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Human biological variation at Nagada: an analysis of dental morphological traits

Abstract

Cemetery T at Nagada has been postulated as being the internment site of a Predynastic royal or ruling elite due to its small, localized area and the richness of its burial goods. In order to examine possible biological differentiation between the individuals buried in cemetery T and those buried in other, possibly lower status, cemeteries at Nagada, non-metric dental morphological data were analyzed using the Mean Measure of Divergence statistic. Results indicate that cemetery T shows some biological distinction from both Cemetery B and the Great cemetery separately and from a pooled sample of all three cemeteries. The size of the difference supports the archaeological interpretation that Cemetery T represents a ruling or elite segment (or lineage) of the local population at Nagada, rather than a ruling or elite immigrant population.

Introduction

The Upper Egyptian site of Nagada was excavated by Petrie in 1895 and, along with nearby Ballas, served as the basis for his pottery sequence dating system. Nagada therefore has become the standard typological reference for the Predynastic era. The site includes at least four cemeteries, which are commonly designated B, G, T, and the Great cemetery (Davis 1983). Cemetery T often has been seen as an elite cemetery because of its small size and the richness of the material culture found in its burials. Petrie attributed the burials to the wealthy citizens of Nagada (Petrie & Quibell 1896), while Hoffman (1979) proposed a comparative connection between cemetery T and the royal tombs of First Dynasty Abydos. Alternatively, Davis suggested that, although cemetery T might represent the burials of a special status group, the material culture included no evidence of a royal elite. Cemetery B, for example, is similarly small, localized and contains some rich deposits, making it equivalently likely as a status differentiated burial ground (Davis 1983: 27).

That cemetery T may be an elite cemetery raises the possibility that the individuals buried there may be biologically distinct from the general population; a ruling elite may consist of a family lineage, or may have come from outside the local population. The purpose of this study, therefore, is to employ biological data, namely non-metrical morphological traits of the teeth, to address the question of whether any degree of biological differentiation can be detected among skeletal samples obtained from cemeteries B, T, and the Great cemetery.

Biological differentiation often results when geographic barriers separate populations, but cultural factors, such as religious affiliation, linguistic group, and social structure, also tend to isolate human groups into regional and local breeding populations, which can lead to the divergence of these groups in genetic and phenotypic features. The resulting variability can be used to solve questions about the biocultural history of human groups. Populations that share similar morphogenetic attributes, for example, are interpreted as being more closely related than are populations that exhibit numerous differences.

Biological distance studies of Egyptian skeletal populations began in the 1960s, with the development of a method for assessing genetically controlled non-metric traits of the cranium (Berry & Berry 1967), and for using these to evaluate the relationships of prehistoric populations (Berry et al. 1967). Prior to this time, most studies were based on measurements of the cranium and adopted a racial typological approach for interpretation. Although more sophisticated statistical measures have improved the interpretive possibilities from metric data (Keita 1990; 1992), many researchers are reluctant to rely on such data since cranial shape has been shown to be affected by non-genetic variables, such as chewing stresses associated with diet (Carlson 1976; Carlson & Van Gerven 1979; Van Gerven 1982; Van Gerven et al. 1976). Certain properties of dental morphological traits make them ideally suited for biological distance analyses; i.e., they are usually independent of each other as well as independent of age and sex, there is a high genetic component in occurrence and expression, and the amount of intergroup variation in trait frequencies is high (Irish & Turner 1990).

Teeth also are often better preserved than are bones and are rarely altered by postmortem diagenesis, so data can be obtained from incomplete, fragmentary or distorted remains that are unsuitable for study by other methods. The best known dental morphology studies are those of ancient and modern Asian and American populations, from which the manner and timing of the peopling of the Americas from Asia has been modelled (Turner 1983; 1986a, b). The advantage of using dental morphology traits as opposed to serological or other genetic traits is that data can be obtained easily from ancestral populations, i.e., skeletal remains. DNA analysis of preserved soft tissues, bone, and teeth is an exciting development in the study of genetic relationships, but the current costs of analyses prevent their widespread application to skeletal populations at present; for the time being they will be most useful in examining the familial relationships among

a few individuals whose proposed affinity derives from historical allusions or their burial as a group.

The most common dental morphological traits take the form of accessory ridges, tubercles and cusps that can be seen macroscopically on the surfaces of the tooth crowns. Some characteristics of tooth roots also are important for biological distance analyses and usually are manifested as variations in root number; these may be difficult to score without the benefit of radiographs if the tooth is held fast in its socket, as multi-rooted premolar and molar teeth tend to be, and thus are less widely discussed in the dental anthropological literature.

