

# DNA and Etruscan Identity

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## Introduction

The question, ‘Who were the Etruscans?’ has long been a knotty problem. From Herodotus to the present day it has been debated (Aigner Foresti, 1974). Putting aside for now romantic notions of ‘mysterious Etruscans’, in recent decades the academic debate has been largely settled. Since Massimo Pallottino (1947), redefined the question, a convincing academic consensus has been built that defines the Etruscans as an autochthonous, non-Indo-European speaking people, with roots that can be traced back to at least the Late Bronze Age in Italy. So much so that the label ‘Villanovan’ given to their predecessors is now, gradually giving way to the pseudo-evolutionary title Proto-Etruscan (Ward-Perkins 1959, 11), emphasising the continuity of population in Etruria between the Prehistoric Iron Age and the slightly more historical Etruscan period. The situation is summed up by Sybille Haynes: ‘The Early Iron Age civilization of the villages from which the later Etruscan communities developed *in an unbroken sequence* is known as the Villanovan ...’ (Haynes 2000, 4, my emphasis). Any academic opinion that diverges from this orthodoxy is generally automatically viewed as ill-considered and outside of the mainstream of Etruscology.

It therefore came as something of a surprise in early 2007 to read in the world’s media that we are all wrong. The story was scooped by the *Turkish Daily News*: ‘DNA shows Etruscans come from Anatolia’ (9th February 2007); followed by the *New Scientist* reporting ‘On the origin of the Etruscan Civilisation’ (14th February 2007); *Economist.com* ‘The origins of the Etruscans. Cowabunga’ (15 February 2007); *Telegraph.co.uk* ‘Genes prove Herodotus right about the Etruscans’ (18 February 2007); *The New York Times* ‘DNA Boosts Herodotus’ Account of Etruscans as Migrants to Italy’ (3 April 2007); and finally *Guardian Unlimited* ‘The enigma of Italy’s ancient Etruscans is finally unravelled’ (18 June 2007). Clearly the media thought a scientific breakthrough had occurred. This essay investigates the matter and explores the recent contributions of molecular biology to Etruscology.

The root of the stories lies in two academic articles: Achilli *et al.* (2007) ‘Mitochondrial DNA Variation of Modern Tuscans Supports the Near Eastern Origin of Etruscans’ published in *The American Journal of Human Genetics*, and Pellecchia *et al.* (2007) ‘The mystery of Etruscan origins: novel clues from *Bos taurus* mitochondrial DNA’ published in the *Proceedings of the Royal Society B*. These two articles are in authoritative and respected scientific journals but they are not widely read by Etruscologists, hence the media stories were surprising. The titles of the articles provided the inspiration for the headlines: a heady mix of ancient mystery and 21st-century science. The articles themselves directly challenge a widely held consensus in Etruscan studies, and what is more, they were both written as the latest episode in a growing body of new scientific studies

of Etruscan origins that challenge the consensus. The challenge was first met in late 2006, by Jean MacIntosh Turfa, before the two latest articles appeared, who concluded ‘Certainly, in the light of current expertise on DNA, there is no more reason to believe Herodotus now than there ever was’ (Turfa 2006, 5). We will return to the detailed consideration of the scientific articles, but first of all it is important to examine the current archaeological consensus and consider why the academic world, outside of molecular biology, is so convinced that it has already solved the problems of defining the Etruscans through the study of their origins.

Even before studying the consensus, it is useful to ask why we are at all interested in the origins of the Etruscans, apart from natural human curiosity, after all, as David Ridgway observed ‘Not many authors of general books about the Romans feel bound to discuss the alleged Trojan ancestry of their subject’ (1993, 109). The clearest answer to the question comes from ancient words: the words of the Etruscans themselves, and the words of the Greeks and Romans who wrote about them, often much later. It is widely believed that the Etruscans wrote, and so spoke, a non-Indo-European language (see Penney this vol.). This would seem to mark them out as different from all of their neighbours, who did speak Indo-European languages. The frequent rôle of language as an indicator of ethnic identity reinforces the suggestion that the use of the Etruscan language might distinguish a distinct ethnic group.

This language difference demands an explanation, and one possible answer is that the Etruscan speakers were migrants to prehistoric Italy from elsewhere, where people used a now lost, precursor of the Etruscan language. This explanation gains support from Herodotus (I, 94): the ‘Father of History’ says the Etruscans came to Italy from Lydia, now in South Western Turkey. He wrote this explanation in the mid-5th century BC, and it was repeated by all but one ancient source. This version of Etruscan ethnogenesis was, as far as can be told, believed in the ancient world and continued to be the accepted consensus up until the mid-twentieth century. The Herodotean consensus was not however unchallenged: several competing explanations emerged.

One, first put forward by Nicolas Fréret in AD 1741, suggested an origin in Germanic areas North of the Alps (Stenger 1994; Pallottino 1985, 86). An apparent support for this theory is shared elements of material culture that are found in the Iron Age Urnfield Cultures of circum-Alpine areas that extend as far south as central Italy. These connections certainly exist, for example Gabriele Zipf has recently examined the similarities – and differences – in figurative decoration of artefacts in France and Italy between the Late Bronze and Early Iron Ages (Zipf 2004). Another study of Italian metalwork has identified connections, particularly in

the sun-boat / bird protome motif, that suggest the movements of artisans from central Europe and the Baltic between the 10th and the 8th centuries (Iaia 2005, 238–43). The similarities are usually not now considered to be the result of the mass movements of peoples, but rather the result of shared cultural traits, similar, tribal, levels of social complexity and trade (Peroni 2004, 166–71). However, from the Villanovan period onwards, as Etruscan culture develops, study of the Urnfield phenomenon in Etruria tends to be rather compartmentalized from its study north of the River Po, and potentially rewarding systematic comparative study between the two areas is rarely undertaken, despite the recent spectacular growth in knowledge of the Iron Age in Italy north of the Po and neighbouring areas (Marzatico and Gleirscher 2004, 161–449). In the Etruscan period it is the Mediterranean connections that take centre stage, although cultural and economic exchange across the Alps is well documented and studied, even if there are still gaps in the archaeological record (Aigner Foresti 1992; Parlavacchia 1992, 157–221; Camporeale 2004).

An alternative theory to the northern origin has been a suggestion that the Etruscans were originally Phoenicians. This theory, derived from skull measurements, was proposed by Giustiniano Nicolucci (1865), and hesitantly promoted in detail by Luigi Calori (1873) with interpretations of Greek history and Egyptian records, and analysis of religious structures and subsequently criticized by Richard Burton (1876, 187–211). Comparative anatomy as a tool for identifying Etruscan origins was popular in the second half of the 19th century, and data collected then, and later, suggested that Etruscan skulls were more dolicho-mesocephalic than brachycephalic (Claassen and Wree 2004, 163). In the early 20th century Boas (1910) convincingly suggested that local environmental factors perhaps had more influence upon the cephalic index than genetic heritage, thereby casting doubt upon the viability of identifying geographical origins from cranial metrics. Subsequently, as a result, in Etruscan studies, the Etruscan phenotype, here their physical anthropology, has not played a major rôle in the debates about Etruscan ethnogenesis. However, recent re-evaluations of Boas' data have suggested that too much emphasis was given to environmental factors and that genetic inheritance does indeed play a significant rôle in skull shape of the phenotype (Sparks and Jantz 2002; Holloway 2002). Metrical studies of Etruscan skeletal materials continue, although emphasis has turned from identifying geographical origins or typological studies to documenting the variations and patterning in the skeletal remains of Etruscan populations (e.g. Moggi-Cecchi *et al.* 1997; Pacciani, *et al.* 1996; Rubini *et al.* 2007). Recently, cranial metrics have indicated that Etruscan skulls from Tarquinia are similar to Hallstatt period skulls from Hallstatt in Upper Austria and La Tene period skulls from Manching Southern Bavaria, and therefore less likely to be the skulls of people from the Levant (Claassen and Wree 2004). These observations might refute Nicolucci's theory of a Phoenician origin but have not yet been used to resurrect the hypothesis of northern origins for the Etruscans. In contrast another study of Pre-Roman Italian skulls (Rubini *et al.* 2007) has demonstrated that the principle difference is between skulls from east and skulls from west of the Apennines, with further differences between skulls from Etruria / Latium and those from sites in

Campania (Pontecagnano and Sala Consilina). This study does not suggest that the Etruscans were an intrusive population, but it does identify unexpected differences between skulls from Etruria and from sites in Campania that are usually considered as the prime exemplars of Villanovan / Etruscan presence (if not colonization) in that area. A colonization of Campania from Etruria in the Iron Age would lead to the expectation that skulls from the two areas would be similar if the colonization involved any movement of people. However, it should be noted that the dating of the skulls is not precise and the data presented (Rubini *et al.* 2007, 120) does not enable an assessment of the likelihood that the Tuscan and Campanian samples are contemporary. Osteoarchaeological studies do not yet provide an unequivocal answer: an earlier study of early first millennium teeth from central Italy found homogeneity in central Italic and Etruscan populations (Coppa *et al.* 1997) and did not find significant East – West differences (Coppa *et al.* 1998) and another suggested skeletal material from Tarquinia was similar to that from other parts of Italy (Rubini *et al.* 1997). Preliminary studies of Etruscan teeth, compared to others from Osteria dell'Osa and Alfedena do not demonstrate significant dental differences between Etruscan and Italic populations (Moggi-Cecchi *et al.* 1997). The physical anthropology of the Etruscans does not currently provide evidence for an origin outside of Italy.

The theory that the Etruscans were, in effect, Phoenicians did not find much favour. Particularly as Etruscan and Phoenician are different languages. However, there are Oriental connections in Etruria that are indicated by the presence of Near Eastern cultural traits and of material culture either imported from the Eastern shores of the Mediterranean or stylistically deriving its inspiration from Anatolia, Syria, Phoenicia and Palestine: the phenomena we use to characterize the Orientalizing Period (720–575 BC), (Burkert 1992, 14–25; Torelli 1985, 17–74; Haynes 2000, 47–134). It is these Oriental connections, and a faith in Herodotus, that help to keep alive the notion that the Etruscan peoples themselves might have also originated in the Near East. If not in Phoenicia itself, then perhaps in Lydia as Herodotus recounts, even if conflation of Lydia with the Near East requires a rather hazy notion of where Lydia actually was, in Western Turkey.

