5 % bleach solution. The cleaned surfaces were then drilled with a dental drill at low speed to prevent overheating and/or milling was performed in a Retsch grinding mill MM400 (Retsch GmbH, Haan, North-Rhine Westphalia, Germany). A total of 50 mg of the resulting powder was lysed and DNA was extracted following the modified Dabney protocol described in Xavier et al. (2021). MtDNA-specific quantitation was performed using *SD quants* (Xavier et al. 2019) that co-amplify a nuclear target (70 bp), two differently sized mtDNA targets (69 and 143 bp) and an internal PCR control to test for inhibition in a tetraplex real-time PCR quantitation system. Those samples that provided the highest mtDNA quantities were further subjected to mtDNA sequence library preparation using the IonXpress Fragment Library Kit (ThermoFisher Scientific, Waltham, Massachusetts, USA; *TFS*) according to the protocol described in Eduardoff et al. (2017). Massively Parallel Sequencing was performed on an Ion S5 (*TFS*) with automated template preparation using the IonChef pipeline (*TFS*) according to the manufacturer's protocol. Raw data were analysed as described in Strobl et al. (2019). MtDNA consensus haplotypes were aligned relative to their known phylogenetic neighbours following the concept outlined in Bandelt/Parson (2008) and reported relative to the revised Cambridge Reference Sequence (Andrews et al. 1999), as outlined in Parson et al. (2014). Polynucleotide stretches were ignored for interpreting the haplotypes. Haplogroups were estimated using SAM2 (Huber et al. 2018) based on Phylotree (mt) haplogroup nomenclature (van Oven/Kayser 2009), using the haplogrouping function in EMPOP (Parson/Dur 2007).

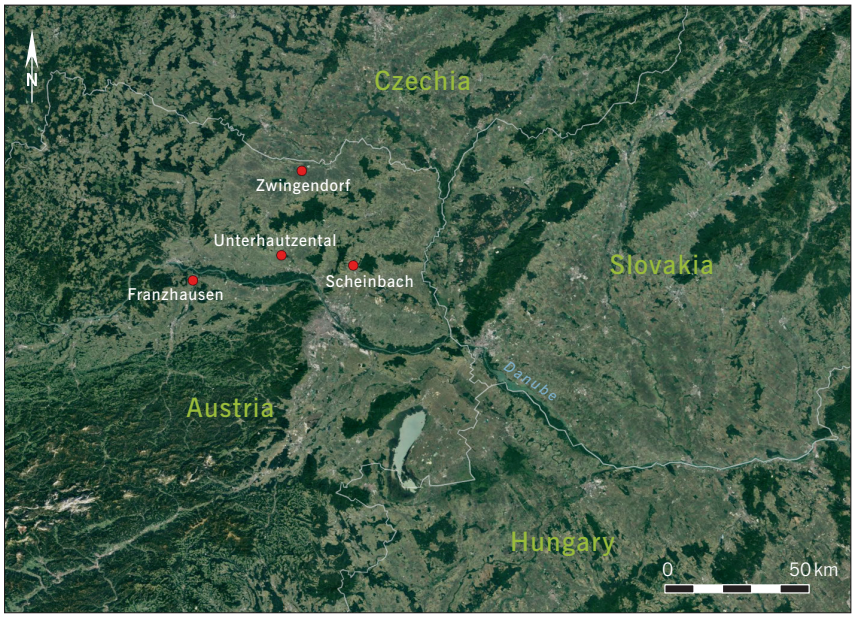


Fig. 1 Map of the study region with the Early Bronze Age sites of Franzhausen, Schleinbach, Unterhautzenthal and Zwingendorf in today's Austria.

Abb. 1 *Karte des Untersuchungsgebiets mit den frühbronzezeitlichen Fundstellen Franzhausen, Schleinbach, Unterhautzenthal und Zwingendorf im heutigen Österreich.*

Site	Context	Individual	NHM AA Inv. Nr.	Grinding Method	Quant.		
					nDNA (70 bp) pg/µl	143 bp mtGE/µl	69 bp mtGE/µl
Zwingendorf							
1	Grave 8	8A	–	drill	423.0	214.6	1556.3
2		8B	–	mill	0.9	216.4	2101.2
Schleinbach							
3	Grave 30/31	30	27635	mill	0.3	2.9	147.7
4		31	27636	mill	0.8	21.6	305.1
5	Pit 60	60	27642	mill	1.0	14.0	98.4
6		60A	27643	drill	0.2	5.4	188.8
7		60B	27644	drill	0.2	16.8	197.0
8		60C	27645	drill	0.1	4.6	102.9
Franzhausen							
9	Grave 599	599A	24076	drill	1.3	18.2	316.8
10		599B	24077	drill	10.7	4.6	166.0
11		599C	24078	drill	46.8	31.2	651.9
12	Grave 860	860/4	24183	drill	0.2	358.0	6346.9
13		860/1+2	24182	drill	0.4	0.7	20.5
14		860/3	24182	drill	0.2	69.9	1352.7
Unterhautzenthal							
15	Pit 27	27A	24904	drill	0.4	473.6	2634.0
16		27B	24905	mill	1.3	113.9	1101.7
17	Grave 38	38A	24908	mill	0.2	NA	4.3
18		38B	24908	drill	0.3	0.5	1.4
19	Grave 95	95	24921	mill	1.5	7.3	55.5
20		95A	24922	mill	0.3	2.8	46.3
21		95B	24923	mill	0.8	1.9	9.7
22	Grave 103	103A	24929	mill	8.3	9.5	171.8
23		103B	24929	mill	0.4	0.3	0.9
24	Grave 109	109A	24933	mill	0.6	0.5	8.2
25		109B	24933	mill	11.5	178.0	1124.3
26	Grave 122	122A	24937	drill	0.9	1.1	6.7
27		122B	24938	mill	2.2	2.1	41.3
28		122C	24938	mill	0.4	0.2	0.5

Tab. 1 Summary of nuclear DNA (70 bp target) and mitochondrial DNA (143 and 69 bp targets) quantitation results.

Tab. 1 *Zusammenfassung der Quantifizierungsergebnisse für Kern-DNA (70-bp-Fragment) und mitochondriale DNA (143- und 69-bp-Fragmente).*

DNA preservation

The solid tissue samples were subjected to both milling and drilling methods, depending on the amount and nature of the available tissue (Tab. 1). Nuclear DNA quantities (70 bp target) were found between 0.2 and 423 pg/µl; mtDNA quantities ranged between 0.4 and 473 copies/µl and 0.5 and 6346 copies/µl for the 143 bp and the 69 bp target, respectively. The extracts contained roughly 10–20 times more of the 69 bp mtDNA template compared to the 143 bp mtDNA target, which reveals and confirms the expected degraded state of the mtDNA extracted from the ancient tissues. This result suggested the application of capture-based mtDNA typing (Primer Extension Capture, *PEC*; see Eduardoff et al. 2017) instead of PCR-based schemes that require larger DNA templates. Samples 18, 23 and 28 were not further sequenced due to the low mtDNA quantities.

We were able to obtain interpretable mtDNA results from 34 of 46 samples (74 %) and 25 of 28 (89 %) tested individuals (Tab. 2). DNA preservation was found to be highest in the pulp cavity of the teeth (all successful) and lower for petrous bone (62 %) and femur (60 %). We only took two samples from ribs and one each from a humerus and tibia. The humerus appeared green, apparently due to copper salts from bronze

Site	Context	Individual	Age	Sex	Haplogroup	Haplotype	EMPOP Query (reduced to CR)*
Zwingendorf							
1	Grave 8	8A	14–16	—	K1a4b[1]	73G 263G 280G 315.1C 497T 524.1A 524.2C 750G 3480G 8860G 11299C 11719A 12308G 12372A 13590A 14167T 14766T 14798C 15326G 16093C 16224C 16311C 16519C	none in 38361/15782
2		8B	4	—	K1a4b[2]	73G 263G 280G 315.1C 497T 524.1A 524.2C 750G 1189C 1438G 1811G 2706G 3480G 4769G 6026A 6899A 7028T 8029T 8860G 9055A 9448G 9698C 10398G 10550G 11299C 11467G 11485C 11719A 12308G 12372A 13590A 14167T 14766T 14798C 15326G 16093C 16224C 16311C 16519C	none in 38361/15782
Schleinbach							
3	Grave 30/31	30	30–35	♂	H+152[3]	152C 263G 315.1C 750G (4769G) 8860G 15326G 16519C	162 in 38361/ 129 in 15782
4		31	27–30	♂	H+152[4]	152C 263G 315.1C 750G 4769G 8860G 15326G 16519C	162 in 38361/ 129 in 15782
5	Pit 60	60	30–35	♂	H2a1[5]	263G 315.1C 750G 8860G 16354T	30 in 38361/ 23 in 15782
6		60A	8–9	♂**	U2e3 (U2e3a)[6]	73G 152C 217C 263G 315.1C 394T 508G 524.1A 524.2C 750G 1811G 3170A 4769G 5390G 5426C 8860G 10876G 11719A 12308G 12372A 13020C 13734C 14180C 14766T 15326G 15721C 15907G 16051G 16129C (16182M) 16183C 16189C 16260T 16356C 16362C 16519C	none in 38361/15782
7		60B	12	♀**	J1c2[7]	73G 185A 188G 228A 263G 295T 315.1C 462T 489C 750G 14766T 14798C 16069T 16126C 16519C	52 in 38361/ 40 in 15782
8		60C	3–4	♀**	U2e3 (U2e3a)[8]	73G 152C 217C 263G 315.1C 394T 508G 524.1A 524.2C 750G 5390G 5426C (10876G) (11467G) (12372A) 13734C 15907G 16051G 16129C (16182M) 16183C 16189C 16260T 16356C 16362C 16519C	none in 38361/15782
Franzhausen							
9	Grave 599	599A	20–25	♂	T2e[9]	73G 150T 195C 263G 315.1C 709A 750G 1888A 2706G 4216C 4769G 4917G 8697A 8860G 10463C 11251G 11719A 11812G 13368A 14233G 14766T 14905A 15326G 15452A 15607G 15928A 16126C 16153A 16294T 16296T 16519C	1 in 38361/ 1 in 15782
10		599B	14–16	—	R1[10]	54C 73G 146C 150T 152C 189G 195C 241G 263G 315.1C 750G 15940C 16235G 16311C 16519C	none in 38361/15782
11		599C	12–14	—	H[11]	263G 315.1C 750G 16519C	791 in 38361/ 630 in 15782
12	Grave 860	860/4	3–5	♀**	K1a4a1i[12]	73G 263G 309.1C 315.1C 497T 524.1A 524.2C 573.1C 750G 9698C 11299C 12308G 12372A 13740C 14167T 14766T 14798C 15880G 16224C 16311C 16519C	15 in 38361/ 12 in 15782
13		860/1+2	35–50	♀	U5a1d2a[13]	73G 195C 263G 315.1C 573.1C 750G 16145A 16189C 16192T 16256T 16270T 16399G	5 in 38361/ 5 in 15782
14		860/3	7–8	—	U5a1d2a[14]	73G 195C 263G 309.1C 315.1C 573.1C 750G 8860G 12372A 13617C 14766T 14793G 16145A 16189C 16192T 16256T 16270T 16399G	5 in 38361/ 5 in 15782
Unterhautzenthal							
15	Pit 27	27A	2	—	H5a1[15]	263G 315.1C 456T 523del 524del 750G 4769G 4336C 8860G 15326G 15833T 16129A 16183C 16189C 16304C	none in 38361/15782

Site	Context	Individual	Age	Sex	Haplogroup	Haplotype	EMPOP Query (reduced to CR)*
16		27B	6	—	H5a1[16]	263G 315.1C 456T 523del 524del 750G 4336C 4769G 8860G 15326G 15833T 16129A 16183C 16189C 16304C	none in 38361/15782
17	Grave 38	38A	14–15	—	T2e[17]	263G 315.1C 709A 750G 15928A 16126C 16153A 16519C	1 in 38361/ 0 in 15782
18		38B	0–0.3	—		NA	
19	Grave 95	95	35–45	♀	HV[18]	150T 152C 263G 315.1C 750G 8860G 16222T 16519C	none in 38361/15782
20		95A	3–4	♀**	T2[19]	73G 207A 263G 315.1C 709A 750G 8697A 15928A 16126C 16294T 16296T 16519C	none in 38361/15782
21		95B	4–5	♂**	T2[20]	73G 207A 263G 315.1C 709A 750G 794C 15928A 16126C 16294T 16296T 16519C	none in 38361/15782
22	Grave 103	103A	16–20	♀	U5b[21]	73G 150T 263G 315.1C 750G 12308G 12372A 14182C 15326G 16147T 16189C 16270T	1 in 38361/ 1 in 15782
23		103B	2.5–3.5	—		NA	
24	Grave 109	109A	40–60	♀	U2e1[22]	73G 152C 217C 263G 315.1C 340T 508G 750G 15907G 16051G 16129C 16189C 16362C 16519C	none in 38361/15782
25		109B	0–0.2	—	J1c1[23]	73G 185A 228A 263G 295T 315.1C 462T 482C 489C 750G 3394C 4216C 4769G 8860G 11251G 11719A 13708A 14766T 14798C 15326G 15452A 16069T 16126C 16352C	none in 38361/15782
26	Grave 122	122A	35–40	♂	I2'3[24]	73G 152C 199C 204C 207A 250C 263G 315.1C 750G 15924G 16129A 16223T 16391A 16519C	22 in 38361/ 18 in 15782
27		122B	17–20	♀	T1a1'3[25]	73G 152C 195C 263G 315.1C 709A 750G 15928A 16126C 16163G 16186T 16189C 16294T 16519C	136 in 38361/ 113 in 15782
28		122C	0.25–0.5	—		NA	

1 1–982 3434–3575 5059–5541 8126–9007 10731–11402 11712–12477 13499–14873 15285–16569
2 1–16569
3 1–907 1652–2100 3392–3924 3967–4524 4592–4795 4848–5670 5854–6005 6351–6624 7268–7982 8157–9263 9364–9696 9777–9916 10734–11367 11485–12676 12787–12986 13027–14946 15262–15732 15764–16569
4 1–930 1694–1757 1816–1950 2051–2374 3419–3604 3765–3912 4123–4246 4639–4790 5019–5715 6131–6260 6405–6630 7343–7499 8031–8989 9207–9321 9505–9715 10173–10332 10681–11368 11922–12186 12255–12620 13059–14944 15315–16569
5 1–950 8220–8581 8775–8953 10833–10962 15764–16569
6 1–882 1618–1757 1793–1974 2149–2463 2750–2890 3150–3622 3765–3897 3983–4307 4362–4531 4599–4782 4894–5665 6392–6660 7319–7510 7645–7911 8167–9017 9090–9692 10083–10319 10766–11397 11514–11761 11902–12575 12835–15080 15273–16569
7 1–897 8195–8709 14727–14854 15744–16569
8 1–900 5109–5461 8217–8749 10853–10973 11220–11355 11425–11555 12036–12235 12351–12424 13724–13888 15787–16569
9 1–978 1616–2490 2670–2758 3173–3621 3725–4287 4369–5728 6363–6702 8130–9693 10204–12594 12792–14989 15250–16569
10 9–897 8187–8701 15704–16569
11 10–978 8098–8773 15663–16569
12 1–948 8153–8817 9490–9731 10701–11342 12285–12504 13610–14878 15715–16569
13 1–862 2181–2390 8156–8466 8521–8679 10782–11041 13760–14615 15699–16569
14 1–924 8101–8986 12310–12567 13277–14830 15605–16569
15 1–1017 1570–2619 3071–6701 7307–10397 10479–15081 15187–16569
16 1–1283 1601–2522 3095–5771 5860–6707 7288–15040 15207–16569
17 216–519 602–802 15821–16270 16406–16567
18 1–901 8207–9073 15811–16569
19 1–841 8273–8440 8582–8711 15816–16569
20 20–460 557–865 15799–16569
21 1–954 8097–8785 10609–11389 11904–12537 14060–14697 15300–16569
22 1–950 8192–8465 15718–16569
23 1–1075 1589–1980 2100–2415 3271–5521 6273–6660 7397–9730 10581–11758 12824–14985 15259–16569
24 1–862 8276–8698 15809–16569
25 1–935 8194–8537 10813–11036 15700–16569

* Haplotypes were restricted to the control region (16024-576) for EMPOP frequency query purposes; Total numer of samples in EMPOP: 38361; number of samples belonging to Westeurasian Metapopulation: 15782.
** Sex identified by nanoflow liquid chromatography-tandem mass spectrometry of sexually dimorphic amelogenin protein fragments in dental enamel.

Tab. 2 Summary of mtDNA haplotype results and estimated haplogroups based on the successful sequencing ranges.

Tab. 2 *Zusammenfassung der mtDNA-Haplotyp-Ergebnisse und geschätzten Haplogruppen basierend auf den erfolgreichen Sequenzierungsbereichen.*

grave goods that had stained the bone; this sample did not return results. In addition to the tissue choice, the age of the individuals seemed to affect DNA preservation. The only individuals that did not return interpretable results included the foetus from Unterhautzenthal 38, the neonate from Unterhautzenthal 122 and the 2.5–3.5-year-old from Unterhautzenthal 103 (Tab. 2). The limited sample size for sub-adults may be an additional reason why these samples did not return results.

Early Bronze Age burial practices in the Lower Austrian study region (c. 2200–1600 BC)

The Danube separates two distinct early Bronze Age cultural groups in Lower Austria that differ by the way they buried their dead (cf. Fig. 1). The area north of the Danube is part of the Únětice complex, where male and female bodies were most often placed in flexed positions on their right side, with the head to the south and looking towards the

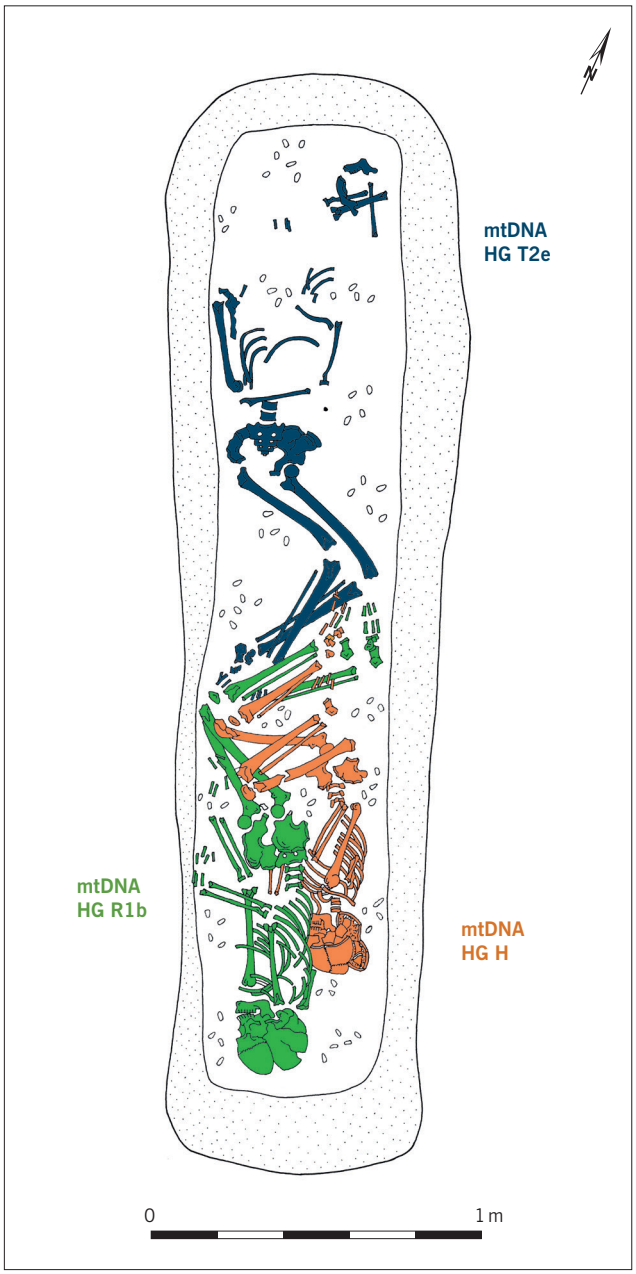


Fig. 2 Triple grave 599 at Franzhausen I, Austria, with the bodies of a 20–25-year-old male individual and two adolescents, aged 14–16 and 12–14.

Abb. 2 *Dreifachgrab 599 aus Franzhausen I, Österreich, mit den Skelettresten eines 20–25-jährigen Mannes und zweier Jugendlicher im Alter von 14–16 und 12–14 Jahren.*

east. Graves with single burials were the norm, but double and multiple burials were frequent; our study includes burials from Schleinbach (Pany-Kucera et al. 2020), Unterhautzenthal (Lauermann 1991; Lauermann 1995; Rebay-Salisbury et al. 2018b) and Zwingendorf (Wewerka 1982). Cemeteries of the Únětice complex are usually located near settlements in Lower Austria and comprise a dozen to several dozen graves (Lauermann 2003).

South of the Danube and west of the Viennese woods, the Unterwölbing Group connects to the Straubing Group farther west. In this region, burials were strongly gendered, even for children (Rebay-Salisbury et al. 2022a). Men were normally placed in a flexed position on their left side with the head to the north, women were usually positioned on their right side with the head to the south – both looked towards the east. Cemeteries may include hundreds of individuals, such as at Franzhausen I and II, but double and multiple burials are rare (Neugebauer/Neugebauer 1997; Neugebauer 1991). Social differences were marked by the depth of graves and the inclusion of bronze and other grave goods; the re-opening of graves and removal of objects was very common (Sprenger 1999).

Franzhausen

The cemeteries of Franzhausen I (Neugebauer/Neugebauer 1997) and II (unpublished) in the Traisen valley, one of the most important archaeological landscapes of Lower Austria, encompass over 2200 burials. Only four of the 716 excavated graves at Franzhausen I contained double or multiple burials. The triple burial 599 in a narrow wooden coffin held the remains of a 20–25-year-old male individual (599A) placed on the left side, head north-west; the upper part of the body was found severely disturbed and the cranium of the man was missing. Two young individuals, 14–16 (599B) and 12–14 (599C) years at death, were also placed on the left side of their bodies, but head south-east, at the feet of the adult, so that the lower legs came to rest in close contact. The man had been placed in the coffin first, followed by the older adolescent; the youngest was placed behind the older one's back in a single act of deposition (Rebay-Salisbury 2018). We found no indication of maternal relatedness through mtDNA in Grave 599 and can exclude siblingship via the mother; the individuals may, of course, have had the same father (Fig. 2).

In the ten documented consecutive graves of Franzhausen, burials were found on top of each other within the same grave pit and frequently with a substantial build-up of soil between the bodies. Grave 860 contained the body of a 3–5-year old girl (860/4) who was buried first; the burial was found severely disturbed, but the location of the bowl and skull indicated a female burial (confirmed by peptide analysis of dental enamel, see Rebay-Salisbury et al. 2022a). The remains of a 35–50-year-old woman (860/1+2) and a 7–8-year-old child (860/3) were found 117 cm higher up in the grave. The excavators suggested that these were the bodies of two individuals that had been removed from other graves in the course of grave robbing whilst the bones were still partly articulated (Neugebauer/Neugebauer 1997). Testing if and what kinds of kinship relations existed between these individuals also contributes to the debate of whether grave re-opening in the Early Bronze Age served primarily material gain, perhaps even from groups unrelated to the ones burying the dead (Jankuhn 1978; Neugebauer 1988), or whether it was a socially accepted ritual practice within the community (Aspöck et al. 2020; Rittershofer 1987).

Through mtDNA analysis, we found no maternal relatedness between the 3–4-year-old girl buried first and the other two individuals buried over a meter higher up in the same grave shaft in Grave 860. The other two individuals, a 35–50-year-old female and a 7–8-year-old child, however, share the same haplotype assigned to haplogroup U5a1d2a. This is remarkable, as the upper two individuals are thought to be secondary deposits within this grave (Neugebauer/Neuge-

bauer 1997). The results of the mtDNA analysis indicate that relatedness was a factor in the final deposition even for multi-staged burials.

Unterhautzenthal

Unterhautzenthal is an Únětice Culture site with settlement features and graves of 57 individuals (Lauermann 1991; Lauermann 1995; Rettenbacher 2004). Five burials of women with children had been discovered at the site and the skeletal preservation was excellent, which is why it served as a pilot study for our work on pelvic modifications through pregnancy and childbirth (Pany-Kucera et al. 2019; Rebay-Salisbury et al. 2018).

Grave 95 included the burial of a 35–45-year-old woman adorned with some twisted bronze wire hair rings and buried in a flexed position on the right side of their body; directly in front of her face, a 3–4-year-old girl[3] wearing a bronze neck ring and a dress pin was placed in a similar position. The heads of both individuals were covered by a large ceramic bowl. Behind the legs of the adult woman, a 4–5-year-old boy was deposited wearing a bronze bracelet. Seven complete ceramic vessels and fragments of other vessels had been placed around the individuals in the grave. Despite being buried in close physical contact, mtDNA analysis was able to rule out a biological mother-child relationship: whilst the children share a T2 mitotype, the female's mtDNA belongs to HV. The burial context and the placing of the individuals nevertheless suggest social kinship between the adult and the children, who could have been siblings. The closest possible relation based on the age difference between the persons buried together is that the woman was their paternal grandmother; she might have been a member of the father's kin or entirely unrelated (Fig. 3).

The body of a 50–60-year-old female buried in a flexed position on the right side of their body and adorned with jewellery, a bronze dress pin and ten twisted bronze wire hair rings, was deposited in Grave 109. The pottery set included a decorated cup, a jug, and a bowl. This grave also contained the left femur of a neonate. The mtDNA lines of the two individuals are entirely unrelated (U2e1 and J1c1), which clarified that the woman was not the newborn's mother. Single human body parts, particularly of foetuses and small children, are not uncommon in Early Bronze Age grave fill; it remains unclear if they were deliberate additions to the grave assemblages.

A foetus/neonate of 34–36 weeks gestational age was found with a 14–15-year-old adolescent in Grave 38, buried with the legs tightly flexed towards the right. The grave contained three bowls, a handled cup and a jug, and was spacious in relation to the size of the body.

Remains of a slightly older child, estimated at between 2.5 and 5.5 years at death, comprised fragments of a *scapula*, *humerus* and *ulna*. They accompanied the 16–20-year old in Grave 103, whose body was found in a loosely flexed position

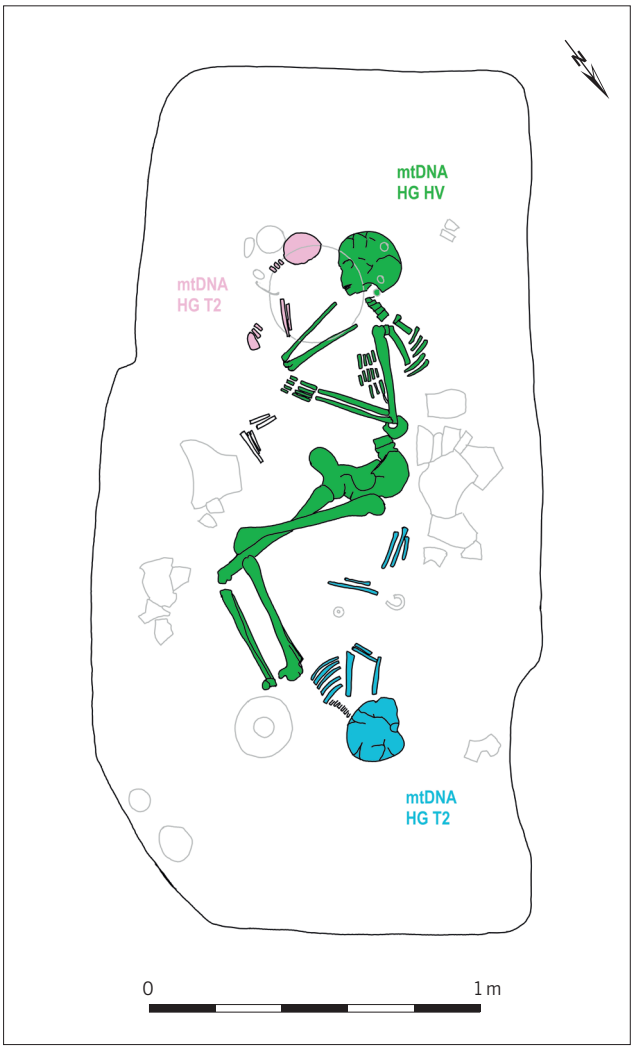


Fig. 3 Grave 95 from Unterhautzenthal, Austria, with the bodies of a 35–45-year-old woman buried with a 3–4-year-old girl and a 4–5-year-old boy.

Abb. 3 *Grab 95 aus Unterhautzenthal, Österreich, mit den Skelettresten einer 35–45-jährigen Frau, bestattet mit einem 3–4-jährigen Mädchen und einem 4–5-jährigen Jungen.*

with legs tilted to the right. A bronze pin and two small bronze rings were found in the chest area; a pottery set with a large bowl and three small cups as well as a bone awl and a chipped stone tool were placed at the feet.

Grave 122, the double burial of a 35–45-year-old male and a 17–20-year-old female, included a 3–6-month-old infant. With both adults' bodies placed in flexed positions on the right side of their body, the woman lay in front of the man; it is unclear where the remains (cranial fragments and *tibia*) of the infant were found. The burials were heavily disturbed, but the remnants of bronze jewellery and pottery suggest a well-furnished grave.

We were not able to confirm or reject the hypothesis that the female individuals in graves 38, 103 and 122 were the mothers of the foetuses or newborns whose remains they

3 The sex of the children was determined by sexually dimorphic amelogenin protein fragments in dental tooth enamel by nanoflow liquid chromatography-tandem mass spectrometry (Rebay-Salisbury et al. 2020; Rebay-Salisbury et al. 2022a).

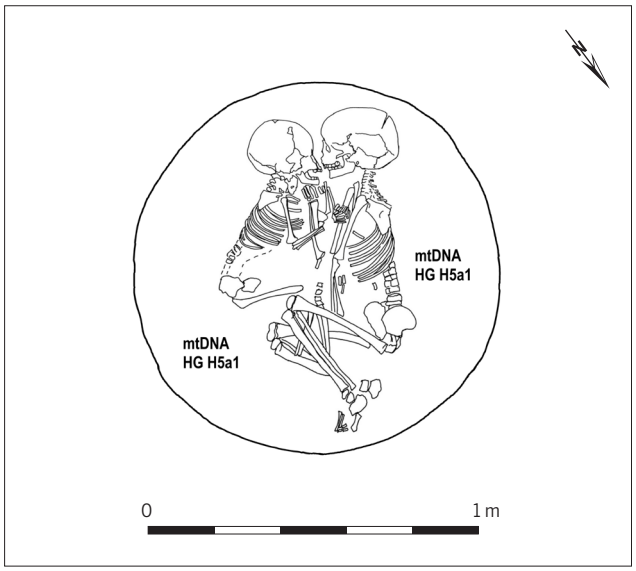


Fig. 4 Burial of a 2- and a 6-year-old child in settlement pit 27 from Unterhautzenthal, Austria.

Abb. 4 *Bestattung eines 2- und eines 6-jährigen Kindes in der Siedlungsgrube 27 aus Unterhautzenthal, Österreich.*

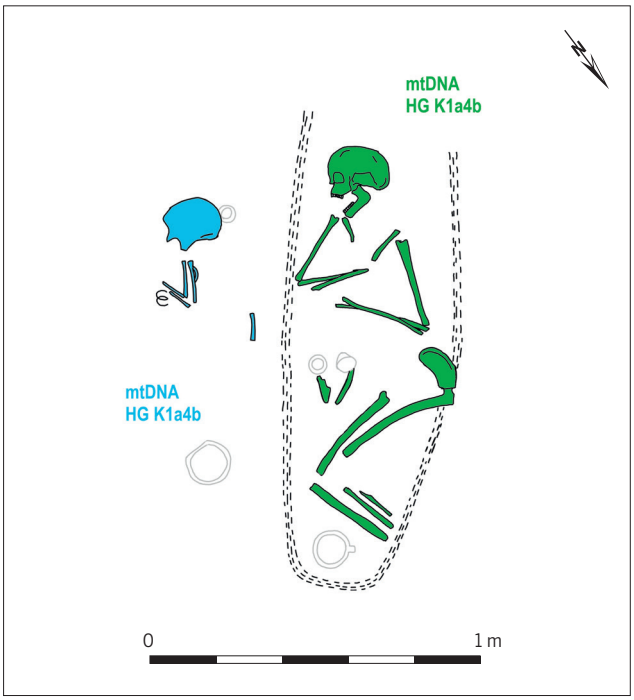


Fig. 5 Burials of a 14–16-year-old adolescent and 4-year-old child at Zwingendorf, Austria.

Abb. 5 *Bestattungen eines 14–16-jährigen Jugendlichen und eines 4-jährigen Kindes in Zwingendorf, Österreich.*

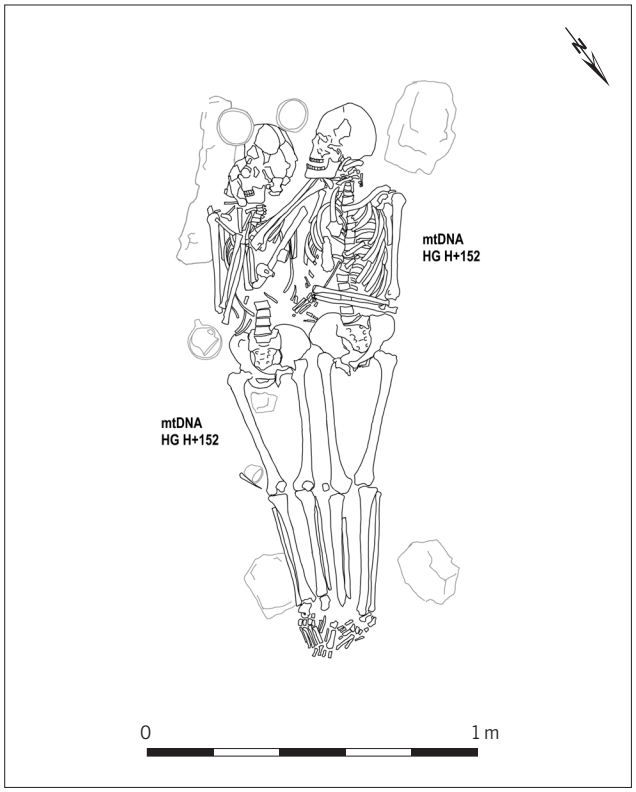


Fig. 6 Double burial of a 27–31-year-old and a 30–35-year-old male in close bodily contact at Schleinbach, Grave 30/31.

Abb. 6 *Doppelbestattung eines 27–31-jährigen und eines 30–35-jährigen Mannes in engem Körperkontakt in Schleinbach, Grab 30/31.*

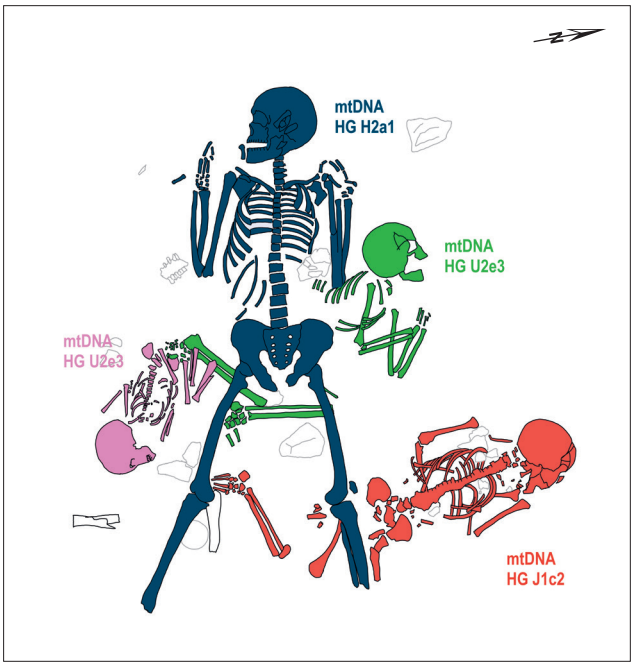


Fig. 7 Quadruple burial of a 30–35-year-old male, a 3–4-year-old girl, an 8–9-year-old boy and a 12-year-old girl from pit 60 at Schleinbach. No scale.

Abb. 7 *Vierfachbestattung eines 30–35-jährigen Mannes, eines 3–4-jährigen Mädchens, eines 8–9-jährigen Jungen und eines 12-jährigen Mädchens aus Grube 60 in Schleinbach. Ohne Maßstab.*

were found with, as the preservation did not suffice to recover their mtDNA profile.

The complete skeletons of a 2- and a 6-year-old child were found in storage pit 27. They were placed face to face in a firm embrace, which suggests a close emotional bond expressed through the burial position. The children in an embrace were found to share an H5a1 mitotype – they were maternally related and could have been siblings, although other types of relations, such as cousins and more distant relations, are also possible (Fig. 4).

Zwingendorf

Nine Early Bronze Age graves were excavated at Zwingendorf, Austria, in 1977 (Grefen-Peters 1982; Wewerka 1982). Although there are no radiocarbon dates available from Zwingendorf, typo-chronological dating places the site within the developed Únětice Culture at around 2000–1600 BC. The north-south oriented grave pits contained ten undisturbed individuals placed in flexed positions on the right sides of their bodies with heads to the south. Grave 8 contained the double burial of an adolescent aged between 14 and 16 years at death and a 4-year-old child. Although the individuals appear to share a grave, traces of a wood coffin were only documented around the adult. The child had been placed about 20 cm away; pottery was deposited at the feet and in the abdominal space of the adolescent and at the feet and head of the child. A bronze *Noppenring* was placed around the child's arm. The close positioning of the two individuals in Grave 8 suggests a personal relationship, even if the age difference between the individuals is probably not enough to suggest a mother-child relationship. MtDNA analysis confirmed a (close) maternal relationship between the adolescent and the child based on an identical K1a4b mitotype. A sibling/cousin relationship appears most likely (Fig. 5).

Schleinbach

Two small groups of graves and settlement features with more than 60 individuals were discovered at Schleinbach in the first half of the 20th century[4]. Grave 30/31 was found within a group of 18 graves arranged in two rows. Unusual for the Únětice context, two men were buried with the head in the south-west, in extended positions on their backs and very closely together; shoulders and legs were touching, whilst the arms and hands of the individual were folded over their upper bodies and partly overlapped (Fig. 6). The two male individuals, a 27–30-year-old and a 30–35-year-old, had identical fractures on the skull, probably inflicted by the same tool. Two ceramic bowls and two cups were found in association with the individuals. Their identical fate and shared treatment after death prompted an investigation of their genetic relationship. The individuals buried closely together in Grave 30/31 indeed share the same haplotype (H+152), suggesting a close maternal relationship.

The deposition of four individuals in a former storage pit at Schleinbach (Weninger 1954) included a 30–35-year-old male (60) and three children, an 8–9-year-old boy (60A), a 12-year-old girl (60B) and a 3–4-year-old girl (60C). The youngest girl had a perimortem impression fracture of the left parietal bone and was the only one placed according to the prevailing burial customs on the right side with the head towards the south-east. The boy was found on the left side of their body, oriented to the north-north-east, and the 12-year-old girl with the upper body in an extended position oriented to the north-east. The body of the adult male was deposited last, in an extended position with the head in the north-west, the upper arms next to the body, with elbows bent and hands adjacent to the shoulders, and legs slightly open (Fig. 7). The age gaps between the individuals and the haphazard mode of deposition suggest the eradication of a whole family.

MtDNA analysis revealed that the 8–9-year-old boy and 3–4-year-old girl from pit 60 share the same haplotype (U2e3a), whereas the 30–35-year-old male individual and 12-year-old girl belong to haplogroups H2a1 and J1c2. The male was not maternally related to the children but could have fathered the children with two different women.

Maternal relatedness

Within this study, we identified 18 unique mitochondrial haplogroups in 25 individuals, seven of which were represented in two individuals (Fig. 8). The haplogroups were estimated based on partial mitogenome sequences (see sequencing ranges in cf. Tab. 2), most of which represent almost full mitogenomes. Age estimates were determined according to Behar et al. (2012) and are listed (Tab. 3). All samples fall within modern European genetic variation and are also found at other archaeological sites. Haplogroup H, for example, is one of the most common mtDNA clades in Europe and is present in about 40 % of today's Europeans, and is thought to have resulted from demographic changes in the Middle Neolithic to Bell Beaker period (Brotherton et al. 2013). The sub-clade H2a1, found in the male individual from Schleinbach, Pit 60, has recently been found in three of 80 genetically typed individuals from the Lech River Valley in Bavaria (Knipper et al. 2017) and is present once in samples from Bronze Age Hungary (Allentoft et al. 2015). The subclade H2a1, as seen in the two children buried in an embrace from Unterhautzenthal 27, has also been identified in Bronze Age Estonia and Russia (Allentoft et al. 2015).

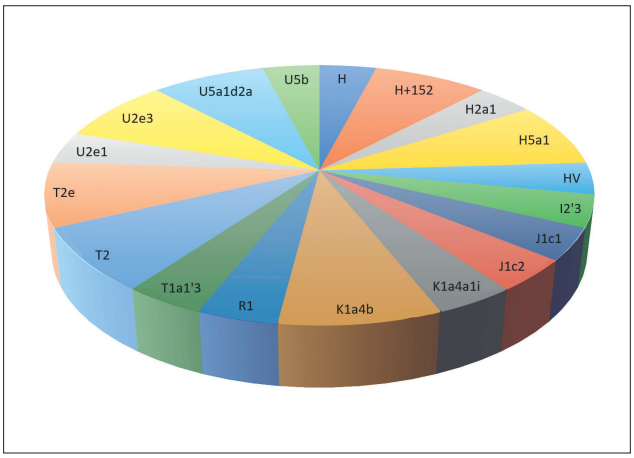


Fig. 8 Graphical representation of the 18 unique mitochondrial haplogroups in 25 individuals in this study.

Abb. 8 *Grafische Darstellung der 18 einzigartigen mitochondrialen Haplogruppen bei 25 Individuen in dieser Studie.*

4 Pany-Kucera et al. 2020; Rebay-Salisbury 2018a; Weninger 1954; Weninger 1954a

HG	Observations	Time Estimate [years]*	SD [years]*	
H	1	12846.0	773.4	
H+152	2	12846.0	773.4	
H2a1	1	7713.4	1754.3	
H5a1	2	6567.1	1533.8	
HV	1	21905.8	2832.7	
I2‘3	1	11307.6	4153.7	
J1c1	1	10090.8	2228.7	
J1c2	1	9762.5	2010.7	
K1a4a1i	1	9617.5	2327.5	for K1a4a1
K1a4b	2	12051.5	3524.3	
R1	1	11420.5	3550.4	
T1a1‘3	1	6997.3	2088.1	for T1a1
T2	2	19316.5	2545.1	
T2e	2	11858.8	3234.1	
U2e1	1	17873.5	3392.1	
U2e3	2	1047.3	4500.8	
U5a1d2a	2	3451.5	2709.3	
U5b	1	22794.0	3590.3	

* according to Behar et al. 2012

Tab. 3 Observed mtDNA haplogroups and time estimates (SD = standard deviation).

Tab. 3 *Beobachtete mtDNA-Haplogruppen und Zeitschätzungen (SD = Standardabweichung).*

In summary, we were able to provide mtDNA results for 11 archaeological contexts that included two or more individuals (Tab. 2) buried together at the same time or in close succession and referring to one another. The practice of burying two or more people together as part of the funerary ritual is not equally common during all prehistoric periods and in all areas. In Early Bronze Age Austria, double and multiple burials occur more often north of the Danube as part of the Únětice Culture than in areas that are culturally affiliated with Bavarian groups south of the Danube (Neugebauer 1994).

Our hypothesis of a close genetic relationship between co-buried individuals, based on the grave contexts, was corroborated by ancient mtDNA analysis in six out of 11 investigated archaeological contexts. For all but Franzhausen 860, we assume that the individuals lived contemporaneously and died in close succession. Taking the ages at death into account, we can propose the most likely types of kinship relations between individuals. In six contexts, we found identical haplotypes, which may suggest (close) maternal relatedness. The exact nature of relatedness, however, cannot be determined; mother/grandmother-child, aunt-niece/nephew, sibling and cousin relationships are possible, as well as more distant relationships.

Potential mother-child dyads were more difficult to trace than sibling/cousin relationships. At Franzhausen, the 35–50-year old female may have been the mother/grandmother or maternal aunt of the 7–8-year old child. We could reject the hypothesis that the 35–45-year-old female at Unterhautzenthal 95 was a maternal relative of the 3–4 and 4–5-year-old children, who were likely siblings. For three possible mother-child pairs, the mtDNA yield of the sub-adult was insufficient to investigate the relationship more closely.

Siblings or close maternal relatives like cousins via the maternal line were also found in Grave 30/31 from Schleinbach, in which two adult men with identical head traumata were buried, and in Pit 60 from the same site, which included four persons; two of the three children, the 3–4 and 8–9-year-olds, were related. The two children from Unterhautzenthal 27, 2 and 6 years old when they were buried embracing each other, also shared the mitochondrial haplotype.

Comparanda

How do our findings compare with other burial contexts of Late Neolithic/Bronze Age Europe? A study of the genetic relationship in four multiple burials of the Corded Ware complex (c. 2700–2200/2000 BC) from Eulau, Burgenlandkreis district, (Saxony-Anhalt, Germany) (Haak et al. 2008), revealed similar results. The burials followed a violent incident and the individuals were placed in meaningful positions to each other. Two graves contained four, one three and one two individuals. Grave 99 was that of a nuclear family, with a 40–60-year-old adult man and 35–50-year-old woman buried with children aged 4–5 and 8–9 at death; the woman shared the same mtDNA haplogroup with the children, and the boy shared the same Y chromosome haplogroup with the man. Grave 98, however, held the remains of a 30–38-year old woman who was excluded as being the biological mother of the three children in the grave (0–0.5–1, 4–5 and 7–9 years), two of which were found to share an mtDNA haplogroup. In the two remaining grave contexts, the DNA of the sub-adult individuals was not preserved well enough to prove further links between individuals.

The Bell Beaker cemeteries of Alburg and Irlbach, Straubing-Bogen disctrict (Bavaria in Southern Germany) (Sjögren et al. 2020), dated to c. 2750–2000 BC, comprising 24 and 18 single burials, respectively. The male individuals belong to a single Y-chromosome lineage, but again there is high vari- ability in the mtDNA, with 14 different mitochondrial haplotypes documented at Irlbach and nine at Alburg. Two pedigrees of four to six generations were linked primarily through the male line; and although there is strong evidence for fe- male exogamy, both through mtDNA diversity and isotope data, there are no direct matches between the mitochondrial haplotypes of the two communities located a mere 15 km apart. An exact match of the mitochondrial H5a1 haplotype was found in two individuals from Irlbach, a young child and a mature woman, but first- and second-degree relations could be excluded based on the full genome data.

Corded Ware (c. 2750–2460 BC), Bell Beaker (c. 2480–2150 BC) and Early Bronze Age (c. 2150–1700/1500 BC) individuals from several cemeteries in the Lech River Valley, Germany, have recently been subject to intensive interdisciplinary analysis, including kinship analysis using genome-wide data (Mittnik et al. 2019). Of 104 individuals, 39 first- and second-degree relationships were identified. Since single burials were the norm in this cultural context, related individuals were found in different graves, but in all but one case buried at the same site. Amongst the ten parent-offspring pairs, six were those of mothers and sons. Whereas the paternal lineage could be traced for four or five generations, with one exception, the maternal line lasted only one generation. The high diversity of mtDNA and the fact that mitochondrial haplotypes were shared almost exclusively between first-degree relatives (Mittnik et al. 2019) are important; this and the corroborating isotope evidence points to patrilocal residential rules. Non-local, high-status women have been identified at the burial sites, but curiously, none of their offspring; low-status individuals were found to be unrelated to the main families.

Of 312 excavated individuals from the Early Bronze Age cemetery of Mokrin, North-Banat disctrict (Serbia; 2700–1500 BC), 24 were tested and 15 were found to be involved in nine family relationships (Žegarac et al. 2021). These included three parent-offspring, two sibling and four second- and third-degree relationships. Related individuals were gen-erally buried close to one another. The population seemed genetically unstructured, with high diversity in both the Y-chromosome and mitochondrial haplogroups; 14 distinct mtDNA haplotypes were identified. The nine individuals with no genetic links to others were all female. Here too, female exogamy is suspected as a social mechanism underpinning the genetic findings.

A study of 80 mitochondrial genomes of Bronze Age individuals from Poland (c. 2400–1100 BC) found eight possible kinship connections in burial sites of the Trzciniec Cultural Circle, in which collective graves are common, as well as two pairs of possible maternal relatives at a Mierzanowice Culture site that include mostly single or double burials (Juras et al. 2020).

Of seven individuals deposited in a pit at Stillfried, Lower Austria in the Late Bronze Age c. 900–800 BC (Parson et al. 2018), a 45-year-old woman was found to share the established mitotype with the 5–6-year-old boy buried in close bodily contact. The archaeological context (Hellerschmid 2015) suggests the child was placed on her hip, with a second, 7–8-year-old boy next in the depositional sequence. A 30-year-old male, a three-year-old boy and a nine-year-old girl were also deposited in the pit; the other, a 40-year-old female of this context could be excluded as the mother of any of the children.

The published studies of Late Neolithic/Early Bronze Age kinship summarised above demonstrate both common traits and cultural variation. Bell Beaker, Corded Ware and Early Bronze Age communities all appear to be characterised by a high level of diversity in mitochondrial DNA but show differences in the way the population is otherwise structured. Genetic kinship could be more reliably traced through the male line, with individuals often buried in the vicinity of their relatives. This and supporting archaeological and isotopic evidence suggest a high level of female mobility, perhaps within super-regional marriage networks, but also for other reasons (Rebay-Salisbury 2023).

The increased use of vessels suitable for feeding infants in the Bronze and Early Iron Ages might indicate not only a change in childcare practices but also a change in mother-child relationships. Successful breastfeeding requires the mother and child to be physically connected most of the time, but with feeding vessels that contained milk from sheep, goats or cattle (Dunne et al. 2019), other members of the community could take over the task of feeding infants. This may have made mothering a more collective, shared responsibility within the community (Rebay-Salisbury et al. 2021).

Conclusion

Close personal relationships such as the mother-child bond were expressed through the way bodies were placed in relation to one another in the grave and frequently broadly based on kinship. Kinship is not the same as biological relatedness, even if there are overlaps, and we need to consider both the archaeological context information and the genetic data to understand how families were composed in the past. Double, multiple and consecutive graves (cf. Duday 2009) appear to be indicative of personal relationships, in particular when the placement of the bodies suggests love and care (Rebay-Salisbury 2018). What this means remains difficult to define – close bodily contact, embrace, interlocking limbs etc. may be part of how the burying community staged a close connection after death. It is perhaps easiest to define the expression of love and care in the burial practice by the clear contrast to its absence.

Not all burial evidence speaks of maternal love. On the contrary, evidence of abuse and neglect is frequent. A 3–4-year-old child from Unterhautzenthal 133, for example, had a broken humerus that was not corrected and healed in the wrong place. Nevertheless, the child was afforded a regular burial in the cemetery, and placed with care (Rebay-Salisbury et al. 2018b). At Schleinbach, a 5–6-year-old boy suffering from middle ear infections was disposed of in an Early Bronze Age storage pit. He died from no fewer than four blunt-force traumata to the skull, inflicted by at least

two different kinds of objects or weapons (Rebay-Salisbury et al. 2020). Body parts of foetuses, infants and young children frequently appear in other graves, seemingly out of context, and most likely testify to the low social significance of some children within Central European Bronze Age communities.

In this study, we tested the genetic relationship between co-buried individuals through the maternal line by mtDNA analysis. Matches of mtDNA of individuals buried together in one grave are a strong argument that biological relatedness was a factor in kinship, a factor that was respected beyond death. However, several instances demonstrate that women appear staged in a mothering role in the burial context even when they were not directly biologically related. Ideologically at least, childcare was not exclusively associated with their biological mothers, which suggests that caregiving was likely organised communally, with the extended family – and perhaps entirely unrelated individuals – playing a significant role in bringing up children.

Acknowledgements

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1 base map © Google 2009
2 after Neugebauer/Neugebauer 1997, 287 Pl. 269
3 redrawn after Lauermann 1995, 33 Pl. 12; Lauermann 1996, 36 Fig. 17–19
4 redrawn after Lauermann 1991, 74 Fig. 22; and photos of the individuals on display in the MAMUZ Schloss Asparn/Zaya, Museum Mistelbach, Austria (taken by K. Rebay-Salisbury)
5 redrawn after Wewerka 1982, 29 Fig. 4
6 redrawn after Weninger 1954, 57 Fig. 4
7 redrawn after Weninger 1954a, 3
8 authors

Tab. 1 authors , NHM AA Inv. Nr. = inventory number of the Anthropological Department of the Natural History Museum in Vienna, Austria
Tab. 2 authors
Tab. 3 authors after Behar et al. 2012

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Lifeway narratives of a Bronze Age community from Balatonkeresztúr (Western Hungary) based on bioarchaeological analyses

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Zusammenfassung

Lebensgeschichte einer bronzezeitlichen Gemeinde aus Balatonkeresztúr (Westungarn) anhand bioarchäologischer Analysen

Dieser Artikel konzentriert sich auf die bioarchäologischen Analysen von 19 Individuen aus bisher wenig untersuchten Populationen der frühen und mittleren Bronzezeit (2200–1600 cal BC), die in Balatonkeresztúr-Réti-dűlő (Westungarn) während der Ausgrabungskampagne vor dem Bau der Autobahn M7 2003 entdeckt wurden. 13 frühbronzezeitliche Bestattungen eines kleinen Friedhofsteils der Kisapostag/frühesten Kultur der inkrustierten Keramik wurden in zwei Grabgruppen mit zwei isolierten Körperbestattungen angeordnet. Die Bayessche Analyse weist darauf hin, dass der Friedhof zwischen 2120 und 1900 v. Chr. genutzt wurde. Die meisten Bestattungen enthielten keine weiteren Grabbeigaben. An dieser Stelle wurde auch eine ungewöhnliche Mehrfachbestattung mit acht Personen entdeckt, die in die mittlere Bronzezeit zwischen 1770 und 1620 cal BC datiert wird. Analysen dieser menschlichen Überreste sind wichtig für die Zeit, in der die Feuerbestattungspraxis in der Region des heutigen Westungarn üblich war. Archäologische, anthropologische und Radiokarbonuntersuchungen wurden durch Strontiumisotopenmessungen und alte DNA-Daten ergänzt, um die Dynamik der am Fundort Balatonkeresztúr entdeckten Gemeinschaften zu rekonstruieren. Die aDNA-Analysen ergaben, dass die Population der Kisapostag/frühesten Kultur der inkrustierten Keramik die genetische Grundlage der nachfolgenden Gemeinschaft der Kultur der inkrustierten Keramik war und dass die soziale Struktur beider Kulturen patrilokal war, ähnlich wie bei den meisten untersuchten zeitgenössischen Gruppen.

Summary

This paper focuses on the bioarchaeological analyses of 19 individuals from previously understudied Early and Middle Bronze Age (2200–1600 cal BC) populations, discovered at Balatonkeresztúr-Réti-dűlő (Western Hungary) during the excavation campaign preceding the construction of the M7 motorway in 2003. Thirteen Early Bronze Age burials of a small cemetery part of the Kisapostag/earliest Encrusted Pottery culture were arranged into two grave groups with two isolated inhumations. Bayesian analysis indicates that the cemetery was used between 2120 and 1900 cal BC. Most of the burials contained no remaining grave goods. An unusual multiple burial with eight individuals was also discovered at this site, dated to the Middle Bronze Age period between 1770 and 1620 cal BC. Analyses of these human remains are important in the period, when the cremation burial practice was common in the region of modern-day Western Hungary. Archaeological, anthropological and radiocarbon investigations were complemented by strontium isotope measurements and ancient DNA data to reconstruct the dynamics of the communities discovered at the site of Balatonkeresztúr. The aDNA analyses revealed that the population of the Kisapostag/earliest Encrusted Pottery Culture was the genetic basis of the succeeding community of the Encrusted Pottery Culture and the social structure of both cultures were patrilocal, similarly to most studied contemporaneous groups.

1. Introduction

In the last centuries of the 3rd millennium BC (2200–2000/1900 cal BC; parallel with the beginning of Central European Early Bronze Age; Bertemes/Heyd 2015; Fischl et al. 2015), during the final phase of the Early Bronze Age in Hungary, the population groups of the Kisapostag/earliest Encrusted Pottery Culture existed in Western Hungary, while the population of the tell cultures inhabited the Great Hungarian Plain. During this period, fahlore copper jewellery are the most characteristic metal finds (Kiss 2020; Kiss 2020a). Before the 1990s, the practice of urn cremation burials was solely associated with this culture. In the last decades, in addition to urn burials and scattered cremations, around 90 inhumation burials of this culture have been documented. Interpretation of the biritual burial practice have been proposed with both chronological and social explanations (s. Kiss 2015; Kiss 2020). The results of new excavations and radiocarbon dating of these recently discovered inhumations indicate that the dominant burial tradition in the earlier phase was inhumation. Deceased were placed in the grave on their sides in a sleeping position, or sometimes on their back, with their legs pulled up, often without any grave goods. Less frequently, a small mug next to the head and personal orna-

ments/jewellery (e.g., tiny tubular beads made of sheet copper or hair rings) were found as grave goods. In a later period of the culture (Kisapostag phase 2), cremation began to be practiced and became dominant (Somogyi 2004; Szabó 2010; Kiss 2012; Hajdu et. al 2016).

The Middle Bronze Age in Hungary (parallel with the younger phase of the Central European Early Bronze Age, Reinecke Br A2; 2000/1900–1600/1500 cal BC) is the flourishing period of the tell-settlements in the Great Hungarian Plain, and the Transdanubian Encrusted Pottery Culture in large areas of Western Hungary, e.g., beside Lake Balaton. Tin bronze weapons and tools appear in all spheres of everyday life during this period, including the Tolnanémedi type hoards in the western part of Hungary, and the Hajdúsámson type metallurgy in the northeastern region of the Carpathian Basin. Fahlore copper is continuously used, while at the end of the Middle Bronze Age chalcopyrite raw material is more widespread. Local production of metallurgy is proven by the moulds found in the settlements[1]. Cremation burial practice (urn graves and scattered cremation burials) were applied nearly exclusively among the groups of the Transdanubian Encrusted Pottery Culture, with cemeteries separated from the settlements (Kiss 2012).

Early and Middle Bronze Age settlements at Balatonkeresztúr

The Balatonkeresztúr-Réti-dűlő site is located 3 km from the southern shore of Lake Balaton. In 2003–2004 an area of 45 000 m² was investigated at this site, preceding the construction of the M7 motorway. As a result, the traces of occupations associated with nine archaeological cultures spreading over eight chronological periods were identified by the analysis of 2976 archaeological features. These include: the Middle and Late Copper Age (Balaton-Lasinja, Furchenstich, Boleráz and Baden Cultures); Early Bronze Age (Somogyvár-Vinkovci and Kisapostag/earliest Encrusted Pottery Cultures); Middle Bronze Age (Transdanubian Encrusted Pottery Culture); Late Iron Age (La Tène D); Migration period (Langobards); Árpádian Age (12th–13th century); and Late Middle Ages (14th–15th century; Fábián/Serlegi 2009).

The settlement of the Kisapostag/earliest Encrusted Pottery and Transdanubian Encrusted Pottery Cultures at the site of Balatonkeresztúr can be interpreted as part of open settlements, consisting of a few buildings, storage and refuse pits (Kiss 2012).

Early Bronze Age cemetery of the Kisapostag/earliest Encrusted Pottery Culture at Balatonkeresztúr

Ancient DNA analyses of the remains of Copper and Bronze Age individuals discovered at Balatonkeresztúr-Réti-dűlő and Balatonlelle-Rádpuszta have revealed the genetic ancestry of the population living on the southern shore of Lake Balaton during that period (21 individuals, between 3500 and 1600 cal BC; Kiss et al. 2015; Bondár/Szécsényi-Nagy 2020; Gerber et al. 2023). Based on these results, this paper focuses on the bioarchaeological analyses of 19 Early and Middle Bronze Age (2200–1600 cal BC) burials from Balatonkeresztúr (Fig. 1). Due to the lack of grave goods, human remains were dated based on ^{14}C dates. Altogether 13 burials of the Kisapostag/earliest Encrusted Pottery Culture were discovered (~ 2200–1900 cal BC), 12 inhumations and one cremation burial, from which 11 were suitable for bioarchaeological analyses. We conducted physical anthropological, stable isotope, and aDNA analysis of these burials from Balatonkeresztúr. Burials without grave goods were not typically evaluated during earlier research, however, these inhumations provide the basis for understanding social processes, possible kinship ties and the genetic makeup of the Bronze Age, due to the widespread cremation burial practice of the study period.

The preservation condition of the human remains (stored in the Rippl-Rónai Museum, Kaposvár) was medium to poor. In the case of most of the skulls, the facial part was reconstructed only in a few cases, while the postcranial remains were relatively well preserved (Fig. 2; Fig. 3a–e). The estimation of age-at-death and the sex determination were based on the methods commonly used in physical anthropology[2]. The paleopathological lesions were investigated macroscopically (Manchester 1983; Aufderheide/Rodríguez-Martín 1989; Ortner 2003).

At the northeastern part of the excavated settlement of the Kisapostag/earliest Encrusted Pottery Culture at Balatonkeresztúr, a small cemetery with 13 burials was discovered with one cremation burial (S12) among them. Most of the burials were spatially distributed into two grave groups (Group A: individuals S1, S2, S3, S5, S6, S7, n = 6; and Group B: individuals S4, S8, S11, S13, n = 4), while one inhumation, found a little further from the two burial groups, was a grave of a young male individual (S10). Another older male (S45) was found further west. All inhumations were sampled for bioarchaeological analyses except S3, due to the nearly complete destruction of the body (Fig. 1; Tab. 1). Most burials contained no grave goods; however, in three cases, small non-diagnostic pieces of copper jewellery were found (Grave S10, S13 and S12 cremated). The deceased were placed in a flexed position, laying on their side (Fig. 2; Fig. 3a–b). Most skeletons show slight or modest distortion. Though the skeletal material was poorly preserved, and osteological sex determination was difficult in a few cases (e.g., children), the biological sex could be determined through aDNA analysis. Group A consists of three juveniles and three adults, five males and a female (individual S7), while in Group B we found one juvenile male, and three adults, two males and one female (Grave S13). Inhumation burials altogether represented four juveniles and eight adults. Radiocarbon dates place these inhumations between 2200–1800 cal BC (95.4 %); however, with Bayesian analysis using the OxCal software the timespan of the burials from this period can be reduced

1 Kiss 2009; Kiss 2012; Fischl et al. 2013; Dani et al. 2016; Dani et al. 2019; Dani et al. 2020.

2 Fazekas/Kósa 1978; Ferembach/Schwidetzky et al. 1979; Işcan/Loth et al. 1984; Işcan/Loth et al. 1985; Ubelaker 1989; Bernert et al. 2007.

