Table 1

Nucleotide Diversity and Age Estimates for mtDNA Belonging to the Four Founder Haplogroups of New World Natives

Haplogroup	No. of Sequences	Genetic Diversity[a] (SE)	Mean Age in Years[b] (95% CI)
A	10	0.73 (0.15)	15,398 (12,052–18,744)
B	11	0.75 (0.14)	15,819 (12,659–18,970)
C	9	0.64 (0.13)	13,520 (10,616–17,425)
D	5	0.86 (0.18)	18,144 (14,137–22,151)
Weighted mean		0.75 (0.15)	15,720 (12,366–19,074)

[a] $\pi(\times 10^{-3})$.
[b] Calculated as in Silva et al. (2002).

to show similarities between the four haplogroups and does not differ significantly from the previously published values (table 1). This supports our primary conclusion in favor of a single migration wave, with a mean age for the four haplogroups of 12,366–19,074 years before present.

The revised versions of the sequences have been submitted to GenBank.

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Electronic-Database Information

The URL for data presented herein is as follows:

MITOMAP, http://www.mitomap.org (for a human mitochondrial genome database)

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Reply to Silva et al.

To the Editor:

Silva et al. (2003 [in this issue]) have certainly improved their data by eliminating many of the errors in the current version of the data matrix, and they have admitted most of their innocent mistakes. Their efforts and atti-

tude should be encouraged (cf. Forster 2003). However, we are still skeptical about the corrected results presented in figure 1, for some idiosyncrasies remain and others seem to have been newly introduced. For example, some sites (e.g., 8584, 14318 [YAN0591; C type] and 14783 [TYR0004; D type]), at which Silva et al. (2003 [in this issue]) have now corrected some of the entries in their original data table, still show back mutations. Homoplasy in the coding region is much less than in the control region and may have only a few hot spots (see, e.g., table 2 of Herrnstadt et al. [2002]); the reference to Eyre-Walker et al. (1999) is not really relevant, since those authors have taken quite problematic data at face value (Kivisild and Villems 2000). The recorded variation at 10400 remains highly suspicious. It is hard to believe that 10400 has actually mutated in two B types (KRC0033 and QUE1880) and one L2a type (NGR0522) and reverted in two C types (QTE1875 and YAN0650) and two D4 types (JAP1045 and GRC0131), because no single homoplasious change at this site has been observed in >900 coding-region sequences or fragments that cover site 10400 from Ingman et al. (2000), Maca-Meyer et al. (2001), Derbeneva et al. (2002), Herrnstadt et al. (2002), and Yao et al. (2002). Moreover, site 11177 is found in only 2 of 10 B4b mtDNAs of Silva et al., which contrasts to the co-occurrence of 11177 and 9950 in all 14 B4b mtDNAs of Herrnstadt et al. (2002). To thoroughly settle these anomalies, it is imperative that the authors take notice of the potential processes that might introduce errors, as listed in our letter (Yao et al. 2003 [in this issue]), especially sample crossover. We would encourage the authors to resequence some short fragments that cover the sites listed above.

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A Multicolor FISH Assay Does Not Detect DUP25 in Control Individuals or in Reported Positive Control Cells

To the Editor:

Gratacòs et al. (2001) reported recently that the co-occurrence of panic and phobic disorders with joint laxity was associated with an interstitial duplication of the chromosomal region 15q24-q26 (named "DUP25"). DUP25, which encompasses a region of the size of 17 Mb, was observed only as mosaicism in three different forms (designated as "direct telomeric," "inverted telomeric," and "centromeric"). In each reported case, cells with DUP25 represented the majority (>50%). In addition, DUP25 mosaicism was also observed in 7% of control individuals, indicating that it could represent a