The argument about the origin of the Etruscans is probably interminable, but the current consensus was initiated by Massimo Pallottino who argued that the real issue was not where the Etruscans came from nor the origins of their language, but the study and the understanding of formation of the Etruscan people (Pallottino 1947). Since the 1940s an immense amount of archaeological evidence has demonstrated, cultural and spatial continuity between Etruscan communities in Etruria and their Iron Age, Villanovan, predecessors. The consensus, derived from archaeological research, favours the account of Dionysius of Halicarnassus (I, 28–30) who says the Etruscans were aboriginal in Italy (written c. 9 BC). A detailed account of the problems and issues surrounding the origin of the Etruscans can be found in the authoritative Italian manual of Etruscan studies 'Etruscologia' (Pallottino 1985 or summarily in Camporeale 1997). In addition to the archaeological consensus, Dominique Briquel (1991) has meticulously dissected the historical sources and found that the Herodotean tradition of a

Lydian origin is rooted in the 6th century politics of Sardis, and has nothing to do with actual origins of the Etruscans (Ridgway 1993).

Despite the strength of the consensus it is still challenged in scholarly publications. Challenges are usually either rooted in linguistic arguments, or hypotheses based on re-readings of historical sources and unconventional readings of archaeological data (e.g. Beekes 2002; 2003; criticized by Turfa 2006, 4–5, reviewed as speculative by Wallace 2005). A key piece of evidence used to challenge the autochthonous consensus is the Lemnos stele, a fragmentary relief found on Lemnos and inscribed with an Etruscan-like language (van der Meer 2004). This may provide evidence that an Etruscan-like language may have been in use in the Eastern Aegean, close to Lydia, and so provide support to the theory of Eastern origins, as reported by Herodotus. The significance of the inscription is debated, but it has been used as one plank of a theory that suggests that future Etruscans migrated from Western Anatolia around about 1200 BC. Their arrival might be detected in Italy in the changes in the archaeological record that may be seen at the start of the Proto-Villanovan period. These putative migrants may have combined with others, from the North, who brought with them the 'Urnfield' culture, that appeared in Italy at this time (Beekes 2003; Briquel 2000; van der Meer 2004). In effect this explanation is pushing back the arrival of Etruscan migrants from the East from a time around 700 BC, when archaeology has demonstrated that it did not happen, to a time around 1200 BC when archaeology is uncertain enough that it might have happened. This hardly resolves the controversy, it only changes its chronology to a period when we know even less than we do about the Etruscan period.

#### DNA studies and molecular archaeology

Now, into this controversy come the DNA studies. Over the past 30 or so years advances in biomolecular science have revolutionized the understanding of the genetic make-up of humans and other organisms. The new knowledge and techniques that have been developed have often been controversial, partly due to their absolute scientific complexity, a daunting combination of sampling, chemistry, biology, statistics and computing, but also to their social and cultural implications, many of which are yet to be assimilated. Genetic fingerprinting is now a routine forensic procedure, even if it is sometimes contested for technical reasons; governments dream of national DNA databases to protect and control their people; genetically modified organisms are polarized as either a miracle or a plague on human health and nutrition. Clearly, social and cultural understanding and acceptance (or indeed rejection) of the results of biomolecular science have tended to lag behind the pace of scientific advances. Alongside these advances a new branch of archaeology has grown: molecular archaeology. This investigates biological molecules, particularly from DNA, that have the potential to inform about the human past. These may be actual ancient molecules, ancient DNA (aDNA), or contemporary DNA that contains molecules that can reveal aspects of an individual's genetic inheritance, most commonly features of the maternal bloodline, through studies of non-recombinant mitochondrial DNA – mtDNA (Richards *et al.* 1998; Richards and Macaulay 2001). Details of the potential and pitfalls of aDNA studies have

been discussed by Graham (2007) and Hummel (2003) and molecular archaeology more generally by Jones (2001; 2006). This is itself a new and emerging area of molecular biology and many of its findings are experimental, provisional and debated: this is the normal process of the advancement of knowledge in the sciences (Barbujani 2007), interpretations of its findings are also, naturally enough, impeded by disciplinary boundaries between archaeology and molecular biology (Jones 2006).

A controversial achievement of molecular archaeology has been the observation of a potential relation between the spread of farming from south-western Asia to north-western Europe in the Neolithic Period and the geographical distribution of distinctive, and variable groups of genes (haplogroups) that can be identified in mtDNA – whether ancient or modern. This has resurrected diffusionist models for explaining culture change that were unpopular in the second half of the 20<sup>th</sup> century, and also added an ingredient to the debate over the origin and distribution of Indo-European languages, which could be linked to the spread of farming (Bellwood 2004) and the spread of human DNA haplogroups (Ammerman and Cavalli-Sforza 1984; Renfrew 1992; Renfrew and Boyle 2000; Cavalli-Sforza 1997b; Cavalli-Sforza 1998; Clark 1998; Otte 1998; Zvelebil 1998 with relative bibliographies). The debate continues as techniques are refined, data sets grow and different approaches to the study of human biological material are integrated. Current theories may be polarized into two camps, those who promote the Neolithic as introduced into Europe by movements of *peoples* from the Near East (the demic diffusion model) (e.g. Cavalli-Sforza 2003; Belle *et al.* 2006a; Barbujani and Chikhi 2007) and those who advocate the transmission of *ideas* to Mesolithic populations (the cultural diffusion model) (e.g. Haak *et al.* 2005), with others preferring a blended model of explanation (e.g. Renfrew 2001; Torroni *et al.* 2006). It may be observed that the molecular biologists preferring the demic diffusion model tend to work less closely with archaeologists. The most recent developments in the analysis of complete mtDNA sequencing seem to have established that the basic human population of Europe was established in the Late Palaeolithic, and subsequent gene flow from the east has been limited, therefore seriously undermining the theory of demic diffusion (Torroni *et al.* 2006).

This is not the place to engage with the details of a Neolithic argument that would usually pass by Etruscologists as a squabble from the mists of prehistory. However, its ingredients, the distribution of Indo-European languages, movements of people, and diffusion from the East are actually the same factors that combine in the debate over Etruscan origins. The Etruscan correlates of the Neolithic debate are the combination of the hypothetical Anatolian origin of Etruscan language and the Herodotean account of Lydian origins for the Etruscan people. These are the same elements that were combined in Briquel's discussion of Etruscan origins that placed potential Etruscan ethnogenesis in the Bronze Age (2000). Disregarding the archaeological consensus of an autochthonous origin, the population geneticists have taken the opportunity to solve the mystery of Etruscan origins, by adding a final ingredient: the distribution of molecules in DNA in Italy and neighbouring areas. Viewed without the context of archaeological interpretation, the Etruscans form an attractive laboratory for

studying ancient population genetics. They were, potentially, a people different from their neighbours, they spoke a different language, they came from elsewhere. Therefore it should be possible to identify a genetic heritage that both characterizes the Etruscans and differentiates them from their neighbours and to analyse their genetic inheritance and heritage.

Interest in Etruscan human biology predates the new genetic techniques. In 1959 a conference addressed the issue, bringing together experts in the archaeology with human biologists (Wolstenholme and O'Connor 1959). Particular attention was paid to the infant genetic science and to blood groups, although no firm conclusions were reached. Interest in the scientific approach to the question was revived in the late 1980s. Piazza *et al.* (1988; 1997) analysed blood group gene frequencies of modern populations in Italy using principle components analysis and identified that the second principle component was distributed within ancient Etruria. Although acknowledging some of the methodological limitations, the authors went on to note similarities between the distributions of the genes, and the peoples of pre-Roman Italy, as surmised from the distribution of ancient languages, and to suggest that the similar distribution patterns would have had similar causes. The distribution and identification of language groups was only discussed using high level generalizations and the automatic association of particular languages with pre-Roman ethnic groups was assumed rather than demonstrated. Perhaps this association is not surprising; it is a common assumption, underlying most histories of pre-Roman Italy, (e.g. Pallottino 1984; 1991), that has been only subsequently investigated more subtly and questioned (Wilkins 1990; Penney this vol.). Nevertheless, compared to more recent studies, the authors go into greater depths to explore the linguistic evidence and come to the remarkable conclusion that the distribution of pre-Roman peoples is the major determinant in the distribution of blood groups in modern Italy (Piazza *et al.* 1988, 211–12).

A subsequent study (Barbujani and Sokal 1991) re-used some of the same data as Piazza *et al.* (1988) but tested different hypotheses. Barbujani and Sokal (1991) demonstrated an association between sharp changes in the geographic distribution of blood group genes and early 20th century dialect boundaries in Italy (some of which coincided with geographic boundaries). The clearest coincident boundaries were found between Sardinia and Corsica and the mainland, and between Friuli and the Veneto. A lesser association was found between the boundaries of the distribution of Tuscan dialect and genetic variations. This association would seem to have little direct relevance to Etruscan genetics given the apparently limited relation between the Etruscan language and the *gorgia toscana*, the Tuscan dialect (Izzo 1972; Agostiniani and Giannelli 1983), although some relationship does remain a possibility (Bonfante 2004). However, later studies have gone on to demonstrate a correlation between genetic variation in the Y (male) chromosome and language families (Poloni *et al.* 1997). This study also developed statistical approaches that applied quantitative methods capable of comparing populations more objectively and offering the possibility of a reduced reliance on *a priori* theoretical assumptions of, for example, an evolutionary, geographical or linguistic nature (Barbujani 1997). Although the correlation between gene variability and language has

been demonstrated beyond reasonable doubt, discussion of the possible explanations for the correlation has been limited. General observations have been made about the limitations that language barriers might present to the exchange of genetic materials, the power of geographical obstacles (mountains and seas) to keep individuals apart (Barbujani and Sokal 1991, 408) and possible resultant endogamy in archaic societies (Rubini *et al.* 2007, 120). The distribution of Italian surnames has also been used to investigate genetic, geographical and linguistic barriers in Italy (Zei *et al.* 1993) and they were found to be interrelated, but the study provided no strong evidence that may be related to arguments about the Etruscans.

