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Reply to Bandelt and Forster

To the Editor:

It is well known (and is clearly stated in our article [Watson et al. 1996]) that patterns in mismatch distributions can be influenced by many evolutionary scenarios other than population growth. In our study, we therefore applied two other approaches to the analysis of demographic history, a graphical method developed by Nee et al. (1995) and a statistical test developed by Tajima (1989). The results of both approaches were compatible with the hypothesis that the food-producing populations have expanded their size, whereas the other populations have not.

Concerning other issues discussed by Bandelt and Forster, we refer the reader to our original article (Watson et al. 1996), which we believe clarifies all relevant points.

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mtDNA Mutation Rates—No Need to Panic

To the Editor:

Readers of the recent paper by Howell et al. (1996) might be forgiven for thinking that, after all the controversy surrounding the reconstruction of the original mitochondrial gene trees (e.g., see Maddison 1991; Templeton 1993), the field was once again in difficulties because of (*a*) a serious underestimation of the mutation rate by a factor of almost nine and (*b*) the resulting misdating of past divergences. We believe that such an interpretation would be unduly pessimistic.

Conventional approaches have calibrated the mutation rate by reference to the divergence between humans and chimpanzees. For the phylogenetically informative first hypervariable segment of the control region (HVSI),