

Population genetic structure of Dog Conch (*Strombus canarium*) in Southern of Thailand

Abstracts

Population genetic structure and demographic history of the Dog Conch (*Strombus canarium*) living along the southern of Thailand coast was analysed based on the variation of the nucleotide sequence of mitochondrial DNA in cytochrome oxidase subunit I (*COI* gene). The mtDNA sequences of 140 individual collecting from 9 sampling sites: Satun, Trang, Krabi, Phuket, Phang Nga, Ranong, Pattani, Surat Thani and Chumporn province, were analyzed. A total of 24 haplotypes, consisting of 11 shared and 13 rare haplotypes, were identified. An excess of rare haplotypes indicated that the female effective population size of *S. canarium* living in the Thailand coast is large. Estimated values of haplotype diversity and nucleotide diversity were 0.746 and 0.003, respectively. The results of neutrality tests, both Tajima's D and Fu's F_S statistics, yielded negative values (-1.843 and -15.815, respectively) and statistically significant deviation from the neutrality, indicating that the *S. canarium* living in the Thailand coast had experienced population expansion. Mismatch distribution analysis indicated that a possible expansion that would occur 98,979 years ago during Pleistocene glaciations period. The analysis of molecular variance (AMOVA) showed the genetic structure of the *S. canarium* population living in southern Thailand into Andaman sea population and Gulf of Thailand population. This study are necessary information contributing to efficient strategies to conserve this species in southern Thailand.