and central European communities. There are several fundamental and interesting differences:

(1) The human impact, especially the effects of treatments such as coppicing, grazing and browsing, has been and still is much more severe in Britain than in central Europe, and obviously far fewer samples could be collected in 'high forests' than on the continent. Consequently, the species richness of British trees and shrubs – even in beech communities – is all the more striking.

(2) The climatic contrasts between the British Isles and the continent seem much larger than the contrasts between southeast and northwest Britain. Indicators of oceanic climate such as *Hyacinthoides non-scripta* are unknown, and others such as *Ilex aquifolium* very rare, in central Europe. On the other hand, indicators of subcontinental climate are absent in Britain, for instance, *Lathyrus vernus* and *Hepatica nobilis* in the *Fagus sylvatica–Mercurialis* woodland.

(3) The indicator value of species and their ecological behavior differ. This is clearly seen from the floristic tables and the community descriptions, which provide an interesting view into the different combination of site conditions suitable for individual species. The species combinations sometimes seem strange to the continental ecologist. For instance, the combination of *Pteridium aquilinum, Melica uniflora, Carex sylvatica* and *Euphorbia amygdaloides* (*Fagus sylvatica–Rubus fruticosus* woodland) will never be found in the more easterly regions of mainland Europe, but is familiar to the phytosociologist of the more oceanic northwestern continent.

(4) Another striking difference is in the role of beech in British communities. This species, which is dominant on a wide range of sites from rich to poor on the continent, is replaced by oak and ash in Great Britain, except in the southeast. These oak and ash communities are more or less unknown in subcontinental central Europe.

Despite these differences, there are correspondences between British and continental vegetation units, especially with regard to beech communities. The classification of the five groups mentioned above into three subgroups on rich, intermediate and poor sites has its parallel in the classification of continental communities and is characterized by a nucleus of the same species.

**G. Jahn**

Institut für Waldbau II, Büsgenweg 1, D-3400 Göttingen-Weende, Germany

**References**

1 Braun-Blanquet, J. (1964) *Pflanzensoziologie* (3rd edn), Springer-Verlag

2 Oberdorfer, E. (1957) *Süddeutsche Pflanzengesellschaften*, VEB Fischer Verlag

3 Tüxen, R. (1937) *Beih. Ber. Naturhist. Ges. Hannover* 3, 1–170

## Molecular Evolution

**Fundamentals of Molecular Evolution**

by W-H. Li and Dan Graur, *Sinauer Associates, 1990. £16.95/$22.95 pbk (275 pages) ISBN 0 87893 452 9*

**Evolution at the Molecular Level**

edited by R.K. Selander, A.G. Clark and T.S. Whittam, *Sinauer Associates, 1991. £44.00/$55.00 hbk, £23.95/$28.95 pbk (xii + 350 pages) ISBN 0 87893 818 4*

Writing a textbook on molecular evolution should entail the construction of two bridges – one from molecular evolution to molecular biology and the other from molecular evolution to population genetics. Li and Graur have made nice work of the former bridge, and many students of molecular biology will find their book helpful and easy to read. The significance of gene duplication, exon shuffling and transposition, as well as nucleotide substitutions and phylogenetic trees, is succinctly presented with the help of many figures. This book will also be attractive to teachers, for a glossary is attached at the end of the book and several problems are given in each chapter (though not all of them have answers).

The bridge between population genetics and molecular evolution, however, is considered in only one chapter (on dynamics of genes in populations) and one section of a chapter (on gene trees and species trees). Therefore, short-term evolution seems to be beyond the scope of this book. Yet, this may not be a shortcoming. There are already many textbooks on population genetics, while we have not had a good introductory textbook on molecular evolution. Because of this strategy, this book contains far fewer mathematical formulas than a textbook of population genetics. This may be attractive to students.

The structure of this book is somewhat similar to that of Nei's *Molecular Evolutionary Genetics*[1]. For example, chapters 1, 3, 5 and 8 of their book correspond to chapters 3, 5, 11 and 6 of Nei's book, respectively. But this resemblance may be inevitable, because both authors were Nei's students. Overall, this is a good textbook for newcomers to molecular evolution, especially for those with a background in molecular biology. The cover design is beautiful and illustrates the current momentum of this field.

*Evolution at the Molecular Level* is the outcome of a symposium held in June 1989 at Pennsylvania State University. The first four chapters deal with the evolution and population genetics of bacteria. Chapters 5–7 are on viral and organelle genes. *Drosophila* is covered in Chapters 8–10, and nuclear genomes of higher organisms, including humans, are discussed in the last three chapters. Overall, population-genetic aspects are stronger than molecular-evolutionary ones. The following chapters particularly caught my interest.

Woese provides a detailed history of bacterial taxonomy as well as a discussion of the controversy on the divergence of eubacteria, eukaryotes and archaebacteria. However, it is now clear that eubacteria diverged first, especially because of the gene-duplication events studied by T. Miyata's group (e.g. Ref. 2). Their work is given scant attention here, and the fact that H. Hori and colleagues[3] had already proposed this branching pattern based on 5S rRNA sequence data should also have been noted.

Selander *et al.* studied evolutionary relationships of many serovars of *Salmonella*. This type of work is not only academically interesting but also practically important. Alkaline phosphatase genes of *Escherichia coli* were studied by DuBose and Hartl. They used oligonucleotide site-directed mutagenesis and showed that the resulting amino acid replacements were selectively neutral or only very slightly deleterious.

