

More than one species? Exploring the possibility of cryptic species in the giant clam *Tridacna maxima* using complete mitochondrial DNA sequences

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Giant clams from the family *Tridacninae* are ecologically significant species that are currently threatened both by global changes and anthropogenic activities. Currently, there are seven extant species of giant clams distributed globally, all of which are listed under Annex II of the Convention on International Trade in Endangered Species and Flora (CITES). To effectively conserve these species, a proper species delimitation approach is needed. However, the most recent studies regarding the phylogeny of giant clams rely on the use of a certain number of mitochondrial and nuclear markers (i.e. COI, 16S, 18S), which does not allow for the detection of possible cryptic species. Additionally, deep divergent lineages have been detected in phylogeographic studies based on COI sequences in the small giant clam *Tridacna maxima*, suggesting cryptic species. This study will focus on the intraspecific genetic diversity in *T. maxima* using complete mitochondrial genomes generated by next-generation sequencing (NGS). Phylogenetic analysis will be conducted using Bayesian approaches, allowing us to investigate the presence of cryptic species.

Keywords

Species Delimitation; Next-generation Sequencing; Intraspecific Genetic Diversity; Phylogenetic Analysis; Bayesian