

Population structure and connectivity patterns of Giant Clams (*Tridacna* spp.) along the Western Indian Ocean

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Connectivity among populations reflects the influence of natural processes, such as community dynamics, community structure, and genetic diversity, but also plays a significant role for the resilience of populations to natural and anthropogenic impacts. Understanding the population structure of a species can give an insight to the connectivity of populations and it offers an opportunity to implement effective conservation and management priorities. *Tridacna* spp. are protected under Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) and many species are locally extinct in many regions due to overexploitation. Only a few studies have been conducted so far to understand their gene flow in the Western Indian Ocean (WIO) and hence critical information is still missing. This study aims to address this data inadequacy by assessing the genetic population structure of three *Tridacna* spp; *Tridacna maxima*, *Tridacna costata* and *Tridacna squamosa* and their differentiation in the WIO. 251 individual tissue samples were collected from Red Sea, Kenya, Tanzania, Mozambique and Madagascar. Genomic DNA was extracted with Chelex method and cytochrome oxidase I gene was used as the molecular marker. The obtained sequences will be compared with sequences in GenBank using BLASTN to verify the orthology and will be combined with the published sequences. Haplotype diversity, nucleotide diversity and statistical tests will be performed by using the program Arlequin to determine the genetic differentiation among populations. Based on the results, the possible patterns of ecological and evolutionary processes of the species will be discussed which is necessary for their protection.

Keywords: population structure; connectivity; gene flow; Western Indian Ocean