



The Ghost of Crises Past: A Reply to Mooi and Gill*

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**In: Carvalho, M.R. de & Craig, M.T. (Eds) (2011) Morphological and Molecular Approaches to the Phylogeny of Fishes: Integration or Conflict?. Zootaxa, 2946, 1–142.*

The conclusion one might draw from all this is that the criterion used to define homology – i.e., the criterion of common ancestry – is a theoretical construct. Like truth, we must approximate it as best we can, and we have no touchstone to tell whether we have found it.---Colin Patterson, 1988: 621

Mooi & Gill (2010; hereafter M&G) presented a discussion of current methods in molecular systematics and contended that methodologies employed in the analysis of molecular data do not identify homology or synapomorphy, are phenetic in nature, and have resulted in a categorical movement “away from an intimate understanding of character distribution, homology, and the meaning of evidence” (M&G, p. 26). If they are correct in their assessment, systematic ichthyology (and systematic research in general) truly is in a state of crisis, and many of the advancements that have been made in the last two to three decades have, in reality, been steps backward. As with any discipline, papers pointing out the dangers of dogmatic thinking and the perils of uncritical analysis are often welcome “wake up calls” and serve a genuine and necessary purpose in scientific literature. Unfortunately, the paper by M&G appears nothing more than a rehashing of long-settled debates with not-so-subtle hints of deeply rooted animosity towards a few specific researchers. Their paper not only misses their intended mark (presumably to ensure the scientific integrity of systematic ichthyology), but also demonstrates a clear misunderstanding of how molecular data are accumulated, analyzed and interpreted.

The criticisms presented by M&G are numerous (so numerous, in fact, that it appears that the authors would be quite satisfied if genetic data were simply thrown out with the baby AND the bathwater) and many will be discussed in other papers in this issue. I will therefore focus on what I interpret as their chief concern, that molecular data and their resulting phylogenetic hypotheses do not provide evidence to support hypotheses of homology. Most of the comments herein are reviewed from literature written decades ago in which the theoretical basis for statements of homology in genetic data were discussed and associated concerns clarified, and in most cases, alleviated. Hypotheses of homology are at the heart of modern phylogenetic theory and systematic research; in fact, hypotheses of homology are central to all of comparative biology whether morphological or molecular. With the general acceptance of Darwin's thesis that all life is related through common ancestry, Sir Richard Owen's "homology" (Owen, 1843) has come to mean similarity *due* to common ancestry. This definition, however, does not highlight or aid in the discovery of homology, but rather is an explanation for it (Patterson, 1982). Homology may also be a relational term that defines groups; for example, the relation among winged forelimbs in tetrapods, genes in the genome, or base pairs in a gene (Forey et al., 1992). However one treats a statement of homology, there is a need to test the statement, and if a statement is testable, it is, by definition, a hypothesis. M&G repeatedly fail to recognize this important aspect of homology in their review, and seem to imply that they are more comfortable with *statements* of homology being made by those who have an “intimate understanding of character distribution” (M&G pg. 26). Does this imply that geneticists who have studied the structure, organization and evolution of the genome for decades do not have an intimate understanding of genes?

Since the dawning of the modern genetic era in biology, geneticists have studied genomes in ever increasing detail, and numerous orthologous genes have been identified. Orthologous genes and their sequences are homologues that reflect the descent of species (Fitch, 1970). They pass the congruence and similarity tests (Patterson,