

Preface

The objective of this book is to synthesize and explore current theory and practice of molecular evolution and systematics focusing on birds. Chapters are written by active practitioners discussing current controversies, demonstrating methods, reviewing new findings, and assessing directions for future research.

As indicated by the title, *Avian Molecular Evolution and Systematics*, studies of organismal phylogeny and of evolution at the molecular level have become closely linked. This stems from widespread use of molecular characters that are believed to be homologs (similar due to common descent) in phylogenetic inference and from reciprocal use of phylogenetic trees in studying the evolution and hypotheses of homology for the characters themselves. The mutually informing nature of organismal and molecular evolution (Fig. 1) is general, applying to all of life and across taxonomic levels. This generality bodes well for the field, signifying a shared research agenda for many evolutionary biologists, in using analyses of molecular evolution to inform phylogenetic analyses and vice versa. Indeed, a great deal has been learned about the evolution of both organisms and molecular sequences during the past decade in this fashion.

However, all change at the molecular level is not so impervious to convergence, natural selection, varying functional constraints, or chance events as to provide a linear measure of the passage of time or of relatedness of taxa. It is increasingly clear that evolution of some molecular characters can be as quirky and unique to individual lineages as that seen for some phenotypic characters. The need to reconcile evolutionary inferences across numerous molecular and phenotypic analyses presents biologists with both challenges and opportunities. For example, assessing discord between molecular and morphological analyses challenges biologists to provide well-corroborated phylogenies based on both molecular and nonmolecular characters, and provides the opportunity to learn about the different constraints on change for different data sets. Assessing discord between gene trees and species trees

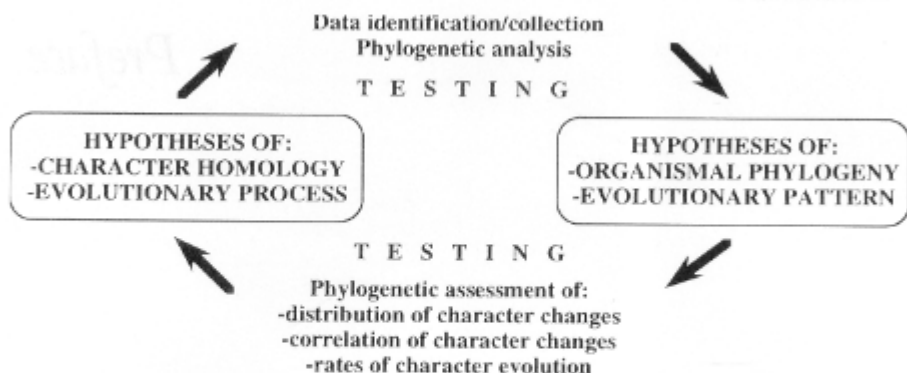


FIGURE 1 Diagram indicating the mutually informing nature of hypotheses of organismal phylogeny and processes of molecular evolution.

provides the same challenge, as well as the opportunity to learn about potential character divergence within and among populations prior to speciation. A degree of uncoupling for evolutionary change across data sets can complicate recovery of the actual phylogenetic pattern; however, this reflects differences in evolutionary processes operating at different levels of organization and on different character sets, and an understanding of both process and pattern is key in a comprehensive view of evolution (Fig. 1).

Birds have long been a source of insight into the workings of nature. This may be attributed, at least in part, to birds being both conspicuous and widespread, attracting numerous field observers. This has in turn yielded detailed understanding of many facets of avian behavior, distribution, and ecology. As an indication of the historical role of ornithology, observations of birds figure prominently in Aristotle's 4th-century BCE *History of Animals*, in which he lays the groundwork for the eventual organization of biology into physiology, morphology, systematics, embryology, ethology, and ecology. In the 13th century, Frederick II was an ardent natural historian of birds and falconer and pioneered a return to direct observations in seeking explanations for the natural world, when nearly all others sought explanations in the revealed word of the churches. Darwin's observations of finches on the Galapagos Islands were vital in development of thought on evolution by means of natural selection. In recent times, birds have been central to work in many fields relevant to evolutionary biology, including studies of species formation and species definition; comparative morphology, physiology, and endocrinology; studies of mating systems and reproductive strategies; roles of kinship in evolution; population and community ecology; effects of environmental change and conservation strategies for populations and species; and the roles of vicariance and dispersal in biogeography. As a consequence, researchers undertaking new molecular studies of birds have available a wealth of background material on comparative avian biology to provide

context and inform interpretation of the molecular findings. Thus, there is good reason to be optimistic about the prospects for further insight into evolutionary patterns and processes to be gained from the continued study of birds.

This volume had its beginnings in the symposium "Avian Molecular Evolution" held at the 113th stated meeting of the American Ornithologist' Union, August 15–19, 1995 in Cincinnati, Ohio. Six of the chapter authors (Edwards, McDonald, Mindell, Quinn, Sheldon, Zink) gave presentations in the symposium, and subsequently, seven others were invited to contribute chapters along with their collaborators. As organizer and editor of this book, I have attempted to seek some balance in coverage of topics, taxa, and taxonomic levels. However, this volume is not intended to be encyclopedic in its coverage, being restricted by the current interests and expertise of the various authors. It is my hope that this volume will stimulate inquiry and promote understanding among researchers and students working in this area, as well as provide specialists and nonspecialists alike with useful topic reviews and empirical examples.

The chapters are divided into two sections: (I) Molecular Sequences and Evolutionary History in Birds and (II) Applying Phylogeny and Population Genetics to Broader Issues. Authors focusing on the evolution and utility of molecular markers consider current understanding of the evolution of the mitochondrial genome in birds and closely related vertebrates (Quinn), the inherent difficulties and applications for nuclear DNA microsatellites (McDonald and Potts), the applicability of mitochondrial control region sequences to studies of population structure (Baker and Marshall), and the range of taxonomic resolution for mitochondrial cytochrome *b* (Moore and DeFilippis). Investigators consider methodological issues in systematics and variously present new data and analyses of phylogeny for select species or populations of Charadriiformes, Apodiformes, and Passeriformes (Baker and Marshall, Edwards, Sheldon and Whittingham, Zink); for species of Piciformes (Moore and DeFilippis), Gruiformes (Houde *et al.*), Pelecaniformes (Siegel-Causey), and ratites (Lee *et al.*; Cooper); and for Falconiformes, Strigiformes, Anseriformes, Galliformes, *Tamias*, *Opisthocomus*, and *Phoenicopterus* (Mindell *et al.*). Application of phylogeny and population genetics studies to broader issues include an assessment of the relevance of population-level processes to phylogeny at the species-level and above (Edwards); uses of phylogenetic hypotheses in studying evolution of behavior, morphology, and ecology (Sheldon and Whittingham); patterns of geographic variation and their potential causes (Zink); speciation (Roy *et al.*); and paleoecology and conservation biology using DNA from extinct taxa (Cooper).

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