Another feature of the distribution of gene variability in Europe that has been demonstrated by many studies is a gradient of variability, or cline, from the South West of Asia towards the North West of Europe (e.g. Belle *et al.* 2006a; Rosser 2000), and particularly in the Mediterranean region (Simoni *et al.* 2000). This cline is a central support of the demic distribution model for the Neolithic colonization of Europe by farmers spreading from the Near East (Ammerman and Cavalli-Sforza 1984). The variability in the mtDNA haplotypes in modern samples from southern Tuscany has been demonstrated to lie between the low variability found in Basque samples and the high variability in the Near East, at either extreme of the cline (Francalacci *et al.* 1996; 1997). This observation, the authors suggested, demonstrated that the Etruscan population was effectively descended from the Neolithic population, an observation supported by the interpretation of their language as a relic of pre-Indo-European times, and that a higher genetic diversity in Etruscans, when compared to other populations, was due to later contacts with other peoples (Francalacci *et al.* 1996, 458). This study therefore suggested that the ancestors of the Etruscans were resident in Italy from the Neolithic onwards, supporting the current archaeological consensus of an autochthonous origin.

### Population genetics

Since about 2000 the study of population genetics has made significant advances in its methodology, particularly in the adoption of statistical techniques to interpret laboratory findings, the development of computer simulation techniques to model population histories, the extraction and analysis of ancient DNA and the development of techniques that can analyse sections of the genome that are larger than the single molecules that were the focus of earlier studies (Barbujani and Bertorelle 2001; Excoffier 2004; Bandelt 2005; Gilbert 2005; Jobling *et al.* 2004; Richards and Macaulay 2001).

In 2004 the first major investigation of an ancient population using ancient DNA analysed 80 samples of Etruscan bone from ten cemeteries in Etruria and samples from Adria in the Po Valley and Capua in Campania (Vernesi *et al.* 2004). Despite its general title, the article asked two specific questions: 1) were the Etruscans a biological population or just people who shared a culture but not ancestry, and 2) what is their relationship to modern populations and are they linked to other Eurasians (Vernesi *et al.* 2004, 695). The first question is interesting because it directly addresses a basic assumption, that the Etruscans were a people. The assumption is rarely questioned in Etruscology, after all the Roman sources identify the Etruscans (the *nomen Etruscum*) as a group, even if they are

then sub-divided into the *duodecim populi Etruriae* (twelve peoples of Etruria) (Torelli 1985b; Colonna 2000; Perkins 2005, 110), and so we assume they were a people. Vernesi *et al.* are, of course, investigating a technical meaning of ‘a people’, as having actual shared genetic ancestry. They found, in answer to the first question, that the internal genetic diversity in the Etruscan DNA was low, similar to modern European populations. This conclusion is important to genetic studies of the Etruscans since it validates the comparative approach that compares Etruscan DNA signatures with those of other peoples. However, it must be noted that the conclusion is only comparative – Etruscan genetic diversity is only comparable to the diversity found in other peoples: there is no distinct Etruscan ‘fingerprint’ this study identifies that can be equated with the Etruscans. Before moving on, it is also worth noting that most Etruscologists would question the premise that Etruscans might be *either* a biological population *or* just people who shared a culture but not ancestry. Etruscan culture was diverse and geographically variable, and the notion that Etruscans shared ‘a culture’ is an imprecise generalization. At best a collection of cultural traits, features, artefacts etc. may, in combination, be used to characterize Etruscans, but the principle of equating a people with a culture is now outmoded and typical of culture-historical approaches that were prevalent in the mid-20th century (Trigger 1989, 148–206). Furthermore, Etruscans palpably did share an ancestry: at a local level the existence of the gentilicial system of family structures based on blood-lines is directly observable in onomastics and shared chamber tombs over several generations. Genetic relationships between individuals from the same chamber tomb have also been demonstrated using mtDNA evidence (Cappellini *et al.* 2004a; 2004b). Indirectly, cultural and settlement continuity from the Late Bronze Age to the Etruscan period would have undoubtedly led to a shared ancestry extending over at least 10 generations. This might not, in itself, be sufficient to generate the levels of genetic diversity found in the Etruscan DNA samples, but it would have been extremely surprising to discover that the Etruscans, whether historically or archaeologically defined, were not genetically related to one another. In effect the first hypothesis of Vernesi *et al.* is a further test of the observations made by Piazza *et al.* (1988) and Barbujani and Sokal (1991) concerning the association of genetic variability, language and geography, using the special case of Etruria and the Etruscans and analysing ancient, as opposed to modern, DNA. The confirmation of the first hypothesis not so much establishes the existence of an Etruscan population as confirms low levels of genetic diversity within skeletal material of people who presumably spoke Etruscan, in a limited geographical area of Italy, c. 2500 years BP, and the confirmatory low levels of genetic diversity are established with reference only to modern populations. Rather perplexingly, the discussion of the results concludes ‘the genetic data of this study suggest that either the people whom we call “Etruscans” shared a set of ancestors ... or they were mixed with people whose mitochondrial features did not differ from theirs’ (Vernesi *et al.* 2004, 701). So ‘the Etruscans’ either had shared ancestors or they had ancestors whose maternal genetic legacy was not ‘Etruscan’ but is indistinguishable from ‘Etruscan’ mtDNA. This conclusion calls into doubt the first question, that the Etruscans can be

distinguished as a genetically isolated people, by the results of this study, even though their mtDNA genetic diversity is low.

### Ancient and modern genetic diversity

The second aspect of the paper, that can be formulated a little more precisely than is done by the authors (Vernesi *et al.* 2004, 695), is the investigation of the relationship between the genetic diversity in the ancient DNA extracted from skeletal material from ancient Etruria (rather than just ‘the Etruscans’) and the genetic diversity observed in modern populations. This, too, is an interesting question to ask. The sub-text of the investigations is made apparent by the second part of the question ‘Do these relationships suggest any *genealogical or migrational* links between the Etruscans and other Eurasians?’ (my emphasis). Clearly the results are expected to contribute to establishing the origins of the mysterious Etruscans. The results are not clear-cut: at the level of alleles Etruscans were found to have less genetic resemblance to modern Tuscans than there is resemblance between randomly chosen modern European populations (Vernesi *et al.* 2004, 699). However, analyses of DNA sequence alignments indicate that the shortest genetic difference in the samples that were compared is between the Etruscans and the Tuscans, with the Turks, other Mediterraneans and the Cornish following after. An alternative means of comparison – the admixture coefficient (Dupanloup and Bertorelle 2001) – suggests Etruscans are more closely related to Turks and North Africans than to Basques and North East Europeans. The authors admit that this measure should not be taken at face value: this is particularly the case because the coefficient used requires the assumption that the Etruscans were a hybrid of long-separated parent populations (Dupanloup and Bertorelle 2001, 672), and there is no archaeological justification for this assumption. At best, this analysis suggests that the Etruscans are more likely to have components of Turkish or North African DNA than the Tuscans, Southern Italians and Sicilians, and it should be noted that the standard errors are very large.

In summary, Etruscan DNA has affinities with some modern European populations, including Tuscans and these ‘do not seem to point to any migrational contact but rather to a common origin of various European gene pools’ but there might be more genetic inheritance ‘from the eastern (and possibly southern) Mediterranean’ than has been observed in modern Italian populations (Vernesi *et al.* 2004, 702). Therefore these summary conclusions would tend to support an autochthonous origin for the Etruscans – autochthonous that is in as much as their DNA is similar to that of other Europeans, but without excluding some component of female derived DNA originating in the eastern or southern Mediterranean.

### Reception and reaction

The novel paper by Vernesi *et al.* was immediately controversial in biomolecular circles. Bandelt (2004) identifies some unlikely mutations that suggest the DNA samples were suffering from post-mortem damage, technical errors in the HVR-I mitochondrial sequences and the network of haplotypes, and unclear application of quality assurance criteria in identifying the Etruscan authenticity of the DNA sequences. Bandelt (2004) concludes by expressing reservations over the

comparability of the ancient DNA with modern samples. Malyarchuk and Rogozin (2004) reanalyzed the nucleotide sequences of the Etruscan skeletal material and noted that many of the previously observed mutations were specific to the Etruscan aDNA and either rare or absent in modern populations, this led them to suggest that significant post-mortem changes to DNA may lead to unreliable identification of modern haplogroups in sequences in the ancient samples. Subsequently, the authors of Vernesi *et al.* (2004) defended their position, largely by assertion, and corrected the errors that they accepted had been observed (Barbujani *et al.* 2004). The point was also made that understanding of the mutation rate of mtDNA and quality assurance in aDNA studies is still developing. Essentially the criticism, and defence, of Vernesi *et al.* (2004) illustrate the healthy practice of scientific debate and criticism. The criticisms do not, necessarily, invalidate the various rather tentative conclusions of Vernesi *et al.* (2004).

Serious procedural and quality assurance concerns were subsequently identified by Bandelt (2005) for aDNA investigations in general, often citing Vernesi *et al.* (2004) as a particular instance. Bandelt's principal concern was that aDNA studies fail to demonstrate that the DNA sequences they recover are authentically ancient and not the result of post-mortem modification, pre-sampling contamination, in excavations or museum stores, contamination in the laboratory setting, or they are not artefacts created by analytical procedures (Bandelt 2005, 1110). Similar reservations were also raised by Thomas *et al.* (2005) who suggest that the simple application of protocols to assure authentication of aDNA is not sufficient and that researchers should also take 'a more cognitive and self-critical approach' and explain why their data should be believed. There has, then, been some re-evaluation of the optimistic early results of aDNA studies, but there is still much potential in the study of aDNA, as methodologies and theoretical approaches develop (Jones 2006, 42).

