variant in haplotypes 20T and 21T and as a singleton mutation in another sample. Haplotype 21T is represented by a combination of variants 16228T and 16229C, which has not been found in modern human HVS-I sequences.

Therefore, the mutational spectrum derived from the Etruscan mtDNA sequences shows some degree of similarity to modern human mtDNA sequences. However, many of the singleton mutations, as well as some consensus mutations found in the cloned sequences, represent substitutions that are very rare in living individuals or do not even exist. The possibility that these haplotypes underwent extinction (Vernesi et al. 2004) cannot be excluded. However, many of these mutations might be due to postmortem damage of mtDNA. The assignment of postmortem mutations in consensus variants of the haplotypes can lead to misidentification of mtDNA sequences. In addition, some phylogenetically informative nucleotide positions are highly susceptible to postmortem damage (Gilbert et al. 2003). These problems may lead to misassignment of mtDNA sequences to haplogroups and, consequently, to biased opinions about genetic history of human populations.

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Electronic-Database Information

The URL for data presented herein is as follows:

Mitomap: A Human Mitochondrial Genome Database, http://www.mitomap.org/

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Etruscan Artifacts: Much Ado about Nothing

To the Editor:

Malyarchuk and Rogozin (2004 [in this issue]) and Bandelt (2004 [in this issue]) question the authenticity of

the sequences in the study by Vernesi et al. (2004), because these sequences contain substitution motifs that are seldom observed in modern samples. Before answering their criticisms in detail, we would like to make three general points: (1) in the study of ancient DNA, the presence of artifacts is inevitably hard to rule out with certainty, and this also applies to our Etruscan data; however, (2) the Etruscan sequences were determined using a very strict set of standards, and, hence, we are confident that they are rather reliable; and (3) many of Bandelt's speculations are based on sites with a high mutation rate, where substitutions have been observed in various associations. For instance, positions 16126, 16219, 16278, and 16362, found in Etruscan haplotypes that Bandelt (2004 [in this issue]) considers with suspicion, are described as mutational hotspots by Wakeley (1993), Hasegawa et al. (1993), Meyer et al. (1999), and even (three of them) Bandelt et al. (2002). Multiple occurrences of those mutations on different lineages does not prove, or suggest, sequencing artifacts.

To test the reproducibility of the results, in our Etruscan study, we cloned the PCR products and sequenced multiple clones from the same individuals (Handt et al. 1996). *Taq* polymerase errors may lead to the apparent occurrence of mutations unique to a single clone (singletons). These errors are, as completely as possible, eliminated by comparing clones and identifying a consensus sequence. Malyarchuk and Rogozin (2004 [in this issue]) compared variation across modern humans with that observed in the 575 clones derived from 28 Etruscan specimens. They noticed that the mutations in the two data sets overlap only in part and that mutations never observed in modern humans occur in the Etruscan clones. However, by making this comparison they were comparing incomparable quantities. On the one hand, they have the spectrum of mutations carried by modern individuals; on the other, they have a set of mutations comprising both those that were actually in the Etruscans' DNA and those that probably result from *Taq* errors. There is no reason to expect the two spectra to be similar. As mentioned on page 698 of our article (Vernesi et al. 2004), the misincorporation rate was 0.27% for the Etruscans—that is, less than observed, for instance, by Handt et al. (1994). Therefore, Malyarchuk and Rogozin (2004 [in this issue]) are wrong when they say that the clones of the Etruscan data set show an excess of singletons. On the contrary, if the appropriate comparisons are made, singleton sequences are relatively rare among them. Malyarchuk and Rogozin (2004 [in this issue]) also notice that two mutations (16229 and 16334) independently occurring twice in the Etruscan network are rare or absent in almost 8,000 modern samples. Their observation is correct, but, given the methodologies that we applied, at this stage, we do not think it implies that these mutations are necessarily laboratory artifacts.

Bandelt (2004 [in this issue]) makes five comments, which we list here along with our responses.

