Book review

Genetics and the Search for Modern Human Origins

JH Relethford

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Human population geneticists love a two-horse race. In their hands, the various rather subtle processes conceived of in the modern archaeological and anthropological literature to explain human dispersal patterns have often been whittled down to a stark choice between two monumental alternative models. We see this, for example, in the controversies between Neolithic and pre-Neolithic origins for Europeans and for Southeast Asian islanders, which continue to make the news. Here John Relethford tackles the mother of all battles between origin myths for modern humans: the 'multiregional' *vs* 'recent Out-of-Africa' models, which tell, respectively, that, modern humans evolved throughout the Old World over the course of the last 2 million years, stuck together by recurrent gene flow; or that they evolved in Africa in the last ~200 000 years, and in a population fission, colonized the rest of the world less than 100 000 years ago, their *erectus* relatives becoming extinct there.

This book is an accessible guide through the models and the data, which I suspect will be a popular recommended text for introductory courses in biological anthropology. The style is amiable, and in general not too much precision has been lost in the effort to explain the methods. What swiftly becomes apparent is that, given the data and the statistical approaches that have been employed in the short history of the subject, there is very limited power to distinguish even these two caricatures of human prehistory.

Although coalescent methods – which model the effect of demography on the genealogy of a stretch of DNA – are given lip service, their potential for making maximum use of the data is not stressed here. This gives much of the book a rather old-fashioned feel, since the days of weaving stories out of summary statistics such as F_{ST} , which throw away a lot of the information in the data, are surely over – there are just too many alternative explanations of the patterns in such summaries.

Although the volume is quite well referenced – in chapter notes that also contain some of the mathematical derivations and modelling assumptions – I would have relished a more critical take on the literature. Rehashed examples include the back-to-Africa story constructed from a very unresolved Y-chromosome phylogeny in 1998 that does not hold water in the light of the much better resolved tree of Peter Underhill and colleagues from 2000; and the strange inferences about patterns of gene flow by Alan Templeton based on an incorrectly rooted mitochondrial DNA phylogeny and a statistical procedure (nested cladistic analysis) which remains unproven.

This particular race will not be over until worldwide data sets from a large number of genomic regions and the statistical methods powerful enough to distinguish recurrent gene flow from a recent population split are available. That is not far away and I know which horse I am backing. Perhaps then we can move on and start formulating and testing more imaginative models, as Relethford begins to do at the end of his book.

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