Thomas *et al.* (2005, 543) also reserve particular criticism for DNA population studies (including Vernesi *et al.* 2004), noting that 'diachronic interpretation of ancient samples, as representatives of past ethnic entities that can be directly compared with modern samples of present ethnic or national groups, is done largely in an a theoretical vacuum'. In addition to the absence of theory, one might add that most studies are carried out in the absence of archaeologists, thus the conclusions derived from the genetic studies are not, typically, subjected to archaeological critique, as for example the above generalized discussion of Vernesi *et al.* (2004). Thomas *et al.* (2005, 543) go on to criticize the 'interpretive gap between reconstructing a complex series of historical processes and measuring genetic differences', or to put it another way the 'interpretive gap' between the domain of the archaeologist and the geneticist. The gap does not need to exist: it results from the limited interdisciplinarity of the population studies (Jones 2006, 49). This essay will go on to attempt to build a bridge across that gap, as it occurs – starting from the archaeological side.

The implications of the conclusions of Vernesi *et al.* (2004) that, amongst modern populations, Tuscans have the shortest genetic distance from the Etruscan aDNA but share only two genetic lineages (haplotypes), have been investigated further by Belle *et al.* (2006b). This study attempts to simulate possible

population histories that could have led to the degree of relatedness between Etruscans and Tuscans that was observed by Vernesi *et al.* (2004). The validity of the comparison between the aDNA with the modern DNA has methodological difficulties, given the reservations about the validity of the aDNA as truly representative of 'Etruscans' (Bandelt 2005, 1110; Thomas *et al.* 2005). However, Belle *et al.* do consider the implications for their modelling, and assert that systematic errors and inappropriate comparisons would not affect the conclusions derived from their modelling. In essence they argue that altering the parameters of their simulation does not alter the conclusions they come to concerning the models they are testing (Belle *et al.* 2006, 8015). The study is therefore best considered more as modelling possible population histories rather than a systematic comparison of aDNA and modern DNA samples.

From an archaeological perspective, a more cogent criticism of the paper is that the assumptions used to develop the various hypothetical population trajectories that are tested are not valid for the Etruscan period. The key assumption that the authors make is that social stratification is 'the existence of genetic differences between a small social elite and the bulk of the population' (Belle *et al.* 2006, 8012) and that the Etruscans are only a social elite within a more general, but unspecified, population. In effect the authors are assuming that the Etruscans are a 'transnational isolate', that is an endogamous, genetically coherent population, geographically shifted into a surrounding population (Jobling *et al.* 2004, 388–96) in effect an immigrant elite. The notion of the Etruscans as solely a social elite seems to have been picked up by Belle *et al.* from Vernesi *et al.* (2004) who note when discussing their results:

Social structure may have affected these results. All skeletons we typed were found in tombs containing artifacts that could be attributed with confidence to the Etruscan culture. Those tombs typically belong to the social elites (Barker and Rasmussen 1998), and so the individuals we studied may represent a specific social group, the upper classes. (Vernesi *et al.* 2004, 701–2).

This generalisation that social structure may have affected these results is a truism for any archaeological work, and much of our evidence for the Etruscans does indeed derive from the social elite. However, as it happens, the cemeteries from which the samples of Vernesi *et al.* were taken do not appear to have represented the highest classes in Etruscan society. It is not possible to be certain because the precise archaeological contexts are not provided, but the six samples labelled Magliano/Marsiliana are from cemeteries more likely to represent middle classes of society (Perkins 1999, 80–96). The bones are unlikely to be from the élite Banditella cemetery at Marsiliana since bone is poorly preserved there (Minto 1921). The bones sampled by Vernesi *et al.* could well be biased towards 'upper classes', but there is no archaeological reason to assert that they therefore represent Etruscans as opposed to a distinct, more general, class of individuals living in Etruria.

The definition of social stratification as having a genetic basis is not widely shared in archaeology. Support for the assertion by Belle *et al.* is provided with a general reference to Renfrew (1989). Presumably Belle *et al.* intend to refer to Renfrew's 'élite dominance' model for language replacement as an illustration of social stratification (Renfrew 1989, 124–5), but this does not include any suggestion that social status has a

genetic component. The assumption by Belle *et al.* that a social elite is a genetically distinct population within a separate non-elite population is not a scenario commonly suggested by archaeologists. It is a theoretical possibility that might be tested in the historical period, for instance in the Anglo-Norman aristocracy of the 11th–12th centuries AD, and in this case the elite also introduced a dominant language. Genetic studies of Indian castes in a small area of south India have demonstrated that higher ranking castes have features of their genetics that are systematically distinct from lower ranking castes (Bamshad *et al.* 2001). Yet these genetic differences are not reflected in the external phenotype in India and so cannot have been a conscious basis for social stratification. The contemporary genetic differentiation between castes is a result of the long term maintenance of partially endogamous social stratification rather than its cause (Bamshad *et al.* 1998). The findings that higher ranking castes have closer genetic affinity to West Eurasian populations than lower ranking castes (Bamshad *et al.* 2001), is evidence for the complexity of human population genetics in the subcontinent rather than the genetic legacy of a wave of Indo-European immigrants establishing an elite dominating Dravidic-speaking ‘natives’ in a colonialist reconstruction (Cavalli-Sforza *et al.* 1994). However, the assumption could only be applicable to ancient Etruria if the Etruscans were an immigrant, endogamous population, socially dominating an autochthonous subject population who adopted the Etruscan language. Alternatively, a genetic distinction might emerge through genetic drift, if the Etruscan aristocracy were to have been a long term endogamous social group. None of these conditions are accepted by the current archaeological consensus.

### Trajectories of the Etruscan population

Despite these theoretical misgivings and the doubts about the interpretation of the aDNA as a starting point representative of an Etruscan population, the simulations of various trajectories for the Etruscan population are interesting, and can be subjected to archaeological scrutiny. Belle *et al.* identify 10 different models (2006b, 8012–14). The first three, of a large, a small and a growing population bridging the genetic differences between the aDNA and the modern DNA are rejected, as not consistent with the observations. The fourth assumes a ‘founder effect’ whereby a small (and therefore with limited genetic diversity), initial population of ‘Etruscans’ are represented in the aDNA. The parameters that provided a best fit with the modern DNA requires an initial population of 770 females in a population of 9,240 Etruscans founding the genealogy of modern Tuscans, 6000 years ago, if a high rate of genetic mutation is assumed. This 12:1 male to female ratio seems rather unlikely, but the model is archaeologically interesting in that it proposes a common genealogy for Tuscans and Etruscans that stretches back into the Neolithic period along with a continuity of population and a lack of admixture from other populations. Such a model would be consistent with an autochthonous Etruscan origin at least as far back as the Neolithic, and therefore also the suggestion that the Etruscan language might be a Neolithic survival (Renfrew 1993).

The fifth model introduces a ‘bottleneck’ into the simulation, positing that ‘Etruscan’ population levels were severely reduced in the 2nd century BC because the Etruscans

suffered a ‘reproductive disadvantage associated with poor living conditions for the Etruscan population after their political assimilation into the Roman state’ (Belle *et al.* 2006, 8013). Bottlenecks are a mechanism used in population genetics to explain a reduced gene pool in a population: a bottleneck is a key part of the ‘out of Africa’ theory that suggests that only a limited number of humans emerged from Africa to colonise the remainder of the world, and consequently only a limited range of human haplogroups are found in descendant populations outside of Africa. Applying a bottleneck to the Etruscan gene pool could explain why so few Etruscan aDNA genes seem to occur in modern Tuscans. However, from an archaeological point of view the parameters of the simulation are not realistic. There is no consistent evidence that Etruscans suffered a ‘reproductive disadvantage’ in the late Roman Republic: for example, some individual Etruscans rose to positions of power, Maecenas (Horace *Carm.* 1.1.1), or the Emperor Otho for example (Suetonius *Otho* 1) (Ramelli 2003). Furthermore, the 2nd century BC is an unlikely date for Etruscan population loss. The 3rd century BC would be better, where there are at least military massacres and deportations of Etruscans recorded at Roselle, Volsinii and Falerii (Harris 1971, 75, 115–18; Salmon 1982, 172–4) and field survey indicates reduced rural and urban settlement in the Albegna Valley and Ager Cosanus that could be interpreted, simplistically, as a 75% reduction in population (Perkins 1999, 169). However, there is no evidence that Etruscans were *systematically* disadvantaged and suppressed as the Romans removed political autonomy from Etruscan city states and expanded political control over the Italian peninsula. Nevertheless, despite its lack of historicity the model was found to be consistent with the DNA data (Belle *et al.* 2006, 8014).

The next five models make a different assumption: that Etruscans and modern Tuscans are unrelated populations. The sixth model assumed there was no mixing between an Etruscan population and the ancestors of the modern population of Tuscans. The best-fit between these assumptions and the observations in the genetic data occurred when a separation between Etruscans and the ancestors of the Tuscans was hypothesized c. 7500 BP. The authors note that this would coincide with the early Neolithic, commenting that this would fit well with an influx of Indo-European speaking Neolithic farmers predicted by the demic diffusion model (the incoming ancestors of Tuscans) not mixing with an already autochthonous population of non-Indo-European speaking Etruscans. The Neolithic date for the emergence of an Etruscan genotype might be compatible with the archaeological model, but the notion that there would have been no genetic exchange between Etruscans and neighbouring Indo-European ancestors of the Tuscans, for over seven millennia, would seem extremely unlikely.

The seventh model assumed low levels of mixing between two populations between c. 4000 and 500 BC, and this was found to be the best fit of all the models to the observed data. The eighth model also assumed mixing but only between 500 BC and the present: to fit the data this model required an extremely low level of mixing of the population. The seventh model simulates genetic exchange between distinct Etruscans and the descendants of another population, who in an archaeological interpretation would have to be the

descendants of Neolithic incomers. As such it would entail some degree of assimilation between the two populations whilst the Etruscans retained their cultural identity. The closure of genetic exchange c. 500 does not seem to be a credible historical feature of the model since archaeological evidence indicates a high level of contact between Etruscans and other peoples of the Mediterranean for centuries after this date. Equally, the eighth model, that precludes genetic exchange before c. 500 BC, seems unlikely as there is evidence for foreign elements integrated with Etruscan society well before 500 (e.g. Ampolo 1976–7).

