Population genomics and phylogeographic structures of Tridacna maxima in the Indo-Pacific region

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Giant clams provide food, shelter, and protection for various marine species, economic benefits for local communities, and are valuable targets for the international aquarium trade. Despite their importance, giant clam species are declining in abundance. Understanding their genetic population structure is important for their conservation and management. Here, we provide insight into the genetic population structure of the giant clam Tridacna maxima across its entire range, spanning the Indo-Pacific.

Samples were collected from Red Sea, Kenya, Tanzania, Madagascar, Maldives, Sri Lanka, Indonesia, and French Polynesia and analysed using genome wide SNPs obtained by low-coverage whole genome sequencing, aiming to investigate both genetic diversity and the genetic population structure.

Eight distinct genetic groups, with three subgroups in the Western Indian Ocean (WIO) were identified. Indonesia itself shows substantial genetic structure, with four subgroups, some of which are highly differentiated. Overall, T. maxima populations from the Red Sea, Tanzania, and Madagascar show marked differentiation from each other, underscoring the species' genetic diversity across its range and highlighting the need for more specific conservation strategies.

Keywords
Whole Genome Sequencing; Population Genomics; Connectivity; Giant Clams