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Editorial

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Will the Real Phylogeneticists Please Stand Up?*

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Abstract

In a recently published commentary, Mooi & Gill asserted that there is a crisis brewing in systematic ichthyology caused by a failure of investigators to apply the basic tenets of outgroup comparison to recover clades based solely on shared apomorphic characters. The result, they claim, is that many recent analyses disregard real synapomorphies and discover clades by phenetic rather than phylogenetic principles. We take the opportunity to refute this claim and assert that matrix-based analyses, whether parametric or nonparametric, satisfy the basic tenets of Hennig's methods, resulting in monophyletic groups confirmed by synapomorphies.

Introduction

Mooi & Gill, (2010; hereafter M&G) claim that molecular phylogenetics is not true phylogenetics but rather "phylophenetics." If true, this serious charge casts doubt on the efforts and results of all systematic studies that employ optimization methods to analyze molecular data. Before we get into specifics of the criticisms levied by M&G, we need to make it clear that the foundation of their arguments rests not on scientific rigor, but rather on opinions about the re-classification of fishes using molecular data. This bias is the reason that they only targeted researchers who proposed changes in the higher-level taxonomy of fishes using phylogenetic hypotheses based on DNA sequence data (Miya et al., 2007; Smith & Craig, 2007; Thacker, 2009). In criticizing these studies, they do not suggest any alternative relationships or provide any counter evidence to the proposed relationships. Despite the limitations of their critique, M&G would have a point if molecular systematists were truly practicing phenetics. Here we show, in no uncertain terms, why that is not the case.

The M&G thesis rests on the following four points: 1. The reliance on optimization algorithms is the modern incarnation of authority-based taxonomy. 2. Outgroup comparisons no longer play a critical role in determining character polarity. 3. The use of optimizations to build trees is not "cladistic." 4. Not showing synapomorphies on a phylogeny obscures the readers' ability to judge alternative hypotheses, and measures of node support do not refer to the quality of individual characters and their states. Instead these nodal supports refer to more abstract measures, such as bootstrap support or conditional probabilities.

We will demonstrate that each of these points is either false or irrelevant.

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