



Phylogenies without Synapomorphies—A Crisis in Fish Systematics: Time to Show Some Character

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Abstract

We contend that the move away from providing character evidence with phylogenies has diminished fish systematics and systematics in general, and amounts to a crisis. Present practices focus on solutions to matrices rather than on character homology, and rely on algorithms and statistics rather than biology to determine relationships. Optimization procedures in tree-building programs are phenetic and no longer employ homology, the original foundation of cladistics. Evidence for phylogenies is presented in a manner that obscures character conflict and makes meaningful debate difficult. The role of morphological characters has largely been reduced to their optimization and reinterpretation on the revealed “truth” of molecule-based topologies. All of this has resulted in a schism between molecular and morphological phylogeneticists. We examine several examples, focusing on Percomorpha and Gobioidae, to illustrate the shortcomings of recent approaches. We feel that phylogenetics can only move forward by recognizing that molecules are small-scale morphology; molecular data are not substantively different from larger-scale morphological data and should be treated in much the same manner. Careful investigation of homology and transparent presentation of evidence will keep our work and our science relevant. We suggest four measures that need reintroduction to phylogenetic practice in order to bring systematics back to its fundamental principles: (1) examine data quality, character distribution, and evidence; plot characters to identify and examine character conflict, and weigh evidence for homology, (2) explore the nature of character information—data become characters only after they are understood, (3) question assumptions of methods, common practice is not necessarily indicative of the ideal analysis, (4) in particular, question and investigate optimization as a method and what its impact is on character homology and the meaning of synapomorphies; use biology, not algorithms to make homology decisions.

Key words: molecular systematics; morphology; character conflict; optimization; Gobiiformes; Percomorpha

Since, in principle, a data matrix containing characters for different minerals can be analyzed with PAUP to obtain a dendrogram, the application of cladistic techniques alone does not make an analysis phylogenetic.

—Wägele, 2004

Introduction

Over the last decade, there have probably been more fish phylogenies published than in any previous decade in the history of systematics. Worldwide projects tackling the relationships of enormous taxonomic groups such as the siluriforms and cypriniforms, along with more general surveys employing DNA barcoding, have directed substantial resources into data collection and phylogeny reconstruction. Fish systematics appears to be healthy and vibrant. So how can we suggest it is in crisis? Over the last decade or two, molecular approaches have come to dominate phylogenetics. This, of course, is not bad in and of itself—the more data, the better. But processing this volume of data has moved workers away from an intimate understanding of character distribution, homology, and the meaning of evidence. de Carvalho and Ebach (2009) similarly lamented the emphasis on quantitative analyses and the abstraction of characters and organisms alike as statistical values and models.