

lection. Names like Dobzhansky, Mayr, Simpson, Rensch, and Huxley are just a few that might bring back memories of an undergraduate history of biology class.

Dr. Smocovitis orients her book around a narrative. In her mind science is a narrative, and in the "more reasoned narrative of evolution, we will find existence within such narrative frameworks that structure (*sic*) lived experience. Within those narratives, which tell themselves through us, lies the meaning of life." What we do find, though, is that the story of how evolutionary thought came to unify biology is not a linear tale, but more like Darwin's tangled bank, a narrative with many intertwined subplots.

The narrative, located in Chapter Five, represents about 40% of the book. It begins post World War I and ends in post-Sputnik times. In it Smocovitis describes how population genetics and natural selection came to be fused into the modern synthesis, how evolution came to be thought of as the unifying aspect of biology, and even how biology came to be, in the minds of some, the unifying element of all science. We learn how biologists were weaned away from mechanism and physics envy and brought to a vision of living creatures as phenomena beyond physics and chemistry. The narrative is complex but well supported with references to the pertinent literature and the author's own conversations with some of the founders. It is tightly woven and holds not only water, but the reader's attention.

The narrative is supported in earlier chapters by a section Smocovitis calls an "Exegesis". Those readers not having a background in history or philosophy will find these chapters helpful in understanding how the history and philosophy of biology has grown and how historians and philosophers can tell us more about our science than we might think. The last section brings us to modern times and describes some problems with the evolutionary synthesis. The epilogue goes into the whole question of multicultural diversity and the stress that it has brought into modern existence. Warfare in Bosnia and Central Africa bring to mind two recent episodes of multicultural conflict. The quote used at the beginning of this review is actually on the last page. In Dr. Smocovitis's mind it is the one way in which this narrative of evolution might save us from ourselves.

The book is actually two books, one being the text and the other being the long footnotes that grace almost every page. At the beginning Smocovitis wonders aloud whether she should have taken this approach. Although I found it to be like watching two programs on TV at one time, and got used to moving between footnote and text, some might find the coupling too disconcerting. There are no diagrams or figures other than the frontispiece by William Blake, *Fall of Man*. The bibliography, in addition to the references to primary and secondary materials given by the footnotes, is broken into general areas, e.g., history and theory.

The book might be a bit tough for an undergraduate to follow, but surely biology graduate students and faculty will find it enlightening. It should also be read by the general public, particularly those who fear evolu-

tion, as it provides a wonderful story of how the unification of biology came about and how evolution might tell us more about our existence on this globe.

LARRY T. SPENCER  
Natural Science Department  
Plymouth State College  
Plymouth, New Hampshire 03264

Avian Molecular Evolution and Systematics, DAVID P. MINDELL, ed. Academic Press, San Diego, 1997, xx + 382 pp., \$84.95, (ISBN 0-12-498315-4).

Birds represent one of the few large groups of organisms where knowledge of species diversity (about 10,000 living species) is nearly complete. Yet the evolutionary history of birds is not well known, in part because of a poor fossil record, ease of dispersal (obscuring historical distributional patterns), and many cases of apparent morphological convergence. For these reasons they have been an ideal group for the application of molecular techniques, and considerable advances have been made over the last several decades. In particular, Sibley and Ahlquist's (1990) DNA hybridization study of about 1,700 species greatly influenced ornithology. Their phylogeny has become a reference point for comparison in avian evolutionary studies.

This new book on avian molecular systematics represents a cross section of topics, although it focuses on mitochondrial DNA sequences. It is not a textbook, but a collection of 13 papers that touch on many of the methodological issues of interest to molecular systematists. Such topics include detection of nuclear homologs of mitochondrial DNA, use of microsatellites and mitochondrial control region sequences, taxonomic resolution of specific genes, ancient DNA, and applications to behavioral and biogeographic questions. Some of the chapters are reviews and others present new data sets. More than 200 kilobases of new avian sequence data, almost all from mitochondrial DNA, are analyzed in several chapters.

Some controversial aspects of the Sibley and Ahlquist (1990) work, such as the polyphyly of pelecaniform birds and the cuculiform affinities of the hoatzin, garnered additional support from DNA sequence data in two chapters. However, one study (Mindell *et al.*) on higher-level phylogeny, presenting the largest data set, yielded an unexpected result. An analysis of five orders of birds based on nearly complete mitochondrial genomes (13.3 kilobases each; data not yet released to databases) resulted in this well-supported tree: (passeriform(falconiform(ratite(galliform, anseriform))))). It is generally believed that the basal split among living birds separates the paleognaths (tinamous and ratites) from the neognaths (all other birds) so this tree will come as a surprise to most. If confirmed, it would give new meaning to the informal terms "passerine" and "non-passerine," which often are used for convenience but not to imply a phylogenetic split. Although this new result lacks support from morphology and other molecular data sets (including that of Sibley and Ahlquist, 1990), it is based on a large sequence data set and is certain to stimulate further research on the

higher-level phylogeny of birds. Important in that regard will be the inclusion of additional orders and sequences from nuclear genes.

