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Measuring biological affinity among populations: a case study of Romano-British and Anglo-Saxon populations

Jeff Lloyd-Jones
Department of Archaeology, University of Glasgow, Glasgow G12 8QQ, UK
Email: archjlj@dish.gla.ac.uk

12.1 Introduction

Traditionally, when attempting to ascertain the origins of the people who created a village or cemetery that has been excavated, archaeologists examine cultural material found on a site. They tend to compare the types of ceramic, coins, clothing, burial practices or types of housing with other sites and, based on this evidence, date the site relative to the others. On those occasions when absolute dating methods such as C_{14} or dendochronology can be used archaeologists can use these dates to refer to written histories such as those of Gildas and Bede to support their interpretations.

The apparent shift in the cultural material recovered from sub-Roman sites to that recovered from sites dated to the Anglo-Saxon period suggests a drastic change in the ethnic identity of the populations. This, and the historical accounts, led many people to believe that the indigenous populations were slaughtered and replaced by invading hoards of Angles, Saxons and Jutes. A cultural replacement hypothesis has largely superseded this earlier view in current studies of the Anglo-Saxon period. This hypothesis states that ethnic identity is a cultural construct and does not necessarily correspond with biological affinity. The proponents of the cultural replacement hypothesis point first to the difficulties of the logistics of mounting an invasion of sufficient size to completely re-populate Britain. There is also the possibility that shifts in cultural material can occur without an exchange of genetic material. Finally there is the possibility that the early histories were not entirely without bias, which may have caused some of the early archaeologists to ignore or not believe evidence of continuity that may have come to light during excavation. The view that the indigenous populations were replaced does, however, still seem to have currency in the minds of the general public and references to the Anglo-Saxons moving into a depopulated landscape can still be found in some texts and museum exhibits.

The approach taken here is to examine the human remains from sites dated to the Romano-British and Anglo-Saxon periods in an attempt to assess the amount of biological change that occurs with the change in cultural material. This is done by comparing the frequencies of various morphological features of teeth across populations from both periods and then calculating the biological distances between sites. If the invasion hypothesis is true there should be very little biological similarity between Anglo-Saxon sites and Romano-British sites. If the cultural replacement hypothesis is true there is a good chance that the population found at an Anglo-Saxon site would have been derived from the population of a Roman-British site that is geographically similar.

12.2 Past Studies

Other biological distance studies have been carried out comparing various metric and non-metric skeletal traits but most of the results have been equivocal. This is due in part to the fact that changes in bone structure occur throughout life and certain differences may be dependant on the sex, occupation and health of the individual in life, the age at time of death as well as the genetic information received from the parents.

Teeth have most often been used as indicators of age and to gain information of the diet of the people being studied. In addition to this sort of information, however, teeth have many genetically controlled traits that can give clues to the genetic affinity of one group of people to another. Teeth retain their genetic information throughout the life span of the individual without being masked in the way skeletal traits can be because once the enamel has been formed the trait can be modified only by attrition or disease; a trait cannot be enlarged through continued use in the way the site of a muscle attachment on the leg or skull, for instance, can change. Teeth are also very durable and are often the only structures remaining after the rest of the body has disintegrated.

Very broad comparisons of populations have shown that Asian and Asian-derived populations have much higher frequencies of certain traits than Caucasians, and, conversely, Caucasians have higher incidence of other traits. These differences led Hanihara to identify a Mongoloid complex with high frequencies of shovel shaped incisors, deflecting wrinkle, protostylid, cusp 7 and the metaconule, and a Caucasoid complex with high scores for Carabelli's cusp and the canine breadth index (Hanihara 1967). Mayhall *et al* (1982) further refined the Caucasoid complex to include straight or counter winging of the central incisors and to have low scores for protostylid, premolar occlusal tubercle and of cusps 6 and 7 (also in Hillson 1986, 272).

Many studies have used dental morphology to compare the relationships among groups of Amerindians (e.g. Sofaer *et al* 1972, Turner 1967), Amerindians to Asian populations (e.g. Haeussler & Turner 1992, Turner 1985) or variation among Asian populations (e.g. Lukács & Hemphill 1991, Turner 1979). Most of the studies on

European and European derived populations have concentrated on tooth size, but a few have included discussions of morphology (e.g Berry 1976, Goose & Roberts 1982).

12.3 Sites

To test for changes in populations in the British Isles dental material recovered from several Anglo-Saxon sites has been scored together with, wherever possible, data from nearby Romano-British sites. With this model it should be possible to test whether the biological distance between two groups that are geographically similar, but date from different time periods is greater than the biological distance between two groups of similar time, but distant in geography.

