Where did Nemo come from? Exploring the genetic population structure of three clownfish species (*Amphiprion clarkii, A. nigripes*, and *A. sebae*) using next-generation sequencing throughout the central and eastern Indian Ocean

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Clownfish, members of the family Pomacentridae, are iconic inhabitants of coral reefs, characterised by intricate social structures. Despite its importance for conservation, the mechanisms driving dispersal of coral reef fishes is still not fully understood. Previously, genetically highly differentiated populations of *Amphiprion clarkii* have been documented, possibly implying the occurrence of cryptic species. Additionally, human induced stress, both direct (overexploitation) and indirect (climate change), resulted in decreased population sizes, thereby increasing the risk of local extinctions. In order to protect clownfish species, it is essential to unravel the genetic population structure and connectivity among populations, enabling the development and implementation of effective management strategies. This study aims at investigating the genetic population structure and the presence of cryptic diversity of three different clownfish species (*Amphiprion clarkii*, *A. nigripes*, and *A. sebae*). Samples from four distinct geographical regions will be used: Taiwan (10x A. clarkii), Sri Lanka (135x A. clarkii, 25x A. nigripes, 60x A. sebae), the Indo-Malay Archipelago (203x A. clarkii), and the Maldives (to be sampled). Representative genetic diversity is assured by examining approximately 700 individual samples scattered across these regions. Next-generation sequencing (NGS) techniques, using single nucleotide polymorphisms (SNPs) will be applied with the intention of assessing genetic diversity and connectivity in the poorly documented Central Indian Ocean as well as performing species delimitation tests. This research aims to discover critical insights into cryptic diversity and population dynamics of clownfish subpopulations, facilitating conservation and management decisions for marine protected areas in which Coral reef species can thrive.

Keywords
Population Genetics; EzRAD Sequencing; Connectivity; Anemonefish; Indo-Pacific; Marine Protected Areas (MPAs)