

# Connectivity of the skunk clown fish in the Indian Ocean using a combination of microsatellite and mitochondrial genetic markers

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Knowledge of connectivity, the exchange of individuals among populations on coral reefs, is vital for a correct spacing of Marine Protected Areas. For almost all coral reef associated fishes, dispersal between reefs in this patchy environment is limited to a weeks- to months-long pelagic larval stage. This study uses the Skunk Clown Fish (*Amphiprion akallopisos*) as a model species to assess connectivity. It has a disjunct distribution, occurring in the Western Indian Ocean (WIO) and the Eastern Indian Ocean (EIO), separated by more than 4.500 km of open sea. We use a combination of mitochondrial (MtDNA, Control Region) and 15 highly polymorphic microsatellite markers. Fin tissue of 387 individuals from 21 different sites in the WIO (Kenya, Tanzania, Madagascar, and Mozambique) and the EIO (Indonesia) was analysed. Mitochondrial and nuclear markers concurred in detecting strong population structure between the EIO and the WIO populations (AMOVA:  $\phi_{ct} = 0.63$ ;  $F_{ct} = 0.10$  respectively,  $P < 0.001$  both), and panmixia within the EIO. Within the WIO, however, results were different depending on the marker. With MtDNA, a genetic break was detected between the East-Madagascar population of St-Marie and the rest. Microsatellite markers also identified genetic differentiation between Madagascar and the East African coast, but the break was located more to the West of Madagascar. Microsatellites also revealed differentiation between Northern Kenyan populations and the rest, not detected by MtDNA. Both genetic breaks can be explained by dominant sea surface currents that promote larval detention in the Mozambique Channel, creating a barrier to dispersal across the channel, and the influence of the Somali Current which may hamper dispersal towards North-Kenya from populations further south.

Keywords: coral reefs; connectivity; gene flow; clown fish; Indian Ocean