The results presented here are from three of the nine sites studied so far. These sites are located in Oxfordshire and Gloucestershire. Two are classified as Anglo-Saxon and one as Romano-British. The Romano-British site is Queenford Mill (also known as Queenford Farm) near Dorchester-on-Thames in Oxfordshire. This site was excavated in 1972 and again 1981. It yielded approximately 160 inhumations dating from the fourth, fifth and possibly as late as the sixth centuries A.D. (Chambers 1987, 36). Of these 160 inhumations, 70 had teeth that could be examined for crown traits.

Both Anglo-Saxon sites are identified as belonging to the pagan Anglo-Saxon period. Berinsfield in Oxfordshire was excavated in 1974 and yielded 114 inhumations, of which 73 proved usable in this study. Lechlade in Gloucestershire, excavated in 1985, yielded 217 inhumations giving 154 for study. Geographically, Berinsfield and Queenford Mill are separated by only a few miles, Both are approximately thirty miles from Lechlade, and all three are situated on or near the Thames.

12.4 ASU Method

There are several different scales available for scoring the variation of crown morphology. Here, the Arizona State Dental Anthropology scoring method as described by Turner *et al* (1991) is used. The traits included in this method were chosen because they are genetically independent of one another, show very little sexual dimorphism, are easily observed and have been shown to be under strong genetic control (Turner *et al* 1991). Each trait is scored as absent if there is no expression of the trait, and on a graded scale from slightest expression to greatest known expression when the trait is present.

To reduce the level of subjectivity inherent in the study of non-metric traits, the teeth are compared to plaster reference casts which have examples of each trait and the score for each size of expression. To test the repeatability of the observations the recommendations of Nichol and Turner (1986) were followed and the traits from one of the cemeteries in this study (Queenford Mill) were scored twice. The sessions were separated by approximately two months. The scores from the two sessions were compared by paired T-Tests with the critical value set at alpha=.05 for a two tail test. The results of the T-Tests showed significant differences in just 16 of the 336 variables tested. These results are comparable to the results obtained by Nichol and Turner, the only difference being that they allowed a difference of one grade in the score to be treated as matching scores, whereas I required an exact match.

12.5 Statistical Analysis

The 11 traits used for this study were chosen because they were shown to be reliably scored by the T-test and because there were enough individuals from each population on whom the trait could be observed to give sufficient n-values for the statistical analysis. To measure the biological distance of these three populations the Mean Measure of Divergence (MMD) was selected. The MMD (eq 1) is based on the Grewal-Smith equation (Grewal 1962) which was introduced into bio-distance studies by Berry and Berry (1967). The equation for the angular transformation is based on the Freeman-Tukey transformation (eq 2) to stabilise variance in small sample sizes (Green & Suchey 1976). The variance (eq 3) and standard deviation are calculated using the formula suggested by Sjovold (1973). Equations 1 and 3 incorporate the modifications suggested by Green and Suchey (1976).

$$MMD = \frac{\sum_{i=1}^{r}(\theta_{1i}-\theta_{2i})^2 - \left(\frac{1}{n_{1i}+\frac{1}{2}} + \frac{1}{n_{2i}+\frac{1}{2}}\right)}{r}$$

Freeman-Tukey transformation:

$$\theta = \frac{1}{2}\sin^{-1}\left(1-\frac{2k}{n+1}\right) + \frac{1}{2}\sin^{-1}1-\left(\frac{2(k+1)}{n+1}\right)$$

where:

r = number of traits considered

n_{1i} and n_{2i} = number of dentitions examined for trait i in populations 1 and 2 respectively.

k = the number of individuals expressing the trait out of n observable individuals in a sample (k/n = observed trait frequency).

Trait frequencies are transformed to the angle Θ (measured in radians) through inverse sine

Θ_{1i} and Θ_{2i} = transformed frequency of trait i in populations 1 and 2 respectively.

$$\frac{2}{r^2}\sum_{i=1}^{r}\left(\left[\frac{1}{n_{1i}+\frac{1}{2}}\right]+\left[\frac{1}{n_{2i}+\frac{1}{2}}\right]\right)^2$$

(adapted from Green and Suchey 1976)

The standardised MMD is obtained by dividing the raw MMD score by its standard deviation (MMD_{stan} = MMD/MMD_{sd}). Sofaer *et al* (1986) suggest that this is a more appropriate measure when comparing populations of different sizes. The null hypothesis is rejected if the MMD is greater than twice the standard deviation, with a significance of approximately 97%. For the standardised MMD scores a value greater than 2 indicates that the populations are derived from different parent populations with the same level of significance.

12.6 Analysis Of Results

The presence/absence frequencies for each trait are shown in Table 12.1. As stated previously, all of these traits have been shown to be genetically independent of one another. This independence means that a change in the frequency of one trait does not require a change in the frequency of another trait. If a small portion of a population migrates away from the main population and becomes isolated, there is a strong possibility that the trait frequencies will differ between the parent and the daughter populations. The more closely related they are the less likely it is that there will be a pronounced variance in the frequencies for each trait. This can be seen by the fact that several of these traits are distributed in a nearly identical way among all three populations which indicates a certain closeness, but variation in others would indicate divergence at some point in their histories.

