

## Molecular phylogenetics of *Chaetodon* and the Chaetodontidae (Teleostei: Perciformes) with reference to morphology

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### Abstract

Butterflyfish are colourful, pan-tropical coastal fish that are important and distinctive members of coral reef communities. A successful systematic scheme and a robust phylogeny is considered essential in understanding further their biogeography and ecology, although recent cladistic treatments of butterflyfish phylogeny, based on soft tissue and bone morphology and coded at the generic and subgeneric levels, differ in character coding and subsequently tree topology. This study provides an independent test of the morphologically based hypotheses, using molecular systematic data from two partial mitochondrial gene fragments, cytochrome b (cytb) and small subunit rRNA (rrnS), for 52 ingroup chaetodontids and seven pomacanthids used to root the molecular trees. Individual gene trees were largely compatible and a combined molecular phylogeny, inferred from Bayesian analysis, was used to test alternative hypotheses suggested by morphological analyses. The tree was also used to map the latest morphological matrix in order to evaluate potential synapomorphies for various nodes defining butterflyfish interrelationships. A clade comprised of *Chelmon* and *Coradion* was sister group to other chaetodontids. *Heniochus* and *Hemitaurichthys* were each resolved as monophyletic groups, and as sister taxa. Of the taxa sampled, *Prognathodes* was resolved as the sister genus to *Chaetodon*. Of the ten *Chaetodon* subgenera sampled, all were monophyletic but their interrelationships differed significantly from that inferred from morphological characters. *Lepidochaetodon* was the most basal subgenus followed by *Exornator* and the remaining subgenera. Molecular data support the sister group relationship between *Corallochaetodon* and *Citharoedus* suggested by morphology, but major differences occur among the remaining more derived taxa. *Chaetodon trifascialis* and *C. oligacanthus* were resolved as sister taxa adding weight to the inclusion of the latter in *C. Megaprotodon*. Of those pairs of taxa known to hybridize and sampled with molecular data, all were closely related phylogenetically, except those hybrids known to occur in the *Rabdophorus* subgenus. Two base changes separated *C. pelewensis* from *C.*