1. **The 16193-16219 motif occurs in association with different substitutions in modern samples and among the Etruscans.** Yes, we already wrote that in the second-to-last paragraph on page 698 (Vernesi et al. 2004). Bandelt notes that the mutation at position 16219 has been observed in two different haplogroups in modern people. We know of at least three (U6a, T*, and H) and, within H, of several different haplotypes with the 16219 mutation (H07, H09, H13, and H16). Meyer et al. (1999) showed that mutation rates at 16219 are fivefold higher than the average mutation rate in this region, and therefore 16219 seems to be a fast-mutating site, which can exist in association with a broad range of other mutations.
2. **The mutation at 16069 occurs in two individuals, 2V and 11C, and in neither is it associated with a mutation at 16126 or with a cut at −766 *Mse*I, which generally characterize haplogroup J.** We published sequence 2V for completeness of information, but we did not consider it in any numerical analyses, because it seemed suspicious to us as well (p. 698). As for sequence 11C, the absence of the restriction cut at 14766 *Mse*I was confirmed by sequencing the region around the restriction site. At any rate, a sequence, SCOT0492, with the 16069-16261 motif but without a mutation at 16126, was described by Helgason et al. (2001). Also, 16126 is considered by Bandelt et al. (2002) to be a "speedy site" and, hence, not a site informative for phylogenetic analysis. Finally, Meyer et al. (1999) showed that position 16069 has a higher-than-average mutation rate; hence, whether to consider it as a fast-mutating site seems largely a matter of taste.
3. **We rejected the hypothesis that postmortem changes may have affected the 16069 or 16294 sites.** No, we didn't. Instead, we wrote (p. 699) that we saw *no compelling reason* to think that postmortem changes had occurred there, because Gilbert et al. (2003) found no instance of changes of that kind in their study. Ruling out postmortem changes completely is probably impossible with the available methodologies.
4. **There are inconsistencies between table 1 and figure 2.** Yes, here Bandelt is right. Haplotype 6AM was erroneously reported in one case with +14766 *Mse*I, whereas it has been observed only in association with −14766 *Mse*I. Another error is a typo in the table, where 13C should be −14766 (as correctly represented in the network). On the other hand, no triangle should be reconstructed for site 95 (as asked by Ban-

