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BOOK REVIEW

Memories from our genes

Genes, Culture, and Human Evolution: A Synthesis

Blackwelll Publishing

ISBN: 978-14051-5089-7 (HB) \$ 94.95/978-14051-3166-7 (PB) \$ 44.95 **Picture to be reproduced**: Plate 4.1 c Bonobos (David Eppstein).

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opulation genetics is often considered the quantum physics of geneticists. Obviously, this is partly due to the scaring hard core of mathematics that is basically ineludible for any population genetics approach. At the same time, we all know how important are the concepts underlying those formulas both in terms of scientific tools for the 'daily genetics' and our vision of human genome characteristics among populations. Linda Stone and Paul F Lurquin from Washington State University and Luigi Luca Cavalli Sforza from Stanford University must have had clear in their mind both hardships and fascinating perspective of population genetics while writing 'Genes, Culture, and Human Evolution: A synthesis.' This pleasant book written by two geneticists including a world renowned scientist and founder of the Human Genome Diversity Project, L Cavalli Sforza, and a socio cultural anthropologist vibrantly draw links between genetic and cultural development. At this purpose, various disciplines such as physical and social anthropology, archeology, demography and linguistics provide complementary approaches to researching questions of human evolution (Cavalli Sforza, 2003).

The book contents include 14 chapters, an introduction and some general conclusion plus some extra materials such as color figures and appendixes. Readers will be taken through the comprehension of the different methodologies and approaches of genetics and anthropology

starting from the very basic concepts gradually to the most complicated ones with a very accessible language. The beginners will find very well done introductory chapters to the principles and theories of anthropology and population genetics and the most curious ones will enjoy appendixes with mathematical demonstrations and focuses at the end of the book. For example, of particular interest for readers is the simulation of drift that is usually difficult for students! These sections of the book allow a deep comprehension of the latest part, which really deserve it all. You will discover how human identity, cultural evolution and medicine are linked to our genes in a unifying theory.

The coevolution or dual inheritance theory that point out a strong connection between genetic and cultural changes, including language, along human evolution is carefully explained in many chapters and from different point of view. As a result cultural and genetic concepts merge on the basis of scientific evidences and recent findings of modern DNA analysis and anthropology.

Indeed, the advances in molecular genetic technology of the past decade allowed an unexpected definition of the variation maps in human populations and primates, expanding our knowledge from the ABO studies to the complete haplotype of human genome in half a century. Furthermore, haploid markers from mitochondrial DNA and the Y-chromosome have proven invaluable for generating a

standard model for evolution of modern humans. In 2005, the completion of the phase I of the HapMap project confirmed the generality of hotspot of recombination, long segments of strong LD and limited haplotype diversity, providing a tool not only for biomedical research but also for the analysis of polymorphisms in population genetics studies through single nucleotide polymorphisms (SNPs). SNPs are in fact the most common and useful genomic biomarkers that can be detected by DNA sequencing and other recently developed methods such as mass spectrometry and array-based resequencing.

Allelic frequencies change in population owing to natural selection (as a result of population variation among individual genotypes in their probabilities of survival and/or reproduction), and random genetic drift (which is due to a finite number of individuals participating in the formation of the next generation) and can ultimately lead to the elimination or fixation of particular allele. Genetic statistics of the substructure underlying human populations can contribute to identifying which genes are candidates to have been under selection. Furthermore, migration is another important factor in human evolution that can profoundly affect genomic variation within a population. The comprehension of these concepts, and the many others that the reader will find explained in this book, allowed the reconstruction of the first population trees.

Early studies showed that genetic differences between populations are relatively small as compared with those within populations. Subsequent analyses, including molecular polymorphisms of 14 populations representing all continents, confirmed that the within-population variance was about 85% of the total. A recent analysis of 377 autosomal microsatellite markers in 1065 individuals from 52 worldwide populations found that only 5-7% of the variation was between populations. Clines (gradual variations of populations in space) are certainly common for many genes, which is one reason to criticize the use of the distinction of races in humans, as already emphasized by Charles Darwin (LL Cavalli Sforza, 2003). It is the remaining 5-15% (the between-population component) that can



be used to reconstruct the evolutionary history of populations. So that, this large amount of genetic data collected in the last few year need to be matched with the anthropologic studies that have been carried on bones, language and culture. Migration can be tracked not only for the cultural and social changes that came with but also as a molecular event written in nucleotide variants. Somehow the knowledge of these variants and the way they organized along human evolution and inside genome structure, which revealed to be such a powerful tool to read our own history, promise even more interesting scenarios in terms of medical applications, reproduction technology, pharmacogenetics, bioethical paradigms and forensics. All these aspect are covered in this intense book.

Finally, but most importantly 'Genes, Culture, and Human Evolution,' has got the merit to remind us how studies of human population genetics and evolution have generated the strongest proof that there is no scientific basis for racism. They demonstrated that human genetic diversity between populations is small, and perhaps

entirely the result of climatic adaptation and random drift. Nothing could be more welcome in a period of cultural fundamentalisms than a thought through and nonpolitical 'manifesto' for cultural diversity ■

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