



Two new cryptogonimid genera *Beluesca* n. gen. and *Chelediadema* n. gen. (Digenea: Cryptogonimidae) from tropical Indo-West Pacific Haemulidae (Perciformes)

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Abstract

A survey of the parasites of Indo-West Pacific Haemulidae revealed the presence of three new cryptogonimid (Digenea: Cryptogonimidae) species warranting two new genera, *Beluesca littlewoodi* n. gen., n. sp. and *B. longicolla* n. sp. from the intestine and pyloric caeca of *Plectorhinchus gibbosus* and *Chelediadema marjoriae* n. gen., n. sp. from the intestine and pyloric caeca of *Diagramma labiosum*, *P. albovittatus* and *P. gibbosus* from Heron and Lizard Islands off the Great Barrier Reef, Australia. *Beluesca* n. gen. is distinguished from all other cryptogonimid genera by the combination of an elongate body, funnel-shaped oral sucker, relatively small number of large oral spines, highly lobed ovary, opposite to slightly oblique testes, uterine loops that are restricted to the hindbody and extend well posterior to the testes and vitelline follicles that may extend from the ovary into the forebody, but do not extend anterior to the intestinal bifurcation. *Pseudallacanthochasmus plectorhynchi* Mamaev, 1970 is transferred to *Beluesca* as *B. plectorhyncha* (Mamaev, 1970) n. comb. based on morphological and ecological (host preference) characteristics. *Chelediadema* n. gen. is distinguished from all other cryptogonimid genera by the combination of a lanceolate body, relatively small number of large oral spines, prepharynx that is much longer than the oesophagus, tandem testes, uterine loops that are extensive in the hindbody and extend well posterior to the testes and vitelline follicles that extend from the ovary to the pharynx. Morphological analysis of the three species described here was augmented with DNA sequence analyses utilizing data from the large subunit (LSU) and the internal transcribed spacers (ITS) 1 and 2, and 5.8S nuclear ribosomal DNA. Sequence data from the LSU and ITS (encompassing the ITS1, 5.8S and ITS2) of the taxa examined here were aligned with those reported for other cryptogonimids, *Caulanus thomasi*, *Latuterus tkachi*, *Neometadena ovata*, four representative species of *Retrovarium* and an undescribed species of *Siphoderina*, for comparative purposes and to explore levels of interspecific and intergeneric variation among these taxa. Minimum evolution analysis was conducted on a combined (LSU and ITS) dataset to explore relationships among these genera. Despite their superficial morphological and host preference similarities, species of *Beluesca* and *Chelediadema* were genetically distant from each other. Interspecific and intergeneric variation among the species described here is similar to that reported for other cryptogonimids.

Key words: Cryptogonimidae, *Beluesca*, *Chelediadema*, *Caulanus*, Haemulidae, Digenea, *Diagramma*, internal transcribed spacers, ITS, Indo-West Pacific, Great Barrier Reef, *Latuterus*, LSU, Lutjanidae, *Plectorhinchus*, *Siphoderina*, *Retrovarium*.

Introduction

The Haemulidae is a relatively large cosmopolitan family of fishes which currently comprises 150 species in 19 genera that inhabit tropical and subtropical waters (primarily marine, but some taxa live in fresh or euryhaline environments) (Froese & Pauly 2007). This family is closely related to species of the Lutjanoidea and Sparoidea (Miller & Cribb in press-a; Orrell & Carpenter 2004), but is distinguished from these by the lack of