

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

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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 eingehirerate 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 1980s¹. 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; Jorgensen 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 ritual². 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 structures³. 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, dis-

crete, 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 kinship⁴. 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 complexes⁵ 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 graves⁶; 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 1970s⁷. 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 traits⁸ 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 Corruccini 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 possible⁹. 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 studies¹⁰. Similar to numerous morphological characteristics, the anatomical traits of teeth (e.g., size, shape, number) vary within populations quasi-continuously¹¹, 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 microevolutionary 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 individ-

dual 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 sub-groups 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 settlement¹⁴.

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 microevolutionary 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. Vach¹⁵. 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 acceptance¹⁶. 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 years¹⁷.

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 samples¹⁸. 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; Jorgensen 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; Johnson/Paul 2016; Sciumi/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; Corruccini 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.
		<i>F</i>	<i>F</i>		(%)
<i>t</i> ₁ :	lingual marginal ridge 42 41 31 32	3	0	120	2.5
<i>t</i> ₂ :	accessory ridge 15 25	7	1	44	18.2
<i>t</i> ₃ :	over developed cusps dist. -ling. 17 27	5	2	106	6.6
<i>t</i> ₄ :	number of cusps ≥ 5 47 37	6	2	125	6.4
<i>t</i> ₅ :	shovel-shaped incisors (strong mongoloid form) 12 22	7	2	77	11.7
<i>t</i> ₆ :	accessory cusplets of the mesial marginal ridge 16 26	4	1	66	7.5
<i>t</i> ₇ :	abnormal size of roots <i>molars</i>	2	1	179	1.7

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

<i>t</i> ₁	<i>t</i> ₂	<i>t</i> ₃	<i>t</i> ₄	<i>t</i> ₅	<i>t</i> ₆	<i>t</i> 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

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

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 gives 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 $G(T)$.

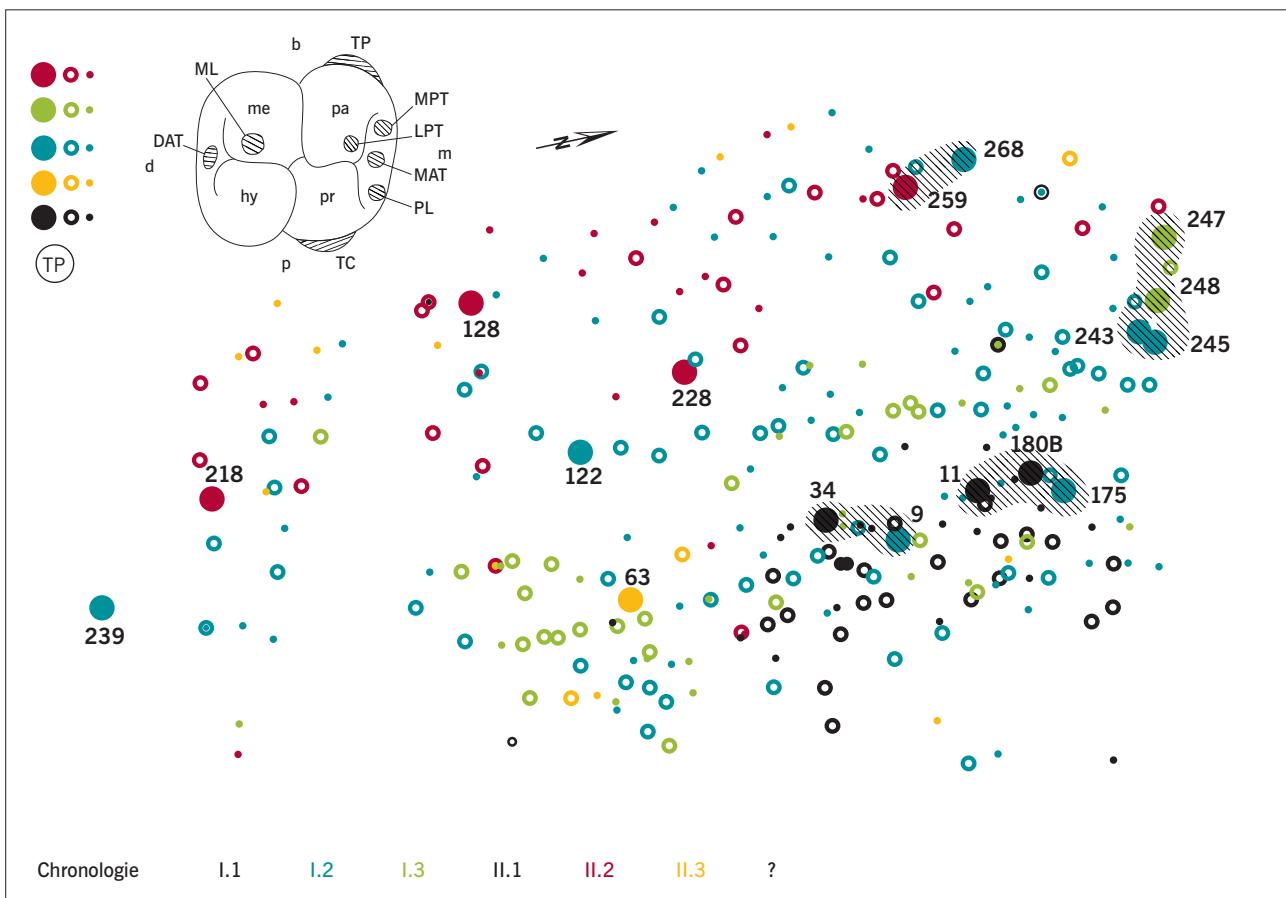


Fig. 1 Example of the spatial distribution of a trait with strikingly increased frequency in the early medieval population of Eichstetten, Breisgau-Hochschwarzwald district (Germany) (land parcel: Wannenberg). The trait, an accessory cusp on one molar, a so-called Tuberculum paramolare (TP) is observed 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 Merkmalsschäften erkläbar (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 (Mitnik 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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Source of figures

1 modified after Sasse 2001,
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Tab. 1 after Vach/Alt 1993, 31,1

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