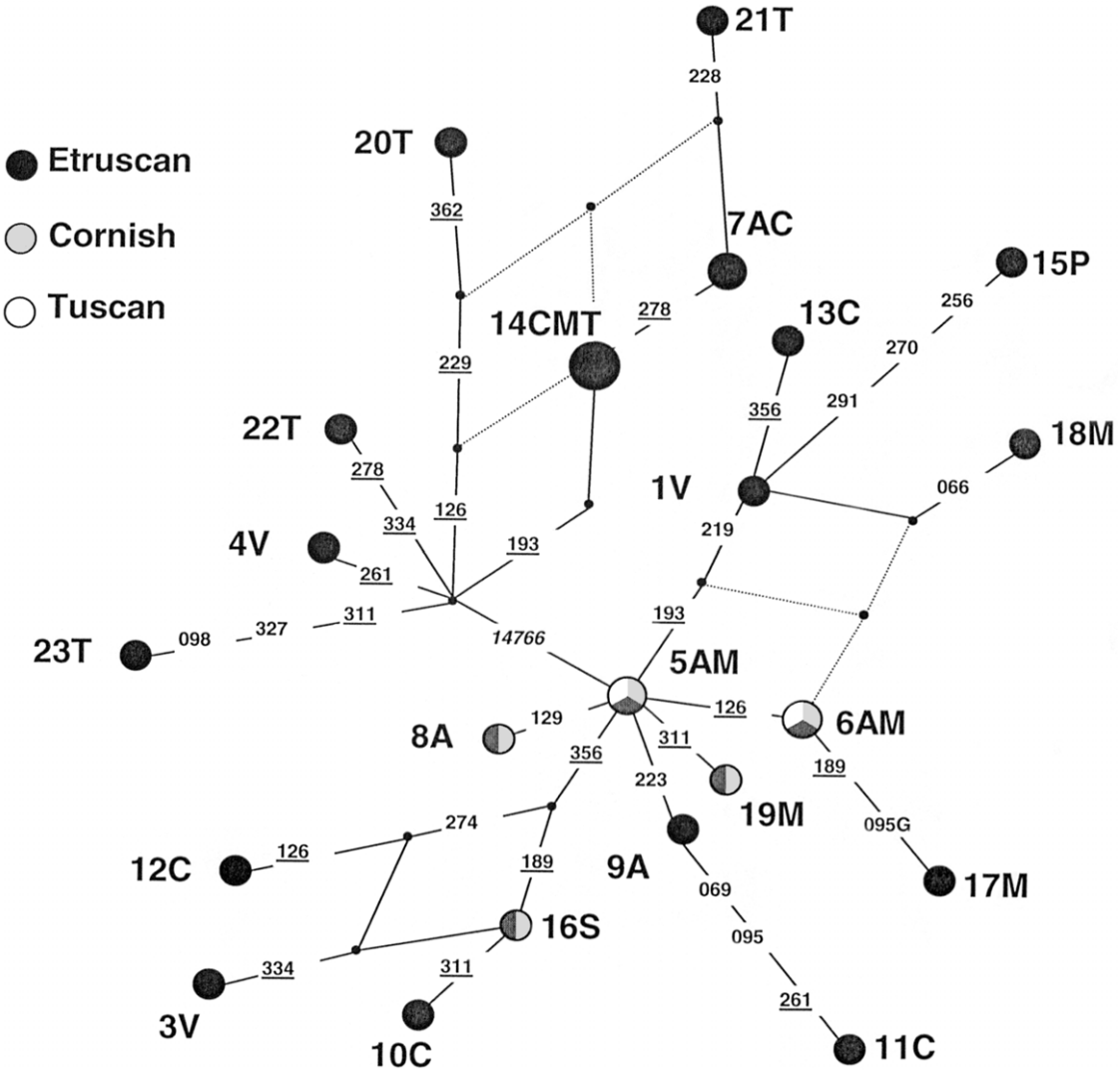

Figure 1 Reduced median network (Bandelt et al. 1995) of sequences identified in Etruscan individuals. The numbers are arbitrary codes; the letters refer to the sites where the sequences have been observed. Haplotype 5AM is the Cambridge Reference Sequence. Nodes are proportional to frequencies. The alleles shared with modern Tuscans and modern Cornish are highlighted.

delt), since the two mutations at this site are different (as correctly reported in the table and on p. 698; a gap in the label in the figure shows that the letter G, indicating a transversion, disappeared in print). He is also right when he points out that there is an error in the network method cited, but the error is in the reference list—namely, Bandelt et al. (1999) is given instead of (1995). However, Bandelt is wrong when he says that the node sizes in figure 2 do not correspond to the haplotype frequencies. Sequences 5AM, 6AM, and 7AC (two occurrences) are represented by big circles, and sequence 14CMT (three occurrences) by a very big circle. The network is a reduced median network (Bandelt et al. 1995, 2000), constructed by hand and checked with the program Network 4.1 for Windows (Fluxus Engineering Web site). Nucleotide positions were weighted using the list of Hasegawa et al. (1993) and following the weighting procedure of Richards et al. (1998). We further reduced the reticulation in the network by a procedure followed in other mitochondrial studies (Richards et al. 1996; Torroni et al. 2001) (see fig. 1). No conclusions of our article change on the basis of this slightly modified network.

5. **Not all of the strictest criteria for the validation of ancient sequences have been followed, because only three individuals were independently sequenced in two laboratories.** All right, then we shall reformulate our sentence as follows: We are not aware of any studies in which the criteria for the validation of an-

cient sequences were followed more strictly. See, for example, Keyser-Tracqui et al. (2003) and Maca-Meyer et al. (2004). Cooper and Poinar (2000) also recommend looking for human DNA in associated faunal material, and we could do that only for one individual, because animal bones were not retrieved from any other burial. We shall try to replicate greater numbers of results in future studies, but it must be understood that it is a very long process and one for which ancient material may not always be easily available.

