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Editorial



Complementary Approaches to Systematic Ichthyology*

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All systematists should be just as comfortable examining and comparing museum specimens as they are at examining and comparing DNA sequences; the future will favor researchers who are not afraid to choose the best approach for any given phylogenetic puzzle – whether it means studying morphological or molecular variation, or both.—Hillis & Weins, 2000, p. 15.

The molecular revolution in phylogenetic biology and its widespread application to fishes has in some ways complicated the task of teaching my craft of ichthyology. Beginning students know nothing of the history of fish classifications, how they were created, how they have changed over the years or how and why they continue to change. On the first day of class I typically bring in the four editions of Joe Nelson's classic *Fishes of the World* (Nelson, 1976, 1984, 1994, 2006) to show students that systematic ichthyology is a vibrant and dynamic science and that these are exciting times. Then I add that the latest of these encyclopedias of our current knowledge has for the most part not incorporated the more radical changes in our understanding of fish relationships suggested by many recent analyses of molecular data. It is not difficult to imagine students' frustration when one moment I tell them that the Scorpaeniformes is a long-recognized lineage of fishes, show them the distinctive morphological features shared by the group, then go on to say that the group is likely not monophyletic and that the character homologies upon which traditional diagnoses of the group were based are homoplasious (Imamura & Shinohara, 1997, 1998; Smith & Wheeler, 2004; Shinohara & Imamura, 2007). That realization may be exciting to some but must be nothing short of maddening to a novice. But in time, if my students and I do our jobs well, they too will learn to relish the vibrant science that systematic ichthyology continues to be.

It is common knowledge that the basis of virtually all phylogenetic hypotheses is morphology (Weins, 2004; Jenner, 2004) and that the exponential growth in molecular phylogenies relies on this foundation. The tension between practitioners of morphological and molecular methods of phylogenetic analysis has been thoroughly discussed and debated (e.g., Patterson, 1987; Patterson et al., 1993; Scottland et al., 2003) and in the minds of many, a consensus has been reached. Most have achieved a realization that while neither approach provides infallible proof of relationships, they are complementary, having their own strengths and weaknesses, but with much to contribute to one another (Hillis & Weins, 2000).

Mooi & Gill (2010) remain unconvinced and seemingly have overlooked many of the contributions of molecular data. Rather they see a crisis in systematic biology because hypotheses of relationships based on molecular data are often not grounded in thorough (or even cursory) morphological analyses and clades lacking morphological synapomorphies are routinely proposed. Rather than viewing this lack of morphological character support for hypothesized clades as a crisis, I see it as a growing pain of the science. In time, if we continue to train and adequately support students of morphology (an uncertain prospect to be sure), the molecular hypotheses will for the most part have their day in the court of morphology.

Rather than critique the many points raised by Mooi & Gill (2010), a task left to others in this volume, I wish to present my own views, similar to those of Hillis & Weins (2000), that morphological and molecular data should be viewed as complementary, each providing potentially novel insights, and that practitioners of both should be