

Clash of cultures? Archaeology and genetics

Mark Pluciennik

University of Leicester, UK

M.Pluciennik@le.ac.uk

ABSTRACT – *This paper examines the ways in which genetic data have been used to interpret the transition to agriculture in Europe over the past two decades, and the relationship of these interpretations to more strictly archaeological explanations. It is suggested that, until recently, those working within the two disciplines have been using not only different data sets and methodologies, but also working within different disciplinary traditions which have inhibited communication and collaboration, and the production of a genuinely integrated field of 'archaeogenetics'.*

IZVLEČEK – *V članku analiziramo pristope, ki so v zadnjih dveh desetletjih uporabljali genetske podatke pri interpretaciji prehoda na poljedelstvo v Evropi ter odnos med temi interpretacijami in striktno arheološkimi razlagami. Ocenjujemo, da so raziskovalci v okviru teh dveh disciplin do nedavna uporabljali različne metodologije in serije podatkov ter delali znotraj različnih raziskovalnih tradicij. To je preprečevalo komunikacijo in sodelovanje ter izdelavo pristno integriranega področja 'arheogenetike'.*

KEY WORDS – *Genetics; archaeology; Neolithic; rhetoric*

Introduction

Archaeology has often had a strange and occasionally fraught relationship to science; the discipline is often described as straddling the humanities-science divide, and many of us would not be averse to being described as social scientists. Nevertheless, on occasions and especially, perhaps, in Anglo-American archaeology, academics have sometimes tried to urge archaeological practice more forcefully in the direction of harder science, or alternatively and perhaps in reaction towards the 'softer' humanities. Such arguments have tended to be about philosophical and epistemological positions rather than methodological ones, and have their basis in the nineteenth century. For example, in 1858 Johann Droysen proposed that there were three types of systematic knowledge: the speculative, which related to the kind of knowledge produced by philosophy and theology; the mathematical or physical, grounded in logic and in empirical facts; and the historical. He suggested that these

three realms of knowledge had what he called three 'essences' or characteristics: respectively, to know (*Wissen*), to explain (*Erklären*) and to understand (*Verstehen*). The last two roughly equated respectively to the 'hard sciences' – physics, chemistry, biology and so forth – and the 'humanities'. The social sciences including archaeology can, however, be seen to partake of both 'essences'. Archaeology is an unusual discipline in drawing on both types of 'knowledge' and their associated theories more or less equally and in an internally-integrated manner; other disciplines such as geography, for example, have ended up with divisions which more or less equate to these distinctions, with physical and human geography. The history of archaeological theory and indeed its disciplinary culture and even status can thus in part be characterised as leaning towards one side or the other – towards science or the humanities for its inspiration.

As usual, though, the picture was and is more complicated: archaeologists are perhaps better described as theoretical magpies. Archaeologists of any persuasion routinely use statistical analysis and scientifically obtained environmental data, for example. In the Anglo-American world, 'scientific' New and processual archaeologists *were* interested in social and cultural phenomena, and not just in explaining energy extraction from the environment. Scientific methodologies and procedures and data are important to all of us; the necessity to be something of a jack-of-all-trades, having to be aware of isotope analysis *and* cultural theory, Bayesian modelling *and* social anthropology, is what makes the discipline particularly challenging. It has therefore been interesting to observe disciplinary reactions when a new and undoubtedly scientific technique from a hitherto unrelated discipline, which I shall here call 'genetics', came to impinge on archaeological understandings of the past.

This seems to have been a particularly divisive area, particularly in addressing the question of the Mesolithic-Neolithic transition, primarily in Europe, and which I shall use as my case study in this paper. By and large, archaeologists were hostile to the outcomes and apparent implications of relevant genetic research: very few archaeologists embraced the genetic data (and controversial 'evidence' from linguistics) with fervour. Equally, geneticists often appeared as though they considered archaeological data irrelevant for studying the prehistoric past. Why should this be? After all, this particular relationship started as collaboration. In this paper I will mainly examine some of the rhetoric and practices associated with this debate as a way of considering whether there are, despite archaeology's hybrid position, fundamentally different disciplinary cultures involved. I shall conclude by looking at some of the implications for methodologies – not for genetics or molecular biology, which I am totally unqualified to offer – but rather ways of collaboration and means of approach.

Genetics and archaeology

Thirty five years ago (and subsequently elaborated in detail), Albert Ammerman and Luigi-Luca Cavalli-Sforza (1971; 1973; 1984) presented an interesting idea relating to a potential new source of evidence about the spread of farming in Europe. Discussing the apparent rate of spread of the Neolithic, and explaining this through an initially exogenous population expansion associated with early farming in Eu-

rope, they mentioned the 'possible genetic implications of the model'.

"The population wave of advance accompanying the spread of early farming should be reflected, if this [demic diffusion] explanation is the correct one, in the genetic compositions of the resulting populations."

