

## Assessing the population genetics and connectivity patterns of reef fauna in Sri Lanka to define conservation priorities

Dissanayake Pulukkutti Arachchige Kushlani Nayanahara<sup>1,2</sup>, Huyghe Filip<sup>1</sup>, Op't Roodt Lode<sup>1</sup>, Akbal Keskin Sezgi<sup>1</sup>, Bergacker Stephen<sup>1,3</sup> and Kochzius Marc<sup>1</sup>

<sup>1</sup> Marine Biology Laboratory, Vrije Universiteit Brussel (VUB), Pleinlaan 2, 1050 Brussel, Belgium  
E-mail: Kushlani.Dissanayake@vub.be

<sup>2</sup> Department of Oceanography and Marine Geology, University of Ruhuna, Sri Lanka

<sup>3</sup> Evolutionary Biology and Ecology, Université libre de Bruxelles (ULB), Avenue Roosevelt 50, 1050 Ixelles, Belgium

Sri Lanka, a tropical island nation, is home to diverse coral reef communities that offer a multitude of reef resources and livelihood opportunities. Nevertheless, they are degrading at an alarming rate due to multiple natural and anthropogenic stressors. Incorporation of population genetics is imperative to manage the coral reefs as well as to guide the establishment of marine protected areas (MPAs). So far, only a handful of molecular studies on corals and their associated biota are available in Sri Lanka. On a broader scale, a critical information gap is identified in the central Indian Ocean to understand the contemporary geographic distributions and connectivity of reef communities in the Indo-Pacific. Therefore, this study aims to address this data inadequacy by providing baseline information derived from population genetics to comprehend the connectivity among reefs in Sri Lanka. Additionally, it seeks to explore the possible contribution and connectivity to the rest of the Indian Ocean regions. A total of 455 branch tips of *Pocillopora damiconis*, 123 mantle tissue of *Tridacna* spp., and 136 caudal fin clips from *Amphiprion clarkii* were collected non-lethal manner and genomic DNA was extracted. DNA barcoding was performed using mitochondrial open reading frame (mtORF) and mitochondrial cytochrome C oxidase subunit I (mtCOI) molecular markers in *P. damiconis* and *Tridacna* spp. respectively. The population genetics and connectivity will be assessed using single nucleotide polymorphisms (SNPs) in all three species. The results will be compared with the published data to elucidate the large-scale connectivity and phylogeography that prevailing in the Indo-Pacific. The data and information generated will be crucial in making informed management decisions for the sustainable administration of MPAs.

### Keywords

Population Genetics; Marine Protected Areas (Mpas); Connectivity; Molecular Markers