The ninth model simulates two separate populations, one of which is a social elite of Etruscans, assuming that the Etruscans were a small, genetically distinct, population (simulating the highly unlikely scenario of a genetically defined social stratification criticized above). Parameters producing a simulated population that was reduced from 25,000 females to 1,000 females through the 5th century BC produced a model that fits the observations, although not as well as models six and seven. This model makes little historical sense, quite apart from the notion that only an elite might be considered genetically Etruscan and produce a genetic heritage, the idea that the Etruscan elite were reduced to 1000 females individuals throughout the 5th century is not sustainable. There is much debated archaeological and historical evidence that suggests that the 5th century was a period of transition in Etruria (Anon. 1990), but there is no evidence to suggest such a massive reduction in population. Furthermore, an approximation of Etruscan population size in the 6th century derived from settlement evidence differs from this starting figure by an order of magnitude: archaeological estimates vary between about 150,000 and 250,000 women (Rasmussen 2005, 86–9).

The tenth simulation, that is not fully explained, seems to combine model nine with model eight testing a model of a social and genetic elite whose descendants only mixed, at a low rate, with another population post c. 500 BC. The model did not improve on model nine and suffers from similar real-world challenges, particularly in the placing of a large-scale Etruscan (elite) population decline in 500 BC.

Summing up, the results of the simulations derived by Belle *et al.* (2006b) can be considered in various ways. An important caveat is that there are doubts as to the extent to which the 'Etruscan' aDNA used in the study, derived from Vernesi *et al.* (2004) is authentically 'Etruscan' DNA. This undermines the basis of all the comparisons, however, the criticisms of the dataset derived by Vernesi *et al.* (2004) are not conclusive and some features of the aDNA they sequenced could still be authentic. Overall Vernesi *et al.* (2004) concluded that the Tuscans were the closest European genetic descendents of the Etruscans: the fourth and fifth models of Belle *et al.* (2006b), in effect, put some simulated parameters on this relation, but suggest that Tuscans can only be the descendants of 'Etruscans' if high levels of mutation are assumed. The sixth to tenth simulations of Belle *et al.* (2006b) that fit the observations made of the aDNA and DNA best of all, presuppose that the ancestors of the Etruscans and the ancestors of the Tuscans were not related. The high level conclusion from the study is then, that the Tuscans are 'largely descended from non-Etruscan ancestors' (Belle *et al.* 2006b, 8015), even if the

conclusion of Vernesi *et al.* (2004) that the Tuscans are the closest European genetic descendents of the Etruscans is accepted. This conclusion relates largely to questions of Tuscan origins and national sentiment and the construction of Tuscan identity. It is only of interest to Etruscologists in so much as it relates to the fate of the Etruscan gene pool. Belle *et al.* suggest this 'raises the possibility that the Etruscans, or at least their maternal lineages, went extinct' (2006b, 8015). The authors themselves seem uneasy with the notion that an entire population might genetically disappear and suggest that it might happen if 'what went extinct was a social class rather than the entire population' (Belle *et al.* 2006, 8016) recalling their idiosyncratic notion of the Etruscans as a genetically defined social elite (models nine and ten). Such a conclusion is archaeologically untenable, there is no evidence for a genocide committed on the Etruscans, or a selective exclusion of Etruscan women from reproductive processes. There is however significant evidence for social and cultural change in Etruria in the post-Etruscan period. There is also specific evidence for the arrival of external settlers in Etruria: this may be accepted in general terms, with the growth of the Roman empire and the subsequent influx of chattel slaves from conquered territories on all fringes of the Mediterranean, or in specific terms with changes in the onomastics in Roman Etruria (Papi 2000, 1–120). Belle *et al.* (2006b, 8016) conclude from their comparison and simulations that the 'mitochondrial gene pool can undergo a drastic turnover in as few as 100 generations' i.e. since 500 BC: if this did happen in Etruria, there is plenty of opportunity to identify episodes of population inflow in these 2,500 years without needing to posit a purposeful elimination of the Etruscans. This conclusion, as the authors note, also has implications for the interpretation of modern genetic distributions as consequences of the prehistoric distributions of people.

Although not a central concern of the study, all of the simulations of Belle *et al.* could also be compatible with a limited number of individuals being ancestral to the Etruscans. The authors briefly consider whether other European populations might be related to the Etruscans, focusing on the tentative suggestion that Etruscans might have some relation to Turks (Vernesi *et al.* 2004, 699), but conclude that just as with the Tuscans, there is 'no evidence of a genealogical continuity between Etruscans and modern people from Anatolia' and that any similarities are a 'consequence of contacts entailing genetic exchanges (as opposed to common origins)' (Belle *et al.* 2006, 8015). The study therefore, does not provide any evidence that ancestral Etruscans might be Near Eastern immigrants to Tuscany. However, all models are also compatible with an autochthonous origin for the Etruscans. Models four and six both indicate the possibility that the 'Etruscans' could have been distinct from other populations in the early Neolithic period, although they cannot say anything about where geographically, the ancestral Etruscans and the ancestral Tuscans were in the Neolithic. The simulated coalescence of the ancestral populations would place the emergence of a distinct Etruscan population in the early Neolithic c. 5500–4000 BC. A continuity of Etruscan population in Tuscany is consistent in general terms with the current reconstruction of Italian prehistory as being rooted in the Neolithic, with a subsequently unbroken sequence of cultural

development (Pallottino 1984, 35–75; Malone 2003). This is not to suggest that there were not movements of people and genetic flow in post-Neolithic Italy, just that a Neolithic ethnogenesis for the Etruscan people is broadly consistent with both the archaeological evidence and these simulations of Etruscan population history. Such reconstructions of population history might not be contradicted by the archaeological record, but there is no strong Neolithic archaeological evidence for a distinctive, single archaeological culture in Etruria, rather there appears to have been a series of developing and changing societies on the western coast of Italy, although none are particularly well known (Malone 2003, figs 5–7).

### Etruscans and Tuscans – no firm link

By 2006 these various investigations of Etruscan genetics had not achieved unequivocal results, but a balanced interim conclusion might be that Etruscans were an autochthonous people as far back as the Neolithic, and only slightly related to Tuscans. The paper by Achilli *et al.* (2007) that attracted so much media attention, ran counter to the previous findings, suggesting findings compatible with a Near Eastern origin for the Etruscans. Undoubtedly the media reports overstate the paper's conclusions, but the authors situate their analyses of 322 modern DNA samples taken from Tuscan individuals from Volterra, the Casentino and Murlo within the debate concerning Etruscan origins. The locations chosen to obtain the samples were selected with the *a priori* expectation that they should contain mtDNA partially inherited from ancestral Etruscans. Volterra is correctly described as 'a former major Etruscan city', the Casentino as 'part of historical Etruria' (Achilli *et al.* 2007, 761) which is probably true, but it was a region peripheral to Etruria, and Murlo is described as 'a rather isolated town of Etruscan origin' (Achilli *et al.* 2007, 759). Modern Murlo does not, however, have Etruscan origins. The Etruscan site on Poggio Civitate is 1 km distant and was abandoned in the second half of the 6th century BC (Phillips 1993, 49), although there is evidence of 4th to 3rd century occupation at Vescovado di Murlo. Any claim for the particularly Etruscan ancestry of the inhabitants of Murlo requires faith in a continuity of population location over the past 2,500 years between an abandoned hill top and a modern village, despite its place as the centre of the estates of the Bishop of Siena through the Middle Ages until the 18th century (Mendozzi 1911; pace Piazza *et al.* 1997, 69–70).

Comparison with DNA samples from other parts of western Eurasia using principal components analysis indicates that the range of haplogroups represented in the Tuscan samples from Volterra and the Casentino is similar to that found in other Italian and Aegean samples. The samples from Murlo lie slightly outside this group with a higher proportion of haplogroups that are commonly found in the Near East (HV without H and HV0, Roa, U7, and U3, Achilli *et al.* 2007, 762, fig. 1, 3). At a more detailed level 11 haplotypes in the Tuscan samples were found to be shared with samples from Near Eastern populations and furthermore these 11 haplotypes are 'absent in a total of 10,589 mtDNAs from Europe, including 2,311 mtDNAs from Italy' (Achilli *et al.* 2007, 766). The origins of the samples containing these 11 Near Eastern haplotypes are spread from the Levant through Jordan, Mesopotamia, Iraq, the Caucasus and one in Turkey (Achilli *et al.* 2007, fig. 5).

Despite this the Tuscan mtDNA has many affinities with European DNA and this is contrasted with the 'Etruscan' aDNA sequences found by Vernesi *et al.* (2004), that 'do not fit anywhere in the mtDNA landscape of western Eurasia' (Achilli *et al.* 2007, 766), because, the authors suggest, of post-mortem changes to the 'Etruscan' DNA. These are the thought provoking findings of the paper.

The conclusions drawn by Achilli *et al.* seem only loosely related to their findings. They suggest that the maternally inherited mtDNA is the 'most appropriate measure of the genetic continuity between Etruscans and modern Tuscans' (Achilli *et al.* 2007, 766). This hypothesis is nowhere tested in the paper, rather it forms an *a priori* assumption. Reconstruction of the phylogeny of the Tuscan mtDNA may seem to provide a better route towards Etruscan DNA than post-mortem modified Etruscan aDNA, but in the absence of a demonstrable genealogy linking Etruscans and Tuscans, the maternally inherited mtDNA provides only genetic information about ancestral Tuscans. It provides no measure, appropriate, or otherwise, of genetic continuity between Etruscans and Tuscans. A correlation between geography and DNA is well established, and specific patterns of genetic mutations have been identified in Tuscany, but the (partial) *spatial* congruity of Tuscans and Etruscans cannot be used to argue for *genetic* continuity that would make Etruscans the ancestors of Tuscans.