(Ammerman and Cavalli-Sforza 1971:687)

This was – and is – a powerful idea. Since that time there has been a huge amount of genetic data and analysis published which is often stimulating, which has undoubtedly raised new questions and perhaps offered new insights, through looking not just at overall genetic frequencies of classical markers such as blood proteins, but subsequently also at different regions and sites within the genome, and suggesting genetic histories – phylogenetics – and putative dates for mutations and haplotypes, and consequently histories of haplogroups; and of differences between female-inherited (mtDNA) and male-inherited (Y-chromosome) genetic material, for example. For the purposes of this paper, though, it is worth noting that the question as posed initially by Ammerman and Cavalli-Sforza was primarily an *archaeological* question: genetic information, it is suggested, may be able to illuminate the process of transition, given certain primarily demographic conditions. The demographic modelling was in part based on ethnographic data relating to hunter-gatherer and small-scale farming societies.

Since then, and especially since the 1990s, the discipline of what some call 'archaeogenetics' (Renfrew 2000:3) has seen the production of large numbers of datasets and numerous interpretations in relation to the transition to and spread of farming, especially in Europe, as well as much evidence related to migratory population movement elsewhere – Polynesia and the Americas in particular (see *e.g.* Jones *et al.* 1999; Renfrew and Boyle 2000). So far, these datasets have been derived primarily from modern populations, and the information explored in terms of their phylogenies – the genetic histories – and modern spatial distribution. Ancient DNA, which would appear to offer much more specific information from individuals and groups of individuals who can be placed, culturally-situated and dated archaeologically, is rarely sought, mainly because of the potential problems of identifying contamination (but see *e.g.* Chandler *et al.* 2005; Haak *et al.* 2005). This is not the place to explore the use (and abuse) of such data in detail: but see Mirza and Dungworth 1995; Fix

1996; Pluciennik 1996, Sims-Williams 1998; MacEachern 2000; Zvelebil 2000; Bandelt et al. 2002). There has been a persistent and major problem of the conflation of genetic, linguistic and cultural 'entities' and (pseudo-)archaeology, with the assumption that these forms of biology, culture and identity almost inevitably go together (see Moore 1994; Terrell and Stewart 1996), at least until 'modern' times.

I would suggest that archaeologists already 'knew', and certainly by the 1980s, that the process of the Mesolithic-Neolithic transition in Europe was complex socially, culturally and therefore almost certainly, biologically. However, one gets little sense of this from looking at the genetic literature, until very recently. And even here the methodology seems, to many archaeologists, rather upside-down. 'We would argue that it would be worthwhile to turn the scientific procedure around', argued Pinhasi et al. (2000: 55). That is, the apparent injunction to start with a simple model – even though obviously, archaeologically-speaking, wrong – is presented as a methodological necessity. In the case examined here, it is that the spread of farming represents *either* population expansion by genetically-distinct farmers, *or* the adoption of farming by genetically distinct foragers. To be fair, a few later publications – led by archaeologists – have asked whether the genetic and other biological signatures supported archaeological interpretations on a regional scale (e.g. Lalueza Fox 1996; Jackes et al. 1997; Pinhasi and Pluciennik 2004; Chandler et al. 2005). Another and arguably more productive approach would be, for example, to model the relevant genetic histories in terms of archaeological understandings of the processes involved (in the plural!), and at least ask what kinds of genetic outcomes we might expect. Yet after 20 and more years of research, this kind of question is apparently only now beginning to be asked. It is these kinds of intellectual propensities and resistances which suggest that at least some of the tensions between 'archaeological' and 'genetic' explanations of the Mesolithic-Neolithic transition are best explained as matters of disciplinary preferences and traditions of thought and practice; that is, of culture.

The great divide

One of the striking aspects of the relevant literature is that for a very long time the 'archaeology' was swept aside and the debate was very largely driven by the genetic data – and hence, de facto, by the geneticists. This was so even though we had here a po-

tentially powerful new set of techniques for saying something about the past, although exactly what they 'say' certainly is not yet clear. Thus in relation to the Neolithic in Europe (the area where many of the best data sets tended to come from), the approach in the publications basically became a question of supporting (or much more rarely disagreeing with) this model of 'demic diffusion'. Even in a recent review, this is still how the question is characterised: 'The primary issue remains whether agriculture spread by contact or by farmers moving into Europe' (Armelagos and Harper 2005:109). So powerful was this drive that some archaeologists, too, decided that the 'truths' of genetics were more plausible than those suggested by the archaeology. The debate became strongly polarised: in general, geneticists (and a few others) accepted the 'fact' of demic diffusion and published evidence which apparently supported it. Meanwhile, many archaeologists had been moving just as strongly away from demic diffusion models and were increasingly arguing for the Mesolithic-Neolithic transition as a highly variable socio-cultural phenomenon (including demographic and other biological processes) on the regional, let alone the continental scale (Zvelebil 1986a; Price 2000). But they were not – and I include myself here – engaging with geneticists through collaboration and joint publication; instead, there were critical papers and conference sessions in which archaeologists were primarily talking to archaeologists, in the same way that geneticists were primarily writing for and speaking to other geneticists. Thus there were a series of papers, referred to above, critical of genetic interpretations which by and large ignored the archaeology and continued to confuse and conflate biological constructs – genetic histories – with social entities, including linguistic and ethnic groups and names.

