



REPORT

Genetic patchiness of the endangered giant clam *Tridacna maxima* from Peninsular Malaysia

Li Keat Lee¹ · Ya Yi Huang² · Chaolun Allen Chen² · Mei Lin Neo³ ·
Kieng Soon Hii¹ · Haifeng Gu⁴ · Po Teen Lim¹ · Chui Pin Leaw¹

Received: 26 July 2024 / Accepted: 18 November 2024 / Published online: 26 November 2024
© The Author(s), under exclusive licence to International Coral Reef Society (ICRS) 2024

Abstract In the marine realm, the interpretation of gene flows is often not as linear as terrestrial but requires an understanding of organisms' life history traits, especially for marine invertebrates with bipartite life stages, as well as the local prevailing seascape features. Giant clams have suffered population decline across the Asia–Pacific region, leading to local extinction. Among giant clam species, *Tridacna maxima* is considered the most widespread. In this study, we investigated the genetic diversity and connectivity of *T. maxima* populations along the east coast of Peninsular Malaysia, using both sequence and microsatellite markers. Overall, high haplotype diversity was observed ($H_d=0.67–1.00$) in the partial mitochondrial cytochrome oxidase *I* gene, but microsatellite markers showed heterozygote deficiency ($H_o=0.40–0.53$) and high inbreeding coefficient ($F_{IS}=0.19–0.53$) among the populations. The possibility of subpopulations was hinted at moderate genetic differentiation among the population. Based on nuclear microsatellite analysis, no

obvious genetic structure was detected in AMOVA between northern and southern zone based on geographic distance, yet subpopulations were revealed in Discriminant Analysis of Principal Component (DAPC) and Bayesian inference with optimal $K=2$. Pairwise genetic distance and migration networks further highlighted fine-scale genetic differentiation despite the close proximity among sites. Results revealed typical genetic patchiness in *T. maxima* populations, a feature often associated with marine bivalves. This study underscores the importance of using genetic tools to assess the genetic connectivity of endangered marine species such as giant clams, which is crucial for the genetic conservation of their populations.

Keywords Genetic differentiation · Marine bivalves · *Small giant clam* · Microsatellite · Marine Protected Area

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1007/s00338-024-02600-x>.

✉ Li Keat Lee
likeat92@gmail.com; 17020873@siswa.um.edu.my

✉ Chui Pin Leaw
cpleaw@um.edu.my

- 1 Bachok Marine Research Station, Institute of Ocean and Earth Sciences, University of Malaya, Bachok, Kelantan, Malaysia
- 2 Biodiversity Research Center Academia Sinica, Taipei, Taiwan
- 3 Tropical Marine Science Institute, National University of Singapore, Singapore, Singapore
- 4 Third Institute of Oceanography, Ministry of Natural Resources, Xiamen, China

Introduction

Marine population recovery and self-organization from disturbances are closely linked to connectivity, facilitated by pelagic larvae dispersal and settlement, which supports their conservation and resilience amid climate change (Jones et al. 2009; Bernhardt and Leslie 2013; Thomas et al. 2015). Most marine population structures fit the model of isolation by distance (IBD) (Planes and Fauvelot 2002; Palumbi 2003; Wright et al. 2015), where the genetic similarity of populations decreases with increasing geographic distance between populations as the dispersive capability of larvae erodes over distance (Wright 1943; Hellberg 2009). However, there are growing instances of nonlinear relationships between genetic differentiation and geographical distance, resulting in genetic structures that appear "patchy" or "chaotic" (Johnson and Black 1982; Hellberg et al. 2002). This phenomenon is