## Concordance of microsatellite and mitochondrial DNA markers in detecting genetic population structure in the boring giant clam Tridacna crocea across the Indo-Malay Archipelago

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Abstract	Mitochondrial DNA (mtDNA) is a single, usually non-recombining locus, and often uniparentally inherited. Therefore, its ability to reveal recent gene flow among populations is usually questioned. In this study, the genetic population structure of 16 populations of Tridacna crocea (n=366) from the Indo-Malay Archipelago (IMA) was examined with 10 microsatellite markers and compared to previous studies using mtDNA, in order to test if the revealed population structure was congruent between the two marker systems. The results showed that the genetic population structure revealed by the two marker systems was mostly congruent, with a high correlation between cytochrome c oxidase subunit I (COI) and microsatellites. The studied populations could be divided by both marker systems as follows: (i) Eastern Indian Ocean, (ii) Central IMA, and (iii) Western Pacific. Populations in the Central IMA showed high gene flow. However, populations in the Java Sea (Karimunjava, Pulau Seribu) were grouped into a separate cluster by mtDNA analysis, while this grouping was not detected by microsatellites. It was also noteworthy that there is obvious heterozygosity deficiency in most of the populations, which may be caused by null alleles, inbreeding or population genetic analysis and precise recovery of connectivity patterns of giant clams. Therefore, the combination of mtDNA and nuclear DNA markers can lead to a more complete understanding of population genetics. Moreover, this study is expected to facilitate fully displaying the population genetic structure of giant clams combining with other researchers' results.
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