This polarisation is seen in Table 1. Here some papers by geneticists and published primarily in journals in that discipline in the 1980's and 1990's are summarised. The fact that these are generally multi-authored is, of course, itself an aspect of disciplinary culture: the convention is for entire laboratory teams to be named as authors. More interesting, perhaps, is the fact that archaeologists were rarely involved in producing these papers: their 'contribution' was limited to a very few items (and those often out of date) cited in the bibliographies. There were notable exceptions: I would single out Martin Richards (see this volume), and also note that where archaeologists were involved (such as Colin Renfrew) appropriate archaeological and other citations were frequent, various and up-to-date. Nevertheless, the widespread

Authors	Date	Geneticists	Archaeologists (linguists)	Subject	Archaeology references (n)
Torroni et al.	1998a	11	–	Late Palaeolithic re-colonization	1990 (1)
Wilkinson-Herbots et al.	1996	4	–	Late Palaeolithic re-colonization	1986, 1995 (2)
Sajantila et al.	1995	13	(–)	Genes & languages	1987, 1988 (2)
Torroni et al.	1998b	11	–	Late Palaeolithic re-colonization	1990 (1)
Sokal & Menozzi	1982	2	–	Neolithic diffusion	1971, 1973 (2)
Richards et al.	1996	10	–	Palaeolithic & Neolithic diffusion	1983–1995 (10)
Semino et al.	1996	5	–	Neolithic diffusion	1889, 1943, 1984, 1989 (4)
Pult et al.	1994	6	–	Modern humans in Europe	–
Rendine et al.	1986	3	–	Neolithic diffusion	1953–1984 (8)
Barbujani et al.	1994	3	1	Neolithic diffusion	1971–1992 (17) plus linguistics
Jones	1991	1	–	Neolithic diffusion	–
Sokal et al.	1991	3	–	Neolithic diffusion	1953–1991 (7)

Tab. 1.

problem amongst geneticists of their ignorance of socio-cultural processes and archaeological interpretations and debates – or perhaps the failure to see their possible relevance – is best epitomised by the astonishing paper by Robert Sokal and colleagues. Rather than seeking archaeological advice, he preferred to use a 'European ethno-history database, developed in our laboratory' which 'documents the known locations and movements of 891 ethnic units over the last 4000 years' (Sokal et al. 1993:56). The database purported to 'list the name of a "gens" or tribe (or that of an archaeological horizon in the case of prehistoric records...)' (Sokal et al. 1993:57).

Thus, even though Renfrew (2000:3) claimed that the new discipline of archaeogenetics involved 'the study of the human past using the techniques of molecular genetics', it tended to be a very partial view. Renfrew continued: 'In practice this is likely to involve the collaboration of molecular geneticists with archaeologists, anthropologists, historical linguists and climatologists'. But so far and despite the integrative work of Renfrew and other grand theorists such as Peter Bellwood (Bellwood 2001; 2004; Bellwood and Renfrew 2002; Renfrew 1992; 1996; 1997) and indeed Cavalli-Sforza himself (1996), such collaboration has not been substantiated, at least in terms of joint authorship, with rare exceptions (e.g. Barbujani et al. 1994). Indeed, even in the volume Archaeogenetics itself, the division between papers by archaeologists, and papers by geneticists, is as strong as elsewhere.

Many other similar papers have been published, of course: those summarised in Table 1 are merely a selection of those claiming to deal explicitly with an archaeological issue, namely the transition to farm-

ing in Europe, or occasionally, the late Palaeolithic re-colonisation of post-Last Glacial Maximum northern Europe. These latter are included because they often discuss the 'Mesolithic' and 'Neolithic' input as compared with 'Palaeolithic' contributions to gene pools. Also excluded are those papers which only allude to possible 'prehistoric scenarios' in passing, and are primarily methodological or papers descriptive of genetic data, and for which the audience will be other geneticists. Other papers not included here examine the supposed relationships between genes and languages. While one could show a similar table for relevant papers written by archaeologists, it would not be so informative. Inevitably, there were up-to-date references for genetics papers (because that is what they were criticising), but (apart from those of Ammerman and Cavalli-Sforza) there were virtually no joint cross-disciplinary papers in the 1980s and very few in the 1990s, but more in the last five years and other evidence of efforts to bring archaeologists and geneticists together (e.g. Bentley et al 2003; ESF 2004; Gamble et al. 2005; this volume).

Apart from the methodological and epistemological facts of the matter, we should also be interested in this as a socio-political phenomenon. Why did the 'debate' unfold in the way that it did? Where are we now? And where we might realistically look for synergies between archaeology and genetics?

Rhetoric and politics

There are other contexts for this, which perhaps also suggests that other more subtle socio-politics are playing a role here. First of all, we can note that of the broadest set being examined, the most high profile archaeogenetics papers and the greatest volume

of work related to either big issues (the origins of modern humans and Neanderthal DNA; origins and spread of agriculture; origins of contemporary peoples such as Polynesians or Native Americans): apparently foundational episodes, rather than the implications of day-to-day demographics and genetic exchange – sex – across or within group boundaries. Overall there are three major groups of relevant papers in order of volume:

- ❶ Papers describing the structure of genetic material and distributions both phylogenetically and geographically: this is basically about genetic data production;
- ❷ Papers dealing with methodologies and model building;
- ❸ Papers dealing with histories: these tend to be stated in terms of ‘Neolithic’, or ‘Indo-European’ contributions; only recently have geneticists started to model admixtures.

