

Connectivity of *Amphiprion akallopisos* (Skunk Clown Fish) in the Indian Ocean

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Like many coral reef associated organisms, *Amphiprion akallopisos*, which lives in mutualistic symbiosis with two species of giant sea anemones, is unable to migrate from one coral reef to another during its adult life stage. Dispersal between reefs in the patchy coral reef environment is assured during the pelagic larval stage. Because small pelagic larvae are extremely difficult to track in the open ocean, population genetics is a useful technique to evaluate gene flow and connectivity between populations of coral reef associated organisms. *Amphiprion akallopisos* has a disjunct distribution, occurring in the Western Indian Ocean (WIO) and the Eastern Indian Ocean (EIO) but not in the Central Indian Ocean (CIO). The WIO and EIO populations are separated by more than 4500km of open ocean. In this study, a 337 base pair long sequence of the Control Region of the mitochondrial DNA is used as a genetic marker to study population genetics and connectivity both between and within the WIO and EIO populations. A total of 263 samples from 17 different sites in the WIO and the EIO have been collected and analysed. Strong population structure ($\phi_{st}=0.28$; $P<0.001$), strong differentiation ($\phi_{ct}=0.61$; $P<0.001$), and low gene flow between the EIO and the WIO populations was observed. A haplotype network was created in which 76 haplotypes were identified. Not one of these haplotypes simultaneously occurred in individuals sampled in the EIO and the WIO populations. This further confirms the genetic differentiation between both populations already observed using F-statistics. Within both the WIO and EIO populations, low population structure was observed. Selective neutrality tests indicate that the WIO population underwent a population expansion. The EIO population was identified as the source population based on higher genetic diversity. Two possible explanations exist for the disjunct distribution of *A. akallopisos*. In the first hypothesis, the WIO was directly colonized from the EIO. However, it is rather improbable that larvae would be able to cross the large distance between both populations during a pelagic stage of less than 2 weeks. Furthermore, our results indicate low gene flow between WIO and EIO populations, making this scenario unlikely. In the second hypothesis, *A. akallopisos* migrated from the EIO towards the WIO in a stepwise manner. Suitable sea anemone habitat occurs in the CIO but is occupied by another species, *Amphiprion nigripes*, in this region. It is currently unclear whether *A. akallopisos* disappeared from the CIO due to competition with *A. nigripes* or whether *A. nigripes* evolved as a new species out of a common ancestor with *A. akallopisos* as a result of isolation of the CIO from the other two regions.