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Archaeogenetics: DNA and the Population Prehistory of Europe. Edited by Colin Renfrew and Katie Boyle. Cambridge: McDonald Institute for Archaeological Research, 2000. Pp. 342. $80.00 (hardcover).

The rapid advances in molecular genetics during the final decade of the past century have brought about a veritable explosion in the number of publications on human population genetics. As ever more information on the fine genetic structure of nuclear DNA and mtDNA of different ethnic groups from all over the world has accumulated, population geneticists have used it to infer prehistoric demographic events and to corroborate accounts from historical sources. In doing so, they have had to reconcile their findings with those of past purveyors of prehistoric information—archeologists, linguists, and paleoanthropologists. Some of the workers in these fields have gladly welcomed the contributions of geneticists, whereas others have shown the expected resistance to the new approaches and paradigms. Perhaps the most enthusiastic champion of genetics in archeology is the first of the two editors of this volume, the distinguished archeologist Colin Renfrew. He considers the field sufficiently advanced to have given it a new name, "archaeogenetics," which he defines as the study of the past by use of the techniques of molecular genetics.

A field so rapidly growing outruns any attempt at a summary, but the present volume furnishes an excellent snapshot of the state of the new discipline in 1999, when a conference entitled "Human Diversity in Europe and Beyond: Retrospect and Prospect" was convened in Cambridge, England. It is appropriate that Europe should be studied, since it is the continent whose human genetic population structure has been most intensively sampled and researched. The book consists of 41 separate contributions organized into six themes. It is obviously impractical even to list, let alone discuss, each contribution. Instead, I shall describe the general tenor of each theme, singling out the occasional contribution for praise or criticism. Part I is introductory. In it, the goals and approaches of the field are outlined, and there is a concise tutorial in molecular genetics and in the analysis of its data (intended for archaeological newcomers to the field—not for regular readers of the *Journal*), as well as a historical survey of the field.

In part II, six contributions treat the current archaeological and climatic findings and paradigms for Europe, based on other than genetic methods. I found this to be the most intellectually challenging—but also the most stimulating—section of the volume. All of the contributions in part II are linked by a common theme: the biological, cultural, and environmental processes involved in the peopling of Europe are far more complex than is indicated by the simple models investigated by the geneticists. Thus, in his contribution (chapter 7), Marek Zvelebil points out that the process of neolithization is unlikely to have been brought about by 100% population replacement (the migrationist position) or, alternatively, to have been generated fully in situ (the indigenist position). It is more likely, he states, that heterogeneity of the demographic processes will engender some of each (the integrationist position). Although some such response from the archaeological community can be expected as a Luddite reaction to newcomers poaching in their preserves, I cannot believe that this is the predominant reason. Rather, it is a manifestation of a common tension, found in many fields of science, between researchers who simplify models so that they can carry out tests of sufficient power to demonstrate the validity of their model while ignoring the contributions of subsidiary factors, and others, who perceive the complexity of the processes under study but who are unable to demonstrate their model convincingly because adequate tests for their complex hypotheses may not exist or their data are inadequate to the task of testing them. The correct approach will vary with the problem being investigated and will depend on the size distribution of the importance of the various factors affecting the process. In an L-shaped distribution, such as a decaying exponential function, the (over)simplification approach will probably provide a good explanation of the process, but this is not so in an approximately uniform or gradually declining distribution of factor importances.

The six contributions in part III illustrate the types of data that human population geneticists analyze and the different analytical approaches that have been pursued, applied to data sets ranging from global to continentwide but always with an emphasis on Europe. We encounter mtDNA and Y chromosomes as well as autosomal nuclear variation of diverse types to which are applied (1) mismatch distributions (Excoffier and Schneider), (2) ordination (principal-components analysis and nonmetric multidimensional scaling), (3) spatial autocorrelation analysis (of gene and haplotype frequencies as well as of DNA data, following the AIDA methods of Bertorelle and Barbujani), and (4) phylogenetic analysis, including phylogeography. Parts IV and V are collections of regional studies of prehistory, based on molecular genetics for western and eastern Europe, respectively. Each part contains eight contributions.