In the absence of any external suitably precise chronological control on mutation in the Tuscan mtDNA, there is no more reason to posit an Etruscan pedigree for any particular haplotype in Tuscan DNA than there is for any other. Archaeological and historical evidence of contact between Tuscany and the Mediterranean world between the Bronze Age and the Early Modern period provides a wide choice of contexts for the genetic flow into Tuscany demonstrated by Achilli *et al.* without needing to involve the Etruscans at all. Research into a chronological control is under way (Endicott and Ho 2008), but is still far from precise enough to identify a genetic flow that may be contemporary with Etruscan civilization. The conclusion of Achilli *et al.* that their data 'support the scenario of a post-Neolithic genetic input from the Near East to the present-day population of Tuscany' (Achilli *et al.* 2007, 767) seems sure enough, but their continuation that this is 'a scenario that is in agreement with an Anatolian origin of Etruscans' outstrips the evidence. 'An Anatolian origin of Etruscans' is not a hypothesis tested by the paper, in any case the archaeological consensus does not accept this as a likely hypothesis. Additionally only one of the haplotypes identified has also been found in Anatolia, the others have been found in an extensive area of south-western Asia. Furthermore, the findings are compatible with any scenario that places females with a Near Eastern genetic heritage in the population ancestral to the Tuscans (particularly the people of Murlo) at any time between (at least) the Neolithic and the near present. The title of the article 'Mitochondrial DNA variation of modern Tuscans supports the Near Eastern origin of Etruscans' therefore bears little, if any, relation to the contents of the article. Unfortunately, journalists only seem to have read the title, and shortly after, another article with an equally attention grabbing title 'The mystery of Etruscan origins: novel clues from *Bos taurus* mitochondrial DNA' (Pellecchia *et al.* 2007) added to the

mystery of how journalists interpret DNA evidence.

### The evidence of cattle-breeds

Pellecchia *et al.* (2007) sequenced bovine DNA from 11 breeds of Italian cattle, identifying Near Eastern haplotypes in Tuscan breeds. Setting this data within a discourse of the mysterious origins of the Etruscans leads to the hypothesis that the cattle arrived in Tuscany with human settlers in the Late Bronze Age. As with Achilli *et al.* (2007) it is necessary to separate the data from the unsupported hypothesis. The authors problematize Etruscan origins by stating 'Etruscan ethnogenesis still remains to be unravelled' (Pellecchia *et al.* 2007, 1175), emphasising the rôle of either Eastern cultural influence or an Eastern Mediterranean provenance, citing the Herodotean account, unconventional accounts of the origins of the people (Beekes 2003) or the language (Semerano 2003), reviving the thesis of a Semitic origin. The inconclusive DNA studies of Francalacci *et al.* (1996) and Belle *et al.* (2006) are briefly discussed and undue emphasis placed upon the suggestion by Vernesi *et al.* (2004, 702) that there may be more Eastern DNA in Etruscan aDNA than in modern Italian DNA. The authors then introduce their sequencing of bovine DNA by noting that the survival, and therefore the dispersion, of domestic cattle was dependent on human intervention, and therefore the geographic distribution of bovine genetic diversity should be influenced by human activities.

Genetic distances were calculated between samples from 164 cattle drawn from 11 Italian breeds. These were then compared with 467 samples drawn from cattle breeds across western Eurasia. Multi-dimensional scaling revealed a pattern in the results that separated most Near Eastern, Anatolian and Balkan breeds from most of the European breeds with six Italian breeds falling between (Pellecchia *et al.* 2007, fig. 1c). This geographic patterning in the genetic distance is emphasized by separating northern and southern Italian breeds from four Tuscan and Ligurian breeds (Chianina, Calvana, Maremmana and Cabannina), with the former falling closer to the European breeds and the latter between European and Eastern breeds. Geographic patterns are also detected in the distribution of haplogroups and frequencies of haplotypes in the samples (Pellecchia *et al.* 2007, 1178, fig. 2). Haplogroup T3 predominates in western and northern European breeds and also northern and southern Italian breeds. In the Tuscan, Balkan, Anatolian and Near Eastern breeds haplogroups are more mixed with T, T1 and T2 in more balanced proportions. The authors do not comment on this partial association between the external phenotype-derived classification of breeds and the haplogroup distribution in the genotype. Presumably, the association is the result of intensive selection of maternal phenotype characteristics that conform to an ideal for the breeds, restricting the genetic diversity of the breeds of cattle. The phenomenon is broadly analogous to the geographical distribution of human haplogroups with the exception that the cattle are strongly selected for the characteristics of their phenotype.

The authors estimate, through admixture analysis, that if the Tuscan cattle are considered as hybrids of European Anatolian/Near Eastern and African breeds, then 60% of their mtDNA derived from haplotypes associated with Anatolian/Near Eastern breeds, whereas the figure was close to zero for

the northern and southern Italian breeds (Pellecchia *et al.* 2007, 1178, table 1). Interpreting these observations the authors hypothesize that the bovine genetic material could only have been transferred from the Near East to Italy by either seaborne trade or by being herded by human migrants from the Near East. In the latter case, human mtDNA would be found in the same (Tuscan) locations as the bovine mtDNA. This DNA is duly found in the dataset published by Achilli *et al.* (2007), leading the authors to conclude 'the most parsimonious explanation is a single and contemporaneous arrival of humans and cattle' (Pellecchia *et al.* 2007, 1178). They suggest that this migration was pre-Roman because of the 'persistence of the same cattle breeds in Tuscany since the 1st century AD' citing Columella (*De re rustica*, VI, 1–2), as a source. The argument is difficult to follow since Columella states the cattle in '*Etruria et Latium compactos, sed ad opera fortes*' (Etruria and Latium are small but strong for work) and goes on in the next sentence to say '*Parandi sunt boves novelli*' (new types of cattle are appearing). Columella can hardly be describing the very large Tuscan breeds and directly contradicts Pellecchia *et al.*'s assumption of continuity between pre-Roman and contemporary breeds. In a further attempt to date the arrival of the Near Eastern genes in Tuscany Pellecchia *et al.* (2007, 1178) estimate the occurrence of a distinctive mutation in  $3970 \pm 2400$  years BP, i.e. 4420 BC - AD 380, with a mean of 2020 BC, that is somewhere between the middle Neolithic in central Italy (Malone 2003, 243) and the time of the Emperor Theodosius I. They reject a Neolithic date because haplotype T2 has not been found in south Italian breeds and the Neolithic is thought to have spread from southern Italy northwards to Tuscany and beyond. The authors suggest that the most likely date for the arrival of the hypothetical human migrants and their cattle would be the Final Bronze Age where there is a 'cultural gap' at the 'birth of Protovillanovan culture' (Pellecchia *et al.* 2007, 1179; c.f. Beekes 2003; Briquel 2000; van der Meer 2004 discussed above). This timing would tie in with putative 'catastrophic environmental events like the earthquake storms which occurred in the Late Bronze Age in the Aegean and Eastern Mediterranean' that drove migrants to Italy, citing Nur and Cline who only tentatively suggest the possibility of earthquake storms (Nur and Cline 2000, 61). So the media were wrong and Pellecchia *et al.* (2007) prove nothing about Herodotus, despite the Seneca quoted at the conclusion of their abstract '*Asia Etruscos sibi vindicat*' (Asia claims the Etruscans back).

Earlier studies of cattle DNA have also detected genetic variation in European cattle that can be associated with cattle from south-west Asia. Cymbron *et al.* (2005) identify the highest levels of alleles associated with *Bos Indicus* (Zebu) in Italian cattle and differentiate Mediterranean cattle from northern European cattle. The study did not aim to differentiate between different Italian cattle breeds, taking a high-level view of the question of cattle origins, suggesting two general routes of cattle diffusion into Europe in the Neolithic: via the Danube corridor and via the Mediterranean seaways. Relatively high levels of *Bos Indicus* alleles were also found in Greek cattle and these are believed to have entered populations of *Bos Taurus* in Anatolia where the taurine cattle were originally domesticated. Cymbron *et al.* (2005) point at the long term cultural associations between Anatolia, Greece and Italy over

the past three millennia as a context for this genetic exchange rather than isolating the single episode of the Etruscan period as the likely context, as do Pellecchia *et al.* (2007).

In 2006 a more comprehensive study than either Cymbron *et al.* (2005) or Pellecchia *et al.* (2007) investigated a larger dataset of European, south-west Asian and North African *Bos Taurus* cattle (Beja *et al.* 2006). This study used 520 samples and concluded that a single origin for European cattle (e.g. in the Near East) was not likely. It also concluded that the cattle originating in the Neolithic in the Near East also have mtDNA deriving from North African cattle and wild Aurochs. The study presents a circum-Mediterranean distribution of cattle DNA illustrating that the African (T1) and Near Eastern (T and T2) haplotypes are found around most of the northern shores of the Mediterranean and suggests that the distribution is possibly of pre-Bronze age origin. This interpretation of the data implies that the spatial distribution of cattle haplotypes was established in the Neolithic subsequent to what is currently believed to be a single domestication event in the Near East about 10,000 years ago (Beja *et al.* 2006, 8116; Achilli *et al.* 2008). These findings are broadly in line with the distribution map produced by Pellecchia *et al.* (2007, fig. 2), but illustrate that the genetic variation across the northern Mediterranean is complex, making it more difficult for Pellecchia *et al.* (2007, 1178) to claim that the genetic variation in Tuscan cattle is a special case and a 'sudden burst of diversity'. Even if Tuscan cattle have a combination of haplotypes not shared with other Italian cattle, the variation they demonstrate fits within the broader geographical pattern of variation observed by Beja *et al.* (2006). Therefore, it is less likely that a single hypothetical migration of (Etruscan) people from the Near East is required to explain the genetic makeup of Tuscan cattle, as Pellecchia *et al.* (2007) would contend. In the absence of any chronological control for the genetic flow of bovine haplotypes into Tuscany there is currently no reason, beyond approximate geographic coincidence, to attempt to associate it with a movement of Etruscan people that is neither confirmed by studies of human mtDNA nor supported by any archaeological consensus.

