Distribution patterns of Indo-Pacific mtDNA lineages of coral-eating sea star (*Acanthaster* spp. and *Culcita spp*.) in the coral triangle region

Mizuki Horoiwa[1], Coralie Taquet[2], Suharsono[3], Miguel Fortes[4], Handoko Adi Susanto[5], Niphon Phongsuwan[6], Ywee Chieh Tay[7], Davide Seveso[8,9], Enrico Montalbetti[8,9], Satoshi Nagai[10], Kazuo Nadaoka[11], Nalinee Thongtham[12], Nina Yasuda[1]

[1]University of Miyazaki [2]University of French Polynesia [3]Research Center for Oceanography, Indonesian Institute of Sciences [4]University of the Philippines [5]Rare, Indonesia
[6]Department of Marine and Coastal Resources [7]National University of Singapore [8]University of Milano-Bicocca [9]Marine Research and High Education Center [10]National Research Institute of Fisheries Science [11]Tokyo Institute of Technology [12]Phuket Marine Biological Center Cape Panwa

E-mail: nina27@cc.miyazaki-u.ac.jp

Key Words: Crown-of-thorns sea star, Cushion sea star, mtDNA, Species distribution, Coral Triangle

Abstract

The center of the Coral Triangle harbors the highest marine biodiversity in the world. The high biodiversity in this region is partly explained by vicariance and allopatric speciation between the Indian and Pacific Ocean habitats during glacial periods, followed by secondary contact of the two lineages. Knowledge of the distribution patterns of Indian and Pacific lineages is, however, limited in the Coral Triangle, hindering the precise evaluation of biodiversity. To reveal the distribution patterns of Indo-Pacific Ocean lineages in the center of the Coral Triangle region, we targeted two genera of corallivorous sea stars, namely, *Acanthaster* spp. and *Culcita* spp., as keystone species in the coral reef environment. In the present study, we collected a total of 388 samples from 12 locations across the Indo-Pacific, including the center of the Coral Triangle. The partial CO1 mtDNA gene was sequenced to determine mitochondrial Indo-Pacific lineages. Haplotype network analysis revealed distinct genetic clades in both *Acanthaster* spp. and *Culcita* spp. Based on their geographic distributions, one of the clades corresponds to the Pacific Ocean clade, while the other corresponds to the Indian Ocean clade. The divergence time of Indo-Pacific *Acanthaster* spp. was 2.40-3.72 million years ago, while that of *Culcita* spp. was 1.81-2.82 million years ago, both of which fall within the Plio-Pleistocene glacial period. Furthermore, we found that *Acanthaster* spp. and *Culcita* spp. showed similar distribution patterns. The major secondary contact zone of the Indo-Pacific Ocean lineages was found in the western Java Sea. Pacific Ocean lineages of *Acanthaster* spp. and *Culcita* spp. are mostly distributed in the center of the Coral Triangle region, while the Indian Ocean lineages of the two genera were found only west of the Java Sea, except for Singapore. The similarity of the distribution patterns and divergence times found between *Acanthaster* spp. and *Culcita* spp. may be attributed to similar ecological features, such as similar life cycles, habitats, and pelagic larval durations. Because different species may have different ecological requirements, the distribution patterns of the coral predator sea stars revealed in this study may be useful in coral reef conservation in the center of the Coral Triangle region.