I am troubled by the lack of statistical-significance tests in some of the contributions (e.g., chapters 8 and 9) and by incorrect applications in some others. Geographically sampled data such as the ones presented in this volume are almost invariably spatially autocorrelated (Sokal and Oden 1978*a,* 1978*b;* Upton and Fingleton 1985). Typically, such data respond liberally when subjected to conventional significance tests; that is, they will indicate statistical significance much more frequently, even when the null hypothesis is true. Tables 6.1 and 6.2 in chapter 6 are examples: here, the radiocarbon dates are undoubtedly spatially autocorrelated, yet their correlations with longitude and latitude are tested at conventional significance levels instead of by the Clifford-Richardson-Hémon test (Clifford et al. 1989). For the same reason, the significance values of the χ^2 tests comparing frequencies of nonmetric cranial traits between Basque populations and other European populations (table 21.1 in chapter 21), as well as the significance values of the $\delta\alpha$ tests of the genetic impact of linguistic boundaries (table 40.1 in chapter 40), are questionable. Contributors in several parts of this volume mention synthetic maps for the representation of summaries of the variation of multiple genetic information (prominently featured in the book by Cavalli-Sforza et al. [1994]), with the implication that this is a reliable method to be emulated. Yet Sokal et al. (1999*a*, 1999*b*) have demonstrated clearly that the interpolation step in the preparation of synthetic maps introduces an added, frequently large component of spurious spatial autocorrelation, which falsely enhances or distorts true trends in such data. Furthermore, they showed that the spurious contribution is often so large that even random data suggest the presence of apparent but entirely artifactual geographic trends. These properties make trends exhibited by synthetic maps quite suspect. (For a contrary view, see the report by Rendine et al. [1999].)

Finally, part VI is a catchall section of contributions, most of which are relevant to European archaeogenetics. They range from four purely methodological papers to another four discussing the insights gained into prehistoric human population structure from studies of the genetic origins of European domesticated animals and plants. The section concludes with two contributions on the relations between genetic and linguistic variation, and the volume ends with concluding remarks by Cavalli-Sforza, who discusses the prospects of the Human Genome Diversity Project.

The editors are to be congratulated for assembling an excellent collection of contributions that accurately reflect the state of this relatively new field at the turn of the century. The editors and publishers have turned out a handsome, profusely illustrated volume, remarkably free of printing errors. For a number of years to come, this book will be a benchmark that will indicate what workers in other regions of the world need to accomplish. However, it will not remain a standard for too many years. The advances in the field are now so numerous and rapid that both techniques and knowledge in the study of European prehistory will surely have drastically changed by the end of this decade. In welcoming and advocating the employment of molecular genetic methods in archeology for quite a few years already, Colin Renfrew has shown considerable prescience and remarkably good judgement.

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References

Cavalli-Sforza LL, Menozzi P, Piazza A (1994) The history and geography of human genes. Princeton University Press, Princeton, NJ

Clifford P, Richardson S, Hémon D (1989) Assessing the significance of the correlation between two spatial processes. Biometrics 45: 123–134

Rendine S, Piazza A, Menozzi P, Cavalli-Sforza LL (1999) A problem with synthetic maps: reply to Sokal et al. Hum Biol 71:15–25

Sokal RR, Oden NL (1978*a*) Spatial autocorrelation in biology. I. Methodology. Biol J Linn Soc Lond 10:199–228

——— (1978*b*) Spatial autocorrelation in biology. II. Some biological implications and four applications of evolutionary and ecological interest. Biol J Linn Soc Lond 10:229–249

Sokal RR, Oden NL, Thomson BA (1999*a*) A problem with synthetic maps. Hum Biol 71:1–13

——— (1999*b*) Problems with synthetic maps remain: reply to Rendine et al. Hum Biol 71:447–453

Upton GJG, Fingleton B (1985) Spatial data analysis by example. Vol 1. Point pattern and quantitative data. John Wiley & Sons, Chichester, England

0002-9297/2001/6901-0029$02.00