Certain crown and root traits, such as incisor shovelling and the expression of Carabelli's cusp, vary so widely in their frequencies in some geographically separated populations that they have proved to be useful in the forensic investigation of an individual's ethnic ancestry. Not all populations are so strongly divergent, however, and distance statistics are used to estimate the relative similarities among less divergent groups; it is generally agreed that appropriately selected dental traits can discriminate among tribal groups, for example.

There are four evolutionary forces that may be invoked in explaining the variation in dental morphology among different populations: mutation, natural selection, gene flow, and genetic drift. Mutation usually cannot explain the differences in the major morphological features of the teeth because these features have long evolutionary histories, extending back to hominid, or perhaps even hominoid, ancestors. An exception is a rare and very distinctive trait, termed the Uto-Aztec premolar, which occurs only among Indians of the New World and may reflect a specific mutation that occurred after the peopling of the Americas from Asia. Natural selection explanations for dental morphological traits propose that certain traits enhance the size and shape and hence the masticatory efficiency of teeth that are subjected to high levels of attrition and use as "tools". Shovel-shaped incisors, for example, have been cited as an example of morphological variation that might have been selected for in populations in which the anterior teeth were subjected to unusual functional stress. Such selective pressures have not been demonstrated, however, and the morphological variants used in this analysis are assumed to be adaptively neutral. Gene flow often is referred to alternately as migration. Rates of gene flow that have been calculated from dental trait frequencies have been shown in many cases to be close to those obtained from gene frequencies such as blood group data, and consistent with known history. Genetic drift, the accumulation of random genetic changes in small populations, probably has played a significant role in human dental differentiation as a result of both colonization events and cultural definitions of appropriate mates within subgroups of a population.

Material and methods

Skeletal samples from Cemeteries B and T and the Great Cemetery were examined at the Department of Biological Anthropology at Cambridge Univer-

sity: 38 skulls from Cemetery B, 26 skulls from Cemetery T, and 67 skulls from the Great Cemetery. Forty-three morphological traits of the permanent dentition were scored by Lovell in accordance with the criteria set out by Turner and colleagues (1991). The data collection took place over a period of one month. Intraobserver variation was assessed by repeated scoring of 25 tooth-trait combinations in a randomly selected subsample of 20 individuals. All available teeth were scored individually, but only the antimere showing the highest degree of trait expression was used in the analysis, according to the individual count method of Scott (1980). Unfortunately, many of these tooth-trait combinations had to be eliminated from the present study due to the small samples of observable teeth within the cranial samples for each cemetery; premortem tooth loss due to periodontal disease or infectious abscessing, severe tooth wear, and postmortem tooth loss and breakage are the causes of the small samples of teeth. As well, any tooth trait combination that was wholly unobservable in any of the cemetery samples was necessarily ignored. Thus, the final data set for statistical analysis was reduced to 11 morphological traits, scored as 24 tooth-trait combinations. Since anterior teeth, i.e., the incisors and canines, are most easily lost or broken in the burial environment, it is not surprising that these 11 traits are all found on the posterior molar and premolar teeth. Table 1 lists the traits analyzed, sample frequencies for each cemetery, and the pooled sample frequencies. Any expression of a trait was scored as presence of the trait except for the following: Cusp # (all) presence = 5 or greater; Root # (UPM1) presence = 2 or greater; Root # (UM3) presence = 3 or greater; Hypocone (UM3 & UM2) presence = 3-5; Hypocone (UM1) presence = 5; Metacone (all) presence = 5. The reason for scoring in this fashion was to avoid the use of traits which have constant frequencies (i.e., are expressed to some degree) in all groups being compared: rather than dropping them from the analysis, those traits were dichotomized by scoring only full expressions of the trait as present.

Chi-squared statistics were calculated to evaluate sex differences in trait frequencies, and since none of the traits were found to have any significant degree of heterogeneity the sexes were pooled for further analysis. Traits then were arcsine transformed using the Freeman and Tukey transformation recommended by Green & Suchey (1976) for small sample sizes. Comparisons were made among the three samples using the multivariate Mean Measure of Divergence (MMD) statistic (Berry & Berry 1967; Sjøvold 1973; Green & Suchey 1976), and the variance and standard deviations were calculated according to the mathematical method of Sjøvold (1973).

Standardized distances were then calculated by dividing the raw MMD score by its standard deviation, since standardized distances are most appropriate for evaluating and comparing relative distances among samples of different sizes (Sofaer et al. 1986). Multidimensional scaling is often used in dental morphological analyses to better visualize the distance relationships, but is not necessary in this study since only three samples are being compared.

