

Population structure and gene flow of *Tridacna maxima* across the Indo-Pacific: new insights from the Central Indian Ocean

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Giant clams are charismatic invertebrates that play crucial ecological and economic roles in coral reef ecosystems. However, many species incur high risks of overexploitation and climate change, which has led to their inclusion in CITES Appendix II. *Tridacna maxima* is a cosmopolitan species that is also vulnerable to these pressures and has experienced local extinctions in certain regions. Despite numerous studies on its population structure and gene flow across the Indo-Pacific, there remains a significant data gap in the central Indian Ocean, a region connecting the eastern and western Indian Ocean. This study aims to fill this gap by providing new molecular data from the Maldives, Red Sea, and the Western Indian Ocean, using two molecular markers and comparing the results with previously published data. We analysed 1,874 mitochondrial COI sequences from 89 localities, yielding 520 unique haplotypes. The haplotype network revealed eight distinct haplogroups: (1) Red Sea, (2) Coastal East Africa, (3) Madagascar, (4) Maldives, (5) Eastern Indian Ocean, (6) Indo-Malay Archipelago and South China Sea, (7) Western Pacific, and (8) Central Pacific. All populations exhibited moderate to high gene diversity (h) and low nucleotide diversity (π), with overall values of 0.966 and 0.043, respectively. Microsatellite data from 10 loci and 510 samples across 30 localities further corroborated these findings. STRUCTURE and DAPC plots identified five distinct populations: (1) Red Sea, (2) Western Indian Ocean, (3) Maldives, (4) Eastern Indian Ocean, and (5) Indo-Malay Archipelago and Western Pacific. Genetic diversity was high (average gene diversity over loci = 0.789 +/- 0.452, mean HE = 0.841 ± 0.107, mean Na = 22.200 ± 7.300), while moderate differentiation ($F_{ST} = 0.123$) suggested restricted gene flow among populations. These restrictions may be due to large geographic distances, short pelagic larval duration, and natural barriers such as ocean circulation patterns, island chains, and archipelagos. Isolated populations, particularly those with limited larval exchange, might experience reduced genetic flow and increased genetic divergence, potentially hindering the species' ability to adapt to environmental changes. Our results provide valuable insights into the evolutionary history and connectivity of *T. maxima*, which are crucial for informing conservation strategies aimed at the sustainable management of this threatened species.

Keywords

Tridacna Maxima, Central Indian Ocean, Population Structure, Genetic Diversity, Conservation Management