

# GENETIC STRUCTURE AND BIOGEOGRAPHY OF THREE WRASSE SPECIES (LABRIDAE) WITHIN THE WESTERN INDIAN OCEAN

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## ABSTRACT

The biogeography of wrasses within the Western Indian Ocean (WIO) is poorly understood, with regard to origins and genetic differentiation or connectivity among the regions of the WIO. This region is a good model for studying the influence of physical complexities and biogeographic breaks in shaping patterns of differentiation in wrasses. Three reef-associated fish species, *Cheilio inermis*, *Thalassoma hebraicum* and *T. lunare*, were selected to examine the factors that have influenced patterns of differentiation across the WIO. Each species was sampled from various localities of the WIO, the Red Sea and Indo-West Pacific Islands. Sequence data were generated from two mitochondrial gene fragments (cytochrome b and ATPase 6) and one nuclear locus (the first intron of the ribosomal protein S7 gene). Genetic analyses were used to calculate genetic diversity indices within species, which were then compared among species. The relationships among haplotypes and alleles were constructed using median-joining networks. Where necessary, neighbour-joining trees (NJ) were constructed to examine relationships among haplotypes and alleles for the *Thalassoma* species. Population structure was analysed using AMOVA and pairwise  $\Phi_{ST}$  to compare and calculate differentiation between the WIO localities. Mismatch distributions were used to examine population growth and decline or stability, and demographic parameters were used to calculate time of population expansion. There was high haplotype ( $h = 0.88$  to  $0.98$ ) and low nucleotide diversities ( $\pi = 0.003$  to  $0.008$ ) among all species for mitochondrial markers. For S7 intron I, high allelic ( $A = 0.95$  to  $0.98$ ) and low nucleotide diversities ( $\pi = 0.002$  to  $0.014$ ) were observed for all species. The pairwise  $\Phi_{ST}$  values revealed little to great ( $\Phi_{ST} = -0.02$  to  $0.67$ ) genetic differentiation between localities, across all species for the three gene regions. The pairwise comparisons indicated the differentiation in *C. inermis* of Tanzania and Kenya from Mozambique and Nosy Be (Madagascar). The widespread *C. inermis* also revealed the differentiation of Kenya and Tanzania. For *C. inermis*, the AMOVAs of ATPase 6 and cytochrome b data indicated high differentiation among defined locality groups. The groups were defined according to geographic proximity. However, the AMOVA of the nuclear gene (S7 intron I) did not find variation among defined locality groups. *Cheilio inermis* revealed a sequence divergence of 0.4%. The divergence that was found in *C. inermis* was not enough to suggest a cryptic species within the WIO. Overall, the widespread and monotypic *C. inermis* revealed genetic differentiation within the WIO. *Thalassoma hebraicum* generally revealed little genetic iii

differentiation across the WIO. The AMOVAs of the three gene regions showed no variation among specimens of the defined locality groups. However, some differentiation was found between localities. The pairwise comparisons of *T. hebraicum* revealed the differentiation of Seychelles from the African mainland and Madagascar. Southern Africa was observed to be differentiated from Nosy Be and Zanzibar. The observed differentiation could be caused by oceanic barriers such as the South Equatorial Current (SEQC), East African Coastal Current (EACC), and the Comoros Gyres and eddies in the Mozambique Channel, and Agulhas Current. *Thalassoma lunare* revealed genetic isolation between the WIO and the Red Sea as well as within the WIO. The genetic isolation between the WIO and the Red Sea is probably due to the historical isolation by the Bab al Mandab and contemporary barriers such as the cold upwelling cells in Somalia. The differentiation of Maldives from the African mainland and Seychelles could be due to distance and the upwelling cells created by monsoon winds. Mismatch distributions suggested that *C. inermis* and *T. hebraicum* had undergone demographic expansion during the Pleistocene (92 678 to 40 219 years ago). The results of the current study are similar to those from previous studies of WIO reef fish species, and the results of the present study could have potential implications for conservation and fisheries management. Single genetic markers and single species studies do not detect all barriers to dispersal in the WIO, thus they are insufficient to inform conservation management. Thus, the use of multispecies and genetic markers in the current study can be adopted by other studies of the marine taxa of the WIO.