



Phylogenetic analysis of Western Atlantic *Bathygobius* (Teleostei: Gobiidae)

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Abstract

The phylogenetic relationships of the Western Atlantic species of *Bathygobius* are inferred from DNA sequence data from two mitochondrial genes (cytochrome *b*, cytochrome *c* oxidase-I) and one nuclear gene (Recombination Activating Gene I). The phylogeny inferred from the concatenated dataset of the three genes uncovered the following major findings: (i) the Western Atlantic species of *Bathygobius* as a whole are not monophyletic; (ii) a well-supported monophyletic group containing *B. soporator*, *B. lacertus* and the Eastern Pacific *B. andrei* was recovered (termed the *B. soporator* group); (iii) a well-supported monophyletic group was recovered that contains *B. curacao*, the Eastern Pacific *B. ramosus* and *B. lineatus*, and *B. antilliensis* (termed the *B. antilliensis* group); (iv) the relationships between the several lineages of new world *Bathygobius* and some species of old world *Bathygobius* could not be resolved, and monophyly of a clade of all new world species could not be determined. The evolutionary history of the Western Atlantic species involves periods of diversification that occurred both before and after the closure of the Isthmus of Panama.

Key words: frill-fin goby, molecular phylogeny, Gobiinae, Gobiiformes, cyt-b, Rag1, COI, concatenated, gene tree

Introduction

The gobiid genus *Bathygobius* contains 29 currently recognized species, six of which occur in the Western Atlantic (Tornabene *et al.* 2010): *Bathygobius soporator* (Valenciennes 1837), *B. curacao* (Metzelaar 1919), *B. mystacium* Ginsburg 1947, *B. lacertus* (Poey 1860), *B. geminatus* Tornabene *et al.* 2010, and *B. antilliensis* Tornabene *et al.* 2010. *Bathygobius* are typically intertidal species that are common in tropical and subtropical oceans worldwide. In the Western Atlantic, *Bathygobius* species inhabit both sheltered and exposed rocky shorelines, rock jetties, sea-grass beds, mangroves, and reef crests (Tornabene *et al.* 2010). The developmental and reproductive biology of *B. soporator* has been extensively studied (Tavolga 1950, 1953, 1954, 1955, 1956), as has the ability for these fish to avoid desiccation by jumping between tidepools (Aronson 1951, 1971). Systematic reviews exist for the species from Japan (Akihito 1980), West Africa (Miller & Smith 1989), the Eastern Pacific (Ginsburg 1947; Miller & Steffani 2001) and the Western Atlantic (Ginsburg 1947; Tornabene *et al.* 2010). Although considerable information is available regarding the general biology and alpha taxonomy of *Bathygobius*, information regarding the phylogeny of this genus, particularly the Western Atlantic members, is incomplete. The diversity of species within this genus coupled with their cosmopolitan distribution makes *Bathygobius* an excellent genus for studying patterns of evolution within and among ocean basins.

The earliest works investigating interspecific relationships within *Bathygobius* were hybridization and allozyme electrophoresis studies on Atlantic and Pacific species of Panamanian *Bathygobius* (Rubinoff & Rubinoff 1971; Gorman *et al.* 1976). Miller and Smith (1989) later analyzed 46 morphological characters to investigate relationships between West African *Bathygobius* and several members from the Indo-Pacific, Eastern Pacific, and Western Atlantic, using both cladistic and phenetic methods of phylogenetic inference. The different methods of phylogenetic reconstruction used by Miller and Smith (1989) yielded conflicting topologies. The study was also missing a large number of species from the Indo-Pacific, as well as from the Western Atlantic, as *B. lacertus* was considered a synonym of *B. soporator*, and *B. geminatus* and *B. antilliensis* were not yet described. Both *B. lacertus* and *B. antilliensis* may have been present in the Western Atlantic *B. soporator* material of Miller & Smith