Traits*	Cemetery B	Great Cemetery	Cemetery T	Pooled
Protostylid LM3	2/7	10/28	0/3	12/38
Protostylid LM2	6/16	17/32	4/7	27/55
Protostylid LM1	3/12	11/24	1/4	15/40
Cusp 5 UM3	3/9	21/35	1/7	25/51
Cusp 5 UM2	4/18	6/38	5/14	15/70
Cusp 5 UM1	1/13	8/33	1/9	10/55
Carabelli's Cusp UM3	1/10	7/31	1/5	9/46
Carabelli's Cusp UM2	3/16	10/36	1/11	14/63
Carabelli's Cusp UM1	2/11	6/29	3/10	11/50
Third Molar Absence UM3	0/22	2/49	3/17	5/88
Third Molar Absence LM3	2/20	4/46	2/13	8/89
Root Number UPM1	9/14	24/29	8/15	41/58
Root Number UM3	8/10	6/18	2/8	16/36
Cusp Number LM3	1/6	14/26	2/3	17/35
Cusp Number LM2	0/15	4/31	2/7	6/53
Cusp Number LM1	6/9	17/25	4/5	27/39
Accessory Cusp UPM2	1/8	6/16	0/5	7/29
Accessory Cusp UPM1	1/7	2/13	0/3	3/23
Hypocone UM3	5/6	23/32	4/4	32/42
Hypocone UM2	15/15	32/37	10/14	57/66
Hypocone UM1	3/14	4/37	0/11	7/62
Y-Groove LM2	6/14	9/26	0/7	15/47
Metacone UM1	7/16	25/37	3/11	35/64
Metacone UM2	16/19	33/44	11/14	60/77

Table 1. ~ Frequencies of nonmetric dental traits for the Nagada cemeteries

~ Frequencies are given as the number of expressions of the trait over the number of observable teeth.

* The tooth for which the trait is scored is reported according to standard procedures: the first letter, L or U, indicates whether the tooth is in the upper or lower jaw; the tooth type follows, indicated by M for molar and PM for premolar; the numerical suffix indicates the position of the tooth relative to others of the same type. Thus, LM3 refers to the lower 3rd molar, while UPM2 designates an upper 2nd premolar.

Results

The MMD distances were calculated using all 24 tooth-trait combinations. The distances, their standard deviations, and the corresponding standardized distances are presented in Table 2.

Cemeteries:	B-Great	B-T	T-Great
MMD:	0.0276	0.0870	0.0778
SD:	0.0365	0.0714	0.0555
Standardized MMD:	0.754	1.2183	1.4017

Table 2. Between cemetery distances using 24 traits

Sjøvold (1973) suggests that a standardized MMD greater than 2.0 denotes a significant difference at the $\alpha = .05$ level. A negative distance is interpretable as a Chi-squared variable not exceeding its expectation and thus signifies no distinction between the samples (Sjøvold 1973). It can be seen that when all 24 traits are used, cemetery T is somewhat differentiated from the other two cemeteries, though not significantly so. When distances are calculated from each cemetery to the pooled sample (Table 3), however, cemetery T demonstrates a

Cemeteries:	B-Pooled	Great-Pooled	T-Pooled
MMD:	-0.0242	-0.1319	0.1156
SD:	0.0326	0.0527	0.0169
Standardized MMD:	-0.7430	-2.5019	* 6.8436

* indicates significance at $\alpha = .05$

Table 3. Cemetery to pooled distances using 24 traits

significant departure from the pooled sample, while cemetery B and the Great cemetery show no distinction from the pooled sample.

Since many of the 24 traits have very low sample sizes, with a greater likelihood of sampling error, distances were recalculated using only those 10 traits with sample sizes greater than 10 individuals in each cemetery, in order to retain a reasonable number of traits in the data set. The resulting distances are shown in Tables 4 and 5 for the between cemetery distances and the cemetery distances to the pooled sample, respectively. As both sample size and the number of traits affect the variance, the reduction of traits to increase sample sizes has had little effect on the standard deviations. The between cemetery distances in Table 4 now show an even stronger pattern of divergence, reinforcing the obser-

Cemeteries:	B-Great	B-T	T-Great
MMD:	0.0054	0.0840	0.0992
SD:	0.039	0.0619	0.0462
Standardized MMD:	0.1365	1.3563	2.1454*