The emphasis in the last group seems to me to demonstrate the well-known prevalence of historical questions dealing with origins – what led to ‘us’ (e.g. *Piazza 1993*). Were this archaeology, one might argue that this focus also relates to the continued influence of stadial social evolution, and hence on apparent moments of transition understood as radical change. In archaeology these biases have at least been considered and critiqued, while geneticists, in a different tradition, typically, are not necessarily *au fait*, or used to dealing with such political and critical issues of structures of thought and narratives. However, it seems that within genetic studies the more likely explanation is that, to begin with, at least, the methodological need to distinguish between populations led to and maintained the focus on the ‘new’ or distinctive, genetically speaking.

Other factors

In the late 1980s Ammerman (*1989*) and Zvelebil (*1989*) exchanged views on how to approach the Mesolithic-Neolithic transition in Europe, and what was structuring those views. Ammerman suggested, broadly, that the bias towards and interest in processes of cultural diffusion and adoption of Neolithic traits by indigenous forager populations *à la* Zvelebil was a result of post-colonial guilt within Europe (see also *Keeley 1992*). Whatever one’s view about the influence of politics on archaeological interpretations, no such doubts assailed many looking at demic diffusion from the genetic point of view. The important thing about the Mesolithic-Neolithic tran-

sition was the incoming, novel populations: the interest was in the ‘contribution’ of farmers, a bias which has been noted in the construction of modern European identities (*Zvelebil 1996*). Thus presentations tended to be couched in terms of Neolithic (or Indo-European) immigrants, rather than of mixing, or hybridism. This was so when estimates of the ‘Neolithic contribution’ through a ‘wave of advance’ were higher than the consensus is now – in Cavalli-Sforza et al’s famous map obtained from Principal Components Analysis it was suggested that the Neolithic contribution to the gene pool might be of the order of 28% (*Cavalli-Sforza et al. 1994:291*). Subsequently revised downwards, most genetic models now suggest a ‘Neolithic’ genetic contribution of perhaps 15%–20% on the continental scale (*Richards 2003*; but see *Barbujani and Dupanloup 2002*; *Chikhi 2002*). This initial estimate was in marked contrast to archaeological interests and, indeed, models developed over the same period (e.g. *Zvelebil 1986b*; *Gronenborn 1990*; *1999*; *Skeates 1994*; *Zilhao 1993*), all of which suggest marked variation in the nature of ‘Neolithic’ distribution, although authors do not necessarily agree on the form that it took). Nevertheless, even on the basis of the earlier figure it is clear that the overall ‘Neolithic’ contribution was a minority, regardless of whether other ‘contributions’ derived from earlier or later demographic and genetic events and processes. It is less certain whence this apparent bias towards farmers derives. One argument would be that from a genetic point of view researchers were, as a matter of practical methodology, necessarily looking for markers of change (understood as some form of colonisation), and that the underlying substrate (equated with indigenous and relatively static Mesolithic populations) was simply less interesting. Work on mtDNA, in fact, subsequently raised the question of the genetic impact of late Palaeolithic re-colonisation. Nevertheless, it is interesting to note (assuming the 20% figure is roughly correct) that, inadvertently or not, such a focus on the impact of the ‘new’ is a continuation of long-established culture historical interpretations: the role and identification of colonisers and invaders assumes priority over processes of cultural hybridism and mixing. More generally, for archaeologists, periods of non-migration or colonization (or demographic or other forms of stability) are just as interesting as any other.

The present scenario

It seems to me that in relation to the Mesolithic-Neolithic transition, the way that this source of informa-

tion has been utilised has not been a happy one: there appear to have been a series of lost opportunities especially throughout the 1990s. Unfortunately, I am unable to engage in debates about the best way to model and (re)construct phylogenies, and the relationship they have to demographic processes. But it is noticeable that from the 1980s onwards, the consensus *in archaeology* about the Mesolithic-Neolithic transition has been that this process, or rather this set of processes, was highly variable in time, space, tempo and nature; and that demic diffusion as originally defined was probably always only part of the answer in specific locales. Thus it is arguable that archaeologists and others should collaborate in modelling the production of genetic diversity relating to this period by

- Identifying relevant demographic, biological, social, and cultural processes on a variety of regional and temporal scales;
- Identifying potential variability in parameters;
- Considering the problem of equifinality (and lack of resolution in genetic data);
- Discussing the limits of resolution, and identifying appropriate techniques and modelling;
- Modelling potential genetic outcomes.

It is surprising that no-one was doing at an earlier stage in the development of ‘archaeogenetics’ what Ammerman and Cavalli-Sforza set out to do in their initial model: namely, this is what the archaeology (in their case, the radiocarbon dates) suggests might be happening in this period; these are the kinds of cultural (and demographic, and social, and biological) processes: what might the genetic outcomes of these kinds of small-scale, regionally variable biological and demographic processes be like? A similar plea was made by three archaeologists (or physical anthropologists) at the conference from which the Renfrew and Boyle *Archaeogenetics* volume derived:

“Instead of generating historical hypotheses from the present genetic patterns, and trying to fit the archaeological record onto these, it would be useful to build hypotheses from the actual record of the past in time and space, which could then be tested with genetic data.”

