The contribution of human DNA studies to the debate on Anglo-Saxon migration

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Introduction
Since the end of the Second World War archaeology has enjoyed an increasing contribution from the physical and chemical sciences. One of the more recent developments is in the application of biochemistry and molecular genetics to the study of issues such as evolution, social structure and population history (Renfrew & Bahn 2008, 37 & 228). One particular use of these methods has been to study the movement of populations, for example in the Prehistoric settlement of Australia (Hudjashov et al. 2007).

This essay will discuss the use of genetic science to study the particular problem of the scale and nature of the Anglo-Saxon migration period. It will begin with an overview of the study of the migration period through the varied historical, linguistic and archaeological evidence, followed by a brief account of the use of DNA evidence in archaeology. Following this is a description and discussion of some of the work that has been done in applying genetic science to the migration question.

The Migration Period
The fifth to sixth centuries A.D. was a period of major transition for Britain, with the collapse of Roman power giving way to settlement and eventual domination by Germanic migrants across much of what is now England (Arnold 1997, 20; Heather 2005, 437; Russell 2005, 1). This transition is strikingly evident in the archaeological record, with considerable differences appearing in the nature of the settlement, burial and material culture evidence (Russell 2005, 1). The nature of this transition is one of the most extensively studied and hotly debated topics in Anglo-Saxon archaeology (Russell 2005, 1; Harke 1998, 19-21; Arnold 1997, 31-32).

In the past this change was studied mainly using the historical sources (e.g. Bede, Gildas and the Anglo-Saxon Chronicle), but these accounts are fragmentary and mostly date from later periods (Hills 1999, 178-9; Arnold 1984, 6-7). This traditional historical view of the migration being due to a single large-scale invasion in the mid fifth century lacks any real evidence (Arnold 1997, 20; Russell 2005, 2), and so consequently historically based studies (e.g. Collingwood and Myres 1936) have tended to give way to modern studies that rely far more heavily on archaeological and linguistic evidence (Arnold 1984, 6-7; Russell 2005, 1-2).
The chief debate lies over the extent of Germanic immigration, and tends to vary between two opposing positions: that the native population was largely displaced (or killed) and replaced by large-scale Germanic migration, or that a small number of Germanic elites established cultural and political dominance over a still largely native British population (Arnold 1997, 21; Harke 1998, 19; Richards et al. 1993, 19; Weale et al. 2002, 1008).

The linguistic evidence certainly indicates strong Germanic influence in post-Roman England - for while some place-names are Brittonic, Old English remained strongly Germanic in its vocabulary, with only about 30 words of Britonic origin being included (Ward-Perkins 2000; Tristram 2007, 192). However, it is worth noting that the preservation of Old English in writing was carried out by a small number of people from amongst the elites (primarily monks), and so the predominance of Germanic language in the surviving literature does not necessarily indicate Old English was the dominant language amongst the rest of the population (Tristram 2007, 203).

In archaeological studies, the varied origins of Germanic migrants can be identified through material culture - pottery, metalworking, and burial rites (Arnold 1997, 23). For example, the Jutish settlement of Kent described in the historical sources is supported by the presence in eastern Kent of diagnostic artefacts such as cruciform brooches and Jutish pottery (Arnold 1997, 23; Hawkes 82, 70). Likewise, settlers from the Saxon region around the river Elbe appear to have settled in the Thames Valley and lands to the south, while ‘Anglians’ from the Schleswig-Holstein region occupied middle, eastern and northern England at the same time (Arnold 1997, 23; Hawkes 82, 71). However, this is a simple description of a very complex reality; there are many areas of apparently mixed settlement, and material evidence identified as Frankish, Thuringian, Frisian, Scandinavian and Alammanic has also been found at cemetery sites such as Bifrons, in Kent (Hills 1999, 184; Hawkes 1982, 70; Wood 2003, 42). This is unsurprising since it is unlikely that people described as ‘Saxon’, for example, were single homogenous ethnic groups – in reality such names likely represented fluid and diverse tribal groupings united under a particular leader or leaders (Wood 2003, 42-43).

The problem of assessing the scale of migration from an archaeological viewpoint is complicated by the question of ethnicity; the fact that a body was interred with identifiably ‘Saxon’ artefacts does not mean the person in question was in fact a Saxon by descent (Arnold 1997, 24). Ethnicity can be seen as a social rather than a biological attribute, and as such an ethnic identity can be changed or adopted (Renfrew & Bahn 2008, 193; Jones 1997, xii). Language, location and material culture can all
be used to determine ethnicity and this makes the task of identifying individuals and settlements as Germanic migrants simply from the material culture they are associated with problematic (Arnold 1997, 21; Jones 1997, 84).

New scientific developments in biochemistry and genetics can, however, allow the possibility of identifying an individual’s origin from skeletal remains.

