
Mathematical study of population genetics began with the pioneering work of R. A. Fisher, J. B. S. Haldane, and S. Wright, who dominated the field until the late 1950s. Since that time, the major contributor to the field has been Motoo Kimura, who has demonstrated the power and wide applicability of diffusion methods in population genetics. In 1968, Kimura proposed the neutral theory, suggesting that the main cause of evolutionary change at the molecular level is random fixation of selectively neutral or nearly neutral mutations rather than positive Darwinian selection. Since then, the properties of the theory have been studied extensively by Kimura and many other evolutionary biologists. The validity of the theory has been tested by using data from protein polymorphism, amino acid sequences, and DNA sequences. It is delightful to see that the advances in nucleic acid techniques now generate the kind of data for which Kimura's theoretical works can be applied so profitably.

Population Genetics and Molecular Evolution is based on the Oji International Seminar held in Mishima, Japan, in November of 1984 on the occasion of Kimura's sixtieth birthday. The book introduces a fascinating and rapidly developing field, where population genetics and molecular biology are combined to elucidate the mechanisms of evolution and variation at the molecular level. Twenty-six papers in the book cover almost all aspects of evolutionary genetics, and four additional essays focus more on Kimura's personal side.

In the opening paper, J. F. Crow discusses why the proposal and refinement of the neutral theory are important not only in the development of population genetics but in the history of evolutionary theory. This is followed by a variety of data analysis papers for prokaryotes and eukaryotes. R. K. Selander shows that natural populations of Escherichia coli and Shigella have clonal structure and that their genetic diversities are consistent with the prediction of the neutral theory. Chemostat experiments with E. coli by D. L. Hartl and D. E. Dykhuizen provide the only available example of an experimentally determined distribution of selection coefficients, which again supports the neutral theory. T. Mukai's extensive analyses of natural populations of Drosophila melanogaster reveal no evidence for either overdominance, frequency-dependent selection, or diversifying selection at polymorphic structural loci. T. Yamazaki presents an example of genetic variability at a putative regulatory-gene locus (or loci) subject to natural selection while genetic variability at the structural gene locus under its control is neutral. Analyses of codon usage in E. coli, yeast, and Salmonella by T. Ikemura and in Mycoplasma by S. Osawa and his colleagues show that choice of synonymous codons is influenced by the availability of isoaccepting tRNA molecules and by the A + T content of the genome. In particular, Ikemura proposes that the constraint arising from tRNA availability decelerates the rates of synonymous substitutions occurring between taxonomically related organisms, which is consistent with the prediction from the neutral theory. R. Milkman presents a unified theory of population genetics and molecular evolution, which reconciles neutrality at the gene level with stabilizing selection at the phenotypic level. Particularly refreshing is Selander's demonstration that protein electrophoresis, an often abused technique, is a powerful method in the fields of bacterial epidemiology, pathology, and systematics.

Phylogenetic studies have been presented by M. Nei for human and other primate
populations and by H. Hori and his colleagues for organisms such as bacteria, multicellular animals, and green plants. Using data such as amino acid and nucleotide sequences, restriction-site maps of mitochondrial DNA, and electrophoretic allele frequencies from man, chimpanzee, gorilla, orangutan, and gibbon, Nei concludes that the phylogenetic tree obtained from DNA sequence data is most reliable and that the species that is closest to man is probably the chimpanzee and that the next closest species is the gorilla.

Statistical analyses of molecular evolution have been presented by three groups of authors. T. Miyata and his colleagues demonstrate the presence of marked amino acid sequence similarities among polymerases of taxonomically distant organisms, suggesting that a DNA piece with a certain function can be transferred horizontally through a wide range of organisms. Studying duplicate genes, W.-H. Li demonstrates that accelerated nucleotide substitution often occurs in either one or both of the duplicate genes and that this is probably caused by relaxation of selective constraint. T. Gojobori studies the rates of nucleotide substitution for different sets of viral and cellular oncogenes, showing that the rate of evolution of retrovirus genomes can be more than a million times greater than that of DNA genomes.

Mathematical studies of molecular evolution have been presented by a number of authors. Kimura’s analyses on a “compensatory neutral evolution” model of individually deleterious but compensatory mutations at two loci may turn out to be important. If the model is applicable in general, the results will support not only Ohta’s “slightly deleterious mutation model” of evolution but also help to explain some “non-random” evolutionary amino acid substitutions under the framework of the neutral theory. N. Takahata explores population-genetic models of extranuclear genomes, with special reference to the degree of polymorphism, linkage disequilibrium, local differentiation, and introgression over species boundaries. B. Charlesworth discusses population-genetic models of transposable elements on the basis of the selfish-DNA hypothesis. Ohta reviews theories relevant to the evolution of multigene families, with emphasis on dispersed repetitive-DNA families generated by gene conversion, duplicative transposition, and interchromosomal recombination.

Traditional population-genetic topics include population dynamics of mutant genes in nonequilibrium populations, by T. Maruyama and P. A. Fuerst; migration patterns of human populations, by N. Yasuda; and some topics in sociobiology, by Aoki. Three papers, one each by A. Shimizu, S. Itatsu, and T. Shiga, are oriented toward more mathematical rigor. Different genetic-distance measures, estimators for the numbers of nucleotide substitutions from DNA sequence data, and methods for the construction of evolutionary trees are discussed by G. A. Watterson, F. Tajima, and Y. Tateno, respectively.