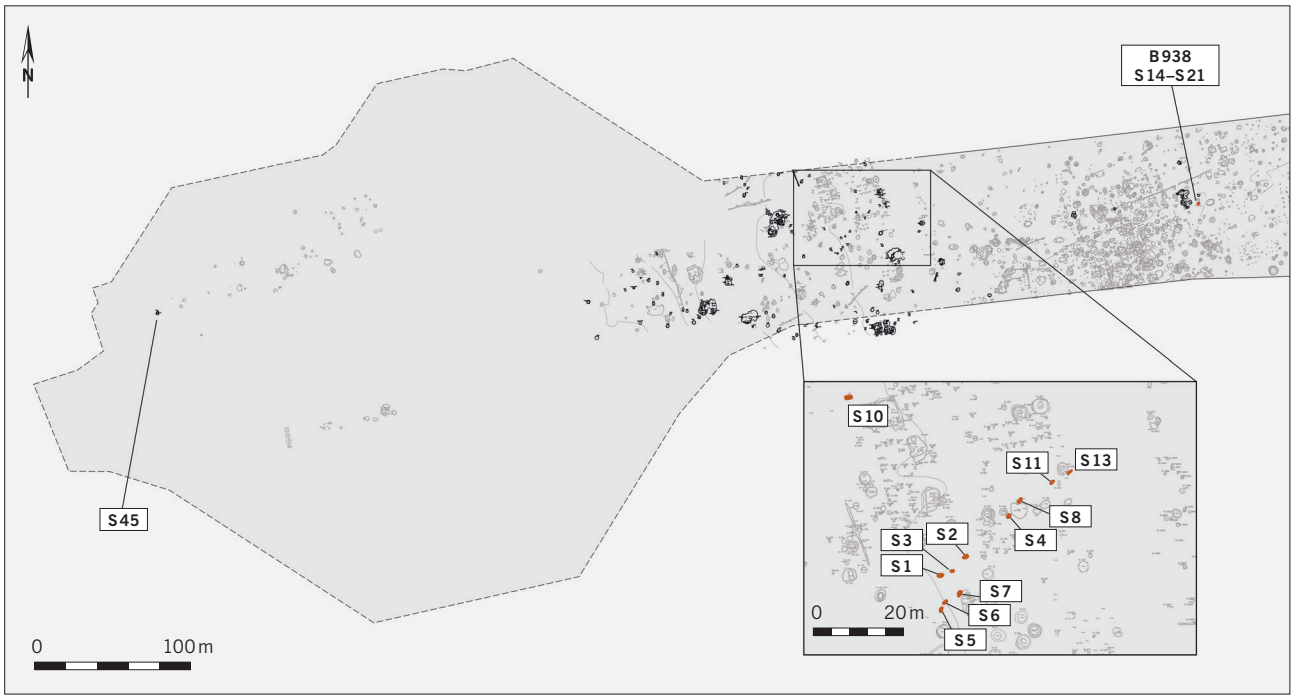


Fig. 1 Early and Middle Bronze Age settlement features (with black) and burials (with numbers) at Balatonkeresztúr-Réti-dűlő site, Somogy County.

Abb. 1 *Siedlungsbefunde der frühen und mittleren Bronzezeit (schwarz) und Bestattungen (s. Ziffern) am Fundort Balatonkeresztúr-Réti-dűlő, Komitat Somogy.*

Group	ID	Grave group	^{14}C (cal BC) 2σ (95.4 % CI)	Age	Sex	MtDNA	ChrY	Degree of genetic relatedness
Kisapostag/ earliest Encrusted Pottery Culture	S1	A	2120–1880	40+	M	V	I2a-L1229	2nd to S2 (& S8?)
	S2	A	2120–1880	30–35	M	U5a2b1a	I2a-L1229	2nd to S1 (& S8?)
	S4	B		17–19	M	H10a1	I2a-L1229	1st to S8
	S5	A		16–18	M	T1a4	I2a-L1229	1st to S6 & S11
	S6	A	2030–1770	17–18	M	T1a4	I2a-L1229	1st to S5 & S11
	S7	A	2120–1880	35–50	F	V		
	S8	B		30–40	M	T2b	I2a-L1229	1st to S4; (2nd to S1 & S2?)
	S10		2140–1940	7–8	M	K1a4a1g	I2a-L1229	None
	S11	B	2200–1980	34–43	M	T2b	I2a-L1229	1st to S5 & S6
	S13	B	2120–1890	35–45	F	J2b1		None
	S45		2200–1980	45–55	M	U5a1g	I2a-L1229	None
Transdanubian Encrusted Pottery Culture	S14	Mass Grave B-938		7–8	F	H10a1		None
	S15			21–23	M	U4b1b1	I2a-L1229	2nd to S17
	S16		1890–1640	35–44	M	T2g2	I2a-L1229	None
	S17		1870–1540	26–35	M	U5b1b1+@16192	I2a-L1229	1st to S19; 2nd to S15
	S18			3–4	M	U4a2	R1b-Z2103	None
	S19			9–10	M	T2b	I2a-L1229	1st to S17
	S20			1.5–2	M	K1a+195	R1b-Z2103	1st to S21
	S21			1.5–2	F	K1a+195		1st to S20

Tab. 1 Balatonkeresztúr-Réti-dűlő. Summary of the data of investigated human remains.

Tab. 1 *Balatonkeresztúr-Réti-dűlő. Zusammenfassung der Daten der untersuchten menschlichen Überreste.*

to 2050–1940 cal BC with an 84.4 % probability, whereas only two graves were possibly slightly earlier. The overall pathological makeup of the population does not show evidence for significant disease and the average biological age of the adults was high (s. Tab. 1).



Fig. 2a–i Human remains from the Bronze Age at Balatonkeresztúr-Réti-dűlő. a S1; b S2; c S4; d S5; e S6; f S7; g S8; h S10; i S11.

Abb. 2a–i *Menschliche Überreste aus der Bronzezeit in Balatonkeresztúr-Réti-dűlő. a S1; b S2; c S4; d S5; e S6; f S7; g S8; h S10; i S11.*

Anthropological data

Grave S1, Group A (Fig. 2a). The body was placed on the right side in a flexed position, with a north-east–south-west axis orientation. One piece of a flint was found in the grave pit. Sexualisation index: -0.18. The remains consist of fragmented skeletal bones and a skull, which were ^{14}C-dated to 3611 ± 31 BP (2120–1880 cal BC, 95.4 % CI), and determined to be a male of over 40 years (determination of age at death based on tooth abrasion: level 5). Among the 29 teeth present, three upper and one lower molar were decayed *(caries)*. The lower right first molar is missing *ante mortem*, indicated by the healed *alveolus*. Other pathological conditions were not revealed. The skull has a *brachycranic* and likely *planoccipital* shape, a feature which is almost ubiquitous within this group.

Grave S2, Group A (Fig. 2b). The remains and endogenous DNA are poorly preserved and fragmented. The body was placed on the left side in a flexed position, with a north-east–south-west axis orientation. Several non-diagnostic pieces of Bronze Age pottery were found in the burial pit. In absolute terms the grave was dated to 3609 ± 32 BP (2120–1880 cal BC, 95.4 % CI). The body was determined to be a male of 30–35 years (determination of age-at-death based on tooth abrasion: level 3). Sexualisation index: -0.50. No molar decay was determined on the remaining 12 teeth, and the skull type is brachycranic and likely planoccipital. A rare anatomical variation of perforated fossa olecrani can be observed on the left humerus.

Grave S3, Group A. Human bone frangments in a grave pit. The remains were not suitable for the bioarchaeological analyses.

Grave S4, Group B (Fig. 2c). The deceased was placed on the right side in a flexed position, with a slight north-east–south-west axis orientation. The human remains consisted of only a small amount of fragmentary bone material and teeth. Sexualisation index: -0.20. The remains of a 17–19 year-old male individual (determination of age at death based on muscular adhesion surfaces, and tooth abrasion: level 2) had 16 remaining teeth with no visible pathological conditions. One boar incisor and fragmentary pottery were recovered from the grave. Radiocarbon dating was not performed as the remains can be dated by the genetically determined father, individual S8.

Grave S5, Group A (Fig. 2d). Moderately preserved remains of a 16–18 year-old male individual in a flexed position, with a north–south axis orientation. Only several non-diagnostic Bronze Age pottery sherds were found in the grave. The determination of age at death was based on muscular adhesion surfaces, and tooth abrasion: level 2–3. The male had 32 remaining teeth and the skull type was brachycranic and likely planoccipital. Besides some severely decayed molars (left upper first molar: *caries*) no other pathological conditions could be observed. Some fragmentary pottery was also recovered from the grave. The ^{14}C-dating was not performed as the remains can be dated by the genetically determined father, individual S11.

Grave S6, Group B (Fig. 2e). The body was placed on the left side in a heavily flexed position, with a north-east–south-west axis orientation. The moderately preserved bone fragments were ^{14}C-dated to 3571 ± 31 BP (2030–1770 cal BC, 95.4 % CI), and belonged to a 17–18 year-old male individual (sexualisation index: +0.71; determination of age-at-death based on muscular adhesion surfaces, and tooth abrasion: level 2). The male had 24 remaining teeth, and besides one decayed molar (right lower first molar: *caries*), no other visible pathological conditions were revealed on the skeletal remains.

Grave S7, Group A (Fig. 2f; Fig. 3c). Moderately preserved remains of a 35–50 year-old female individual (sexualisation index: -0.18; determination of age-at-death was based on sutures ossification, and tooth abrasion), who was ^{14}C-dated to 3611 ± 32 BP (2120–1880 cal BC, 95.4 % CI). The skull was of brachycranic type with a long facial structure. Besides 28 remaining teeth (with no *caries*), some were missing ante mortem (right lower second premolar and second molar, and left lower second premolar). Extended porotic lesions were found in the skull (os frontale and parietale), in addition to some enthesopathy, i.e., bone spikes caused by heavy labour on the right calcaneus (left was not examined because of its fragmentary condition). No grave goods were recovered from the grave besides some non-diagnostic Bronze Age pottery sherds.

Grave S8, Group B (Fig. 2g). The body was placed on the left side in a flexed position, with a north-east–south-west axis orientation. The poorly preserved bones belonged to a 30–40 year-old male (sexualisation index: +0.80; determination of age-at-death based on abrasion of teeth: level 4, sutures ossification and the surface of *facies auricularis*) with a calculated stature of 168.2 cm. Just like individual S2, the body had an anatomical variation of perforated fossa olecrani on the right humerus, likely as a result of biological relationship. Only four teeth remained, showing no signs of decay *(caries)*. On the diaphysis of his right tibia periostitis was observed, while both calcanei showed signs of enthesopathy.

Grave S10, which was located farther from Group A, was the only child grave among the burials of this period (Fig. 2h). The moderately preserved remains of a 7–8-year-old male individual (determination of age-at-death based on teeth, and size of long bones) were found and ^{14}C-dated to 3661 ± 30 BP (2140–1940 cal BC, 95.4 % CI). The skeleton was placed in a flexed position, with a north-east–south-west axis orientation. The bones did not show any sign of pathological conditions. A copper or bronze bracelet on the arm suggested a higher social status for this individual.

Grave S11, Group B (Fig. 2i; Fig. 3d). Moderately preserved remains of a 34–43-year-old male (sexualisation index: +1.16, determination of age-at-death based on the trajectory of the proximal epiphysis of the *humerus* and *femur* and abrasion of the remaining 26 teeth: level 3), which was ^{14}C-dated to 3705 ± 30 BP (2200–1980 cal BC, 95.4 % CI). The skeleton was placed in a flexed position, with a north-east–south-west axis orientation. The dolichocranic skull was highly deformed under soil pressure. The bones are distorted, similarly to many other individuals from this archaeological culture. The calculated stature of the individual was 171.9 cm. He had a severe walking disabililty of the left leg owing to an early-life injury or a developmental



Fig. 3a–f Human remains from the Bronze Age at Balatonkeresztúr-Réti-dűlő. a S13, b S45; c S7 skull; d S11 skull; e S13 skull; f S15 skull.

Abb. 3a–f *Menschliche Überreste aus der Bronzezeit in Balatonkeresztúr-Réti-dűlő. a S13, b S45; c S7 Schädel; d S11 Schädel; e S13 Schädel; f S15 Schädel.*

disorder. The grave contained some non-diagnostic Bronze Age pottery sherds.

Grave 12, Cremation burial; not included in the bioarchaeological analyses.

Grave 13, Group B (Fig. 3a,e) included the well-preserved remains of a 35–45-year-old female. The body was placed on the left side in a flexed position, with a north–south axis orientation. The remains had a strange body placement compared to other individuals, with her right arm covering the face, implying special treatment for this individual. Several fragments of metal beads made of copper sheet were placed at the left side of the head along with a small burnt animal bone fragment, and traces of green patina on the right side of the skull were found. Copper or bronze bead fragments associated with the headdress or cap ornament found in the grave suggest that she had a relatively high social status within the community. According to radiocarbon dating (3618 ± 30 BP; 2120–1890 cal BC, 95.4 % CI), her burial

most probably can be dated to between 2040 and 1890 cal BC (90.9 %). Sexualisation index: -0.81; determination of age-at-death was based on sutures ossification, the surface of *facies symphyses* and tooth abrasion: level 4–5. The skull is of *brachycranic* type, the calculated stature of the body was 158.7 cm, which can be considered the average stature of females during this era. This individual had a rare anatomical variation of extra sutural bones and maxillary prognathy. While 29 of her teeth remained, *caries* was observable only on the lower left second molar; the lower left third molar had fallen out *ante mortem*. The only pathological conditions were one missing and one decayed tooth. There was no sign of an external injury or illness on her body, so the cause of her death is currently unknown. Analyses on pelvis bones suggest no or few birth-giving events during her lifetime. The remains of the skull were the best preserved among all individuals in the site, which enabled facial reconstruction, grave reconstruction and a detailed anthropological description for this individual using genetic data (Kustár et al. 2022; Gerber et al. 2023).

Grave S45 (Fig. 3b) The moderately preserved remains of a 45–55-year-old male individual were laid next to a typical Kisapostag-associated pit with a west–east axis orientation. It was located a significant (more than 300 m) distance from the other Kisapostag-associated graves. Broken pottery and considerable amounts of shell fragments were also recovered. The individual had no grave goods, although shell fragments could be observed right next to the human bones, and the individual was buried in a heavily flexed position facing towards the North. The remains were ^{14}C-dated to 3702 ± 28 BP (2200–1980 cal BC, 95.4 % CI). A significant abrasion of the upper teeth can be observed with slight mandibular prognathism, likely in association with some sort of profession or behavioural anomaly that caused bruxism (Gerber et al. 2023). The skull is curvoccipital and mesochycranic, the mandibles are slightly protruding, perhaps in relation with the bruxism.

Middle Bronze Age multiple burial

The later horizon of the human remains is represented by a multiple pit burial of eight individuals including three adults and five children (cf. Fig. 1; Tab. 1, S14–21; Fig. 4–5) from the period of the Transdanubian Encrusted Pottery Culture. Due to the lack of other finds, the feature was formerly defined as a household refuse pit used for mortuary purposes sometime in the Late Copper Age or the Early Bronze Age (Fábián 2006). However, based on the *brachycran taurid* type skull, anthropological analyses suggested a Bronze Age dating (Köhler 2006). Radiocarbon dates proved that this multiple burial can be dated to between 1870–1620 cal BC (95.4 %; cf. Tab. 1; also Gerber et al. 2023), parallel with the developed Early Bronze Age in Central Europe (Reinecke Br A2; Fischl et al. 2013; Kiss et al. 2019). The physical anthropological examinations detected the presence of the *planoccipital brachycranic taurid* type *crania*, a physical trait which could be linked to the Bell Beaker Group (Zoffmann 2000; Köhler 2006). The discovery of this multiple burial is significant in the context of cremation burial tradition (urn burials and scattered cremations), which was practised nearly exclusively by the population of the Transdanubian Encrusted Pottery Culture during this period (Kiss 2012). Prior to our examination, only a few data were available concerning the physical anthropological makeup of these communities (Zoffmann 2000; Zoffmann 2008).

Anthropological data of the multiple burial B-938

Individual S14 (Fig. 4; Fig. 5a) revealed a 7–8-year-old female child, whose body was placed on the right side, with a south–north axis orientation. The upper body was in a prone position with heavily flexed legs. The skull and skeletal bones were relatively well-preserved and determination of age-at-death was based on the teeth and the length of long bones.

Individual S15 (Fig. 3f; Fig. 4; Fig. 5a) was a 21–23-year-old male, whose body was lying on the right side with flexed legs, oriented on a north–south axis. The remains consisted of medium-preserved skeletal bones and a skull. Determination of age-at-death was based on the trajectory of the proximal epiphysis of the *humerus* and *femur*. Based on the sexualisation index (-0.43) the individual was osteologically determined as a female (Köhler 2006). The skull was short, broad, and *hyperbrachycyran* according to the index; alveolar prognathism was moderate (for details see Köhler 2006, Tab. 1). The calculated stature of the body on the basis of the size of the long bones was in the tall category: 174.2 cm (Köhler 2006, Tab. 2). Pathological conditions included hip dysplasia (*luxatio coxae congenita*) in both *femurs* and the pelvis. The heads of both *femurs* are severely deformed, with thinning of the diaphysis, and the thickened *fibulae* are also characteristic for this illness. No *caries* was observed on the 32 teeth; level 2 tooth abrasion.

Individual S16 (Fig. 4; Fig. 5b) was a 35–44-year-old male whose body was lying on the right side with slightly flexed legs, with west–east axis orientation. The remains consisted of a medium-preserved skull and relatively well-preserved skeletal bones. The characteristics of the skull were determined to be moderately masculine but the gracility of the skeleton suggested a female with a sexualisation index of (± 0.00). Determination of age-at-death was based on the trajectory of proximal epiphysis of the *humerus*, the surface of *facies symphyseos ossis pubis* and abrasion of the teeth and *femur* (Köhler 2006). The skull was short and very broad in absolute dimensions and *hyperbrachycranic*; alveolar prognathism was moderate (Köhler 2006, Tab. 1). The calculated stature of the body on the basis of the size of the long bones indicates the individual fell within the small-medium category of 151.2 cm (Köhler 2006, Tab. 2). Anatomical variation revealed *ossa wormiana* on both sides of the skull. Pathology: sacralisation of the final part of the vertebra and entesopathy on both *calcaneus* were observed. No *caries* was observed on the 31 remaining teeth, but a small amount of *calculus* was visible; level 4 tooth abrasion.

Individual S17 (Fig. 4; Fig. 5b). A 26–35-year-old male. The upper body was in a supine position, with bent legs on the right side. The body was oriented on an east–west axis. The remains consisted of a medium-well preserved skull, and a relatively well-preserved postcranial skeleton. Determina-

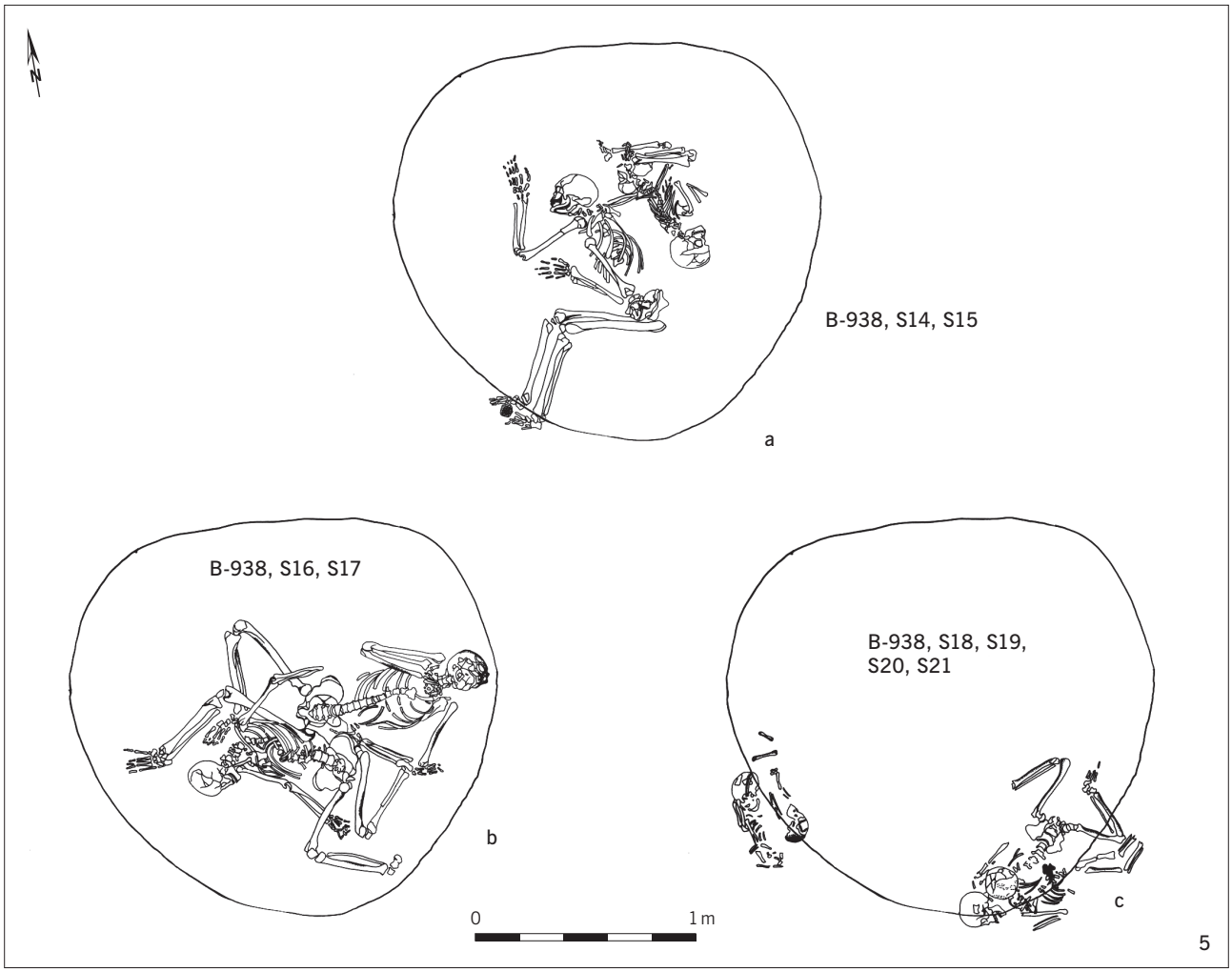


Fig. 4 Human remains from the Bronze Age at Balatonkeresztúr-Réti-dűlő, multiple burial B-938: S14–S21.

Abb. 4 *Menschliche Überreste aus der Bronzezeit in Balatonkeresztúr-Réti-dűlő, Mehrfachbestattung B-938: S14–S21.*

Fig. 5 Three layers of human remains from the Bronze Age at Balatonkeresztúr-Réti-dűlő, multiple burial B-938: S14–S21.

Abb. 5 *Menschliche Überreste aus der Bronzezeit in Balatonkeresztúr-Réti-dűlő, Mehrfachbestattung B-938: S14–S21.*



tion of age-at-death was based on the ribbed surface of the *facies symphy-seos ossis pubis*, the trajectory of the proximal epiphysis of the *humerus*, and the abrasion of the teeth. The sexualisation index was average (+0.70). The skull was short, broad, *hyperbrachycephalic*, and had a planoccipital profile (Köhler 2006, Tab. 1). The calculated stature was high: 173.5 cm (Köhler 2006, Tab. 2). Anatomical variations: *ossa wormiana* on the sides of the skull were visible. Pathology:

incomplete *sacrum bifidum*, enthesopathy on both *tibiae*. On the inner side of the left medial surface of the pelvis a 1.8 × 1.8 cm area suggests the presence of a tumour during life. No *caries* was observed on the 31 remaining teeth, with small amount of *calculus*, tooth abrasion level 3.

Individual S18 (Fig. 4; Fig. 5c) was a 3–4-year-old male child, whose body was lying on the right side with slightly flexed legs, and a west–east axis orientation. The remains consisted of a fragmentary skull with moderately preserved, incomplete postcranial skeletal bones. Determination of age-at-death was based on the abrasion of teeth and the length of the long bones.

Individual S19 (Fig. 4; Fig. 5c) was a 9–10-year-old male child, whose upper body was in supine position, with bent legs on the right side, and oriented on a south–north axis. The remains consist of a fragmentary skull and skeletal bones. Determination of age-at-death was based on the abrasion of teeth and the length of the long bones. Anatomical variation revealed *ossa wormiana* on both sides of the skull.

Individual S20 (Fig. 4; Fig. 5c) was a 1.5–2-year-old male child, whose body lay on the right side with slightly flexed legs and oriented from south–north. The remains consisted of a poorly preserved skull and fragmentary, incomplete postcranial skeletal bones. Determination of age-at-death was based on the abrasion of teeth and the length of the *humerus*. Pathology: lesions were observed on the long bones, especially along the muscle joints, as well as on the skull.

Individual S21 (Fig. 4; Fig. 5c) was a 1.5–2-year-old female child with very fragmented bones. The individual was lying in flexed position and oriented on a north–south axis. Determination of age-at-death was based on the length of the tibia (Köhler 2006, Tab. 2). According to genetic analyses individuals S20 and S21 were dizygotic twins.

Bioanthropological analyses: Sr isotope and genetic ancestry of the Balatonkeresztúr populations

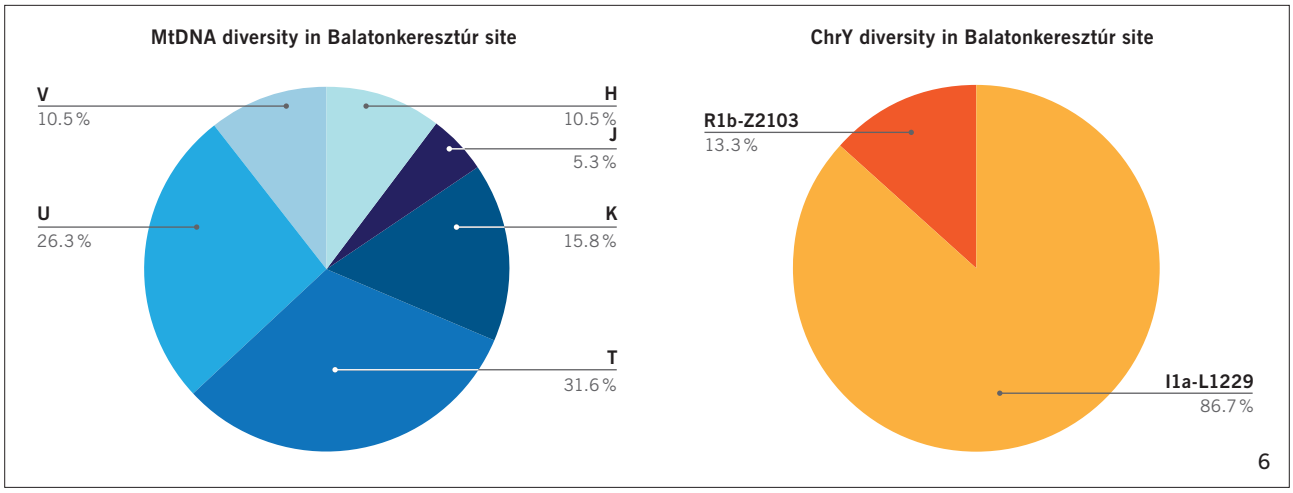
Dental enamel samples from Early Bronze Age burials (S1–13, S45) were analysed for their strontium isotope ($^{87}Sr/^{86}Sr$) ratios by the ICER laboratory, Atomki, Debrecen (Hungary), while samples of the Middle Bronze Age multiple burial (S14–20) were analysed at the Center for Anthropological Research (CAR) at Quinnipiac University and the Yale Metal Geochemistry Center (Department of Geology and Geophysics at Yale University (for details of methodology see Gerber et al. 2023). The first molar was sampled, or the second/third molar if the first was not available. In the case of the multiple burial, the first and third molars were both sampled. According to our results (Tab. 2) the radiogenic strontium isotope data ($^{87}Sr/^{86}Sr$) from all of the Balatonkeresztúr individuals were consistent with »local« values of the biologically available strontium ratio measured from plants, water and soil from the region to the south of Lake Balaton (calculated by taking the mean value of the published plant and water samples: Alt et al. 2014) plus or minus two standard deviations. There were no significant differences between males and females or subadults versus adults. The samples from the multiple burial of the Transdanubian Encrusted Pottery culture (Pit: B-938, S14–20) were slightly less radiogenic and more variable than the earlier time periods. This is particularly apparent for samples from three individuals (S15, S16, and S17) where the first and third molars were sampled. While both values could have come from the region south of Lake Balaton, they exhibit some spread, indicating movement within the region during the early adolescence period of their life.

The archaeogenetic studies were carried out in the Institute of Archaeogenomics, Research Centre for the Humanities in Budapest, Hungary with state of the art NGS (Next Generation Sequencing) methodology (for details see Gerber et al. 2023). Samples were taken from Early Bronze Age human remains in accordance with the international standards: from the *pars petrosa* of the temporal bone or, in the absence of it, from tooth material. DNA library preparation for shotgun sequencing was carried out in dedicated sterile laboratory facilities following the most recent methodology (Dabney et al. 2013; Rohland et al. 2015; Lipson et al. 2017). An average of 5 million DNA fragments (reads) were randomly shotgun-sequenced per sample, using the sequencing platforms Illumina MiSeq and NovaSeq. Bioinformatical analyses consisted of raw sequencing read-filtering and mapping to the human reference genome (hg19 version) and post-filtering data processing. We called for 1.240 million Single Nucleotide Polymorphisms (SNPs) from the genomes, a frequently used genomic SNP panel in ancient DNA analyses (Mathieson et al. 2015), from which an average of 101 thousand SNPs per sample were retrieved from the population of this study. This was a sufficient amount for various population genetic analyses, including PCA and allele-frequency-based methods, and even for a – limited – phenotypic variant discovery (Walsh et al. 2014; Walsh et al. 2017; Chaitanya et al. 2018).

Male dominance (~ 78 %) in both periods suggest distinctive funeral treatment for males and females. However, in other cemeteries of the same community (e.g., Ordacsehi and Bonyhád in Hungary), males, females and children were buried close to each other, suggesting high variance of burial practices (Somogyi 2004; Hajdu et al. 2016).

According to the results, the Kisapostag/earliest Encrusted Pottery population had a high level of hunter-gatherer (HG) genetic ancestry, compared to other Bronze Age groups of the region, beside genetic material of the Anatolian farmers and the Yamnaya component from the steppe[3]. Based on the extensive population genomic analyses (for details see Gerber et al. 2023) the origin of this outstandingly high HG ancestry can be traced back to previously overlooked regions in Eastern Europe, such as today's Ukraine, Moldavia, Romania or Belarus Belarus. New results (Chyleński et al. 2023) supports this assumption. Biological connections of this population in the wider area could have been traced back via this peculiar ancestry. Population

3 Gamba et al. 2014; Allentoft et al. 2015; Brandt et al. 2015; Haak et al. 2015; Lipson et al. 2017; Mathieson et al. 2018; Olalde et al. 2018.



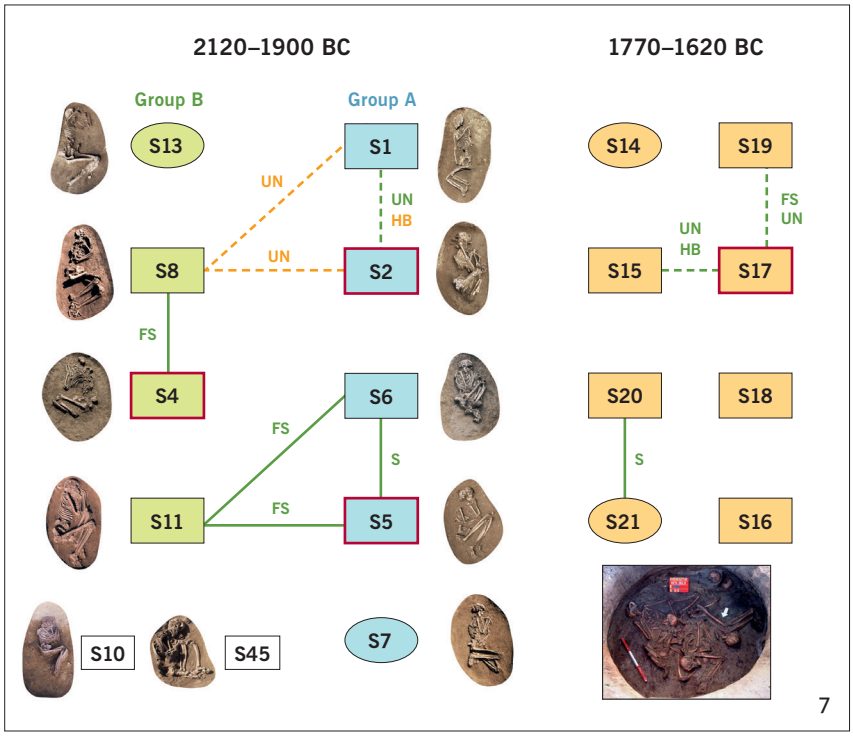


Fig. 6 Mitochondrial DNA and Y chromosomal haplogroups or the ratio of maternal and paternal lineages in the genetic dataset of Balatonkeresztúr-Réti-dűlő from the Bronze Age.

Abb. 6 *Mitochondriale DNA und Y-chromosomale Haplogruppen oder das Verhältnis der mütterlichen und väterlichen Abstammungslinien im genetischen Datensatz von Balatonkeresztúr-Réti-dűlő aus der Bronzezeit.*

Fig. 7 Genetic relatedness network of Early and Middle Bronze Age burials at Balatonkeresztúr site (solid lines represent first degree, dashed lines second degree relationships; green line represents proven, orange unproven but possible relationships; FS: father-son, UN: uncle-nephew, S: siblings, HB: half brother). In three cases, more than one relation type can explain the scarce genetic data.

Abb. 7 *Genetisches Verwandtschaftsnetzwerk von Bestattungen aus der frühen und mittleren Bronzezeit am Fundort Balatonkeresztúr (durchgezogene Linien stellen Beziehungen ersten Grades dar, gestrichelte Linien zweiten Grades; FS: Vater-Sohn, UN: Onkel-Neffe, S: Geschwister, HB: Halbbruder). In drei Fällen kann mehr als ein Beziehungstyp die knappen genetischen Daten erklären.*

genetic analyses uncovered that the main ancestry component (~ 60 ± 8 %) for the Transdanubian Encrusted Pottery Culture individuals was the Kisapostag/earliest Encrusted Pottery Culture population. Differences mostly driven by female-biased admixture with various local populations, which was genetically best represented in the currently available dataset by Transdanubian Late Bronze Age or Early and Middle Bronze Age Maros Culture data from modern-day Serbia (Freilich et al. 2021; Patterson et al. 2022; Gerber et al. 2023). This indicates not only cultural but also genetic continuity between the two communities (detected by archaeological and anthropological data also in the cemetery of Bonyhád; Hajdu et al. 2016).

Accordingly, numerous contemporaneous populations show admixture with the Kisapostag/earliest Encrusted Pottery and/or Transdanubian Encrusted Pottery associated population from Czechia to Serbia. The transition of Kisapostag to Encrusted Pottery in the Balatonkeresztúr site was followed by the dilution of their characteristic ancestry most likely by female-biased admixture of local populations, as paternal lineages remained mostly unchanged between periods (cf. Tab. 1; Fig. 6). This supports that female exogamy, detected elsewhere as a general phenomenon in the Bronze Age (Mittnik et al. 2019), can also be observed among this population living in the vicinity of Lake Balaton, although this may have been limited in distance according to the local strontium isotope signature.

Biological relatedness and Bayesian modelling of radiocarbon dates

Biological relatedness analyses are important to reveal social structures in prehistory lacking written records or human documentation. Kisapostag/earliest Encrusted Pottery Culture is represented by three relationships; green line repre-

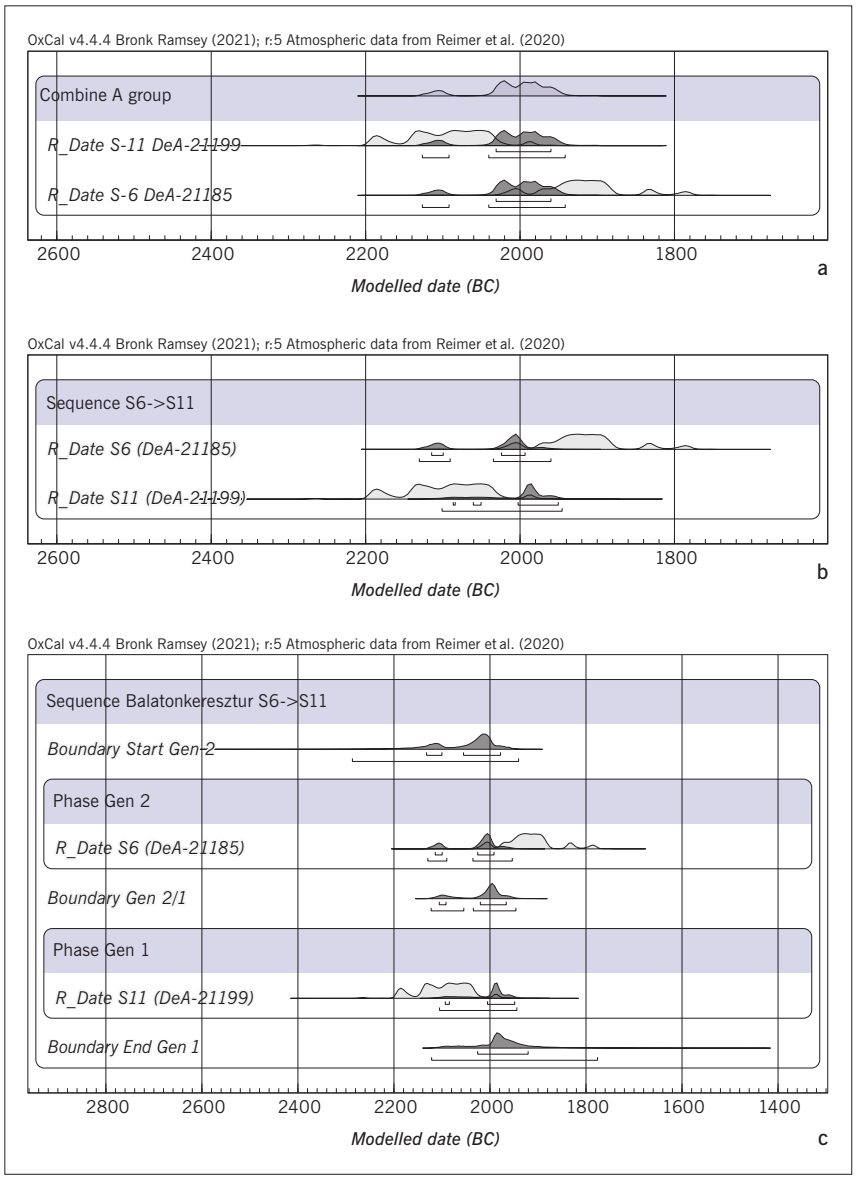


Fig. 8a–c Modelled radiocarbon dates. a Modelled radiocarbon dates of samples S6 and S11 from the Balatonkeresztúr site; b Modelled radiocarbon dates of samples S6 and S11 from the Balatonkeresztúr site (a multiplot, where S6 precedes S11); c Modelled radiocarbon dates of samples from the Balatonkeresztúr site for individuals S6 and S11.

Abb. 8a–c *Modellierte Radiokarbondaten. a Modellierte Radiokarbondaten der Proben S6 und S11 vom Fundort Balatonkeresztúr; b Modellierte Radiokarbondaten der Proben S6 und S11 vom Fundort Balatonkeresztúr (ein Multiplot, bei dem S6 vor S11 steht); c Modellierte Radiokarbondaten von Proben aus der Fundstelle Balatonkeresztúr für die Individuen S6 und S11.*

sents proven, orange unproven but possible relationships; FS: juveniles (16–19 year-old) and seven adults (30+ year-old) distributed into two spatial groups: Grave Group A and B (cf. Fig. 1; Tab. 1). One child grave (individual S10) and the burial of another adult male (S45) were further away from the others. The absence of children from the site is a phenomenon which often can be observed in the cemeteries of prehistoric and early historic periods and can be traced back to different preservation dynamics or burial practices of adults (Mende 2000), while the reason for the absence of young adults (~ 20–30 year olds) is unknown.

According to the results of the uniparental and the autosomal *READ* (Monroy Kuhn et al. 2018; cf. Günther in this volume)/MPMR (Modified Pairwise Mismatch Rate, Gerber et al. 2023) genetic relatedness analyses, a number of first- (parent-offspring, siblings) and second-degree paternal (on the Y-chromosomal lineage identical) relations were found within the Kisapostag/earliest Encrusted Pottery Culture Group. The kinship network of the population approximately follows the distribution of individuals in Grave Groups A–B, which were likely established along family relationships and chronology (Fig. 7): ascendants, i.e., the earliest members of the group, were also the genetically most distant (i.e., highest huntergatherer ancestry component) individuals compared to others represented in Grave Group B, while their children and likely grandchildren and/or nephews were in Grave Group A. The distant inhumations (S10, S45) did not show a biological relationship to any other individuals up to second degree.

Individuals from the Middle Bronze Age multiple burial also showed a few blood relations (Fig. 7): a half-brother or uncle-nephew, a father-son and dizygotic twins (the oldest detection of such relatedness to our knowledge). Based on these results, this pit cannot be considered as a single blood-related family »mass grave«. However, we also have to bear in mind that possible further connections may have remained hidden due to low genomic coverages of the samples. Several recent archaeological studies emphasise that prehistoric social kinship relations were not necessarily determined by biological links (Brück/Frieman 2021; Mittnik et al. 2019), and it is possible to assume second marriage due to higher female mortality (Rebay-Salisbury 2017). So we

have to note that the interpretation of an extended family group cannot be excluded in the case of the multiple burial.

Most male individuals in both periods belong to the Y chromosome haplogroup I2a-L1229, except for two haplogroups R1b-Z2103 (cf. Tab. 1). This uniparental makeup shows a patrilocal social structure that is similar to previously reported Bronze Age findings (Mittnik et al. 2019; Schroeder et al. 2019; Žegarac et al. 2021), and results also resemble to previous observations about the Encrusted Pottery Culture's population at the Jagodnjak site, Croatia (Freilich et al. 2021).

Radiocarbon dating was performed for all Bronze Age horizons of the site at the HEKAL AMS ^{14}C facility of the Institute for Nuclear Research, Debrecen (Molnár et al. 2013; Molnár et al. 2013a), except for individual S16, which was measured at the VERA AMS facility in Vienna. The dates were calibrated with the OxCal v4.4 software using the IntCal20 Northern Hemisphere radiocarbon calibration curve (Bronk Ramsey 2009; Reimer et al. 2020; all calibrated dates are presented at 2σ range, unless indicated otherwise). Overall 10 samples have been radiocarbon-dated from the 19 burials published here: eight samples from Kisapostag/earliest Encrusted Pottery period (four from Grave Group A: S1, S2, S6 and S7, two from Grave Group B: S11 and S13, and two from isolated graves, S10 and S45), while two individuals were sampled from the Middle Bronze Age mass grave (S16 and S17). The dates from the graves of the Kisapostag/earliest Encrusted Pottery Culture range between 2200 and 1770 cal BC, however, with Bayesian analysis using the OxCal software the timespan of the burials can be reduced to ca. 2120–1900 cal BC (95.4 % CI), with two graves (individuals S10 and S11) possibly being slightly earlier (s. Gerber et al. 2023).

In recent years it has been recognized that archaeogenetic analysis and information on relatedness can provide further prior chronological information (Fig. 8a–c) that can be built into the Bayesian modelling of radiocarbon dates (Sedig et al. 2021; Massy et al. 2022). A new software, refinedate, was developed to perform such analyses. Nevertheless, OxCal software is also perfectly capable of including and analysing such information. Here we used Oxcal, following an earlier study (Massy et al. 2022). There is a first-degree (father-son) relationship between indiviual S11 from Grave Group B and individual S6 from Grave Group A. Since the father (S11) died at the age of 34–43, and the son at the age of ca. 17–18 years, it may be assumed that their dates of death were rather close, if not even simultaneous. Although we obviously cannot be certain of this, we combined these to date a single event. The combined date for their deaths (Fig. 8a) is 2130–1940 cal BC (95.4 % CI), within this boundary dates between 2050 and 1940 cal BC have a significantly greater probability (84.4 % CI).

In the case of a 17 year-old son and a 43 year-old father it is also possible that the son died earlier, which we may use as prior chronological information (Massy et al. 2022). This scenario was also modelled. Since this prior information seems to reverse the order of these two dates (which is also indicated by OxCal through the poor agreement values), modelling them should actually place significant constraints on their ranges. We can model them in two ways. We may simply place these dates into a sequence where individual S6 precedes individual S11 (Fig. 8b). In this case the 2σ date for S6 is 2140–1960 cal BC, where the period of 2040–1960 cal BC has greater probability (68.9 %). The date for S11 is 2110–1940 cal BC.

The other way is to place these two dates into a model with two phases, where the data of the son represents the earlier phase (generation), and that of the father the latter (Fig. 8c). Here S6 is dated to 2130–1950 cal BC, where the range between 2040 and 1950 has greater probability (73.5 %), and S11 is dated to 2110–1940 cal BC. Thus, both models indicate roughly the same dates for the deaths of these individuals.

The dates of the Middle Bronze Age multiple burial fall between 1890 and 1540 cal BC (Tab. 1). Since the context and the full articulation of the skeletons indicate that the individuals deceased at the same time or within a short time of each, the two dates were combined to date a single event. The combined date for the mass grave is 1870–1620 cal BC (95.4 % CI), within this boundary the timespan between 1770 and 1620 cal BC has a significantly greater probability (93.1 % CI; s. Gerber et al. in press, Suppl.).

Lifeway narratives of the Bronze Age community from Balatonkeresztúr

The cultural relations and origin of the Early Bronze Age communities in the Carpathian Basin have been explained with various ways, mainly with the arrival of population groups from the east (Yamnaya Culture), from the west (Bell Beaker Groups), and from the south (Vučedol and Somogyvár-Vinkovci Groups). According to these views newcomers also brought with them the technology and know-how of bronze metallurgy (Bóna 1975; Bóna 1992). The pottery decoration technique (the so-called reeled-stick decoration) of the Kisapostag/earliest Encrusted Pottery Culture, appearing in the last phase of the Early Bronze Age according to the Hungarian relative chronology (c. 2200/2150 cal BC; RBA1), was connected to the Middle Dnieper region (Ukraine) or epi-Corded Ware Groups (northern Carpathians, e.g. Chłopice-Veselé, Slovakia). Similarities of burial positions in connection with the Corded Ware were also were pointed out (Bóna 1961; Bándi 1984; Hajdu et al. 2016). However, local development of communities connected to eastern (Makó-Kosihy-Čaka Culture) or southern (Somogyvár-Vinkovci Culture) origins, as well as western and southwestern contacts (with the Litzenkeramik or Guntramsdorf-Drassburg Group in Eastern Austria, Slovenia, and western Croatia) were also raised in the archaeological literature (Bóna 1992; Črešnar 2010; Kiss 2015). Moreover, the Bell Beaker influence was mentioned in relation to the craniometry data: the so-called *Glockenbecher* or *brachycranic* skull type (Mozsolics 1942; Zoffmann 2000; Köhler 2006).

Bioarchaeological analyses of the Early and Middle Bronze Age burials from Balatonkeresztúr (cf. Tab. 1) indicate that the genomic ancestry of the Early Bronze Age Kisapostag/earliest Encrusted Pottery Culture population was previously unknown from Central Europe (from a later

Laboratory ID	Laboratory	Burial/Specimen	Tooth Sampled	$^{87}Sr/^{86}Sr$
I/2584/2	ICER Laboratory, Atomki	Balatonkeresztúr, S1	Second molar	0.709843
I/2584/3		Balatonkeresztúr, S2	Second molar	0.709790
I/2584/4		Balatonkeresztúr, S4	Second molar	0.709797
I/2584/5		Balatonkeresztúr, S5	Second molar	0.709896
I/2584/6		Balatonkeresztúr, S6	First molar	0.709778
I/2584/7		Balatonkeresztúr, S7	First molar	0.709969
I/2584/8		Balatonkeresztúr, S8	Second molar	0.709802
I/2584/9		Balatonkeresztúr, S9	Third molar	0.709692
I/2584/10		Balatonkeresztúr, S10	Second molar	0.709716
I/2584/11		Balatonkeresztúr, S11	Second molar	0.709763
I/2584/12		Balatonkeresztúr, S13	Second molar	0.709757
I/3273/1		Balatonkeresztúr, S45	Third molar	0.709820
CAR0995	Quinnipiac University, Yale Metal Geochemistry Center	Balatonkeresztúr, S14 (Pit B-938)	First molar	0.709413
CAR0991		Balatonkeresztúr, S15 (Pit B-938)	First molar	0.709562
CAR1016		Balatonkeresztúr, S15 (Pit B-938)	Third molar	0.708721
CAR0992		Balatonkeresztúr, S16 (Pit B-938)	First molar	0.709482
CAR1015		Balatonkeresztúr, S16 (Pit B-938)	Third molar	0.709284
CAR0993		Balatonkeresztúr, S17 (Pit B-938)	First molar	0.709530
CAR1014		Balatonkeresztúr, S17 (Pit B-938)	Third molar	0.708945
CAR0994		Balatonkeresztúr, S18 (Pit B-938)	First molar	0.709588
CAR0990		Balatonkeresztúr, S19 (Pit B-938)	First molar	0.709613
CAR0996		Balatonkeresztúr, S20 (Pit B-938)	First molar	0.709432

Tab. 2 Radiogenic isotope data for Balatonkeresztúr site samples.

Tab. 2 *Radiogene Isotopendaten für Proben von dem Fundort Balatonkeresztúr.*

period see: Freilich et al. 2021). The aDNA analyses revealed that the Kisapostag/earliest Encrusted Pottery population can be connected to newcomers in the Carpathian Basin, most probably arriving from Eastern Europe, in line with the earlier archaeological assumptions of several scholars (Bóna 1961; Hajdu et al. 2016). Strontium ($^{87}Sr/^{86}Sr$) isotope ratio data from molars (Tab. 2) indicate that every individual investigated in this study was raised and lived in at least close proximity to the Balatonkeresztúr site in their childhood and early adolescence. This suggests that individuals of this grave group do not represent the first generation of the Kisapostag/earliest Encrusted Pottery Culture associated population in Transdanubia (Western Hungary). This group, which had settled in the southern shore of Lake Balaton, was the genetic basis of the succeeding community of the Transdanubian Encrusted Pottery Culture, which was also suggested by Bronze Age research based on pottery typochronology (Kiss 2012; Hajdu et al. 2016). The specific genetic makeup of newcomers diluted the culture generation by generation, but it remained characteristic for centuries in the region (in details: Gerber et al. 2023). The homogeneity of paternal lineages suggests a social organisation similar to the patrilocal residence system during the Early and Middle Bronze Ages of the region (Schroeder et al. 2019; Freilich et al. 2021). Local values of strontium isotope data, along with similar genomic makeup of both sexes suggest exogamy most probably occurred between communities of the same population living in distant villages. Grave groups were established along family relationships. Genetic data from other Encrusted Pottery Culture sites (e.g., Jagodnjak, Croatia; Freilich et al. 2021) also support that communities belonging to the culture may have been based on families along the male line or a clantype society.

Considering the unstructured age and kinship distribution in the multiple burial compared to the earlier phase, the coetaneous death of at least eight people and the absence of traumatic or ritual events on bones (in contrast e.g., with what was detected by Meyer et al. 2009; Szeverényi et al. 2019), and the non-normative (non-cremated) nature of the burial all point to a sudden tragic event in the Transdanubian Encrusted Pottery period (between 1800–1600 cal BC), as first suggested based on the anthropological analyses (Köhler 2006). The position of the deceased placed in the pit, similar to earlier inhumations of the same society, support an interpretation that these individuals were buried by their own community for a special reason (most probably an infection caused by pathogens not detectable on their bones).

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Bronze Age relations: genetics, kinship, and gender in Britain

Joanna Brück

Zusammenfassung

Beziehungen in der Bronzezeit: Genetik, Verwandtschaft und Geschlecht in Britannien

Das bronzezeitliche Europa wird oft als eine Zeit angesehen, in der führende Adelsschichten entstanden, die um die Kontrolle des Handels und die Anhäufung von Reichtum in Form von Bronzegegenständen und anderen Prestigegütern konkurrierten. Jüngste archäogenetische Studien stützen diese Sichtweise auf die Bronzezeit, in der expansive Kriegergesellschaften in patrilinearen Verwandtschaftsgruppen organisiert waren und der Austausch von Frauen als Bräute zwischen mächtigen Männern dazu diente, politische Loyalitäten zu festigen. Aber gibt es Alternativen zu diesem geschlechtsspezifischen Narrativ der Vergangenheit? Obwohl archäogenetische Analysen spannende neue Erkenntnisse erbracht haben, basieren deren aktuelle Interpretationen häufig auf biogenetischen Formulierungen von Verwandtschaft und Identität, die das Erbe der kolonialen Geschichte repräsentieren. Im Gegensatz dazu weist die anthropologische Forschung darauf hin, dass Vorstellungen von Verwandtschaft nicht immer auf biologischer *Verwandtschaft beruhen müssen und dass die Zusammenhänge zwischen Abstammung, Ehe und Geschlecht komplex und variabel sind. Am Beispiel Britanniens in der Zeit des Chalkolithikums und der Bronzezeit sowie der Zusammenführung der genetischen und archäologischen Nachweise werden in diesem Artikel alternative Möglichkeiten zur Einordnung der genetischen Daten und zur Erforschung der sozialen Prozesse untersucht, durch die Identitäten in der Vorgeschichte konstruiert wurden. Obwohl in dieser Region paternale Bindungen offensichtlich von Bedeutung waren, lassen sich auch andere Formen der Verwandtschaft erkennen, was darauf hindeutet, dass die Stellung der Frauen in Verwandtschaftsgruppen unterschiedlich war; dass soziale Prozesse wie Rituale und Austausch für die Etablierung von Beziehungen von zentraler Bedeutung waren; und dass auch nicht-menschliche »Andere« als Verwandte betrachtet werden konnten. Diese Betrachtung vom europäischen Randgebiet legt nahe, dass es gewinnbringend sein könnte, alternative Wege zur Interpretation der archäogenetischen Evidenz aus anderen Regionen Europas in den Untersuchungen zu berücksichtigen.*

Summary

Bronze Age Europe is often seen as a period which saw the emergence of chiefly aristocracies who competed to control trade and to accumulate wealth in the form of bronze objects and other prestige goods. Recent archaeogenetic studies have supported this vision of the Bronze Age, in which expansionist warrior societies were organised into patrilineal kin groups and the exchange of women as brides between powerful men was used to cement political allegiances. But are there alternatives to this gendered narrative of the past? Although archaeogenetic analyses have yielded exciting new insights, current interpretations of the evidence are often based on biogenetic formulations of kinship and identity that are the legacy of colonial history. In contrast, anthropological research indicates that ideas of kinship are not always based on biological *relatedness and that the links between descent, marriage and gender are complex and variable. Taking Chalcolithic and Bronze Age Britain as an example, and bringing together the genetic and archaeological evidence, this paper will consider alternative ways of interpreting the genetic data and of exploring the social processes by which identities were constructed in prehistory. In this region, although paternal links were evidently significant, other forms of kinship can be discerned, suggesting that the position of women in kin groups varied; that social processes such as ritual and exchange were central to the making of relations; and that non-human others could also be considered as kin. This view from the margins suggests that it may be fruitful to consider alternative ways of interpreting the archaeogenetic evidence from other regions of Europe.*

Introduction

Bronze Age Europe is often viewed as the first globalised economy, a period in which technological innovation and long-distance trade facilitated the creation of wealth, increasing inter-personal competition and the emergence of institutionalised forms of social difference. According to this perspective, the Bronze Age is a stepping-stone towards the modern world. Central to developments of the period, it is argued, were the activities of male warriors, traders and chiefs. Women, in contrast, are viewed as objects of masculine control, displaying the wealth of their husbands in bronze

and gold ornaments, and traded as wives to bolster the political aspirations of male kin.

This vision of the Bronze Age foregrounds certain aspects of the evidence, such as the appearance of wealthy burials, the development of specialised weapons like swords and rapiers, and the accumulation of scrap metal hoards used for recycling and exchange. It also interprets that evidence from a very particular perspective. Men buried with bronze or gold grave goods are chiefs, traders or craftsmen; women buried with bronze or gold grave goods are bartered brides (Frieman et al. 2019). Although it is widely accepted that bronze was not always commodified, even socially significant items exchanged as gifts have primarily been viewed as objects to be manipulated in strategies of social and political aggrandisement (Brück/Fontijn 2013).

However, a different image of the Bronze Age is presented when one examines other aspects of the evidence. In Britain, the focus of this paper, the expansion of developer-funded archaeology over the past 30 years has reframed our perspective away from the hoards and burials that dominated narratives of the Bronze Age for much of the 20th century. The most common finds now recovered during developer-funded excavations are the residues of everyday life: some 8000 settlements of Middle Bronze Age date have now been recorded, for example (Caswell 2018). These present an alternative reading of Bronze Age life in which competition between warrior elites is far from everyday experience, and in which both women and men were co-participants in complex social and cultural worlds. At the same time, recent discussion of hoards and burials has interpreted such finds in new ways. It is now recognised that bronze artefacts, for example, were not commodities to be weighed and measured for the purposes of trade, nor were they simple markers of status; rather, they were inextricably bound up with the life-histories of the people through whose hands they passed (Fontijn 2019).

In fact, it can be argued that colonial and dualist thinking lies at the heart of traditional narratives of the Bronze Age. The competitive individualism and economic intensification imagined for the period are predicated on modes of thinking characteristic of the modern Western world, in which self is divided from other, subject from object, culture from nature, and men from women (Olwig 1993; Thomas 2004). In this way, artefacts, women, animals and land are constituted as objects to be manipulated and exploited for economic and political gain. But such dualisms are more than conceptual categories: they are the product of recent colonial histories. European colonialism was legitimated by figuring land, natural resources and indigenous peoples as objectified »others« without history or agency, beyond the bounds of normal social and moral relations (e.g., Thomas 1994; Harley 2009); thus, they could be transformed into commodities to be bought, sold and controlled.

But how do these general comments on the Bronze Age relate to recent advances in archaeogenetics? The potential for ancient DNA to yield extraordinary insights into human mobility, interaction and social structure has been hailed as a scientific revolution (Kristiansen 2022). At the beginning of the Bronze Age, the appearance of populations whose genetic ancestry ultimately derived from the Eurasian steppes (Allentoft et al. 2015; Haak et al. 2015) has been interpreted as indicating the large-scale migration of young men – described by archaeologists as »war bands« seeking new territories and intermarrying with local women (Kristiansen et al. 2017). These men are viewed as agents of significant social and economic change, introducing new technologies such as metalworking, new modes of transport, and intensive exploitation of secondary products (Wilkin et al. 2021). Beyond the macro-level of population dynamics, the past few years have seen increasing fine-grained analyses of prehistoric burials to understand Bronze Age kinship structures, marriage and residence rules. To date, most of these studies have argued that the primary unit of kinship was the monogamous nuclear family, and that patrilineal descent, patrilocal residence and female exogamy were the norm (e.g., Mittnik et al. 2019; Sjögren et al. 2020). The results of archaeogenetic research therefore appear to support views of male-dominated, hierarchical Bronze Age societies in which women are figured as passive objects of exchange, while male mobility is viewed as the result of activities such as warfare and trade.

Other perspectives on kinship and marriage

Contemporary Western understanding of kinship, marriage and gender are, however, profoundly interconnected with colonialism and its legacies. Indigenous and queer theorists have demonstrated how the imposition of settler sexuality on Indigenous communities was a core component of European colonialism in recent centuries (e.g., Smith 2005; Rifkin 2011). Colonial ideologies defined patriarchal, heteronormative and monogamous family structures as a moral imperative, central to the civilising mission of European settlers. By controlling women and identifying certain types of intimate relations as immoral, the ownership and transmission of land and other forms of wealth could be regulated, class boundaries maintained, and certain forms of labour – notably, reproductive labour – obscured and appropriated. Central to the colonial endeavour was a dualistic conceptual framework which distinguished culture from nature: by positioning women, Indigenous peoples and natural resources as part of the latter, the seizure of land could be legitimised, and land, animals and women could be defined as property (Stoler 2002; Descola 2013; TallBear 2018).

Indigenous theorists and anthropologists describe how in other cultural contexts, kinship extends to include non-human others, including animals and plants, sustained through relations of care, obligation and interdependency (Kimmerer 2013; TallBear 2018). In many Indigenous communities, it is not sexual relations that determine rights over resources. Rather, relations with non-human others are central to the constitution of kinship: abiding, emotional attachments to place or links to totemic and ancestral animals define identity and ensure access to resources (e.g., Sissons 2013). Western concepts of kinship consider it possible for kin relations to exist only between humans. This is due to the distinctions that are drawn between culture and nature, self and other, and humans and animals. By stripping the non-human world of agency, Western forms of kinship legitimise extractive, rather than meaningful, social relations between humans and non-human others (Haraway 2016). In contrast, Indige-

nous scholars propose expansive definitions of kinship that encompass relations beyond those centred on procreation, ownership and control. These perspectives underscore the ties of mutual care and interdependency between humans and non-humans, which must be nurtured to ensure a sustainable world (Kimmerer 2013; TallBear 2018).

Anthropologists have long recognised the extraordinary cross-cultural variability of kinship. There is always an element of cultural selection built into kinship systems: some relationships are considered more significant than others. For example, S. Kahn's study (Kahn 2000) of the new reproductive technologies in Israeli Orthodox communities in the 1990s demonstrated that because Jewishness is considered to be transmitted exclusively through the mother, and non-Jewish paternity is not recognised in religious law, children born to different women using sperm from the same non-Jewish donor are considered to be unrelated. In south India, C. Busby (1997) has shown that the children of a woman and those of her brother are also considered to be unrelated, as men pass on male substance to their children in the form of semen, while women pass on female substance in the form of blood and breast milk. The children of a brother and sister therefore do not share the same substance. Genetic relatedness, in other words, does not translate directly to social relatedness. This is because in many societies, although the physical process of procreation is acknowledged, it may not be considered socially salient, and the production of babies may be understood in other ways. E. Evans-Pritchard's classic study of the Nuer in the early 20th century illustrated how cattle are said to beget children (Evans-Pritchard 1951). Nuer fatherhood was not predicated on sexual relations with the mother, but on the transfer of cattle in bride-wealth transactions. If a woman's husband died, she could take a new partner, but any children from this second relationship were considered to be the children of the man on whose behalf her bride-wealth was originally paid.

In many other societies, too, biological parentage is not the primary determinant of kinship. Instead, kinship is viewed as *socially* and *culturally* constituted – as the outcome of social not sexual relations. Kinship is understood to be a product of social practices including ritual, exchange and the sharing of food. J. Carsten (1997) describes how, on the island of Langkawi in Malaysia, kinship is viewed as an ongoing process that involves the sharing of substance. By living and eating in the same house, and by having children together, the blood of the husband and wife becomes increasingly similar over time. Foster children and other affines (people related by marriage) who eat food together also come to share the same blood. Because kin are made, not determined by birth, kinship can be strategic and situational. In many parts of highland New Guinea, immigrants are quickly absorbed into local descent groups, as residence (and not genetic links) is the most important factor in determining kinship (e.g., Held 1957). Although most societies in this region are patrilineal in principle, in practice co-resident maternal kin and affines may be considered members of the descent group. Elsewhere, different forms of kinship may be important in different contexts: among the Yakö of eastern Nigeria, land is passed down the paternal line, but cattle, money and cult membership are inherited from maternal kin (Ford 1950). Indeed, although broad »types« of kinship organisation can be identified (for example patrilineality), their socio-political implications vary significantly: gender ideologies and the position of women in patrilineal societies are extremely variable (Stone 2010), for example, yet the pictures we are presented with on the basis of the archaeogenetic data remain highly stereotypical.

These observations have several significant implications for our interpretation of the archaeogenetic evidence. Firstly, dominant Euro-American binary and heteronormative models of gender and kinship have their origins in a particular historical context and cannot be assumed to be universal. Secondly, genetic relationships are not the sole determinant of kinship: rather, social practices of various sorts make kin, and kinship transcends biological links. The material world is often central to the creation of kin, and non-human others can be considered to be kin. This suggests that there may be other ways of understanding how kin relations were constructed in the past that may be archaeologically accessible beyond the identification of biological links.

Making relations in Bronze Age Britain

In this paper, I will consider how to interpret the evidence for biological kinship presented in a recent study of archaeogenetic change in Chalcolithic and Bronze Age Britain (Olalde et al. 2018). I will then discuss how archaeologists can move beyond genetics to explore how social practice made kin in the past. I. Olalde et al.'s primary focus is on genetic change at the population level and their samples were not selected in order to consider kinship. Nonetheless, genetic links were incidentally identified between sixteen individuals in their dataset. Twelve of these were related through the paternal line (Booth et al. 2021), suggesting that patrilineal descent was a significant factor in the reckoning of social identity. These included three sets of paternal relatives from Amesbury Down in Wiltshire. Here, the inhumation burials of an adult male and subadult male from adjacent pits were 1st degree relatives and shared a paternal but not a maternal lineage, indicating that they were genetic father and son (Booth et al. 2021). The inhumation burials of two adult males found close together near a Neolithic timber post-setting were 2nd–3rd degree genetic relatives belonging to the same patrilineages but different matrilineages. Radiocarbon dates from these burials are statistically indistinguishable, suggesting that they may have been paternal cousins or half-brothers. A third pair of paternal relatives from Amesbury Down was identified from the so-called »Boscombe Bowmen« grave, a collective burial that contained both articulated and disarticulated remains (Fig. 1; Fitzpatrick 2011). Here, the inhumation burial of an adult male (burial 2504) was probably the paternal cousin or half-brother of an individual whose disarticulated skull had been placed at his feet (ON 10) (Booth et al. 2021).

