

# 琉球大学学術リポジトリ

## インド・太平洋産シマイセエビの遺伝的集団構造と系統解析に関する研究

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## 論 文 要 旨

## Abstract

## 論 文 題 目

Title : Studies on genetic population structure and phylogenetic analysis of pronghorn spiny lobster in the Indo-Pacific

Among the spiny lobsters, the pronghorn spiny lobster, *Panulirus penicillatus* (Olivier 1811), probably has the widest distribution. It is found in tropical and adjacent regions from South-eastern Africa, the Red Sea, Southern India, the Southeast Asian Archipelago, Japan, Northern Australia, and the Southern and Western Pacific islands, to Hawaii, the Galápagos Islands, and other islands of the Eastern Pacific. Sequence data derived from the mitochondrial DNA control region, 16S rRNA and COI genes were used to determine the phylogenetic relationships among populations of *Panulirus penicillatus* inhabit Indo-Pacific Ocean. A combined Maximum Likelihood analysis based on 1444 bp recovered the most resolved phylogeny with  $\geq 99\%$  bootstrap support for associations among clusters. The populations from southwestern-central-western Indian Ocean to western and central Pacific Ocean consistently clusters nested within the Indo-west-central Pacific clade. Combined phylogenetic tree suggest that evolutionary history of Indo-west-central Pacific probably had settled from Red Sea cluster with east Pacific population as the most separated cluster

Study of population genetics between western Pacific region and eastern Pacific region of Pronghorn spiny lobster *Panulirus penicillatus* was conducted to provide a better understanding in explaining population structure of *P. penicillatus* in these areas. Analysis of molecular variance (AMOVA) shows a clear genetic difference between two regions (Western/Central Pacific and Eastern Pacific). High gene flow was found within localities in Western/Central Pacific region. The present study detected genetic structure between Eastern Pacific populations and Western Pacific populations, indicating that despite the nearly 1-year larval period for this species, larvae generally do not pass over the East Pacific Barrier.

Mitochondrial DNA control region sequences were determined to investigate the population genetic structure of this species in the Indian Ocean. We observed distinct genetic isolation of population located in at the northwestern and southwestern edge of the species range. Gene flow was found within localities in central and eastern region of Indian Ocean, probably resulting from an extended planktonic larval stage and prevailing ocean currents.

In these studies we also successfully to develop ten novel di- and tri-nucleotide polymorphic microsatellite loci for *P. penicillatus*. Analyses using microsatellite showed no significant genetic differences among *P. penicillatus* in the northwestern Pacific and concordant with the previous study on mitochondrial DNA.

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