
Molecular identification of selected species of family Carangidae in Sri Lanka: An initiation for establishment of barcoding library

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Economically important fish groups in family Carangidae have been identified as potential candidates for aquaculture. The phenotypic similarity of many species may lead to misidentification of species. The objectives of this study were to use partial sequence of mitochondrial Cytochrome c Oxidase I (COI) gene (650bp), also known as the DNA barcoding gene region to confirm the species status of selected carangid fishes and to initiate the first Sri Lankan Barcode Library for native Carangid species. Eight fish species, namely, *Caranx ignobilis*, *Caranx heberi*, *Caranx sexfasciatus*, *Gnathanodon speciosus*, *Carangoides hedlandensis*, *Carangoides malabaricus*, *Selaroides leptolepis* and *Selar crumenophthalmus* were collected from fish landing sites. Three samples from each species were amplified for the DNA barcoding gene region and sequences were submitted to both databases, the National Center for Biotechnology Information (NCBI) and Barcode of Life Database (BOLD) to initiate the formation of library. The mean length of the generated sequences was 655bp. Calculated using the P-distance model, the pairwise distances within species ranged from 0 to 1.4% and between species ranged from 6.1 to 17.1%. The resulted distance levels were consistent with the reported values for marine fish species and revealed that DNA barcoding gene region was successful in discriminating the selected fish species. The species phenotypically identified in the current study as *Carangoides malabaricus* showed only 88.2% similarity (11.8% divergence) with *Carangoides coeruleopinnatus* under NCBI Blastn option. Further studies are recommended for confirmation of its species status and to identify remaining Carangid species in Sri Lanka using DNA barcoding data.

Keywords: Barcoding library, Carangidae, Cytochrome c Oxidase I, Pairwise P-distance.

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