Paternal links are evident not only in the burial of men. An older adult female buried on a wooden bier or in a wooden coffin at Yarnton (Hey et al. 2016) was the probable paternal grandmother of a male infant who had been buried close by (Booth et al. 2021). This suggests that the position of women in ancestral genealogies may also have been important. This

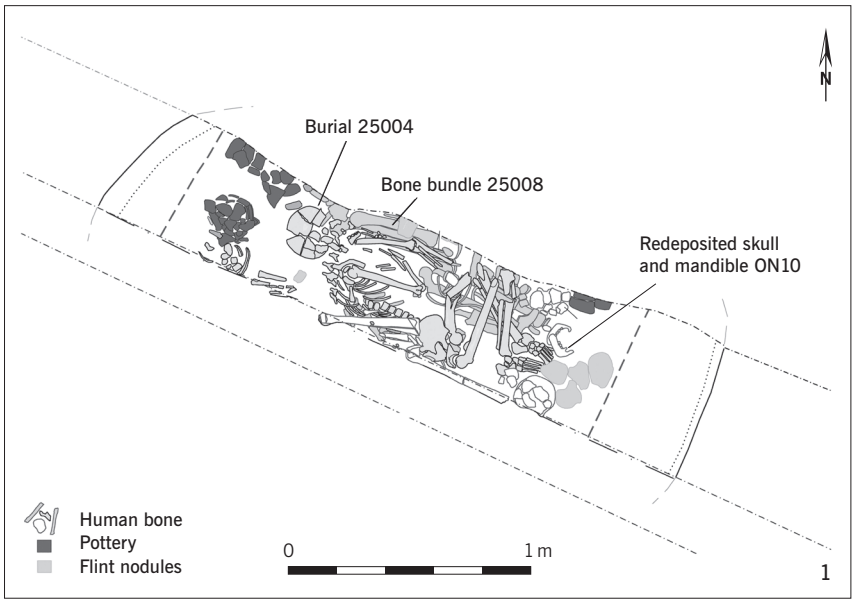


Fig. 1 The Boscombe Bowmen, Wiltshire.

Abb. 1 *Die Bogenschützen von Boscombe, Wiltshire.*



Fig. 2 Double burial, Trumpington Meadows, Cambridge.

Abb. 2 *Doppelbestattung, Trumpington Meadows, Cambridge.*

is supported by evidence for the deliberate curation of bones belonging to both men and women during this period. On Amesbury Down, a grave containing the inhumation burial of an adult woman was reopened to facilitate the removal of some of her bones and the rearrangement of others (Gibson 2013). Similar practices have been well documented elsewhere and have been interpreted as a means of engaging with, and retrieving, ancestral remains belonging to known and significant individuals for curation and redeposition (Brück/Booth 2020).

Anthropological studies of kinship demonstrate that even where there is patrilineal descent in principle, relationships with maternal kin continue to be highly important, facilitating access to land, goods, titles, and so on (e.g., Held 1957). It is therefore no surprise that maternal relations were sometimes also foregrounded. For example, the articulated skeleton of a 9–11-year-old female from Amesbury Down was placed in a pit adjacent to another pit containing an adult female skull and vertebrae (Powell/Barclay 2022). Ancient DNA and radiocarbon evidence suggests that the child was probably the genetic maternal aunt of the neighbouring burial (Booth et al. 2021). Elsewhere, a young man and woman buried together in the same grave at Trumpington Meadows, Cambridge (Fig. 2; Evans et al. 2018) were 2nd–3rd degree relatives belonging to the same matrilineage. It is possible that matrilineal descent was the key principle of kinship organisation in this community, hinting at regional variability in kinship structures. Radiocarbon dates on the remains of these two individuals are statistically indistinguishable. They may have been half-siblings related through their mother (Booth et al. 2021). In matrilineal societies, a woman's loyalty is to her brother not her husband (Schneider 1961). Alternatively, they may have been the children of two sisters. Parallel cousins (the children of same-sex siblings) are regarded as siblings in many societies and marriage between them is prohibited (e.g., Busby 1997).

As previously noted, many scholars have suggested that women were exchanged as marriage partners by their male relatives. The argument that Bronze Age societies were patrilineal and practiced virilocal marriage (where a woman moves to join her husband on marriage) is perhaps supported by the identification of the genetic daughter of one of the cousins from Amesbury Down (Booth et al. 2021). She had been buried on Porton Down, some 6.5 km to the southeast. However, the reconstruction of residence patterns is complicated by evidence for residential mobility during this period: we cannot assume that relatives who were buried together actually lived together during life. Isotope analysis indicates that both

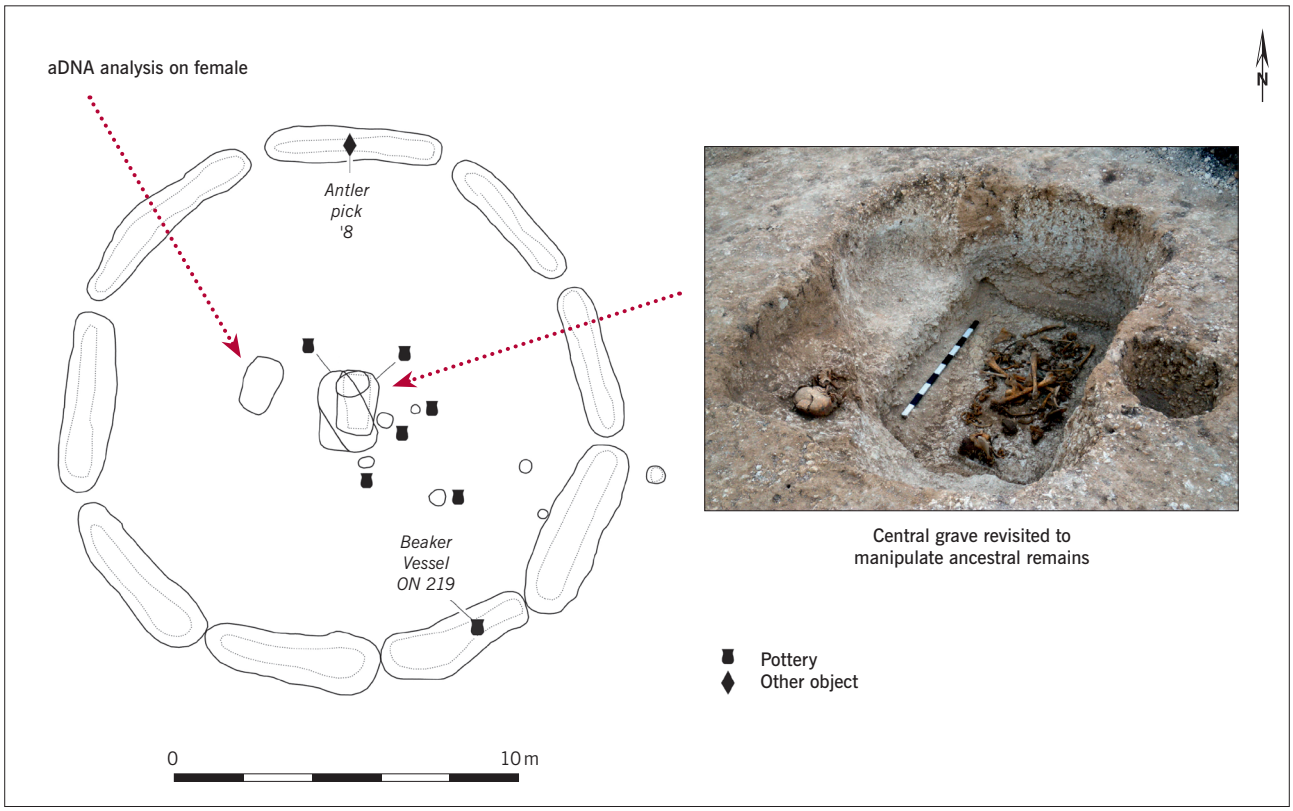


Fig. 3 The Porton Down (Wiltshire) ring-ditch and associated burials.

Abb. 3 *Der Ringgraben von Porton Down (Wiltshire) und die dazugehörigen Bestattungen.*

men and women moved (Parker Pearson et al. 2019). Of the seven burials (six male and one female) from Amesbury Down that have been subjected to both genetic and isotope analysis, the female and four males were all identified as non-local. It is clearly problematic to assume that the woman buried on Porton Down moved for the purpose of marriage when mobility (for a variety of reasons) might in fact have been a common life experience regardless of gender. The burial of an adult woman close to the grave of her paternal uncle or grandfather at Netheravon Flying School in Wiltshire (Cunnington 1929) also indicates that women did not always move away from their paternal kin. In this case, isotope analysis suggests that both individuals were non-local (Montgomery et al. 2019) and may have travelled together into this area.

Evidence for the curation and redeposition of ancestral remains (Booth/Brück 2020) also suggests that those who were buried together may not have lived together during life. Certainly, Chalcolithic and Early Bronze Age cemeteries cannot be assumed to represent all members of a particular residential or kin group, and other priorities may have determined the place of burial. The woman from Porton Down, for example, was one of a group of burials of four adult females and six children in a segmented ring-ditch (Fig. 3; Andrews/Thompson 2016). She lay approximately 1 m to the north-west of a large grave at the centre of the monument that contained the disarticulated remains of another adult female. The central grave had been revisited to access and manipulate this woman's bones; her skull was missing, suggesting that it may have been retrieved for deliberate curation or redeposition elsewhere. This latter individual may have been considered a significant ancestor and likely occupied a position of authority during life. The women buried in this monument were not accorded social positions relative to men, but rather, on their own terms.

Other evidence suggests that concepts of kinship were not always based on biological relatedness. At several sites, close spatial relationships between burials that likely reflected intimate inter-personal ties in life are not mirrored in the genetic data. Four individuals (Sk 2, Sk 4, Sk 7 and Sk 8) from Windmill Fields, Ingleby Barwick, North Yorkshire, were buried within a few metres of one another (Annis et al. 1997). Sk 2 and Sk 7 comprised articulated single burials of an adult male and an adult female. Sk 4 was a disarticulated adult male cranium excavated from a collective deposit of disarticulated bones in a wooden cist. Sk 8 comprised a disarticulated adult female cranium that formed part of a bundle of disarticulated crania and long bones (Fig. 4) accompanying an articulated adult female burial (Sk 6; which was not subject to archaeogenetic analysis). Their radiocarbon dates suggest they were broadly contemporary, but they were not close genetic relatives (Booth et al. 2021). It is possible that these burials were genetic relatives too distant to be recognised by the methods used by Olalde et al. (2018), although the probability of this is reduced given that they all belong to different paternal and maternal lineages. It seems likely that the individuals buried at Windmill Fields belonged to a single small community and that they may have viewed each other as kin. Here, co-residence may have determined kinship, as is common in many contemporary societies (e.g., Schneider 1984). The careful deposition of the disarticulated bundle of bones with articu-



Fig. 4 Windmill Fields, Ingleby Barwick, Stockton-on-Tees, Durham: inhumation burial (Sk 6) accompanied by a bundle of disarticulated bones, including disarticulated cranium (Sk 8).

Abb. 4 *Windmill Fields, Ingleby Barwick, Stockton-on-Tees, Durham: Körperbestattung (Sk 6), vergesellschaftet mit einem Bündel disartikulierter Knochen, einschließlich disartikuliertem Schädel (Sk 8).*

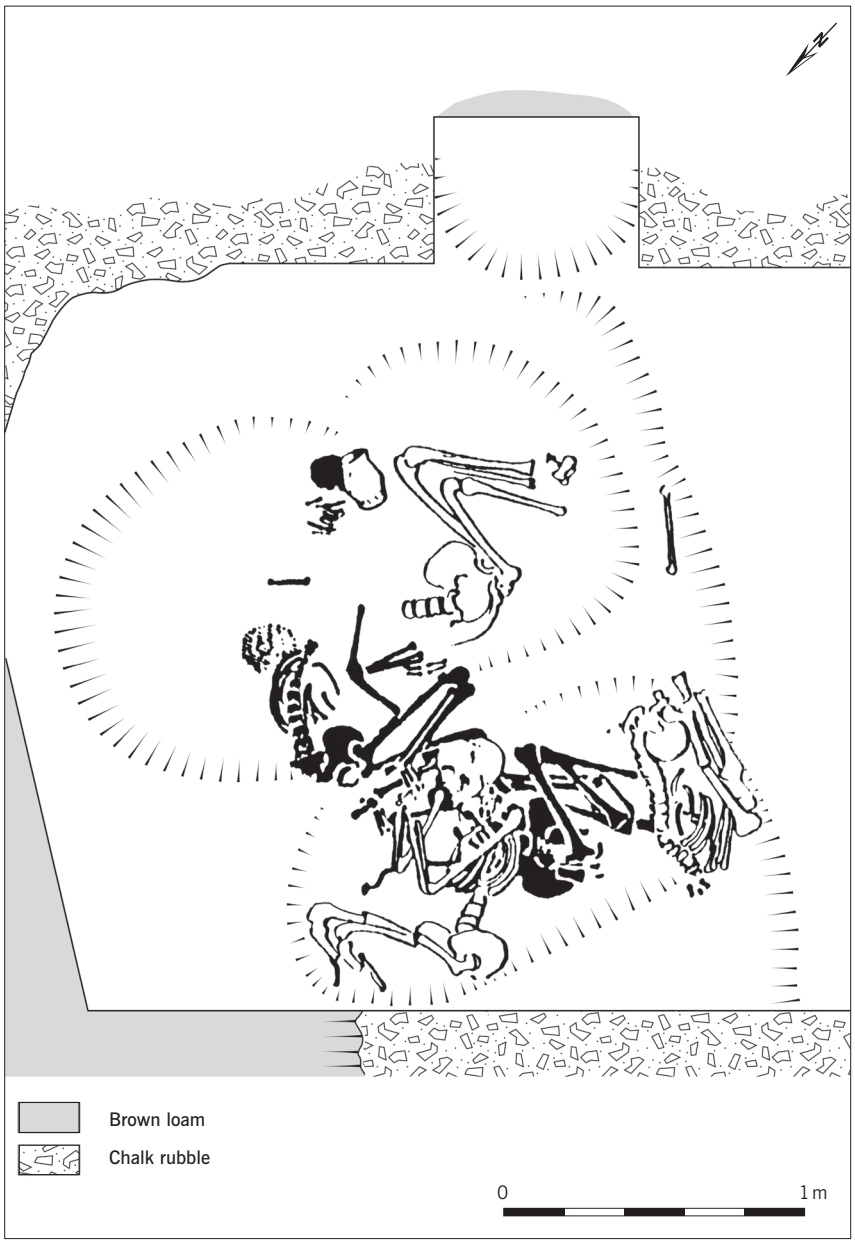


Fig. 5 Sequence of inhumation burials at South Dumpton Down, Kent.

Abb. 5 *Abfolge der Körperbestattungen in South Dumpton Down, Kent.*

lated burial Sk 6 illustrates how here, social practices involving the manipulation of the bodies of the dead were central to the creation of kin relations.

I have already pointed out how the heteronormative character of kinship in the contemporary Western world serves particular purposes, supporting a view of gender identity that is integral to colonial and capitalist modes of political and economic power. This means that it is important to be open to exploring the archaeological evidence for other types of relationship. At Needingworth Quarry, Cambridgeshire, an adult female aged 18–25 years was laid at the base of a deep grave (Olalde et al. 2019, 84; Suppl. Inf. 2). The grave was subsequently recut and received the burial of a second adult female more than 40 years old. Their deaths were not many years apart, but they were not genetically closely related. Anthropological studies of kinship and gender suggest there are various different ways in which this grave might be interpreted. It is possible that they were co-wives in a polygamous marriage. Alternatively, these burials might represent an instance of woman-to-woman marriage. Historically, woman-to-woman marriage was widespread in Africa (Levine 2008, 378). A woman presumed to be barren could divorce her husband and remain in her father's home. She could herself then marry a woman whose children would count her as their father and who would be members of her patrilineage. Woman-to-woman marriage enhanced women's status and offered greater social and sexual freedom. It is also possible that the women from the Needingworth Quarry grave were in an intimate same-sex relationship: this is something that is rarely considered in discussions of kinship and marriage in the Bronze Age.

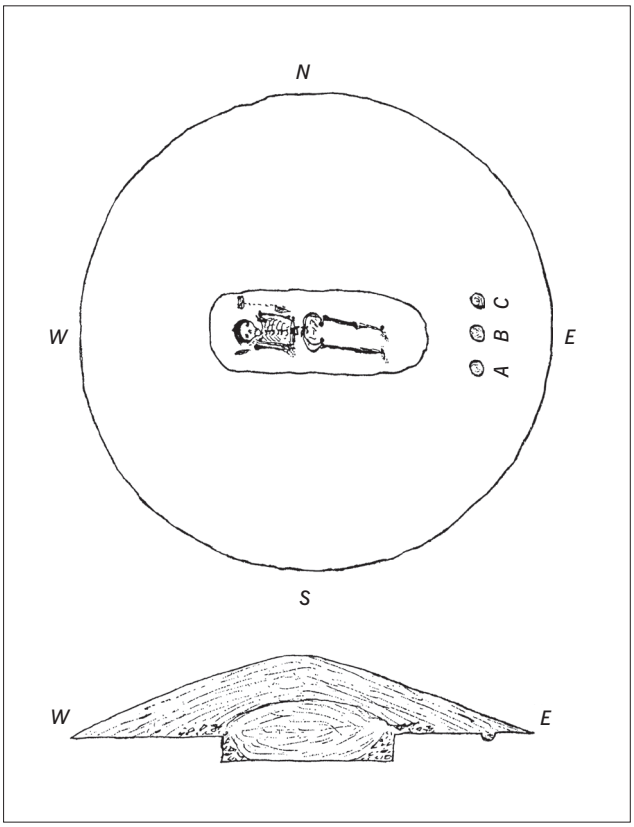


Fig. 6 Antiquarian drawing of the barrow at Towthorpe, East Yorkshire.

Abb. 6 *Antiquarische Zeichnung des Hügelgrabes in Towthorpe, East Yorkshire.*

Performing kinship

Archaeogenetics clearly provides extraordinary new opportunities to understand kinship in the past. However, because of the valorisation of science in contemporary academia, there is a danger of prioritising scientific data over other archaeological evidence for the making of kin in the past. Making kin involves material technologies: in the contemporary world, direct-to-consumer genetic testing kits do not so much reveal kin as make them (Wolf-Meyer 2020), just as the material economies of love create and sustain ideologies of kinship in the present. M. Di Leonardo (1987), for example, shows how the task of making and maintaining kin relations is primarily assigned to women in contemporary North America, and how the material world is central to that process, for example by sending greeting cards and organising holiday gatherings. Archaeologists are particularly well placed to investigate technologies of kinship in the past for these are directly reflected in material practice.

In Bronze Age Britain, as we have already described, kinship is created in the spatial articulation and manipulation of the bodies of the dead. At South Dumpton Down in Kent, for example, a deep pit at the centre of a ring-ditch contained seven crouched inhumations deposited in sequence (Fig. 5; Perkins 1995). All but one of these burials were placed so that they lay perpendicular to the body of the previous interment, and in most cases the skull had been removed when the subsequent burial was deposited. Here, not only were spatial and bodily relations employed to foreground particular relationships, but the bones of the dead were also retrieved for curation, display or deposition elsewhere. Nearby, the inhumation burial of an adult was accompanied by the mandible of another individual, and we can surmise that this might have been recovered from the multiple deposit. A recent programme of radiocarbon dating indicates that such »relic« fragments of human bone were curated for around two generations before final deposition, suggesting that they derived from known individuals, possibly significant ancestors (Brück/Booth 2022). Here, the remains of the dead were manipulated to foreground, sustain and transform kinship links: engaging with the bones of dead individuals figured as ancestors acted as a means of performing kinship.

Kinship was not located solely in the human body, however. The archaeological record also provides rich evidence for different technologies of kinship, illuminating how kinship was conjured and enacted in material practices. For example, at Towthorpe, East Yorkshire (Fig. 6), a barrow covering the inhumation burial of an adult male was built of materials from three distinct sources: soil from the immediate vicinity of the barrow; clay from the area around Burdale, a mile to the west; and clay from the vicinity of Duggleby, a mile and a half to the north (Mortimer 1905, 6). The mound was composed of layers of these clays, alternating with layers of soil from the immediate vicinity of the barrow, and each kind of clay predominated at the side of the mound nearest the place from which it had been brought. Here, kin were



Fig. 7 Inhumation burial of a subadult female from Cliffs End Farm, Kent. Her head resting on a cattle skull.

Abb. 7 *Körperbestattung einer subadulten Frau von der Cliffs End Farm, Kent. Ihr Kopf ruht auf einem Rinderschädel.*

made not through the bodies of the dead themselves, but through other forms of social practice, in this case, when people brought baskets of different materials from significant places in the landscape. In doing so, they marked the contribution of different kin groups (perhaps maternal and paternal kin, for example) to the substance of the deceased.

Beyond the mortuary context, material practices in the world of the living also made kin. I have described elsewhere how the assemblage of shale armlets from the midden at Potterne in Wiltshire were standardised in size (Brück/Davies 2018). Their internal diameters lay in the region of 5–7 cm – a size that will fit over the hand of a modern 8- to 10-year-old child of slim build, but will not fit someone older. The standardised diameter of these artefacts suggests that they may have been given to mark particular life-cycle rites, perhaps in mid-late childhood. Some of these items have been snapped in half or broken into quarters. Potterne has been interpreted as a ceremonial site at which large groups of people came together for feasting and other ritual activities (Lawson 2000; Madgwick/Mulville 2015). As such, these broken shale bracelets can perhaps be interpreted as the residues of age-grade ceremonies or initiation rites in which fragments of socially-significant artefacts were gifted to important kin: here, kinship was the outcome of social practice.

Archaeologists are also well-placed to consider the implications of Indigenous scholars' call to move beyond models of kinship rooted in the heteronormative, patriarchal, and anthropocentric structures of settler sexuality (Kimmerer 2013; TallBear 2018). More expansive and inclusive definitions of kinship that are not predicated on sexual reproduction but instead foreground ongoing acts of mutual care can make space for other-than-humans as kin. In Bronze Age Britain, R. Johnston (2021) has explored how kin relations were rooted in places invested with animate and ancestral powers. These relations can be traced in material interventions in the landscape, such as the deposition of bronzes and other objects at striking landmarks. For example, on Dartmoor in Devon, a complete pot was found placed in a crevice, part-way up the face of an imposing granite outcrop (Pettit 1974, 92). This can be interpreted as an offering to ancestral spirits whose powers were vested in this place – a gesture of care towards ancestral lands and a manifestation of kin relations with both human and non-human persons. Relations with animals may also speak of kinship links.

Sometimes, those were the intimate interconnections of everyday life: at Cliffs End Farm in Kent (Fig. 7; McKinley et al. 2014), for example, a subadult female lay flexed on her right-hand side, her head resting on a cattle skull. It is possible that this animal had been gifted as part of the bride-wealth of this young woman; anthropologists have frequently described how cattle transferred as part of marriage transactions are considered a crucial component of the self, with close personal links existing between particular people and animals (e.g., Evans-Pritchard 1951). Other relations may be more totemic in character. For example, the cremation burial of a child at Skilmafilly, Aberdeenshire, included a pair of burnt golden-eagle talons and a perforated bone or antler object (Johnson/Cameron 2012, 30); these items may have been worn together as part of a necklace. Totemic animals are usually understood as kin, the original progenitors of their human descendants, their frequent slippage between human and non-human form reminding us that the boundary between human and animal is not always viewed as categorically elsewhere as it is in our own cultural context (Descola 2013).

Conclusion

In this paper, I hope to have demonstrated that bringing together theories of social practice with critical perspectives on the social salience of the biological links revealed by ancient DNA has much to tell us about kinship. Ancient DNA analysis has come to be viewed as the most accurate means of revealing prehistoric kinship structures, yet it is crucial that we avoid reading the genetic evidence in ways that unthinkingly impose modern conceptions of kinship and gender relations onto the past. A century of anthropological analysis of kinship and marriage demonstrates the extraordinary diversity of ways in which humans organise and understand their relationships with one another. We need to remain open to that diversity and consider alternative ways of interpreting the archaeogenetic evidence that go beyond our own lived experience. Moreover, kinship cannot be viewed as a direct reflection of genetic links. Kinship is not a given, or »natural fact«, but is a process: the outcome of culturally prescribed social practices that require careful nurture, work and commitment. Archaeological evidence provides many insights into how relations were created and maintained through varied technologies of kinship, both focused on the body and beyond it. This is a different but complementary perspective to that offered by archaeogenetics, which identifies genetic links but does not immediately reveal their social salience. It allows us to move beyond biogenetic determinism to consider the ways in which social practice generated enduring affective bonds and the sharing of substance with both human and non-human others. These points have implications for our understanding of the Bronze Age more generally. They require us to question established anthropocentric and androcentric notions of agency and to consider alternative concepts of gender, personhood and kinship. Set within this context, it becomes easier to understand evidence that appears to challenge accepted models of Bronze Age society, such as the discovery of wealthy female burials (e.g., <https://www.wessexarch.co.uk/news/beaker-burial> [23.04.2023]); the decentralised production of »high-status« weaponry like swords (Webley et al. 2020); or the evident regional and contextual variability in how social identity was constructed (Haughton 2018).

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FALLSTUDIEN – EISENZEITEN

CASE STUDIES – IRON AGES

Intramural child burials in Iron Age Navarra: How ancient DNA can contribute to household archaeology

Luka Papac, Patxuka de Miguel Ibáñez, Adam B. Rohrlach, Javier Armendáriz, Marcello Peres, Thiseas C. Lamnidis, Angela Mötsch, Stephan Schiffels, and Roberto Risch

Zusammenfassung

Intramurale Kinderbestattungen im eisenzeitlichen Navarra: Wie alte DNA zur Archäologie von Hausgemeinschaften beitragen kann

Am Übergang von der späten Bronze- zur Eisenzeit vollzog sich auf der Iberischen Halbinsel ein Wandel in der Bestattungspraxis von der bis dahin überwiegenden Körperbestattung zur Brandbestattung. Die schlechten Erhaltungsbedingungen verbrannter Knochen haben molekulare Analysen wie Isotopen- und aDNA-Analysen von endbronze- und eisenzeitlichen Bevölkerungen bislang verhindert. Gelegentlich wurden jedoch Kleinkinder, oft Neugeborene, von dem vorherrschenden Brandbestattungsritus ausgenommen und stattdessen unverbrannt innerhalb von Gebäuden bestimmter Siedlungen beigesetzt. Die Diskussion über die Bedeutung und Interpretation dieses besonderen Bestattungsritus hat sich in der iberischen Archäologie über einen langen Zeitraum hinweg entwickelt, wurde aber immer durch die begrenzten anthropologischen, archäologischen und molekularen Daten, die von diesen intramuralen Körperbestattungen zur Verfügung standen, behindert. Im vorliegenden Artikel untersuchen wir die Genome von 37 intramural bestatteten Kindern aus drei früheisenzeitlichen Siedlungen (ca. 800–450 v. Chr.). Populationsgenetische Analysen haben unser Verständnis der genetischen Vielfalt auf der vorgeschichtlichen Iberischen Halbinsel erweitert, weil eine bis dahin nicht gekannte genetische Vielfalt – mit viel weniger mediterranem Einfluss, als in den bisher veröffentlichten eisenzeitlichen Individuen aus derselben Region – identifiziert werden konnte. Wir liefern ebenfalls Erkenntnisse zu Geschlecht und biologischer Verwandtschaft der Kinder und erhellen so verschiedene Aspekte des Bestattungsritus intra muros *und der Nutzung von Gebäuden in Siedlungen. Die genetischen Daten dieser Individuen füllen eine wesentliche Lücke in der Archäologie Nordspaniens und bieten die einzigartige Gelegenheit, die genetische Zusammensetzung und Veränderungen innerhalb der Bevölkerung von der Bronzezeit bis zur Antike zu untersuchen.*

Summary

The transition from the Late Bronze to the Iron Age on the Iberian Peninsula saw a shift in mortuary customs from mainly inhumation to cremation of the deceased. The poor preservation characteristic of cremated skeletal remains has hindered molecular analyses (isotope analyses, ancient DNA) of the Iberian Final Bronze and Iron Age communities of Iberia. Incidentally, a limited number of young children, often newborns, were exempt from the predominant cremation ritual, in favour of intramural inhumations inside buildings at certain settlements. The discourse surrounding the meaning and interpretation of this particular burial rite has developed over a long time in Iberian archaeology but has always been hampered by the limited anthropological, archaeological, and molecular data from these intramural inhumations. Here, we study the genomes of 37 intramurally buried children found in three Early Iron Age settlements, dated between c. 800–450 BC. Population genetic analyses on the newly reported individuals extend our understanding of ancient Iberia by revealing previously unsampled genetic diversity as well as showing a lesser influence of Mediterranean ancestry than on previously published Iron Age individuals from northern Spain. We also provide insights into the sex and biological relatedness of the children, and in so doing, elucidate different aspects of the intramural burial ritual and building use in settlements. More broadly, the genetic data from these individuals fill an important gap in the archaeogenetic record of northern Spain and offer a unique opportunity to study the genetic makeup and population changes from the Bronze Age to Antiquity.

Introduction

Although intramural burials represent a relatively rare funerary practice in human societies, they offer a unique opportunity to explore the relationship between certain members of a community and specific living spaces and buildings. A recurrent aspect of this practice, since its earliest known practice at the beginning of sedentary life in stable settlements, is its restriction to a relatively small subset of society, while the majority of a community's deceased were granted a different mortuary ritual or remain invisible in the archaeological record[1]. The number of intramural

1 Borić/Stefanović 2004; Boroneant/Bonsall 2012; Boz/Hager 2013; Cavanagh/Mee 1998; Lull 2000; Lichter 2001.

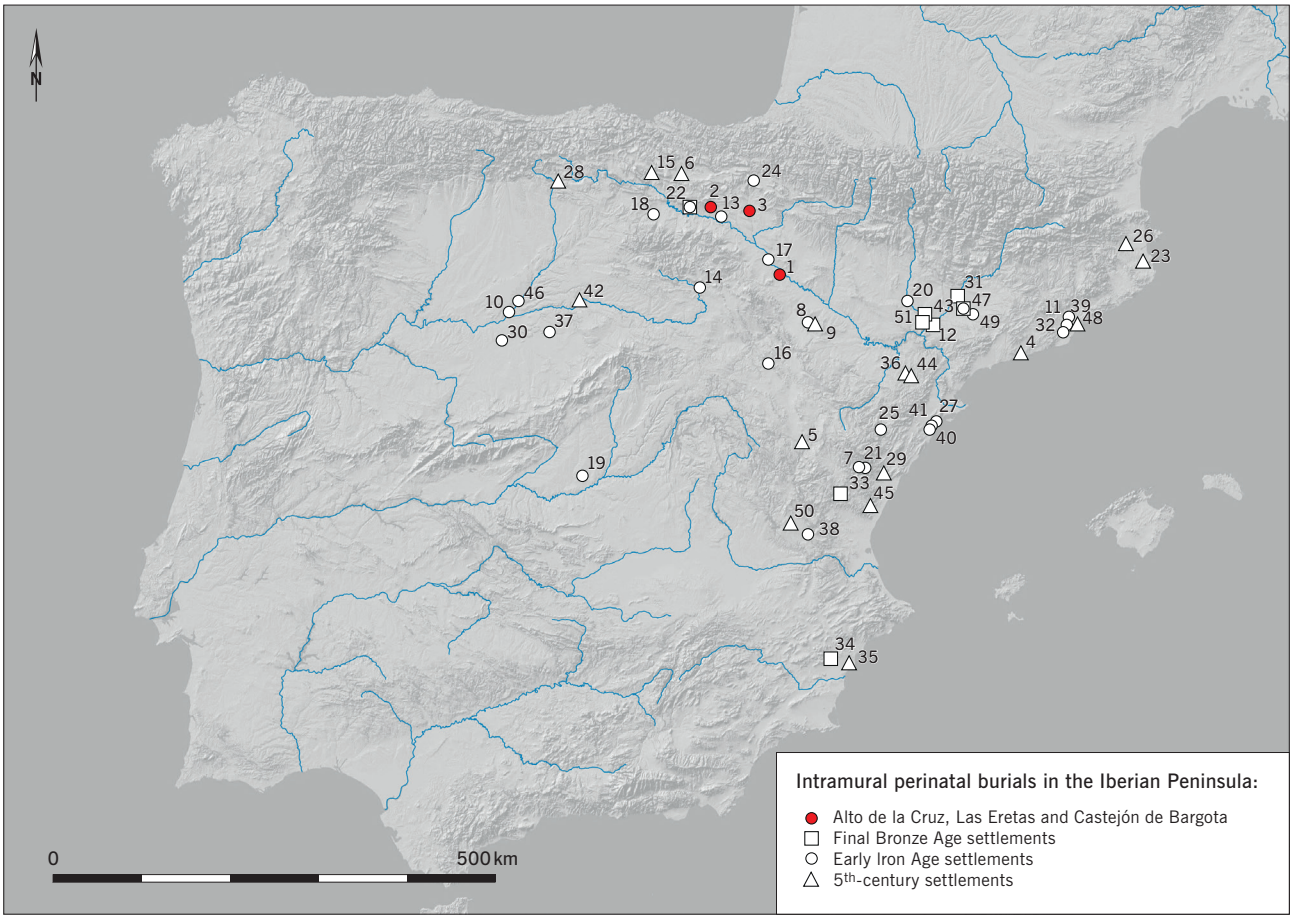


Fig. 1 Map of Final Bronze Age, Early Iron Age and 5th-century settlements with intramural perinatal burials in the Iberian Peninsula. 1 Alto de la Cruz (Cortes, Navarra); 2 El Castejón (Bargota, Navarra); 3 Las Eretas (Berbinzana, Navarra); 4 Alorda Park (Calafell, Tarragona); 5 Alto Chacón (La Muela, Teruel); 6 Atxa (Vitoria-Gasteiz, Alava); 7 Los Cabañiles (Zucaina, Castellón); 8 Cabezo de la Cruz (La Muela, Zaragoza); 9 Cabezo de las Minas (Botorrita, Zaragoza); 10 Calle Atrio de la Iglesia (Simancas, Valladolid); 11 Can Roqueta (Sabadell, Barcelona); 12 Carretelà (Aitona, Lleida); 13 El Castillar (Mendavia, Navarra); 14 El Castillejo (Fuensaúco, Soria); 15 Los Castros de Lastra (Caranca-Càrcamo, Alava); 16 Cerro de Santa Barbara (Cubel, Zaragoza); 17 Cerro de Santa Bàrbara (Tudela, Navarra); 18 Cerro Piquillo (Libia) (Herramélluri, La Rioja); 19 Cerrocuquillo (Villaluenga de la Sagra, Toledo); 20 La Codera (Alcolea de Cinca, Huesca); 21 La Escudilla (Zucaina, Castellón); 22 La Hoya (Laguardia, Alava); 23 Illa d'en Reixac (Ullastret, Girona); 24 Leguin Chiqui (Echauri, Navarra); 25 La Lloma Comuna (Castellfort, Castellón); 26 Mas Castellar (Pontós, Girona); 27 La Moleta del Remei (Alcanar, Tarragona); 28 Monte Bernorio (Villarén, Palencia); 29 Montmirà (Alcora, Castellón); 30 La Mota (Medina del Campo, Valladolid); 31 La Pedrera (Vallfogona de Balaguer-Térmens, Lleida); 32 Penya del Moro (Sant Just Desvern, Barcelona); 33 Peña de la Dueña (Teresa, Castellón); 34 Peña Negra (Crevillente, Alicante); 35 La Picola (Santa Pola, Alicante); 36 Piuró del Barranc Fondo (Valdeltormo, Teruel); 37 Plaza del Castillo (Cuellar, Segovia); 38 Plaza del Castillo (Requena, Valencia); 39 Puig Castellar (Montcada i Reixac, Barcelona); 40 Puig de la Misericordia (Vinaròs, Castellón); 41 Puig de la Nau (Benicarló, Castellón); 42 Rauda (Roa de Duero, Burgos); 43 Safranals (Fraga, Huesca); 44 San Antonio (Calaceite, Teruel); 45 Sant Josep (Vall d'Uixó, Castellón); 46 El Soto de Medinilla (Valladolid, Valladolid); 47 Tossal de les Tenalles (Torregrossa, Lleida); 48 Turò de ca n'Olivé (Cerdanyola, Barcelona); 49 Els Vilars (Arbeca, Lleida); 50 Los Villares (Caudete de las Fuentes, Valencia); 51 Vincamet (Fraga, Huesca).

Abb. 1 *Karte der Siedlungen mit intramuralen perinatalen Bestattungen aus der späten Bronze-, frühen Eisenzeit und dem 5. Jh. v. Chr. auf der Iberischen Halbinsel. 1 Alto de la Cruz (Cortes, Navarra); 2 El Castejón (Bargota, Navarra); 3 Las Eretas (Berbinzana, Navarra); 4 Alorda Park (Calafell, Tarragona); 5 Alto Chacón (La Muela, Teruel); 6 Atxa (Vitoria-Gasteiz, Alava); 7 Los Cabañiles (Zucaina, Castellón); 8 Cabezo de la Cruz (La Muela, Zaragoza); 9 Cabezo de las Minas (Botorrita, Zaragoza); 10 Calle Atrio de la Iglesia (Simancas, Valladolid); 11 Can Roqueta (Sabadell, Barcelona); 12 Carretelà (Aitona, Lleida); 13 El Castillar (Mendavia, Navarra); 14 El Castillejo (Fuensaúco, Soria); 15 Los Castros de Lastra (Caranca-Càrcamo, Alava); 16 Cerro de Santa Barbara (Cubel, Zaragoza); 17 Cerro de Santa Bàrbara (Tudela, Navarra); 18 Cerro Piquillo (Libia) (Herramélluri, La Rioja); 19 Cerrocuquillo (Villaluenga de la Sagra, Toledo); 20 La Codera (Alcolea de Cinca, Huesca); 21 La Escudilla (Zucaina, Castellón); 22 La Hoya (Laguardia, Alava); 23 Illa d'en Reixac (Ullastret, Girona); 24 Leguin Chiqui (Echauri, Navarra); 25 La Lloma Comuna (Castellfort, Castellón); 26 Mas Castellar (Pontós, Girona); 27 La Moleta del Remei (Alcanar, Tarragona); 28 Monte Bernorio (Villarén, Palencia); 29 Montmirà (Alcora, Castellón); 30 La Mota (Medina del Campo, Valladolid); 31 La Pedrera (Vallfogona de Balaguer-Térmens, Lleida); 32 Penya del Moro (Sant Just Desvern, Barcelona); 33 Peña de la Dueña (Teresa, Castellón); 34 Peña Negra (Crevillente, Alicante); 35 La Picola (Santa Pola, Alicante); 36 Piuró del Barranc Fondo (Valdeltormo, Teruel); 37 Plaza del Castillo (Cuellar, Segovia); 38 Plaza del Castillo (Requena, Valencia); 39 Puig Castellar (Montcada i Reixac, Barcelona); 40 Puig de la Misericordia (Vinaròs, Castellón); 41 Puig de la Nau (Benicarló, Castellón); 42 Rauda (Roa de Duero, Burgos); 43 Safranals (Fraga, Huesca); 44 San Antonio (Calaceite, Teruel); 45 Sant Josep (Vall d'Uixó, Castellón); 46 El Soto de Medinilla (Valladolid, Valladolid); 47 Tossal de les Tenalles (Torregrossa, Lleida); 48 Turò de ca n'Olivé (Cerdanyola, Barcelona); 49 Els Vilars (Arbeca, Lleida); 50 Los Villares (Caudete de las Fuentes, Valencia); 51 Vincamet (Fraga, Huesca).*

interments is restricted by the physical limitations of a settlement or constructed space in which they are placed, meaning socially established criteria likely governed who was granted such a burial. Criteria may have been based on sex, age, class, or other socially recognised indicators. They may have also derived from astronomical or meteorological observations, relating ritual practices to specific years, months, or days. In any case, the interment of individuals in specific living spaces likely signalled a relationship between the individual and the space, which presumably needed to

be ritually and socially sanctioned. This study explores these relationships and rituals by combining archaeological, anthropological, and genetic data from Early Iron Age (c. 800–450 BC) Navarra, northern Spain, where this intramural funerary rite was restricted to some perinates or children of a very young age. We study ancient DNA data from 37 intramurally-buried children from the Early Iron Age villages of Alto de la Cruz (n = 29), Las Eretas (n = 6), and El Castejón (n = 2), which allows a better understanding of the social criteria governing these funerary practices. We provide insights into the sex and biological relatedness of these children, as well as the mating patterns and genetic affinities of the communities they belonged to. We discuss the implications of our results on the interpretations of this burial rite and social organisation at these sites, as well as the population genetic changes in northern Spain more broadly.

Intramural child burials in Iron Age western Mediterranean

Intramural child burial was a funerary ritual practised during the Final Bronze Age and Iron Age in the western Mediterranean coastal regions, from Murcia in the southwest to the Languedoc in the northeast, including the entire Ebro Valley and parts of the Spanish northern Meseta (Fig. 1)[2]. Absolute dates confirm that infants started to be interred in settlements around 1000 BC in the Ebro Valley (Moya et al. 2015, 44), although a slightly earlier date can be proposed based on stratigraphic observations[3]. The ritual continued to be practised at least until the end of the 1st millennium BC, when the Iberian Peninsula came under Roman rule after a series of wars and violent repression. In certain settlements, intramural child inhumations have been documented even at the beginning of the 1st millennium AD (e.g., Mínguez 1990; Rodrigo 2022). Despite widespread evidence of dense human occupation during the Iron Age, the low number of known intramural and inhumation burials implies the existence of other funerary practices. While low, the precise rate of intramural interments remains difficult to infer.

Given its introduction to a region where cremation became the dominant funerary ritual, the intramural interment of children has often been linked to the influence, or even presence, of central European »Urnfield Culture« groups (Gusi/Muriel 2008; Armendáriz/de Miguel 2006; Lorrio et al. 2010). In contrast, it has also been speculated that this practice was an influence of the Phoenician and Greek colonisation of the Iberian Peninsula after 900 BC[4]. However, neither the spatiotemporal distribution, nor the funerary practice itself seem entirely compatible with either hypothesis. While newborns were cremated in the Eastern Mediterranean derived *Molk* sacrificial ritual, the Iberian communities inhumated their bodies in pits. No intramural burials are found in colonial settlements[5]. Anthropological data has also not provided evidence for violent sacrificial rituals. Finally, intramural child burials appeared in Catalonia and the Ebro Valley well before the Phoenician presence in Andalusia or in the founding of Greek colonies along the coast of Catalonia and Languedoc.

Archaeological evidence indicates that perinatal infants in settlements emerged as a funerary practice at the end of the 2nd millennium BC among communities settling in the north-western Mediterranean regions and the Ebro Valley. Later, by the middle of the 1st millennium BC, it became a distinctive funerary practice of populations identified in archaeology as »Iberian«, based on their settlement pattern, artefact typology, the Northeastern Iberian script, and pre-Roman toponymy of the Iberian Peninsula and southern France.

So far, around 800 intramural burials of young children have been identified in nearly 90 Final Bronze Age and Iron Age settlements, mostly in the north-eastern part of the Iberian Peninsula (Fig. 1). While the site of La Hoya, Álava, has provided an exceptionally large number of intramural inhumation burials (n = 260), in more than half of the known sites only one or two intramural burials have been found. Less than 20 settlements present 10 or more intramural burials. Even in larger and extensively excavated settlements, such as Els Vilars, Lleida (0.26 ha) or Alto de la Cruz, Navarra (0.75 ha), a maximum of between 16 and 45 infant burials have been found, respectively. In other Final Bronze Age and Iron Age settlements, no inhumation burials have been identified so far, as some authors have pointed out (Moya et al. 2015, 42). Considering the timespan over which this burial rite was regularly used (c. 800–200 BC), as well as the number and size of the settlements excavated, c. 800 individuals can only represent a small fraction of the Final Bronze Age and Iron Age population in that age group. Even taking into account that some burials probably passed unnoticed during excavations due to poor preservation and the small size of perinatal skeletons, or due to the applied excavation method (no sieving of sediments, etc.), the total number of children who died at a young age in this time period must have been considerably larger, leaving the majority of perinatal deaths unaccounted for.

A common trait of these intramural burials, which indicates the existence of a shared funerary rite for the whole area, is the young age of the children. Anthropological studies reveal that the majority of the individuals who were interred intramurally were perinatal infants, who either died before reaching full term, or during the first months of extra-uterine life. Most of the c. 70 skeletons that have been studied anthropologically died around 40 weeks of intrauterine life, probably during or shortly after birth[6]. Children older than six months of age were rarely interred in the set-

2 Gusi 1970; Gusi 1992; Gusi/Muriel 2008; Dedet 2008a; Dedet 2008b; Armendáriz/de Miguel 2006; Lorrio et al. 2010; Belarte 2010.

3 This is the case in the Late/Final Bronze Age settlements of La Pedrera, Vallfogona de Balaguer-Térmens, Lleida (Gallart/Junyent 1989) and La Hoya, La Guardia, Álava (Galilea/García 2002).

4 Oliver/Gómez 1989; Barrial 1990; Ruiz Cabrero 2008; Gusi/Murial 2008.

5 No such burials have been detected in extensively excavated colonies such as Villaricos, Almería, or Morro de Mezquitilla, Toscanos, or Cerro del Villar, in Málaga (Siret 1906; Schubart/Maass-Lindemann 2017; Schubart 2002; Delgado/Aubet 2003).

6 Risch/Carbonell 1986; Guérin/Martínez 1988; Gómez/Oliver 1989; Gracía et al. 1989; Maluquer de Motes et al. 1990; Augustí et al. 2000; Lorrio et al. 2010; Armandáriz/de Miguel 2006; de Miguel 2009; Carnicero-Caceres/Torres-Martínez 2021.



Fig. 2 The Ebro Valley at the height of Tudela (Navarra). In the background, on the right, the town of Alto de la Cruz.

Abb. 2 Das Ebrotal auf der Höhe von Tudela (Navarra). Im Hintergrund rechts die Stadt Alto de la Cruz.

tled areas. Although anthropological studies of cremations are still not sufficient to account for the majority of deceased children (e.g., Gómez 2011; Uroz/Uroz 2010), the available information suggests that these were rarely cremated, especially if one takes into account that child mortality in Later Prehistory probably affected between one quarter and one third of the population. If this is confirmed in future studies, it follows that young children buried in settlements or in cremation necropoleis probably received special ritual attention compared to most of the children who died at a young age and received no archaeologically recognisable burial. Regardless, the main question concerning the Iron Age intra-mural burials of Eastern Iberia remains: *what made these few children »special« to so many communities and over such an extended spatial and temporal range?*

Another aspect shared by most of the perinatal intramural inhumations is their placement in simple pits under the floors of living quarters[7]. Only in the Spanish Levante were they occasionally buried in pottery vessels (Gómez/Oliver 1989; Moneo 2003, Fig. 6; 19). Careful excavations have confirmed that human remains are usually found in a primary position. The disturbances observed in some cases are probably the result of post-depositional processes. Their identification and excavation are further hampered by the fact that these tombs were rarely marked in an archaeologically visible way, although stone settings have been identified in some cases (e.g., Risch/Carbonell 1986; Gracía et al. 1989; Armandáriz/de Miguel 2006; etc.). Grave goods, such as bronze rings and bracelets, appear in a small number of cases, even accompanying premature children, as in Alto de la Cruz, Navarra (Maluquer de Motes et al. 1990). The presence of young animals, particularly ovicaprines, seems to have been more frequent (Gómez/Oliver 1989; Nieto 2013). Complete animals, or parts thereof, have been found either in direct association with, or in close proximity to, the infant burials. However, animals were also interred individually with no relation to perinatal burials, suggesting that different, but related rituals, were carried out inside the settlements and buildings (Belarte/Valenzuela-Lamas 2013).

The spatial location of the burials has been studied in order to gain insights into the meaning of this ritual practice. Although some buildings or rooms contain more interments than others, no common pattern has been identified concerning their size, architecture, or the function of the spaces. Constructions interpreted as domestic realms, storage rooms, or as specialised workshops, such as tanneries, metal workshops, winepresses etc., as well as buildings with a possible ritual use, were chosen as funerary spaces in an apparently arbitrary way. So far, it has not been possible to recognise any pattern or logic behind the spatial distribution of the skeletons within the settlements. In the case of the extensively excavated site of Els Villars, Lleida, children and horse foetuses were buried in mutually exclusive sides of the fortified settlement, at least during its occupation phase II, dated between 550/525–425/400 BC (Nieto 2013). However, the reasons behind such a spatial segregation remain unclear. Furthermore, the number of burials in each building and the number of individuals interred in each burial pit does not seem to follow any obvious rule. While most tombs contained single inhumations, double and triple burials, which are well-documented in c. a dozen settlements, have been interpreted by some authors as twins or triplets, who died more or less simultaneously at a perinatal age[8]. However, such a hypothesis becomes less likely in the rare cases where more individuals have been found together, such as in a possible ritual building of La Moleta del Remei, Tarragona, where five newborns were buried in the same pit (Gracia et al. 1989). In this and similar contexts, a lethal epi-

7 A burial in fillings during the preparation of the floors of living quarters in the building cannot be excluded. However, the identification of the pit features and their limits is not always easy in archaeology, especially if the fillings are indistinguishable from the surrounding sediment.

8 Augustí et al. 2000; Armandáriz/de Miguel 2006; de Miguel 2009; Lorrio et al. 2010; Subirà/Molist 2016; Blasco/Montón 2019.



Fig. 3 Aerial view of Alto de la Cruz during the 1989 excavation campaign.

Abb. 3 *Luftaufnahme von Alto de la Cruz während der Ausgrabungskampagne 1989.*

demic outbreak might provide a plausible explanation for the simultaneous death of a larger number of newborns.

The apparent randomness concerning the number of tombs, the number of inhumations per tomb, and their location inside the settlements suggests that the event or circumstances leading to intramural burial practices were unforeseeable or erratic, as well as selective in view of the limited number of skeletons found in living spaces. Different interpretations have been proposed, but none accounts for the rareness, restricted age, and the widespread chronological and geographical practice of intramural inhumation during the Final Bronze Age and Iron Age of eastern Iberia. Sacrificial rituals have been suggested for a long time (Gusi 1970), but these are not supported by available anthropological evidence. Human sacrifices could be expected in the ritual buildings identified in many Iron Age settlements, but are less likely to have taken place in simple houses, and even less so in workshops or storage rooms. Some authors have related the burials to offerings during the construction or remodelling of buildings, as this would account for the regular placement of the burials next to the house or fortification walls (Guérin/Martínez 1988; Dedet/Schwaller 1990). A third way to interpret these interments is simply to consider them as a selection of children who died of natural causes during or shortly after birth (Armendáriz/de Miguel 2006, 41; Lorrio et al. 2010). So far, no archaeogenetic investigation has been conducted to determine the circumstances under which, perinates and children younger than one year old, were given special burial rites in built areas of settlements.

The Early Iron Age villages of Alto de la Cruz, Las Eretas and El Castejón

The intramural child burials studied here come from the archaeological excavations carried out in three fortified villages located in northern Spain, in the modern towns of Cortes, Berbinzana and Bargota, in present-day Navarra. They were recovered in the archaeological levels of the Early Iron Age and are dated in a chronological range between the 8th and 5th centuries BC (c. 800–450 cal BC).

The three sites are typical of a new occupation pattern emerging in the northeast of the Iberian Peninsula during the last stage of the Final Bronze Age under the influence of the local Urnfield Culture and which developed during the Early Iron Age: fortified villages with blocks of rectangular houses organised around a central street, and extramural cremation necropolis, sustained by a largely agricultural economy. Els Vilars d'Arbeca, Lleida, located in the alluvial plain of the lower Segre, is the best studied site in the Ebro Valley and a paradigmatic example of this phenomenon (Alonso et al. 2018). In a relatively short time this model of territorial setting expanded up the Ebro River throughout the valley until reaching Navarra in its upper course, with numerous intermediate examples, such as the most recently studied Cabezo de la Cruz in La Muela, Zaragoza (Picazo/Rodanés 2009) and La Codera in Alcolea de Cinca, Huesca (Montón 2004).

In Navarra this new territorial planning took place somewhat later than in Catalonia, but it was quickly implemented in the alluvial plains of the Ebro River (Fig. 2) and its main tributaries in the 8th century BC. Hilltop settlements – *castra* – were also established at the foot of mountains and interfluves that close and structure this great fluvial basin (Armendáriz 2008). While Alto de la Cruz and Las Eretas are good examples of exquisitely fortified villages in plains located at the bottom of valleys next to the Ebro and Arga Rivers, respectively, El Castejón de Bargota is a fortified hilltop settlement that occupies one of the heights in the southern foothills of the Cantabrian Mountains.

Alto de la Cruz (Cortes)

Better known internationally as »Cortes de Navarra«, this Iron Age town is located just over 4.5 km from the current course of the Ebro, next to the Huecha River, which runs only 1.5 km away and is a tributary of the Ebro on its right bank (Fig. 3; UTM: 629.007/4.462.981). It occupies the centre of a wide alluvial plain at 260–267 m a.s.l., formed by deep,

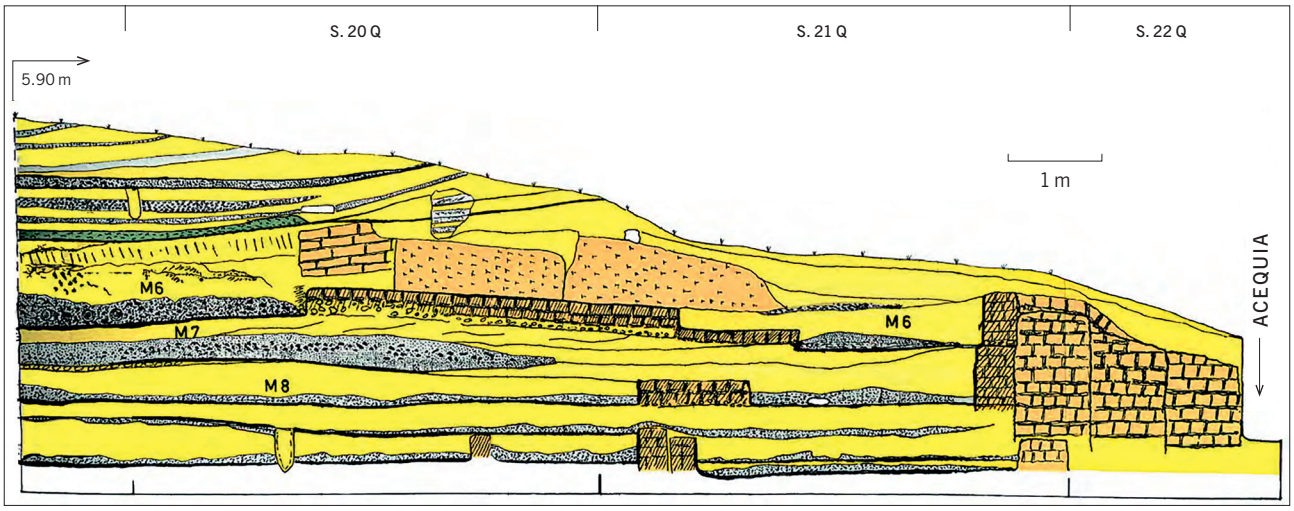


Fig. 4 Stratigraphic section of the Early Iron Age layers and mud brick wall of Alto de la Cruz. M8 corresponds to settlement phase PIIIb, while M6 is PIIb.

Abb. 4 *Stratigrafischer Abschnitt der früheisenzeitlichen Schichten und der Lehmziegelmauer von Alto de la Cruz. M8 entspricht der Siedlungsphase PIIIb, während M6 PIIb ist.*

humid and highly fertile soils, which are highly agriculturally productive both today as well as in the past. Technically, the site can be defined as a »tell«, which is an accumulation of archaeological levels that reaches a stratigraphic record of 6.25 m high, and that developed from the Late Bronze Age (10th–11th centuries BC) to the beginning of the Middle Iron Age in the 4th century BC (García et al. 1994). This tell is actually the result of the superposition of 14 building phases on the same site, which makes it the widest and most representative sequence of all the settlements of this type that have been studied so far in the Ebro Valley. It was the habitat of a peasant population, specialised in the production of cereals, although it also had an important livestock, artisanal and metallurgical development.

Discovered accidentally in 1946 during clearing works on the southern slope of the hill for the construction of a rural hut, a year later the Provincial Council of Navarra began its systematic research, which continued until 1957. Initially excavated by B. Taracena and O. Gil (1951; Gil 1953), the responsibility later passed to J. Maluquer de Motes (1958). Three decades later Maluquer resumed fieldwork in Cortes in 1985, with the purpose of excavating the lower levels of the site, which were scarcely explored in the first campaigns (Maluquer de Motes et al. 1988). After his death in 1988, F. Gracia and G. Munilla (1996) continued the work. They opened a new stratigraphic survey (C1) in the core of the site, which was excavated to the bedrock, in whose profiles (Fig. 4) a complete chrono-stratigraphic sequence of the first construction phases, or moments of occupation, of the site was recognised. These were added to the one established by Maluquer in 1958 (García et al. 1994). No further excavations have been carried out on the site since 1992.

In general, the architecture of the town follows an *a priori* design, since it reproduces the same model seen in Els Vilars d'Arbeca: a fortified oval enclosure of about 7500 m² with blocks of attached houses built against the peripheral wall and another block of houses of identical type in the centre, delimited by a street that provides access to all the houses of the town (Fig. 5; Armendáriz 2008, Cat.-N°. 244). The fortification is less studied because excavations focused mostly on the inner space. It consists of a solid adobe with a width that varied between 1.20 m (in phase PIIIa, 9th century BC) and 2.50 m (PI, 4th century BC). Solid adobe bastions or equidistant towers of c. 3 m deep must have been attached to the wall. An outer ditch was dug into the ground around the wall, though it has not been possible to prove if it was floodable. The population of Alto de la Cruz had at least one cremation necropolis (La Atalaya), which was discovered in a hill of the land less than 1 km away from the town in a southerly direction (Maluquer de Motes/Vázquez de Parga 1956).

Maluquer, in his famous synthesis published after the last campaign of the first period of excavations (Maluquer de Motes 1958), concluded that the chronological sequence of the site was roughly articulated in three major construction phases, separated by destruction levels caused by generalised fires, which required the integral reconstruction and new urban planning of the hamlet: Village PIII (850–700 BC), Village PII (700–500 BC), and Village PI (550–350 BC). The new radiocarbon dates obtained from the infant remains studied here mostly correspond to these levels, except for perhaps the initial period (phase PIIIa), confirming a chronology between c. 800–400 cal BC *(infra)*. According to the new radiocarbon results, one child burial excavated in 1949 dates to 992–1032 cal AD. Unfortunately, nothing is known about the archaeological context. Although the ^{14}C date fulfils the usual quality standards[9], a new sample of the same individual is being prepared for radiocarbon dating.

What characterises the domestic architecture of these three superimposed villages and their different intermedi-

9 C:N ratio: 3.2; C: 24.1 %; Collagen: 3.6 %.

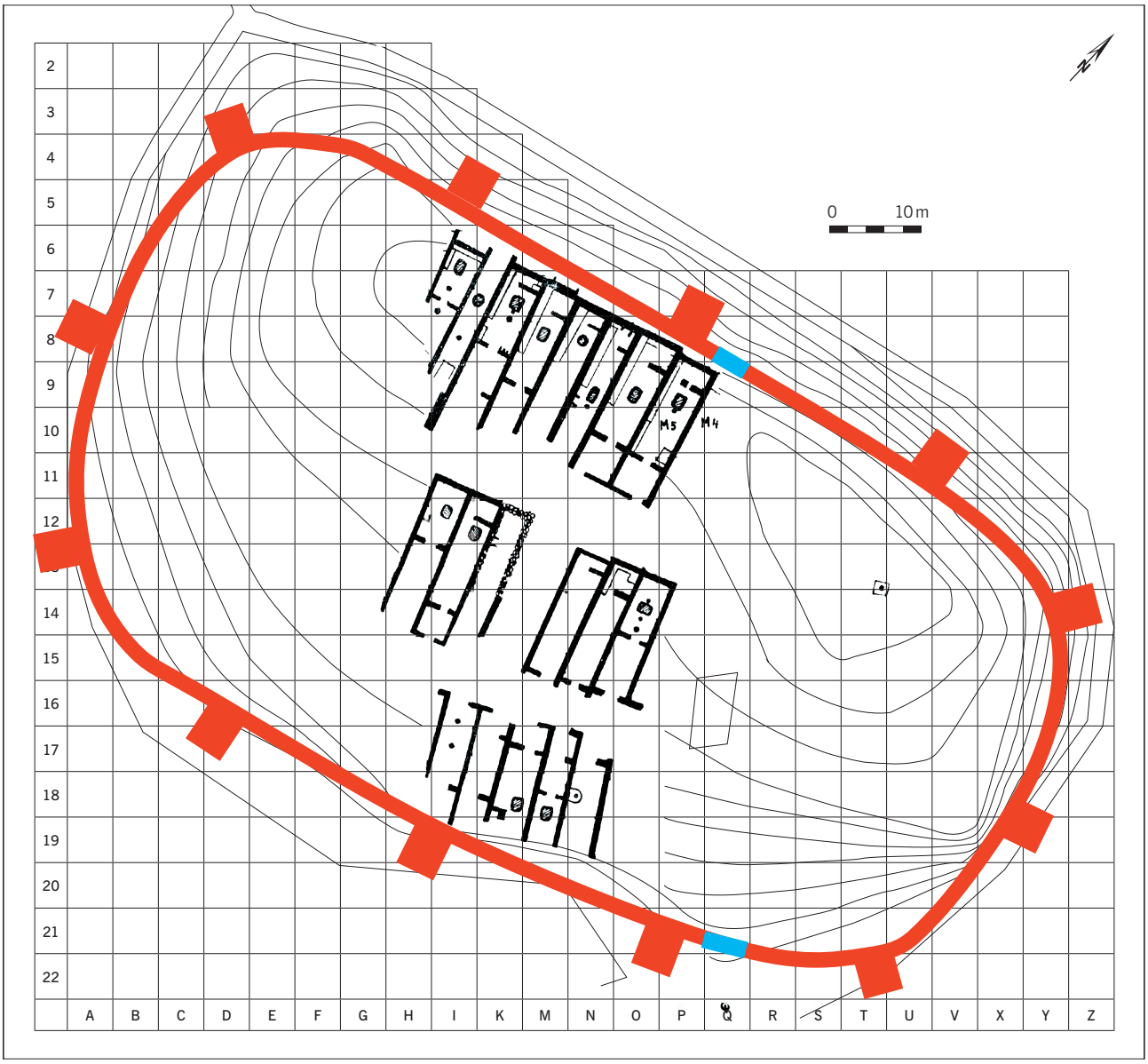


Fig. 5 General plan of Alto de la Cruz Village PIIb with our proposal for the reconstruction of its possible fortification. Blue: documented parts of the wall; red: proposed layout.

Abb. 5 *Gesamtplan des Dorfes Alto de la Cruz PIIb mit unserem Vorschlag für die Rekonstruktion seiner möglichen Befestigung. Blau: dokumentierte Teile der Mauer; rot: der vorgeschlagene Grundriss.*

ate remodelling phases is that they all reproduce the same house model (Fig. 6) with a rectangular ground plan of tripartite division, involving a lobby at the entrance, a central room and a pantry in the back, and this model hardly changed over time. If anything, there was a loss of the isometry of the ground plans of the most recent phases of the settlement (García 1994). However, the last excavation seasons (1989–1992) identified three new construction phases below Village PIII, in the lower levels of the stratigraphic cuts C1. Therefore, in the Final Bronze Age layers, called PIV, PV and PVI, a very different building pattern developed. This consisted of a dispersed habitat pattern (or unstructured village) made up of huts of square or trapezoidal ground plan, built with small intestate posts vertically covered by mud (García 1994), which are typical in the region during the Bronze Age. Therefore, in the period between Villages

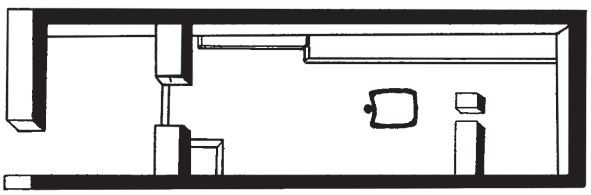


Fig. 6 Plan of the house M5 of the PIIb.

