Population genomics the clownfish Amphiprion clarkii in Indo-Pacific coral reefs

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Clownfish, iconic members of the family Pomacentridae, are well-known coral reef inhabitants characterized by complex social structures and lifecycles. Despite their ecological significance, the mechanisms driving coral reef fish dispersal remain incompletely understood. Previous research on *Amphiprion clarkii* has revealed high genetic differentiation among populations, suggesting substantial regional isolation or potential cryptic speciation. Furthermore, human-induced stressors, including climate change and overexploitation (e.g., ornamental fisheries), have contributed to declining population sizes. Understanding the genetic structure and connectivity of these populations is essential for developing effective, site-specific management strategies to protect coral reefs and their biodiversity.

This study investigates the population genetic structure of *A. clarkii* across the Indo-Pacific, focusing on underexplored regions in the Central Indian Ocean. We analysed samples from five regions: Taiwan (6), Japan (7), Sri Lanka (73), the Indo-Malay Archipelago (62), and the Maldives (33). Using whole genome sequencing (WGS) and single nucleotide polymorphisms (SNPs), we uncovered significant genetic diversity and distinct population structures.

Our findings identify four clearly differentiated population clusters across these regions: Sri Lanka, the Maldives, Eastern and Western Indonesia, and the Western Pacific. Interestingly, individuals from Eastern Indonesia and the Western Pacific form a single genetic cluster despite their geographic separation, while other regions show pronounced genetic differentiation. This large-scale study builds upon previous research, shedding new light on the genetic structure of *A. clarkii* populations in the Indo-Pacific.

The restricted connectivity observed highlights the importance of managing differentiated and geographically separate *A. clarkii* populations as distinct units. Conservation measures, such as establishing and enforcing marine protected areas (MPAs), must account for these genetic differences to ensure the species' resilience and long-term survival amid environmental challenges.

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