(Pinhasi et al. 2000.55)

But although many of us were critical of many of the assumptions associated with the wave of advance – or at least its continent-wide application – none of us went on (or was able to) develop [in collaboration!] the kinds of models that were actually requi-

red to make ‘sense’ of much of the genetic data. Zvelebil (2000) described the variety of relevant potential processes and problems with genetic approaches, but could not be expected to deal with the genetic aspects of population modelling.

Perhaps one reason for this lack of explanation (or interpretation) of the genetic data as the result of complex processes is simply the difficulty of conceiving and producing such models. It is also part of a wider disciplinary cultural difference: the use of binary logic to begin an explanation or modelling process (either p or not-p; either demic diffusion or adoption). But even though much has changed in attitude at least over the last five years or so, the underlying problems remain. For example: Currat and Excoffier (2005) examine some of the reasons for contradictory signals from different types or sources of genetic data (e.g. Y chromosomes, mtDNA, ‘classical’ markers). They build a model which simulates various scenarios of genetic exchange between indigenous ‘Palaeolithic’ and exogenous ‘Neolithic’ populations. But this, archaeologically well-informed, paper also notes:

“Our simulations were performed in a homogeneous environment with g [a measure of forager-farmer genetic interaction] identical in every deme, regardless of its location. While this assumption may seem unrealistic at a regional scale, it is quite reasonable at a continental scale... It would be interesting to test ... the influence of some heterogeneity of the migration wave, and to incorporate, with considerable additional work and computer power, more realism in the simulation... It, however, appears necessary to understand the genetic signature expected under a relatively simple demographic scenario, before considering more complex ones.” (Currat & Excoffier 2005.684)

We find very similar phrases used by Dupanloup et al. (2004), but again working on the effects of ‘admixture’ on a continental scale:

“In the future, it will be important to incorporate detailed archaeological information into the population models, so that the assumptions will become both more complicated and more realistic.”

(Dupanloup et al. 2004.1370)

It is a rather sad commentary on academic communication that it appears to have taken some twenty years to reach this conclusion.

Discussion

This raises a whole series of other questions. One of which is: even if such detailed archaeological information were incorporated, what effect might it have on our *archaeological* interpretations? That in turn suggests another: what is it that we, as archaeologists, are interested in, what kinds of phenomena? Clearly, demographic processes *per se* are only a part of the answer – it is cultural and social process (which, of course, incorporates demographic and other biological factors and outcomes). There remain, as described above, marked cultural differences between ‘sciences’; as a social science looking at and interested in primarily social phenomena, archaeology always deals with the already complex; to apply ‘harder’ science criteria to cultural processes is often unhelpfully reductionist.

“When historians look back on the 21st century, they may well conclude that this was the moment when the biological and medical sciences finally began to appreciate the multi-layered complexity of all living things... As Francis Crick put it: “While Occam’s Razor is a useful tool in the physical sciences, it can be a very dangerous implement in biology. It is thus very rash to use simplicity and elegance as a guide in biological research.”

(Weatherall 2006)

Archaeology is very much a mixture of disciplines, methods, techniques and approaches. Pinhasi & Pluciennik (2004) also examined the mesolithic-neolithic transition in southern Europe using relatively ‘hard’ data (skeletal morphometrics), which is partly related to genotypes and gene frequencies. However, we suggested that such data are rather another point of triangulation in the complex debate about some aspects of the demographic and cultural processes in this period of prehistory. It is a necessarily woolly picture. In that paper we wrote:

“Neither skeletal, nor genetic, nor archaeological [nor linguistic] data alone will provide “solutions” to questions about the nature of the Mesolithic-Neolithic transition. Different data sets address a variety of processes at different scales and chronological and geographical resolutions.”

(Pinhasi & Pluciennik 2004, 74)

What does seem to tell us much more of interest as archaeologists is when we can start talking with some degree of certainty about regional and local processes, whether through excavation, dating, or

combinations of such things as genetic and skeletal isotope and archaeological information (*e.g. Bentley et al. 2003*). This is because larger continental or even global phenomena are emergent from and dependent on the local. The global usually does not necessarily tell us that much of interest on its own, although it may also give us a framework; we need at least to tack back and forth between the local and ‘global’ to answer the kinds of questions about cultural shift and social change with which many of us are concerned. Genuine archaeogenetics must be informed by the archaeological, just as the archaeological should draw on the genetic.

There remain problems of chronological resolution and scale. For much of prehistory we are often constrained to discuss general, structural, relatively long-term change (in settlement patterns, in modes of exploitation, in patterns of material culture, in belief systems as evidenced in burial practices, and so on); however, we can and often do illuminate these structural shifts by tightly-constrained contexts (in duration and location) which act as snapshots of practices at a particular place and time. We have the macro-scale and we have the micro-scale; what archaeology often finds difficult is the meso-scale, at which much social change could be argued to manifest itself most clearly.