Abb. 6 *Grundriss des Hauses M5 der Phase PIIb.*

PIV and PIII (around the 9th century BC) an evident social change occurred among its inhabitants that led to the construction of a fortified town with clusters of houses of rectangular ground plan (PIII). The lack of continuity in the investigation of the lower levels of Alto de la Cruz since 1992

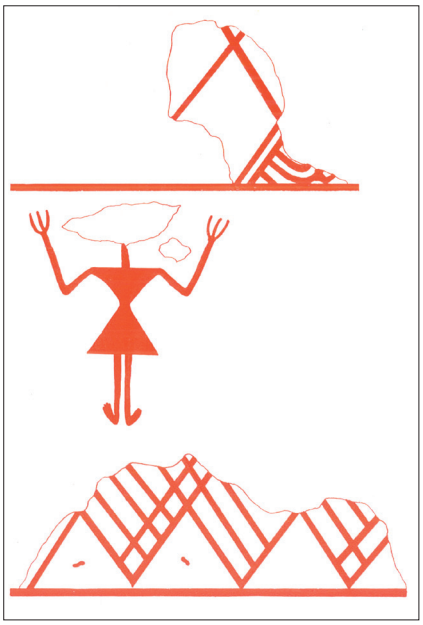


Fig. 7 Detail of the plaster of the whitewashed wall painted with red motifs of the lobby of house 8 of the PIIb.

Abb. 7 *Detail des Putzes der weiß getünchten, mit roten Motiven bemalten Wand dem Eingangsbereich des Hauses 8 der Phase PIIb.*



Fig. 8 Wall painting at Alto de la Cruz Iron Age house.

Abb. 8 *Wandmalerei im eisenzeitlichen Haus von Alto de la Cruz.*

prevents us from verifying how this change occurred. However, it introduced new ways of life and a shift from the hut to the house in a fortified and urbanised town. Whether this implied a break in continuity of the previous Bronze Age communities, and whether there were contributions from migratory settlers of trans-Pyrenean origin remains a debated issue, which this study will start to address from an archaeogenetic perspective.

Of all the research carried out in Alto de la Cruz perhaps the best-known feature is the internal structuring of their houses. These were rectangular in shape with only one entrance from the street. The houses were organised around a central room that had one or more hearths and sometimes an oven with a clay vault attached to the walls. In some cases, benches appear along the walls at the back of the house, where the roof is higher and a loft, mezzanine or a first floor might have been raised. The walls were plastered and whitewashed, and sometimes decorated with colourful geometric decorative motifs painted in red and black (Fig. 7–8). Few variations of this building scheme are observed between the different phases of the town

From the first excavation campaigns, infant burials in simple pits were detected under the floor of these houses, some of which were accompanied by personal ornaments and funeral offerings (Fig. 9). Although not all of these burials were well defined because of the methods used in earlier excavations, this was not the case for burials recovered in the last excavation campaigns (1985–1992). In any case, from all of the data collected to date, a continuous practice of burying children of perinatal age from the levels of Village PIIIb (8th century BC) to Village PIb (5th–4th centuries BC) has been attested.



Fig. 9 Perinatal inhumation with large limestone bead, which could correspond to individual CRU016.

Abb. 9 *Perinatale Bestattung mit großer Kalksteinperle, die dem Individuum CRU016 entsprechen könnte.*



Fig. 10 Arga River Valley from the south (Miranda de Arga). In the background, next to the river, is the town of Berbinzana.

Abb. 10 *Arga-Flusstal von Süden (Miranda de Arga). Im Hintergrund, neben dem Fluss, liegt die Stadt Berbinzana.*

Las Eretas (Berbinzana)

The site of Las Eretas is located in the middle-lower stretch of the Arga River, which provides the Ebro with an important water flow on its left bank. It is in a valley bottom that is characterised by its deep and well-drained soils of high agricultural productivity (Fig. 10; UTM: 596.082/4.709.202). Located on the right bank, at the edge of the first alluvial terrace next to the town of Berbinzana, the hilltop settlement rises 310 m a.s.l. Discovered originally in 1991 during the works prior to an urbanisation project, the archaeological excavations began in the same year and continued for five years. In the year 2000 excavations resumed. These excavations have allowed us to study the defensive structures and several houses of a fortified town founded *ex novo* around the 8th century BC and which was continuously inhabited until the 1st century BC, although the levels corresponding to the final phase of the Iron Age are preserved in a testimonial way. It is estimated that it may have occupied an interior area of about 4500 m^2, of which only 600 m^2 have been excavated (Armendáriz 1998; Armendáriz 2007; Armendáriz 2008). At present its ruins have become an archaeological park containing a monographic museum[10].

Like Alto de la Cruz, Las Eretas is a fortified lowland village showing the same defensive pattern and a similar urban plot. Its robust outer stone wall with foundations made of large 1.60 m wide dry stone blocks was reinforced on the outside with solid square towers raised with dry ashlar stone masonry. On the outside to the west there must have existed a defensive ditch dug in the gravels of the land, while to the east the Arga River offered a natural defence to the village. The urban structure featured a central street, initially paved with boulders and then with stone slabs, around which a rectangular line of attached houses was built against the outer wall.

The stratigraphic analysis of the site allows us to conclude that, unlike at Alto de la Cruz, Las Eretas was not occupied before the construction of the town, as both the wall and the houses are directly built on the natural terrain. Stratigraphic observations confirm that the first houses were already attached to the interior side of the fortification wall. This indicates a planned founding of the site adhering to the well-known village pattern in the Ebro Valley. Initially, the houses were isolated from each other and were built in the traditional manner with small wooden posts driven into the ground covered with mud (Village I, late 9th entury or early 8th century BC), but they were already elongated and rectangular, although soon they were destroyed by fire. The hamlet was rebuilt on the ashes, with the new houses leaning against the wall (Villages II and III, 8th–5th century BC) and with different construction phases and partial adaptations on the same road axis. This settlement was also subsequently destroyed by fire. The superficial erosion due to pressure from human occupation in historical times has hampered preservation of the settlements of the Late Iron Age (4th–1st centuries BC), although this site's continuous occupation is documented by a few remains until the first third of the 1st century BC, when there is a level of destruction that can be associated with the Sertorian wars.

In total, four houses have been completely excavated (Fig. 11), and many others partially, and these correspond to the two lower (earlier) levels of the stratigraphic record. The typical house of Las Eretas is a replica of those of the Alto de la Cruz, if perhaps even more formal and repetitive, as they are also divided into three rooms that are separated by light internal partitions connected by doors and include: a vestibule, where the oven is usually placed; the central room, which has a square fireplace of clay plate with a flange in the centre and at the side of the door and in the back of the room, next to the wall, a storage area that

10 <https://eretas.es/es/informacion/introduccion.php> (14.06.2023).



Fig. 11 Ground plan of the area excavated in Las Eretas.

Abb. 11 *Grundriss der ausgegrabenen Fläche in Las Eretas.*

always has a bench running in the background and sometimes makes an angle to the central room. In terms of construction, they are based on a continuous stone plinth about 60 cm high on which the dividing walls between houses and the façade are raised with a wooden framework and adobe or earth wall work. Two large central posts in the interior supported the wooden beams on which the roof was held and this was made of clay and organic materials. It was arranged with a slope so that rain could drain to the street. A loft is believed to have existed above the storage area in the back of the houses. Like at Alto de la Cruz, the houses had their inside walls plastered with mortar and were painted white; decorative motifs coloured in black and red have been preserved on the lateral benches.

In Las Eretas five child graves have been recovered under the floor of two houses belonging to the second construction phase of the town (Armendáriz/de Miguel 2006). These tombs were excavated as single pits in different parts of the house. The first contained a double, simultaneous burial (Fig. 12), while the rest contained single individuals. Recently, these burials have been ^{14}C-dated to between 800 and 550 BC *(infra)*. The care with which tomb 5 (inhumation 6) was constructed in the pantry of house 2 is striking, because there was a stone slab closing the tomb of a child aged just a few months and to whom a ceramic cup was offered as funerary *trousseau*.

El Castejón (Bargota)

El Castejón is a fortified and artificially plateaued hilltop settlement located on a steep rocky mountainous elevation of the piedmont of the Yoar and Cantabrian Mountains (Fig. 13), between the ravines of Cornava and Marimañas. Its outstanding topographical position (635–649 m a.s.l.; UTM: 557.125/4.711.677) gives it an exceptional perspective of its immediate surroundings, which allows it to exercise long-distance control of the territory and to establish visual contact with other fortified villages and other contemporary settlements in the region.

Unfortunately, the site has not been well preserved due to several factors. In particular, this is due to the opening of several quarry sites in historical times, the reforestation of the site in the 20th century, which destroyed much of the western sector of the *castrum*, the agricultural exploitation of the site, natural erosion, and plundering since ancient times. Even so, it preserves part of the eastern side of the fortification that follows the natural perimeter of the hill where the wall that rests on the bed was cut along the defensive perimeter to increase the fortification's height. The access ramp to the enclosure is also visible on the eastern slope (Armendáriz 2008).

The site presents an occupation sequence from the Early to the Late Iron Age (8th–2nd century BC), as attested by the recovered archaeological remains. No preceding material



Fig. 12a–b Burial 1 of Las Eretas. a Excavation of the infant double burial; b Skeletons 1 and 2.

Abb. 12a–b *Grab 1 von Las Eretas: a Ausgrabung der Säuglingsdoppelbestattung; b Skelette 1 und 2.*

dating to the Final Bronze Age has been identified so far. Based on the topography of the relief, an area close to 7700 m² could have been occupied during the site's zenith in the Late Iron Age.

Between 1992 and 1994, A. Castiella led his archaeological team from the University of Navarra in the excavation and investigation of this site (Castiella et al. 2009). An excavation was undertaken in an area of about 500 m² in which, on the one hand, confirmed the very poor conservation of the western part of the site, where numerous intrusions and loss of its architectural structure occurred. On the other hand, it allowed the study of parts of its urban layout, documented and recorded the occupational sequence throughout the Iron Age, and, lastly, recovered representative domestic material culture of the Early Iron Age and the Celtiberian Late Iron Age.

The excavations confirmed that only the eastern sector of the settlement was relatively well preserved, including a 2.60 m wide ashlar stone wall. Rectangular houses were leaning against the inner side of this fortification (Fig. 14a), of which only two could be – partially – delimited. Houses were raised on a stone plinth to keep the accommodation dry and the roof was supported by internally divided walls and central posts that aligned along the axis of the house. The preserved surface of house 1 is only 44 m² and in house 2 it is estimated that it could have reached 70 m². Inside, hearths and numerous post holes have been discovered. They would have supported the roof, although they do not follow the regular placement that has been seen in the houses of Alto de la Cruz or Las Eretas. Unfortunately, the doors of the houses and the entrance hall have not been preserved, nor has the street from which they would have been accessed because this area of the site has been completely lost. Despite the above caveats, we believe that the urbanism of the *castrum* must have been interconnected by a central street that would have followed the longitudinal axis of the hill, as has been seen in other contemporary settlements in the region.

The double child burial that we analysed in this work was located next to the wide door of the entrance space of house 1 (Fig. 14b–c), which is a compartment of 8.50 m² that is attached to the fortification wall and is separated from the eastern part of the house by a masonry wall. The burial was a circular pit of 70 cm in diameter, delimited by an alignment of stones. Apparently, in the course of the excavation two fragments of Celtiberian ceramics were associated with this burial, and this allowed dating to the Late Iron Age (Castiella et al. 2009, 95–96; 111; de Miguel 2009). However, the absolute dates (^{14}C) of both children *(infra)*, provide calibrated dates between 790 and 546 BC, therefore corresponding to the Early Iron Age of El Castejón and contemporary with the graves of the towns Alto de la Cruz and Las Eretas.



Fig. 13a–b View of El Castejón from the east (a) and south (b).

Abb. 13a–b *Ansicht von El Castejón von Osten (a) und Süden (b).*

The anthropology of intramural child burials

Alto de la Cruz

The 36 intramural child burials from the Alto de la Cruz site have been studied, 9 of these from the excavations carried out in the 1980s, of which a detailed report is available (Mercadal et al. 1990). The remains of the excavations performed between 1948 and 1957 have been identified from the references found in the database of the storeroom of the Archaeological Service of the Government of Navarra. The surviving data (they lacked the documentation recovered at the time of the excavation) have frequently provided imprecise information on the levels and location of the remains. However, it is almost exceptional that such remains of children from archaeological excavations should still survive, as researchers in the first half of the 20th century generally regarded children's remains as not providing relevant information on past populations.

The state of preservation is good in those remains recovered in the campaigns of the 1980s (Mercadal et al. 1990), in which it is obvious that the bones were recovered with great care. When it comes to materials from the oldest excavations, different bones are represented among the various individuals. The material preserved ranges from a single bone to various sets of bones, in which it was possible to differentiate at least two individuals, generally in a partial form. One individual was split between two sets with two different labels (with fragments of the same bone found in each set). It must be pointed out that in some cases animal bones and elements from the grave goods were recovered along with the human remains. No burnt bones have been identified, nor have bones of persons older than 2 or 3 years been found.

Determining the minimum number of individuals (MNI) has been complicated by the coexistence of at least two individuals in some sets, and by the presence of remains with imprecise references regarding their location. This latter fact hinders the possibility of unequivocally asserting or refuting whether the loose remains or the barely represented sets of bones correspond to the missing remains in some of the better-preserved burials. This is why one must take into account that there may be limitations when determining the MNI.

Fig. 14a–c (right page) a Ground plan of the excavated area of El Castejón settlement; b excavation of the twin child burial of house 1; c Skeleton 1 and 2.

Abb. 14a–c (rechte Seite) *a Grundriss der ausgegrabenen Fläche der Siedlung El Castejón; b Ausgrabung der Zwillingskinderbestattung von Haus 1; c Skelett 1 und 2.*


N
House 1
auxiliary room 1
House 2
auxiliary room 2
0
5 m
a
b
10 cm
10 cm
c

The identification of two individuals in several bone assemblages needs to be highlighted, as it would imply their interment in the same funerary feature, either simultaneously or successively (CRU013.1–CRU013.2, CRU015.1–CRU015.2, CRU020–CRU021, and CRU030.1–CRU030.2; Tab. 1). In all cases a certain asymmetry of skeletal development is observed, an aspect which is particularly marked in the case of CRU015.1 and CRU015.2, where the age difference is more than two years. Of these double burials, only in the case of CRU020 and CRU021 both individuals could be genetically analysed.

The difficulty in determining age stems from the variety of available methods. For early ages, such as moments linked to foetal life and full-term pregnancies (37/40 weeks), bone measurements are viewed as giving a reliable approximation of age. In this study we have used two methods to determine age, one of them being that proposed by I. Fazekas and F. Kósa (1978), which includes common and easy to establish parameters. Their proposals stem from the forensic study of a high number of children all of whose skeletal bones were measured, establishing averages by gestational weeks, on the basis of their classification according to lunar months, which identifies 40 weeks of gestation with the 10 lunar months. Likewise, this method discriminates by sex, even if we rarely have this information in archaeology. Although the biological sex has been identified for most of the individuals included in this study, we have opted to use the general tables for age assignment in order to make the work comparable to other studies. For age determination, we have given priority to the measurements obtained from the humeri and femora; whenever we had no valid measurements for these other bones were used. A second method has been proposed by P. Jeanty et al. (1984), who made use of the radiological record of foetuses to create tables in which the lengths of the long bones are differentiated into three categories in accordance with the foetal development percentiles currently available in the perinatal diagnosis. In our study we used the 50th percentile (P50), as we were aware of the errors implied because foetal development can be subject to considerable variation. Given the inherent difficulty in predicting the age of the infants, we made a mean age estimation with the parameters from Jeanty et al. (1984), and we decided to use the guidelines of Fazekas and Kósa (1978) whenever possible.

The data recovered from the burials indicate that a considerable portion of the individuals correspond to children with an age above that of birth. In such cases we have taken into account the length of the long bones as an age-discriminatory element, using the values offered by M. Maresh (1970), taken from L. Scheuer and S. Black (2000). Further considerations should be made when adopting these methods. The determination of age derived from dental development, for which we have used D. Ubelaker (1994, 64) as well as S. AlQahtani et al. (2010) should be considered. Occasionally, we found evidence of ossification phases indicating older ages than those suggested by the length of the long bones, and this was viewed as the most accurate value, along with that of dentition, particularly for infants who have survived beyond the first month of life. The most relevant markers considered were the fusion of the mental symphysis of the mandible and the presence of fused vertebral arches.

Another parameter we took into consideration is that of size, applied to perinatal individuals and on the basis of the formulae proposed by V. Balthazard and H. Dervieux (1921). In our case, they make it possible to contrast the differences in size both in relation to developmental age and to the verified evidence of asymmetries between the bones of the upper and lower limbs of some of the individuals.

The presence of clear pathological signs in several of the individuals studied is noteworthy. Hyperostosis and periostitis are the main signs that allow us to identify health status. It is difficult to relate these alterations to a specific pathology; however, the most common causes are nutritional deficit, with various ultimate causes (malnutrition, anaemia, infections etc.; Lewis 2018, 131–223).

The early death of the infants can be related to possible pregnancy complications for those who died before reaching gestational maturity (less than 37 weeks). Those who died at the end of gestation, a possible cause of death might be related to birth complications. However, some skeletons show pathologies possibly linked to pregnancy problems. During the first month of extra-uterine life, deaths are frequently related both to the after-effects of a complicated birth, and to genetic and congenital alterations that limit the development of the babies, leading to their death. It is also during the first year of life that there is a higher mortality rate both in weakened infants, as a result of poor adaptation to life, and due mainly to respiratory and digestive infectious disease states. Identifying the reasons for the death of those who survive the first year of life is complex, although they are often related to infectious causes.

Some individuals show discrepancies in bone development, occasionally with several months of *decalage*, which must be related to health conditions that prevented normal bone development. In these cases, we have prioritised dental age over bone age for their classification. Similarly, in some individuals, differences in bone development have been observed, generally between the humeri and femora, although the specific cause of these asymmetries has yet to be determined. In the case of CRU013.1, morphological anomalies were identified in the humerus and femur, as well as in the scapula and one hemi-vertebra, and in another incomplete bone, probably a fibula, initially indicating a clear alteration in body morphology. It was difficult to relate these bone pathologies to a specific syndrome, having raised the possibility of osteogenesis imperfecta. As we shall see below, the genomic study of this individual revealed a case of trisomy of chromosome 18, or Edward's syndrome, the first documented in archaeological contexts.

On the basis of the minimum number of 36 child remains in Alto de la Cruz (cf. Tab. 1), we obtain a demographic profile which, despite possible limitations, we believe may be representative of the population buried in the settlement. The distribution of the age of death is significant due to the limited representation of individuals who died before the age of foetal maturation (37 weeks).

In the light of the data obtained, we believe that the distribution of age and sex could be explained by complications arising during pregnancy and the first weeks of life

(Tab. 2; Fig. 15). More difficult to explain is the slight increase of children over six months of age, some of whom were noted for a clear asymmetry between dental and bone development.

Las Eretas (Berbinzana)

The presence of perinatal burials in the Las Eretas site was documented during the excavations made under the supervision of one of the authors J. Armendáriz, a published initial study being already available (Armendáriz/de Miguel 2004). Recently, the possibility of carrying out genetic studies that make it possible to obtain data on sex and kinship relationships has led us to revise the initial data and modify some of the results in order to make them comparable to those obtained at the sites of Alto de la Cruz (Cortes de Navarra) and Castejón de Bargota (de Miguel 2009).

Following the same methodology to determine the approximate age of death, we have created a table with the data obtained from the length of the humerus and the femur, using the parameters proposed by Balthazard and Dervieux (1921) and Fazekas and Kósa (1978). The results obtained from the genetic study have been included, as has the determination of the sex, the identification of two twin brothers and a case of trisomy 21 (Down's syndrome) (Tab. 3–4).

El Castejón (Bargota)

Excavations at this Iron Age site obtained partially preserved skeletal remains of two young children. They were preserved partially in the anatomical position, although most of the bone remains were moved from their original position.

In order to determine their ages, the measurements of various long bones – such as tibiae, a femur, a humerus and two clavicles – were used. The determination of which remains belonged to which individual proved challenging as the skeletons were found in a disordered state. Subsequently, the complexity of laboratory assignment of some of the remains to each one of the individuals limited the measurement of bone sizes and estimation of ages (de Miguel 2009).

On the basis of the results, we verified the presence of two individuals who had been buried under the floor of the house, close to each other. The data available allow us to regard them as primary deposits, close to each other in time, though it was not possible to determine whether the deposits were simultaneous or separated by a period of time – clearly, however, it was a short time-period judging from the approximate ages documented. From the measurements recovered, it is obvious that both very probably survived for some time following birth (Tab. 5).

The results obtained from the available analyses of different bones indicate that the age of both new-born children was above that of the expected 40 weeks of gestation. Likewise, the size, independently of the correspondence between one individual or the other, indicates figures of above 51 cm. This leads us to believe that both individuals survived for an undetermined period of time after birth. It is likely that they died during the first month of life. In the study of the surviving remains, there were no signs of any significant alterations that might offer clues as to the cause of death.

The genetic analysis of the Early Iron Age infant burials

A total of 37 Iron Age (800–40 BC), intramurally buried children were sampled from Alto de la Cruz (CRU, n = 29 individuals), Las Eretas (ERE, n = 6), and Castejón de Bargota (BGO, n = 2) in the Navarra region of present-day northern Spain.

Preferentially, petrous parts of the temporal bone (Gamba et al. 2014; Pinhasi et al. 2015; Parker et al. 2020) were sampled for ancient DNA (aDNA), after which single-stranded non-UDG treated libraries (Gansauge/Meyer 2013; Rohland et al. 2015) were generated and screened for aDNA preservation on an Illumina HiSeq machine. Endogenous human aDNA preservation was exceptional (Tab. 6), meaning only a subset (n = 10) of the libraries needed to be 1240K captured (Mathieson et al. 2015) before deeper Illumina sequencing. All sequencing data produced were processed using nf-core/eager version 2.4.5[11]. Briefly, the sequenced reads were preprocessed with AdapterRemoval (v2.3.2) and mapped to the human reference genome (hs37d5) using bwa-aln (v0.7.17-r1188). Duplicates originating from PCR amplification during laboratory processing were then removed using picard MarkDuplicates (v2.26.0). Pseudohaploid genotypes were called using pileupCaller (from sequenceTools v1.5.2)[12] by randomly sampling one allele at each 1240K site. To eliminate the effects of deamination damage on the resulting genotypes the additional parameter ›--singleStrandMode‹ was used, which restricts the reads used when calling transitions to only forward- or reverse-mapped reads, depending on the alleles of the genotyped SNP. Enough data was produced from 35 children (> 40 000 1240K SNPs) for downstream autosomal, Y-chromosomal, and mitochondrial analyses (Tab. 6).

Population genetic analysis

In order to assess the genetic affinities of the newly studied Iron Age individuals from Navarra (n = 35), we conducted a principal components analysis (PCA; Fig. 16) on modern-day west Eurasian genetic diversity onto which ancient Bronze Age and Iron Age individuals from northern Spain were projected[13].

The new Iron Age Navarra individuals plot closely to previously published Bronze Age and Iron Age individuals from northern Spain (Fig. 16). The Bronze Age individuals (green) form a cline along PC2, which has been shown to be correlated with steppe-related ancestry. This is most plausibly indicative of recent admixture between Spanish Chalcolithic individuals, who are lower on PC2, with incoming central European individuals carrying steppe-related ancestry, who

11 <https://github.com/nf-core/eager/tree/2.4.5> (14.06.2023).

12 <https://github.com/stschiff/sequenceTools> (14.06.2023).

13 Lazaridis et al. 2014; Günther et al. 2015; Valdiosera et al. 2018; Olalde et al. 2019; Patterson et al. 2022.

LabID	Archaeological label	Reference	HUR	HUL	FER	FEL	Age	Sex	Observations
CRU001	1948	mm	58.3	58.4			38 w	M	TIL: 59.3 mm (38 w; 47.04 cm (Balthazard/ Dervieux 1921)
		Fazekas/Kósa 1978 (w)	36	36					
		Balthazard/Dervieux 1921 (cm)	45.89	45.96					Asymmetric development between humerus/tibia
									Down's syndrome
CRU002	1948. Hab saliente piso D. 23.III.48	mm	68.5				0/1 m	F	
		Fazekas/Kósa 1978 (w)	> 40						
		Balthazard/Dervieux 1921 (cm)	52.52						
		Maresh 1970 (m)	< 1.5						
CRU003	1949. 8.10.49. Estrato C-2. Esqueleto infantil al nivel superior de los muros de dicho estrato, junto al ángulo NE.	mm	61.3	61.2	68.8		38 w	M	Hyperostosis
		Fazekas/Kósa 1978 (w)	38	38	38				
		Balthazard/Dervieux 1921 (cm)	47.84	47.78	46.52				
CRU004	1949.10.10.49. C2. Corresponde C1. Junto al muro oriental cerca del ángulo NE	mm	48.3			51.2	31 w	F	Asymmetric development of long bones
		Fazekas/Kósa 1978 (w)	31			30			
		Balthazard/Dervieux 1921 (cm)	39.39			36.67			Hyperostosis
CRU005	10-IX-1949. Estrato B. Hab. 21. Pero enterrado desde el estrato A, inferior	mm	71.3	71.2	82.2	81.8	0/1 m	M	
		Fazekas/Kósa 1978 (w)	> 40	> 40	> 40	> 40			
		Balthazard/Dervieux 1921 (cm)	54.34	54.28	54.03	53.80			
		Maresh 1970 (m)	≤ 1.5	≤ 1.5	< 1.5	< 1.5			
CRU006	1949. 17.9.49. Estrato A. Corte norte Cortes. 11.11.48. 2. H.8. C. Relación con R1	mm	65.7	65.4	72.6	72.9	0/1 m	M	Excavated in different seasons
		Fazekas/Kósa 1978 (w)	> 40	> 40	38	38			
		Balthazard/Dervieux 1921 (cm)	50.70	49.86	48.65	48.82			
		Maresh 1970 (m)	< 1.5	< 1.5	< 1.5	< 1.5			
CRU007	1949. 14-10-49. Estrato C-2. Hab.6. por encima del suelo C-2	mm	68.5	69	79.9	80.3	0/1 m	F	Hyperostosis
		Fazekas/Kósa 1978 (w)	> 40	> 40	> 40	> 40			
		Balthazard/Dervieux 1921 (cm)	52.52	52.85	52.744	52.96			
		Maresh 1970 (m)	< 1.5	< 1.5	< 1.5	< 1.5			
CRU008	1949. 6-X-49. Esqueleto infantil. Estrato C-2. Hab. 11. Bajo muro de la habitación 11 a 17. (Corresponde a C-1)	mm	68.3	68.3	80.08	80.07	0/1 m	F	Hyperostosis
		Fazekas/Kósa 1978 (w)	> 40	> 40	> 40	> 40			
		Balthazard/Dervieux 1921 (cm)	52.39	52.39	52.84	52.83			
		Maresh 1970 (m)	< 1.5	< 1.5	< 1.5	< 1.5			
CRU009	1950. 5.9.50. Hab.15. Estrato A. Sobre suelo						40 w	M	According to teeth ± 40 (Ubelaker 1994 1999, 64)
									Pars basilaris: 40 w (Scheuer/Black 2000, 62)

LabID	Archaeological label	Reference	HUR	HUL	FER	FEL	Age	Sex	Observations
CRU010	1950. 19-IX-1950. B.27. Enterramiento infantil	mm	76.3		88	87.3	0/1.5 m	M	Criba orbitaria, Hyperostosis
		Fazekas/Kósa 1978 (w)	> 40		> 40	> 40			
		Balthazard/Dervieux 1921 (cm)	57.59		57.28	56.88			
		Maresh 1970 (m)	< 1.5		< 1.5	< 1.5			
CRU011	1951.10.9.51. Hab13.Est-rato Z	mm	79.9			≥ 92.4	6/9 m	M	Asymmetric development between long bones and teeth. Teeth/chin 6/9 m Costal notch
		Fazekas/Kósa 1978 (w)	> 40			> 40			
		Balthazard/Dervieux 1921 (cm)	59.93			59.78			
		Maresh 1970 (m)	3			± 3			
CRU012	1952. 52. 1. Hab.56	mm	70.6	71.1	78.5	78.4	± 4.5 m	M	Asymmetric development between long bones and teeth Asymmetric development between long bones Long bones 0/1,5 m Clavicular long 0/6 m (Black/Scheuer 2000) Dentition: ± 4,5 months (AlQahtani et al. 2010) Hyperostosis/ periostitis
		Fazekas/Kósa 1978 (w)	> 40	> 40	39	39			
		Balthazard/Dervieux 1921 (cm)	53.89	54.21	51.96	51.90			
		Maresh 1970 (m)	< 1.5	< 1.5	< 1.5	< 1.5			
CRU013	1953. 53. Est.A. Corte A-A', esqueleto infantil. 1	mm	64.5	65	71.1		± 40 w	F	Edward's syndrome Asymmetric development between long bones Same assemblage as CRU013.2
		Fazekas/Kósa 1978 (w)	40	40	38				
		Balthazard/Dervieux 1921 (cm)	49.56	50.25	47.81				
		Maresh 1970 (m)	< 1.5	< 1.5	< 1.5				
CRU013.2	1953. 53. Est.A. Corte A-A', Esqueleto infantil 2	mm	66.6	67.2	80	80.2	0/1 m	UD	Same assemblage as CRU013.1
		Fazekas/Kósa 1978 (w)	> 40	> 40	> 40	> 40			
		Balthazard/Dervieux 1921 (cm)	51.29	51.68	52.8	52.91			
CRU014	1953. 53.m Est.Y.	mm	68.6	69.1	77.2	78.2	0/1 m	F	Hyperostosis
		Fazekas/Kósa 1978 (w)	> 40	> 40	> 40	> 40			
		Balthazard/Dervieux 1921 (cm)	52.59	52.91	51.23	51.68			
		Maresh 1970 (m)	< 1.5		< 1.5	< 1.5			
CRU015.1	1955. M6.1	Ubelaker 1994					2/3 y	M	Age according to teeth; Stored together with CRU015.2
CRU015.2	1955. M6.2	mm	68		75.6		0/1 m	UD	Stored together with CRU015.1
		Fazekas/Kósa 1978 (w)	> 40		> 40				
		Balthazard/Dervieux 1921 (cm)	50.3		52.2				

LabID	Archaeological label	Reference	HUR	HUL	FER	FEL	Age	Sex	Observations
CRU016	1957. 13.8.57. Sector B (8 metros) sección A-A1-A2	mm		78.3		90.8	6/9 m	M	Asymmetric development between long bones and teeth Age by teeth: 6/9 m Age by long bones: ± 3 m Age by clavicle (D: 57.1 mm): 7/12 m (Black/Scheuer 1996)
		Fazekas/Kósa 1978 (w)		> 40		> 40			
		Balthazard/Dervieux 1921 (cm)		58.89		58.84			
		Maresh 1970 (m)		± 3		± 3/6			
CRU017	1957. 14.8.57. N.1. »Chiquillo de la anilla«	mm	60.3				37 w	F	Possible grave good
		Fazekas/Kósa 1978 (w)	37						
		Balthazard/Dervieux 1921 (cm)	47.19						
CRU018	1957. 29-8-57. »Huesos de Niña/fondo con grafito«	mm	79	78.6	92	91.6	± 3 m	M	Costal notch
		Fazekas/Kósa 1978 (w)	> 40	> 40	> 40	> 40			
		Balthazard/Dervieux 1921 (cm)	59.35	59.09	59.52	58.96			
		Maresh 1970 (m)	± 3	± 3	± 3	± 3			
CRU019	1949. Sin número	mm	98.49	98.8	121.25	121.3	18 m	F	Asymmetric development between long bones and teeth; Age by teeth: 18 m Age by long bones 6/12 m
		Maresh 1970 (m)	6/12 m	6/12 m	6/12 m	6/12 m			
CRU020	1949. Sin r eferencia 2	mm			73.3	72.6	40 w	F	Possible double burial (with CRU021).
		Fazekas/Kósa 1978 (w)			40	40			
		Balthazard/Dervieux (cm)			49.04	48.65			
CRU021	21. 1949. Sin referencia 2	mm	70.4	71	77.6	77.5	0/1 m	M	Asymmetric development between long bones, Possible double burial (with CRU020).
		Fazekas/Kósa 1978 (w)	> 40	> 40	> 40	> 40			
		Balthazard/Dervieux 1921 (cm)	53.76	54.15	51.45	51.4			
		Maresh 1970 (m)	< 1.5	< 1.5	< 1.5	< 1.5			
CRU022	Individuo n.° 1. H. 87/8 N. P.II.a.	mm	63.6	64	75.8	75.8	0/1 m	F	Slight asymmetric development between long bones
		Fazekas/Kósa 1978 (w)	40	40	> 40	> 40			
		Balthazard/Dervieux 1921 (cm)	49.34	49.6	50.44	50.44			
		Maresh 1970 (m)			< 1 m	< 1 m			
CRU023	Individuo n.° 2. H. 87/8. N. P.II.a	mm		62.9	73		39 w	F	
		Fazekas/Kósa 1978 (w)		39	39				
		Balthazard/Dervieux 1921 (cm)		48.88	48.88				
CRU024	Individuo n.° 3: H. 86/19. N. P.III.b	mm	41.1	41.5	47.1	47.1	28 w	F	Down's syndrome; asymmetric development between long bones
		Fazekas/Kósa 1978 (w)	26	26	28	28			
		Balthazard/Dervieux 1921 (cm)	34.71	34.97	34.37	34.37			
CRU025	Individuo n.° 4: H. 87/8. N. P.II.a	mm	80	81.6	96.3	96.7	7 m	M	Asymmetric development between long bones and teeth
		Maresh 1970 (m)	3	3	3	3			

LabID	Archaeological label	Reference	HUR	HUL	FER	FEL	Age	Sex	Observations
CRU026	Individuo n.° 6. H. 87/8. N. P.II.a (bajo pavimento)	mm	61.2	61.8	66.1		38 w	M	Asymmetric development between long bones
		Fazekas/Kósa 1978 (w)	38	38	36				
		Balthazard/Dervieux 1921 (cm)	47.78	48.17	45.01				
CRU027	Individuo n.° 7. H. 87/8. N. P.II.a (bajo pavimento).	mm				65.5	37 w	M	
		Fazekas/Kósa 1978 (w)				37			
		Balthazard/Dervieux 1921 (cm)				44.68			
CRU028	Individuo n.° 8 (ver n.° 5). H. 88/21. N. P.III.b (bajo pavimento)	mm			69	69	38 w	M	
		Fazekas/Kósa 1978 (w)			38	38			
		Balthazard/Dervieux 1921 (cm)			46.64	46.64			
CRU029	Individuo n.° 9. H. 88/21. N. P.III.b (17 cm. bajo pavimento)	mm		60.5	63.4	63.5	37 w	M	
		Fazekas/Kósa 1978 (w)		36	37	37			
		Balthazard/Dervieux 1921 (cm)		47.32	43.504	43.56			
CRU030.1	Cortes. 3.11.48. Estrato A. habitación 3.	mm	71.1			77.6	± 1.5 m	UD	Could correspond to the same space of CRU030.2. Remains from two individuals.
		Fazekas/Kósa 1978 (w)	> 40			> 40			
		Balthazard/Dervieux 1921 (cm)	54.60						
		Maresh 1970 (m)	± 1.5						
CRU030.2	Cortes 8.11.48. Estrato A. habitación 3. »Fauna«	mm		67.7	71.8		≥ 40 w	UD	Asymmetric development between long bones could correspond to the same space of CRU030.1. Remains from two individuals
		Fazekas/Kósa 1978 (w)		> 40	39				
		Balthazard/Dervieux 1921 (cm)		52	48.20				
		Maresh 1970 (m)		< 1.5 m					
CRU031	Cortes. 21.10.49. Estrato B. huesos.	mm	73.4				1.5 m	UD	
		Fazekas/Kósa 1978 (w)	> 40 w						
		Balthazard/Dervieux 1921 (cm)	55.71						
		Maresh 1970 (m)	1.5 m						
CRU032	Septiembre 1955. Esqueleto niño. Fuera W a M6 bajo piso	mm	60.2	60.4	68.9		38 w	UD	
		Fazekas/Kósa 1978 (w)	37	37	38				
		Balthazard/Dervieux 1921 (cm)	47.19	47.26	48.58				
CRU033	Cortes. 15.X.49. Habitación 29. Estrato C-2. Bajo muro oriental.	mm		90.5		115	1 y	UD	Asymmetric development between long bones and teeth. Two bronze bracelets
		Maresh 1970 (m)		6/12 m		6/12 m			

Tab. 1 Infant individuals from Alto de la Cruz. Age and height obtained from the long bones and dentition. The formula used to obtain the results is specified. Sex was determined according to genetic analysis. HU: humerus, FE: femur, TI: tibia; R: right, L: left; M: male, F: female; UD: undetermined; w: weeks (gestational age); m: months (postnatal age); y: years (postnatal age).

Tab. 1 *Säuglingsindividuen aus Alto de la Cruz. Alter und Größe werden anhand der Langknochen und des Gebisses ermittelt. Die zur Ermittlung der Ergebnisse verwendete Formel ist angegeben. Das Geschlecht wurde anhand genetischer Analysen bestimmt. HU: Humerus, FE: Femur, TI: tibia; R: rechts, L: links; M: männlich, F: weiblich; UD: nicht bestimmt; w: Wochen (Gestationsalter); m: Monate (postnatales Alter); y: Jahre (postnatales Alter).*

Age	Undetemined	Female	Male	Total
24–28 weeks		CRU024		1
31–34 weeks		CRU004		1
35–36 weeks				0
37–40 weeks	CRU030.2 CRU032	CRU013.1 CRU017 CRU020 CRU023	CRU001 CRU003 CRU009 CRU026 CRU027 CRU028 CRU029	13
0–1.5 month	CRU013.2 CRU015.2	CRU002 CRU007 CRU008 CRU014 CRU022	CRU005 CRU06 CRU010 CRU021	11
1.5–3 months	CRU030.1 CRU031		CRU018	3
3–6 months			CRU012	1
6–12 months	CRU033		CRU011 CRU016 CRU025	4
2–3 years			CRU015.1	1
Total	**7**	**11**	**17**	**35**

Tab. 2 List of the individuals from Alto de la Cruz according to sex and age at death. Weeks = fetal age; months and years = postnatal age.

Tab. 2 *Liste der Individuen aus Alto de la Cruz, geordnet nach Geschlecht und Alter zum Zeitpunkt ihres Todes. Wochen = fetales Alter; Monate und Jahre = postnatales Alter.*

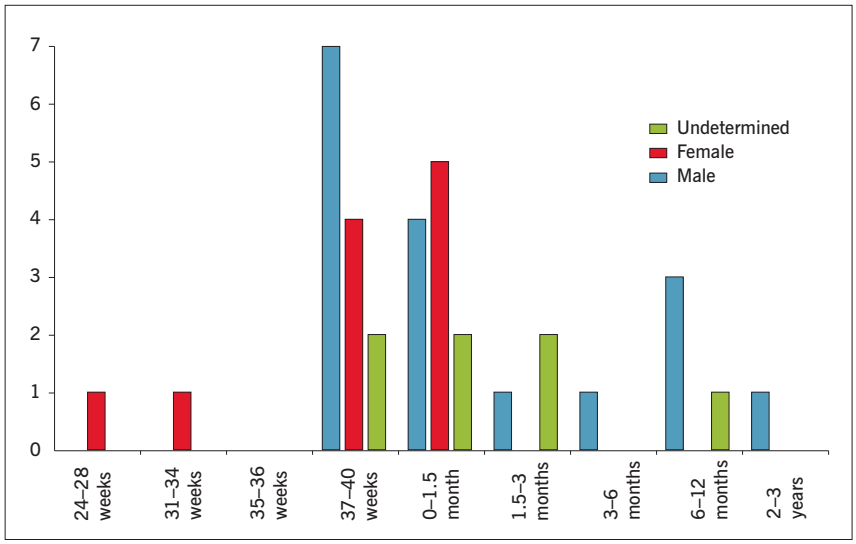


Fig. 15 Histogram of age and sex of the child burials from Alto de la Cruz. Weeks = fetal age; months and years = postnatal age.

Abb. 15 *Histogramm von Alter und Geschlecht der Kinderbestattungen in Alto de la Cruz. Wochen = fetales Alter; Monate und Jahre = postnatales Alter.*

are higher on PC2 (Olalde et al. 2019). In contrast to the Bronze Age individuals from northern Spain, the Iron Age Navarra individuals tend to occupy higher PC2 values indicative of more steppe-related ancestry compared to the Bronze Age individuals. This is also seen in qpAdm modelling of the Iron Age Navarra individuals, who cannot be modelled as being genetically indistinguishable from the preceding Middle and Late Bronze Age individuals from northern Spain ($p < 2.4E-03$), but instead are better modelled as a two-way mixture of 89.1 % (82.5–95.7 % two standard errors) Middle and Late Bronze Age northern Spanish-like ancestry admixed with 10.9 % (4.3–17.5 % two standard errors) French Bell Beaker-like ancestry ($p = 4.3E-02$).

In terms of genetic variation along PC1, the new Iron Age children from Navarra tend to occupy lower values than the previously published Iron Age individuals from northern Spain (Welch Two Sample t-test $p < 1.3e-03$, Wilcoxon rank sum test with continuity correction $p < 5.3e-05$; Fig. 16). In the context of post-Bronze Age Spain, PC1 is correlated with Mediterranean ancestry (Olalde et al. 2019; Villalba-Mouco et al. 2021), suggesting that the published Iron Age individuals ($n = 8$) were more influenced by Mediterranean gene flow compared to the new intramurally buried Iron Age children from Navarra. This is supported by the f_4-statistic of the form f_4(Mbuti, test; Iron Age_Navarra, Iron Age_published), which is significantly positive for Near Eastern test populations such as Turkey_SoutheastByzantine ($Z > 4$) and Iran_GanjDareh ($Z > 5$). We note that geography does not explain this shift, as the new Iron Age Navarra children are geographically closer to the Mediterranean coast than the published Iron Age samples from northern Spain. One interpretation is that the Iron Age children from Navarra may have belonged to groups that resisted gene flow from communities with higher Mediterranean ancestry, perhaps suggesting some level of relative isola-

LabID	Archaeological label	Reference	HUR	HUL	FER	FEL	Age	Sex	Observations
ERE001	Eretas Indiv. 1	mm	59.2	56.6	65.1	65.1	37 w	M	Twin of ERE002
		Fazekas/Kósa 1978 (w)	37	36	37	37			
		Balthazard/Dervieux 1921 (cm)	46.48	44.79	44.456	44.456			
ERE002	Eretas Indiv. 2	mm	50.2	50.5	53.9	50.5	32 w	M	Twin of ERE001
		Fazekas/Kósa 1978 (w)	32	32	31	31			
		Balthazard/Dervieux 1921 (cm)	40.63	40.82	38.18	36.28			
ERE003	Eretas Indiv. 3	mm		63.6		71.6		M	
		Fazekas/Kósa 1978 (w)		39		39			
		Balthazard/Dervieux 1921 (cm)		49.34		48.09			
ERE004	Eretas Indiv. 4	mm	40.6				26 w	M	Down's syndrome
		Fazekas/Kósa 1978 (w)	26						
		Balthazard/Dervieux 1921 (cm)	34.39						
ERE005	Eretas Indiv. 5	mm	41.2				0/1 m	UD	
		Fazekas/Kósa 1978 (w)	26						
		Balthazard/Dervieux 1921 (cm)	34.78						
ERE006	Eretas Indiv. 6	mm			79.7	76	> 40 w	F	
		Fazekas/Kósa 1978 (w)			> 40	> 40			
		Balthazard/Dervieux 1921 (cm)			52.63	50.56			

Tab. 3 Infant individuals from Las Eretas. Genetic sex, age (gestational weeks) and size obtained (cm) from the length of humeri and femurs (mm) for intramural child burials from Las Eretas. HU: humerus, FE: femur, TI: tibia; R: right, L: left; M: male, F: female; UD: undetermined; w: weeks (gestational age); m: months (postnatal age); y: years (postnatal age).

Tab. 3 *Säuglingsindividuen aus Las Eretas. Genetisches Geschlecht, Alter (Schwangerschaftswochen) und Größe (cm), ermittelt aus der Länge der Ober- und Unterschenkelknochen (mm) für intramurale Kinderbestattungen aus Las Eretas. HU: Humerus, FE: Femur, TI: tibia; R: rechts, L: links; M: männlich, F: weiblich; UD: nicht bestimmt; w: Wochen (Gestationsalter); m: Monate (postnatales Alter); y: Jahre (postnatales Alter).*

tion from coastal south-eastern areas. Another possibility is that the Iron Age children from Navarra predate the published Iron Age individuals and this Mediterranean influence.

Kinship analysis

In order to identify close biological relatedness in Iron Age Navarra, we used READ (Relationship Estimation from Ancient DNA; Kuhn et al. 2018; cf. Günther in this volume) along with calculating rates of pseudo-haploid genotype mismatch in all pairwise comparisons of both published and newly reported individuals (Tab. 7; Fig. 17). We identified nine cases of biologically closely related pairs of individuals, ranging from 0^{th}- to 2^{nd}-degree related.

We identified two cases (BGO001–BGO002 and ERE001–ERE002) of identical twins. In addition to having a high rate of identical genotypes on the autosomes (Fig. 17), they also share the same mitochondrial and Y-chromosome hapw-

Age	Male	Female	Undetermined	Total
26 w	ERE004	ERE005		2
32 w	ERE002			1
37/39 w	ERE001 ERE003			2
≥ 40 w			ERE006	1
Total	4	1	1	6

Tab. 4 Sex and age distribution of intramural child burials at Las Eretas; w: weeks (gestational age).

Tab. 4 *Geschlechts- und Altersverteilung der Kindergräber in Las Eretas; w: Wochen (Gestationsalter).*

LabID	Reference	HUR	HUL	FER	FEL	Age	Sex	Observations
BGO001	Individual 1	mm				0/6 m	M	Clavicle left 47 mm (Black/ Scheuer 1999). Twin of BGO002
BGO002	Individual 2	mm	69.6			0/1 m	M	Twin of BGO001
		Fazekas/Kósa 1978 (w)	> 40					
		Balthazard/Dervieux 1921 (cm)	53.24					

Tab. 5 Infant individuals from El Castejón (Bargota). Measurements of the preserved remains that were recovered. HU: humerus, FE: femur, TI: tibia; R: right, L: left; M: male, F: female; UD: undetermined; w: weeks (gestational age); m: months (postnatal age); y: years (postnatal age).

Tab. 5 *Säuglingsindividuen aus El Castejón (Bargota). Maße der erhaltenen Überreste, die geborgen wurden. HU: Humerus, FE: Femur, TI: tibia; R: rechts, L: links; M: männlich, F: weiblich; UD: nicht bestimmt; w: Wochen (Gestationsalter); m: Monate (postnatales Alter); y: Jahre (postnatales Alter).*

Individual ID	Site	Period	C^{14} Date	Shotgun Endogenous DNA Post (%)	5' C-to-T damage 1st base	Number of SNPs on »1240K«	Genetic Sex	Mitochondrial Haplogroup	Y-chrom Haplogroup
BGO001	Castejón de Bargota	Iron Age	790–567 cal BC	59.31	0.285	559.108	Male	J1c1	R1b–151
BGO002		Iron Age	779–546 cal BC	60.73	0.287	508.624	Male	J1c1	R1b–P310
CRU001	Alto de la Cruz	Iron Age	—	18.12	0.356	619.206	Male	H1e1a	R1b–P312
CRU002		Iron Age	—	25.12	0.383	205.154	Female	H17	—
CRU003		Iron Age	—	59.75	0.334	498.150	Male	HI	R1b U51
CRU004		Iron Age	771–544 cal BC	24.88	0.353	195.426	Female	H4a1	—
CRU005		Iron Age	—	56.03	0.341	449.823	Male	T2b	R1b–2272
CRU006		Iron Age	—	36.39	0.332	226.316	Male	J1c3g	R1b–2266
CRU007		Iron Age	726–407 cal BC	26.83	0.369	192.208	Female	J2a1a1	—
CRU008		Iron Age	—	53.89	0.31	426.467	Female	T2e	—
CRU009		Iron Age	—	7.6	0.331	491.909	Male	H1ak1	R1b–P312
CRU010		Iron Age	—	41.65	0.308	338.699	Male	H1ae2	R1b–P312
CRU011		Iron Age	—	10.08	0.338	231.190	Male	J1c1	R1b–2272
CRU012		Iron Age	800–593 cal BC	22.7	0.342	160.253	Male	K1a3	I2a1
CRU013		Iron Age	—	55.08	0.329	443.640	Female	H1ae2	—
CRU014		Iron Age	—	13.96	0.292	477.865	Female	H1ae2	—
CRU015		Iron Age	—	44.13	0.344	282.166	Male	H1ah	R1b–U51
CRU016		Iron Age	—	22.86	0.358	163.053	Male	T1a1	R1b–U51
CRU017		Iron Age	—	25.91	0.345	187.803	Female	T1a1	—
CRU018		Iron Age	—	53.04	0.294	390.581	Male	H1t	R1b–P310
CRU019		Medieval	992–1032 cal ACE	20.12	0.22	690.655	Female	U5b1	—
CRU020		Iron Age	—	51.23	0.326	475.669	Female	H3y	—
CRU021		Iron Age	—	7.85	0.344	392.560	Male	K1a4a1	R1b–2195
CRU022		Iron Age	—	47.23	0.303	310.099	Female	T2a1a	—
CRU023		Iron Age	774–544 cal BC	26.67	0.342	203.563	Female	T2a1a	—
CRU024		Iron Age	779–549 cal BC	38.71	0.32	294.884	Female	J2a1a1	—
CRU025		Iron Age	—	36.11	0.294	270.491	Female	K1a4a1	—
CRU026		Iron Age	—	12.16	0.351	571.749	Male	J1c1	R1b–2295
CRU027		Iron Age	—	0.49	0.418	43.447	Male	J1c1	R1b–2195
CRU028		Iron Age	—	30.4	0.342	300.276	Male	H4a1	R1b–P310
CRU029		Iron Age	—	41.97	0.332	272.017	Male	J1c1b	R1b–M269

Individual ID	Site	Period	C^{14} Date	Shotgun Endogenous DNA Post (%)	5' C-to-T damage 1st base	Number of SNPs on »1240K«	Genetic Sex	Mitochondrial Haplogroup	Y-chrom Haplogroup
ERE001	Las Eretas	Iron Age	758–479 cal BC	34.31	0.372	282.642	Male	T1a1	R1b–M269
ERE002		Iron Age	—	37.55	0.355	308.220	Male	T1a1	R1b–U51
ERE003		Iron Age	—	11.13	0.403	6.516	Male	U2e1	Unknown
ERE004		Iron Age	801–764 cal BC	22.14	0.388	198.307	Male	J1c2	R1bP312
ERE005		Iron Age	775–549 cal BC	32.58	0.388	178.682	Female	J1c2	—
ERE006		Iron Age	—	1.56	0.484	134	Unknown	Unknown	Unknown

Tab. 6 General overview of ancient Navarra individuals studied from a genetic perspective.

Tab. 6 *Allgemeiner Überblick über prähistorische Individuen aus Navarra, die unter genetischen Gesichtspunkten untersucht wurden.*

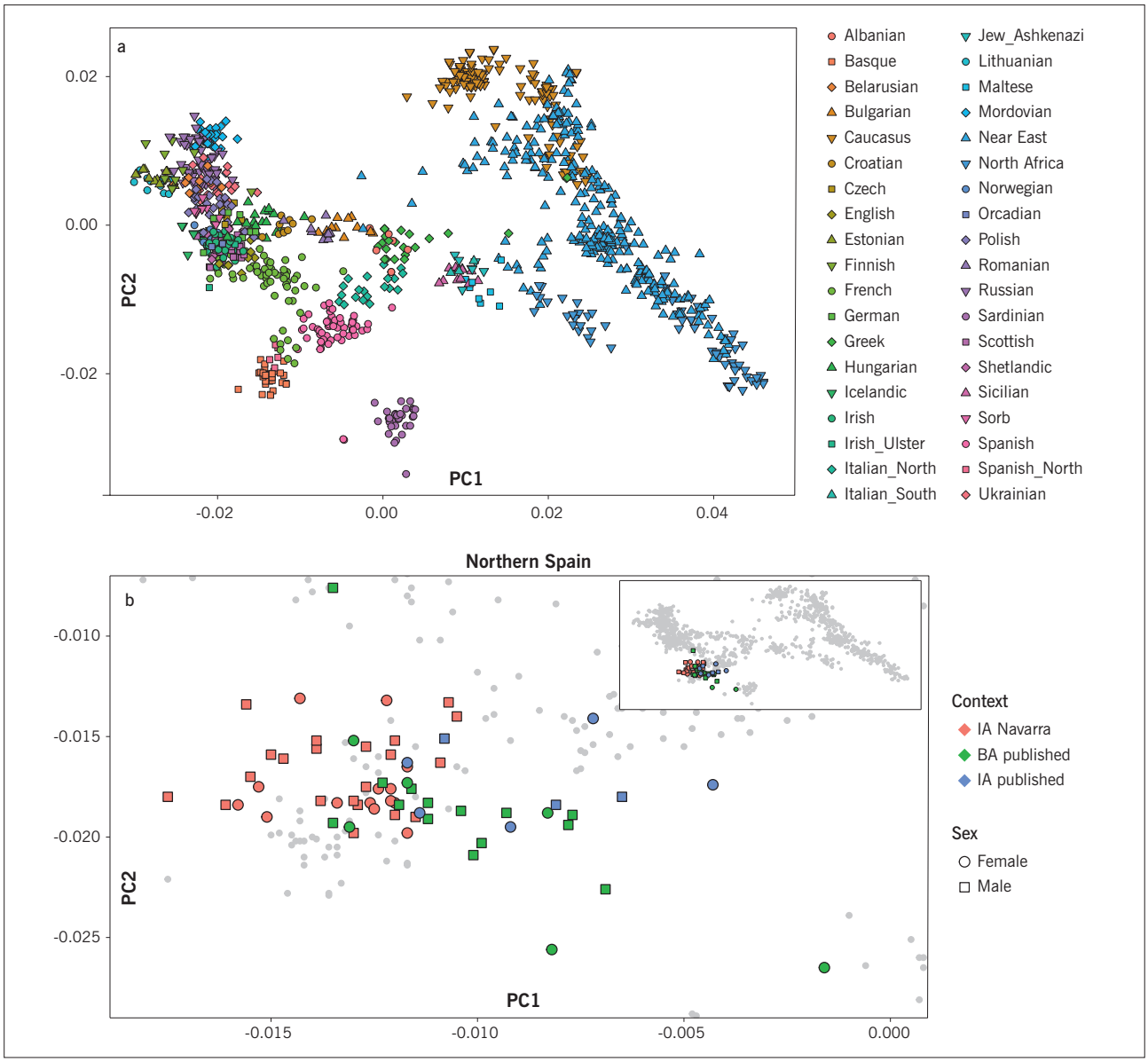


Fig. 16a–b a) Principal component analysis (PCA) of contemporary West Eurasian genetic variability, with b) projections of diverse prehistoric individuals: intramural buried children in Iron Age Navarra (red, n = 34), Bronze Age (green, n = 20) and Iron Age (blue, n = 8) individuals from northern Spain presented in this study (previously published data). Enlarged image (see small graphic above right).

Abb. 16a–b *a) Hauptkomponentenanalyse (PCA) der heutigen westeurasischen genetischen Variabilität, mit b) Projektionen diverser prähistorischer Individuen: in dieser Studie vorgestellte intramural begrabene Kinder im eisenzeitlichen Navarra (rot, n = 34), bronzezeitliche (grün, n = 20) und eisenzeitliche (blau, n = 8) Individuen aus Nordspanien (bereits veröffentlichte Daten). Vergrößerte Darstellung (siehe kleine Grafik oben rechts).*

Pairindividuals	Relationship	Z upper	Z lower	Mitochondrial Haplogroups	Y Haplogroups
BG0001–BG0002	Identical Twins/ Same Individual	29.68	NA	J1C1-J1C1	R1b-LI51-R1b-P310
ERE001–ERE002	Identical Twins/ Same Individual	22.78	NA	T1a1-T1al	R1b-M269-R1b-L151
CRU022–CRU023	First Degree	5.2	-10.5	T2a1a-T2a1a	NA-NA
CRU026–CRU027	First Degree	3.80	-7.95	J1Cl-J1C1	Rlb-Z295-R1b-Z195
CRU010–CRU014	Second Degree	7.19	-7.83	H1ae2-H1ae2	R1b-P312-NA
CRU008–CRU015	Second Degree	7.49	-6.10	T2e-H1ah	NA-R1b-L151
CRU027–CRU029	Scoond Degree	1.55	-3.49	J1c1-J1c1b	R1b-Z195-R1b-M269
ERE004–ERE005	Second Degree	6.77	-1.661	J1c2-J1c2	R1b-P312-NA
CRU026–CRU029	Unrelated	NA	-0.18	J1cl-J1c1b	R1b-Z295-R1b-M269

Tab. 7 Output from READ (columns 1–4) quantifying the degree of genetic relationships for pairs of relatives. Z-scores smaller than 3 and larger than 3 indicate uncertain assignments. Mitochondrial and Y-chromosomal haplogroups (columns 5–6) match in cases where matches based on autosomal relatedness are expected. Note that due to different and uneven Y-chromosomal coverage between relatives, the resulting Y haplogroup assignments might be slightly different, but all pairs of male relatives are consistent with carrying the same lineage.

Tab. 7 *Ergebnis von READ (Spalten 1–4), die den Grad der genetischen Verwandtschaft von Verwandtenpaaren quantifiziert. Z-Scores kleiner als 3 und größer als -3 zeigen unsichere Zuordnungen an. Mitochondriale und Y-chromosomale Haplogruppen (Spalten 5–6) stimmen in den Fällen überein, in denen Übereinstimmungen auf der Grundlage der autosomalen Verwandtschaft zu erwarten sind. Zu beachten ist, dass aufgrund der unterschiedlichen und ungleichmäßigen Y-Chromosomenabdeckung zwischen den Verwandten die resultierenden Y-Haplogruppenzuordnungen leicht unterschiedlich sein können, aber alle Paare männlicher Verwandter stimmen mit der gleichen Abstammung überein.*

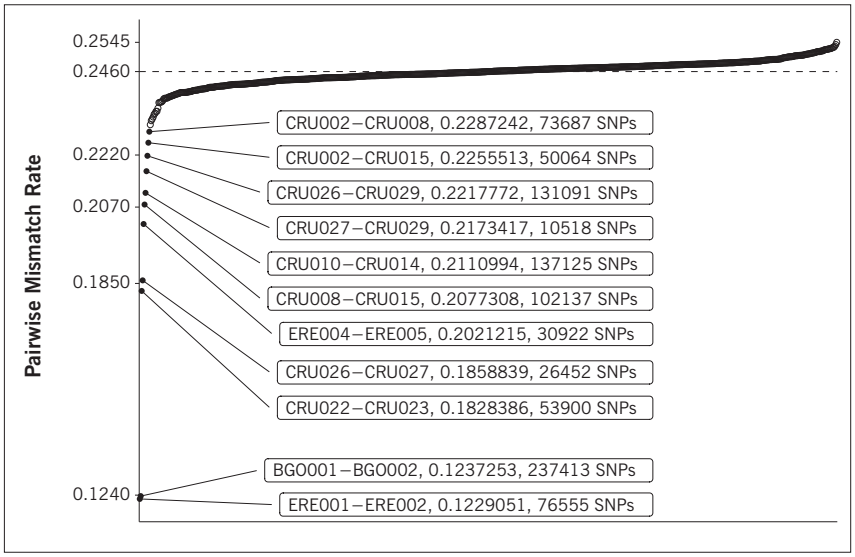


Fig. 17 The distribution of autosomal pairwise genotype mismatch rates in in studied individuals from Iron Age northern Spain. Lower mismatch rates indicate closer biological relatedness. The median mismatch value (0.246) is indicated by the dashed line, and the number of overlapping SNPs is shown for selected pairwise relationships.

Abb. 17 *Die Verteilung der autosomalen paarweisen Genotyp-Mismatch-Raten in hier untersuchten Individuen aus dem eisenzeitlichen Nord-Spanien. Niedrigere Mismatch-Raten weisen auf eine engere biologische Verwandtschaft hin. Der mediane Mismatch-Wert (0,246) ist durch die gestrichelte Linie gekennzeichnet, und die Anzahl der überlappenden SNPs ist für ausgewählte paarweise Beziehungen dargestellt.*

logroups (cf. Tab. 6). Adding further confidence to the assignment of identical twins (as opposed to potentially sampling different elements from the same individual twice) is the fact that in both cases the same skeletal element from both individuals was sampled (i.e., the left petrous bone), which rules out any possibility of a sample mix-up. It is noteworthy that the two individuals originating from another possible double burial (CRU020–CRU021) were not related in a first or second degree, implying that not all multiple Iron Age infant burials need to be seen as twins, siblings or half-siblings. However, this conclusion needs to be taken with caution, as no information on the context of both skeletons, found in 1949, has been published.

We also identified two cases of first-degree relatives (CRU022–CRU023 and CRU026–CRU027). *IcMLkin* (Maximum Likelihood Estimation of Relatedness; Lipatov et al. 2015) did not yield enough overlapping SNPs between the pairs of relatives to distinguish between parent-offspring or siblings, but the fact that all four individuals are newborns implies they must be siblings (too young to be parent-offspring). The assignment to siblings is also consistent with both pairs sharing mitochondrial and Y-chromosome haplogroups (cf. Tab. 7).

Five cases of second-degree relatives (ERE004–ERE005, CRU008–CRU015, CRU010–CRU014, CRU027–CRU029, CRU026–CRU029) were also found. The CRU026–CRU029 relationship is ambiguously placed between the 2nd and 3rd degree by *READ* (cf. Tab. 7), however given that CRU026 and CRU027 are brothers, CRU029 must be equally related to both. The CRU027–CRU029 relationship is assigned to

the 2nd degree, making it more likely that CRU026–CRU029 are also 2nd-degree related.

All identified pairs of relatives were interred at the same site, and pairs show overlapping dates where both individuals were ^{14}C-dated (BGO001–BGO002, ERE004–ERE005).

Runs of Homozygosity

Runs of homozygosity (ROH) in genomes inform on patterns of consanguinity and effective sizes of the population from which individuals are sampled. We analysed ROH of various haplotype lengths using HapROH (Ringbauer et al. 2021).

Most of the new children from Navarra show patterns of ROH indicative of low levels of consanguinity in their recent family history (lacking ROH > 20 cM), as well as having come from communities with effective population sizes of several thousand (lacking ROH > 8 cM; Fig. 18). However, patterns typical of consanguineous mating behaviour can be seen in at least three individuals. ERE004, CRU022, and CRU023 harbour long stretches of ROH (≥ 33 cM) totalling ≥ 62 cM in length, suggesting that they are the offspring of parents who were related to one another in approximately 3rd degree (possibly 1st cousins). CRU022 and CRU023 are siblings with the same parents, making a similar ROH pattern in both of them an expected result.

Sex bias

The archaeogenetic study of Iron Age intramural burials from Navarra allows us, for the first time, to test if perinatal children were preferentially selected according to their biological sex. Our results reveal 22 of 36 children were male, indicating a ratio of 1.57:1 towards male interments, which is not significantly different from 1:1 (p = 0.24, binomial test).

Cases of trisomy as a possible approach to past demography

The individuals studied here were also subject to a recent screening project involving 9855 ancient samples with genetic data for chromosomal trisomies (Rohrlach et al. in preparation). Notably, the individuals included in this study revealed 4 cases of trisomies. In particular, individuals CRU001, CRU024, ERE004 were identified as having three copies of chromosome 21 (Down's syndrome), while CRU013 had three copies of chromosome 18 (Edward's syndrome). Only three other cases of trisomy 21 were identified among the 9855 screened samples. While a more detailed assessment of these conditions in light of anthropological information is beyond the scope of this paper, we discuss in the following some implications of these findings for demographic interpretations.

To investigate whether the number of observed cases of trisomy 18 and 21 was higher than might be expected by chance, we simulated cases for Alto de la Cruz and Las Eretas in the following way. We accounted for both variability of case numbers due to the randomness of developing a trisomy, and for the uncertainty of the simulation parameters themselves. Moreover, this simulation allowed us to test paleodemographic models that have been proposed by archaeology and anthropology, and which have been in use for a long time (Hassan 1981).

