



A molecular phylogeny of the Grunts (Perciformes: Haemulidae) inferred using mitochondrial and nuclear genes

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Abstract

We infer a phylogeny of haemulid genera using mitochondrial COI and Cyt *b* genes and nuclear RAG1, SH3PX3, and Plagl2 genes from 56 haemulid species representing 18 genera of the expanded haemulids (including the former inermiids) and ten outgroup species. Results from maximum parsimony, maximum likelihood, and Bayesian analyses show strong support for a monophyletic Haemulidae with the inclusion of *Emmelichthys atlanticus*. The former inermiids did not form a clade indicating that the highly protrusible upper jaw specialization to planktivory evolved more than once within Haemulidae. The subfamilies Haemulinae and Plectorhinchinae, currently diagnosed by eight morphological characters, most notably the number of chin pores and the origin of the retractor dorsalis, are also recovered from these analyses with the Haemulinae sister to the Plectorhinchinae. *Plectorhinchus* is monophyletic only with the inclusion of *Diagramma*. Within the Haemulinae, *Pomadasyss* and *Conodon* are polyphyletic. In addition, *Anisotremus* is monophyletic only with the inclusion of *Genyatremus* and *Conodon nobilis*, and *Haemulon* is monophyletic only with the inclusion of *Xenistius*. These results suggest that further morphological and molecular studies are needed to revise the limits of several haemulid genera.

Key words: Inermiidae, taxonomy, biogeography, partitioned dataset

Introduction

The family Haemulidae, or grunts, include 18 genera and about 145 species (Nelson 2006) in the ill-defined order Perciformes, suborder Percoidei (sensu Nelson 2006). Grunts are circumglobal and often prominent in both hard- and soft-bottom nearshore tropical, subtropical, and warm temperate waters (McKay 1984; McKay & Schneider 1995; McKay 2001; Lindeman & Toxey 2003). Most are carnivorous, feeding opportunistically on a wide variety of benthic invertebrates including crustaceans, polychaete worms, clams, and echinoids, while smaller species primarily feed on plankton (Konchina 1977; Ogden & Ehrlich 1977; Williams *et al.* 2004).

Johnson (1981) used a number of characters to define Haemulidae and its subfamilies, Haemulinae and Plectorhinchinae (Appendix 1). He proposed the superfamily Haemuloidea to include the mostly bottom feeding Haemulidae and the planktivorous Inermiidae. The latter family, commonly known as bonnetmouths, contains only two species that are reef-associated, typically small, and specialized for planktivory with highly protrusible jaws and fusiform bodies (McEachran & Fechhelm 2005; Lindeman 2006; Nelson 2006). Johnson (1981) found that the families Haemulidae and Inermiidae share a suspensorium similar to that of the lutjanoids in having little direct osseous articulation and a simple symplectic but having a unique projection on the margin of the metapterygoid, which projects posteriorly as a vertically oriented rounded flange that overlaps the medial side of the lower arm of the hyomandibular. This, in addition to other osteological characters such as the number of branchiostegals; number of openings in pars jugularis; presence of chin pores and scales on lacrimal, snout, and preopercular margin; absence of subocular shelf and trisegmental pterygiophores; and specializations in their infraorbitals, suspensorium, and procurent spur provide morphological evidence for a monophyletic Haemuloidea.