

BOOK REVIEW

Molecular Systematics and Phylogeography of Mollusks

Edited by Charles Lydeard and David R. Lindberg

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This volume makes a contribution to the scientific literature on molluscs that will remain valuable for many years, providing excellent summaries of how studies of DNA sequence variation have informed understanding of the evolutionary relationships and biogeography of molluscs. Nearly all chapters can be considered as the most comprehensive and up-to-date treatments of their respective fields, especially as many include substantial amounts of new data. The editors are to be particularly congratulated on two aspects of the excellent work they have done in the compilation of the volume. These are the choice of contributors and the integration of the book's individual chapters. All of the contributors would be included in any consideration of the most active and insightful researchers in their respective fields.

With regard to the second aspect, much thought was clearly given to the delineation of subject areas, so that overlap between chapters is minimised and most of the subjects suggested by the title are actually covered in the book's pages. Additionally, the effort to format individual contributions consistently has been well rewarded. The presentation of tables in a standardised manner and the equal weight to branches in phylogenetic trees in the several chapters greatly assist legibility. The figures generally are very pleasing – the diagram of mitochondrial gene order (fig. 2.2) makes the complex evolutionary rearrangements of these sequences much easier to understand and the maps of species' distribution and bioclimatic modelling in the chapter by Hugall *et al.* on *Sphaerospira* are striking indeed.

Building on a general introduction on molluscan molecular investigations, the second chapter deals with the implications of such studies for the relationships of the phylum to other multi-celled animals, the inter-relationships of molluscan classes and, since there is a concentration on DNA sequence *per se* in much of the book, on other ways in which molecular information such as gene order or patterns of expression may be informative. The following chapters dealing with the phylogeny of individual groups comprise the bulk of the book. These consider bivalves in general, freshwater mussels, scaphopods, gastropods in general, Euthyneura and opisthobranchs. The book concludes with two chapters on biogeography; one a broad treatment of the topic with respect to aquatic Mollusca and the second a generic-level investigation of the evolution of the terrestrial pulmonate *Sphaerospira*.

Diverse analytical approaches are reflected in the book. In their major investigation of bivalve evolution, Giribet and Distel employ a cladistic approach, using the programme POY, that both aligns the DNA sequences and searches for optimal phylogenetic relationships. McArthur and Harasewych employ maximum likelihood, Bayesian, and supertree techniques in their similarly important study of gastropods. It is not the book's ambit to canvas the merits of the various analyses but the brief introductions to the

techniques offer a valuable recognition of the ongoing developments available to modern systematists.

As a practitioner in molecular systematics, I have encountered many odd ways in which DNA data can be contaminated by sequences of similar genes from other individuals or species. Few are as unusual as the example offered by Steiner and Reynolds in their chapter on Scaphopoda. Although published as a scaphopod sequence, subsequent investigation showed that it actually derived from a sipunculan inhabiting a scaphopod shell. The authors are to be congratulated for both establishing the source of this contamination and making its existence known.

Euthyneuran phylogeny is treated in two chapters. The earlier, by Dayrat and Tillier, concentrates on the implications of molecularly generated phylogenies for the evolution of morphological characters, such as the presence of an operculum, and for general questions, such as the invasion of freshwaters or land. I particularly liked the counsel in the introductory paragraph of this chapter that obtaining phylogenetic trees is a preliminary step rather than a goal in the understanding of evolutionary patterns. In this context, attempts to remove the lack of resolution in a tree can be seriously misleading about character evolution. Why this is so critical to Euthyneura is demonstrated in the second chapter on their phylogenetics.

Wägele *et al.* investigate the Opisthobranchia adding substantial amounts of new data to the compilation of DNA sequences available. The basal evolutionary relationships of the group are not clarified robustly by a dataset that must be regarded as impressive, even if only 27 of 178 studied species are represented by all three genes used in the investigation. For instance, the very interesting question of the relationship of opisthobranchs and pulmonates is not resolved. The data includes sequences from more than twenty pulmonates. In the 18S rDNA analysis, the studied pulmonates (Lymnaeidae and Planorbidae) are shown as the sister group (with high probability) to a group of Sacoglossa, Anaspiidea, and Cephalispidea. In 16S rDNA analyses, however, the pulmonate representatives are the monophyletic sister group to all of the Opisthobranchia, except Actaeonidae. The data are more informative at slightly lower phylogenetic levels, with consistently high support for several taxa such as Doridoidea and Cladobranchia.

Biogeography is addressed less comprehensively than phylogenetics, with only two chapters and some discussion about the family level in the Roe and Hoeh chapter on freshwater mussels devoted specifically to the subject. Many future investigations will apply DNA sequences to molluscan phylogenetics, so the topic will likely be given additional coverage in any subsequent edition. As the state of knowledge now stands, however, biogeography is a subject where the decision (whether by the editors or individual contributors) to exclude allozyme electrophoretic studies significantly underplays the contribution of genetic studies. The power of combining allozymes with DNA sequence data is shown in the summary by Wares and Turner of the fascinating situation in the *Mytilus edulis* species complex in the North Atlantic. Molecular studies have shown that all the species identified originally by allozyme electrophoresis derive from the Pacific mussel *M. trossulus* following a migration through the Arctic Ocean between three and four million years ago.

The general subjects of Wares and Turner's chapter are the consequences for biogeography and evolutionary diversification of differences between intrinsic and extrinsic factors operating in marine and freshwater habitats. They cite numerous relevant examples – the intriguing case of *Biomphalaria* amongst them.

Hugall *et al.* concentrate on the use of mitochondrial DNA and bioclimatic modelling to investigate the biogeography of a single genus of camaenids in rainforests along the eastern

seaboard of Queensland. The diversity of the group is high, with 24 lineages separated clearly in geography and DNA sequence. The particular details of this investigation are related to several general questions. Amongst these is the relation of the distribution of phylogenetic diversity to biogeographic gaps. This is a methodological advance in conservation biology and a worthy conclusion to the volume.

The collection of DNA sequence data will continue to grow in importance in molluscan studies, as it will in other areas of zoology. Future studies will generally refer to works in this volume: it will continue to be an excellent entree to contemporary molluscan research.

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