



Comments on the establishment of the one to one relationship between characters as a prerequisite for homology assessment in phylogenetic studies

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The importance of the homology theorem for the whole of biological research can easily be conceived...It will shortly appear, however, that almost everything essential was said by Goethe, among early morphologists, and by Remane, among modern ones (Riedl, 1978: 32)

The most vociferous advocates of alternative methods are not biologists, but statisticians and computer programmers (Schuh & Brower 2009: ix)

In two recent papers Mooi & Gill (2010a, 2010b) stressed that the evaluation and discussion of character homologies and their significance as synapomorphies has disappeared from current molecular phylogenetic analyses in ichthyology (see Chakrabarty (2010) and Smith (2010) for a different perspective). Synapomorphies represent the evidence that allows us to postulate phylogenetic groupings under the paradigm of Hennig's (1950, 1966) phylogenetic systematics. Therefore, their absence would indeed indicate an absence of evidence and hence a reason for serious concern. In the following paragraphs we provide a brief review of the differences between morphological and molecular approaches in relation to the establishment of homology.

Homology—the basis for synapomorphy

Homology is the central concept in and the foundation of comparative anatomy and phylogenetic systematics, with numerous papers and several books dedicated to this topic (e.g., Remane, 1952; Patterson, 1982, 1988; de Pinna, 1991; Hall, 1994; Bock & Cardew, 1999; Scotland & Pennington 2000). While agreement on the precise definition of homology has not been reached, there seems to be a general consensus that the recognition of homology is at least a two step process (see e.g. Patterson 1982, de Pinna 1991, Wägele 2005; Schuh & Brower 2009). The first step establishes a 'one to one relationship' between two structures to be compared (Hennig 1966: 94 citing Woodger; Rieppel & Kearney 2002) by identifying arguments for considering these structures to be the 'same.' The evidence required to show they are the same is the possession of one or more recognizable similarities. If the two structures are hypothesized to be the same they are said to belong to a transformation series (= character of authors), as for example structures a and a' (= character states of authors). To be phylogenetically informative the transformation series a to a' must be represented by at least two of the taxa under investigation. The second step assesses whether this transformation series of character state a to a' occurred only once among the study taxa and thus characterizes a single monophyletic group, or, if it occurred more than once and characterizes more than one group. In the first case we conclude that the transformation series a to a' is homologous in the lineage that possesses it, and thus the presence of character state a' in taxa of this lineage is a synapomorphy of them. In the second case we conclude that the transformation series a to a' is not homologous among the lineages that share it, and thus the presence of character state a' in taxa of the different lineages is a homoplasy. This second, evaluating step, was called congruence test by Patterson (1982) and is performed by testing the congruence between the distribution of