When, however, we look at the dating of events – demographic or genetic – drawing on strictly genetic data, we are even less likely to be able to discuss meaningfully events or processes in socio-cultural terms, simply because the standard deviation associated with such ‘molecular clocks’ is much greater even than that associated with radiometric dating. And in any event, even if, say, mutations can be dated, it does not necessarily help an understanding of the subsequent process of geographical and biological dispersal on the kinds of scales with which we are concerned for socio-cultural processes. Similar issues arise from the lack of spatial resolution. I would suggest that it is still the case that we cannot discuss prehistoric demographic ‘events’ in a meaningful social scientific (rather than biological) way, certainly not from modern genetic data. The kinds of resolution which might help us as archaeologists to discuss the socio-cultural and biological processes in the past might be available from palaeogenetic data (especially if allied with other techniques such as isotope analysis), but so far there are simply insufficient surviving samples of old DNA, and I suspect that (archaeo)geneticists have also found it easier and more profitable in the academic sense to work

through the much more accessible modern data. This perhaps suggests that we have sometimes asked the wrong questions, and that we should be able to use this new data source in more illuminating ways than simply in terms of the old dichotomies of colonisation and adoption in which both geneticists and some archaeologists seem to be entrapped. The potential use of genetic data in conjunction with archaeological, and in this case other palaeoclimatic evidence is admirably demonstrated by Gamble et al. (2005) discussing the archaeology of Late Glacial (re)colonization. Although the methodologies will not be the same for the early Holocene and the Mesolithic-Neolithic transition, there are equally relevant ‘databases’ which can be used to investigate questions of population history and human and cultural dispersals and shifts.

Conclusion

There has been a welcome shift from the description and exploration of genetic data sets (e.g. genetic structure of Europe) to interpretations of ‘real world’ history. But this is still a limited focus, from an archaeologist’s point of view, on demography and biological history and structure, which is perfectly understandable, and also interesting and relevant, but also only part of the kinds of histories we are interested in. For various reasons, the intellectual investment by some (archaeologists and geneticists) in modelling or explaining ‘the Neolithic’ as demic diffusion has proved a hindrance. As Gamble et al. note (2005:218):

“When the genetic data were first suggested to support Late Glacial expansions in the mid-1990s, the dominant view in population genetics was that the major signal was Neolithic. This came as something of a surprise and seems to have been resisted by some ever since.”

This paper has been an attempt to understand why genetic data have been presented in the way that they have in the debate on the Mesolithic-Neolithic transition; and to discuss some problems of cross-disciplinary communication and the effects of different disciplinary aims and cultures. Is it just that genetics is too large, too self-sufficient, too complex a field? Or is it that ‘archaeogenetics’ was initially an interesting sideline to most geneticists, and the historical (or socio-cultural) side was simply not worth the intellectual investment? Or is it that (anthropologically-trained) archaeologists have in the main found it difficult to engage with the data and impli-

cations of the methodologies – such as the modelling of population genetics and molecular biology – at the level of detail required? If geneticists may have been disappointed in the inability of most archaeologists to be able to engage at the technical/methodological level, on the archaeological side such frustration and even resentment was compounded by the lack of consultation from geneticists and the minimal or dated use of archaeological data, publications and relevant theory. Equally, geneticists may have found the comparatively slow productivity of archaeologists and relevant archaeological data irritating: anecdotally, Cavalli-Sforza was said to want to stop working with archaeologists because they took so long to produce results, as compared with genetic analyses. National and international disciplinary expectations (surely compounded by exercises such as the UK government’s system of measuring and rewarding research output, or similar systems in other countries such as citation counts), really do structure different norms of activity, especially across very different disciplines, and what it is intellectually worth ‘investing’ in. Such barriers are likely to be particularly high at the inception of a new and initially unrelated technique/approach.

Nevertheless, we have to find ways of not just talking to, but communicating with each other in meaningful ways in which we can all start to understand the challenges and limitations as well as possibilities of new methods and ideas. Genetics is, of course, also a continually changing field, with new data and new techniques continually being produced, explored and refined. We certainly have not reached the limit of what genetics can tell us about some past processes. Such studies also often act to stimulate new archaeological approaches and interpretations, or suggest boundaries to existing explanations, and this will continue to happen. Archaeology is an especially multi-disciplinary practice; genetics will for the foreseeable future be one of a battery of techniques, approaches, ideas and datasets that we will incorporate into our interpretations.

