**Genetic history of human populations, the frequencies and gene frequency maps.**

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I have two comments that are more substantive. (1) The authors' consistent use of UPGMA (i.e. unweighted pairgroup method with arithmetic means) for constructing phylogenetic trees seems to be inappropriate. This is because, although UPGMA assumes a constant rate of evolution, most human populations have undergone extensive size fluctuation in the past, so that the average heterozygosity at present varies considerably with population. Therefore, any distance measure is affected by change in the population size. (2) Their argument

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**Book Review**

**Human evolution**

The History and Geography of Human Genes

edited by LL Cavalli-Sforza, P. Menozzi and A. Piazza

Princeton University Press, 1994. £120.00/$150.00 hbk (viii + 1068 pages) ISBN 0 691 08750 4

At the International Congress of Genetics in 1963, Luca Cavalli-Sforza and Anthony Edwards presented the first phylogenetic tree of human populations produced from gene frequency data. Many human geneticists were skeptical of their results at that time, but this was the start of phylogenetic analysis of human populations that fascinated many population geneticists and anthropologists in subsequent years. During the past 30 years, the extent of gene frequency data has expanded and the statistical methods for studying the history of human populations have improved. Cavalli-Sforza has been a major figure in this growing field and has conducted extensive data analyses, introducing new ideas, new hypotheses and new methodologies. This book is a compilation of his collaborative work with Menozzi and Piazza over the past 14 years. It is a huge book, with 362 pages of text and the rest devoted to, for example, tables of gene frequencies and gene frequency maps. Although this book is about the genetic history of human populations, the authors cover various aspects of human evolution, including paleontology, archeology, anthropometry, linguistics and known history. In this sense, the book is a product of an interdisciplinary study encompassing an enormous amount of knowledge accumulated in recent years. The authors have studied the history of genes and human populations using several different statistical methods but the most important one is phylogenetic analysis. Using this technique, the authors reached the conclusion that the first split of human populations occurred between Africans and the rest of the human population, whereas the second split occurred between the Northeurasian populations (including Amerindians) and the southeast Asian and Oceanian populations. By comparing their phylogenetic tree with Ruhlen's classification of languages in the world, they also concluded that genes and languages coevolved in the early stages of human evolution. Furthermore, application of their statistical methods to gene frequency data in populations from various parts of the world generated a number of interesting findings and hypotheses concerning human evolution, including the origins of Europeans, Lapps, Khoisans and southeast Asians. The authors cover a wide range of subjects, so it is not difficult to find some criticisms. For example, the FST distance used by the authors is possibly not the best one available for constructing a tree. The pure-drift model used for detecting natural selection is probably inappropriate. It is also possible to disagree with the authors' view of the origins of European or Indo-European languages. The description of archeological data in northeast Asia seems to be outdated. However, these criticisms are unlikely to affect their main conclusions and thus are of minor importance. I have two comments that are more substantive. (1) The authors' consistent use of UPGMA (i.e. unweighted pairgroup method with arithmetic means) for constructing phylogenetic trees seems to be inappropriate. This is because, although UPGMA assumes a constant rate of evolution, most human populations have undergone extensive size fluctuation in the past, so that the average heterozygosity at present varies considerably with population. Therefore, any distance measure is affected by change in the population size. (2) Their argument
BOOK REVIEW

about the coevolution of genes and languages in the early stages of human evolution is weak. As the authors themselves state, languages evolve much faster than genes and it is difficult to construct a phylogenetic tree of languages that differentiated more than 10,000 years ago. Thus, the authors do not really compare the genetic tree with the language tree. In fact, they compare the genetic tree with Ruhlen's taxonomy of languages. Furthermore, recent studies of genetic trees on a global basis, including that by Cavalli-Sforza (Bawcock et al., Nature 368, 455, 1994), do not support the authors' UPGMA tree (p. 99) on which the idea of coevolution of genes and languages was based.

In the last chapter, the authors state: 'We obviously do not claim that all our interpretations are correct. At least, some of them are provocative, and we offer them for further testing by other techniques or, perhaps more usefully, by a large number of data.' At present, gene frequency data are collected rather haphazardly by different investigators and the genetic loci and populations studied vary extensively with investigators. To derive more definitive conclusions, it is important that gene frequency data are collected more systematically. It is well known that Cavalli-Sforza is a proponent of the human genome diversity project, the purpose of which is to study many polymorphic loci for the same set of human populations. If this project is funded and completed, we would be in a much better position to study the history of human genes and populations.

This book will be a landmark in the study of human evolution and any investigator in this field should read it carefully whether or not he or she agrees with the authors. It is a product of the authors' painstaking work and contains a wealth of information that will be useful for the further study of human evolution.

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Errata

The maize mitochondrial genome: dynamic, yet functional
by Christiane Fauron, Mark Casper, Yan Gao and Barry Moore (Trends Genet. 11, 228-235)

Figure 3 in this review was incorrect due to an error in the production process. The correct figure together with the legend is shown below.

FIGURE 3. Recombination between repeats within a circular DNA molecule. (a) Recombination between a single pair of inverted repeats generates an isomeric form of the master chromosome characterized by a flip-flop of the sequences located between the two copies of the repeat (abcd versus acbd). (b) Recombination between a single pair of direct repeats converts the master chromosome into two subgenomic circular DNA molecules, each containing one copy of the repeat. (c) Recombination between a three-copy direct repeat produces six subgenomes. (d) Recombination between a three-copy repeat (two direct copies; one inverted), as found in the cmsT mtDNA, generates four isomeric forms of the master chromosome (each one contains the entire genetic information but the sequences have been permuted) and two sets of subgenomic circular molecules.

Genetic approaches to nuclear pore structure and function
by Valérie Doyle and Eduard C. Hurt (Trends Genet. 11, 235-241)