The strength of the book lies in the diversity of the topics covered by leading researchers in theoretical and experimental population genetics, molecular biology, molecular evolution, and mathematics. Despite the diversity, Population Genetics and Molecular Evolution is a coherent book, thanks in no small part to the work of the editors, Ohta and Aoki. Essays written by N. Calder, Y. Yamada, Kimura, and Crow add a personal touch to the book, making it comfortable to approach. Population Genetics and Molecular Evolution is exciting and stimulating to read and is an important addition to the current evolutionary literature.

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This large book presents the results of a NATO Advanced Research Workshop organized by the editors and held in Paris during July of 1984. The symposium goal was to better understand the phylogenetic relationships of the rodents, both within the Rodentia and the other mammalian orders, by utilizing many kinds of biological information. Participants were encouraged to use character analyses based on cladistic methodologies. Data from the fields of paleontology, comparative anatomy, embryology, cytogenetics, and biochemistry are presented.

Following a general introductory chapter, there are 26 chapters by the symposium participants and then a summary by the editors. This volume is heavily biased toward morphological rather than molecular studies. Seven chapters contain information on fossil rodents. Twelve articles deal primarily with anatomical and embryological data, and one chapter is a cytogenetic analysis of the genus Mus. Only five chapters (13% of the text) are concerned with the evolutionary stories suggested by proteins.

These molecular studies cover a broad range of phylogenetic comparisons. Sho-shani and colleagues present a phylogeny of the rodents and other eutherians based on amino acid sequences of the alpha and beta globins. The superordinal affinities of the rodents and other mammals are also examined using the sequences of the α-crystallin A protein (De Jong). An albumin immunological study of the relationships between rabbits and rodents and the relationships among the rodents is presented by Sarich. Beintema analyzes the amino acid sequences of pancreatic ribonuclease and insulin, to produce phylogenetic trees of these proteins as expressed in the commonly studied laboratory murids and the hystricognaths (the group including porcupines and guinea pigs). Electrophoretic data on 77 rodent species are analyzed by Bonhomme and colleagues.

Based on remarks in the summary chapter, the symposium was considered at least a social success. The participants listened to and discussed the wide variety of reported results. In its format and writing style the volume is also successful. The editors are to be complimented on achieving a technically pleasing volume. The papers are nearly all well written, and results are presented across the chapters in comparable types of data tables and figures. The graphics are well done throughout the book. However, my impression from reading the data chapters and the editors' resume is that this multidisciplinary symposium was unsuccessful in resolving most of the major controversies that existed before July of 1984.

Major questions posed for the symposium were: the relationships of rabbits and rodents, the origins of the earliest rodents, and the relationships among extant rodent groups. The paleontologists report on important new fossil material and describe the morphology of the earliest rodent-like animals from Asia. But consensus as to whether the rabbits and rodents are more closely related to one another than to other mammalian orders is not forthcoming from the different data sets, nor is it satisfactorily resolved where some of the anomalous rodent families should reside on the phylogenetic tree. This uncertainty arises in part from the considerable amount of parallelism and convergence that occurs in the anatomy of these creatures.

The papers dealing with molecular data do not break much new scientific ground.
Only the works by Sarich and Bonhomme et al. are largely new, the other materials having appeared in earlier reports. The sequence data used in the interordinal comparisons (Shoshani et al. and De Jong) do not suggest a common lineage for the rabbit and rodents versus other orders such as the Primates. The chapter by Sarich seems to me the most appropriate and successful of the molecular biology studies. The resolving power of immunological studies of albumin is ideal for answering the phylogenetic questions posed for this symposium. A surprising finding is the great molecular difference between two mouse genera (*Mus* and *Acomys*) that are considered very closely related on morphological grounds. This discovery emphasizes how misleading phylogenetic conclusions can be when based on systems in which so much parallelism exists. Beintema's analysis of insulin and ribonuclease genes is limited in part by insufficient diversity of sequences available to make many statements about intrafamilial relationships and by the confounding effects of duplication of the insulin gene in different lineages. The last paper utilizes information on the relative mobilities of electromorphic alleles from starch-gel electrophoresis of tissue extracts. This is an ambitious attempt by Bonhomme et al. to deduce the phylogenetic relationships of many rodent taxa, an attempt at which they are only partly successful. Phenetic methods, multivariate analyses, and cladistic techniques are all employed. But the resolution of relationships among many genera remains inconclusive by all of these methods. The authors offer three explanations for these results: electrophoretic convergence, ancestral polymorphisms, and/or reticulate evolution. They conclude that the nearly simultaneous splitting into many branches of an ancestral stock best explains their results.

The book represents a useful overview by many of the major figures in this field and brings together in one place references to most of the relevant paleontological and anatomical literature. For a complementary treatment of the rabbits and rodents by some who did not contribute to the NATO volume, one should see the six pertinent chapters in Anderson and Jones (1984).1 Almost certainly the future insights into the questions posed at this symposium will come from the comparative molecular biologists, as they apply their powerful tools to these same questions. At its extravagant price this book is a poor investment for the biologist of a molecular bent. But it should be available for reference in the local library.

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