

## Submerged giants through time: A phylogenetic analysis of the giant clam subfamily Tridacninae using whole mitochondrial genomes

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Giant clams are species at risk of extinction due to their high economic value. They are a coastal resource exploited by both local fishing communities and commercial markets. It is for this reason that *Tridacna gigas* and *T. derasa* were listed in appendix II of CITES. Later the family Tridacnidae, now recognized as the subfamily Tridacninae, was added to appendix II due to the similar morphology between species (CITES 2019). This subfamily houses all 12 currently recognized giant clam species (Noe *et al.* 2017). To inform conservation efforts a good understanding of the genetic distribution, population connectivity, cryptic species and species boundaries is essential. These aspects are also essential knowledge for enforcement of CITES regulation. For instance, there is demand for easy-to-use, inexpensive, forensic tools to determine the species and spatial origin of unidentified samples.

In an international collaboration between Belgium, Hawai'i (USA), Florida (USA), American Samoa (USA) and Australia we use the next generation sequencing technique ezRAD (Toonen *et al.* 2013) to approach several of these issues. Here we focus on a phylogenetic analysis that can lend itself as scaffold for other facets of the overarching project as well as future research. Molecular phylogenetic analyses have been performed on giant clams, however these are either limited in species number or marker data. The goal of this MSc thesis is to construct a molecular phylogeny of all Tridacninae using whole mitochondrial genome sequences. This would also result in many first complete mitochondrial giant clam genomes as there are only five currently published (Gan *et al.* 2015; Ma *et al.* 2018a, 2018b, 2019; Cia *et al.* 2019).

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