For each simulation at each site, we required a (cumulative) population size, denoted, which represents the total

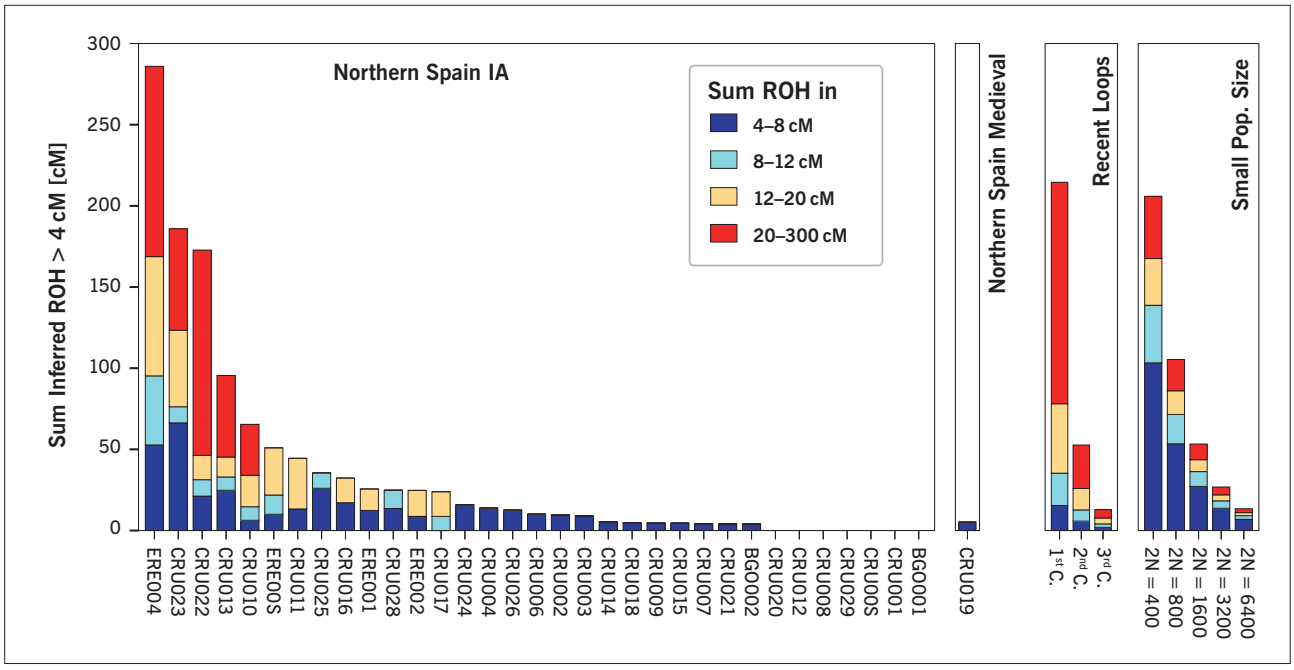


Fig. 18 Runs of Homozygosity (ROH) in the Iron Age Navarra individuals. Most of the individuals have low levels of ROH indicative of effective population sizes of several thousands. A few individuals also show evidence of consanguineous mating behaviour, indicative of being offspring from first-cousin unions.

Abb. 18 *Umfang homozygoter Genom-Abschnitte (Runs of Homozygosity, ROH) in den eisenzeitlichen Individuen aus Navarra. Die meisten Individuen weisen niedrige ROH-Werte auf, was auf eine effektive Populationsgröße von mehreren Tausend hinweist. Einige wenige Individuen zeigen auch Anzeichen sexueller Verbindungen zwischen Blutsverwandten, die darauf hindeuten, dass sie die Nachkommen von Cousin/Cousine-Paaren ersten Grades sind.*

number of individuals born at the site and can be found via the well-known paleodemographic formula proposed by G. Acsádi and J. Nemeskéri (1970):

$$D = \frac{PT}{e^0}.$$

Where P is the population size of individuals living at any point in time in the settlement, T is the time span of the settlement in years, and e^0 is the mean life expectancy in years. First, we used four methods for estimating the initial population size P[14] from the settlement area (A). A random integer $K = 1,2,3,4$ was chosen, and then the associated population size estimator was used to account for the uncertainty in the literature in estimating P (Tab. 8).

Based on the ^{14}C dates produced at each site, we estimated the site usage period using the Normal distributions $N(400,25/3)$ and $N(250,25/3)$ for Alto de la Cruz and Las Eretas, respectively, from which T was sampled. The standard deviations are set such that 99.9 % of the weight falls inside of 50 years around 400 BC and 250 BC, respectively. Finally, the mean life expectancy obtained using 26 anthropological studies of 3rd–1st millennium BC cemeteries[15] is $e^0 = 24,86$ years, with a standard deviation of 4.04 years. However, as infant deficits can be expected in several case studies, a corrected life expectancy of 22.90 ± 1.37 years is obtained when the formula proposed by C. Masset/J. Bocquet (1977) is used, and hence we sampled $e^0 \sim N(22.9,1.37)$.

Once we have sampled P, T, e^0, and actually used the rounded value of D, we simulated a number of cases of trisomy 18 and 21 using the binomial distributions:

$$X^{18} \sim Bin(D, p^{18})$$

and

$$X^{21} \sim Bin(D, p^{21}),$$

k	P	Study
1	A , where C ~ N(250,50/3)	Renfrew 1972
2	146√A	Kramer 1978
3	DA , where D ~ N(180,60/3)	Schreiber/Kintigh 1996
4	–441.37 + 149.89 x log (Ax10^4)	Curet 1998

Tab. 8 The estimators for the census population size per average lifespan used with equal probability in the simulation study.

Tab. 8 Die Schätzwerte für die Größe der Bevölkerung in der Erhebung pro durchschnittlicher Lebensspanne werden mit gleicher Wahrscheinlichkeit in der Simulationsstudie verwendet.

$p^{18} = 1/3226$ and $p^{21} = 1/1282$ (Mai et al. 2013).

We generated five million simulations according to the above description. We report the mean and standard deviation of the simulated number of cases, and 95 % empirical confidence intervals for all sampled simulation parameters, as well as for the simulated number of cases of each trisomy (Tab. 9).

By considering the remaining area to be excavated, and the proportion of samples that have yielded aDNA, we corrected the observed number of cases of each trisomy at each site. After a careful examination of all the published archaeological information[16], it appears that c. 45 individuals were identified during the excavations of Alto de la Cruz carried out between 1947–1988, of which 29 have now been genetically screened. Then, air photographs and the published site plans were used to determine the area excavated over the years. This allows us to conclude that 0.23 ha of this 0.75 ha-large site or 0.7 ha-large settled area, if we exclude the fortification wall, have been explored. Las Eretas has a well delimited, more or less oval, 0.5 ha large surface area, of which 0.075 ha have been thoroughly excavated. The resulting correction factor for the unex-

Site (% excavated)	Ha	P	T	D	$\underline{t}_{18}$ Mean (upper 95 % CI)	t_{18} Observed	$\hat{t}_{18}$ Observed corrected	$\underline{t}_{21}$ Mean (upper 95 % CI)	t_{21} Observed	$\hat{t}_{21}$ Observed corrected
Alto de la Cruz (32.5 %)	0.75	126–197	383–417	2040–3738	0.827 [0,3]	1	4.72	2.08 [0–5]	2	9.43
Las Eretas (15 %)	0.5	49–80	233–267	520–934	0.227 [0,1]	0	0	0.57 [0,2]	1	16.67

Tab. 9 Results comparing expected numbers of cases of trisomy 18 and 21, based on simulations of settlement sizes, to (corrected) observed numbers of cases. Ha is the settlement area in hectares, P is the census population size per average lifespan, T is the time of use for a settlement, and D is the cumulative census population size over the site's use. Ha, P, T and D are reported with 95 % confidence intervals for simulation parameters, $\hat{t}$ and $\bar{t}$ represent the observed, corrected and empirical sample mean number of cases of trisomies 18 and 21.

Tab. 9 Ergebnisse des Vergleichs der erwarteten Fallzahlen von Trisomie 18 und 21, basierend auf Simulationen der Siedlungsgrößen, mit den (korrigierten) beobachteten Fallzahlen. Ha ist die Siedlungsfläche in Hektar, P ist die Volkszählungsbevölkerungsgröße pro durchschnittlicher Lebensspanne, T ist die Nutzungsdauer einer Siedlung und D ist die kumulative Volkszählungsbevölkerungsgröße über die Nutzungsdauer des Standorts. Ha, P, T und D werden mit 95 % Konfidenzintervallen für Simulationsparameter angegeben, $\hat{t}$ und $\bar{t}$ stehen für die beobachtete, korrigierte und empirische mittlere Anzahl von Fällen der Trisomien 18 und 21.

14 Renfrew 1972; Kramer 1978; Schreiber/Kintigh 1996; Curet 1998.

15 Kunter 1990, Tab. 30; Alesan et al. 1999; Nicklisch 2017, Tab. 1.6; Aytek 2020; Lukasik 2020.

16 Taracena/Gil 1951; Gil 1953; Maluquer de Motes 1954; Maluquer de Motes 1958; Maluquer de Motes et al. 1990.

plored area in both settlements is 78.8 % and 85 % at Alto de la Cruz and Las Eretas, respectively (cf. Tab. 9).

The results based on the frequencies of trisomy shown in Tab. 9 suggest that in both settlements the cases of trisomy are over-represented in relation to the estimated population. As the recent screening of 9855 genomes (Rohrlach et al. in preparation) does not suggest that trisomy frequencies were significantly different in the past than in the present, this over-representation implies that these children where preferentially buried intramurally in these sites. Though not quantifiable in the same way, the same situation seems to be observed in relation to twins. These over-representations imply that the population from which these children originated was notably larger than ***D*** (and ***P***). The only explanation for such an excess in population is the participation of a much larger community in the intramural burials practice. Given the spatial limits of the living space in both fortified settlements, such a population must have come from a larger territory surrounding the settlements.

Child burials and household organisation

The ritual placement of the genetically related children inside buildings provides further insight into the social organisation of these Early Iron Age communities. Unfortunately, spatial information is only available for the recent excavations of Alto de la Cruz and Las Eretas. Few of the archaeological labels of the anthropological remains recovered between 1948 and 1957 provide sufficient information to relate them, at least tentatively, to some of the individuals mentioned in the excavation reports (Taracena/Gil 1951; Gil 1953; Maluquer de Motes 1958).

While the stratigraphic sequence of Las Eretas only consists of a single occupation phase, Alto de la Cruz was a multiperiod site occupied from the Final Bronze Age until the end of the Early Iron Age. During the latter period, the settlement went through four major building phases interrupted by generalised destructions and burning down of the houses. Such sequences typically pose two questions in archaeology with historical and social implications: 1) How much time elapsed between the phases of occupation?; and 2) Was the settlement rebuilt by the same community or did a population replacement take place? The genetic study of Alto de la Cruz sheds light on both issues thanks to a second-degree relation between children from two successive and stratigraphically overlapping buildings. While CRU029 was buried under building H88/21 of phase IIIb, CRU027 (and probably CRU026) is associated with the more recent building H87/8, belonging to the subsequent phase IIa (Maluquer de Motes et al. 1990). Although an »uncle-nephew« relationship seems as likely as a half-sibling relationship, it can be concluded that the same kin group was present in both settlements and, more specifically, in two buildings constructed at practically the same spot, a pattern which in archaeology is often understood as an architectural expression of property rights. The time elapsed between both burials and, consequently, the destruction of settlement IIIb and construction of IIa could only have lasted a few decades or even years. Regardless of what caused the burning down of the older settlement, this did not imply a hiatus in the occupation of the site, nor a (large) population replacement.

The biological relationships between the infants also allow us to delve into the size and organisation of the social group connected to the buildings. Two of the three perinatal burials of the older building H88/21 have been analysed in this study and a first and second relation can be excluded. In the successive building H87/8 DNA from all five children could be sequenced. In this case, a set of brothers (CRU026–CRU027), a set of sisters (CRU022–CRU023), as well as a female infant with no 1st or 2nd degree relation with the other children can be identified (Fig. 19).

A similar situation is observed in one of the square buildings of Las Eretas (Fig. 20). Only two of the four interments were related to the 2nd degree (ERE004–ERE005), while the other two were unrelated at a 1st or 2nd degree level. Although, the causes for the variable number of burials in houses remains unresolved, it appears that some of them were used as funerary spaces and, expectedly, occupied by more than one adult couple and maybe even with as many as three. While further analysis of the biological relatedness is required to identify more distant links, the present results do not support the identification of individual dwellings with nuclear families, as conventional archaeological models would assume. Rather, the Early Iron Age square buildings seem to have been built and used by extended groups formed by several couples and their offspring. Such a model would also explain the so far puzzling presence of two or more fireplaces and kilns in some of the buildings, which are usually related to basic subsistence units formed by a couple of adults and their close relatives.

Equally revealing is the burial of children with trisomy 18 or 21. CRU001 and CRU013 probably belonged to the youngest occupation phase (settlement I), but cannot be located in the excavation reports. Instead CRU024 was found in building 86/19 of settlement IIIb, which corresponds to the beginning of the Iron Age. This perinatal girl with Down's syndrome died at a very premature age (c. 27 weeks) and was buried with comparatively rich grave goods, formed by three bronze rings and one *Glycymeris glycymeris* shell (probably brought from the Mediterranean Sea). Moreover, the child seems to have been buried with three complete sheep/goats in the central part of this large, rectangular building, in which no other children were found. This special burial and the discovery of a large, decorated fireplace, which is unique at Alto de la Cruz, has led archaeologists to interpret this building as a possible ritual space.

The third case of Down's syndrome (ERE004) was found in Las Eretas in a burial under a large stone block that had been intentionally placed in the south-western corner of a large rectangular building (Fig. 21). The skeleton was recognised as very immature and gracile in the initial anthropological study (Armendáriz/de Miguel 2006). This might be due to the young age of the child or a case of delayed intrauterine growth restriction (IUGR).

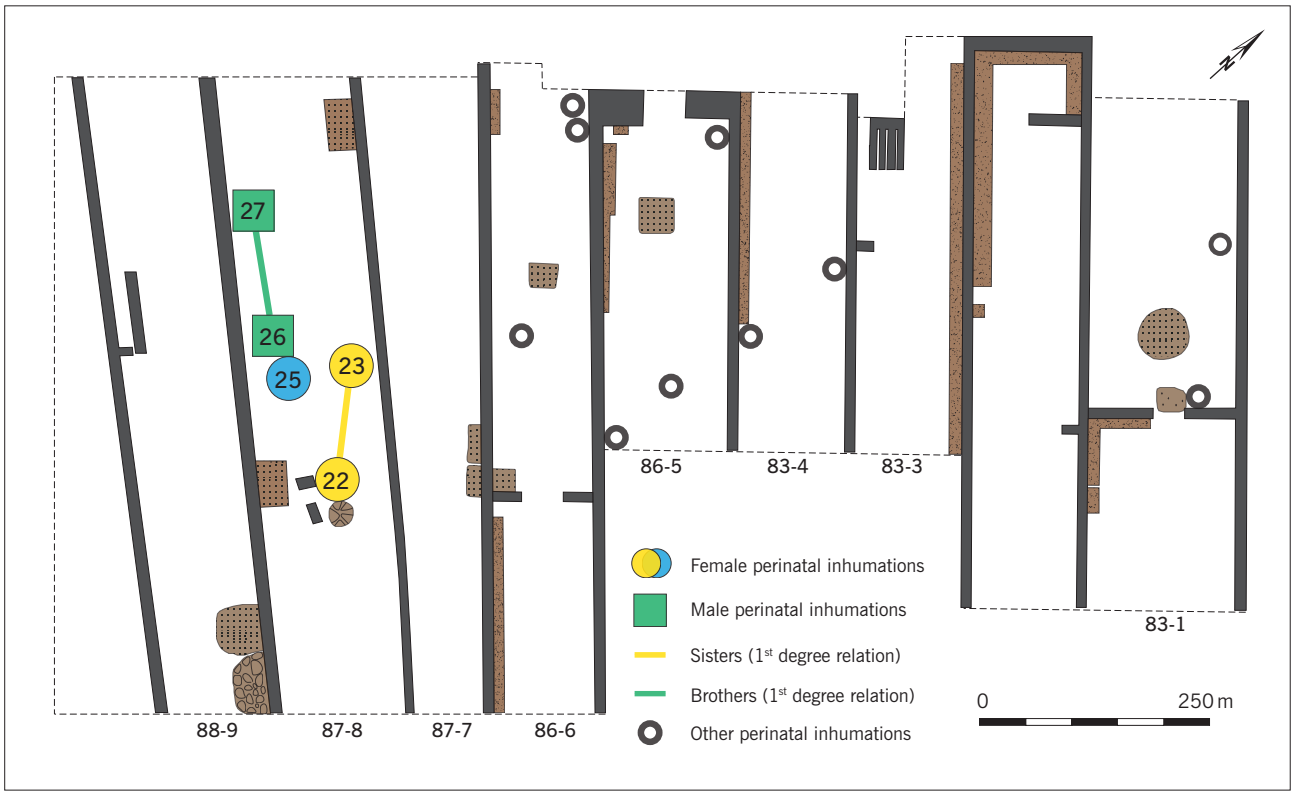


Fig. 19 Buildings at Alto de la Cruz settlement of the PIIa and 1st degree relationships between perinatal inhumations identified in the buildings.

Abb. 19 *Gebäude der Siedlung Alto de la Cruz des PIIa und Verwandtschaftsbeziehungen 1. Grades zwischen den in den Gebäuden identifizierten perinatalen Bestattungen.*

Conclusions

The intramural inhumation burials from Iron Age Navarra provide an important opportunity to study aspects of human behaviour and ritual practices at the local level, as well as aspects of population dynamics from the Bronze to the Iron Age in northern Spain more broadly. This burial practice seems to have emerged at the end of the Bronze Age in the north-eastern and eastern sector of the Iberian Peninsula among communities which are identified by archaeology with the local Urnfield Culture (cf. Fig. 1). The burial practice became widespread during the Iron Age and endured well into Roman times, although it always remained restricted to a small part of the communities. Cremation burials outside the settlements were the regular funerary practice. The genetic data provide, for the first time, some indications why certain children, usually under one year of age, were placed under the living floors inside settlements and houses.

In the first place, no clear selection in terms of sex is observed. Despite more male than female intramural child inhumations being recovered, the ratio did not deviate statistically significantly from 1:1. However, an exceptionally high number of twins (4/35) and cases of chromosomal trisomies (4/35) were genetically identified. These high case numbers suggest that only children with unusual traits, or that were born under special circumstances, remained in the settlement domain instead of being cremated when they died at young age. The discrepancies that were observed between dental and post-cranial growth in some individuals, and the pathological signs observed in others, would support the idea that intramural child burials were limited to cases of recognisable and exceptional diseases, birth conditions or physical traits, in contrast to the more common causes of infant mortality, which would leave no visible sign on the children, such as due to infectious diseases.

The combination of genetic and archaeological information also provides new insights into the social organisation of the typical Early Iron Age houses and settlements of the region. The presence of infants who were not closely related to one another (1st–2nd degree) in at least two of the houses at Alto de la Cruz, and one at Las Eretas, suggests that these buildings may have been used by extended families or by multiple, biologically-unrelated kin groups. This cohabitation would also explain the discovery of two or more fireplaces or ovens (or both) in many houses.

Additionally, the population size required to observe the high incidence of trisomies and identical twins found at the studied sites must have been much larger than what would be anticipated by demographic models for the sites, based on settlement size. In fact, we estimated that a population size of about five times larger than what could be modelled would be required to explain the increased number of chromosomal trisomies. As 625–1000 inhabitants would be an excessive population size for a pre-urban settlement of 0.75 ha (such as Alto de la Cruz), both socio-archaeological categories (*community* and *settlement*) do not seem to have been equivalent in the Early Iron Age of Navarra. It is more likely that the community engaged in these settlements, including aspects such as the intramural burials, settled

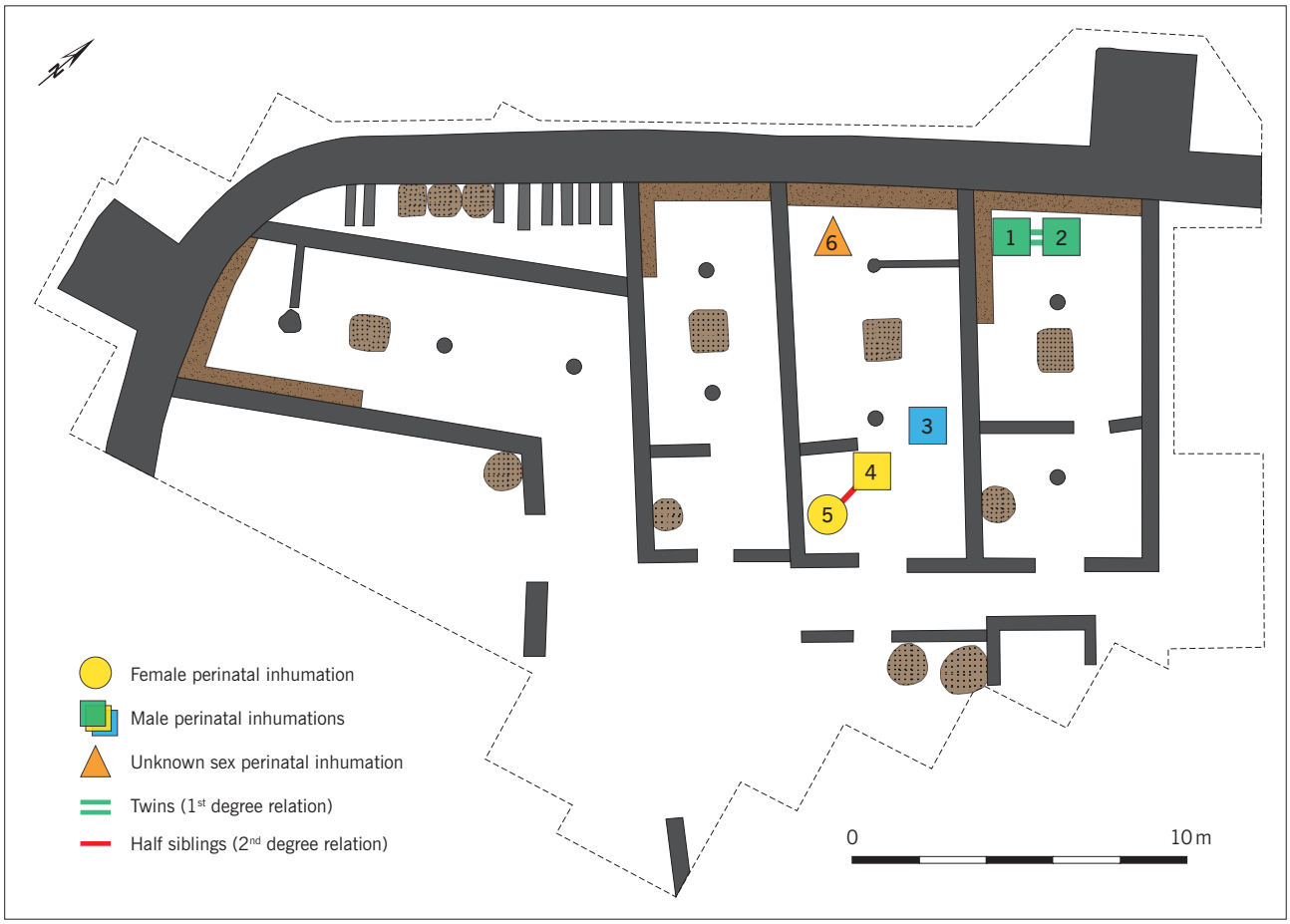


Fig. 20 Buildings and infant burials of Las Eretas. Besides the twins ERE001 and ERE002, only inhumations ERE005 and ERE006 revealed a 2nd degree relationship.

Abb. 20 *Gebäude und Säuglingsbestattungen von Las Eretas. Neben den Zwillingen ERE001 und ERE002 zeigten nur die Bestattungen ERE005 und ERE006 eine Verwandtschaft zweiten Grades.*

beyond the fortified area. The sharing of buildings by biologically unrelated groups, otherwise residing in a wider area, suggests a complex economic and political use of the fortified *tell* space, which challenges the usual household-based models envisaged by archaeology. The existence of dispersed dwellings, nearby villages, or in extramural quarters should be identified in the future through geophysical and archaeological surveys.

Finally, population genetic analyses revealed a relatively homogeneous group of individuals, with an increase of approximately 10 % of steppe-related ancestry, relative to the preceding Middle and Late Bronze Age individuals in northern Spain. Compared to published Iron Age individuals from northern/eastern Spain, the newly analysed individuals from Las Eretas, Alto de la Cruz, and El Castejón yielded less evidence of Mediterranean-related ancestry. This, in conjunction with elevated runs of homozygosity in these newly studied individuals may suggest some degree of isolation from individuals carrying Mediterranean-related ancestry. It would also be consistent with migration bringing more steppe-related ancestry into the region. Deeper sampling of this time period is necessary to test these hypotheses more carefully.

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The raw sequencing data will be publicly available upon further publication of genetic results.

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2 M. Ángel García
3 after Maluquer de Motes et al. 2009, 14
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10 J. Armendáriz
11 Armendáriz/de Miguel 2006, 11 Fig. 3
12 a after Armendáriz/de Miguel 2006, 18 Foto 7; b J. L. Larrión, Gobierno de Navarra
13 J. Armendáriz
14 a after Castiella et al. 2009, Fig. 4; b after Castiella et al. 2009 Fig. 5,4; c J. L. Larrión, Gobierno de Navarra
15–18 P. de Miguel Ibáñez
19 M. Peres based on Maluquer de Motes et al. 1990, 247 Pl. 38
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Scythian »families« – biological and/or social kinship. An overview of the research problem

Anton Gass

Zusammenfassung

Skythische »Familien« – biologische und/oder soziale Verwandtschaft. Ein Überblick zur Forschungsproblematik

Die früheisenzeitlichen reiternomadischen Verbände des skythischen Kulturkreises waren im 1. Jt. v. Chr. im gesamten eurasischen Steppengürtel durch eine neue soziale Schicht gekennzeichnet – eine kriegerische Elite. Deren Macht spiegelte sich in den monumentalen Grabbauten und prunkvollen Grabbeigaben. Bereits im 19. Jh. führten diese Machtzeugnisse die Wissenschaft zur Frage nach der Sozialstruktur der nomadischen Verbände. Man suchte zuerst nach Hinweisen in den antiken Schriftquellen und verknüpfte sie mit Ergebnissen erster Ausgrabungen von großen Grabhügeln der Führungsschicht der skythenzeitlichen Nomaden. Im Laufe der Zeit stützte sich die Forschung auf die Analysen der Fund- und Befundsituation früheisenzeitlicher Nekropolen mit monumentalen Grabhügeln der »Könige/Fürsten«, auf ethnologische Forschungen zu eurasischen Nomaden jüngerer Zeit und auf antike Schriftquellen.

Eine der zentralen Forschungsfragen zur skythenzeitlichen Gesellschaft war und bleibt immer noch, wie die gesellschaftliche Stellung legitimiert und weitergegeben wurde. Zur Klärung dieser Frage bot man verschiedene Modelle gesellschaftlicher Entwicklung zum Erreichen einer herausgehobenen Stellung durch Verdienste oder biologische Verwandtschaft sowie aufgrund eines postulierten Verwandtschaftsverhältnisses zu einem mythischen Urahn. Jedoch blieb offen, inwieweit die Verwandtschaftsbeziehungen der skythenzeitlichen Eliten bereits auch zu Dynastiebildungen geführt hatten. Einen Durchbruch für solche theoretischen Überlegungen verspricht ein Einsatz der Naturwissenschaften, vor allem der Archäogenetik, der noch in der Zukunft liegt.

Summary

In the 1st millennium BC, the early Iron Age equestrian nomadic societies of the Scythian cultural sphere were widespread across the Eurasian Steppe and were characterised by a new social class – a warrior elite. Their power was reflected in monumental tombs and magnificent grave goods. As early as the 19th century, these testaments to power led scholars to question the social structure of these nomadic societies. At first, they searched for clues in the ancient written sources and linked these to the results of early excavations of large burial mounds of the leading stratum of the Scythian nomads. Over time, research has focused on analyses of finds and features of Early Iron Age cemeteries with large »royal/princely« kurgans, as well as ethnological research on contemporary Eurasian nomads and on ancient written sources.

One of the central research questions about Scythian society was, and remains, how social status was legitimised and passed on. To clarify this question, scholars offered various models of social development and different explanations for achieving a prominent position. These included merit or biological kinship, as well as a postulated relationship to a mythical ancestor. However, to what extent the kinship relations of the Scythian elites had already led to the formation of dynasties remained unanswered. The use of natural sciences, especially archaeogenetics, promises future breakthroughs to help answer these theoretical considerations.

Introduction

The early Iron Age equestrian nomadic societies of the Eurasian Steppe between the 9th/8th and the 3rd centuries BC are referred to as »Scythians«. In some areas further east, they are also referred to as »Sauromats«, predominantly from the Volga-Don interfluve to the southern Urals, or as »Saks«, especially in Kazakhstan (Parzinger 2004, 55 f.; 64 f.; Parzinger 2007, 31 f.; cf. Jettmar 1964). Ancient written texts, such as the tradition of Herodotus, describe the Scythians as a confederation of different tribal groups north of the Black Sea (Herodot IV, 17–31; 47–57). The equestrian nomadic societies further east, from the southern Urals far into southern Siberia, had their own cultural characteristics and more regional traditions; however, based on their way of life and economy, their art, their social structure and their ideas about the afterlife, they can be included in the Scythian cultural sphere in a broader sense. Nevertheless, the term »Scythian« and related concepts are not precise ethnic attributions, but rather serve as a designation for groups with similar cultural characteristics (Menghin/Parzinger 2007, 23; Parzinger 2013, 539).

The economy and way of life of the Scythian equestrian nomads was based on livestock breeding. The size of the



Fig. 1 Burial site Issyk, Almaty Region (Kazakhstan). View over the Scythian kurgans. View from south.

Abb. 1 *Gräberfeld Issyk, Gebiet Almaty (Kasachstan). Überblick auf die skythenzeitlichen Kurgane. Blick von Süden.*

herds, consisting mainly of sheep and horses, and attractive nutritious grazing areas played a central role in their life. The constant search for new grazing areas often led to conflicts, therefore warlike confrontations formed part of everyday life. The increasing emphasis on a warlike element in these societies during that period is striking, which is why they have also been termed »equestrian warrior nomads« (Parzinger 2006, 541; Parzinger 2013, 540). Charismatic and energetic leaders probably stood at the head of these societies, as Herodotus's writings also suggest. They enjoyed a high reputation and their power was based on the allegiance of warrior elites (Parzinger 2013, 541). This development led to a strong stratification within society, which was not evident in the preceding Bronze Age. The mortuary cult in particular reflects these

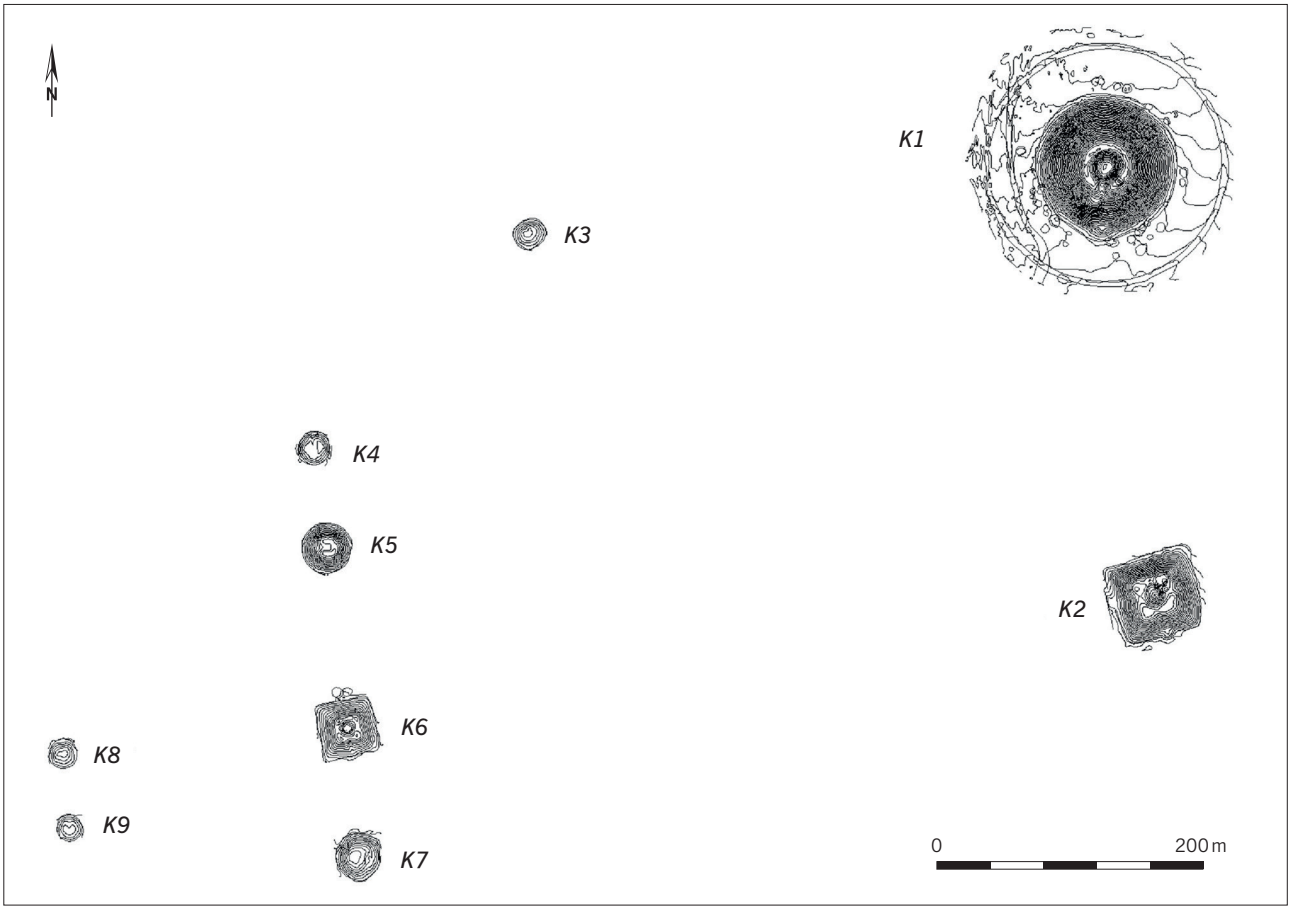


Fig. 2 Burial site Zhoan Thobe, Almaty Region (Kazakhstan). Plan of the necropolis with three rows of kurgans.

Abb. 2 *Gräberfeld Žoan Tobe, Gebiet Almaty (Kasachstan). Plan der Nekropole mit drei Kurganenreihen.*



Fig. 3 Burial site Asy Saga, kurgan 1, Almaty Region (Kazakhstan). Kurgan 1 had a height of 21 m and a diameter of 149 m. View from west.

Abb. 3 *Gräberfeld Asy Saga, Kurgan 1, Gebiet Almaty (Kasachstan). Der Kurgan 1 maß 21 m in der Höhe und hatte einen Durchmesser von 149 m. Blick von Westen.*

processes in an impressive way: the prominent position of the Scythian elites is expressed throughout the entire Eurasian Steppe by monumental burial structures (burial mounds = know as kurgans [Fig. 1]) and magnificent grave goods.

The importance of these tombs for the equestrian nomads is well documented by the ancient Greek historian Herodotus in his »History« when he reports on the Persian-Scythian war. When asked by the Persian King Darius I (549–486 BC) to fight, Scythian King Idanthyrsos replied as follows: »It is like this with me, Persian: I never ran from any man before out of fear, and I am not running from you now; I am not doing any differently now than I am used to doing in time of peace, too. As to why I do not fight with you at once, I will tell you why. We Scythians have no towns or cultivated land, out of fear for which, that the one might be taken or the other wasted, we would engage you sooner in battle. But if all you want is to come to that quickly, we have the graves of our fathers. Come on, find these and try to destroy them: you shall know then whether we will fight you for the graves or whether we will not fight. [...]« (Herodotus IV, 127).

Scythian burial grounds usually consisted of several kurgans arranged in rows, the location and orientation of which depended on landscape conditions, but they were predominantly prominently positioned so as to be visible from a distance. The number of kurgans within a row varied, as did the size of the burial mounds in each necropolis (Fig. 2). The dimensions of the kurgans ranged in size from very small, with a moderate height, to monumental, with a diameter of up to almost 150 m[1] and a height of 21 m[2]. Such outstandingly large and ostentatiously furnished kurgans, the first of which were excavated as early as the 19th century, are often referred to as »princely« or »royal« kurgans (DGS 1866, II; Zabelin 1876, 619; Talbot Rice 1957, 91–103).

Social-anthropological, historical and archaeological approaches to the problem of kinship relations in equestrian nomadic society

Early in research history, the monumentality of the graves and the splendour of the grave goods raised the question of the social structure of these early equestrian nomadic societies. Since the Scythian culture was itself without writing, 19th century scholars focused on ancient written sources, especially Herodotus, in order to be able to interpret the extraordinary archaeological findings. They thought that the formation of dynasties and kinship relations played a decisive role in shaping the equestrian nomadic society of the Scythian period. Apparently, the idea of a divine origin of royal power existed among the Scythians and played



Fig. 4 Kurgan Alexandropol, Dnipropetrovsk oblast (Ukraine). Drawing between 1850 and 1860. The kurgan was 21 m high and 100 m in diameter. View from west.

Abb. 4 *Kurgan von Alexandropol, Oblast Dnipropetrowsk (Ukraine). Zeichnung zwischen 1850 und 1860. Der Kurgan maß 21 m in der Höhe und hatte einen Durchmesser von 100 m. Blick von Westen.*

1 E.g., kurgan 1 of the Asy Saga cemetery, Kazakhstan (Fig. 3): Gass 2016, 254.

2 E.g., kurgan Alexandropol in Ukraine (Fig. 4): Polin/Alekseev 2018, 22.

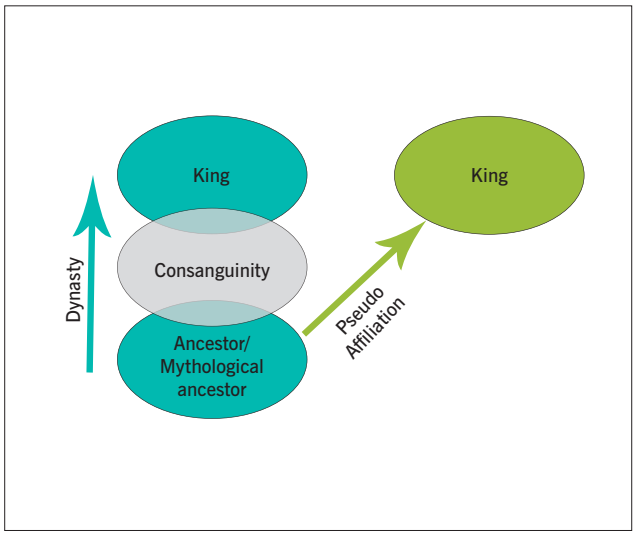


Fig. 5 Diagram of familial relations between the Scythian elite according to theory by A. Khazanov (1975).

Abb. 5 *Schema der verwandtschaftlichen Beziehungen skythischer Elite nach der Theorie von A. Chazanov (1975).*

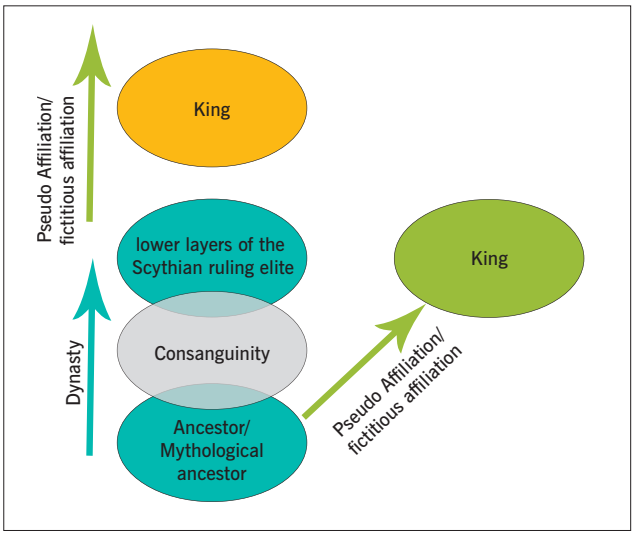


Fig. 6 Diagram of familial relations between the Scythian elite according to theory by N. Orekhova (2003).

Abb. 6 *Schema der verwandtschaftlichen Beziehungen skythischer Elite nach der Theorie von N. Orechova (2003).*

an important role in this. Much, however, remained speculative, because considerations about Scythian society, although plausible, were difficult to verify, either with the help of written texts or through the findings of excavations.

The historian and sociologist A. S. Lappo-Danilevsky assumed as early as 1887 that kinship relations had played a central role in Scythian society. This applied to the ordinary population and to the leading stratum and the royal families. Accordingly, each kurgan cemetery was suggested to represent a Scythian clan. This thesis has been put forward repeatedly by researchers up to the present day (Gass 2011, 68; Alexejew 2020, 181), but without any definitive evidence to support it.

Lappo-Danilevsky was convinced that power within society could only have passed from father to son. He divided society itself into three groups. The first group was the leading stratum. It consisted of great kings, kings and princes as well as *nomarchs* (provincial administrators). *Nomarchs* could only attain this position by belonging to a noble family or through their own merits. For all others it was exclusively hereditary. The second group consisted of the priests. The third and last group included so-called free Scythians and slaves. Lappo-Danilevsky based his considerations on an analysis of ancient Greek written sources that described everyday Scythian life, beliefs and social structure. Furthermore, he included the results of the first excavations of great Scythian kurgans in the 19th century, such as Kul-Oba, Autonomous Republic of Crimea (Ukraine), Alexandropol and Chertomlyk, both Dnipropetrovsk oblast (Ukraine) (Lappo-Danilevsky 1887, 145–147).

In 1925, historian and archaeologist Y. V. Got'e divided the Scythian graves into three groups based on the grave goods: Tombs of kings and princes, those of warriors and those of common people (Got'e 1925, 229 f.). The archaeologist V. I. Ravdonikas was also convinced in 1932 that the power of a Scythian prince or king was hereditary, because Scythian society was patriarchal (Ravdonikas 1932, 62–69). In 1985, the archaeologist E. P. Bunyatyan also assumed that the status of king was hereditary and that Scythian royal dynasties existed. She also considered it possible that the Scythians could have had both dynastic nobility with hereditary power and a warrior nobility with acquired power (Bunyatyan 1985, 21 f.).

In 1975, the evaluation of ancient written texts, results from archaeological excavations and ethnological research on Eurasian nomads of more recent times also led historian and social anthropologist A. M. Khazanov to the conclusion that Scythian society was probably led by kings. These kings either belonged to a dynasty or displayed a pseudo-affiliation to legitimise their power (Fig. 5). In his opinion, in the territory of the European Scythians (predominantly southern Ukraine and the southern Russian steppe) there was only one royal dynasty based on genealogical kinship. In any case, overall, genealogical kinship determined the configuration of the social structure, which reinforced the prominent position of the leading stratum. This process, also referred to in ethnography as the »conical clan« (Sahlins 1958, 132–142), transformed genealogical kinship into a self-contained noble class whose membership was hereditary (Khazanov 1975, 193).

Based on Greek written sources, Khazanov defined some parameters that should characterise a Scythian king. In particular, these include the splendour of the burial, evidence of human sacrifice (or *Totenfolge*[3]) and opulent grave goods. According to this definition, he counted about 40–45 great kurgans from the 5th–3rd century BC for the area of the European Scythians. Khazanov considered it unlikely that

3 This German term describes practices in which other persons in some way related to a deceased person (e.g., a spouse or a servant) follow the deceased to the grave. This can be connected to the suicide or the ritual killing of the aforementioned related person.

40–45 Scythian kings of one and the same dynasty would have been buried there during a three-hundred-year period. Rather, he explained this high number of great kurgans by the fact that not all contained graves of kings, but that also the highest nobility might have been buried in some of them (Khazanov 1975, 193).

However, written sources could not provide an answer to the question of whether or not this high nobility belonged to the ruling royal family. In contrast, Khazanov noted that Herodotus, Hippocrates of Kos, Lucian of Samosata and Klearchos of Soloi described a very diverse Scythian aristocracy. A distinction was made between an aristocracy by birth, i.e., a so-called »aristocracy of bloodline« (tribal leaders and leaders of tribal coalitions) and an aristocracy of merit (in the army or the administration), whereby the social position of the latter was determined by proximity to the king and their position within the administrative apparatus (Khazanov 1975, 179–187).

N. A. Orekhova developed A. Khazanov's statements further in 2003, applying general sociological approaches and concepts as well as historical-comparative and historical-systematising analyses. She concluded that only the lowest strata of the Scythian elite were actually related to each other by blood within the framework of a family or tribe. The higher a social position, the more conditional was the consanguinity, or family relationship (Fig. 6). The top of the leading stratum resorted to fictitious genealogical relationships in order to remain associated with a leading family with mythological ancestors (Orekhova 2003).

Dimensions of the Scythian kurgans *versus* social differentiation

Since the 1960s and 1970s, research on Scythian culture has been concerned with the question of the relationship between the interred people. When looking at the kurgan-size of Saka burial mounds in the catchment area of the River Ili in the south-eastern Zhetysu in Kazakhstan, the archaeologist K. A. Akishev from Almaty proposed in 1963 to divide the constructions into three size categories. In his model, each kurgan size was associated with a particular social group of the leading stratum of society. In his opinion, the socially elevated groups included people interred in the burial mounds with a height of over 1–2 m (Fig. 7). These were particularly successful and respected warriors who could be called heroes. In Akishev's opinion, the Saka nobility was buried in larger kurgans with a height of over 5–6 m (Fig. 8). In very large burial mounds (Fig. 9) with a height of 8–17 m the kings or princes rested (Akishev/Kushaev 1963, 86; cf. Gass 2016, 76). He did not, however, provide a detailed definition of these three strata of the Saka elite. In consequence, the division into three groups on the basis of the sizes of kurgans and the associated social interpretation must remain speculative.

A few years later, Akishev revised his subdivision. He no longer considered the exact measurements of the burial mounds to be the only decisive factor to determine the social differentiation of the interred. Nevertheless, he continued to refer to three group-sizes of burial mounds for members of the upper class and designated them as »small«, »medium« and »large« kurgans. He interpreted the small ones as the burial sites of warriors, who *per se* held an elevated position in a warlike society. He equated the ›heroes‹ who came from the ranks of the warriors with the nobility. Thus, both acquired and inherited power were treated in a similar way in the early Iron Age societies of the Asian equestrian nomads. In his view, medium-sized kurgans were erected for the deceased of both groups. At the top of the social scale were kings or princes, for whom the monumental royal or princely kurgans were built (Akishev 1978, 56; cf. Gass 2016, 76).

In the course of his analysis of Scythian-period great kurgans in the Altai and Tuva, the archaeologist A. D. Grach made a similar proposal for the classification of kurgan sizes and their correlation with the social position of those interred within them, albeit including classification based on grave goods (Grach 1975, 158–174; cf. Gass 2016, 76). Here too, however, many questions remain unanswered.

In 1979, the observation that the size of Scythian kurgans from the Lower Dnieper in southern Ukraine did not always correlate with the quality of the grave goods led archaeologist B. N. Mozolevsky to conclude that the kurgans' dimensions alone would not be sufficient to draw conclusions about the actual status of those buried there. In his view, social status would be expressed by the combination of several elements,



Fig. 7 Burial site Torgunsky-III, kurgan 2, Transvolga, Volgograd Region (Russia). View from east. With its height of 1.9 m and a diameter of 59 m kurgan 2 is a representative of kurgans of the higher Scythian society – warriors and heroes according to K. Akishev's sizing of kurgans.

Abb. 7 *Gräberfeld Torgunsky-III, Kurgan 2, Transwolga, Gebiet Wolgograd (Russland). Blick von Osten. Mit einer Höhe von 1,9 m und einem Durchmesser von 59 m steht Kurgan 2 stellvertretend für die Kurgane der gehobenen skythenzeitlichen Gesellschaft – für Krieger und Helden nach K. Akiševs Kurganengrößenaufteilung.*



Fig. 8 Burial site Issyk, kurgan 11, Almaty Region (Kazakhstan). View from north. With its height of 6.4 m and a diameter of 69 m kurgan 11 is a representative of kurgans of the Saka nobility according to K. Akishev's sizing of kurgans.

Abb. 8 *Gräberfeld Issyk, Kurgan 11, Gebiet Almaty (Kasachstan). Blick von Norden. Mit einer Höhe von 6,4 m und einem Durchmesser von 69 m steht Kurgan 11 stellvertretend für die Kurgane des sakischen Adels nach K. Akiševs Kurganengrößenaufteilung.*

including: Height of the kurgan; depth and size of the burial grave; complexity of the kurgan structure; presence and dimension of stone constructions; the number of accompanying graves *(Totenfolge)* and co-buried horses; and lastly, opulent grave goods and indications of a rich funeral feast or ritual acts at the burial site (Mozolevs'kyy 1979, 156 f.; cf. Gass 2016, 76).

In a study of the large kurgans of the Scythian Gerrhos, the so-called area of the Scythian Heroes on the lower Dnieper, B. N. Mozolevsky and S. V. Polin presented a size classification into four groups of Scythian kurgans of the northern Pontic region, which they immediately interpreted accordingly: Group 1 – monumental kurgans (14–22 m high) for the main kings (the *Basileia*); Group 2 – kurgans with a height of 8–11 m for family members of the main king, or for secondary kings (also *Basileia*); Group 3 – kurgans with a height of 4.5–7.0 m for the *nomarchs* (chiefs) of the *nomoi* (administrative subdivisions); and lastly as Group 4 – kurgans with a height of 2.0–4.5 m for tribal elders and other respected tribal members (Mozolevsky/Polin 2005, 299 f.; cf. Parzinger 2004, 90; Gass 2016, 76 f.).

In 2016, A. Gass suggested that the size of the burial complexes in the Saka kurgans of the south-eastern Zhetysu in Kazakhstan, which he evaluated, should not be considered in isolation from the overall findings and the find material. He suggested that the special social position of the interred, which was underlined by the construction of large kurgans by the community, did not always depend only on certain achievements of the deceased, but may also have been based on the heritability of social position (Gass 2016, 79).

There is no doubt that the large kurgans were built for persons of note. However, the question of the exact status within society of the interred person remains open. For example, the »Golden Man« of Issyk in south-eastern Kazakhstan,



Fig. 9 Burial site Vinogradny 2, kurgan 1, northern Caucasus, Stavropol Region (Russia). View from west. With its height of 10.6 m and a diameter of c. 90 m kurgan 1 is a representative of kurgans of the Scythian kings and princes according to K. Akishev's sizing of kurgans.

Abb. 9 *Gräberfeld Vinogradny 2, Kurgan 1, Nordkaukasus, Region Stavropol (Russland). Blick von Westen. Mit einer Höhe von 10,6 m und einem Durchmesser von ca. 90 m steht Kurgan 1 stellvertretend für die skythenzeitliche Königs- und Fürstenkurgane nach K. Akiševs Kurganengrößenaufteilung.*



Fig. 10 Burial site Issyk, Almaty Region (Kazakhstan). View from north. Left: »Golden Man of Issyk«, reconstruction by K. Akishev.

Abb. 10 *Gräberfeld Issyk, Gebiet Almaty (Kasachstan). Blick von Norden. Links: »Goldener Mann von Issyk«, Rekonstruktion von K. Akišev.*

which, until 2001, was considered the richest scientifically studied Scythian burial east of the Ural Mountains, was discovered in an adjacent (or secondary) chamber of a 6 m high burial mound (Gass 2016, 283). The fact that the interred individual lay in an adjacent chamber could be an indication of his secondary status (Fig. 10).

On the other hand, the investigations at the royal kurgan of Arzhan 2 in Tuva, Southern Siberia (Russia), which, since 2001, has been considered the richest scientifically studied Scythian burial east of the Urals, showed that the main burial does not always have to be placed exactly in the middle of a kurgan (Fig. 11) (Čugunov et al. 2010, 16–22). Moreover, the kurgan of the »Golden Man« with a height of 6 m is not the largest kurgan in the necropolis, as some kurgans here reach a height of up to 10 m. However, it is somewhat higher compared to an average kurgan height of 4 m for all other great kurgans of Issyk. Thus, with regard to this feature, the social status of the »Golden Man« remains unclear. Furthermore, the question arises whether the special status, which was supposed to be emphasised by the community through the construction of the tomb, is actually due to the deceased's own achievements, especially since the »Golden Man« of Issyk had already died at a young age[4]. It is more likely that the high social standing of the »Golden Man« was inherited.

If one considers Scythian cemeteries with large kurgans as cemeteries of a leading class, or even a dynasty (Gass 2011, 68), then the question arises whether the different sizes of graves in one and the same necropolis could indicate an internal social stratification among the buried elite. However, as long as such kurgan cemeteries have not been fully excavated and investigated, such considerations inevitably remain speculative. The same applies to the question whether there might have been a genetic relationship between the burials in the central tombs of the linearly arranged kurgans of a particular necropolis; if this were confirmed, we might well be dealing here with dynasties (Gass 2016, 81).

Input from the natural sciences

Scientific methods, especially archaeogenetic analyses on aDNA, promise completely new insights. While archaeogenetic studies and isotope analyses in the Eurasian Steppe region have so far been very successfully used to solve questions of population history and mobility[5], there are now also promising new approaches to clarify biological relationships between the burials within one and the same kurgan, or indeed between several kurgans within the same necropolis (Mary et al. 2019).

The only pilot study conducted so far to investigate genetic relationships in the Scytho-Siberian world, which was carried out by a Russian-French team in 2018, included 28 individuals of the ordinary population from five Early Iron Age cemeteries in the southern Siberian Republic of Tuva. The researchers were able to prove family relationships of the first degree, involving parent-child pairs; a man and his two parents, a woman with two daughters, or full sibling pairs. Second degree family relationships verified included siblings and paternal uncles, while third degree relationships included siblings, uncles and grandparents and great uncles (Mary et al. 2019, 418). Further results of the studies indicate that the »Siberian Scythians« were organised in patrilocal and patrilineal societies, in which the men remained within the family and the women left the families after reaching marriageable age. Thus, burial practices of the ancient equestrian nomads in southern Siberia were linked to both kinship and paternal lineage (Mary et al. 2019, 411).

Conclusion

If we look back at the discussion of the past hundred years, we can see that the repeated attempts to evaluate ancient written texts in conjunction with the findings of archaeological excavation have hardly advanced beyond unprovable hypoth-

4 16–18 years; according to Akishev 1978, 62; cf. Parzinger 2006, 660.

5 Unterländer et al. 2017; Krzewińska et al. 2018; Gnecchi-Ruscone et al. 2021; Ventresca Miller et al. 2021.

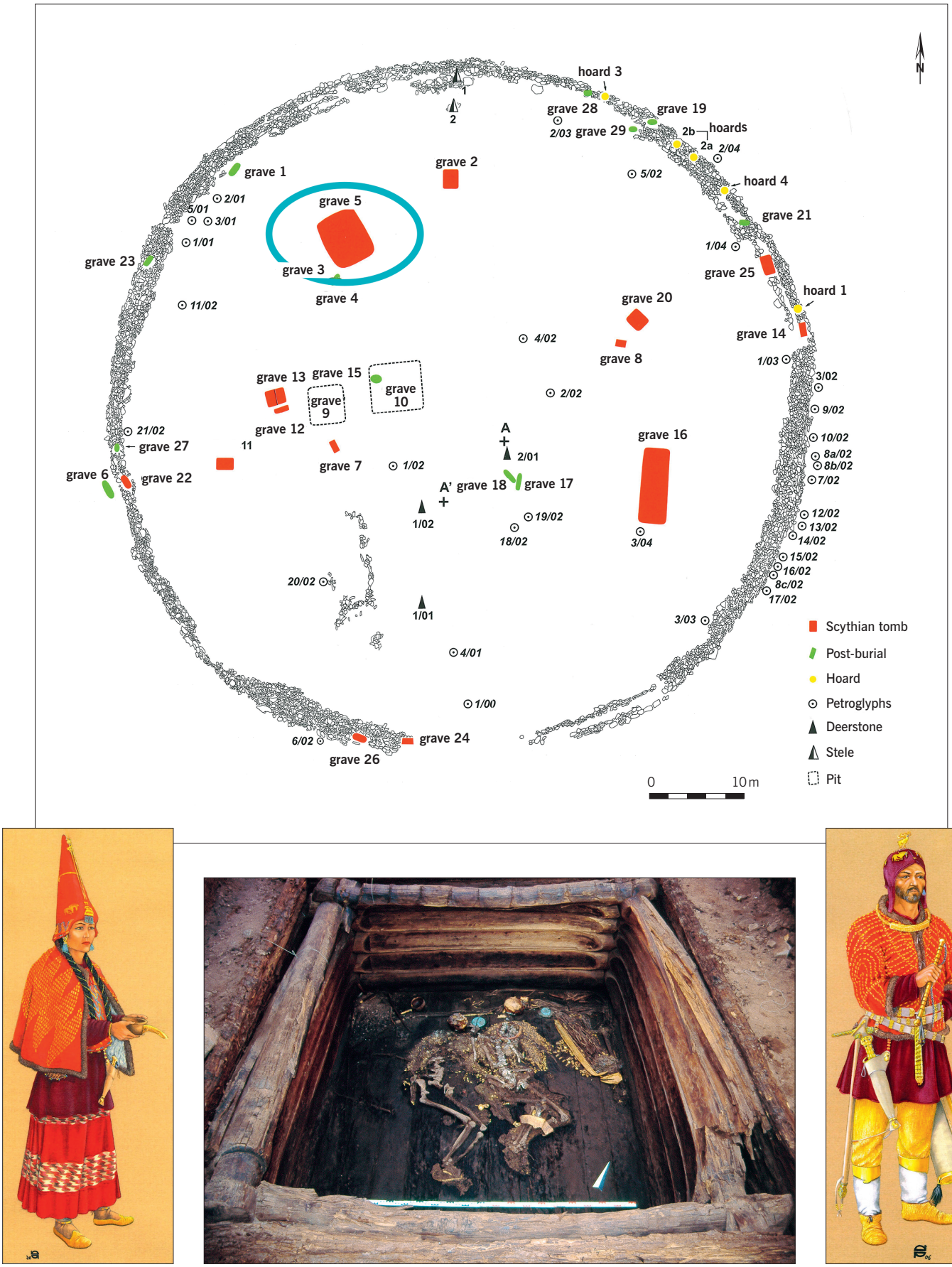


Fig. 11 Royal kurgan Arzhan 2, Tuva Republic (Russia). Map of the site. Grave 5 with the burial of the royal couple. View from south-east. Reconstruction of the costumes and equipment of the prince and princess from grave 5.

Abb. 11 *Fürstenkurgan Aržan 2, Republik Tuva (Russia). Plan der Anlage. Grab 5 mit der Bestattung des Fürstenpaars. Blick von Südosten. Rekonstruktion der Bekleidung und der Ausrüstung vom Fürsten und von der Fürstin aus dem Grab 5.*

eses or even pure speculation. It is obvious that the sometimes very large differences in the size of the tombs and the opulence of the grave goods reveal social stratification. However, we know no more today than we did a hundred years ago about what might be behind this, because neither ancient written sources nor excavation results alone can provide unambiguous and reliable answers to questions about social structure, kinship relations and early dynasty formation (Kunichika 2012, 242–245). The written evidence is not very reliable and often reflects a distinctively Greek view on social conditions amongst the Scythian equestrian nomads, as already expressed in the terminology used by Herodotus. Any attempts to reconcile his statements with archaeological findings and to develop a picture of Scythian society from them are therefore either limited to generalities or doomed to failure, just as they were a hundred years ago.

In addition, theoretical discussions on the phenomenon of early Iron Age elite or royal tombs in Eurasia (Parzinger 1992; Eggert 2007; Schier 2010) have so far hardly been able to draw upon results from investigations using natural sciences (Čikiševa 2010). Initiating an interdisciplinary, theory-based debate in the field of Scythian studies still remains a future endeavour.

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Auf der Suche nach den feinen Unterschieden. Die awarischen Gräberfelder von Leobersdorf und Mödling – An der Goldenen Stiege

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Für Karl Matzner (†), Hermann und Lotte Schwammenhöfer, den Ausgräbern der Nekropole von der Goldenen Stiege

Summary

In search of subtle differences. The Avar burial grounds of Leobersdorf and Mödling – An der Goldenen Stiege

The international project »HistoGenes: Integrating genetic, archaeological and historical perspectives on Eastern central Europe 400–900 AD« has been running for three years. Its goal is to integrate historical, archaeological and genetic data from around 6000 skeletons from the Carpathian Basin and neighbouring regions and thus write a completely new population history for the area. From 568 to around 800, the Avar Empire was located here, from which we now know about 100 000 graves, most of them with significant inventories.

Within the framework of »HistoGenes«, two Avar burial grounds from Lower Austria were also completely sampled. The necropolises of Mödling – An der Goldenen Stiege and Leobersdorf appear similar as far as the generally used means of representation are concerned, but differ in numerous other details.

The article presents the large, yet still unpublished cemetery of Mödling, and compares it with the smaller one of Leobersdorf. It then goes into the ongoing archaeogenetic investigations and shows how genetics makes it possible to explain certain archaeological phenomena. Two excursions on special earring types and another on the development of pottery forms in Mödling complete the overview.

Zusammenfassung

Seit drei Jahren läuft das internationale Projekt »HistoGenes: Integrating genetic, archaeological and historical perspectives on Eastern central Europe 400–900 AD«. Sein Ziel ist es, historische, archäologische und genetische Daten von rund 6000 Skeletten aus dem Karpatenbecken und den angrenzenden Gebieten zusammenzuführen und so eine völlig neue Bevölkerungsgeschichte zu schreiben. Von 568 bis um 800 befand sich hier das Awarenreich, aus dem wir heute rund 100 000 Gräber, zumeist mit aussagekräftigen Inventaren, kennen.

Im Rahmen von »HistoGenes« wurden auch zwei awarische Gräberfelder aus Niederösterreich vollständig beprobt und die Stammbäume der Bestatteten rekonstruiert. Die Nekropolen von Mödling – An der Goldenen Stiege und Leobersdorf zeigen sich ähnlich, was die allgemein üblichen Repräsentationsmittel betrifft, unterscheiden sich jedoch in zahlreichen anderen Details.

Der Beitrag stellt das noch nicht publizierte große Gräberfeld von Mödling vor und vergleicht es mit dem kleineren von Leobersdorf. Anschließend wird auf die laufenden archäogenetischen Untersuchungen eingegangen und gezeigt, wie es die Genetik ermöglicht, bestimmte archäologische Phänomene zu erklären. Zwei Exkurse zu besonderen Ohrringtypen und ein weiterer zur Entwicklung der Keramikformen in Mödling ergänzen den Überblick.

Vorbemerkung: Chronologie und Datierung

Eine relative Chronologie der awarenzeitlichen Fundtypen und Bestattungen lässt sich mithilfe von Beobachtungen bei der Grabung (z. B. Grabüberschneidungen), belegungschronologischer Analysen (Kartierungen im Gräberfeldplan), mittels statistischer Verfahren (Kombinationsstatistik etc.) und dem Abgleich mit benachbarten Chronologiesystemen (Kulturkontaktmethode) mit einer gewissen Genauigkeit erstellen. Die Absolutchronologie ist in der Awarenforschung allerdings noch immer ein Problem. Mitgegebene Münzen sind selten, Holzfunde für dendrochronologische Datierungen gibt es (noch) nicht, ^{14}C-Daten sind zu ungenau. Im Grunde wird das relative Chronologiegerüst zwischen zwei historischen Eckdaten eingehängt: Die Übergabe des Karpatenbeckens an die Awaren in der Folge des Abzugs der Langobarden nach Italien 568 und die Zerstörung des Awarenreiches durch Karl den Großen am Ende des 8. Jhs. Doch wie lange dauerte es, bis die jeweils neue politische Lage auf das Siedlungswesen und damit auf die Bestattungen durchschlug?

Wenn andererseits die archäologischen Ergebnisse mit den Schriftquellen in Bezug gesetzt werden sollen, sind absolute Datierungen unverzichtbar. Hier das derzeit meist verwendete Modell (Tab. 1).

