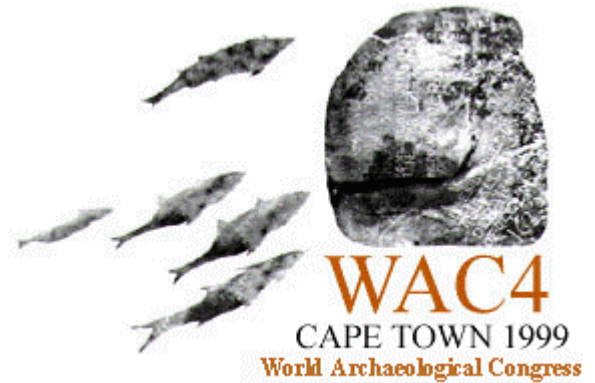


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Symposium: Genetics in Archaeology

Abstract Package

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Symposium Abstract

Developments in molecular genetics continue to be controversial in wider society and much the same can be said for the role of genetics in archaeology. Technological advances have allowed human biological diversity to be measured with increasing resolution, allowing geographical patterns to be discerned at the DNA level. At the same time, ancient DNA can now be recovered from archaeological remains, human and non-human. But have technological developments been accompanied by theoretical sophistication? Does research design and interpretation incorporate anthropological or archaeological knowledge in ways which are realistic or meaningful?

Archaeologists are by now familiar with the flawed doctrines of racial anthropology and its descendants. Both the socio-political context and the research paradigms—in genetics and archaeology—changed drastically with the Second World War and geneticists have contributed considerably to the recognition of racial taxonomy as being scientifically groundless. Nevertheless, the popularity of publications such as *The Bell Curve* indicate that a fertile ground persists for racial science—or

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pseudoscience. Media hyperbole can obscure our attempts to understand the issues—as it can distort the value and meaning of scientific discoveries.

Genetic evidence now plays a role in the study of long-term historic processes in all continents. Importantly, genetic evidence is not derived solely from humans. Considerable evidence has been amassed from the study of domesticated animals and plants. How definite are the inferences geneticists draw from their own evidence and how much distortion might result when these interpretations are co-opted in the study of the past?

Interpretations based on the genetic evidence are often seen to conflict with those based on archaeology alone. To some extent this may be due to conflicting theoretical trends reflected in each discipline. Gradients in gene distributions are normally explained as being the result of diffusion or migration. Their interpretation will inevitably conflict with the indigenist posture widely adopted in post-war archaeology, insisting that changes in material culture patterns are derived from internal social developments. Are these differences more apparent than real?

Molecular genetics now allows us to study human variation at the DNA level, reducing the influence of environment to a minimum. This would seem to offer an unparalleled opportunity for an empirically-based understanding of the nature of biological diversity. But is human genome diversity research founded on flawed and outmoded anthropology? Is it possible to study human biological diversity without being forced to make equations of genes, language and culture or assuming that human groups were once primitive isolates?

Ancient DNA potentially offers a means of resolving many archaeological hypotheses based on demographic and gender or kin-related processes. How reliable are the results? Is it rational or ethical to employ DNA results—modern or ancient—in discussions of identity?

The aim of this symposium is to explore and debate these issues. Papers will be presented which critically discuss historical and contemporary uses of genetics in archaeology, debate conflicts between the aims of population genetics and archaeology, illustrate the potential for use of ancient DNA in archaeology and present new models for the integration of genetic evidence into archaeological research. Papers will refer to theoretical and interpretative matters, and to archaeological and historical case studies in Europe and North America.

Genetics and the Origins of Agriculture

Terry Brown, UMIST, Manchester.

Currently there is little consensus regarding the events that underlay the transition from foraging to farming. At one extreme of the spectrum of possibilities is the notion that agriculture began as a small series of isolated events, at the other extreme agriculture is envisaged as a gradual and dispersed occurrence. At the heart of the debate is the question of crop origins, centring on the number of times that each crop plant was taken into domestication. Relevant information is being obtained by genetic analysis of modern crop cultivars and, to a lesser extent, by direct examination of archaeological varieties via ancient DNA typing. With several crops, the results of these studies have been interpreted as supporting a single domestication event. This paper will argue that for most if not all crops for which a single origin has been

proposed, the genetic data are either too uncertain to draw any conclusion, or lead to a more parsimonious conclusion of multiple origins. The paper will also attempt to define the types of genetic data needed to address the issue of single-multiple origins.

Genetics, prehistory and the Mesolithic-Neolithic transition: problems of resolution and meaning.

Mark Pluciennik, University of Wales, Lampeter.

Two types of genetic analysis and of models associated with their respective data have been produced with implications for the Mesolithic-Neolithic transition: modern gene frequency analysis ('classical' genetic analysis), and lineages derived from contemporary (and potentially from ancient) mtDNA. The two models suggested to represent the processes by which the patterns arose are largely in opposition to each other, reflecting the similar archaeological arguments about colonisation versus adoption. Authors associated with both methods have tended to show confusion over the potential relationships between genetic and other histories and identities. This paper asks what it is that archaeologists are interested in saying about past social relations, practices and histories; at what scale of chronological, geographical and demographic resolution; and what and how current or potential genetic data may contribute to the archaeological understanding of the social processes and the prehistories of Mesolithic-Neolithic transitions.