### Interpretative models

The preceding paragraphs have been a rather negative assessment of the interpretations that have been placed upon the DNA studies of Tuscan and Etruscan organisms as they have been related to the Etruscan people. This critical appraisal has not, and cannot call into question the scientific methods and results, beyond noting where they have been challenged by other specialist, and that the science is rapidly developing. It can, and does, however, question the interpretative framework adopted to both formulate hypotheses relating to the Etruscans and the interpretation of the testing of the hypotheses. What needs to be filled is the 'interpretive gap' (Thomas *et al.* 2005, 543) between the archaeologist and the geneticist. The phenomenon has also been observed in studies of the Neolithic where: '... the genetic data are like a bag of marbles. The marbles themselves say nothing about the cause of their arrangement in the bag. What provides an explanation for the way they are arranged is the model of interpretation. As we know, the fit of a model to the data is not proof of its reality' (Bocquet-Appel 2004, 75). So, what is the nature of the interpretive gap between the genetic studies of the Etruscans

and the archaeological studies?

The long-running question of Etruscan origins is essentially an interdisciplinary problem (Ward-Perkins 1959, 1–16): ancient history, literature, linguistics, archaeology and now molecular biology all bring their separate methodologies to the question. As John Ward-Perkins made clear 50 years ago, none of these disciplines, with its discrete methods and techniques can hope to derive a single solution to the complex mesh of issues that constitute the Etruscan question. The different fields have made great progress addressing the question, even if Theodore Mommsen in 1854 stated that it is 'difficult to determine from what quarter the Etruscans migrated into Italy; nor is much lost through our inability to answer the question' suggesting it was not a profitable pursuit and Massimo Pallottino (1947) advised that the real issue is not where the Etruscans came from nor the origins of their language, rather it is the study and the understanding of their civilization. The current consensus of autochthonicity is now strongly supported by historical, literary and archaeological arguments; linguistic issues also lean that way but are still subject to debate. The molecular biology is isolated in its attempts to demonstrate an Eastern ancestry. The scientific DNA studies have fallen outside of the consensus because they have not fully engaged in interdisciplinary dialogue with the humanities investigating the same issues. This is hardly surprising given the absence of a clearly stated interdisciplinary framework for addressing the question of Etruscan origins.

Fundamentally, the gulf lies between differing conceptions of how the Etruscans can be defined. The Herodotean account identifies Etruscans as alien immigrants to Italy. As such they would be genetically distinct from autochthonous residents in Italy. The notion of the Etruscans defined as outsiders with a distinctive material culture fits well with a model of cultural change in prehistory as driven by movements of peoples is reminiscent of migrationist and diffusionist explanations of cultural change that were current in the 1930s and 40s. More generally, the strict association of a people with an archaeological culture (*Völker = Kultur*) lies behind the expectation that Etruscans might be genetically distinct, because some aspects of their material culture are distinctive. This association also lies at the roots of 'culture-historical archaeology' (Trigger 1989, 148–206), a theoretical approach to the subject that developed in the mid-20th century, precisely at the same time that Etruscology emerged as a discipline, and one that still underlies most studies of the Etruscans. This approach treats the Etruscans as a unique culture with an historical trajectory. Incidentally, this also explains the lasting interest in Etruscan origins, since any historical trajectory requires a starting point. This form of historical particularism that defines the Etruscans as a discrete people occupying a circumscribed stretch of time in the past is what makes the Etruscans an attractive target for the genetic studies. Studies in genetics that seek to explore the ancestry of populations require a target population which might be the source of a genetic signal that can be detected in contemporary populations: the Etruscans, defined in this way, form just such a target.

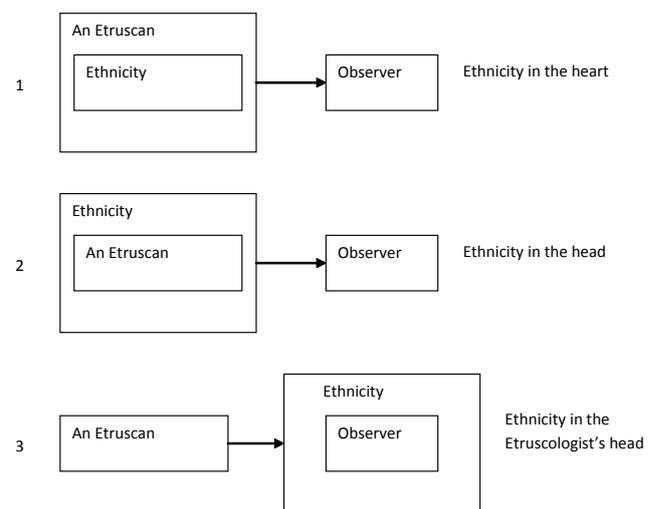
Another root of this mode of interpretation of phylogenetic reconstructions may be traced further back to the 1930s Vienna school of ethnography with the work of Oscar Menghin and

Wilhelm Schmidt who believed that ‘back in the Stone Age there was a greater correspondence between race, language, and culture; subsequently, mixtures and hybridizations constantly occurred, making it impossible today to refer to pure races, languages, or peoples’ (Kohl and Pérez Gollán 2002, 564). Such a view of race, language, and culture leads to the expectation that a genetic history of the contemporary ‘hybridized’ Tuscans might contain a detectable Etruscan component. This early 20th-century conception of archaeological populations also lies behind the interpretation of the genetic variation observed in modern Italians as resulting from the movements of past archaeological cultures in Italy that is favoured by genetic studies, originating with Piazza *et al.* (1988). When allied to a diffusionist interpretation of the cultural connections in the Orientalizing Period that lays emphasis upon the eastern origins of luxuries, arts and ‘higher culture’ the archaeology provides enough to enable the molecular biologists to hypothesize eastern origins for the Etruscans, and to test the hypothesis. This hypothesis is particularly attractive because it enables geneticists to bring a battery of emerging techniques that study genetic admixture to the problem (Jobling *et al.* 2004, 373–97) and these depend upon assumptions that the Etruscans had an identifiable ‘ancestral population’ distinct from that of other inhabitants of Italy.

It is alarming that scholars from a differing, and intellectually distant, discipline should be picking up ideas from Etruscology that are over half a century out of date and currently not at all credible or fashionable in anthropologically aware fields of archaeology. But we, as Etruscologists, of whatever variety, should ask ourselves how is it possible? Perhaps the outward projection of our field of study is deficient, maybe we are not sending out the right messages and communicating our current thinking to other scholars. Or perhaps the molecular biologists *are* reading our work correctly and we are in fact still wedded to early 20th-century views of the people we study. Perhaps in our acceptance of the Pallottino consensus and concentration on understanding of the formation of the Etruscan people (Pallottino 1947) we are accepting the notion of an ‘Etruscan people’ without questioning enough what that means and not paying enough attention to the wider population history of the Mediterranean.

A way forward lies in the examination of what the concept of an ‘Etruscan people’ entails. Help comes from another discipline: anthropology. Anthropologists, and indeed many archaeologists would have little problem identifying the Etruscan people as an ethnic group (Perkins 2005, 109–12). An ethnic group (*ethnie*) can be ‘defined by a set of features or dimensions ... a collective name; a common myth of descent; a shared history; a distinctive shared culture; an association with a specific territory; and a sense of solidarity.’ (Banks 1996, 130; Smith 1986).

The ethnicity of individual members of an ethnic group or community may be considered as being located in a range of conceptual spaces in relation to the subject of investigation, in this case the Etruscan, and the observer, here the Etruscologist or molecular biologist (Banks 1996). The theoretical division of the possible locations of ethnicity characterizes it as being located either 1) within the subject and may be termed ‘ethnicity in the heart’ or primordial ethnicity, 2) outside the subject and so a mental construct of their own – ‘ethnicity in



**Figure 1** Locations of ethnicity (adapted from Banks 1996, 187, fig. 1)

the head’ or 3) outside the subject but a mental construct of an observer – ‘ethnicity in the observer’s head’ (summarized in Fig. 1). Of these three the first two are impossible to be sure about since no Etruscan literature discussing the elements that constitute ethnicity have survived. With an archaeological ethnic group our understanding is largely limited to the third, where we apply our own conceptions of ethnicity as we attempt to define and understand the people we study. So can definitions of the Etruscans be fitted into this schema? The definition of an *ethnie* provided above fits well with what we know of the Etruscans. The criteria can be easily matched, except perhaps that we do not know that all Etruscans had a common myth of descent, and we know their sense of solidarity was sorely tested when they faced external military threats. Now, is it possible to integrate the biomolecular studies in to this pre-genetic way of thinking about ethnicity?

A first point to make is that although the Etruscans were obviously ignorant of their own genetic make up, heredity did play a part in their ethnicity: their common myth of descent (from Tarchon perhaps son of Tyrrhenus) and heredity was a strong force shaping the gentilitial social structure. Locating DNA within the three models of ethnicity raises a number of issues. The most obvious place to locate the DNA would be within the subject, the Etruscan, themselves. Ancient DNA from Etruscans would clearly belong here, although it could play no rôle in the construction of ethnicity in an Etruscan’s heart or head. None of the DNA studies claim to have identified anything as simplistic as an Etruscan ‘genetic fingerprint’ but they do implicitly expect to be able to observe something in the genetic diversity of Etruscans that can be associated with the ethnic group archaeologists identify as the Etruscan people. What they are doing is identifying ‘eastern’ haplotypes and using them as support for the theory of eastern origins and interpreting them as markers of Etruscan ethnicity. In effect the genetic studies are moving the DNA from the subject part of the model into the ethnicity part of the model. The DNA is being used as a indicator of ethnicity by suggesting that features of Tuscan mtDNA derive from the Etruscan ethnic group. The supposition is that the Near Eastern haplotypes in Tuscan DNA are a characteristic of the Etruscan ethnic group.