In brief, we thank Bandelt for detecting some differences between the data reported in table 1 of our article and their graphical representation in the network. However, we suggest that Bandelt read our text more carefully and also consider the lists of fast-mutating sites compiled by authors other than himself. Bandelt is clearly right when he stresses the importance of quality in the data, and we showed that we share the same concern in three ways: (1) by excluding from the analysis 50 of the initial 80 samples, whenever any of eight biochemical tests did not suggest a good probability of obtaining reproducible results; (2) by further excluding two identical sequences from the same burial, to make sure that consanguinity did not bias our results; and (3) by excluding sequence 2V because it showed two sets of mutations previously observed in evolutionarily distant haplogroups, and that could conceivably result from the presence of multiple DNAs in the specimen. On the contrary, the problems Bandelt raises are due to individual substitutions that, he says, are "almost always" observed in different contexts. We suspect science would proceed very slowly, if at all, if scientists agreed to trust only the data they observe almost always. Mitochondrial data sets contain many homoplasies, and sites that were considered mutational hotspots have changed their status over time. Our understanding of mitochondrial variation is still evolving, and it seems bizarre to dismiss as implausible all the data that do not neatly conform to what we think we already know.

Whereas Malyarchuk, Rogozin, and Bandelt think that the Etruscan sequences are too different from modern ones to be good, Serre et al. (2004) argued that ancient mitochondrial sequences should be considered authentic only if they clearly differ from known modern ones. In other words, to make everybody happy, ancient mtDNA sequences should be at the same time *identical to and different from* the sequences of modern people. The famous lines of Joseph Heller's *Catch 22* come inevitably to mind: "Orr was crazy and could be grounded. All he had to do was ask; and as soon as he did, he would no longer be crazy and would have to fly more missions."

With this, we do not mean to deny that problems exist with the validation of ancient DNA sequences. What is necessary, however, is a set of standard criteria that everybody is reasonably happy about. Despite serious attempts to define these criteria (Cooper and Poinar 2000; Hofreiter et al. 2001), the present debate shows that a consensus has not been reached yet. As Helgason and Stefánsson (2003) remarked, errors can and do occur in large-scale DNA studies, either in the laboratory or in the construction of the databases. However, the impact of such errors, or of the possibility of such errors, should be evaluated critically before raising unjustified doubts about the conclusions of a study.

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The URL for data presented herein is as follows:

Fluxus Engineering, http://www.fluxus-engineering.com/sharenet.htm (for Network 4.1 for Windows)

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GDD1 Is Identical to TMEM16E, a Member of the TMEM16 Family

To the Editor:

In the June 2004 issue of *The American Journal of Human Genetics,* Tsutsumi et al. (2004) reported the identification and characterization of the *GDD1* gene, which is mutated in patients with gnathodiaphyseal dysplasia (MIM 166260). They claimed that human *GDD1* is a novel gene without any human homologs (Tsutsumi et al. 2004); however, we found that *GDD1* was identical to *TMEM16E* (MIM 608662), a member of the *TMEM16* gene family (Katoh and Katoh 2003, 2004*a*, 2004*b*).

In 2003, we identified and characterized the *TMEM16A* (*FLJ10261*) gene, which is located within the 11q13.3 amplicon (Katoh and Katoh 2003). The *CCND1-ORAOV1-FGF19-FGF4-FGF3-TMEM16A-FADD-PPFIA1-EMS1* amplicon at human chromosome 11q13.3 is one of the most frequently amplified regions in the human genome (Schwab 1998; Katoh and Katoh 2003). The *FLJ10261, C12orf3, C11orf25,* and *FLJ34272* genes, which encode mutually homologous eight-transmembrane proteins with N- and C-terminal tails facing the cytoplasm, were designated as "*TMEM16A,*" "*TMEM16B,*" "*TMEM16C,*" and "*TMEM16D,*" respectively, on the basis of our communication with the Human Gene Nomenclature Committee (see the HUGO Gene Nomenclature Committee Web site).

We then searched for novel members of the *TMEM16* gene family and identified the *TMEM16E, TMEM16F* (MIM 608663), and *TP53I5* genes (Katoh and Katoh 2004*a*, 2004*b*). TMEM16A, TMEM16B, TMEM16C, TMEM16D, TMEM16E, TMEM16F, and TP53I5 are eight-transmembrane proteins with TMEM16 homologous (TM16H1, TM16H2, and TM16H3) domains. Several Cys residues and Asn-linked glycosylation sites are included in the conserved residues (or the consensus sequence) of the TM16H1, TM16H2, and TM16H3 domains.

The *TMEM16E-NELL1* locus at human chromosome 11p15.1-p14.3 and the *TMEM16F-NELL2* locus at human chromosome 12q12 are paralogous regions (par-