

Genetic population structure of the convict surgeonfish *Acanthurus triostegus* in the Indo-Pacific: insights from mitochondrial DNA

* L. Otwoma, V. Diemel, H. Reuter & A. Meyer

Leibniz Centre for Tropical Marine Research, University of Bremen and Kenya Marine and Fisheries Research Institute, Kenya

Leibniz Centre for Tropical Marine Research, University of Bremen, Germany

Leibniz Centre for Tropical Marine Research, University of Bremen, Germany

Leibniz Centre for Tropical Marine Research, University of Bremen, Germany

levyot@yahoo.com

The convict surgeonfish *Acanthurus triostegus* is widely distributed in the lagoon and seaward reefs of the Indo-Pacific. In coral reefs it feeds predominantly on filamentous algae, thus helps to keep them in the coral-dominated state. The long pelagic larval duration of 44 to 60 days and the wide distribution range makes it a suitable model to investigate the forces that shape the genetic structure and evolution of marine organisms in the Indo-Pacific. This study investigates the genetic population structure and connectivity of *A. triostegus* in Western Indian Ocean (WIO), Eastern Indian Ocean, Western Pacific, Central Pacific, and Eastern Pacific, using mitochondrial ATPase8 and ATPase6 gene regions. In order to assess the phylogeography and genetic population structure of *A. triostegus* throughout its range, 35 individuals were sampled from five localities in the WIO and complemented with 227 sequences from two previous studies (Lessios & Robertson 2006; Liggins et al. 2016). The overall AMOVA without priori grouping showed evidence of significant differentiation in the Indo-Pacific ($\Phi_{ST} = 0.53$, $P < 0.0001$), with 124 (41.3%) out of 300 pairwise Φ_{ST} comparisons being significant. However, the hierarchical grouping of Indian and Pacific populations failed to support the vicariance hypothesis, showing a lack of genetic break between the two ocean basins ($\Phi_{CT} - 0.02$ $P = 0.46$). On the other hand, the correlation between pairwise Φ_{ST} values and geographic distance was significant ($R^2 = 0.19$ $P < 0.001$), indicating that dispersal in Indo-Pacific follows an isolation-by-distance model. Three clades could be deduced from the haplotype network, with clade 1 and 2 dominating Indian and Pacific Ocean respectively.