

Comparative genetic population structure of three endangered giant clams (Cardiidae: Tridacna species) throughout the Indo-West Pacific: implications for divergence, connectivity and conservation

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Title	Comparative genetic population structure of three endangered giant clams (Cardiidae: Tridacna species) throughout the Indo-West Pacific: implications for divergence, connectivity and conservation
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Abstract	Information on the genetic population structure of endangered giant clams is important for conservation programmes and the understanding of ecological and evolutionary processes. In this study, the genetic population structures of three codistributed and ecologically similar giant clam species (<i>Tridacna crocea</i> , <i>T. maxima</i> and <i>T. squamosa</i>) are compared. A fragment of the cytochrome c oxidase I gene was sequenced as a genetic marker in three giant clam species sampled throughout the Indo-West Pacific, from the Western Indian Ocean (WIO) and Red Sea (RS) to the Eastern Indian Ocean (EIO), across the centre of marine biodiversity in the Indo-Malay Archipelago (IMA) to the Western Pacific (WP) and the Society Islands in the Central Pacific (CP). All three species showed limited gene flow and a highly significant genetic population structure. The Phi(st)-values ($P < 0.001$) are 0.46, 0.81 and 0.68 for <i>T. crocea</i> , <i>T. maxima</i> and <i>T. squamosa</i> , respectively. Based on a hierarchical AMOVA they could be divided into three to six groups from West to East: (1) WIO (<i>T. maxima</i> and <i>T. squamosa</i>), (2) RS (<i>T. maxima</i> and <i>T. squamosa</i>), (3) EIO (including Java Sea in <i>T. maxima</i>), (4) central IMA, (5) WP and (6) CP (<i>T. maxima</i>). The distribution of the haplotype clades in the populations and the pairwise <i>Fst</i> -values between populations indicated a high level of gene flow in the central IMA for the three species. The concordant patterns suggest that geological history, sea-level changes during glacial periods of the Pliocene and Pleistocene, and oceanography are important factors shaping the genetic population structure of giant clams. The observed deep evolutionary lineages in the peripheral areas of the IMA might include cryptic species.
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