



Morphological disparity despite genetic similarity; new species of *Lobosorchis* Miller & Cribb, 2005 (Digenea: Cryptogonimidae) from the Great Barrier Reef and the Maldives

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Abstract

Examination of the humpback red snapper, *Lutjanus gibbus* (Perciformes: Lutjanidae), from Lizard Island off the Great Barrier Reef and Rasdhoo Atoll, Maldives revealed the presence of a new species of *Lobosorchis* (Digenea: Cryptogonimidae), *L. polygongylus* n. sp. *Lobosorchis polygongylus* n. sp. is distinguished from the type- and only other species, *L. tibaldiae* by the combination of body size, oral spine number (60–81 in *L. polygongylus*, 47–56 in *L. tibaldiae*) and number of testes (13–25 in *L. polygongylus*, 9 in *L. tibaldiae*). Bayesian inference analysis using data from the internal transcribed spacers 1 and 2 (ITS1 and ITS2), 5.8S and the large subunit (LSU) nuclear ribosomal DNA of *L. polygongylus*, *L. tibaldiae* and species of *Beluesca*, *Caulanus*, *Chelediadema*, *Neometadena*, *Latuterus*, *Retrovarium* and *Siphoderina* was performed to explore phylogenetic relationships of species of *Lobosorchis* with other cryptogonimid taxa. Despite the significant morphological differences between *Lobosorchis polygongylus* and *L. tibaldiae*, these two species differed consistently by only 5 base pairs (bp) over the entire ITS region (3 bp in ITS1, 0 bp in 5.8S and 2 bp in ITS2) and 1 bp in the LSU rDNA regions examined. The ITS2 rDNA region was sequenced from metacercariae obtained from the fins, flesh or body cavities of a number of fishes belonging to the Blenniidae, Pomacentridae and Tetraodontidae and analysed using minimum evolution analysis with *L. polygongylus* and *L. tibaldiae*. This revealed the presence of two additional genotypes (putative *Lobosorchis* sp. A and B), which consistently differed from *L. polygongylus* by 1 and 4 bp, *L. tibaldiae* by 1 and 4 bp and from each other by 3 bp over the ITS2 dataset. Although these genetic differences are relatively small, when evaluated in light of the differences observed between *L. polygongylus* and *L. tibaldiae* (which are morphologically quite distinct) and differences seen in other congeneric cryptogonimid taxa, the ITS2 rDNA data alone suggest that at least two more species of *Lobosorchis* are present at Lizard Island. These data also suggest that the ITS2 rDNA region alone is suitable for resolving operational taxonomic units (OTUs) at the species level within the Cryptogonimidae based on what was observed in this and other cryptogonimid systems. A morphological description of metacercariae of *L. tibaldiae* obtained from two species of Pomacentridae at Heron Island, off the Great Barrier Reef is also provided.

Key words: Biodiversity; Blenniidae; Cryptogonimidae; Digenea; Great Barrier Reef; Lizard Island; *Lobosorchis*; Lutjanidae; *Lutjanus gibbus*; *Lutjanus*; Maldives; Opisthorchiata; Opisthorchioidea; Pomacentridae; ribosomal DNA; Tetraodontidae

Introduction

The humpback red snapper, *Lutjanus gibbus* (Forsskål) (Lutjanidae), is a relatively common inhabitant of Indo-West Pacific coral reef ecosystems from the Red Sea and East Africa to the Line and Society islands, north to southern Japan and south to Australia (Allen 1985). The diet of this long-lived species includes a variety of fishes, benthic crustaceans, echinoderms and mollusks, similar to its sister taxon, the two-spot red snapper, *L. bohar* (Forsskål) (Miller & Cribb 2007a; Froese & Pauly 2008). *Lutjanus gibbus* is known to harbour a