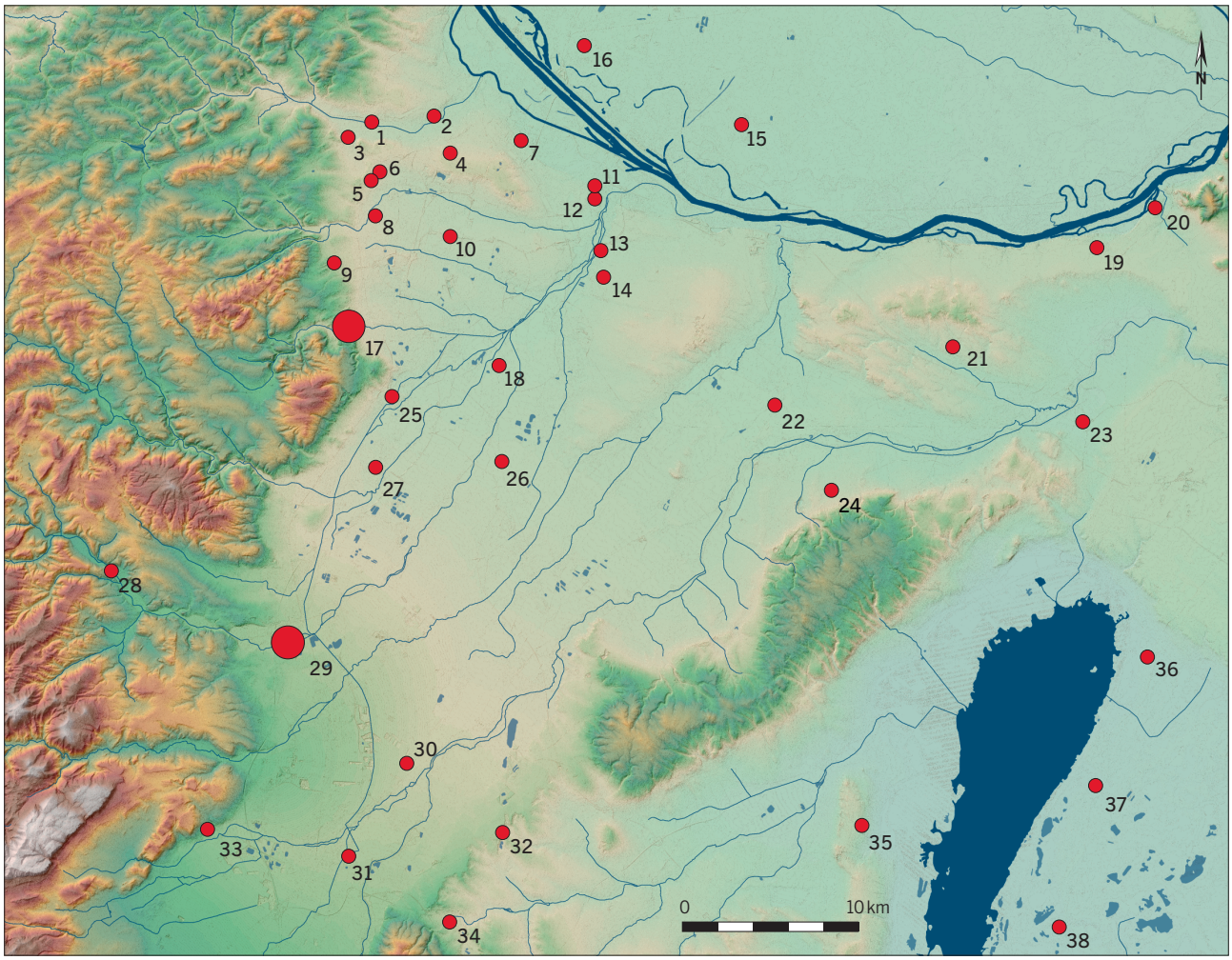


Abb. 1 Awarische Grabfunde südlich von Wien. 1 Wien 14 – Penzing, Penzinger Straße; 2 Wien 06 – Mariahilf, Stumpergasse 7; 3 Wien 13 – Hietzing, Spohrstraße, Wien – Unter St. Veit; 4 Wien 10 – Favoriten, Inzersdorfer Straße 113; 5 Wien 12 – Meidling, Südwestfriedhof; 6 Wien 12 – Meidling, Hervicusgasse; 7 Wien 11 – Simmering, Hauffgasse; 8 Wien 23 – Liesing, Carlbergergasse; 9 Perchtoldsdorf – Marktplatz; 10 Vösendorf – Laxenburgerstraße; 11 Wien 11 – Simmering, Csokorgasse; 12 Schwechat – Wienerstraße; 13 Zwölfaxing I – Feldsiedlung; 14 Zwölfaxing II – Burstyn Kaserne; 15 Oberhausen – Im Kreutzfeld; 16 Wien 22 – Hirschstetten; 17 Mödling – An der Goldenen Stiege; 18 Achau – Haidäcker; 19 Bad Deutsch-Altenburg – Erstes Amphitheater; 20 Bad Deutsch-Altenburg – Mühläcker; 21 Göttlesbrunn – Ortsgebiet, Haus Nr. 62; 22 Margarethen am Moos – Fürhappen; 23 Bruckneudorf – A6 (Dreieck); 24 Sommerein – Steinäcker; 25 Guntramsdorf – Anningerstraße; 26 Münchendorf – Drei Mahden; 27 Traiskirchen – Wienersdorferstraße; 28 Pottenstein; 29 Leobersdorf – Ziegelei Polsterer; 30 Obereggendorf – Haidäcker; 31 Wiener Neustadt – Bulgarengrund; 32 Zillingtal – Unterer Kapellenberg; 33 Brunn an der Schneebergbahn – Hochquellenwasserleitung; 34 Bad Sauerbrunn – Friedhof; 35 Rust – Mitterkräftenwald; 36 Neusiedl am See – Obere Neun Mahd; 37 Podersdorf am See – Winkeläcker; 38 Illmitz – Ortsgebiet.

Fig. 1 Avar burial grounds south of Vienna. 1 Vienna 14 – Penzing, Penzinger Straße; 2 Vienna 06 – Mariahilf, Stumpergasse 7; 3 Vienna 13 – Hietzing, Spohrstraße, Vienna – Unter St. Veit; 4 Vienna 10 – Favoriten, Inzersdorfer Straße 113; 5 Vienna 12 – Meidling, Südwestfriedhof; 6 Vienna 12 – Meidling, Hervicusgasse; 7 Vienna 11 – Simmering, Hauffgasse; 8 Vienna 23 – Liesing, Carlbergergasse; 9 Perchtoldsdorf – Marktplatz; 10 Vösendorf – Laxenburgerstraße; 11 Vienna 11 – Simmering, Csokorgasse; 12 Schwechat – Wienerstraße; 13 Zwölfaxing I – Feldsiedlung; 14 Zwölfaxing II – Burstyn Kaserne; 15 Oberhausen – Im Kreutzfeld; 16 Vienna 22 – Hirschstetten; 17 Mödling – An der Goldenen Stiege; 18 Achau – Haidäcker; 19 Bad Deutsch-Altenburg – Erstes Amphitheater; 20 Bad Deutsch-Altenburg – Mühläcker; 21 Göttlesbrunn – Ortsgebiet, Haus Nr. 62; 22 Margarethen am Moos – Fürhappen; 23 Bruckneudorf – A6 (Dreieck); 24 Sommerein – Steinäcker; 25 Guntramsdorf – Anningerstraße; 26 Münchendorf – Drei Mahden; 27 Traiskirchen – Wienersdorferstraße; 28 Pottenstein; 29 Leobersdorf – Ziegelei Polsterer; 30 Obereggendorf – Haidäcker; 31 Wiener Neustadt – Bulgarengrund; 32 Zillingtal – Unterer Kapellenberg; 33 Brunn an der Schneebergbahn – Hochquellenwasserleitung; 34 Bad Sauerbrunn – Friedhof; 35 Rust – Mitterkräftenwald; 36 Neusiedl am See – Obere Neun Mahd; 37 Podersdorf am See – Winkeläcker; 38 Illmitz – Ortsgebiet.

»HistoGenes«, die Integration von Schriftquellen, Archäologie und Archäogenetik (FD, WP)

Eines der größten interdisziplinären Archäogenetik-Projekte weltweit findet derzeit in Mitteleuropa statt. Der Synergy Grant des Europäischen Forschungsrates »HistoGenes: Integrating genetic, archaeological and historical perspectives on Eastern central Europe 400–900 AD« hat sich zum Ziel gesetzt, die wechselhafte Geschichte der Bevölkerung im Karpatenbecken zu entschlüsseln. Schriftzeugnisse, archäologische Hinterlassenschaften und über 6000 Genanalysen von Skeletten aus dem 5. bis 9. Jh. sollen einerseits helfen, das ganz große Bild von den Verbindungen zwischen Ostasien und dem europäischen Subkontinent neu zu zeichnen und andererseits das konkrete Leben der Menschen in ihren meist kleinen Siedlungen mit ihren kulturellen Traditionen und Regelwerken zu beleuchten. Alle am Projekt beteiligten Disziplinen haben im vergangenen Vierteljahrhundert kräftig dazuge-

Relative Datierung	Entspricht etwa
Frühawarenzeit I	ca. 570–630
Frühawarenzeit II	ca. 630–650
Mittelawarenzeit I	ca. 650–675
Mittelawarenzeit II	ca. 675–700
Spätawarenzeit I	ca. 700–730
Spätawarenzeit II	ca. 730–760
Spätawarenzeit IIIa	ca. 760–790
Spätawarenzeit IIIb	ca. 790–810

Tab. 1 Derzeit übliche chronologische Perioden des awarenzeitlichen Fundmaterials und ungefähre absolute Datierungen.

Tab. 1 Currently common chronological periods of the Avar find material and approximate absolute dates.

lernt und vor allem ihr theoretisches und methodisches Rüstzeug geschärft.

Die Geschichtsforschung musste vor allem die traditionelle Vorstellung überwinden, dass »Völker« weitgehend unverändert über lange Zeiträume bestehen und dass ihre gemeinsame biologische Substanz sowohl ihre kulturellen Äußerungen wie auch ihr gemeinschaftliches historisches Handeln bestimmt. Das bedeutet, dass die Zeugnisse der Schriftquellen, der Bodenfunde und der Genetik nicht von vornherein auf ein Volk bezogen werden können, dessen Name gerade schriftlich überliefert ist. Volksname, Sprache, archäologische Kultur und genetische Cluster können mehr oder weniger, in manchen Fällen aber auch gar nicht, zur Deckung kommen. Nur interdisziplinäre Forschung ist imstande dazu, für jeden einzelnen Fall Kriterien zu entwickeln. Von der Erforschung frühmittelalterlicher Ethnogenesen ist die Geschichtswissenschaft zu einer Erfassung vieler verschiedener Formen und Ebenen sozialer Identitäten fortgeschritten, ohne die großen politischen Entwicklungen und die dahinterstehenden Akteure aus den Augen zu verlieren (Pohl 2018; Pohl 2022).

Die Archäologie hat ihr methodisches Arsenal in den letzten Jahrzehnten massiv erweitert, teils mit neuen theoretischen Ansätzen, aber auch mit Anwendungen aus Nachbardisziplinen, z. B. statistischen Auswertungsverfahren (Stadler 2005), Materialuntersuchungen, mit der geophysikalischen Prospektion oder dem Airborne Laserscanning. Die Herausforderung besteht nun darin, die bewährten Methoden der Interpretation archäologischer Befunde im Gleichklang mit den neuen Möglichkeiten der »Scientific Archaeology« weiterzuentwickeln. Das »HistoGenes«-Projekt hat bereits gezeigt, dass gerade die Integration der verschiedenen methodischen Zugänge viele neue Erkenntnisse verspricht.

Tatsächlich erweitert die rasante Fortentwicklung der Methoden zur Analyse alter DNA und ihrer bioinformatischen Auswertung ständig unsere Forschungsperspektiven. In den 2000er Jahren hat die Entschlüsselung der Menschheitsentwicklung anhand relativ weniger Genproben große Fortschritte gemacht. Es war ein Paukenschlag für die noch junge Paläo- bzw. Archäogenetik, als 2022 Svante Pääbo für seine paläogenetischen Forschungen an Neandertalern und anatomisch modernen Menschen den Nobelpreis gewann. Schon vorher, in den 2010ern, wurde die Besiedlungsgeschichte des neolithischen und bronzezeitlichen Europas und die Vermischung dreier unterschiedlicher daran beteiligter Gruppen archäogenetisch untersucht. Doch erst seit einigen Jahren ist es möglich, auch bei historischen Bevölkerungen, deren Genome sich voneinander oft nur mehr wenig unterschieden, robuste Hypothesen über ihre Herkunft aufzustellen. Darüber hinaus wurden die bioinformatischen Methoden soweit verfeinert, dass aus dem Nachweis von Verwandtschaft unterschiedlicher Grade ganze Stammbäume (*pedigrees*) in komplett beprobten Gräberfeldern rekonstruiert werden können. Das bringt für die archäologische Interpretation von Gräberfeldern ganz neue Möglichkeiten.

Die Grundlage für die archäogenetischen Analysen im Rahmen von »HistoGenes« bilden rund 100 000 Körpergräber aus dem Mitteldonaubecken (vor allem Ungarn, Slowakei und Österreich), wo sich eine Reihe von Herrschaften abwechselte. Als erstaunlich beständig erwies sich das Reich der »Awaren«, das von 568 bis um 800 im Karpatenbecken bestand, und damit auch Zeit genug hatte, eine – bis zu einem gewissen Grad – gemeinsame Reichskultur auszubilden, welche Gegenstände des täglichen Bedarfs, Schmuck und Bilderwelten umfasste.

Die Awaren an der Wiener Pforte

Wenig überraschend führten bedeutende Fernverbindungen aus dem Awarenland in die verschiedenen Richtungen und folgten dabei oft alten Römerstraßen. Die wichtigste Fernstraße zwischen dem Karpatenbecken und »dem Westen« verlief entlang der Donau durch die »Wiener Pforte« zwischen den Voralpenausläufern und dem Bisamberg. Von hier aus gelangte man durch das Alpenvorland in das heutige Süddeutschland, zu den Bayern, Alamannen und Franken. Wohl um diese Route zu kontrollieren ließen sich im Wiener Becken und der »Kleinen Ungarischen Tiefebene« schon bald awarische Krieger mit ihren Sippen nieder (Leobersdorf, Zillingtal, Enzersdorf an der Fischa, Börcs-Nagydomb; Tomka 2005). Aber die Landschaft vom Wiener Becken über das heutige Nordburgenland bis Westungarn bot zugleich gute Bedingungen für die Viehzucht. Sie stellt quasi den westlichsten Ausläufer der Eurasischen Steppe dar – den schier endlosen Streifen von der Mandschurei bis zum Wienerwald.

Eine der frühesten awarischen Bestattungen im Wiener Becken wurde 1953 in Leobersdorf gefunden, rund 200 m westlich des Gräberfeldes. Es enthielt einen kleinen Maskenbeschlag aus Silberguss und die Blechrosette von einem Bogenköcher (Daim 1987). Diese Bestattung wurde wohl noch im 6. Jh. angelegt (Daim 1987, 121–130). Parallelen zu den frühawarischen Funden von Leobersdorf finden sich z. B. im Nordkaukasus (Belinskij/Härke 2018).

In den folgenden Generationen ließen sich laufend neue Gruppen im Wiener Becken nieder, das Siedlungsnetz wurde immer dichter (Abb. 1). Die Ausstattungen der awarenzeitlichen Gräber sind sehr ähnlich, doch bei genauerer Analyse zeigen sich auch viele kleine Unterschiede, die wohl mit den vertrauten Gewohnheiten und sozialen Regeln der einzelnen Siedlungsgemeinschaften zusammenhängen. Inwieweit diese aber auch mit der unterschiedlichen Genese der beiden Bestattungsgemeinschaften zu tun haben, soll im Folgenden diskutiert werden.

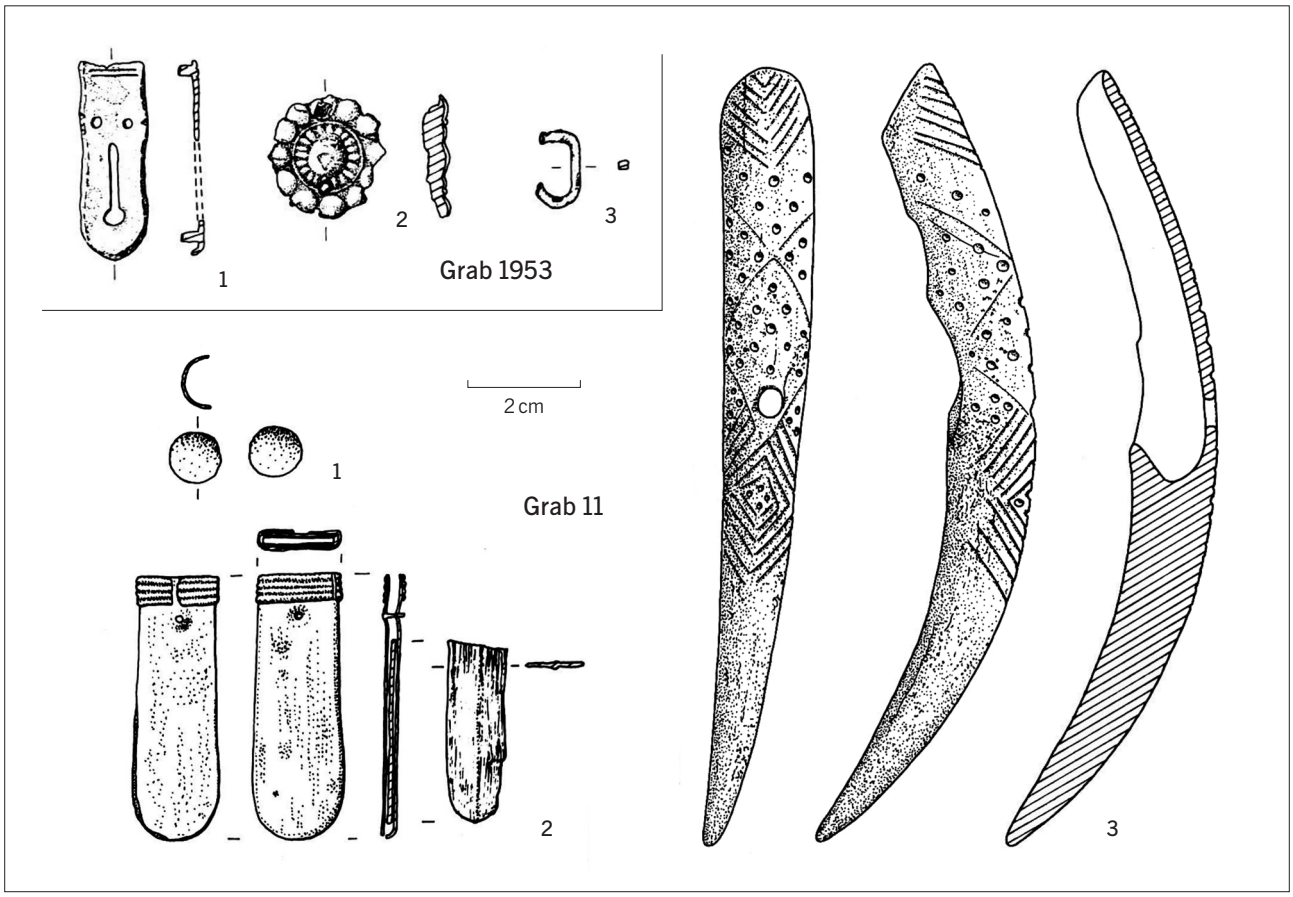


Abb. 2a Leobersdorf. Grab von 1953 (Auswahl): 1 Silberner Gürtelbeschlag; 2 Rosettenbeschlag von einem Köcherriemen; 3 Klammer aus Draht zur Befestigung der Rosette am Riemen. Grab 11 (Auswahl): 1 Zierknöpfe; 2 Riemenzunge aus Bronzeblech, verzinnt, mit Holzlamelle zur Versteifung der Riemenzunge; 3 »Knotenlöser« aus Horn.

Fig. 2a *Leobersdorf. Grave from 1953 (selection): 1 silver belt fitting; 2 rosette fitting from a quiver strap; 3 wire clips for attaching the rosette to the strap. Grave 11 (selection): 1 decorative buttons; 2 strap end made of bronze sheet, tinned, with wooden slats to stiffen the strap end; 3 »knot removers« made of horn.*

Die Gräberfelder Leobersdorf und Mödling – An der Goldenen Stiege. Archäologie und Naturwissenschaften

Die Beprobungsstrategie in »HistoGenes« sieht vor, nach Möglichkeit ganze Gräberfelder zu beproben, also idealerweise sämtliche Skelette einer Nekropole. Und tatsächlich konnten zwei awarenzeitliche Bestattungsplätze in Niederösterreich auf diese Weise vollständig archäogenetisch untersucht werden, und zwar die von Leobersdorf (153 Gräber) und Mödling – An der Goldenen Stiege (553 Gräber). Die Nekropole von Mödling wurde von 1967 bis 1973 von z. B. K. Matzner und H. und L. Schwammenhöfer erschlossen, der deutlich kleinere Friedhof von Leobersdorf zwischen 1976 und 1982. Die beiden Bestattungsplätze (mit den dazugehörigen Siedlungen) liegen nur rund 20 km voneinander entfernt.

Die Analyse der Proben aus Leobersdorf und Mödling brachten fundamental neue Erkenntnisse zu den Gesellschaften im Awarenreich und erlauben uns darüber hinaus die bisherigen kulturhistorischen Erkenntnisse aus den Analysen der archäologischen Hinterlassenschaft schärfer zu interpretieren. Im Folgenden sollen die beiden Gräberfelder archäologisch charakterisiert und einander gegenübergestellt werden. Was verbindet sie, worin unterscheiden sie sich?

Topografie

Während das Gräberfeld von Leobersdorf im Flachland des Wiener Beckens liegt – Reste von älteren Bestattungen wurden nicht entdeckt – hat man die Nekropole von Mödling auf einer Geländestufe am Abhang des Wienerwaldes zwischen prähistorischen Hügelgräbern angelegt. Der Bestattungsplatz war mit hoher Wahrscheinlichkeit von der zugehörigen Siedlung im Tal aus zu sehen[1]. Eine ähnliche Situation liegt in Zillingtal (Burgenland) vor, wo die Nekropole am Abhang der heutigen Flur »Unterer Kapellenberg« angelegt worden war. Etwa 500 m davon entfernt lag eine awarische Siedlung, die sich durch Oberflächenfunde zeigte und wo ein kleiner Ausschnitt mit Pfostensetzungen und einem Eisenverhüttungsofen ergraben werden konnte (Daim 1996, 372–375). Die Sichtverbindung von den Lebenden zu den Ahnen war offensichtlich von Bedeutung.

1 Vermutlich lag die zugehörige Siedlung im Bereich der heutigen Stadt Mödling. Archäologische Reste davon wurden bislang nicht entdeckt.

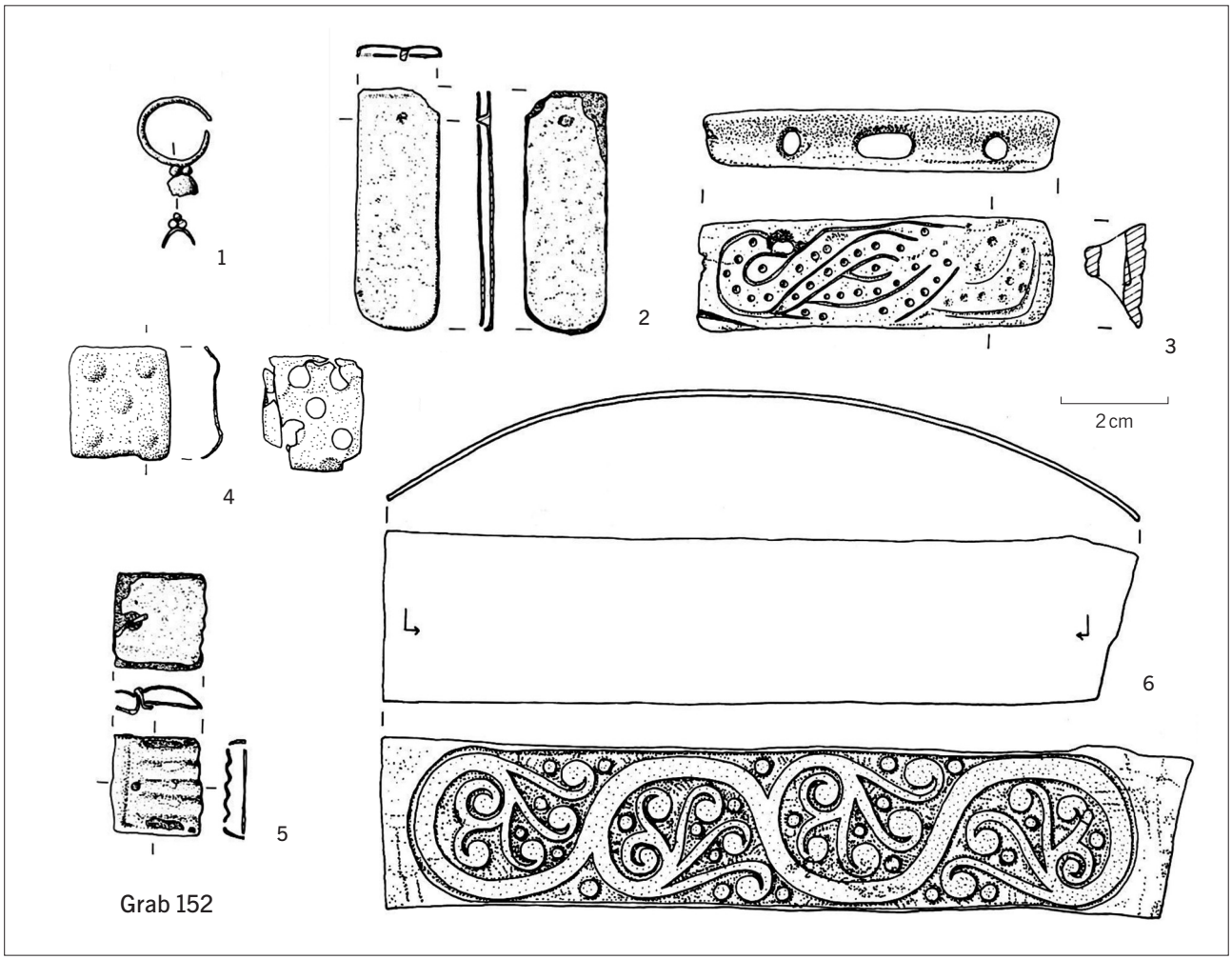


Abb. 2b Leobersdorf. Grab 152 (Auswahl): 1 Ohrring mit kleinem Bommelanhänger; 2 Riemenzunge aus Bronzeblech; 3 »Taschenverschluss« aus Bein; 4 Bronzeblechbeschlag; 5 Beschlagfragment; 6 aus Bein geschnitzter Köcherbesatz.

Fig. 2b *Leobersdorf. Grave 152 (selection): 1 earring with a small bobble pendant; 2 strap end made of sheet bronze; 3 »bag fastener« made of bone; 4 sheet bronze fitting; 5 fragment of fittings; 6 quiver trimmings carved from bone.*

Beide Plätze sind geeignet, wichtige Verkehrsverbindungen zu kontrollieren. In Leobersdorf überblickt man die flachen Weidegründe des Steinfelds, in Mödling speziell den Taleinschnitt des Weißenbachs, wo mit Sicherheit ein Weg in den Wienerwald verlief. Später, im 12. Jh., gründete man dort das Zisterzienserstift Heiligenkreuz. Dass zumindest die letzte Generation der awarischen Bestattungsgemeinde von Mödling den Wienerwald und das nördliche Alpenvorland im Blick hatte, belegt die Verbreitung der Spiralohrgehänge (s. Exkurs 2 in diesem Beitrag).

Die Nekropole von Leobersdorf umfasst 153 Gräber, allerdings gab es vor der Anlage eines typischen Reihengräberfeldes schon eine wohl sehr ausgedehnte frühawarische Grablandschaft mit Bestattungen in großen Abständen zueinander, von der wir nur einen winzigen Teil erfasst haben. Von den 1976 bis 1983 erschlossenen Gräbern gehören mindestens 3 zu den verstreut angelegten »scattered graves« (11, 152–153), und höchstwahrscheinlich gehört auch das bereits 1953 gefundene Grab dazu, rund 200 m westlich davon gelegen (s. o.). Diese Bestattungen datieren vermutlich in das späte 6. und das frühe 7. Jh. (Abb. 2a–b). Das Gräberfeld von Mödling – An der Goldenen Stiege zählt 553 Bestattungen, davon 497 aus der Awarenzeit.

In beiden Fällen konnte wohl der Großteil der kompakten Nekropolen ergraben werden, doch sind auch einige Bestattungen durch Baggerarbeiten (Leobersdorf) und die Anlage von Künetten etc. (Mödling) zerstört worden.

Grabtypen

Beide Nekropolen bestehen aus Körpergräbern, die Bestattungen erfolgten fast ausschließlich in gestreckter Rückenlage. Pferdemitbestattungen gibt es weder in Leobersdorf noch in Mödling, kamen aber im weiteren Umland durchaus vor (z. B. Wien-Liesing; Wien 11 – Csokorgasse). In zwei Fällen kamen in Mödling auch Hunde mit ins Grab, was für awarische Gräber ungewöhnlich ist, nicht aber – z. B. – für die der Langobarden im 6. Jh.[2].

2 Freundl. Hinweis von Bendeguz Tobias, ÖAW.

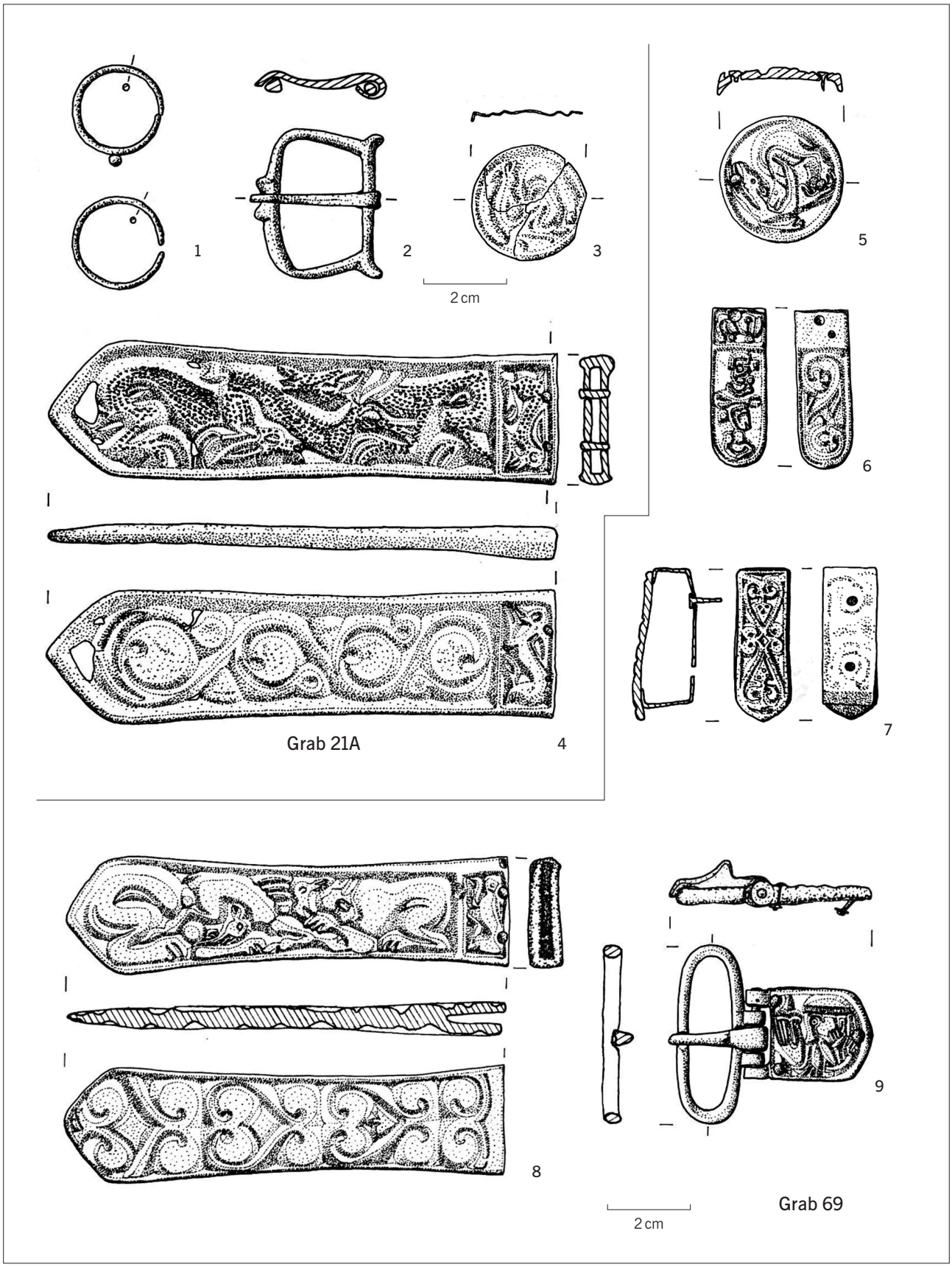


Abb. 3a Leobersdorf. Grab 21A (Auswahl): 1 Ohrringe; 2 Gürtelschnalle; 3 tiefgezogener Gürtelbeschlag, vergoldet; 4 aus Bronze gegossene Hauptriemenzunge mit Tierkampfszene, feuervergoldet. Grab 69 (Auswahl): 5 gegossener Gürtelbeschlag mit Tierkampfszene; 6 gegossene Nebenriemenzunge, vergoldet; 7 gegossene Riemenschlaufe, vergoldet; 8 gegossene Hauptriemenzunge mit Tierkampfszene, vergoldet; 9 gegossene Bronzeschnalle, vergoldet, mit der abstrakten Darstellung des Kaisers im Profil mit Lorbeerbüschel.

Fig. 3a *Leobersdorf. Grave 21A (selection): 1 earrings; 2 belt buckles; 3 deep-drawn belt fittings, gilded; 4 cast bronze main strap end with animal fight scene, fire-gilded. Grave 69 (selection): 5 cast belt fitting with animal battle scene; 6 cast side stap end, gilded; 7 cast strap loop, gilded; 8 cast main stap end with animal fight scene, gilded; 9 cast bronze buckle, gilded, with an abstract depiction of the emperor in profile with a tuft of laurel.*

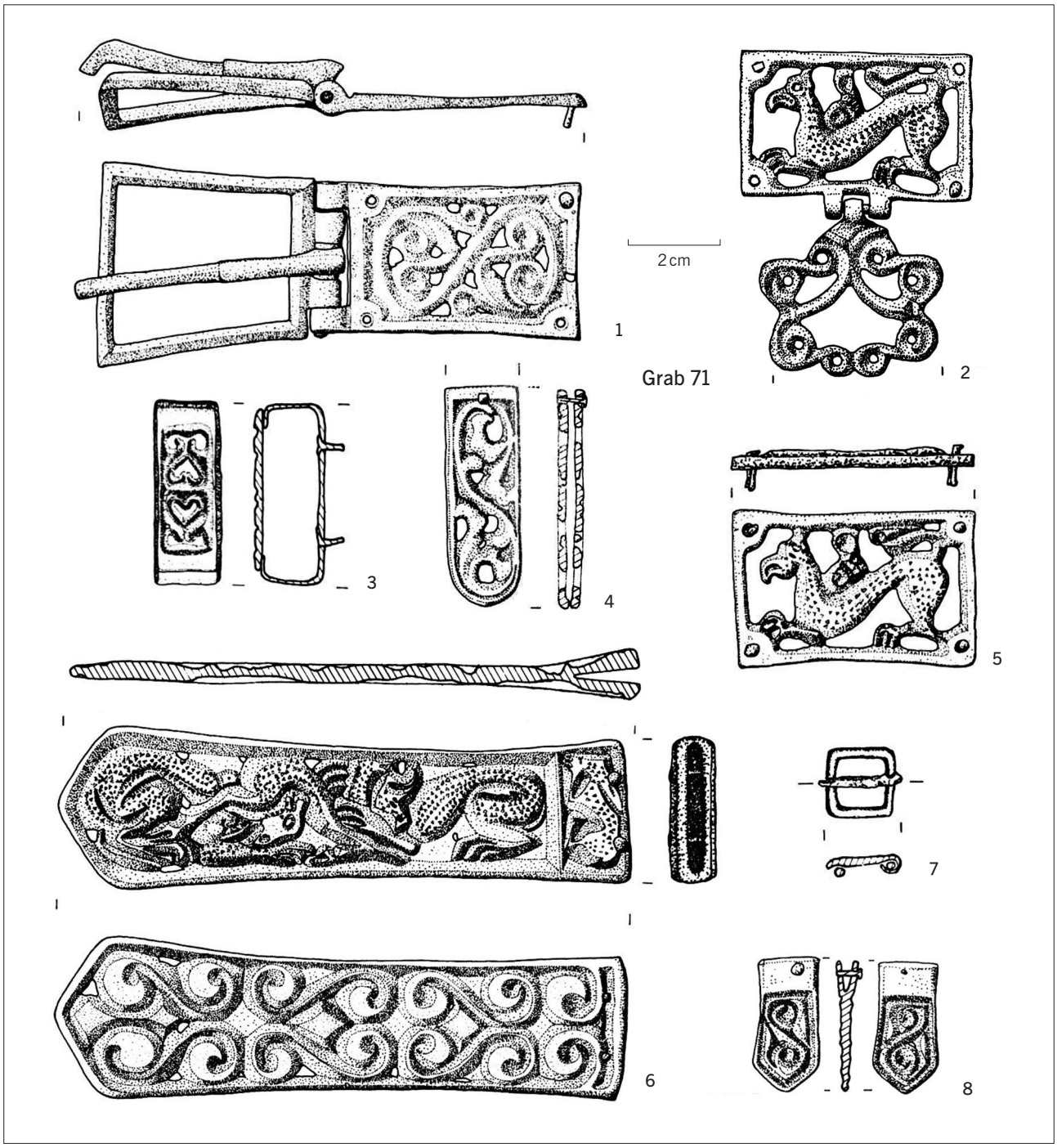


Abb. 3b Leobersdorf. Grab 71 (Auswahl): 1 gegossene Bronzeschnalle, vergoldet; 2 Scharnierbeschlag mit Greif, vergoldet; 3 gegossene Riemenschlaufe, vergoldet; 4 Nebenriemenzunge in zwei Teilen gegossen, vergoldet; 5 gegossener Beschlag mit Greifendarstellung, vergoldet; 6 gegossene Hauptriemenzunge mit Tierkampfszene, vergoldet; 7 Schnalle einer Wadenbinde o. Ä.; 8 Nebenriemenzunge, vergoldet.

Fig. 3b *Leobersdorf. Grave 71 (selection): 1 cast bronze buckle, gilded; 2 hinge fitting with griffin, gilded; 3 cast strap loop, gilded; 4 side stap end cast in two parts, gilded; 5 cast fitting with griffin depiction, gilded; 6 cast main stap end with animal fight scene, gilded; 7 buckle of a calf bandage or similar; 8 side stap end, gold-plated.*

Ausstattung der Gräber – Schmuck

Leobersdorf

Die früheste (beraubte) Bestattung von Leobersdorf enthielt zwar einen silbergegossenen Maskenbeschlag (Grab von 1953), doch ist das Gräberfeld – verglichen mit den awarischen Männergräbern des 7. Jhs. mit reichem Goldschmuck, die man im Zentrum des Karpatenbeckens gefunden hat (z. B. Bócsa, Kunagota, Kunbábony, Igar) – ein eher ärmlicher Friedhof. Aber dennoch hatte man den Wunsch und auch einige Möglichkeiten, sich zu schmücken. Manche Männer zeigten ihr Amt oder ihren gesellschaftlichen Rang durch komplexe Gürtelgarnituren. Das Spektrum des Frauenschmucks ist zwar beschränkt, doch die wichtigsten zeitgenössisch aktuellen Ohrgehänge- und Perlentypen kommen

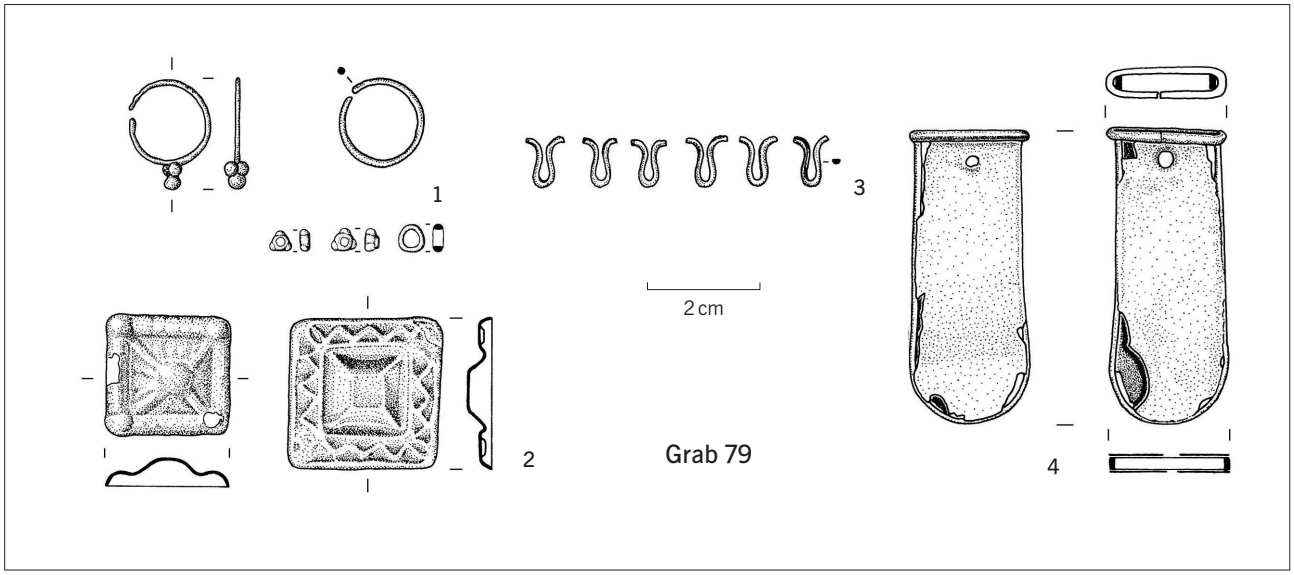


Abb. 4 Mödling – An der Goldenen Stiege. Grab 79 (Auswahl): 1 zwei Ohrringe und zwei Augenperlen; 2 zwei Gürtelbeschläge aus Blech; 3 Klammern zur Befestigung der Beschläge am Gürtel; 4 Riemenzunge aus Blech.

Fig. 4 *Mödling – An der Goldenen Stiege. Grave 79 (selection): 1 two earrings and two eye beads; 2 two belt fittings made of tin; 3 clips for attaching the fittings to the belt; 4 tin strap end.*

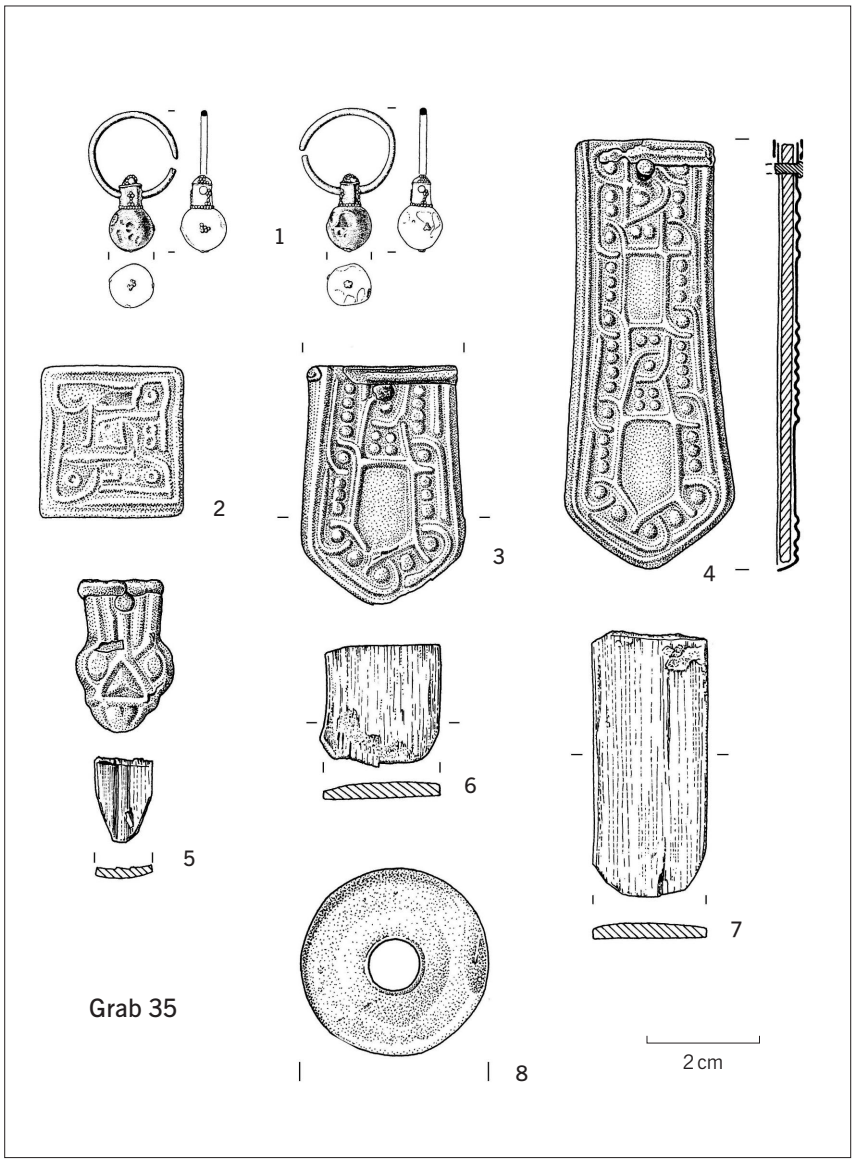


Abb. 5 Mödling – An der Goldenen Stiege. Grab 35 (Auswahl): 1 zwei Bommelohrgehänge; 2 Beschlag mit »Kettenzier« aus Silberblech; 3 Nebenriemenzunge aus Silberblech; 4 Hauptriemenzunge aus Silberblech; 5 Nebenriemenzunge aus Silberblech; 6 Holzlamelle zur Versteifung von 3; 7 Holzlamelle zur Versteifung von 4; 8 Spinnwirtel aus Ton.

Fig. 5 *Mödling – An der Goldenen Stiege. Grave 35 (selection): 1 two bobble ear pendants; 2 fitting with »chain decoration« made of silver sheet; 3 side strap end made of silver sheet; 4 main strap end made of silver sheet; 5 strap end made of silver sheet; 6 wooden slat to stiffen 3; 7 wooden slat to stiffen 4; 8 spindle whorls made of clay.*

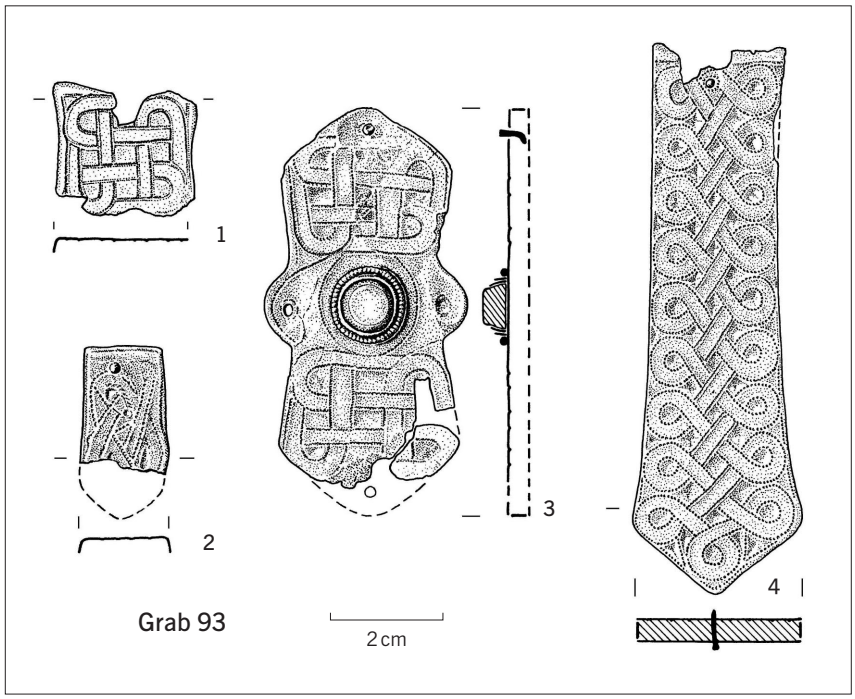


Abb. 6 Mödling – An der Goldenen Stiege. Grab 93 (Auswahl): 1 Bronzeblechbeschlag mit »Kettenzier«; 2 Nebenriemenzunge aus Bronzeblech mit Flechtbandzier; 3 Rückenbeschlag aus Bronzeblech mit »Kettenzier« und blauem Stein.

Fig. 6 *Mödling – An der Goldenen Stiege. Grave 93 (selection): 1 bronze sheet fitting with »chain decoration«; 2 bronze sheet side strap end with plaited decoration; 3 bronze sheet back fitting with »chain decoration« and blue stone.*

vor, besonders kreisrunde Ohrgehänge mit schwarzen Perlenanhängern, die später von ovalen Ohrgehängen abgelöst werden (Spätawarenzeit III) und Halsketten aus Melonenkernperlen. Rascher als der Frauenschmuck wechseln die Typen der Gürtelgarnituren, sowohl was die Konstruktion als auch die verwendeten Verzierungen oder Motive betrifft.

Die einzigen Gräber, die mit ihren feuervergoldeten Gürtelgarnituren hervorstechen, wurden in der Spätawarenzeit II angelegt (Gräber 21A, 69, 71; Abb. 3a–b). Zeigen sie einen größeren Wohlstand an oder eine Umbruchphase mit erhöhtem Repräsentationsbedarf?

Mödling

Die Belegung der Nekropole »An der Goldenen Stiege« beginnt deutlich später als in Leobersdorf. Eines der frühesten Gräber, die man der Frühawarenzeit II zurechnen kann, ist das Grab 79. Der hier bestattete Mann hatte u. a. eine Gürtelgarnitur aus Blech mit einer Hauptriemenzunge, die sich nach dem runden Ende hin leicht verbreitert. Dazu gehörten fünf quadratische Beschläge mit geometrischer Zier. Beim Kopf fanden sich drei Ohrringe, davon einer mit angelöteten Kügelchen, und zwei kleine Perlen (Abb. 4). Der beigegebene Topf ist aus lokalem Ton hergestellt, ohne drehbare Unterlage (vgl. Abb. 26,3)

Das reichste Männergrab der Mittelawarenzeit, Nr. 35, enthielt eine vielteilige Gürtelgarnitur aus Silberblech mit Kettenzier. An den Schläfen lagen zwei Ohrgehänge mit kleinen hohlen Blechbommeln. Neben einer dreiflügeligen Pfeilspitze und den Beinbeschlägen eines Köchers gehörte auch ein Spinnwirtel zum Inventar – normalerweise ein Accessoire in Frauengräbern (Abb. 5).

Der gleichen Zeitstufe gehört das Inventar des Grabes 93 an. Der Gürtelzierrat (Hauptriemenzunge, einteiliger Rückenbeschlag mit blauer Steineinlage und quadratische Gürtelbeschläge) ist extrem fein ausgearbeitet (Abb. 6). Das Gefäß, wohl für eine Flüssigkeit oder einen Brei, war auf einer drehbaren Unterlage hergestellt worden und zeigt zahlreiche Einsprengsel von Karbonaten (vgl. Abb. 27,2).

Was Mödling ebenfalls von Leobersdorf unterscheidet, ist die auffällige Vielfalt an Ohrgehängen und Halsketten in Mödling. Die Leobersdorferinnen hatten offenbar zu manchen Moden, speziell des fortgeschrittenen 7. Jhs., keinen Zugang oder lehnten sie ab. Zu den frühen Ohrringtypen in Mödling zählen der Ohrring mit schwarzer Perle und konischem Mittelteil sowie die auffälligen bommelförmigen Ohrgehänge (Abb. 7a–b). Sie gehen auf ältere Vorformen zurück, die noch keine Glasaugen aufweisen. Einige davon sind aus Silberblech gefertigt. Ihr Verbreitungsgebiet erstreckt sich vom Wiener Raum (Wien 11 – Csokorgasse) und dem heutigen Burgenland (Sommerein am Leithagebirge) über das gesamte Karpatenbecken (s. Exkurs 1 in diesem Beitrag). Halsketten dieser Zeitstufe in Mödling sind auffällig bunt, bestehen aus doppelkonischen oder Augenperlen. Sehr langlebig sind die gelben und – etwas später – dunklen Hirsekornperlen (Abb. 8a–b).

Ungewöhnlich sind auch die zwei Gürtelgarnituren mit gegossenen Riemenzungen und Beschlägen mit geometrischem Dekor, teils vergesellschaftet mit quadratischen Blechbeschlägen. Sie können in die Mittelawarenzeit II datiert werden und bilden eine Brücke zu den meist vollständig gegossenen Garnituren der Spätawarenzeit. Von einer der Garnituren finden sich Teile in zwei Gräbern (100, 242). Im Grab 353 fand sich eine eng verwandte kleinere Schnalle (Abb. 9a–b). Das handgeformte Gefäß in Grab 100 ist mit vermahlener, stark karbonathaltiger Keramik gemagert (Schamott). Im Grab 242 ist die gegossene Hauptriemenzunge mit quadratischen, geometrisch dekorierten Blechbeschlägen kombiniert. Das Grab enthielt auch ein auf einer drehbaren Unterlage hergestelltes dunkelgraues Gefäß mit zahlreichen Karbonateinsprengseln (vgl. Abb. 27,4). Im Grab 353 fanden sich neben der gegossenen Schnalle, zwei Pfeilspitzen und einem Kampfmesser

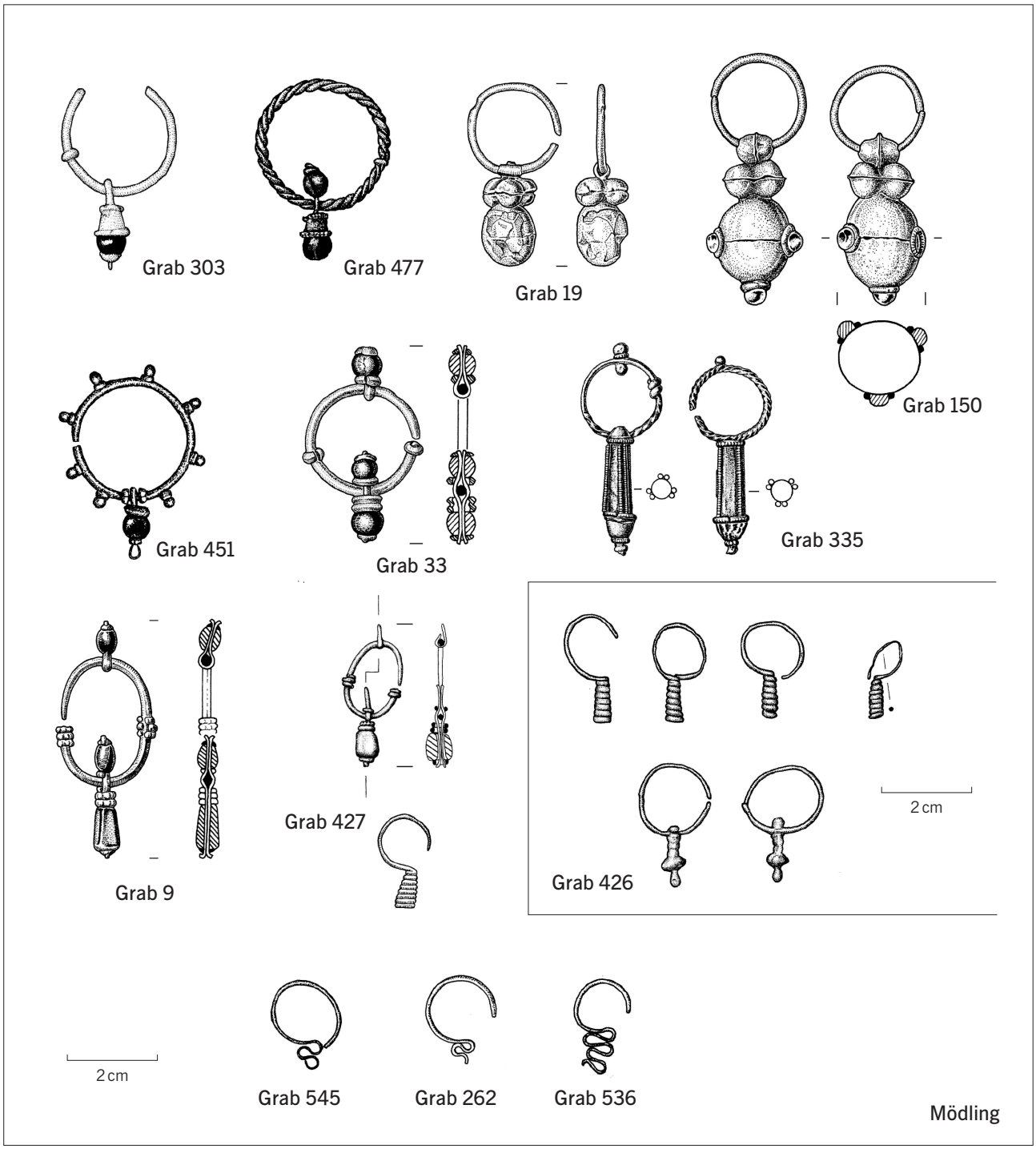


Abb. 7a Mödling – An der Goldenen Stiege. Die Vielfalt der Ohrringtypen (Auswahl). Komplexe: Grab 426 – Kopfschmuckringe mit Spiralfortsätzen sowie zwei Ohrringe (?) mit Anhängern und Grab 427– ovale Ohrgehänge und ein Kopfschmuckring mit Spiralfortsatz.

Fig. 7a *Mödling – An der Goldenen Stiege. The variety of earring types (selection). Complexes: grave 426 – headdress rings with spiral extensions and two earrings (?) with pendants and grave 426 – oval earrings and a headdress ring with spiral extension.*

auch zwei Ohrringe mit angelöteten Kügelchen und eine umfangreiche Kette mit kleinen gelben und schwarzen Perlen (Abb. 9c). Das zugehörende Gefäß aus lokalem karbonatsandhaltigem Ton hatte man auf einer drehbaren Unterlage hergestellt. Es ist rot-gelb gebrannt, dünnwandig und mit waagerechten Linien verziert (vgl. Abb. 27,5).

Während die Güsse der genannten drei Gräber wenig qualitätsvoll sind, erbrachte das Grab 135 eine exzellent ausgeführte Garnitur, bei der die Befestigungsstifte für die quadratischen Beschläge an deren Rückseite mitgegossen worden waren. Bemerkenswert sind auch die aufwendig verzierten Ohrringe und – vor allem – der Teil einer Halskette aus Hirsekornperlen mit sechs aufgezogenen Kugeln aus Bronzeblech (Abb. 10). Das Gefäß aus Grab 135 ist leuchtend rot gebrannt und zeigt viele weiße Punkte von Karbonaten (vgl. Abb. 27,3)

Mit der eisernen, streifenplattierten Gürtelgarnitur aus Grab 240 haben wir einen starken Beleg für Handelsbeziehun-

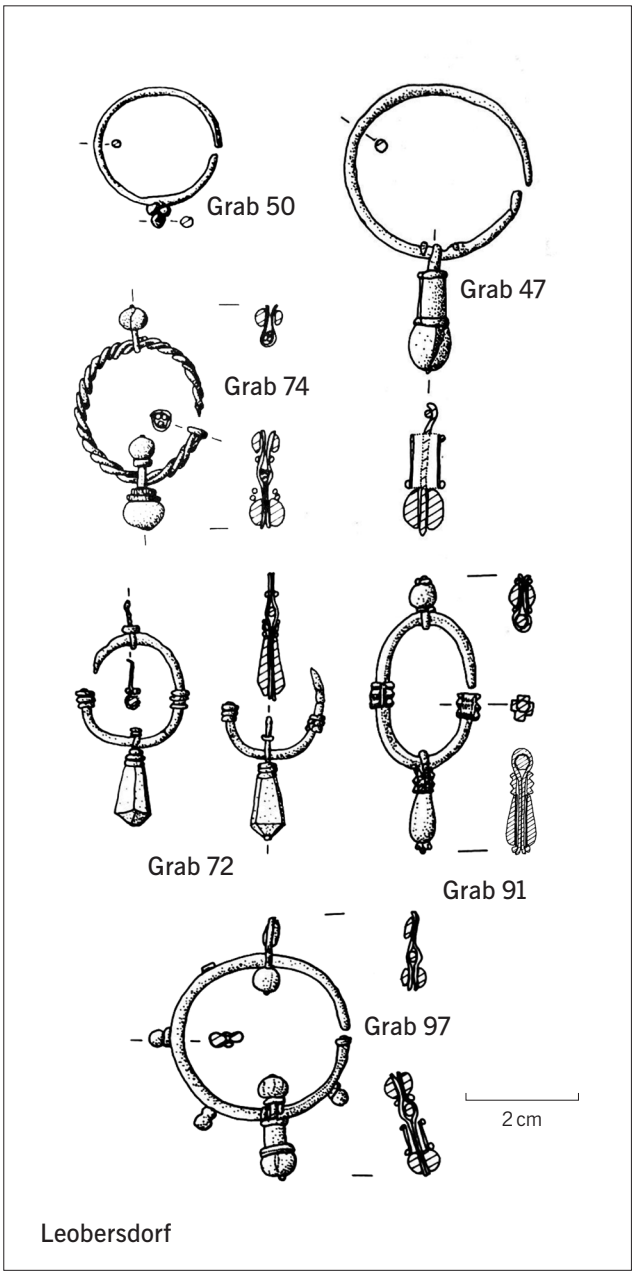


Abb. 7b Leobersdorf. Geringere Vielfalt an Ohrringtypen (Auswahl).

Fig. 7b *Leobersdorf. Smaller variety of earring types (selection).*

gen zwischen Bayern und dem Awarenland im dritten Viertel des 7. Jhs. (Abb. 11). Derartige Gürtel finden sich auch in Sommerein am Leithagebirge und an anderen Orten, sogar bis in das heutige Ostungarn, nach Allatyán, scheint ein Händler gekommen zu sein (Kovrig 1963, Grab 520).

Die spätawarischen Gürtelgarnituren zeigen keine großen Überraschungen. Sie folgen den überregionalen Moden. Im Grab 478 ist die gegossene Hauptriemenzunge mit querrechteckigen Blechbeschlägen kombiniert – typisch für die beginnende Spätawarenzeit (Abb. 12). Das Grab enthielt auch einen nachgedrehten, rot-schwarz gebrannten Tontopf mit zahlreichen Karbonatpünktchen, was beweist, dass diese Tonmischung auch noch nach der Mittelawarenzeit verwendet wurde und dass auch die absichtlich herbeigeführte rote Farbgebung der Keramik gebräuchlich war.

Eine typische frühere Greifengarnitur erbrachte das Grab 326 (Spätawarenzeit I; Abb. 13). Der Adlergreif, die Verbindung zweier mächtiger Tiere, dominiert in der ersten Hälfte des 8. Jhs. die Gürtelmotive. Etwas später (Spätawarenzeit II) datieren die Hauptriemenzungen mit Tierkampfszenen »zwei Greife schlagen eine Hirschkuh« angeordnet im Rhythmus einer Blattranke, z. B. die aus Grab 256A (Abb. 14).

Die Spätawarenzeit III bringt viele Neuerungen, auch in der Bildersprache. Der Greif als Gürtelmotiv ist *passé*, jetzt dominieren Blattranken, Schuppen und figürliche Darstellungen, z. B. die beliebte Zirkusszene der Hauptriemenzunge von Grab 440, wo ein Löwe den Gladiator (?) in das Genick beißt (Abb. 15). Jetzt werden die Riemenzungen meist aus zwei Teilen hergestellt, wohl zur Arbeitsvereinfachung, da so die nicht unproblematische Ausformung der Tülle für den Lederriemen entfällt. Ausnahmen stellen die Garnituren mit Riemenzungen dar, die zwar aus einem Guss hergestellt wurden, aber keine Tüllen haben, sondern Fortsätze an den Zwingen zur Befestigung am Lederriemen. Dieser Typ kommt in Mödling nur im Grab 140 vor (Abb. 16). Interessanterweise fand sich in diesem Grab ein handgeformtes Gefäß, wobei der Ton vermutlich mit zermahlenen Scherben gemagert worden war.