TRAIT	SITE	TOTAL	ABSENT	PRESENT	PERCENT
UI1 SHOVEL	Berinsfield	27	8	19	70.37
	Queenford	20	3	17	85
	Lechlade	83	31	52	62.65
UI1 DOUBLE SHOVEL	Berinsfield	32	19	13	40.62
	Queenford	30	19	11	36.66
	Lechlade	100	77	23	23
UC DISTAL RIDGE	Berinsfield	32	4	28	87.5
	Queenford	22	2	20	90.90
	Lechlade	71	35	36	50.70
UP1 LINGUAL CUSPS	Berinsfield	44	0	44	100
	Queenford	44	0	44	100
	Lechlade	113	35	78	69.02
UM1 METACONE	Berinsfield	52	0	52	100
	Queenford	44	0	44	100
	Lechlade	120	0	120	100
UM1 HYPOCONE	Berinsfield	52	0	52	100
	Queenford	44	0	44	100
	Lechlade	118	1	117	99.15
UM1 CARABELLI'S CUSP	Berinsfield	40	4	36	90
	Queenford	25	2	23	92
	Lechlade	88	25	63	71.59
LP1 LINGUAL CUSPS	Berinsfield	48	4	44	91.66
	Queenford	40	4	36	90
	Lechlade	114	2	112	98.24
LP1 TOME'S ROOT	Berinsfield	34	11	23	67.64
	Queenford	37	17	20	54.05
	Lechlade	111	52	59	53.15
LM1 PROTOSTYLID	Berinsfield	49	5	44	89.79
	Queenford	33	5	28	84.84
	Lechlade	106	37	69	65.0
LM1 CUSP 6	Berinsfield	54	48	6	11.11
	Queenford	42	41	1	2.38
	Lechlade	111	100	11	9.90

Table 12.1: Trait frequencies for the 11 traits in this study listed by site.

Site Pair	MMD	Standard Deviation	Standardised MMD
BERINSFIELD and LECHLADE BUTLER'S FIELD	0.22475392**	0.015047	14.9362
BERINSFIELD and QUEENFORD MILL (FARM)	0.03626664	0.024361	1.48871
LECHLADE BUTLER'S FIELD and QUEENFORD MILL (FARM)	0.28059086**	0.0178829	15.6904

Table 12.2: MMDs for three pairs of sites. **indicates a 97% probability that the sites were derived from different populations. Standardised MMD= MMD/MMD_{sd}

Table 12.2 shows the raw MMD values, the standard deviations for each MMD and the standardised MMD score for all three sites. These scores show that Berinsfield and Queenford Mill are very closely related. The standardised MMD comparisons of Lechlade to Berinsfield is approximately ten times greater, with the comparison of Lechlade to Queenford Mill a little greater still. The statistical probability that people who lived in Berinsfield and Queenford Mill are derived from the same parent population is greater than 97%, and the likelihood of falsely rejecting the hypothesis that Lechlade is the same population as either Berinsfield or Queenford is less than 3%.

12.7 Conclusions

In conclusion, if the invasion hypothesis is correct, it would be expected that there would be a change in biological affinity associated with changes in material culture. If there is continuity of the population, a cultural replacement hypothesis is more likely to explain changes in material culture. By applying the Dental Anthropology method it has been possible to demonstrate that, while some of the morphological features of the teeth are similar in all samples, there are also certain traits which strongly distinguish between samples. In the samples discussed in this paper, it was found that the two samples from the same geographical region but from different time periods (Berinsfield and Queenford Mill) had a very high statistical probability of being derived from the same population. The Anglo-Saxon sample from Lechlade however, showed a high divergence in morphological traits from the Oxfordshire samples.

Under the invasion hypothesis, one would assume that Berinsfield would be morphologically more similar to Lechlade than it is to Queenford Mill. These findings suggest that the cultural replacement theory provides a more accurate representation of what probably occurred during the period of change from the Romano-British to Anglo-Saxon periods. It is interesting that a site such as Lechlade appears to have remained biologically isolated from another Anglo-Saxon site, especially when the fact that both are located on the Thames is taken into consideration. This gives even more weight to the cultural replacement hypothesis because even though there is a natural connection between the two areas (the river Thames) the people living there did not have a noticeable amount of interbreeding.

It will be interesting to see whether, with planned refinements in statistical method and consideration of several other sites, this pattern still holds. It is my suspicion that the final picture will be similar, but rather more complicated than the fairly clear cut results shown here.

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