REFERENCES

- AMMERMAN A. 1989. On the neolithic transition in Europe: a comment on Zvelebil and Zvelebil (1988). *Antiquity* 63: 162–165.
- AMMERMAN A. and CAVALLI-SFORZA L.-L. 1971. Measuring the rate of spread of early farming in Europe. *Man (NS)* 6: 673–688.
1973. A population model for the diffusion of early farming in Europe. In Renfrew C. (ed.), *The Explanation of Culture Change: Models in Prehistory*. Duckworth, London: 343–357.
1984. *The Neolithic Transition and the Genetics of Populations in Europe*. Princeton University Press, New Jersey.
- ARMELAGOS G. and HARPER K. 2005. Genomics at the origins of agriculture, Part two. *Evolutionary Anthropology* 14(3): 109–121.
- BANDELT H.-J., MACAULAY V. and RICHARDS M. 2002. What molecules can't tell us about the spread of languages and the Neolithic. In P. Bellwood and C. Renfrew (eds.), *Examining the Farming/Language Dispersal Hypothesis*. McDonald Institute Monographs, Cambridge: 99–107.
- BARBUJANI G., PILASTRO A., DE DOMENICO S. and RENFREW C. 1994. Genetic variation in North Africa and Eurasia: neolithic demic diffusion vs. palaeolithic colonisation. *American Journal of Physical Anthropology* 95: 137–154.
- BARBUJANI G. and DUPANLOUP I. 2002. DNA variation in Europe: estimating the demographic impact of Neolithic dispersals. In P. Bellwood and C. Renfrew (eds.), *Examining the Farming/Language Dispersal Hypothesis*. McDonald Institute Monographs, Cambridge: 421–431.
- BELLWOOD P. 2001. Early Agriculturalist Population Diasporas? Farming, Languages, and Genes. *Annual Review of Anthropology* 30: 181–207.
2004. *First Farmers: The Origins of Agricultural Societies*. Blackwell. Oxford.
- BELLWOOD P. and RENFREW C. (eds.) 2002. *Examining the Farming/Language Dispersal Hypothesis*. McDonald Institute Monographs. Cambridge.
- BENTLEY R., PRICE T. D. and CHIKHI L. 2003. Comparing broad scale genetic and local scale isotopic evidence for the spread of agriculture into Europe. *Antiquity* 77: 63–66.
- CAVALLI-SFORZA L.-L., MENOZZI P. and PIAZZA A. 1994. *The History and Geography of Human Genes* (Abridged paperback edition). Princeton University Press. Princeton.
- CAVALLI-SFORZA L.-L. 1996. The spread of agriculture and nomadic pastoralism: insights from genetics, linguistics and archaeology. In D. Harris (ed.), *The Origins and Spread of Agriculture and Pastoralism in Eurasia: 51–69*. UCL Press, London.
- CHANDLER H., SYKES B. and ZILHÃO J. 2005. Using ancient DNA to examine genetic continuity at the Mesolithic-Neolithic transition in Portugal. In Arias P., Ontañón R. and García-Moncó C. (eds.) *Actas del III Congreso del Neolítico en la Península Ibérica: 781–786*. Monografías del Instituto Internacional de Investigaciones Prehistóricas de Cantabria 1, Santander.
- CHIKHI L. 2002. Admixture and the demic diffusion model in Europe. In *Examining the Farming/Language Dispersal Hypothesis*. McDonald Institute Monographs, Cambridge: 435–447.
- ESF (EUROPEAN SCIENCE FOUNDATION) 2004. ESF Exploratory Workshop on Archaeology and Genetics: Towards (Integrated) Archaeogenetics. http://www.edb.upstlse.fr/esf_workshop/Programme_final.pdf
- FIX A. 1996. Gene frequency clines in Europe: demic diffusion of natural selection? *Journal of the Royal Anthropological Institute* 2: 625–844.
- GAMBLE C., DAVIES W., PETTIT P., HAZELWOOD L. and RICHARDS M. The archaeological and genetic foundations of the European population during the Late Glacial: implications for 'Agricultural Thinking'. *Cambridge Archaeological Journal* 15: 193–223.
- GRONENBORN D. 1990. Mesolithic/neolithic interactions: the lithic industry of the earliest Bandkeramik culture site of Friedburg-Bruchenbrücken, Wetteraukreis. In P. Vermeersch and P. van Peer (eds.), *Contributions to the Mesolithic in Europe*. Leuven University Press. Leuven: 173–182.
1999. A variation on a basic theme: the transition to farming in southern central Europe. *Journal of World Prehistory* 13: 123–210.
- HAAK W., FORSTER P., BRAMANTI B., MATSUMARA S., BRANDT G., TÄNZER M., VILLEMS R., RENFREW C., GRONENBORN D., ALT K. W. and BURGER J. 2005. Ancient DNA from the first European farmers in 7500-year-old Neolithic sites. *Science* 310: 1016–1018.