Evolutionary rates and divergence time of AIDS viruses (HIVs) are discussed by Yokoyama. It now seems to be established that the evolutionary rate of HIV is a million times higher than that for ordinary DNA genomes, and divergence times of these viral strains are on the order of 100 years. Deeper evolutionary analysis is necessary to tackle AIDS.

The Major Histocompatibility Complex (MHC), a rather special case in molecular evolution, is discussed by Nei and Hughes; in a good combination of molecular-evolutionary and population-genetic analyses, they show clear-cut evidence for the existence of positive darwinian selection at this gene complex. The last chapter, by R.C. Hardison, is a brief review of the evolution of globin genes, and is useful for a quick grasp of the current status of globin research.

Generally speaking, symposium proceedings have several inherent problems. Contents tend to be heterogeneous and not all the chapters are good. Publication is often slow and the contents are already obsolete when the proceedings is published, though this does not apply to this book. And review papers may be less suitable to such books than to journals such as *TREE*.

**Naruya Saitou**

Laboratory of Evolutionary Genetics, National Institute of Genetics, Mishima 411, Japan

**References**

1 Nei, M. (1987) *Molecular Evolutionary Genetics*, Columbia University Press

2 Iwabe, N., Kuma, K., Hasegawa, M., Osawa, S. and Miyata, T. (1989) *Proc. Natl Acad. Sci. USA* 86, 9355–9359

3 Hori, H. and Osawa, S. (1987) *Mol. Biol. Evol.* 4, 445–472

# Epidemiology and Ecology

## Infectious Diseases of Humans: Dynamics and Control

by R.M. Anderson and R.M. May, *Oxford University Press, 1991. £50.00 hbk (viii + 757 pages) ISBN 0 19 854 599 1*

They first met in 1974. After only a brief period of latency, Roy Anderson and Robert May had become the foremost advocates of a population-biological approach to epidemiology that uses simple mathematical models to guide the collection of data, to explain epidemiological phenomena and to help design programmes for disease control. The philosophy is that 'mathematical models are no more, and no less, than tools for thinking about things in a precise way', and that even simple models can embrace those essential nonlinearities that have consequences too complex to be derived from armchair speculation.

In making an impact on epidemiology over the last 15 years or so, Anderson and May have been agents of a synthetic process that has had three main components. First, they have done more than anyone else to reunite mathematical (as opposed to statistical) epidemiology with its empirical base. Bailey's[1] general text is a classic of applied mathematics, but it is simply unapproachable by public health epidemiologists, and is heavy going even for Masters' students in medical statistics. His more recent and more specialized treatment of malaria[2] contains almost no data at all. For practitioners, a fundamental difficulty with these books is their focus on mathematics rather than biology. In 1975, Bailey said he was 'convinced that purely academic investigations are largely a waste of time'. I presume, therefore, that he approves of what has happened since. Anderson and May have led a school that has productively taken the necessary step closer to reality; their approach sacrifices some mathematical niceties by, for example, making more use of deterministic models rather than stochastic ones, but incorporates those key components that characterize the complex ecologies of infectious agents.

Second, although the models have much more biological detail, they remain general enough to keep in perspective the extraordinary variety of parasite life histories. The value of maintaining generality is that it permits comparative study of the dynamical characteristics of different infectious agents: thus, by varying the parameter values of a single model, it is possible to explain the longer interepidemic period of mumps, as compared with measles, as a function of its lower generation case reproductive rate and longer latent and infectious period. More broadly, the new theory has done much to highlight general principles that apply to infectious agents ranging from micro- to macroparasites; in short, to bridge the gap between the traditionally separate disciplines of microbiology and parasitology.

These first two themes dominate the new book. The third component has emphasized the similarities between the aims and methods of ecology and epidemiology. Clearly, this is the area of most direct interest to ecologists and evolutionary biologists, but one which inevitably commands less space here. Under this heading, elaboration of the principles has, for example, added much momentum to practical investigations of the role played by parasites in regulating their host populations, and stimulated much thought about host–parasite coevolution.

All three of these things have been done prolifically and publicly: this has been no quiet revolution. As one source close to the authors recently remarked on discovering first-rate work in a lesser-known journal, 'when Anderson and May do something that good, it's all over the tabloid press'. Well, not quite, but throughout the 1980s there has been a tendency to open one's copy of *Nature* on a Thursday wondering what Anderson and May have been doing this week.

From two such productive authors, we could not have expected a short book, even though they take an admittedly 'personal view'. The personal view means that, despite the length, this is a monograph rather than a textbook: almost every section is dominated by an account of their own work and that of collaborators, generally a resumé of published material (we need no longer turn to that bulging file of reprints), with some new additions, even where other unmentioned authors have made a substantial contribution. So specialists, of whatever group of parasites, should not expect to find a thorough review of their fields. For example, the quantitative epidemiology of malaria is dealt with in 50 illustrative pages, oriented around the material in Anderson's earlier edited book[3]. It excludes all the other good work that could fill a large volume on this disease alone.

Picking up a book for the first time, one inevitably heads for familiar territory, not merely to see whether one's own work has been thought worthy of mention, but most easily to judge