In genetic studies ‘ethnicity’ tends to have a different usage to the one that has been developed here. ‘Ethnicity’ in

biomedical studies is a characterisation of individuals, preferably a self-description, where a subject categorizes themselves as belonging to an ethnic group: usually Asian, African, White, Black, African American or similar. These are essentially racial categories, although they are also sometimes confused by nationalistic categories such as British, Indian or Irish. Geneticists are interested in this form of ethnicity because correlations have been observed between some self-described ethnicities and particular genes that play a rôle in some medical conditions or drug metabolism. Geneticists are at pains to point out that there is no genetic basis for racial categorization (Lewontin 1972) and features of the phenotype such as skin colour are not simply determined by a distinct genotype. Although there is some correlation between some genetic data and broad racial categories based on geographic location, such as Asian, African and European, this is a result of the patterns of gene distribution caused by the gene flow created as humans populated the earth. However other genes are not at all correlated with an ethnicity based on geographic location (Barbujani 2005; Jorde and Wooding 2004; Tishkoff and Kidd 2004). These studies, and others, clearly demonstrate that it is not possible to divide the human species into taxonomic categories and construct a phylogeny of distinct races that have developed in isolation from one another. Race, or ethnicity as commonly conceived in biomedical studies, is not a human characteristic determined by the genotype; it is a 'conceptual construct with historical, biological, and anthropological elements' (Weiss and Fullerton 2005). The same is also true of ethnicity conceived as an artefact in the heart, head or the investigator's head. The genetic component of ethnicity is not an indicator or determinant of ethnicity: it is a new, and developing component of ethnicity that needs to be integrated with both technical and popular constructions of ethnicity.

Therefore Etruscan ethnicity cannot be determined by genetic studies alone, and an 'Etruscan' genetic fingerprint cannot be constructed because 'Etruscan' is the label for an ethnic group, not a configuration of genetic mutations. What the genetic studies can do is reconstruct the genetic ancestry of a sampled population, whether ancient or modern. The important distinction is to keep separate genetic ancestry and ethnic affiliation. Some part of the collective DNA ancestry of Tuscans might well have passed through individuals who would have self-identified themselves as Etruscans, but to identify that DNA as Etruscan is wishful thinking. To associate Near Eastern haplotypes with an Etruscan ethnicity and stories in Herodotus is just an extension of this conflation of genetic ancestry and ethnicity.

### Conclusions

So, in conclusion, what do we, and what can we, know about Etruscan genetics? The investigation of Etruscan ancient DNA has barely started: the study of Vernesi *et al.* (2004) is problematic because there are many questions surrounding the reliability and authenticity of the sequences obtained. The problems are not limited to this study: aDNA analysis is still in its infancy (Jobling *et al.* 2004, 110–18). The work of Capellini *et al.* (2004) makes fewer claims and has demonstrated the potential of aDNA to sex skeletal remains and to establish consanguinity of individuals in the same chamber tomb. The

simulations of Belle *et al.* (2006), although stimulated by the uncertain results of Vernesi *et al.* (2004) raise an interesting question, essentially, 'What happened to the Etruscans?' but also with implications for where they came from. This is not a novel question but the methodology has not, to my knowledge, been previously applied to historical archaeological problems. Archaeology, traditionally, approaches such questions through studying acculturation or culture change, in league with historical sources. Here the methodology is to model the trajectory of a hypothetical founder population of Etruscans. It compounds genetic ancestry and ethnicity, but it does raise the very human question of what became of the genetic legacy of the Etruscans. Generally they are assumed to have 'disappeared' soon after their language (mostly) died in the Augustan period.

Yet the last, self-describing Etruscans will have left descendants, whose genetic legacy will have comprised part of the Roman ethnicity of successor societies in the central Mediterranean. The Roman Empire appears to have consumed the Etruscan identity, for there is no suggestion that an Etruscan ethnicity resurfaces in post-Roman times, even if Etruscan genetic ancestry persisted. This mechanism opens the pathway for Etruscan ancestry persisting to the present day in Tuscany. Yet the study of Achilli *et al.* (2007), rather than broadly exploring the genetic heritage of Tuscans, focuses on Near Eastern haplotypes as supportive of Etruscan origins in the East. Ultimately, however, there is no reason to associate the Near Eastern haplotypes with the Etruscans. The Near Eastern haplotypes could have entered the Tuscan's ancestry at any, or many, points between the Neolithic colonization of Europe and the 20th century AD. Many studies have demonstrated that haplotypes in Mediterranean populations, whether human or bovine, have clinal distributions. Haplotypes are distributed over gradients, some representing gene flows from south-west Asia north-westwards into Europe. These are generally interpreted as resultant upon the Neolithic colonization of Europe. Therefore, it is to be expected that a Tuscan, or indeed Etruscan DNA should contain haplotypes characteristic of south-west Asia. The Tuscans or Etruscans occupy a position on the clines of various distributions of haplotypes just like any other European population. There have not yet been enough studies to reliably distinguish a Tuscan combination of haplotypes as distinct from other combinations in Italy, even if it is now possible to separate northern Italian samples from Bergamo and Tuscan samples (Li *et al.* 2008, fig. 2a). In Achilli *et al.* (2007) only one of the three Tuscan samples appears to be at all divergent from the cluster of other European samples. More samples might help to clearly distinguish a Tuscan population and associate it with elevated levels of south-west Asian haplotypes as the rather crude definition of the clinal distributions improves, but for the present, all that can be safely said is that DNAs from Murlo have a higher than anticipated proportion of south-west Asian haplotypes. A subsequent, more detailed study of 258 samples from Tuscany has identified that approximately 3% of these contain typical Near Eastern haplogroups, significantly reducing the proportion estimated by Achilli *et al.* (Brisighelli *et al.* 2008). Nothing can be added from these analyses concerning Etruscan origins because no link has yet been established between the south-west Asian haplotypes and the

Etruscans. One of the serious impediments to the establishment of such a link is the absence of an accurate or precise chronological control on the rates of mutation that have produced the haplotypes. Achilli *et al.* (2007, 767) claim that the arrival of 'Levantine' genetic material is recent because it occupies 'terminal positions in the phylogeny'; there are however no parameters for 'recent'. Brisighelli *et al.* (2008) have very recently provided a potential terminus ante quem for the arrival of the typical Near Eastern haplogroup U7a2 in Tuscany by analysing the genetic variation within a sub-clade of the haplogroup, U7a2a. This configuration was found in 9 (out of 53) samples from the island of Elba. The analysis suggests a date of between 350±400 BC and AD 850±100 for the emergence of this mutation, found only in Elba. In archaeological terms the date range and associated errors are imprecise: the lower extent of this range coincides with the Etruscan period, but overall, the range would fit better with a Roman, or Early Medieval date for the emergence of the novel, ancestrally Near Eastern haplogroup U7a2a.

Even if the arrival of south-west Asian haplotypes could be dated to c. 2,800 years ago this would not prove anything about Etruscan origins. We already know that people did move around the 1st-millennium BC Mediterranean, either as groups of colonists, as, for example, in the structure of the Herodotean story of Etruscan origins, or the foundation of Phoenician (Levantine), or Greek colonies, or as individuals. Ethnic diversity can be seen in the evidence for the presence of foreigners, particularly Sardinians, in Etruria from the Villanovan period on (10th–9th centuries BC) (Camporeale 1997, 48–9; Bartoloni 1989, 48–9) and there is plentiful evidence for cultural and economic exchange from the Orientalizing period onwards (Cristofani 1996; Giangiulio 1996, 518–25) that has led Jodi Magness to suggest the presence of Near Easterners in the elite of Etruria (Magness 2001). From ethnic diversity it is a small step to genetic diversity and it is not difficult to imagine mechanisms for genetic flow into Etruria from the Eastern Mediterranean. Therefore, the archaeology and history would lead us to expect a detectable south-west Asian gene flow in the central and western Mediterranean dating to the early 1st millennium BC and superimposed on the Neolithic clines of European haplotype distributions.

What is novel in the results of Achilli *et al.* (2007) and subsequent analyses (Brisighelli *et al.* 2008; Li *et al.* 2008) is the observation of south-west Asian haplotypes in the maternal mtDNA. This implies the existence of maternal bloodlines connecting south-west Asia and the central Mediterranean. This mtDNA evidence indicates the mobility of childbearing females across the Mediterranean. In the absence of any evidence to support the Herodotean account of mass immigration to central Italy, we must now accept the immigration of individuals or small groups of females at the very least. Traditional archaeological techniques find it challenging to convincingly identify intrusive alien individuals. Burials of individuals have occasionally been interpreted as foreign in 1st millennium BC Etruria through the study of grave goods. However, grave goods are not a sure indicator of ethnicity and Orientalizing imports are usually interpreted as indicating trade contacts rather than the direct movement of people. Mytho-historical accounts in ancient sources occasionally suggest the movements of people (e.g. see

Winter this volume) and onomastics occasionally suggest a non-Etruscan origin of individuals known either from literary sources or funeral inscriptions (Cristofani 1996). The immigration of craft workers has also been suggested using the presence and production of new styles of decoration or uses of materials to suggest migrant workers (e.g. Pallottino 1971, 83–4; Colonna 1989, 21), a scenario also suggested by the mytho-historical account of Demaratus and companions bringing crafts to Italy (Winter this volume; Ridgway 1992; Ampolo 1976–7). But none of these are indicative of large scale migrations, and none provide clear evidence for female mobility – it is always assumed that craft workers or traders are male. The DNA studies therefore have produced a challenge for the archaeological consensus and it has nothing to do with Herodotus. It is a far more interesting challenge to investigate and explore female mobility across and around the Mediterranean in the 1st millennium BC.

The other point that emerges clearly from this study of the contribution made by DNA studies to the understanding of the Etruscans is that collaboration is desperately needed between the molecular biologists and the Etruscologists. At the moment the molecular biologists are attempting to write a population history of the Mediterranean without the help of archaeologists. Just as the archaeologists, generally, do not understand the methods, theories and approaches of the biologists, the biologists are not aware of the current issues and outstanding problems in Etruscan studies. The methodologies that the molecular biologists are developing have the potential to explore some of the fundamental questions concerning the definition of Etruscan identity and ethnicity. However, the methodologies are not currently matched to the most interesting and appropriate questions in contemporary Etruscology. The molecular biologists currently need the input of Etruscologists to help formulate archaeologically appropriate hypotheses for their methodologies to explore. Population genetics has a significant potential to advance our understanding of the history of Mediterranean populations and to contribute to the definition of Etruscans, but this potential will not be achieved until meaningful interdisciplinary collaborations are developed. Hopefully, this contribution to the centuries-old debate, made from an archaeological viewpoint, will become a starting point for such a collaboration.

### Acknowledgements

I would like to thank Adrian Harrison, Department of Life Sciences, University of Copenhagen, and Judith Swaddling for reading and commenting upon a draft of this chapter.

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