I would identify three areas of common concern which I see as problematic in relation to current genetic approaches to Mesolithic-Neolithic transitions. The first of these relates to identity, and what I see as the remnants of essentialist assumptions about innate identities. In many genetic studies there is a tendency to link genetic, archaeological and linguistic data by assuming their general congruence, while in archaeology the opposite trend has been increasingly emphasised over the last thirty years. Further, one can also note the general assumption that contemporary ethnic labels and origin myths relate in some meaningful way to hypothesised genetic histories.

The second area is the problem of resolution of current genetic data-both in terms of chronologies (dating) and spatial distribution. There are difficulties with not only the historical, but also the spatial resolution possible with current analytical techniques and the associated model-building. Partly this is due to the concentration on contemporary genetic information, a methodological problem which may be surmountable, but which at present produces genetic 'histories' with little independent evidence for dating any correlation with geographically described populations. Another factor producing imprecision is the small sample sizes currently available, which only allow us to produce 'coarse' models of population movement and change; and a further source of potential chronological confusion in the construction of models is the large uncertainty associated with rates of mtDNA change. In effect, the two main methods of genetic analysis are currently producing data which is largely convincing on the very long-term (evolutionary) and the large scale-global and continental; but which is increasingly unconvincing at the sub-continental and regional scale. And I think that this is where there is a mismatch between the frameworks of most archaeologists and most geneticists.

The third area of concern, which grows out of the second, is the notion of what might constitute a 'good'-in the sense of interesting-understanding or explanation of any

particular Mesolithic-Neolithic transition. Archaeologists over the last 10 or 15 years have become increasingly aware of and interested in the heterogeneity of Mesolithic-Neolithic transitions of Europe. Although there are exceptions, such as Colin Renfrew, who has attempted to characterise the transition exactly in terms of grand processes linking archaeological, genetic and linguistic evidence on a global scale, most archaeologists are currently trying to refine their models in both time and space to produce regional and micro-scale approaches. Clearly, in the present state of knowledge, the sample size, analysis and resolution of palaeogenetic material does not allow us even to approach the archaeological problem understood in these small-scale and social terms.

Some of apparent tensions between people working with biological data and those working with archaeological data are more apparent than real, but derive from genuine differences in research culture. This is partly because they are asking different questions, have different understandings of what might constitute an interesting explanation, are driven by different agendas (including funding and other academic politics), and work within different disciplinary histories and trajectories. However, the types of narratives produced also tend to demonstrate these contrasting approaches: the 'scientific' story might start from a relatively simple model because the approximation to a closed experiment with relatively few variables is often more appropriate; the 'social' or 'archaeological' is more likely to begin with the premise that social life is inherently complex, messy and blurred, and so are social prehistories, and that simplifications are always going to be misleading, even as a starting point. Thus there is a major difference in the cultural contexts in which these sorts of knowledges are being produced.

Nevertheless, the current and future production of biological data will inevitably change the context in which prehistories of the Mesolithic-Neolithic transition are written; one hopes that appreciation of recent archaeological debates and interests will also change the context and ways in which biological data are presented, and even the sorts of methodologies used and questions which are being asked. Such interdisciplinary tensions as there are may also be used in constructive ways for productive debates and continuing dialogue.

Ancient DNA and human remains.

Leif Haavard Vikshaaland, University of Tromsø, Norway.

What is ancient DNA? A short summary on what has been done so far. There is cause to be careful when it comes to identifying ethnic groups and races in prehistory. Genetics must not claim to have found the ethnicity of prehistoric human remains without having knowledge about what ethnicity is, or the last 20 years archaeological and anthropological debate on the subject. Ethnic identity is created, and changes over time. It is not unproblematic to identify prehistoric human remains several thousand years old as belonging to a present day ethnic group. Prehistoric Kinship Analysis: Biological relationships versus social relationships. Example: When a woman and child is found buried together it can now be decided whether the woman is the child's biological mother or not. They may still though have had a strong social relationship in the society they lived in, even though they were not mother and child in the way we think of it.

The future: Important tool for sex identification, kinship analysis, studying sickness in prehistory. But be careful with ethnicity. If ancient DNA analysis can be done on a cheap routine basis, archaeologists can look at the past in ways that never has been done before. Archaeologists and geneticists need to work close together.

Sex, Gender and Ancient DNA

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For prehistory, gender archaeology is dependent on the analysis of representations of humans in various media where males and females can be distinguished by the appearance of characteristic sexual features. However, interpreting prehistoric art is fraught with difficulties. Another source of information are burials accompanied by grave goods. Here two types of information can be analysed - the biological sex of the burials, and the nature of the grave goods interred with them. A reliable method for the identification of the sex of human remains is therefore needed in order to investigate gender construction and gender roles from this type of evidence. Current physical anthropological methods of sex identification work well with complete remains, but with incomplete skeletal material, cremations and juveniles/infants the accuracy of these methods decreases and the element of subjectivity increases. Much research effort has been put into the development of a simple, PCR-based test to identify the sex of human remains. The extraction of ancient DNA from bones and the amplification of sequences from the X and Y chromosomes in theory should provide a robust and objective method for identifying the sex of an individual. However, these PCR-based methods also have their own uncertainties, which precludes their routine application to human remains from archaeological sites. The development of new methodologies is required to ensure the wider use of molecular methods of sex identification in archaeology.