Auch die Kleidung der Frauen veränderte sich im Laufe der Spätawarenzeit. Leittypen der Belegungsphasen II und III sind die schwarzen Melonenkernperlen. Erst in der Phase III kommen die ovalen Ohrgehänge mit länglichen Perlanhängern vor (z. B. Grab 144). Diese Schmucktypen findet man auch in größerer Zahl in Leobersdorf. Sowohl in Mödling als auch in Leobersdorf treten in der jüngsten Phase zudem amphorenförmige Perlen mit Längslochung auf (vgl. Abb. 7a–b; 8a–b).

Im Gräberfeld von Mödling – An der Goldenen Stiege wurde eines der reichsten spätawarischen Frauengräber überhaupt gefunden. Die junge Dame aus Grab 144 verfügte über eine Komplettausstattung an Schmuck: Ovale Ohrringe aus Gold und Silber, einen Halsreif, eine Halskette aus schwarzen Melonenkernperlen, Armreife, Spiralfingerringe und die mittlerweile berühmte vergoldete Mantelschließe mit der Darstellung kniender Bogenschützen (Abb. 17a–b). All diese Gegenstände sind charakteristisch für die Spätawarenzeit III. Zu allem Überfluss hatte man der jungen Dame noch ein Glasfläschchen mitgegeben, das man vermutlich in einem römischen Grab entdeckt hatte, und welches nun wohl einen Duftstoff enthielt. Das Gefäß für eine Speisebeigabe hatte man aus Ton hergestellt, der mit zermahlenen Scherben gemagert war. Gleiches beobachteten wir im Fall des Grabes 140 gilt (s. o.). Die hartgebrannten Töpfe, die wohl in einer Manufaktur weiter östlich von Mödling hergestellt wurden, lehnte man offenbar für bevorzugte Begräbnisse ab.

Wie in Leobersdorf kann man auch in Mödling die Belegungsphase Spätawarenzeit III mittels des Frauenschmucks noch unterteilen. Für die Spätawarenzeit IIIa sind Kopfschmuckringe mit Spiralfortsätzen typisch. Im Grab 426 fanden sich vier derartige Ringe mit Spiralenden und zwei mit länglichen Anhängern (Abb. 18), im Grab 427 sind sie mit ovalen Ohrringen mit länglichen Perlenanhängern, einer Halskette mit melonenkern- und amphorenförmigen Perlen, einer blütenförmigen Mantelschließe, Armreifen und einem nachgedrehten Tontopf kombiniert (Abb. 19). Vermutlich zierten die Spiralschmuckringe eine Haube o. Ä. Diesen Kopf-

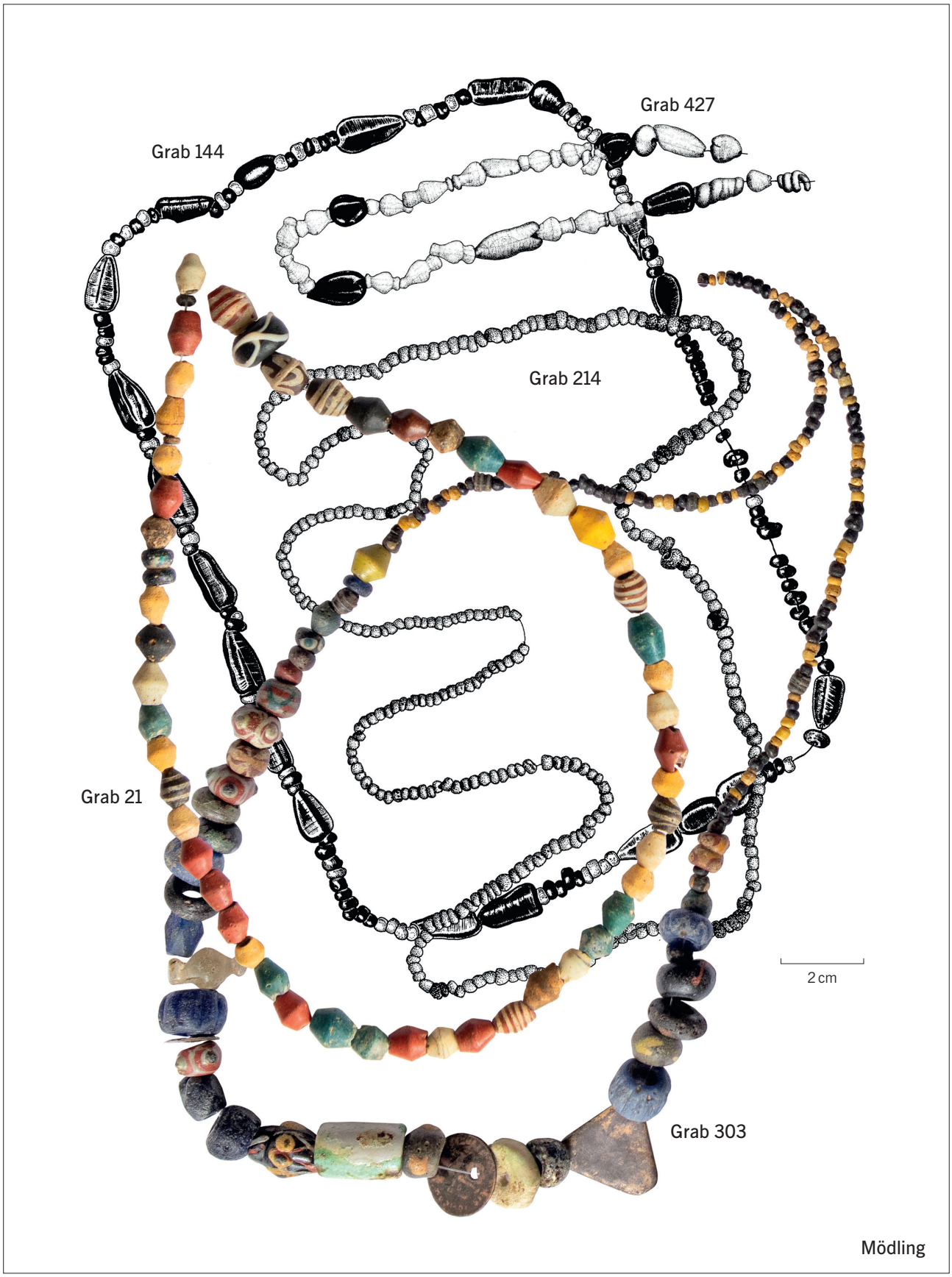


Abb. 8a Mödling – An der Goldenen Stiege. Vielfalt an Halsketten (Auswahl): Bunte Perlen der Früh- und Mittelawarenzeit (Gräber 21 und 303), Hirsekornperlen periodenübergreifend (Grab 214), vorwiegend schwarze Melonenkernperlen (Grab 144) und Amphorenperlen mit Längslochung der Spätawarenzeit (Grab 427).

Fig. 8a *Mödling – An der Goldenen Stiege. Variety of necklaces (selection): colourful beads from the Early and Middle Avar period (graves 21 and 303), millet beads from all periods (grave 214), mostly black melon seed beads (grave 144) and amphora beads with longitudinal holes from the late Avar period (grave 427).*

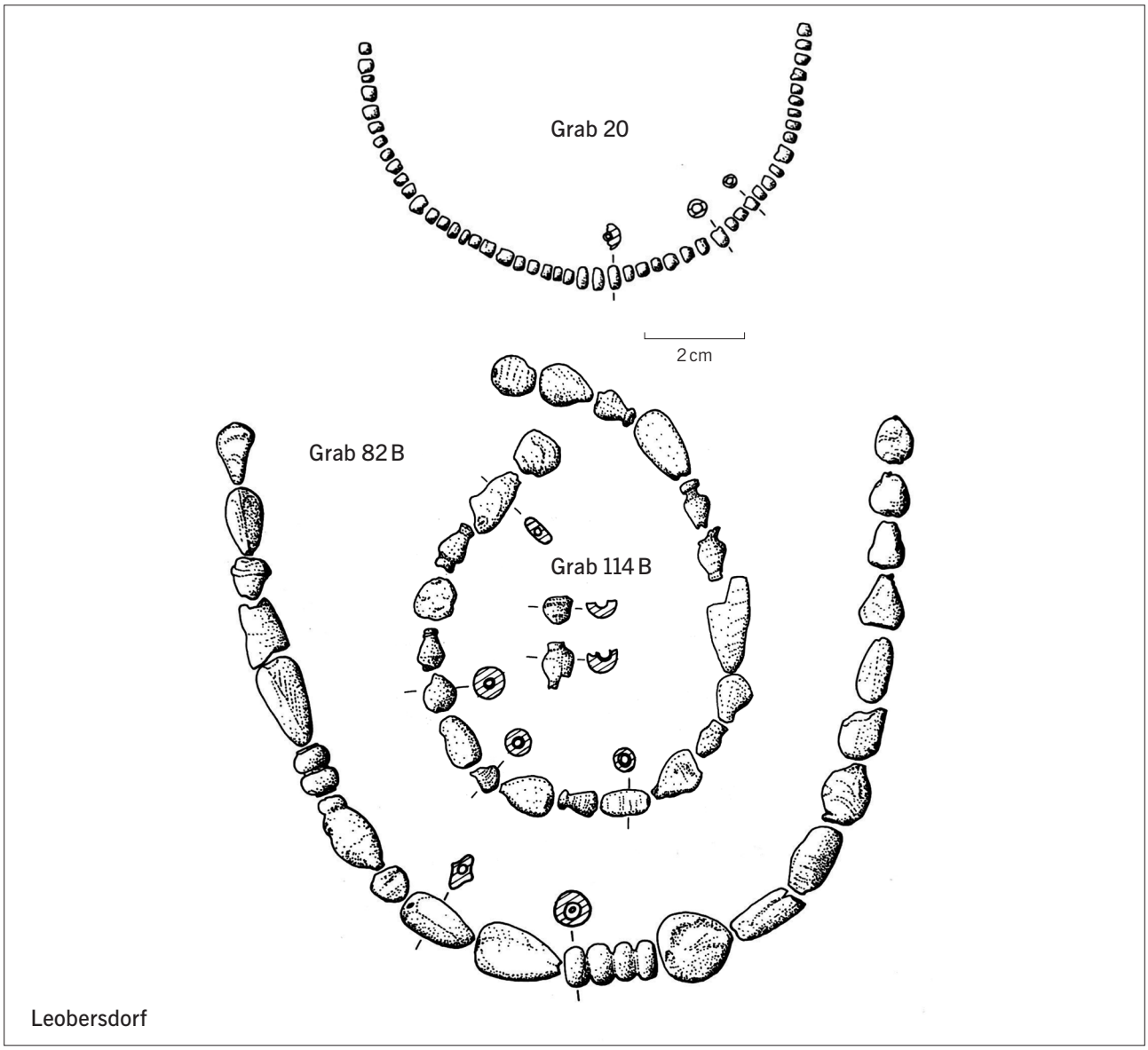


Abb. 8b Leobersdorf. Halsketten (Auswahl). Keine bunten Perlen, Hirsekornperlen periodenübergreifend (Grab 20), schwarze Melonenkernperlen und Amphorenperlen mit Längslochung der Spätawarenzeit (Gräber 82B und 114B).

Fig. 8b *Leobersdorf. Necklaces (selection). No coloured beads, millet beads from all periods (grave 20), black melon seed beads and amphora beads with longitudinal perforation from the Late Avar period (graves 82B and 114B).*

schmuck kennen wir auch aus Gräberfeldern im heutigen Oberösterreich nördlich der Donau (Gusen, Auhof), aber auch in Tulln und Pitten im südlichen Wiener Becken (s. Exkurs 2 in diesem Beitrag).

In der spätesten Phase des Friedhofs von der Goldenen Stiege treten erstmals Ohrringe mit Schleifenenden auf, bezeichnenderweise stammen alle drei aus Gräbern von Kleinkindern: 262, 536, 545 (Abb. 20). Diese Ohrringe erlebten bald eine stürmische Verbreitung, doch sind sie – auch wegen ihrer Einfachheit – schwer zu datieren. Diese Schmuckringe zeigen eine Verbindung der Nekropole von Mödling zu den Gräberfeldern (und Siedlungen) von Einwanderern nach der Beseitigung der awarischen Herrschaft. Waren die Mödlinger Kleinkinder bereits nach den neuesten Kleidungssitten geschmückt? Entscheidend ist, dass sich diese späten Schmucktypen (Spiralschmuckringe und Ringe mit Schleifenenden) in Leobersdorf nicht finden. Wie es aussieht, hat man sich in Leobersdorf nicht mehr angepasst, vielleicht ist man auch gen Osten abgezogen, eventuell zu entfernten oder auch nahen Verwandten östlich der Donau. Noch ist das reine Spekulation, könnte aber bald geklärt werden – mithilfe z. B. der Archäogenetik.

Ausstattung der Gräber – Keramik (FD, RS, KR)

Nahrungsmittelbeigaben spielen in den awarenzeitlichen Bestattungsbräuchen eine große Rolle. Vom Fleisch sind häufig die Knochen erhalten, von flüssiger oder breiförmiger Nahrung die Gefäße, in der Regel Tontöpfe. Aber auch hier zeigen sich zwischen Mödling und Leobersdorf große Unterschiede. In den 152 Gräbern von Leobersdorf fanden sich nur 15 Gefäße, während aus Mödling aus insgesamt 497 awarenzeitlichen Gräbern über 300 Töpfe vorliegen. Leider bleibt uns (noch) verborgen, was sie einst enthielten, umso größer ist ihr

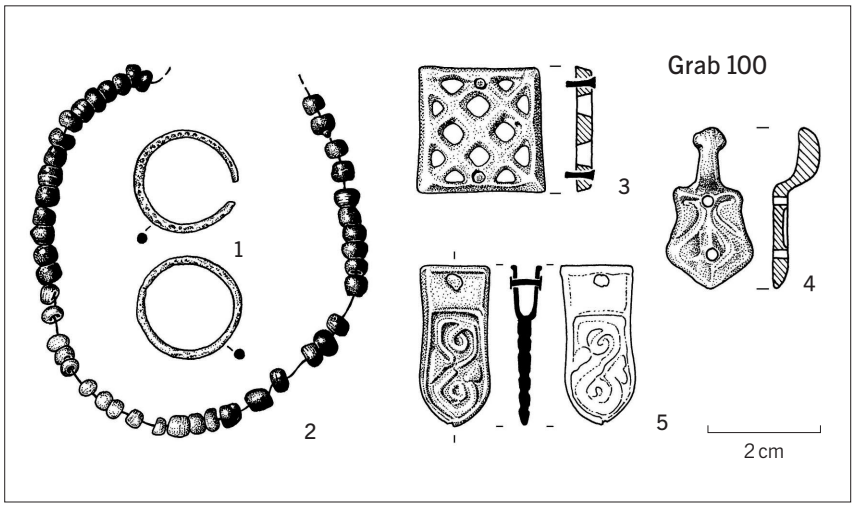


Abb. 9a Mödling – An der Goldenen Stiege. Grab 100 (Auswahl): 1 Ohrringe aus Bronzedraht; 2 Kette aus gelben und schwarzen Hirsekornperlen; 3 Gürtelbeschlag, Bronzeguss, Gitterdekor; 4 Hakenbeschlag (vielleicht zum Tragen eines Messers mit Scheide); 5 Nebenriemenzunge.

Fig. 9a *Mödling – An der Goldenen Stiege. Belt ornaments in cast bronze with lattice decoration. Grave 100 (selection): 1 bronze wire earrings; 2 necklaces of yellow and black millet grain beads; 3 belt fittings; 4 hook fittings (perhaps for carrying a knife with a scabbard); 5 side strap end.*

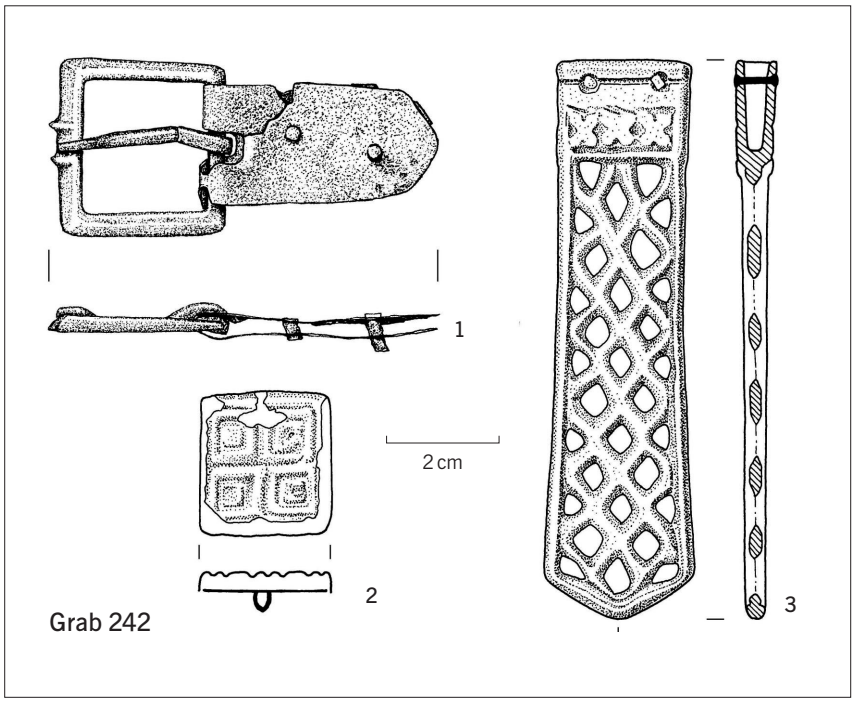
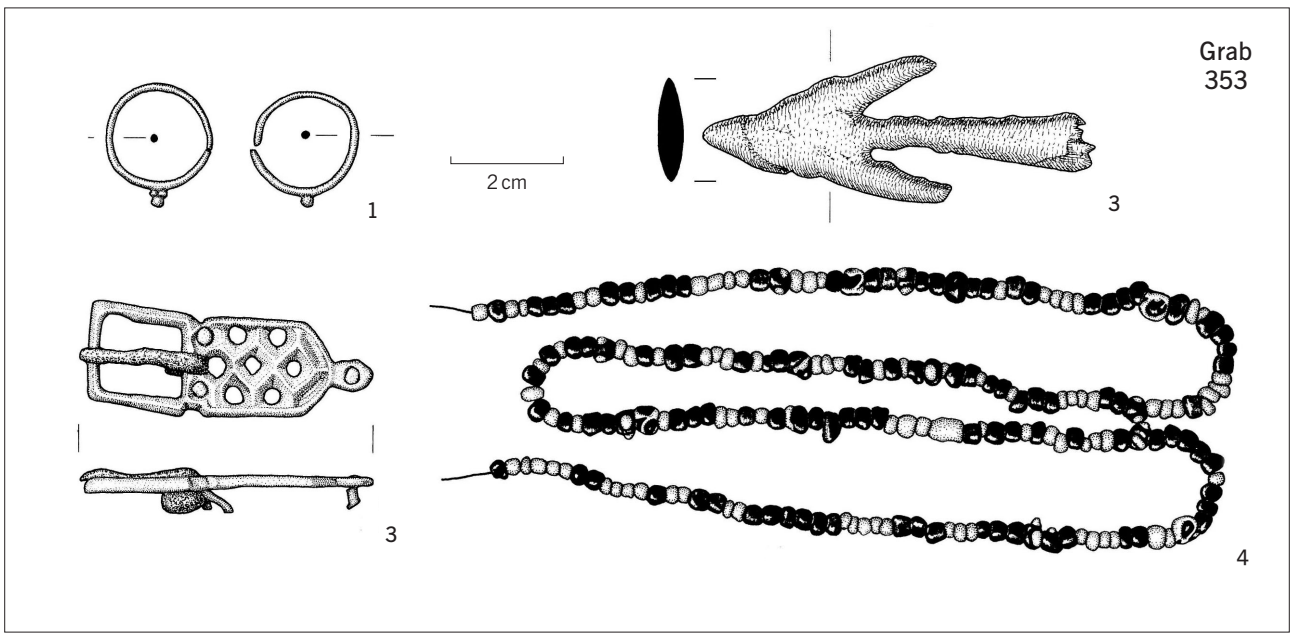


Abb. 9b Mödling – An der Goldenen Stiege. Grab 242 (Auswahl): Gürteldekor. 1 Schnalle; 2 Gürtelbeschlag aus Blech, vermutlich als Ersatz für gegossene Beschläge; 3 Hauptriemenzunge passend zu den Beschlägen aus Grab 100.

Fig. 9b *Mödling-An der Goldenen Stiege. Grave 242 (selection): belt decoration. 1 buckle; 2 belt fittings made of metal sheet, probably as a replacement for cast fittings; 3 main strap end matching the fittings from Grave 100.*

Abb. 9c Mödling – An der Goldenen Stiege. Grab 353 (Auswahl): 1 Ohrringe mit Kügelchen; 2 Bronzeschnalle, gegossen, mit Gitterdekor; 3 zweiflügelige Pfeilspitze; 4 Halskette aus gelben und schwarzen Hirsekornperlen.

Fig. 9c *Mödling – An der Goldenen Stiege. Grave 353 (selection): 1 earrings with beads; 2 bronze buckles with lattice decoration, cast; 3 two-winged arrowhead; 4 necklace of yellow and black millet grain beads.*



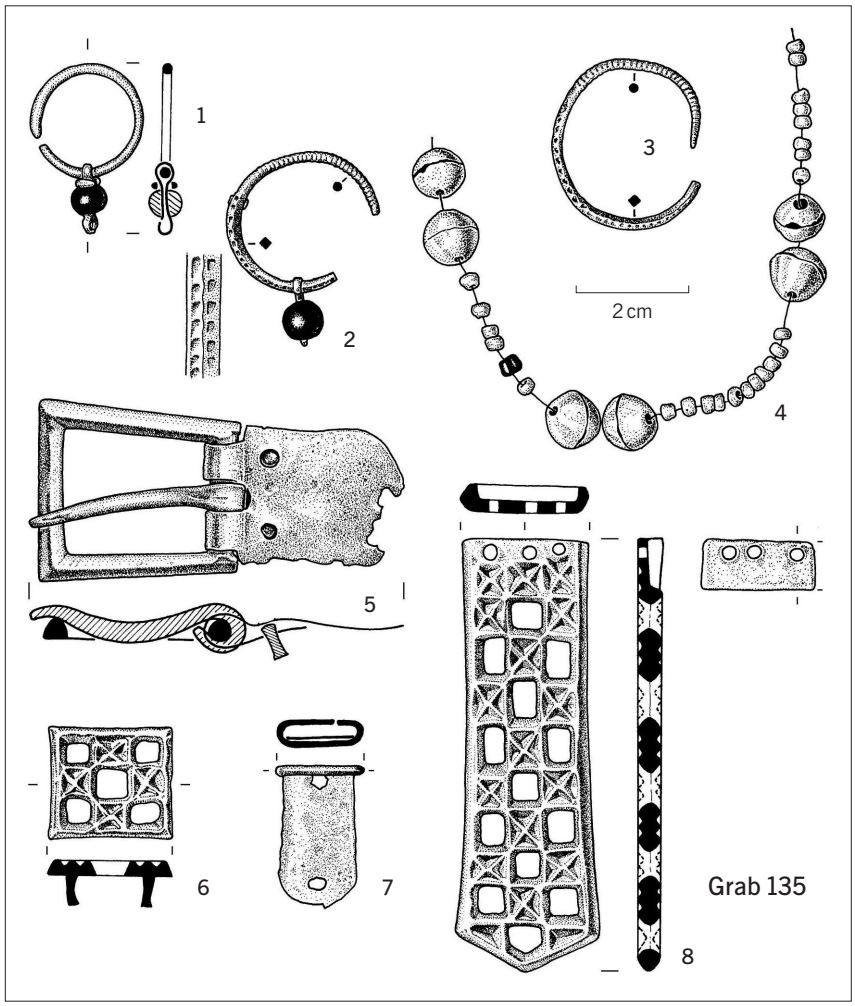


Abb. 10 Mödling – An der Goldenen Stiege. Grab 135 (Auswahl): 1–2 Ohrringe mit schwarzen Perlanhängern; 3 Ohrring; 4 Perlenkette mit zweiteiligen Kugeln aus Bronzeblech; 5 Gürtelschnalle; 6 gegossener Gürtelbeschlag mit Schachbrettdekor; 7 Nebenriemenzunge aus Bronzeblech; 8 Hauptriemenzunge mit Beilageblech zur Befestigung der Riemenzunge am Gürtel.

Fig. 10 *Mödling – An der Goldenen Stiege. Grave 135 (selection): 1–2 earrings with black pearl pendants; 3 earring; 4 pearl necklace with two-part balls made of bronze sheet; 5 belt buckle; 6 cast belt fitting with chessboard decoration; 7 side strap end made of bronze sheet; 8 main strap end with sheet for attaching the strap end to the belt.*

Erkenntniswert zu Handwerk und Symbolik der awarenzeitlichen Bevölkerung. Schon während der Grabung in Mödling zeigte sich die Vielfalt der Keramik in Tonqualität, Aufbereitung durch Zusätze aller Art, Formgebung, Verzierung und Brand. Ein Überblick der awarischen Keramik und ihrer Entwicklung wurde bereits 1994 vorgelegt (Daim 1994). Wegen ihres weiten Spektrums schien es lohnend, eine repräsentative Anzahl der Töpfe aus Mödling durch z. B. R. Sauer mineralogisch-petrografisch untersuchen zu lassen (s. Exkurs 3 in diesem Beitrag).

Außergewöhnlich ist eine Gruppe von dünnwandigen Gefäßen mit sanftem S-Profil, auf der Scheibe nachgedreht, meist rot gebrannt, mit weißen Karbonaten im Ton, wie gesprenkelt. Dieser Keramiktyp datiert in die Mittelawarenzeit, doch finden sich die Karbonate im Ton auch schon wesentlich früher und auch noch in der Spätawarenzeit. Mittels der mineralogisch-petrographischen Analyse konnte auch nachgewiesen werden, dass die ziemlich einheitlichen, nachgedrehten, hart gebrannten und graubraunen Töpfe der Spätawarenzeit nicht in Mödling hergestellt worden sind, sondern vielleicht in der Gegend des Leitghagebirges, wo vermutlich eine Manufaktur existierte, die das Umland mit dieser außerordentlich gebrauchsfähigen Ware versorgte. Für die Bestattung höherrangiger Verstorbener verwendet man allerdings gerne handgefertigte, nicht nachgedrehte Gefäße, so auch für die vorzüglich ausgestattete junge Frau in Grab 144.

Anthropologie und Archäogenetik

Die Anthropologie oder Humanbiologie ist die älteste Partnerdisziplin der Archäologie, und manche Routinen wie Alters- und Geschlechtsbestimmung sowie die Untersuchung der Skelette nach Verletzungen, Pathologien und am Knochenmaterial ersichtlichen Krankheiten gehören nach wie vor zu ihrem Werkzeugkasten. Doch wurde dieser in den letzten Jahren wesentlich erweitert und besonders durch die Archäogenetik, die es möglich macht, die Verwandtschaftsverhältnisse innerhalb von Gräberfeldern und ganzen Entitäten zu ermitteln. Leobersdorf und Mödling bilden zwei Fallstudien, welche die Möglichkeiten und Grenzen der Methode aufzeigen sollen. Doch gerade diese Grenzen werden laufend verschoben. Der erste Knalleffekt war die Feststellung, dass die Bevölkerung von Leobersdorf »ostasiatischer« Herkunft sei und sich in den 150 bis 200 Jahren der Belegung des Gräberfelders nicht mit den umliegenden Sippen vermischt habe (Wang u. a. in Vorbereitung). Da es aber in Leobersdorf auch keine Anzeichen von Inzucht gibt, müssen die Mütter von anderen Gruppen ebenfalls ostasiatischer Herkunft gekommen sein.

Die nächste Überraschung kam erst Ende 2021, da lief »HistoGenes« bereits zwei Jahre, als es erstmals gelang, ganze Stammbäume in den Gräberfeldern zu identifizieren, zunächst ohne das archäologische Fundgut einzubeziehen. Es ist fast unheimlich, denn dadurch wurden Körpergräberfel-

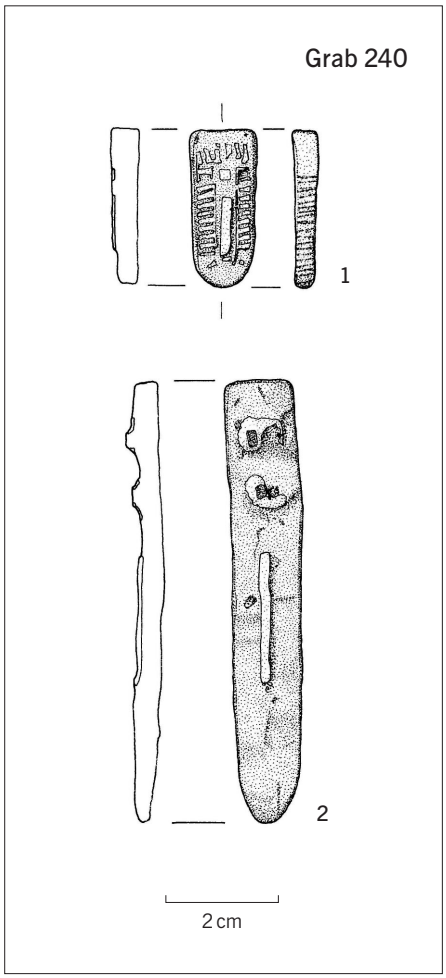


Abb. 11 Mödling – An der Goldenen Stiege. Grab 240 (Auswahl): 1 Riemenzunge aus Eisen mit Streifenplattierung mittel Silberblech; 2 eiserne Riemenzunge mit Silberblechstreifen.

Fig. 11 *Mödling – An der Goldenen Stiege. Grave 240 (selection): 1 iron strap end with strip plating using silver sheet; 2 iron strap end with silver sheet strips.*

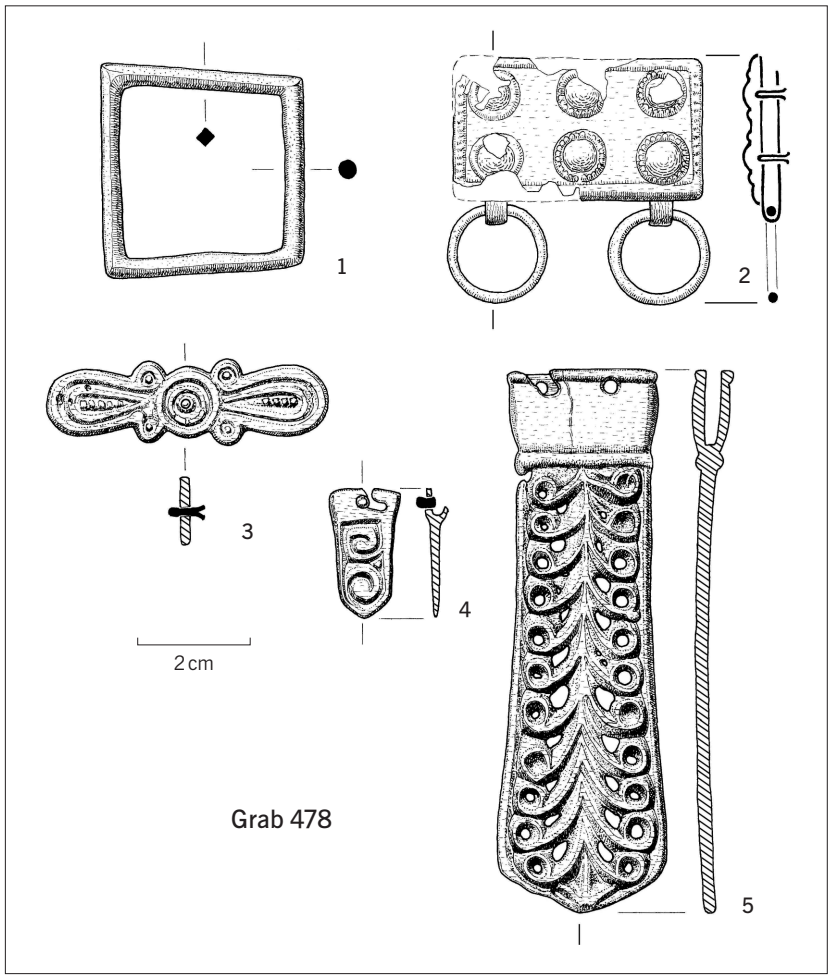


Abb. 12 Mödling – An der Goldenen Stiege. Grab 478 (Auswahl): 1 Schnallenbügel aus Bronze; 2 Gürtelbeschlag aus Bronzeblech mit Ziernieten; 3 Propellerbeschlag, wohl zur Befestigung einer Messerscheide; 4 Nebenriemenzunge; 5 in Bronze gegossene Hauptriemenzunge mit Tülle und Rankendekor.

Fig. 12 *Mödling – An der Goldenen Stiege. Grave 478 (selection): 1 buckle bracket made of bronze; 2 belt fitting made of bronze sheet with decorative rivets; 3 propeller fitting, probably for attaching a knife sheath; 4 side strap end; 5 cast bronze main strap end with socket and tendril decoration.*

der völlig transparent. Großväter und -mütter, Brüder, Schwestern, Kinder, Onkel und Tanten: Sie alle werden für uns sichtbar in der vierdimensionalen Struktur einer jeden Nekropole, das Ergebnis von immer wieder getroffenen menschlichen Entscheidungen während der gesamten Belegungszeit.

Demographie, Verletzungen, Gesundheit (MB, DP)

Im anthropologischen Teil des »HistoGenes«-Projektes untersuchen wir demographische und traumatische sowie Gesundheitsaspekte, um die Lebensumstände der Gemeinschaften zu eruieren. Ein Schwerpunkt stellt der Vergleich der beiden Gräberfelder Mödling und Leobersdorf dar, die jeweils weitestgehend vollständig beprobt wurden. Bei der Reihenfolge der Beprobung lag der Fokus auf dem Felsenbein, an zweiter Stelle wurden Zähne und in einzelnen Fällen, wenn keine Schädelreste vorhanden waren, postkraniale Elemente beprobt.

In Leobersdorf konnten von 181 anthropologisch identifizierten Individuen 20 %, und in Mödling von 536 anthropologisch identifizierten Individuen ca. 10 % aufgrund des schlechten Erhaltungszustandes nicht beprobt werden.

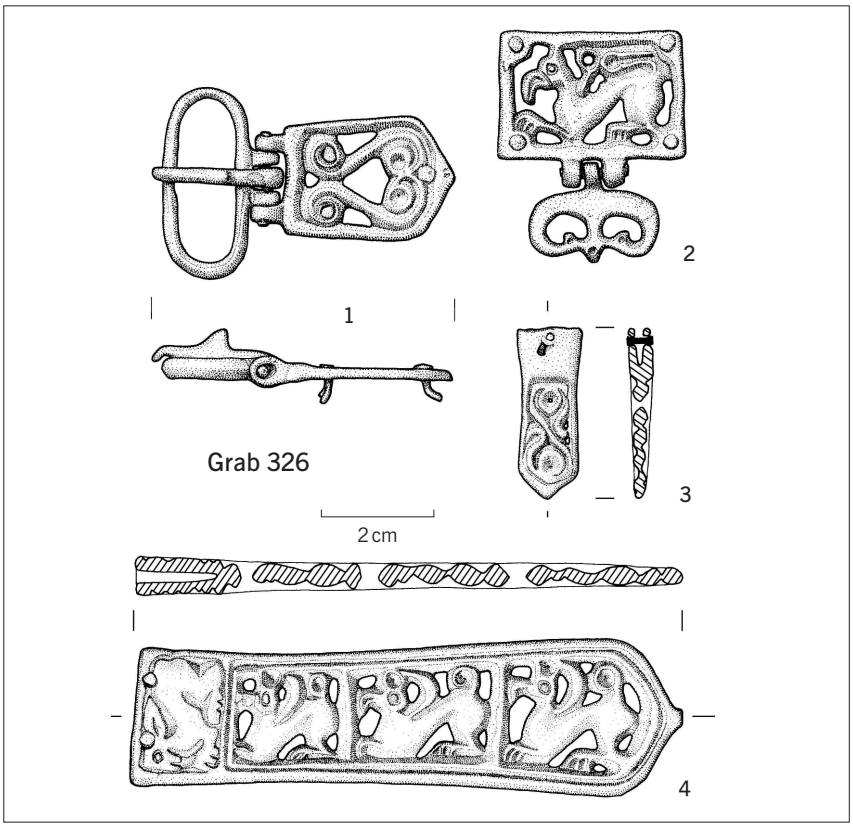
Begleitend zur Probennahme wurde eine neue, systematische anthropologische Untersuchung durchgeführt, um einerseits die von S. Grefen-Peters (1987) erhobenen Daten zu aktualisieren und zu erweitern, andererseits um einen guten Vergleich mit Mödling zu erhalten. Die bereits von K. Wiltschke-Schrotta erhobenen anthropologischen Basisdaten (Wiltschke-Schrotta in Vorbereitung) wurden um die im »HistoGenes«-Projekt vorgesehenen Daten ergänzt.

Interessant ist, dass die bisherigen genetischen Auswertungen bezüglich des Geschlechts der Individuen für beide Gräberfelder eine nahezu vollständige Übereinstimmung mit den anthropologischen Ergebnissen brachten. Abweichungen finden sich lediglich bei sehr schlecht erhaltenen Skeletten. Mit der genetischen Geschlechtsbestimmung der Kinder und Jugendlichen können aber nunmehr die im Rahmen des »HistoGenes«-Projektes untersuchten Gräber detaillierter und besser bioarchäologisch untersucht und interpretiert werden.

In Leobersdorf war bei 162 Individuen eine genauere Schätzung des Sterbealters möglich. Der Anteil der subadulten Individuen bis zum Alter von 18 Jahren beträgt 50 %. In Mödling war bei 523 Individuen eine Sterbealtersbestim-

Abb. 13 Mödling – An der Goldenen Stiege. Grab 326 (Auswahl). In Bronze gegossener Gürtelzierrat mit Greifendekor: 1 Schnalle; 2 Scharnierbeschlag; 3 Nebenriemenzunge; 4 Hauptriemenzunge mit Hase (an der Zwinge) und drei Greifen mit Sichelflügel.

Fig. 13 *Mödling – An der Goldenen Stiege. Grave 326 (selection): belt ornament cast in bronze with griffin decoration. 1 buckle; 2 hinge fittings; 3 side strap end; 4 main strap end with a hare (on the ferrule) and three griffins with sickle wings.*



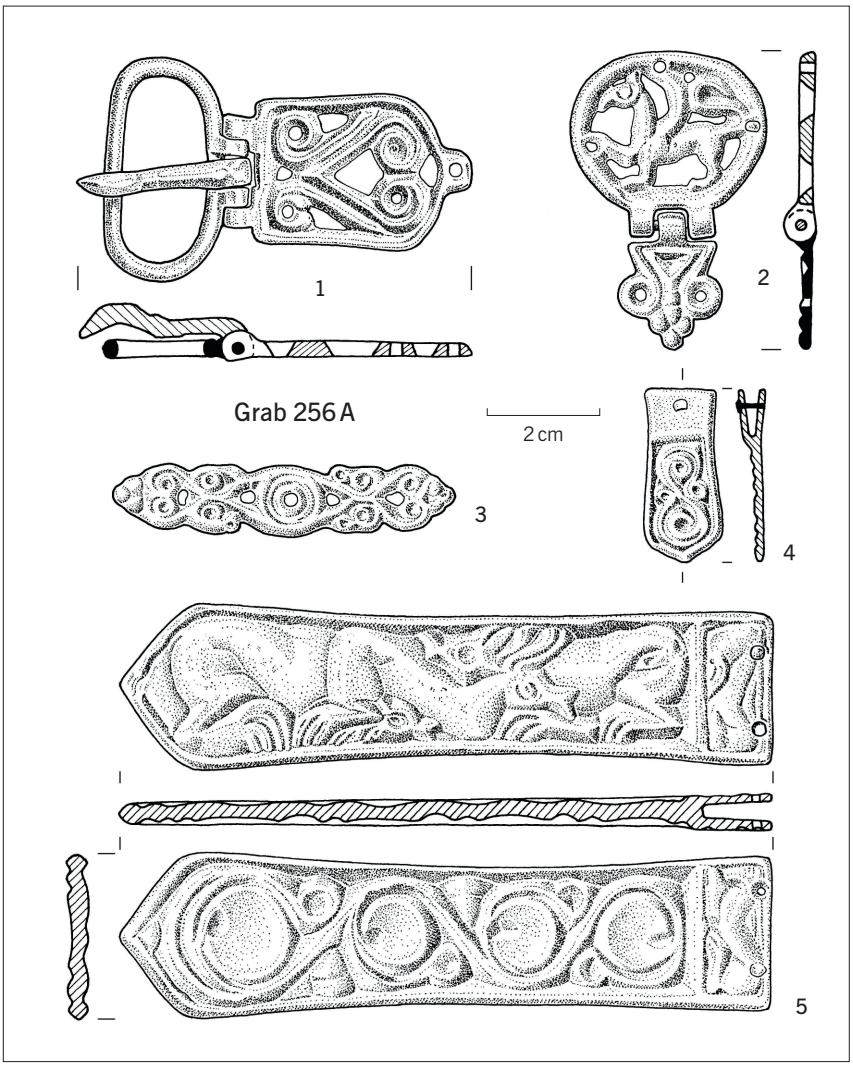


Abb. 14 Mödling – An der Goldenen Stiege. Grab 256A (Auswahl). Gürtelgarnitur, in Bronze gegossen. 1 Schnalle; 2 Scharnierbeschlag, Greif mit Sichelflügel; 3 Propellerbeschlag; 4 Nebenriemenzunge; 5 Hauptriemenzunge mit zwei Greifen, welche ein Reh oder eine Hirschkuh schlagen, verschlungen in Form einer Blattranke.

Fig. 14 *Mödling – An der Goldenen Stiege. Grave 256A (selection): Belt set, cast in bronze. 1 buckle; 2 hinge fitting, griffin with sickle wings; 3 propeller fitting; 4 side strap end; 5 main strap end with two griffins hitting a deer or hind, intertwined in the form of a tendril of leaves.*

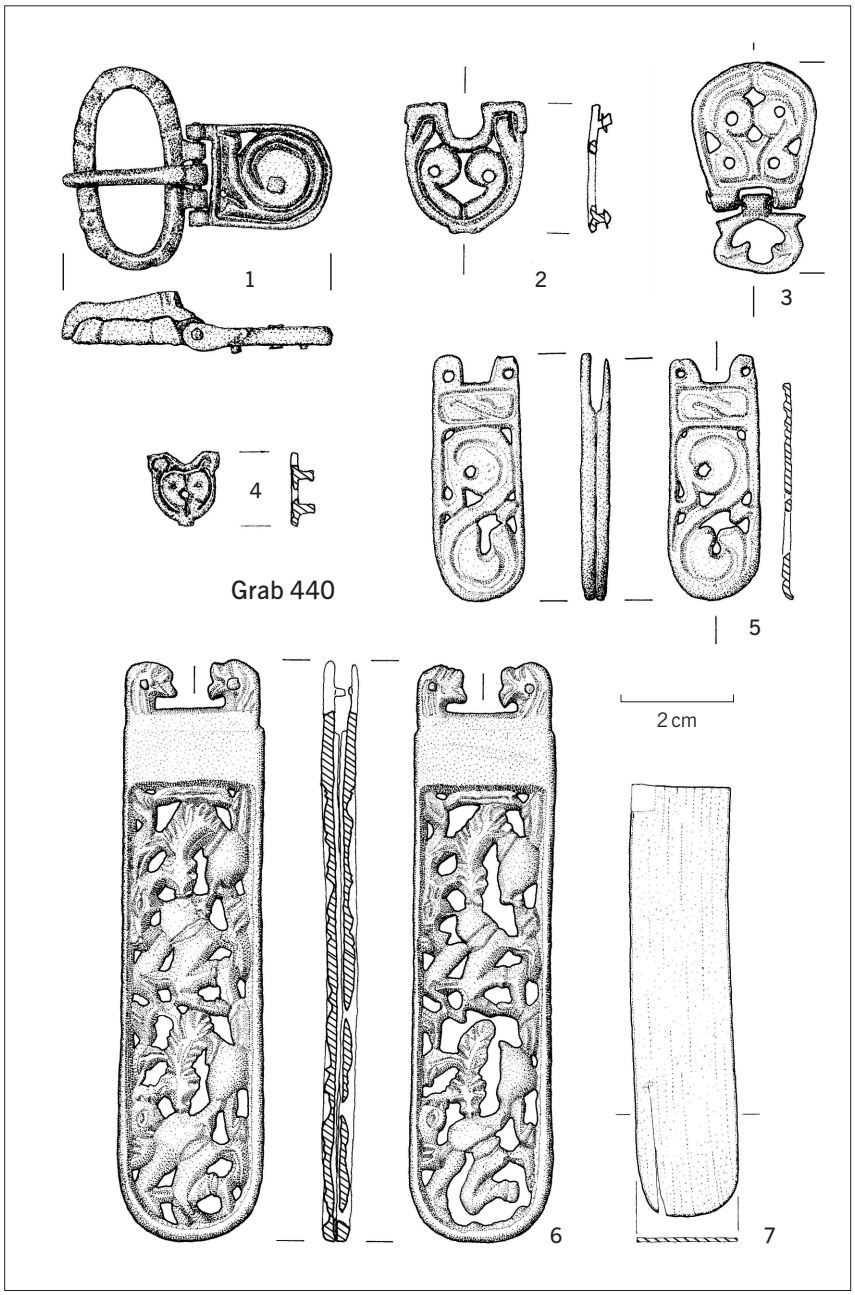


Abb. 15 Mödling – An der Goldenen Stiege. Grab 440 (Auswahl). Gürtelgarnitur in Bronze gegossen. 1 Schnalle; 2 Lochschützer; 3 Scharnierbeschlag; 4 Nebenriemenbeschlag; 5 Nebenriemenzunge, aus zwei Teilen zusammengesetzt; 6 Hauptriemenzunge, aus zwei Teilen zusammengesetzt, dazwischen Holzlamelle (7), vierfache Darstellung, wohl einer Zirkusszene: Ein Löwe beißt einen knienden Gladiator in das Genick.

Fig. 15 *Mödling – An der Goldenen Stiege. Grave 440 (selection): belt set cast in bronze. 1 buckle; 2 hole protectors; 3 hinge fitting; 4 side strap fitting; 5 side strap end, assembled from two parts; 6 main strap end, assembled from two parts, with wooden lamella in between (7), quadruple depiction, probably of a circus scene: a lion bites a kneeling gladiator in the neck.*

mung möglich, bei einem kleinen Teil davon gelang keine genauere Eingrenzung als »erwachsen«. Der Anteil der bestatteten subadulten Individuen ist mit 65 % in Mödling höher als in Leobersdorf. Auffallend ist, dass in beiden Gräberfeldern Bestattungen von Neonaten und Kindern bis zum ersten Lebensjahr stark unterrepräsentiert sind.

Ein besonderer Fokus der anthropologischen Befunde liegt auf physischen Belastungen ab dem Alter von 14 Jahren, besonders auf Knochenbrüchen und traumatischen Veränderungen. Die ersten Ergebnisse in Leobersdorf zeigen eine generell niedrige Frakturfrequenz, auch gibt es nur wenige Hinweise auf interpersonelle Gewalt. Der höchste Prozentsatz verheilter Frakturen war an den Rippen von Männern sichtbar (ca. 21 %), etwas niedriger bei Frauen (ca. 13 %), und der linken oberen Extremität von Männern (ca. 13 %). Ein Mann und eine Frau sind von leichten Schädeltraumata betroffen, während ein Mann eine schwere Gesichtsfraktur mit Beteiligung der Schulter erlitten hatte. Die folgenschweren Gesichtsverletzungen des Mannes könnten durch den Tritt eines Pferdes verursacht worden sein. Die meisten Frakturen sind allerdings gut verheilt, was auf ein gutes Versorgungsnetzwerk in der Gemeinschaft hindeutet. Es konnten in dieser Gruppe keine Dekapitationen und keine Frakturen der unteren Extremität festgestellt werden (Mühlburger 2023; Pany-Kucera u. a. 2022). Abgeleitet vom derzeitigen Untersuchungsstand dürfte die Frakturfrequenz in Mödling ähnlich niedrig sein wie in Leobersdorf (Wagner 2023). Im Unterschied zu Leobersdorf wurden allerdings in Mödling an bisher drei Männerskeletten Spuren einer Dekapitation gefunden (Wiltschke-Schrotta/Stadler 2005).

Weiters wird in beiden Serien der Gesundheitszustand der Menschen betrachtet, z. B. werden systematisch Anzeichen von Tuberkulose untersucht. Die in Mödling – An der Goldenen Stiege und Bruckneudorf bereits festgestellte niedrige Frequenz (Wiltschke-Schrotta/Berner 1999; Pany-Kucera/Wiltschke-Schrotta 2023) zeichnet sich auch in Leobersdorf

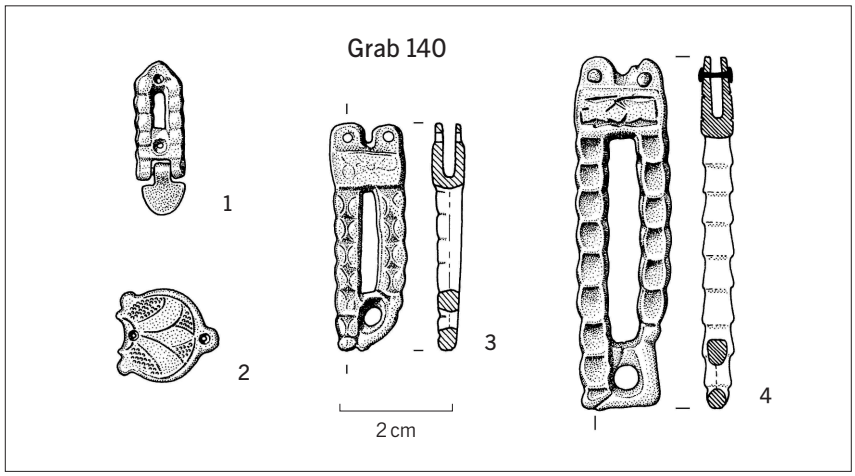


Abb. 16 Mödling – An der Goldenen Stiege. Grab 140 (Auswahl). In Bronze gegossene Gürtelgarnitur. 1 zungenförmiger Scharnierbeschlag; 2 Lochschützer; 3 einteilig gegossene Nebenriemenzunge mit Fortsätzen an der Zwinge; 4 einteilig gegossene Hauptriemenzunge mit Fortsätzen an der Zwinge.

Fig. 16 *Mödling – An der Goldenen Stiege. Grave 140 (selection): belt set cast in bronze. 1 tongue-shaped hinge fitting; 2 hole protectors; 3 side strap end cast in one piece with extensions on the ferrule; 4 main strap end cast in one piece with extensions on the ferrule.*



Abb. 17a Mödling – An der Goldenen Stiege, Grab 144 (Auswahl). 1 und 2 leicht ovale Ohrgehänge aus Gold mit länglichen Glasperlenanhängern und ebensolche aus Silber; 3 Halsreif aus Bronzedraht; 4 Agraffe (Gewandschließe) aus starkem Bronzeblech, vergoldet, mit der Darstellung kniender Bogenschützen.

Fig. 17a *Mödling – An der Goldenen Stiege, grave 144 (selection). 1 and 2 slightly oval gold earrings with long glass bead pendants and same earrings mad of silver; 3 bronze wire neck ring; 4 strong bronze clasps, gilded, depicting kneeling archers.*

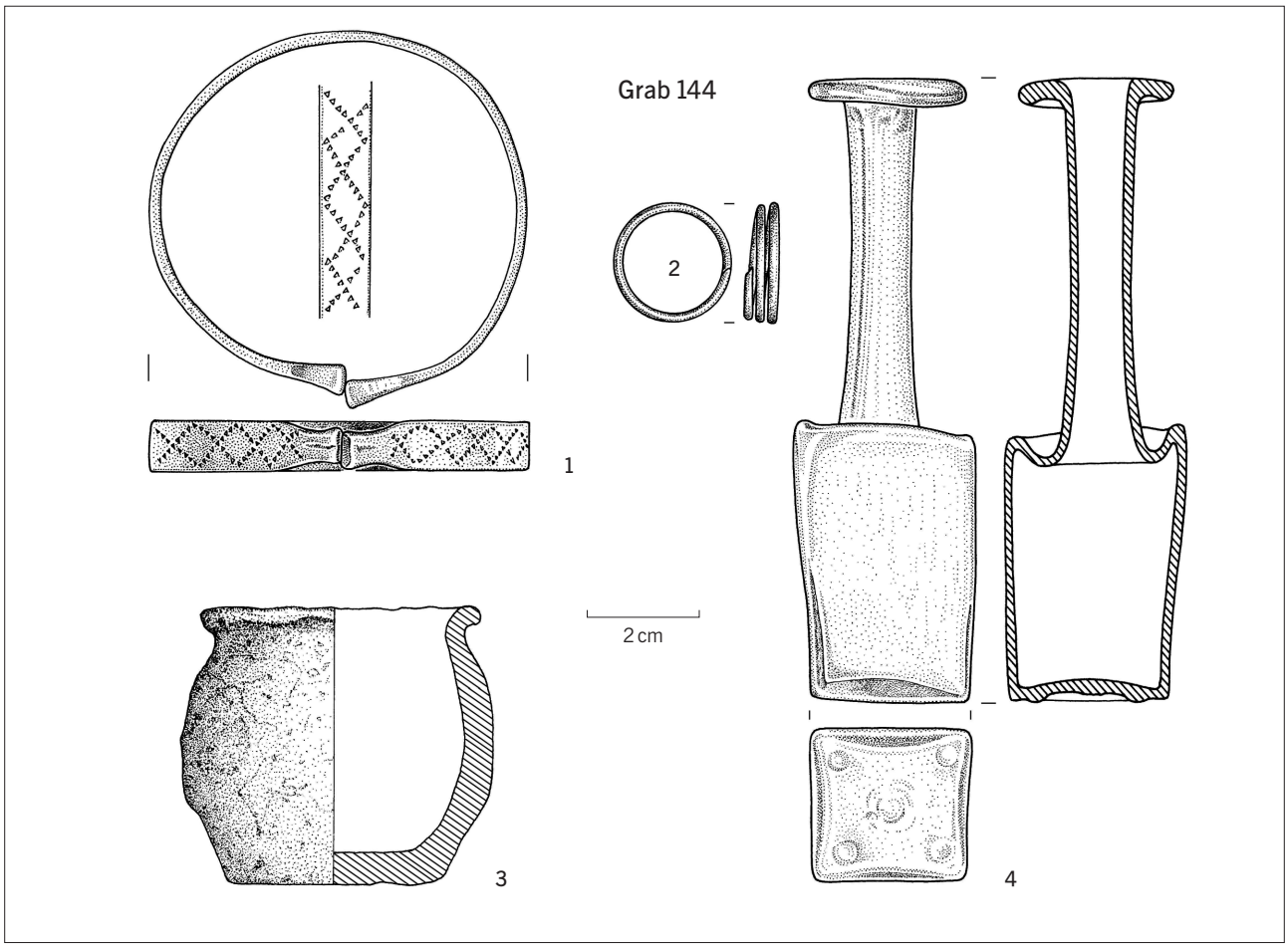


Abb. 17b Mödling – An der Goldenen Stiege, Grab 144 (Auswahl). 1 bandförmiger Armreif; 2 Spiralfingerring; 3 handgefertigtes Töpfchen; 4 römisches Glasfläschchen.

Fig. 17b *Mödling – An der Goldenen Stiege, grave 144 (selection). 1 band-shaped bangle; 2 spiral finger ring; 3 handmade small pot; 4 Roman glass vial.*

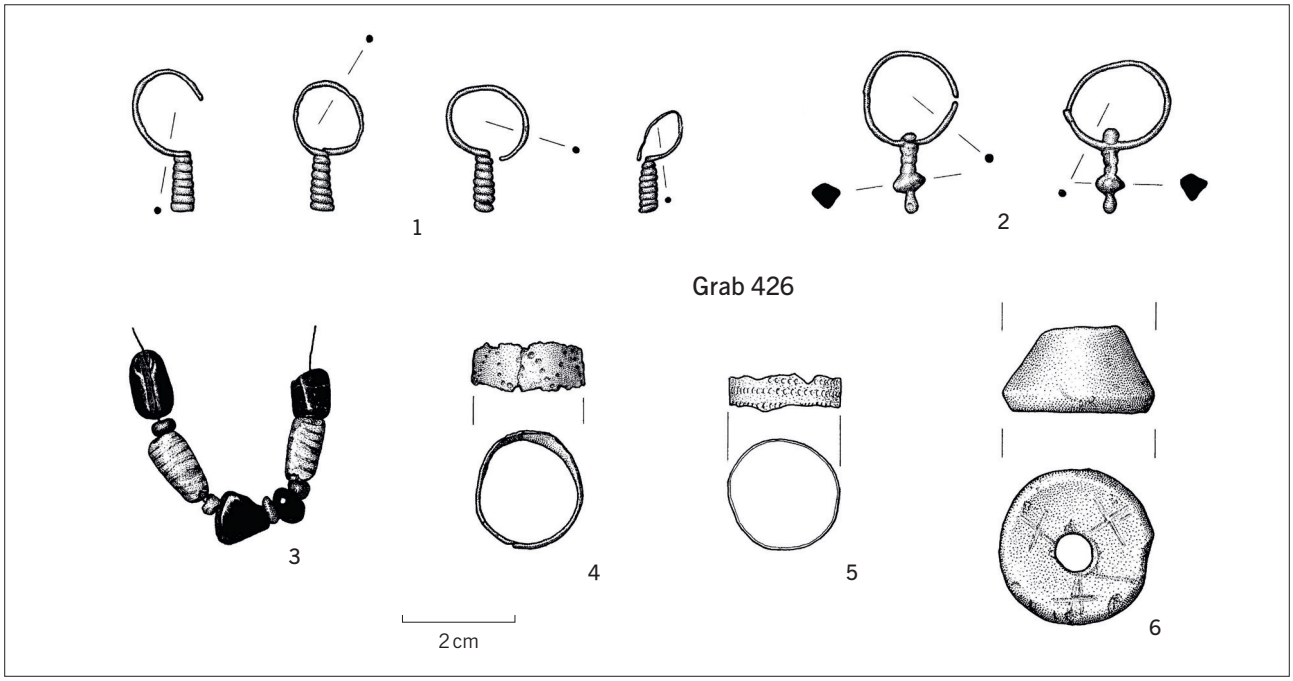


Abb. 18 Mödling – An der Goldenen Stiege. Grab 426 (Auswahl). 1 vier Kopfschmuckringe mit Spiralfortsatz; 2 Ohrringe (?) mit Anhänger; 3 Perlen; 4 und 5 Fingerringe; 6 Spinnwirtel aus Ton.

Fig. 18 *Mödling – An der Goldenen Stiege. Tomb 426 (selection). 1 four headdress rings with spiral extension; 2 earrings with pendants; 3 pearls; 4 and 5 finger rings; 6 spindle whorl made of clay.*

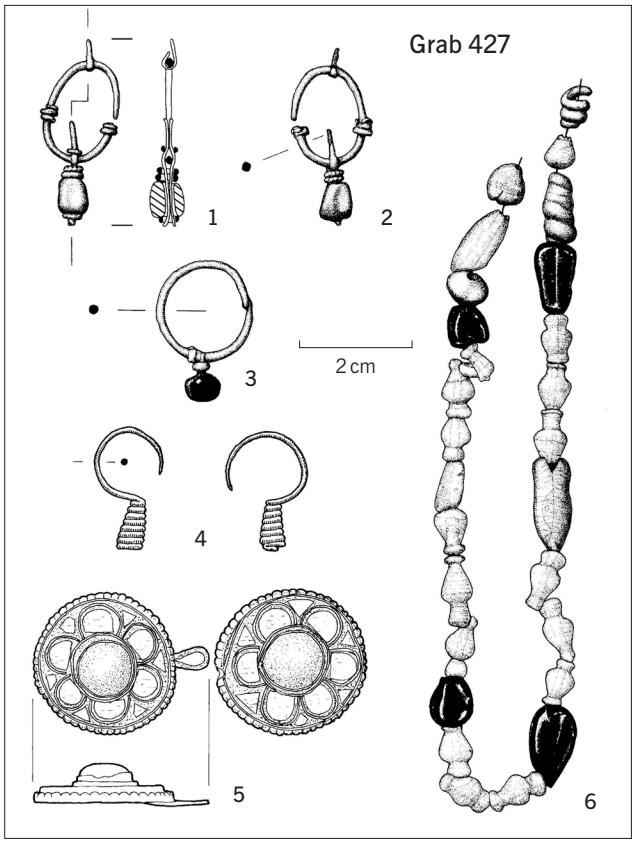


Abb. 19 Mödling – An der Goldenen Stiege. Grab 427 (Auswahl). 1–2 ovale Ohrgehänge mit länglichen Glasanhängern; 3 Ohrring mit schwarzer Glasperle; 4 zwei Kopfschmuckringe mit Spiralfortsätzen; 5 Agraffe (Gewandschließe) mit blütenförmigen Glaseinlagen; 6 Halskette mit schwarzen Melonenkernperlen und amphorenförmigen Perlen mit Längslochung.

Fig. 19 *Mödling – An der Goldenen Stiege. Tomb 427 (selection). 1–2 oval earrings with elongated glass pendants; 3 earring with black glass pearl; 4 two headdress rings with spiral appendages; 5 agraffe (cloak clasp) with flower-shaped glass inlays; 6 necklace with black melon seed pearls and amphora-shaped pearls with longitudinal perforation.*

ab. Diese gehen mit den niedrigen Prävalenzen von unter 1 % für das awarenzeitliche Ungarn einher (Pálfí/Marcsik 1999).

Mithilfe der DNA-Analysen ist es auch möglich, Verwandtschaftsverhältnisse in Form von Stammbäumen zu finden und Heiratsmuster in den Gruppen nachzuvollziehen. In den Pilotstudien wurde ein sehr hoher Verwandtschaftsgrad innerhalb der Serien festgestellt. Isotopenanalysen von Stickstoff und Kohlenstoff werden zusätzlich Aufschluss über die Ernährungssituation der Bevölkerungen geben. Pathogenanalysen an ausgewählten Individuen sollen bei bestehendem Verdacht bestimmte Krankheiten abklären und morphologisch nicht erklärbare Todesfälle aufklären helfen.

