Genetically-guided taxonomic studies of the goatfish genus *Upeneus* (Perciformes: Mullidae) in the Western Indian Ocean

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**Background and approach**

Goatfishes are ecologically- and economically-important inhabitants of sand-associated, shallow-water habitats. The genus *Upeneus* contains around 30 species, occurring in coastal tropical and subtropical waters in all major oceans. A single review of the genus in the Western Indian Ocean (WIO) published in 1994, recorded nine species from this region. The recent description of six species from the WIO and Central Indian Ocean, and preliminary evidence of population distribution within several species indicate the need for more taxonomic research. To investigate aspects of the taxonomy and systematics of WIO (*upeneus*, an analytical) pipeline was established: analyses of sequence data, mostly the “barcoding” fragment of the mtDNA cytochrome c oxidase subunit 1 (COI) gene region, guided morphometric analyses, morphological examinations and eventual taxonomic studies.

**Case study 1:** *Upeneus heemstra* n. sp.

- The hickled goatfish *Upeneus tragula* was known to occur across the Indo-Pacific from South Africa to Japan. There was a distinct possibility of cryptic diversity within this widespread species.
- *Upeneus oligospilus* was described from the Arabian Gulf and U. niebuhr from the Gulf of Suez. Both species were later synonymised with *U*. tragula, but *U*. oligospilus was subsequently resurrected.
- With material becoming available from across the WIO, as well as from other regions, *U*. tragula and the status of *U*. oligospilus and *U*. niebuhr were re-assessed.
- Comparative studies were undertaken using 56 meristic, morphometric and colour characters from 340 specimens of ten phenotypically-similar species, guided by the analysis of a 622 bp fragment of COI.

**Case study 2:** The “vittatus” species group

- To enable comparisons among the many (*upeneus* species, phenotypically-similar species have been arranged into six species groups/complexes2 (Fig. 4).
- Of the four WIO species within the “vittatus” group, *U*. suahelicus and *U*. supravittatus are similar and distinguished only through the combination of a large number of characters. *U*. indicus and *U*. vittatus are identified by single morphometric or colour characters.
- Species delineation in this group, however, is more complex.
- Preliminary analysis indicated a 561 nucleotide alignment of COI from 12 species; a morphometric study will follow, focused on *U*. indicus, *U*. suahelicus, *U*. supravittatus and *U*. vittatus.

**References**


**Figures**

1-3. Phylogeny of evolutionary relationships among species of three *upeneus* species, determined from COI sequence data. *Upeneus* nudibarbus specimens were used as outgroups. Bootstrap supports (> 70%) for relationships from the likelihood, parsimony and neighbour-joining analyses are indicated in the order ML/NJ/UP. Images are of *U*. heemstra n. sp. from Hawaii (Fig. S1A-B) and *U*. tragula from Vietnam (bottom Dirleb-Pathir). (Figure and bottom image copyright Marine Biology Research, Taylor and Francis Publishing)

4. Phylogeny of phylogenetic relationships among representatives of 12 *upeneus* species, constructed using COI sequence data. Bayesian posterior probabilities and bootstrap support from the phylogenetic analyses are indicated in the branches. *Upeneus* suahelicus, *U*. supravittatus and *U*. vittatus are in the vittatus species group. The inset (right) lists the groups, the constituent species and the colour codes used. Groups and species in black font were included in the present analysis.

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