

GENETIC STRUCTURE OF GIANT CLAM, *TRIDACNA MAXIMA*
IN THE ANDAMAN SEA, THAILAND

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ABSTRACT

Three populations of giant clam, *Tridacna maxima*, from Surin, Phuket and Adang Rawii islands were examined for allozyme variation by starch-gel electrophoresis. Four polymorphic loci showed high heterozygosity with the mean values of 36 %, 53 %, and 52 % for Surin, Phuket, and Adang Rawii respectively. The Nei's genetic distance over all loci showed that population difference between Surin-Adang Rawii was highest (0.09132) whereas lesser difference was found between Phuket-Adang Rawii (0.06346) and Surin-Phuket (0.04836). The genetic variation among the populations (F_{st}) showed no divergency between Surin-Phuket whereas significant differences were found between Phuket-Adang Rawii and Surin-Adang Rawii when the genotypic distribution between populations were tested. The results reveal that *T. maxima* in the area is divided into two sub-populations which may be explained by the specific water circulation pattern in the Andaman Sea. Two opposite currents meet and deflect in the vicinity of Phuket Island and this could prevent dispersal of larvae between the north and the south water body. The consequences of restocking or introducing giant clams from other sources should be considered in order to preserve the genetic identity of local sub-populations.