* indicates significance at alpha = .05

Table 4. Between cemetery distances using 10 traits

Cemeteries:	B-Pooled	Great-Pooled	T-Pooled
MMD:	-0.0223	-0.1356	0.0743
SD:	0.0345	0.0851	0.0188
Standardized MMD:	-0.6461	-1.5936	3.9483*

* indicates significance at alpha = .05

Table 5. Cemetery to pooled distances using 10 traits

vation that cemetery T is distinct from the other cemeteries, and significantly so from the Great cemetery. The distances to the pooled sample still indicate no distinction between the Great cemetery or cemetery B from the pooled sample, while cemetery T is still significantly different from the pooled sample. In terms of the distances to the pooled sample, it is unsurprising that the Great cemetery should show no distinction because its higher sample sizes contributed more to the pooled sample in both the 24 trait and the 10 trait analysis. In the 10 trait analysis, however, cemetery B contributes little more than cemetery T to the pooled sample, and yet still shows no distinction from the pooled sample. Cemetery T does show significant differences from both the Great cemetery and the pooled sample in the 10 trait analysis, though much of the distance to the pooled sample must still be interpreted in terms of its distance to the Great cemetery, given the weight of the Great cemetery in the pooled sample.

With regard to the robustness of the MMD statistic, its properties and significance levels apply to "moderate" and "large" samples (Sjøvold 1973). Monte Carlo simulations of various sample sizes drawn from a single parent population, however, indicate that this statistic is quite robust in terms of type I errors under smaller sample sizes and when sample sizes fluctuate between traits within samples (Johnson, in prep.).

Discussion

Although morphological features of the dentitions from the individuals buried in Cemetery T differ significantly from those of Cemetery B and the Great Cemetery in more instances than would be expected by chance alone, the question of the nature of the biological relationships among the people buried in these cemeteries remains. The hypothesis that cemetery T represented an elite or even royal burial ground (Hoffman 1979) is supported over the argument that it merely represents a special status group of some kind (Davis 1983). Cemetery B, in contrast, is much closer to the Great cemetery in affinity than it is to cemetery T and was shown to be not distinct from a pooling of all three samples; it therefore may represent, as Davis (1983) suggested, a status differentiated group which is not biologically distinct from the population using the Great cemetery. Alternatively, cemetery B may reflect a biological intermediary group between the two populations, or segments of the populations interred in the other two cemeteries.

Another possible explanation of the biological distinction among the cemeteries is that it represents temporal variation. Hoffman (1979) suggested that cemetery T was constructed and used in the Late Gerzean (Nagada III) period, while Davis (1983) concluded that cemetery T was used contemporaneously with the Great cemetery throughout the entire Gerzean period and not just the Late Gerzean period. The possibility exists, therefore, that the distinctions found among cemetery T, cemetery B, and the Great cemetery are the result of microevolutionary changes over some temporal span, rather than a contemporaneous distinction of an elite group from the general population. The proposed rate of dental microevolution is conservative, however: roughly 0.01 MMD[raw] per 1000 years based on 28 traits, remaining stable even when only 10 traits are used (Turner 1986a).

While the raw distance from cemetery B to the Great cemetery is well below 0.01 (Table 4), the distances between cemetery T and both of the other two cemeteries is well in excess of this distance, suggesting microevolution over a period of some eight to nine thousand years if indeed the occupants of cemetery T were at one time derived from the same population that is now represented in the other cemeteries. This is an untenable hypothesis given the time period in question, and the idea of cemetery T representing a different, i.e. immigrant, population seems equally unlikely based on the similarity of goods, if not richness, between the cemeteries. Thus, some effect other than local population microevolution or in-migration must be called upon to interpret the magnitude of these distances in terms of Turner's rate of dental microevolution.

Perhaps the most likely explanation for the magnitude of the distances between cemetery T and the other cemeteries is that of inbreeding within a segment or class of a population. Ruling or elite classes or lineages may have preferential, within group, marriage rules. Thus, genetic drift would affect the genetic

structure of the group and could account for the greater than expected distance between this group and the general population.

Conclusions

Results of this analysis of dental non-metric traits indicate that cemetery T shows some biological distinction from both Cemetery B and the Great cemetery separately and from a pooled sample of all three cemeteries. The size of the difference supports the archaeological interpretation that Cemetery T represents a ruling or elite segment (or lineage) of the local population at Nagada, rather than an ruling or elite immigrant population. As demonstrated here, the analysis of morphological variations of human teeth provides a powerful tool for assessing the nature of human biocultural history, and the addition of new data for other Predynastic and archaic populations (Lovell, in prep.) will help us decipher the biological history of the people of the ancient Nile Valley and Delta.

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