- JONES S. 1991. Farming is in the blood. *Nature* 351: 97–98.
- JONES M., BRIGGS D., EGLINGTON G. and HAGELBERG E. (eds.) 1999. *Molecular Information and Prehistory. Philosophical Transactions of the Royal Society B* 354 (1379): 3–5.
- KEELEY L. 1992. The introduction of agriculture to the western North European Plain. In A. Gebauer and T. D. Price (eds.), *Transitions to Agriculture in Prehistory*. Prehistory Press, Madison: 82–95.
- MACEACHERN, S. 2000. Genes, tribes, and African history. *Current Anthropology* 41: 357–384.
- MIRZA M. and DUNGWORTH D. 1995. The potential misuse of genetic analyses and the social construction of ‘race’ and ‘ethnicity’. *Oxford Journal of Archaeology* 14: 345–354.
- MOORE J. 1994. Putting anthropology back together again: the ethnogenetic critique of cladistic theory. *American Anthropologist* 96: 925–948.
- PIAZZA A. 1993. Who are the Europeans? *Science* 260: 1767–1769.
- PINHASI R., FOLEY R. and MIRAZÓN LAHR M. 2000. Spatial and temporal patterns in the Mesolithic-Neolithic archaeological record of Europe. In C. Renfrew and K. Boyle (eds.), *Archaeogenetics: DNA and the population prehistory of Europe*. McDonald Institute Monographs. Cambridge: 45–56.
- PINHASI R. and PLUCIENNIK M. 2004. A regional biological approach to the spread of farming in Europe: Anatolia, the Levant, South-Eastern Europe, and the Mediterranean. *Current Anthropology* 45 (Supplement): 59–82.
- PULT I., SAJANTILA A., SIMANAINEN J., GEORGIEV O. SCHAFFNER W. and PAABO S. 1994. Mitochondrial DNA sequences from Switzerland reveal striking homogeneity of European populations. *Biological Chemistry Hoppe-Seyler* 375: 837–840.
- RENDINE S., PIAZZA A. and CAVALLI-SFORZA L.-L. 1986. Simulations and separation by principal components of multiple demic expansions in Europe. *The American Naturalist* 128: 681–686.
- RENFREW C. 1992. Archaeology, genetics and linguistic diversity. *Man (NS)* 27: 445–478.
1996. Language families and the spread of farming. In D. Harris (ed.), *The Origins and Spread of Agriculture and Pastoralism in Eurasia*. UCL Press, London: 70–92.
1997. World linguistic diversity and farming dispersals. In R. Blench and M. Spriggs (eds.), *Archaeology and Language I*. Routledge, London: 82–90.
- RENFREW C. and BOYLE K. (eds.) 2000. *Archaeogenetics: DNA and the population prehistory of Europe*. McDonald Institute Monographs. Cambridge.
- RICHARDS M., CORTE-REAL H., FORSTER P., MACAULAY V., WILKINSON-HERBOTS H., DEMAINE A., PAPIHA S., HEDGES R., BANDELT H.-J. and SYKES B. 1996. Paleolithic and neolithic lineages in the European mitochondrial gene pool. *American Journal of Human Genetics* 59: 185–203.
- RICHARDS M. 2003. The Neolithic invasion of Europe. *Annual Review of Anthropology* 32: 135–162.
- SIMS-WILLIAMS P. 1998. Genetics, linguistics, and prehistory: thinking big and thinking straight. *Antiquity* 72: 505–528.
- SKEATES R. 1994. Towards an absolute chronology for the Neolithic in central Italy. In R. Skeates and R. Whitehouse (eds.), *Radiocarbon dating and Italian prehistory*. Accordia/British School at Rome, London: 61–288.
- SOKAL R., JACQUEZ G., ODEN N., DIGIOVANNI D., FALSETTI A., MCGEE E. and THOMSON B. 1993. Genetic relationships of European populations reflect their ethnohistorical affinities. *American Journal of Physical Anthropology* 91: 55–70.
- SOKAL R. and MENOZZI P. 1982. Spatial autocorrelations of HLA frequencies in Europe support demic diffusion of early farmers. *The American Naturalist* 119: 1–17.
- SOKAL R., ODEN N. and WILSON C. 1991. Genetic evidence for the spread of agriculture in Europe by demic diffusion. *Nature* 351: 143–145.
- TERRELL J. and STEWART P. 1996. The paradox of human population genetics at the end of the twentieth century. *Reviews in Anthropology* 26: 13–33.
- TORRONI A., BANDELT H.J., D’URBANO L., LAHERMO P., MORAL P., SELITTO D., RENGÓ C., FORSTER P., SAVONTAUS M.-L., BONNE-TAMIR B. and SCOZZARI R. 1998. mtDNA analysis reveals a major Late Paleolithic population expansion from southwestern to northeastern Europe. *American Journal of Human Genetics* 62: 1137–1152.
- WILKINSON-HERBOTS H., RICHARDS M., FORSTER P. and SYKES B. 1996. Site 73 in hypervariable region II of the human mitochondrial genome and the origin of European populations. *Annals of Human Genetics* 60: 499–508.

ZILHÃO J. The spread of agro-pastoral economies across Mediterranean Europe: the view from the far west. *Journal of Mediterranean Archaeology* 6: 5-63.

ZVELEBIL M. (ed.) 1986a. *Hunters in Transition: Mesolithic Societies of Temperate Eurasia and their Transition to Farming*. Cambridge University Press. Cambridge.

1986b. Mesolithic societies and the transition to farming: problems of time, scale and organisation. In Zvelebil M. (ed.) *Hunters in Transition: Mesolithic Societies of Temperate Eurasia and their Transition to Farming*. Cambridge University Press. Cambridge: 167-188.

1989. On the transition to farming in Europe, or what was spreading with the Neolithic: a reply to Ammerman (1989). *Antiquity* 63: 379-383.

1996. Farmers our ancestors and the identity of Europe. In P. Graves-Brown, Jones S. and Gamble C. (eds.), *Cultural identity and Archaeology: The Construction of European Communities*. Routledge, London: 145-166.

2000. The social context of the agricultural transition in Europe. In C. Renfrew and K. Boyle (eds.), *Archaeogenetics DNA and the population prehistory of Europe*. McDonald Institute Monographs. Cambridge: 57-79.