The high price of this book, taking into account that there are no color illustrations, will be a consideration. Nonetheless, it is a well-edited volume that will be of interest to many ornithologists and molecular systematists.

#### REFERENCES

Sibley, C. G. and J. E. Ahlquist. 1990. *Phylogeny and classification of birds*. Yale University Press, New Haven.

S. BLAIR HEDGES  
*Department of Biology*  
*208 Mueller Laboratory*  
*Pennsylvania State University*  
*University Park, Pennsylvania 16802*

*New Uses for New Phylogenies*. PAUL H. HARVEY, ANDREW J. LEIGH BROWN, JOHN MAYNARD SMITH, AND SEAN NEE, eds. Oxford University Press, Oxford. 1996. xi + 349 pp. \$70.00 cloth. ISBN 0-19-854985-7. \$35.00 paper. ISBN 0-19-854984-9.

The integration of phylogenies into areas outside of pure systematics has been one of the most striking developments in evolutionary biology over the past decade or so. Several recent books testify to the strength of such phylogenetic approaches (Eggleton and Vane-Wright, 1994; Martins, 1996; Sanderson and Hufford, 1996). One may wonder, in approaching the edited volume *New Uses for New Phylogenies*, whether another collection of phylogenetic papers will be very useful, especially one with a seemingly arbitrary focus on using trees based on nucleotide sequences. As it turns out the book is useful, presenting an extremely wide range of ideas, methods, and applications that overlaps very little with the volumes just mentioned. Furthermore, although it is not a stated purpose of the book, the 20 chapters together demonstrate the special qualities of molecular data for addressing certain problems.

At least three advantages of molecular data are evident in these papers. First, in some cases what one wants is not a phylogeny of species or other taxa, but a genealogy of a segment of DNA (often a gene); molecular characters generally provide the only means of obtaining such genealogies. It is evident that gene genealogies are often needed when the focus of a study is the history of the gene itself, e.g., in studies of gene duplication, gene conversion, and transfers of genes between taxa. The chapter by Fitch summarizes a variety of studies of this kind and also serves as a reminder that a handful of people were studying gene trees and their implications well before the recent explosion of tree-based studies. Several chapters represent a less obvious, but increasingly common, use of gene genealogies, namely to address problems in population genetics. At the core of these studies is the fact that measures derived from gene trees often contain more information relevant to such problems than do "history-free" measures such as heterozygosity. These

various chapters are largely outside the realm of morphological phylogenetics.

Another advantage of molecular data is that it can provide the variation necessary to infer a phylogeny when, for practical or other reasons, little phenotypic variation can be detected. This advantage is exemplified by Sharp *et al.*'s examination of cross-species transmission of HIV and related viruses. A striking result from this study is that HIV-type viruses apparently have been transmitted from other primates to humans several times independently. Although the authors do not discuss it, an obvious implication of this result is that the eventual infection of humans with HIV may have been in some sense inevitable. It seems unlikely that phenotypic variation among these viruses would have allowed the same kind of analysis.

A final, more general, and more controversial advantage of molecular characters is that their evolution apparently can be modelled more precisely than that of traditional characters. Most of the chapters in the book endorse the use of explicit evolutionary models. This approach is obvious in the chapters on population genetics, since these studies rely on examining the fit of data to expectations under specific genetic and demographic models. Many other chapters rely on estimating dates of divergence based on the assumption of a molecular clock, with the exact dates depending on further assumptions about molecular evolution (e.g., the relative probabilities of transitions and transversions). For example, chapters by Nee *et al.* (on inferring population histories), Purvis (a pithy review of methods for inferring patterns of speciation and extinction), and Holmes *et al.* (applying the approach of Nee *et al.* to the history of disease epidemics) involve plotting the number of lineages against time, which requires dating phylogenetic branching events. It is intuitive that a phylogeny with dated branching events provides more information for the analysis of character evolution and lineage diversification than an undated one. However, the implications of such dated phylogenies can be surprising, as in the discovery that one may be able to infer both speciation and extinction rates from a lineages-against-time plot generated from the analysis of living taxa alone (Harvey *et al.*, 1994, reviewed in the chapter by Purvis).

Interestingly, the most extensive argument for a model-based approach is in a chapter by Martins and Hansen that does not emphasize molecular data. These authors show how various statistical comparative methods (e.g., those used to measure the evolutionary correlation between two traits) are all dependent on assumptions about the evolutionary process. Their findings mirror previous conclusions about the process assumptions underlying methods of phylogeny estimation (e.g., Felsenstein, 1983; Sober, 1988). Under this view, molecular studies currently are ahead of non-molecular ones, but eventually phylogenetic studies using any kind of data should incorporate explicit evolutionary models. Of course, this does not imply that molecular and non-molecular data are interchangeable; it is unclear, for example, whether any class of morphological traits will ever be useful as a clock.

Despite the emphasis on molecular data, *New Uses* does not present an anti-morphological view. For one