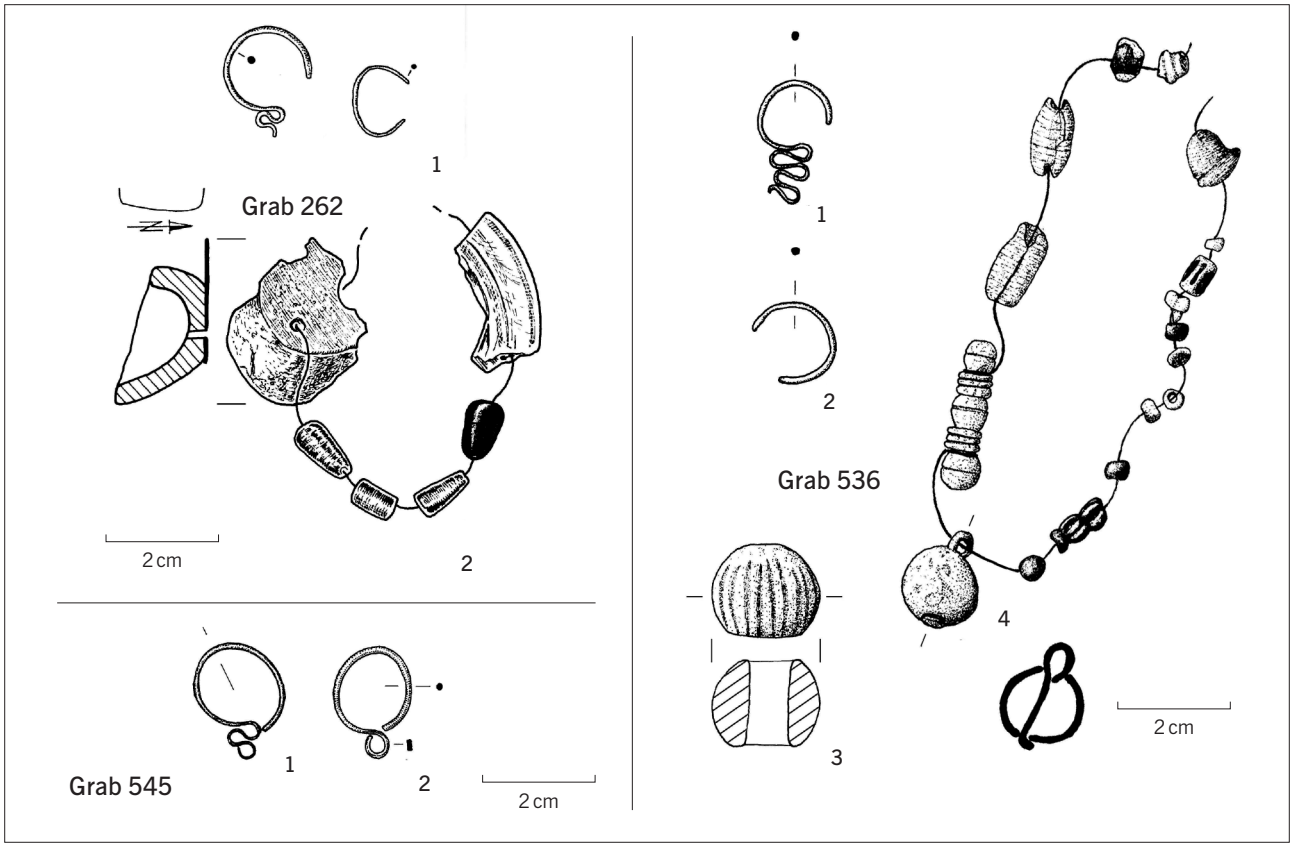


Abb. 20 Mödling – Mödling – An der Goldenen Stiege. Gräber 262, 536 und 545 (Auswahl). Grab 262. 1 Ohrring mit Schleifenende und Ohrringfragment (?); 2 Fragment einer Schelle (?) aus Eisenblech, Perlen, Glasfragment. Grab 536. 1 Ohrring mit Schleifenende; 2 Ohrringfragment (?); 3 Perle; 4 Halskette mit gegossenem Bronzekugelanhänger, beinernem Zierstück und. Perlen. Grab 545. 1 Ohrring mit Schleifenende; 2 Ohrring mit eingerolltem Ende.

Fig. 20 *Mödling – An der Goldenen Stiege. Graves 262, 536 and 545 (selection). Grave 262. 1 earring with loop end and earring fragment (?); 2 Fragment of a bell (?) made of sheet iron, beads, fragment of glass. Grave 536. 1 earring with loop end; 2 earring fragment (?); 3 pearl; 4 necklace with cast bronze ball pendant, bone ornament and beads. Grave 545. 1 earring with loop end; 2 earring with rolled end.*

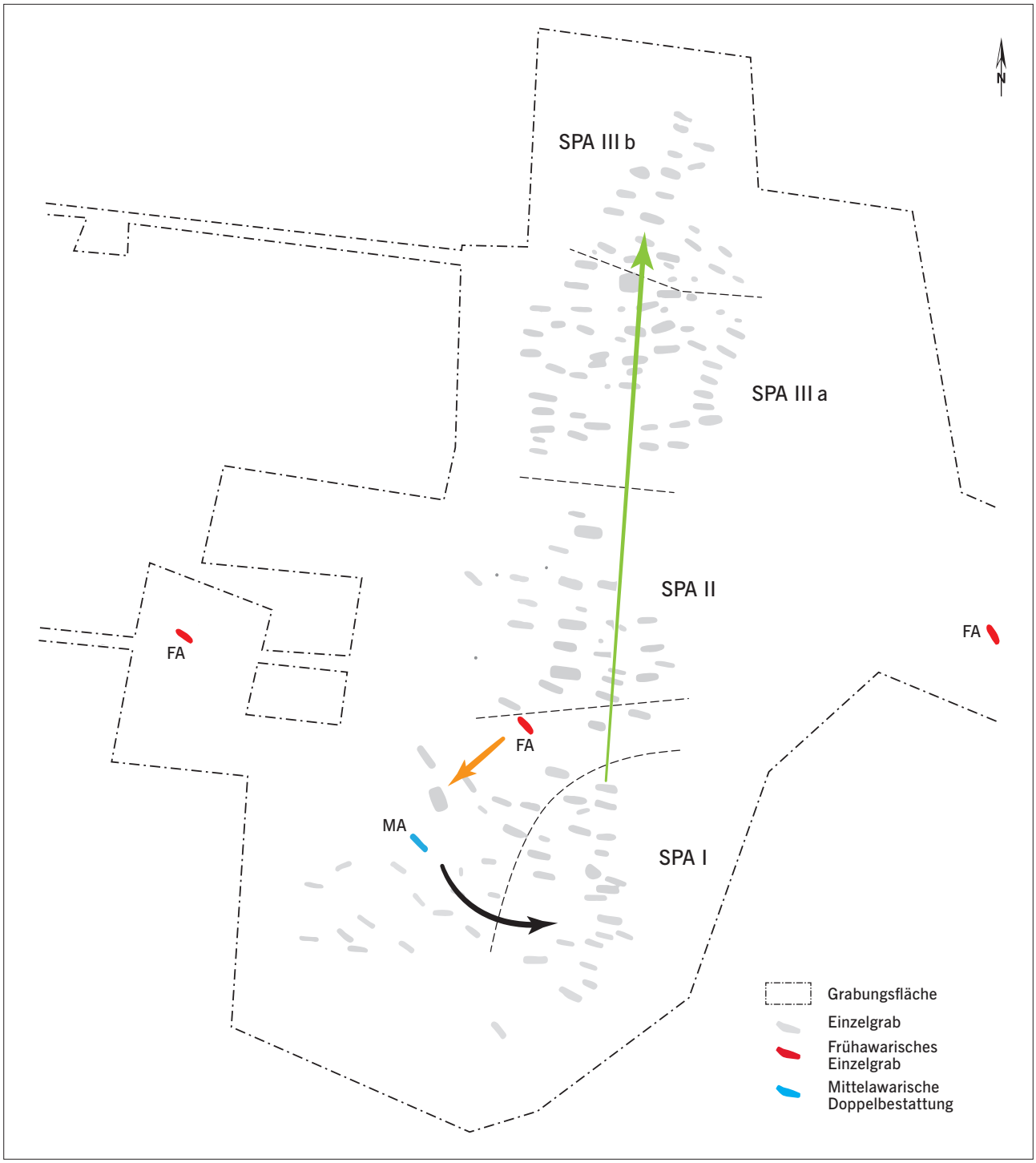


Abb. 21 Leobersdorf. Gang der Belegung der Nekropole. Ohne Maßstab.

Fig. 21 *Leobersdorf. Course of occupation of the necropolis. No scale.*

Die Gene der Krankheitserreger (AHe, AHi)

Darüber hinaus erlauben Methoden der Molekularbiologie Überreste des Erbguts von Krankheitserregern zu identifizieren. Die Anthropologie kann in diesem Zusammenhang Veränderungen am Skelett erkennen, die auf Infektionskrankheiten hindeuten und somit auch die Beprobungsstrategie für die genetischen Analysen aufzeigen. Doch nicht alle Erreger hinterlassen Spuren am Skelett. Falls sie sich im Blut verbreiten, können Reste ihres Erbguts noch nach Jahrhunderten oder sogar Jahrtausenden im Inneren von Zähnen nachgewiesen werden.

Im Rahmen von »HistoGenes« konzentrieren wir uns in diesem Kontext vor allem darauf zu ergründen, welche Infektionskrankheiten zu dieser Zeit vorherrschend waren und wie diese sich innerhalb der Bevölkerung verbreitet haben. Dabei haben wir Erreger wie z. B. Hepatitis B im Blick, welcher bereits in der Bronzezeit und sogar im Neolithikum nachweisbar ist. Hier wird es von Bedeutung sein zu erfahren, ob sich Infektionsketten rekonstruieren lassen und ob sie bestimm-

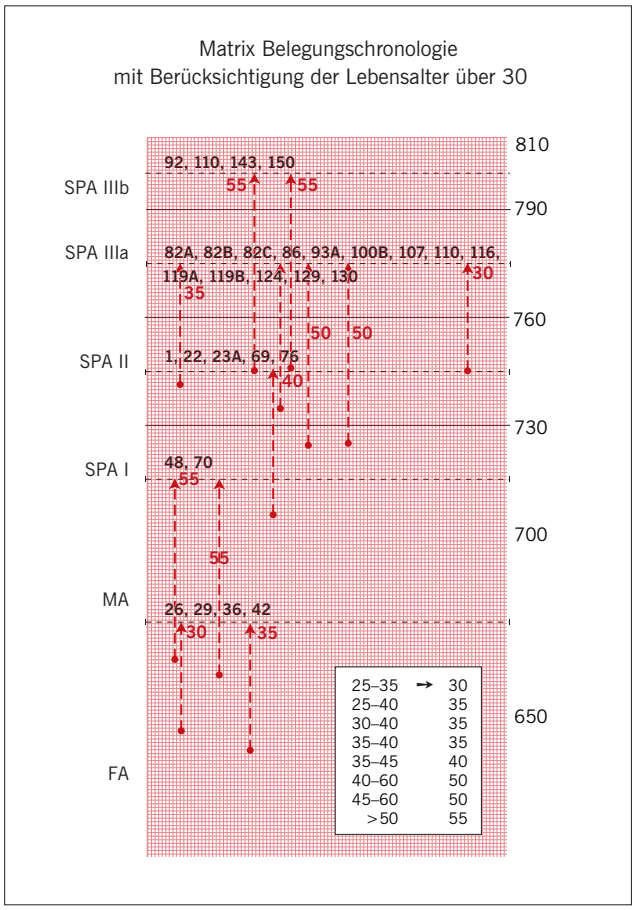


Abb. 22 Leobersdorf. Abstraktes Modell zur Übereinstimmung der Belegungschronologie mit den genetischen Daten. Mit über 30 Jahren Verstorbene werden so in den Gräberfeldbereich ihrer Geburt »versetzt«.

Fig. 22 *Leobersdorf. Abstract model for matching the occupancy chronology with the genetic data. In this way, those who have died over the age of 30 are ›relocated‹ to the cemeteries of their birth.*

ten Mustern innerhalb der Bevölkerung folgen. Dazu ist es von großer Bedeutung, die entsprechenden Ergebnisse mit denen der Archäologie, Anthropologie und Humangenetik zusammenzubringen.

Während Hepatitis B chronisch verläuft, führen andere akut verlaufende Erkrankungen oft schnell zum Tod und können sich epidemisch verbreiten. Entsprechend suchen wir z. B. auch nach dem Erreger der Pest sowie nach Typhus und artverwandten Krankheiten.

Archäogenetik, Archäologie und Geschichte

Geburt und Bestattung (FD)

Die Position eines Individuums im Stammbaum ist ausschließlich von seinem Genom bestimmt, das sich von der Zeugung bis zum Tod nicht verändert. Die Position einer verstorbenen Person im Gräberfeld wird jedoch von den Hinterbliebenen entschieden bzw. hängt sie von Regeln ab, die sich eine Gemeinschaft gegeben hat. Oft wird ein Gräberfeld von einem Zentrum (»Gründergrab«) ausgehend in mehrere Richtungen weiterbelegt, aber es können auch Grabgruppen gebildet werden, z. B. Männer und Frauen getrennt, oder aus nahen Verwandten. Keine zwei Gräberfelder sehen ganz gleich aus. Wird eine Nekropole archäologisch ausgewertet, geht es zunächst hauptsächlich darum herauszufinden, nach welchen Gesichtspunkten die Nekropole entwickelt worden ist. Wir nennen das die »belegungschronologische Analyse«. Dazu werden primär Grabüberschneidungen genützt und Fundtypen kartiert. Am Ende hat man oft hunderte Verbreitungspläne, die man vergleichen kann. Manchmal kommt man zu unsicheren Ergebnissen, z. B. wenn ein Areal mehrfach belegt wird, aber man kann auch Glück haben und erzielt ein klares Bild, wie der Friedhof sukzessive genutzt wurde. Im Idealfall gelingt es dann, jedes einzelne Grab einer chronologischen Stufe zuzuordnen, auch solche, die keine chronologisch relevanten Funde enthalten – einfach aufgrund der Position innerhalb des Friedhofs.

Genau das gilt glücklicherweise für das Gräberfeld von Leobersdorf, das von Süden nach Norden fortschreitend belegt wurde (Abb. 21). Insbesondere die spätawarischen Phasen I bis IIIa und IIIb sind bestens zu verfolgen.

Schwierig wird es jedoch, wenn man die DNA-Daten im Gräberfeldplan kartiert, denn die Menschen sind unterschiedlich alt geworden, manche verstarben bereits im Säuglingsalter, andere hochbetagt. So ein »Methusalem« findet dann möglicherweise seine ewige Ruhe in einem weit fortgeschrittenen Gräberfeldabschnitt, bis zu zwei oder drei chronologische Stufen später als sein verstorbenes Kleinkind. Um also die genetischen Daten und die archäologischen Befunde zu integrieren, brauchte es eine Methode, die chronologische Stellung der Gräber mit den unterschiedlichen Lebensdaten, die von den Anthropologinnen bereitgestellt werden, bildlich darzustellen. Dazu wurde ein abstraktes Modell entwickelt, das quasi die genetischen Stammbäume mit der Gräberfeldanalyse verbindet (Abb. 22).

Dazu trägt man die Gräber auf mm-Papier auf, entsprechend den Ergebnissen der belegungschronologischen Analyse. Dann aber werden Vektoren angesetzt, deren Länge den unterschiedlichen Sterbedaten entsprechen, für 50 Jahre z. B. 50 mm. Ihre Pfeile geben dann in der Matrix die ungefähren Geburtstermine an. Praktisch werden die Gräber grafisch um die Lebensalter verschoben, was im Gräberfeldplan selbst natürlich nicht möglich wäre.

Im Ergebnis zeigt sich dann, welche Individuen etwa zur gleichen Zeit geboren worden sind. Dieses Modell hat sich in der praktischen Arbeit bewährt und wird laufend verbessert, doch funktioniert es nur dort, wo tatsächlich eine systematisch fortschreitende Belegung des Friedhofareals erfolgt ist. So wird es im Fall von Mödling – An der Goldenen Stiege notwendig sein, Teile der Nekropole getrennt voneinander zu analysieren.

Verstehen, was war

Die Archäologie, stets bestrebt große Lebensbilder für die untersuchten Menschengruppen zu entwerfen, hat mit der Archäogenetik die Möglichkeit, ihr Material viel schärfer zu interpretieren. Ein besonderes Beispiel dafür bieten drei Gräber von Leobersdorf, die sich etwa in der Mitte des Friedhofs befinden – die Gräber 21, eine Dreifachbestattung Mann-Frau-Kind, 69 und 71 (vgl. Abb. 3). Sie stechen unter all den spätawarischen Bestattungen durch feuervergoldete Gürtelgarni-

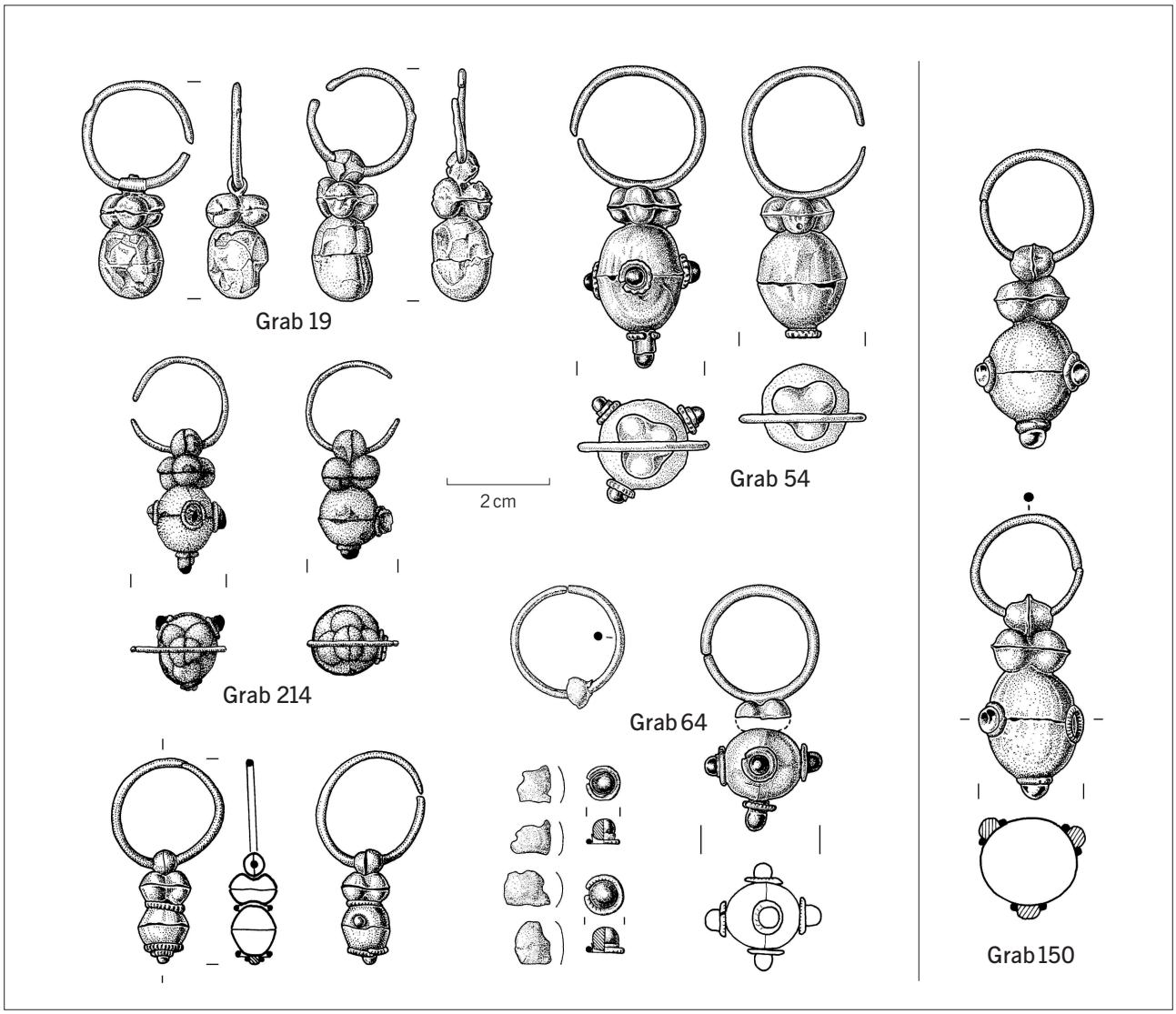


Abb. 23 Mödling – An der Goldenen Stiege. Bommelohrgehänge in Mödling (Auswahl).

Fig. 23 *Mödling – An der Goldenen Stiege. Bobble earrings in Mödling (selection).*

turen hervor, wobei die feinchronologische Abfolge vermuten lässt, dass die Garnitur 69 die zuerst hergestellte war, der die des Grabes 21 folgt. Pikanterweise enthält das Grab 21 nämlich kreisrunde Blechbeschläge, die aber von den gegossenen aus 69 abgeformt (abgeschlagen) worden waren. Die jüngste Garnitur wäre die aus Grab 71, wo eine zweiteilig gegossene Riemenzunge vorliegt, die typologisch bereits in die Spätawarenzeit III gehört. Schon der archäologische Befund lässt vermuten, dass die hier bestatteten Männer eng miteinander verbunden waren. Hier bringen die genetischen Analysen statt bloßen Vermutungen eine klare Aussage (Wang u. a. in Vorbereitung). Die herausstechende Pracht der vergoldeten Garnituren datiert etwa gleich wie die außergewöhnlichen Gräber von Komárno-Schiffswerft (Trugly 1987; Trugly 1993). Das Grab 144 der »Prinzessin« von Mödling – An der Goldenen Stiege ist etwas jünger, gehört der Spätawarenzeit III an, sticht aber ebenfalls aus den sonst üblichen Inventaren heraus. Jedenfalls sieht es so aus, als hätte man gerade in der Mitte und der zweiten Hälfte des 8. Jhs. plötzlich einen größeren Repräsentationsbedarf gehabt. Vermutlich befand man sich bereits in einer Zeit der politischen Umwälzungen, doch wird sich das kaum jemals beweisen lassen, denn schriftliche Nachrichten für diese Periode kennen wir nicht.

Das Projekt »HistoGenes« hat im Grunde genommen erst vor kurzem begonnen. Zwar sind fast alle Proben in Österreich, Ungarn und den anderen kooperierenden Ländern genommen und viele schon sequenziert, aber die sehr aufwendige bioinformatische Datenanalyse ist in vielen Fällen noch nicht abgeschlossen. Aber schon jetzt ist klar: Die zusätzlichen Einblicke in das Leben am Westrand der awarischen Ökumene sind spektakulär und stellen einen qualitativen Sprung in der Forschung dar. Die Publikation der Resultate ist bereits in Vorbereitung (Wang u. a. in Vorbereitung). Obwohl die beiden Gräberfelder bei allen Unterschieden kulturell ziemlich ähnlich sind, unterschieden sich die dort Bestatteten stark in ihrer Herkunft *(ancestry)*. Schon eine 2022 erschienene Studie aus dem »HistoGenes«-Projekt hatte gezeigt, dass die im 7. Jh. im Donau-Theiß-Zwischenstromland bestattete Elite des Awarenreiches überwiegend aus dem östlichen Zentralasien stammte (Gnecchi-Ruscone

u. a. 2022). Nun können wir auch Menschen zentralasiatischer Herkunft erkennen, die bis ins Wiener Becken kamen, und – bei den komplett beprobten Nekropolen – die biologische Verwandtschaft der Bestatteten, die in ausgedehnten Stammbäumen *(pedigrees)* dargestellt werden kann (Gnecchi-Ruscone u. a. in Vorbereitung). Und wir erfahren mehr über die Strategien der Reproduktion, die im Awarenreich gepflegt wurden (s. Beitrag Pohl in diesem Band).

Diese genetischen Informationen können dann wiederum mit den archäologischen und anthropologischen Befunden zusammengebracht und in das historische Bild eingepasst werden. Stammten die Leobersdorfer Awaren letztlich aus dem Reich der Rouran, das die Türken 552 zerstört hatten (Pohl 2018a)? Wie erfolgte in einer recht kleinen Gemeinschaft die Reproduktion, ohne Inzucht zu betreiben? Spielte die engere Verwandtschaft im Alltag eine Rolle? Gab es eine Gruppe, einen Clan, der offenbar privilegiert war? Dazu und zu vielen anderen Fragen, bei denen die menschliche Biologie eine Rolle spielt, wird es bald konkrete Antworten geben.

Es lebe der kleine Unterschied

Ziel archäologischer Forschung ist nicht das Abenteuer oder das Gewinnen von Wertgegenständen, sondern zu verstehen, wie vergangene Gesellschaften gelebt, sich organisiert und gedacht haben könnten. Die Analyse von Gräberfeldern ergibt im Idealfall konkrete Handlungsmuster, die auf Traditionen, gesellschaftliche Regelwerke und – in seltenen Fällen – auch auf kosmologische und religiöse Vorstellungen schließen lassen. Diese Handlungsmuster werden besonders im Vergleich von zwei Bestattungsplätzen deutlich.

Im Fall der Nekropolen von Leobersdorf und Mödling – An der Goldenen Stiege erkennt man viele Ähnlichkeiten im Grabbrauch, aber auch feine Unterschiede, die den damaligen Menschen sicher bewusst und auch wichtig waren – und auch von den anderen Bevölkerungsgruppen in der Umgebung gesehen wurden.

Gleich ist vor allem die Repräsentation von höherrangigen Männern mit Gürtelgarnituren und die Beigabe von Waffen in die Gräber: Reflexbögen, beinverzierte Köcher, Pfeile, selten Schwerter. Bei den Frauen sind es bestimmte Schmucktypen, die in beiden Bestattungsplätzen zur gleichen Zeit auftreten: runde Ohrringe mit Perlenanhängern, später ovale, bestimmte Perlentypen, vor allem die schwarzen Melonenkernperlen, runde Mantelschließen, teils schön verzierte Nadelbüchsen.

Wie es aussieht, konnte sich seit der Mitte des 7. Jhs. im Awarenreich, diesem riesigen Kommunikationsraum, eine recht einheitliche Repräsentationskultur etablieren. Die Sprache der Gürtelgarnituren, Ohrringe, Halsketten und Agraffen wurde überall verstanden. Doch auf der regionalen und lokalen Ebene sehen wir auch das Bestreben, sich von den Nachbarn in kleinen, aber wichtigen Details zu unterscheiden – in der Kleidung aber auch in diversen Praktiken, wie dem Totenbrauchtum. Dabei zeigen sich auch Spielräume für das einzelne Individuum. Wo deren Grenzen zu ziehen waren, könnte zum täglichen Gesprächsstoff gehört haben. Letztendlich erhalten wir so auch Hinweise, wie sich die kollektiven Identitäten ausgedrückt haben und wie weit der Spielraum für Individualismus war.

Auch im Totenbrauchtum sehen wir Unterschiede zwischen den beiden Nekropolen. So kommt in Leobersdorf nur in jedes zehnte Grab ein Tongefäß (mit Inhalt), in Mödling etwa in jedes zweite. In Leobersdorf wird klar zwischen »männlichen« und »weiblichen« Ausstattungen unterschieden. In Mödling dagegen findet man auch in Männergräbern immer wieder Perlen, bisweilen sogar längere Ketten und auch komplexe Ohrringe mit Perlenanhängern sowie Spinnwirtel. Einfache Gräber von Mödling sind daher ohne anthropologische Untersuchung oft nicht als männlich oder weiblich zu bestimmen. Leobersdorfer Männer haben allenfalls einfache Drahtohrringe.

Ganz sicher hatten viele awarische Gegenstände, die wir als Schmuck oder bloß als Tascheninhalt o. Ä. bezeichnen, für die Bestatteten und die Trauergemeinde symbolische oder sogar religiöse Bedeutung, die uns aber meist verborgen bleibt. Doch in manchen Fällen blitzt etwas von der einstigen geistigen Bedeutung durch. So bei drei eisernen Panzerplatten, die in den Gräbern 345, 433 und 464 gefunden worden sind. Höchstwahrscheinlich sollten sie die Verstorbenen vor Unheil schützen, wie einst – ganz praktisch – ihre Besitzer im Kampf. Gleiches könnte auch für mehrere miteinander verbundene Eisenringe gelten, wie sie in mehreren Gräbern von Mödling vorkommen – möglicherweise Fragmente von Ringelpanzern. Allerdings wird es schwierig werden, dafür den Beweis anzutreten. Interessant ist jedoch, dass sich Derartiges, Panzerplatten oder mögliche Teile von eisernen Ringelpanzern, nur in Mödling finden, nicht aber in Leobersdorf. Sicher verfolgte man hier andere Strategien, sich übernatürliche Hilfe zu sichern.

Leobersdorf kennt nur drei sehr gut ausgestattete Männergräber mit vergoldeten Gürtelgarnituren der Spätawarenzeit II. In Mödling stammt das reichste Männergrab 35 aus der Mittelawarenzeit, es enthielt eine feine Gürtelgarnitur aus Silberblech. Herausstechende Frauenbestattungen gibt es in Leobersdorf nicht, dafür haben wir aus Mödling mit der »Prinzessin« in Grab 144 eines der reichsten Frauengräber der Spätawarenzeit insgesamt.

Im Zuge der umfassenden Analyse der Nekropole von Mödling, die derzeit läuft, werden noch viele andere Details lokaler Praktiken zutage treten. Manche davon werden dem Netzwerk geschuldet sein, das die Menschen von Mödling unterhalten haben. Andere werden jedoch eine Subkultur (oder eventuell auch mehrere) erkennen lassen, die Summe von Regeln und Gewohnheiten, die sie von benachbarten Siedlungen (Clans, Haushalten, »Dörfern«) unterscheiden. Indem die Archäogenetik das Beziehungsgeflecht der awarischen Gesellschaft in wichtigen Teilen offenlegt hilft sie zu verstehen, wie die Menschen vor über 1200 Jahren ihr soziales Leben gestaltet haben – bis hinunter auf die Ebene der einzelnen Individuen. Und das ist erst der Anfang.

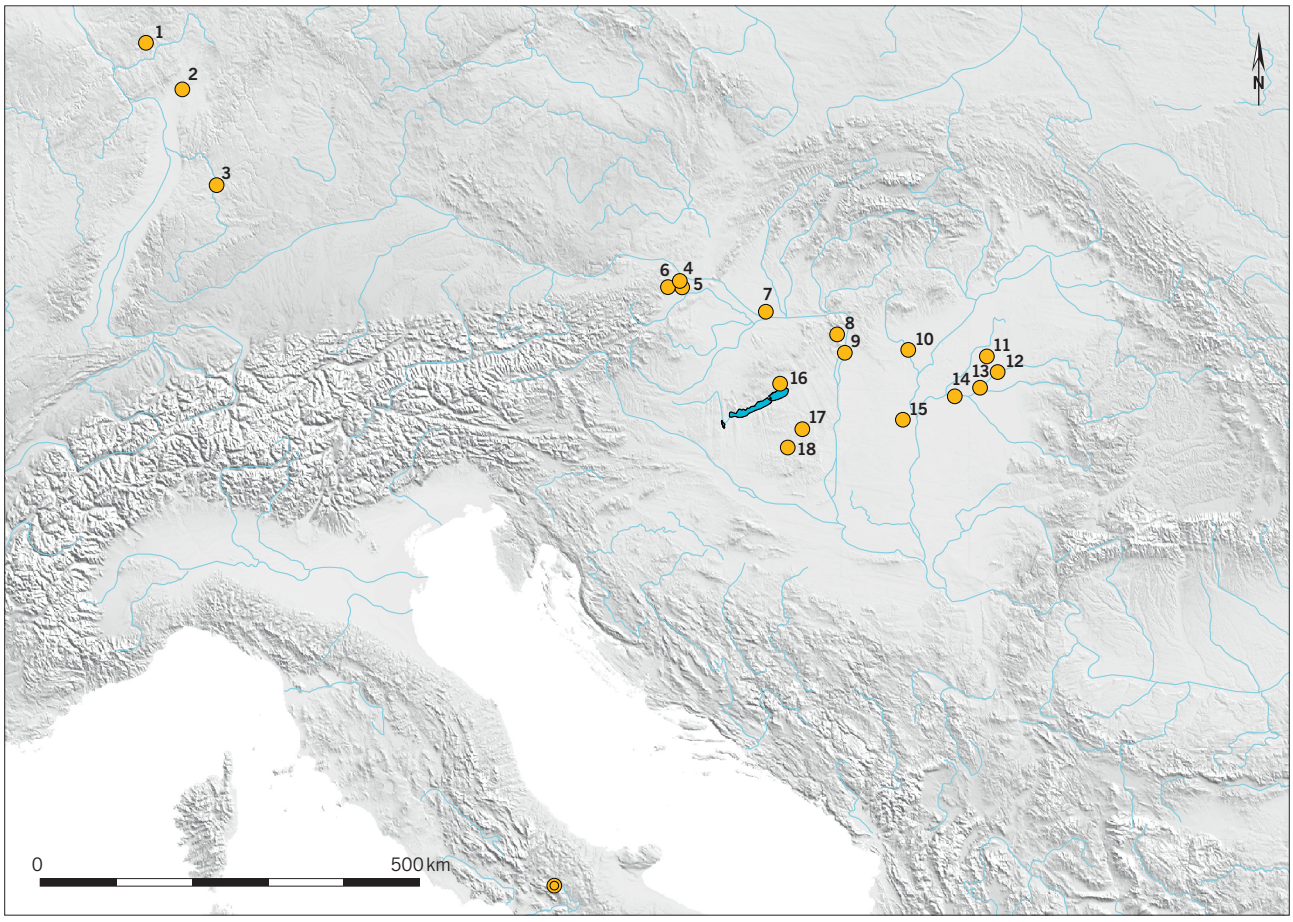


Abb. 24 Bommelohrgehänge mit Dreipaß, teilweise auch mit Glasaugenzier, 2. und 3. Drittel 7. Jh. 1 Mittelhofen (Stork 1997, 307); 2 Frankfurter Domgrab (Hampel 1994, 112–173); 3 Großgartach bei Heilbronn (Steuer 1997, 283); 4 Wien – Csokorgasse (Streinz/Daim 2018); 5 Zwölfaxing (Daim 1977, Taf. 7); 6 Mödling – An der Goldenen Stiege; 7 Holiare (Točik 1968, Taf. LXI,10–11.); 8 Solymár (Török 1994, 9); 9 Csepel-Sziget (Nagy 1998, Taf. 108,41); 10 Alattyán (Kovrig 1963, 27–28); 11 Kaba-belterület (Zoltai 1929, 39–40.); 12 Bakonszeg (Garam 1993, 53 Taf. 3,1); 13 Szeghalom (Ecsedi-Sőregi 1929, 33); 14 Endrőd-Doboskert (Makkay 1989, 137); 15 Gátér (Kada 1906, 135); 16 Balatonfűzfő-Szalmássy telep (Szinyei Merse/Trogmayer 1989, 57); 17 Regöly (Kiss-Somogyi 1984, 130); 18 Dombóvár (Garam 1993, 61 Taf. 33,3–4.); 19 Morrione (Hegewisch 2008, 392 Kat. 198).

Fig. 24 *Bobble ear pendants with trefoil, partially with glass eye ornaments, 2nd and 3rd third 7th century. 1 Mittelhofen (Stork 1997, 307); 2 Frankfurter Domgrab (Hampel 1994, 112–173); 3 Großgartach near Heilbronn (Steuer 1997, 283); 4 Vienna – Csokorgasse (Streinz/Daim 2018); 5 Zwölfaxing (Daim 1977, Taf. 7); 6 Mödling – An der Goldenen Stiege; 7 Holiare (Točik 1968, Taf. LXI,10–11.); 8 Solymár (Török 1994, 9); 9 Csepel-Sziget (Nagy 1998, Taf. 108,41); 10 Alattyán (Kovrig 1963, 27–28); 11 Kaba-belterület (Zoltai 1929, 39–40.); 12 Bakonszeg (Garam 1993, 53 Taf. 3,1); 13 Szeghalom (Ecsedi-Sőregi 1929, 33); 14 Endrőd-Doboskert (Makkay 1989, 137); 15 Gátér (Kada 1906, 135); 16 Balatonfűzfő-Szalmássy telep (Szinyei Merse/Trogmayer 1989, 57); 17 Regöly (Kiss-Somogyi 1984, 130); 18 Dombóvár (Garam 1993, 61 Taf. 33,3–4.); 19 Morrione (Hegewisch 2008, 392 Kat. 198).*

Exkurs 1

Zu den Bommelohrgehängen bzw. Ohrringen mit großem Blechkugelanhänger mit Glaseinlagen oder halbkugelförmigen Buckeln (AB)

Die Bommelohrgehänge in Mödling – An der Goldenen Stiege gehören zu den auffallendsten Schmuckstücken der Frauen (Abb. 23–24).

Es war J. Hampel, der den Ohrring mit großem Kugelanhänger als Erster näher behandelte. Mit Verweis auf das Fundensemble von Szentendre datierte er den Typ in die erste Hälfte des 7. Jhs. und hielt ihn für ein »byzantinisches« Derivat (Hampel 1905, 114; Ormándy 1995, 155). I. Bóna erwähnt Parallelen zu den frühesten Exemplaren im Osten und führt als Belege mittelasiatische Wandmalereien aus dem 6. bis 8. Jh. an, obwohl die Darstellungen typologisch und formal nicht eindeutig sind (Bóna 1980, 39). Allerdings kennen wir aus dem Pontus-Gebiet tatsächlich einige ausgezeichnete Vergleichsfunde zu unseren awarischen Funden. Am nächsten stehen ihnen Ohrringe aus Kamunta, Nordossetien-Alanien, Russland, Kaukasusgebiet (Uvarova 1902).

Die erste feinchronologische Einordnung dieses Ohrringtyps nahm I. Kovrig anhand des Gräberfeldes in Alattyán vor, wo er in der ersten – frühawarenzeitlichen – Gruppe auftritt (Kovrig 1963, 27). Z. Čilinská untergliederte die Bommelohrgehänge anhand ihrer Konstruktion und besonders der Befestigung am Ring. Die mit Glaseinlagen und Halbkugeln verzierten Varianten datierte sie in das zweite Drittel des 7. Jhs., konkret bis 630 (Čilinská 1973, 66–67).

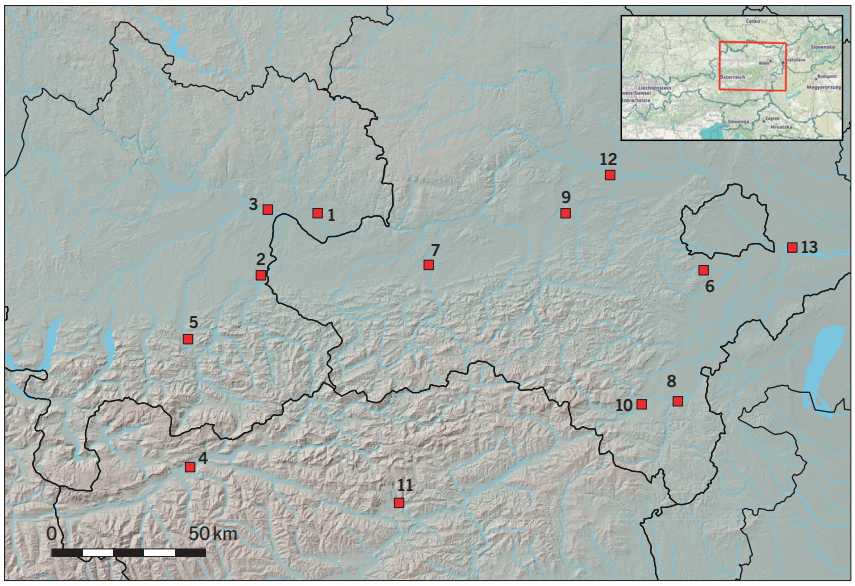


Abb. 25b Verbreitung der Kopfschmuckringe mit Spiralfortsätzen. 1 Auhof (3); 2 Gleink (6); 3 Gusen (1); 4 Hohenberg (3); 5 Kremsdorf (5); 6 Mödling (12); 7 Mühling (2); 8 Pitten (5); 9 Pottenbrunn (26); 10 Pottschach (2); 11 Trofaiach (1); 12 Zwentendorf (1); 13 Zwölfaxing (3).

Fig. 25b *Distribution of headdress rings with spiral extensions. 1 Auhof (3); 2 Gleink (6); 3 Gusen (1); 4 Hohenberg (3), 5 Kremsdorf (5); 6 Mödling (12); 7 Mühling (2); 8 Pitten (5); 9 Pottenbrunn (26); 10 Pottschach (2); 11 Trofaiach (1); 12 Zwentendorf (1); 13 Zwölfaxing (3).*

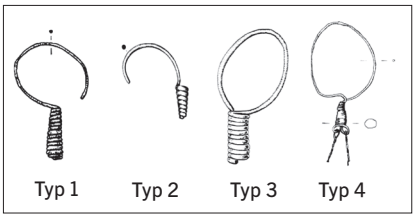


Abb. 25a Typen der Kopfschmuckringe mit Spiralfortsätzen.

Fig. 25a *Types of headdress rings with spiral extensions.*

Die jüngste detaillierte Typologie der Ohrringe mit Kugelanhänger erstellte J. Ormándy (Ormándy 1995, 151–181). Er definierte zwei Haupttypen anhand der Größe der Anhänger, Ohrringe mit großen und kleinen Blechkugelanhängern. Dazu kommen mehrere Varianten aufgrund der Befestigung der Blechkugelanhänger[3].

Betrachtet man die gesamten Fundkomplexe der Bommelohrgehänge mit den Begleitfunden, dann zeigt sich, dass die Mehrheit dieser Ohrringe erstmals im zweiten Drittel des 7. Jhs. auftreten, dann aber während der gesamten zweiten Hälfte des 7. Jhs. getragen werden. Dies wird speziell durch ihre Vergesellschaftung mit Hirsenkornperlen (Zwölfaxing, Városföld) belegt (Lippert 1969; Balogh-Pintér 1998, 104 Taf. 8).

Die einfacheren glatten Varianten, ohne Verzierungen kommen gleichzeitig mit den größeren, aufwändig dekortierten Exemplaren vor, allerdings finden sich die kleineren auch in Männergräbern, während die großen Bommelohrgehänge auf Frauengräber beschränkt bleiben. Sie treten sehr häufig zusammen mit Perlenketten (Augenperlen, aber auch Hirsenkornperlen), mit Eisenmesser, Eisenschnalle, Eisenringen und mit Spinnwirtel auf.

Bemerkenswert ist, dass einige Stücke auch in Süddeutschland und in Italien vorkommen. In einigen Fällen sehen wir eine Tendenz zu länglichen Formen, mit langem, zylindrischem Mittelteil[4]. Auch die langgestreckten, geradezu doppelkonischen Bommelohrgehänge (z. B. Zwölfaxing Gräber 4, 33a, 65) scheinen aus den früh- und mittelawarischen Formen entwickelt worden zu sein (Lippert 1969).

Exkurs 2

Kopfschmuckringe aus Draht mit Spiralfortsatz (SE)

Diese Kopfschmuckringe kommen in den bis dato publizierten österreichischen Gräberfeldern des Frühmittelalters zu 55 Exemplaren vor. Sie lassen sich formal in 4 Typen unterteilen (Abb. 25a–b):

1. Konische Spiralfortsätze, die sich nach unten hin verbreitern
2. Konische Spiralfortsätze, die sich nach unten hin verjüngen
3. Zylindrische Spiralfortsätze
4. Spiralfortsätze, mit einer oder mehreren Schlaufen, in welche Anhängsel eingehängt sind

Die Exemplare vom Typ 4 weisen einen konischen Fortsatz auf, der sich wie Typ 1 nach unten verbreitert, bzw. nach oben verjüngt.

Ein Exemplar aus Gleink ließ sich wegen des Erhaltungszustands nicht eindeutig zuordnen.

Kontext

Auhof: Grab 75, Typ 2; 81, Typ 3; 114, Typ 1[5].
Gleink: Grab 1/1968, Typ ?; 2/1969, 2 Exemplare Typ 1; 4a/1991, Typ 1; 8/1969, 2 Exemplare Typ 1[6].
Gusen: Grab 157B, Typ 1[7].
Hohenberg: Grab 5, Typ 1; 27, Typ 4[8].

3 Ormándy 1995, 155–163. Unsere bezeichnete er als »Untertyp Tószeg«, vgl. Ormándy 1995, 158–159.

4 Weismain-Selitzen (Schwarz 1984, Abb. 54); Kirchheim bei München (Christlein 1981, Abb. 136).

5 Tovornik 1985.
6 Russ 2016.
7 Tovornik 1986.
8 Nowotny 2005.

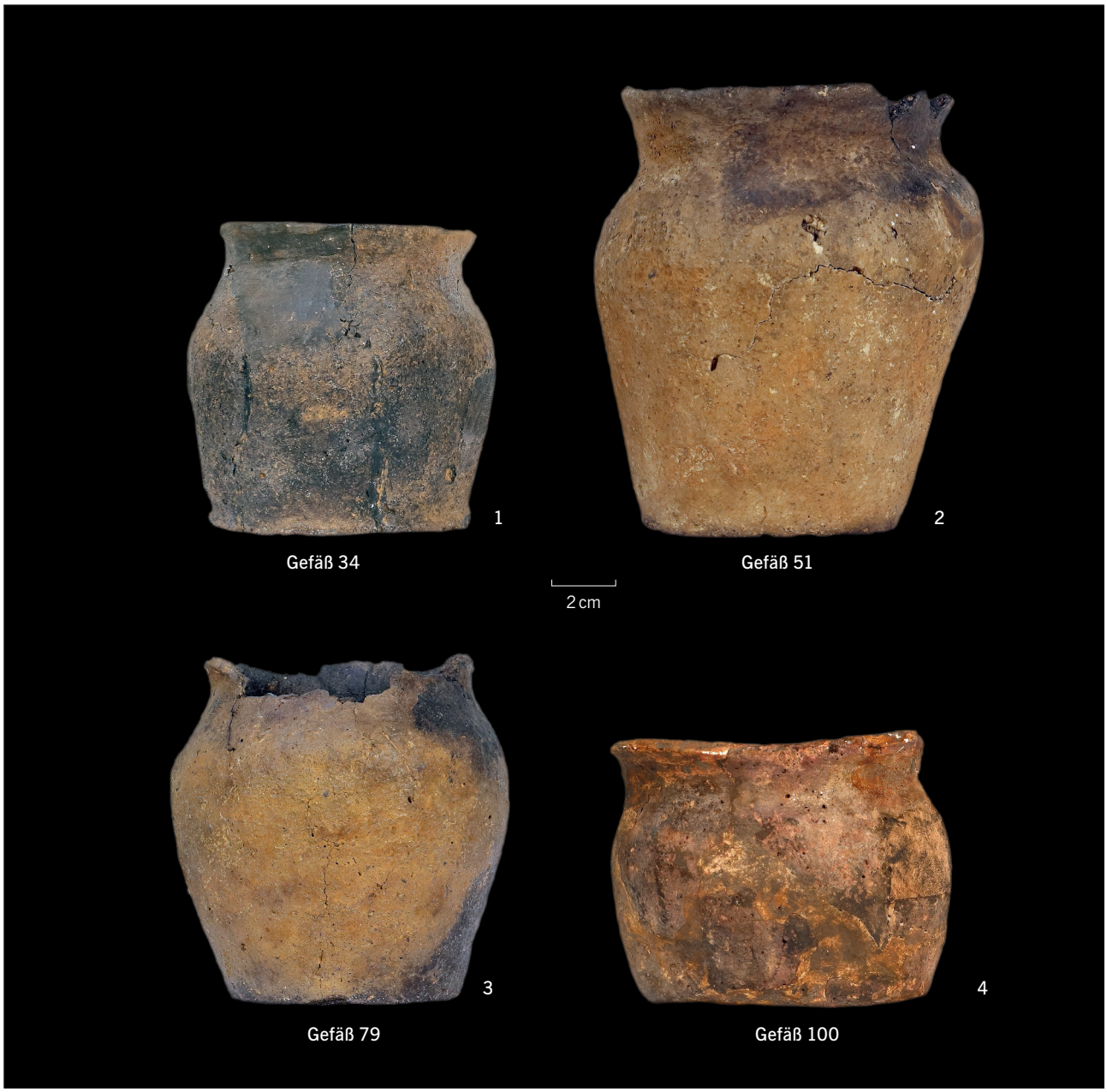


Abb. 26 Mödling – An der Goldenen Stiege. Scherbentyp C nach R. Sauer. 1 Grab 34; 2 Grab 51; 3 Grab 79; 4 Grab 100.

Fig. 26 *Mödling – An der Goldenen Stiege. Ceramic type C according to R. Sauer. 1 grave 34; 2 grave 51; 3 grave 79; 4 grave 100.*

Kremsdorf: Grab 11/1960, Typ 3; 25/1960, 2 Exemplare Typ 3; 30/1960, 2 Exemplare Typ 1[9].
Mühling: Grab 11, 2 Exemplare Typ 1[10].
Pitten: Grab 32, 2 Exemplare Typ 1; 79, 2 Exemplare Typ 1; 83, Typ 2[11].
Pottenbrunn: Grab 4, Typ 1; 11, 2 Exemplare Typ 1; 14, Typ 2; 17, Typ 4; 22, Typ 4; 23, Typ 3; 29, 2 Exemplare Typ 3; 34, 2 Exemplare Typ 1; 41, Typ 1; 43, Typ 1; 43, Typ 1; 46, 2 Exemplare Typ 1; 47, 2 Exemplare Typ 1; 48, Typ 3; 50, Typ 1; 56, 2 Exemplare Typ 1; 92, Typ 3; 94, Typ 1; 102, Typ 1; 103, Typ 1; 195, Typ 1[12].
Pottschach: Grab 8, 2 Exemplare Typ 3[13].
Trofaiach: Grab 4, Typ 1[14].
Zwentendorf: Grab 193, Typ 1[15].
Zwölfaxing: Grab 39, Typ 1; 70, Typ 2 (massiv)[16].

9 Hausmair 2016.
10 Friesinger 1974.
11 Friesinger 1977.
12 Petschko 2013.
13 Friesinger 1977.
14 Gutjahr 2000.
15 Heinrich 2001.
16 Lippert 1969.



Abb. 27 *Mödling – An der Goldenen Stiege. Gefäße mit Karbonatsandmagerung (Scherbentyp B nach R. Sauer). 1 Grab 19; 2 Grab 93; 3 Grab 135; 4 Grab 242; 5 Grab 353.*

Fig. 27 *Mödling – An der Goldenen Stiege. Vessels with carbonate sand tempering (ceramic type B according to R. Sauer). 1 grave 19; 2 grave 93; 3 grave 135; 4 grave 242; 5 grave 353.*



1

Gefäß 290



2

Gefäß 418

2 cm



3

Gefäß 311



4

Gefäß 422



5

Gefäß 144



6

Gefäß 140

Exkurs 3

Mineralogisch-petrografische Analysen von Gefäßen aus der Nekropole Mödling – An der Goldenen Stiege (RS, FD, KR)

Die große Anzahl der Gefäße aus dem Gräberfeld Mödling – An der Goldenen Stiege und insbesondere ihre Vielfalt gaben den Ausschlag, eine größere Anzahl davon eingehend mineralogisch-petrografisch zu untersuchen.

Zunächst erfolgte die Entnahme von Proben aus den Wänden der ausgewählten Töpfe, von denen dann Dünnschliffe und – wenn möglich – Präparate für Schwermineralanalysen und weitere chemisch-mineralogische Untersuchungen angefertigt wurden. Unter dem Polarisationsmikroskop wurden dann die feine Keramikgrundmasse und die verschiedenen sandigen Beimengungen wie Quarz, Glimmer, Feldspäte, Kristallingesteinsbruchstücke, Karbonate, Schwerminerale, zerkleinerte Keramikfragmente sowie pflanzliche Beimengungen etc. sowohl qualitativ als auch quantitativ analysiert.

Die awarenzeitliche Keramik ist für sich genommen nur sehr ungenau zu datieren, doch finden wir in Mödling viele Gefäße, die als Beifunde feinchronologisch empfindliche Gegenstände haben, hauptsächlich Schmuck: Ohrringe, Halsketten, Fingerringe, Mantelschließen oder Gürtelgarnituren bzw. Teile davon. So ist es möglich, die Mödlinger Keramik noch vor der laufenden feinchronologischen Auswertung der gesamten Nekropole in Gruppen einzuteilen, den petrografisch erkannten Scherbentypen gegenüberzustellen und gemeinsam historische Schlüsse daraus zu ziehen (Sauer/Daim in Vorbereitung; Richter in Vorbereitung).

In der Mittelawarenzeit (zweite Hälfte 7. Jh.) kommt zunächst ausschließlich Keramik in die Gräber, die ohne drehbare Unterlage hergestellt wurde. Wir bezeichnen sie hier etwas unscharf als »handgefertigte Ware«. Dazu verwendete man offenbar einen lokal anstehenden Ton, dem man aber typischerweise zermahlenen Keramikgrus zusetzte. Diese Proben wurden unter dem petrografischen Scherbentyp C zusammengefasst. Auf Grund von Unterschieden in der Zusammensetzung der zugesetzten Keramikpartikel können diese noch weiter untergliedert werden (Subtypen C1–C2b). Vereinzelt finden sich im Scherben auch Hinweise auf Reste pflanzlicher Beimengungen, die aber vermutlich bereits natürlich in der verwendeten Keramikmasse enthalten waren. Manchmal wurde der Rand mit umlaufenden Eindrücken oder Einschnitten verziert. Beispiele sind die Gefäße aus den Gräbern 34, 51, 79 und 100 (100 wurde eindeutig mit zerkleinerter, karbonatreicher Keramik des Scherbentyps B) gemagert (Abb. 26).

Bald jedoch taucht hier auch eine sehr qualitätsvolle Keramik auf, dünnwandig auf einer drehbaren Unterlage hergestellt, von der sich öfters am Boden der Abdruck einer Achse zeigt (»nachgedrehte Keramik«). Sie zeigt ein S-förmiges Profil und sticht durch die rot-schwarze Oberfläche mit zahlreichen weißen Einsprengseln hervor. Bei diesen dekorativen weißen Pünktchen handelt es sich um überwiegend intentionell der Keramikmasse beigefügten groben Karbonatsand. Im Dünnschliff wurden Körner bis über 3 mm Durchmesser beobachtet (= petrografischer Scherbentyp B). Dieser Sand besteht aus Dolomitkörnern, die teilweise stärker alteriert und in Kalzit umgewandelt sind, groben Kalzitfragmenten und Kalksinterresten. Dieses Material konnte man jedenfalls leicht aus den, in der unmittelbaren Nähe anstehenden, verwitterten Bereichen des Hauptdolomits (= geologische Formation der Obertrias) durch Sieben gewinnen und dann direkt als Zusatz verwenden. Die verwendeten Tone könnten aus Residuallehmen, wie sie auch in Verwitterungsböden über und an den Randbereichen der Hauptdolomitzone vorkommen, stammen. Eine detailliertere Untersuchung und Vergleiche zu möglichen verwendeten Rohstoffen werden derzeit noch vorgenommen und geprüft.

An den Scherbenoberflächen sind diese Karbonatpartikel durch Auslaugung bzw. Verwitterung teilweise völlig herausgelöst, sodass die Keramikoberflächen dieses Typs meist einen löchrigen Eindruck machen. Diese Löcher stellen daher Hohlformporen der ursprünglich vorhandenen, später jedoch aufgelösten Karbonatkörner dar. Außerdem führte das zu einem Substanzverlust. Die dünnwandigen Töpfe verloren dadurch noch weiter an Gewicht und wiegen dann tatsächlich oft bloß die Hälfte von den harten, schweren Keramiken des petrografischen Scherbentyps A. Beispiele für diesen Gefäßtyp stammen aus den Gräbern 19, 93, 135, 242 und 353 (Abb. 27).

Zu Beginn des 8. Jhs. finden wir weiter handgefertigte Keramik aus lokalen Quellen. Der abgebildete Topf stammt aus Grab 290 (petrografischer Scherbentyp C2; Abb. 28,1).

In die Spätawarenzeit II (Mitte 8. Jh.) datiert der Topf aus Grab 418 (petrografischer Scherbentyp D; Abb. 28,2). Aufgrund der typischen petrografisch-mineralogischen Zusammensetzung kann dieser Scherbentyp nicht in Mödling hergestellt worden sein. Die Magerungspartikel bestehen typischerweise häufig aus diversen Feldspäten und ungeschieferten Kristallingesteinsbruchstücken, die meist reichlich Rutil führen. Diese Zusammensetzung der Magerungskörner kann der-

Abb. 28 (linke Seite) Mödling – An der Goldenen Stiege. 1 Gefäß aus dem Grab 290 (Spätawarenzeit I), Scherbentyp C nach R. Sauer; 2 Gefäß aus dem Grab 418 (Spätawarenzeit II). Auch dieses Gefäß wurde nicht in Mödling hergestellt. Scherbentyp D nach R. Sauer; 3 Gefäß aus Grab 311 (Spätawarenzeit III). Magerung mit Silikatsand, wohl Herstellung in einer Manufaktur östlich von Mödling. Scherbentyp A nach R. Sauer; 4 Gefäß aus Grab 422. Silikatreicher Ton, nicht aus Mödling. Scherbentyp A1 nach R. Sauer; 5 Grab 144. Die »Prinzessin« mit ihrer überreichen Grabausstattung bekam »nur« ein einfaches handgeformtes Gefäß mit. Scherbentyp C nach R. Sauer; 6 Grab 140 eines privilegierten Mannes mit einem einfachen handgeformten Gefäß. Scherbentyp C nach R. Sauer.

Fig. 28 (left page) *Mödling – An der Goldenen Stiege. 1 vessel from grave 290 (Late Avar Period I), ceramic type C according to R. Sauer; 2 vessel from grave 418 (Late Avar Period II). This vessel was also not made in Mödling. Ceramic type D according to R. Sauer; 3 Vessel from Grave 311 (Late Avar Period III). Tempering with silicate sand, probably made in a factory east of Mödling. Ceramic type A according to R. Sauer; 4 Vessel from grave 422. Clay rich in silicate, not from Mödling. Ceramic type A1 according to R. Sauer; 5 Grave 144. The »princess« with her lavish grave furnishings was »only« given a simple hand-made vessel. Ceramic type C according to R. Sauer; 6 Tomb 140 of a privileged man with a simple hand-made vessel. Ceramic type C according to R. Sauer.*

zeit mit keiner anderen Probe aus dem analysierten Material von Mödling verglichen werden. Als Rohstoff kommt wohl nur ein Verwitterungslehm über Kristallin infrage.

Ähnliches gilt auch für andere Gefäße der Spätawarenzeit III (drittes Drittel 8. Jh.), die aus einem Ton gebrannt wurden, der eine charakteristische, siliziklastische Sandmagerung mit zahlreichen metamorphen Kristallingesteinsbruchstücken, meist Quarzite, Gneis und Glimmerschiefer, aufweist, während Karbonatkörner selten sind oder überhaupt fehlen. Beispiele: Grab 311 (petrografischer Scherbentyp A; Abb. 28,3), 422 (petrografischer Scherbentyp A1; Abb. 28,4). Auch die hier verwendeten Rohstoffe kommen nicht lokal bei Mödling vor und könnten am ehesten aus dem Raum oder den Einzugsgebieten des Leithagebirges oder Rosaliengebirges, o. Ä., stammen.

Alle diese Töpfe wurden unter Anwendung von langsamen Drehscheiben oder drehbaren Unterlagen hergestellt. Man formte den unteren Teil des Topfes mit der Hand, glättete aber die Außenseite, vor allem die Schulter und den Rand mit einem Formholz. Häufig wurde der Topf dann noch mit Linienbündel, Wellenbändern oder Kammeinstichen verziert. Die Töpfe wirken alle sehr ähnlich, doch scheint sich eine Tendenz zu immer kräftiger ausgeprägten Mundsäumen zu zeigen. Da sich alle diese Töpfe aus dem Gräberfeld von Mödling gleichen, zugleich hart gebrannt sind und einen robusten Eindruck machen, könnten sie in einer Art Manufaktur hergestellt worden sein, die dann aber sicher einen weiteren Abnehmerkreis beliefert hätte. Dies muss noch in einer größeren Studie geprüft werden.

Gleichzeitig werden aber in Mödling in der Spätawarenzeit III (drittes Drittel 8. Jh.) auch noch (oder wieder?) handgefertigte Töpfe verwendet. Diese haben sicher nicht als minderwertig gegolten, findet man sie doch gerade in einigen sehr gut ausgestatteten Bestattungen. So hat man auch der »Prinzessin« in Grab 144 die Speise in einem derartigen Gefäß mitgegeben (Scherbentyp C, Subtyp C2b; Abb. 28,5) Ein weiteres Beispiel ist das Gefäß aus Grab 140 (Scherbentyp C; Abb. 28,6). Es wird begleitet von einer typischen Gürtelgarnitur der Spätawarenzeit III.

Was lässt sich aus diesem Befund schließen? Könnte es sein, dass man der »Massenware« aus der Fabrik die »persönlichere« handgefertigte vorgezogen hat? Könnte die Herstellung eines Grabgefäßes Teil des Bestattungsrituals gewesen sein?

Im Gräberfeld von Leobersdorf fand sich nur in jedem zehnten Grab ein Gefäß. Umso wichtiger sind die Töpfe aus den Bestattungen 9 und 91, die eine eindeutige äußerliche Verwandtschaft mit den Mödlinger Gefäßen der Scherbengruppen A und C zeigen. Beide stammen aus der Spätawarenzeit. Grab 9 wurde in der Spätawarenzeit II angelegt (Mitte 8. Jh.), das Grab 91 ist durch die Lage im nördlichsten Gräberfeldabschnitt und ovale Ohrringe in die Spätawarenzeit III (drittes Drittel 8. Jh.) datiert. Wenn die Annahme richtig ist, dass wir mit den Gefäßen des Scherbentyps A, C und D eine regelrechte Keramikwerkstätte fassen können, so könnte diese auch Leobersdorf beliefert haben. Die beiden genannten Töpfe aus Leobersdorf werden in allernächster Zeit mineralogisch-petrografisch untersucht.

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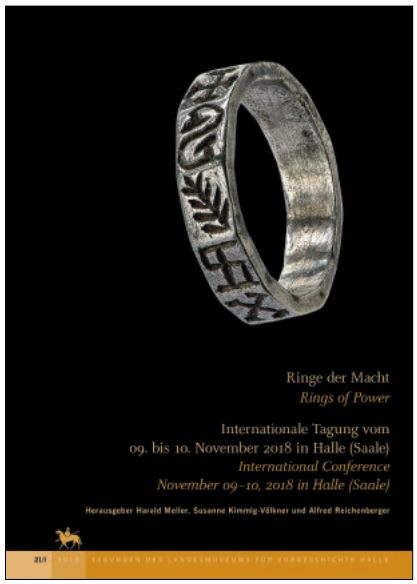
Bislang erschienene Bände in der Reihe »Tagungen des Landesmuseums für Vorgeschichte Halle«

Die Reihe der Tagungsbände des Landesmuseums wurde 2008 ins Leben gerufen. Anlass dazu war die Konferenz »Luthers Lebenswelten«, die im Jahr 2007 in Halle (Saale) ausgerichtet wurde. Bereits der zweite Tagungsband widmete sich mit dem Thema »Schlachtfeldarchäologie« dem Mitteldeutschen Archäologentag, der seit 2008 jährlich vom Landesamt für Denkmalpflege und Archäologie Sachsen-Anhalt veranstaltet und zeitnah publiziert wird. Dem großen Anteil internationaler Autorinnen und Autoren entsprechend, erscheinen viele Beiträge dieser Reihe in englischer Sprache mit deutscher Zusammenfassung.

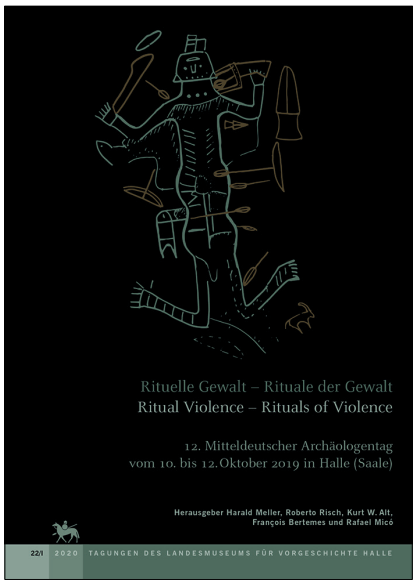
Mit dem zuletzt erschienenen Tagungsband konnten die Vorträge der Internationalen Konferenz »Grenzüberschreitungen – Reiternomaden in Mitteleuropa, ihre östlichen Wurzeln und Verbindungen« in zahlreichen Artikeln renommierter Forscher verschiedenster Fachdisziplinen vorgelegt werden.



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Band 24



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Zwischenmenschliche Beziehungen bilden seit jeher die Grundlage gesellschaftlichen Zusammenlebens. Der Verwandtschaft – ob biologisch oder sozial – kommt dabei eine ganz besondere Bedeutung zu. In der Archäologie konnten diese immateriellen Verbindungen bisher nur selten zweifelsfrei nachgewiesen werden. Die Archäogenetik hat jedoch in den letzten Jahren Methoden und Verfahren entwickelt, die es bei guter DNA-Erhaltung erlauben, den Grad genetischer Nähe zwischen zwei Menschen zu bestimmen, die in der Vergangenheit gelebt haben.
Die hier gesammelten Beiträge schöpfen ihr Wissen zum Thema Verwandtschaft aus Anthropologie, Archäologie, Genetik sowie den Geschichts- und Sozialwissenschaften. Sie verdeutlichen anhand von unterschiedlichen Fundplätzen, welche Rückschlüsse die Integration der neuen naturwissenschaftlichen Erkenntnisse einerseits ermöglichen, zeigen andererseits aber auch die Grenzen bei der Interpretation von (prä-)historischen Gesellschaften auf.

Relationships between people have always been the basis of social coexistence. Kinship – whether it is biological or social – has a very special significance. In archaeology, these immaterial connections have rarely been proven beyond doubt. In recent years, however, the field of archaeogenetics has developed methods and techniques that, given good DNA preservation, make it possible to determine the degree of genetic relatedness between two people who lived in the past.
The studies collected in this book, draw their knowledge on kinship from the fields of anthropology, archaeology, genetics, and the historical and social sciences. They demonstrate, on the basis of various sites, which conclusions the integration of new scientific insights allow, but also point out the limitations in the interpretation of (pre-) historic societies.

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