The use of molecular biology in archaeology

The use of molecular biology in archaeology (or archaeogenetics, a term coined in Renfrew 2000, 3) has advanced in two main stages: originally by using genetic markers such as blood groups and disease incidence, and more recently using DNA-based techniques (Oliveira 2008, 110; Renfrew 2000, 5-6; Weale et al. 2002, 1009). The inheritance of DNA is a complex process that varies between male and female individuals; consequently this allows the study of separate female and male lineages using mitochondrial DNA and Y-chromosome DNA respectively (Renfrew & Bahn 2008, 464; Oliveira 2008, 110). Mitochondrial DNA (mtDNA for short) and Y-chromosome DNA differ from nuclear DNA in that they are not formed from the combination of both parent’s genes, but are inherited solely through a single parent of the same sex. Consequently they preserve a genetic record from individual to individual that is altered only through mutation (Renfrew & Bahn 2008, 464; Sykes & Renfrew 2000, 14).

These mutations occur mainly in the DNA-copying process, and the chance of this occurring and being passed on to the next generation is essentially random. The gradual change in the DNA of a population over time due to mutation is known as ‘genetic drift’ (Sykes & Renfrew 2000, 14), whilst the occurrence of such changes are known as Unique Event Polymorphisms, or UAPs (Weale et al. 2002, 1009). It is the resulting difference in DNA coding (genes) amongst different population groups due to genetic drift that is useful to archaeologists; a variety of statistical analysis methods can be used to interpret such data. Sykes and Renfrew identify three main types of analytical methods: spatial analyses, that show the frequency of particular genes geographically; phenetic dendrograms that compare the similarities and differences of genes between particular population groups (clades) to form a kind of ‘family tree’; and the network-joining method that is similarly used to track the pathways of mutations between different genetic populations, but unlike the phenetic dendrogram method allows for the possibility of previously separated genetic groups to recombine (Sykes & Renfrew 2000, 17-20; Renfrew & Bahn 2008, 128). This last method can be used to estimate the point at time at which two particular clades separated, based upon the assumption of a predictable
rate of mutation (Sykes & Renfrew 2000, 19, Renfrew & Bahn 128).

DNA evidence can be gathered from excavated skeletal and other biological remains (Renfrew & Bahn 2008, 440), but this can be problematic due to chemical degradation of organic matter, or contamination with modern human DNA (often that of the excavators - Hills 2009, 124; Richards et al. 1993, 19; Sykes & Renfrew 2000, 16). However, modern studies tend instead to use a technique of extrapolating backwards from DNA samples of present day populations (Hills 2009, 125; Renfrew & Bahn 2008, 228-9).

Examples: Four archaeogenetic studies of Anglo-Saxon migration
A considerable amount of work has been published in recent years on the use of mtDNA and Y-chromosome DNA as it applies to the Anglo-Saxon migrations, not just on the question of the scale of the migration but on the relationships between the migrants and native Britons.

The Centre for Genetic Anthropology at UCL carried out a study of Anglo-Saxon migration using Y-chromosome data gathered from DNA samples of modern male populations, taken from a transect across central England and Wales, from Anglesey in the west to North Walsham in the east, at intervals roughly 50 miles apart. These were compared with similar samples taken in Friesland and Norway (Weale et al. 2002). Friesland was selected for the study due to it being regarded as a source location for Anglo-Saxon migrants, and because of the similarities between Old English and Frisian. Samples from Norway were also compared, as this is a source of the later Viking migrations (Weale et al. 2002, 1010).

Comparison of the genetic similarities and differences between the sample groups showed that there was little genetic differentiation amongst the English towns, but in the two Welsh towns sampled, Abergele and Llangefni, there was significant difference, both from the other sample areas and from one another. Additionally, there was considerable differentiation between the Norwegian samples and the others, but between the Friesian and English samples there were no significant differences (Weale et al. 2002, 1017).

Various statistical projections were carried out to account for this genetic differentiation, and concluded that without a mass-migration event in the mid-first millennium, an unrealistically high rate of migration between England and Frisia would be needed. Therefore, Weale cautiously proposes that a substantial migration (comprising 50-100% of the resultant male gene-pool) of
Frisian males to England took place, explaining both the similarity between English and Frisian genes and the differences between both areas and Wales: the Welsh border was a greater barrier to population movement than the North Sea (Weale et al. 2002, 1018-19).

However, a further study of Y chromosome data published the following year (Capelli et al. 2003) produced somewhat different results by using a greater number of samples and sampling areas to provide a higher resolution to the data. This data presents a more complex picture than the one from the Weale et al. study, with a less marked differentiation between Welsh and English samples, and less obvious continental introgression except in the central eastern part of England (i.e. York and Norfolk). Capelli et al.’s data argues for a somewhat smaller scale of migration than the Weale et al. report, particularly since this study incorporates Danish data which complicates the matter still further; the incidence of continental genetic markers could be due as much to the later Danish incursion of the ninth century rather than the Anglo-Saxon migrations (Capelli et al. 2003, 982-3).

