

## Exploring phylogeographic pattern in the giant clam *Tridacna maxima* across the Indo-Pacific: insight into connectivity

Akbal Keskin Sezgi, Dissanayake P. A. Kushlani N., Huyghe Filip and Kochzius Marc

Marine Biology, Vrije Universiteit Brussel (VUB), Pleinlaan 2, 1050 Brussels, Belgium

E-mail: sezgiaa@gmail.com

The study of marine ecoregions, influenced by combined biogeographic, geomorphologic, and oceanographic factors, delineates regions with relatively uniform species compositions. The Indo-Pacific, renowned for its unparalleled biodiversity, faces increasing vulnerability due to diverse climatic and human-induced stressors. Giant clams provide food, shelter, and protection for various marine species, as well as economic benefits for local communities. Despite their importance, giant clam species are declining in abundance. Understanding the genetic population structure is important for their effective conservation and management. This study aims at investigating the genetic population structure of the giant clam *Tridacna maxima*, the most prevalent and widely distributed giant clam species.

Samples were collected from the Red Sea, Kenya, Tanzania, Madagascar, Mozambique, Sri Lanka, Indonesia, and French Polynesia. The DNA extracted from these samples will be analysed with genome-wide SNPs obtained by next-generation sequencing, aiming to investigate both genetic diversity and the genetic population structure. These results will be compared with previous studies based on COI sequences and microsatellites. Comparing this extensive phylogeographic data set with ecoregions aims at providing insights into connectivity, genetic diversity and biogeographic pattern in order to provide crucial information for marine protected areas networks, safeguarding the species and genetic diversity effectively.

### Keywords

Connectivity; Giant Clam; SNP; COI; Microsatellite; Next-generation Sequencing