

Taxonomic Complexity and Biogeography of Endemic Channids in Sri Lanka

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Taxonomic status of endemic members of the Sri Lankan snakeheads from family Channidae i.e. *Channa orientalis* complex and *Channa ara/marulius* complex are still plagued with taxonomical ambiguities and complexities. The objectives of this study were to understand and resolve such issues of these two groups of species based on molecular genetics, morphological characters and biogeographical modelling. A field survey was carried out to record their distribution pattern while fin clip samples were collected for molecular genetic study. *C. orientalis* complex has been recorded from Mahawali and southwest ichthyological zones while *C. ara/marulius* complex was recorded from southwest, Mahaweli and dry ichthyological zones of Sri Lanka. Genetic diversity of these two groups were assessed using the mitochondrial COX1 gene. Our findings confirmed the existence of two cryptic lineages within *C. orientalis* complex (with >8% genetic divergence), while these two populations could not be distinguished based on the currently known morphological characters. Further, the study revealed taxonomical and molecular genetics ambiguity within the *C. ara/marulius* complex suggesting the need for further studies. Among the studied lineages of *C. orientalis*, one population is restricted to Mahawali and Kelani basins including coastal flood plain penetration to lower reaches of Kalu and Benthara catchments. The other lineage is distributed in Nilwala, Gin and upper reaches of the Kalu river catchment, without overlapping the previous population. Current taxonomy on *C. ara/marulius* complex has elsewhere suggested to be consisting of three distinct, but puzzling lineages based only on a few morphological characters and COX1 barcoding gene region. However, our findings revealed that morphologically intermediate characters specially in the contact zone of *C. marulius* and *C. cfara*, proposing a genetically and morphologically highly diverse single species than two or three separate species. To resolve the taxonomic puzzles related to these two groups, we proposed to assess the molecular genetics of species by using additional genetic markers such as NT2 and 16s rRNA and also to examine extended morphometric characters.

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