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**Gyliauchenid trematodes and morphometrics: is size phylogenetically informative?**

Kathryn A. Hall, Thomas H. Cribb and Rodney A. Bray

**Abstract:**

Gyliauchenid trematodes have been collected from herbivorous fishes from the Great Barrier Reef, Ningaloo Reef, New Caledonia, and French Polynesia. The taxonomic work arising from these collections has generated a large amount of morphometric data for at least 25 species of gyliauchenid. These data were coded for use in a cladistic analysis. The use of morphometric data in cladistic analyses is still quite controversial; e.g. are continuous data amenable to (able to be efficiently coded for) cladistic treatment? and are these data phylogenetically informative? We performed two morphometric cladistic analyses; the first based on gap coding and the second using a gap-weighting method. Each analysis was then subjected to standard methods of parsimony. In addition to these cladistic methods, we generated phenograms using multivariate cluster techniques. We assessed the performance of both the cladistic and phenetic approaches to the treatment of morphometric data by comparison with phylogenies inferred using sequence information from both mitochondrial and ribosomal genes. Preliminary analysis indicates that morphometric data has a considerable capacity for resolving phylogenies at the specific level.