While the previous studies focus on Y-chromosomes, and therefore male-line lineages only, a study of mtDNA by the School of Biological and Biomedical Sciences at the University of Durham focused instead on the role of women in migrations, using both ancient and modern DNA samples (Topf et al. 2005, 152). The ancient DNA samples came from bones and teeth recovered from burial sites in England dating from the Roman to the late Saxon period, which were compared with modern samples from across Europe and the Near East (ibid., 153). These were compared to measure the genetic differentiation between them.

The results of this survey showed significant differentiation between the early and late ancient samples and modern populations; and, like the Capelli et al. study, they showed limited genetic closeness between samples from northern Germany and the early Saxon samples, although Norwich showed more continental descent amongst its female population (Topf et al. 2005, 157-9). Overall, the study concludes that the main genetic differences and similarities between European populations were established much earlier, possibly as far back as the early Mesolithic period (ibid., 158-9).

In a 2006 study by Thomas, Stumpf and Harke, an attempt was made to explain the large contribution to the English male gene-pool from the northern German/Danish area in social terms, rather than simply the number of immigrants. An apartheid-like society, in which Anglo-Saxon immigrants enjoyed superior social status over the native Britons, could grant the former group
greater reproductive success, while restrictions on marriage between the two groups would prevent their genetic makeup from becoming gradually homogenised over time (Thomas et al. 2006, 1-2). This social structure is to some degree backed up by legal codes and archaeological evidence from the early Anglo-Saxon period (ibid., 4-5); the statistical projections carried out in this study indicate that the genetic contribution of the male immigrant population could rise from 10% to 50% in the space of fifteen generations, and possibly as few as five (ibid., 6).

**Discussion**

It is clear from the previous four studies that DNA evidence cannot provide a simple answer to the question of the scale of Anglo-Saxon migration. Ultimately, like any other form of archaeological evidence the data is open to different interpretations. Three of the four papers listed above, for example, use modern population samples only; the results they produce are statistical projections, theoretical models which do not in themselves prove anything (Hills 2009, 125). The results of the Capelli et al. 2003 study can be interpreted as the result of a single migration event, but also as the consequence of an apartheid-like society (as in Thomas et al. 2006), or even as a natural consequence of low-level immigration up to modern times (Pattison 2008, 2428). The debate remains continuous; Pattison’s argument against an apartheid-like society was refuted in the same journal (*Proceedings of the Royal Society B*) by Thomas et al. (2008, 2419-21).

Many problems can be identified with the conclusions drawn from DNA data. Although the tracing of separate genetic lineages caused by Unique Event Polymorphisms is a reasonably clear principle, the assumption that such events can be dated is problematic. The reliability of such projections based on an average rate of mutation is questionable, particularly when applied to the relatively small period of time (evolutionarily speaking) covered by a subject such as the Anglo-Saxon migrations (Hills 2009, 129). If the dating of migration events is unreliable then observed differentiation between genetic groups cannot easily be attached to any one particular migration event (as in Pattison 2008).

The inherently theoretical nature of models based on modern DNA samples could be countered by the use of ancient samples, but this comes with its own problems. Survival of biological matter is one, as is the contamination of DNA samples with modern DNA (Richards et al. 1993, 20).

In practice the use of DNA evidence has tended to be more successful in areas with less complex patterns of historical and prehistoric migration, such as in Iceland, where DNA studies have found that the majority of the Y-chromosomes are of Norse extraction but the mtDNA is of largely Gaelic
origin (Helgason et al. 2000). In England the picture is considerably more complicated, and therefore drawing definite conclusions from DNA data alone is difficult (Hills 2009, 131).

**Conclusion**

While the use of DNA evidence has certainly added fresh vigour to the debate over the scale of Anglo-Saxon migration, it cannot be said to have provided any definite answers. Arguments using DNA evidence can support either side of the debate; some in favour of mass-immigration (Weale et al. 2002), some for small-scale elite dominance (Thomas et al. 2006), while others argue for a middle-road between the two extremes (Capelli et al. 2003).

It is possible that as further work is done in this field a more detailed picture will emerge, benefiting from larger-scale sampling and a greater use of ancient biological material. The use of data gathered using other scientific processes - in particular the use of Stable Isotope Analysis on skeletal matter to determine the likely origins of an individual - could illuminate another facet of the question (Hills 2009, 140).

A combination of the traditional historical accounts, linguistic, archaeological, isotopic, and DNA evidence together may clarify the issue in the future; however, so far the debate on the scale of Anglo-Saxon migration remains unsettled.

**References**


