

## **Genetic population structure of the blue sea star (*Linckia laevigata*) and the boring giant clam (*Tridacna crocea*) across Malaysia**

### **ABSTRACT**

Various studies on population genetics in the Indo-Pacific that include the Coral Triangle region have revealed phylogeographic patterns in marine species populations. However, little is known about the population structure and connectivity pattern among the coral reefs in four seas surrounding Malaysia: the Strait of Malacca (Andaman Sea), the South China Sea, the Sulu Sea, and the Sulawesi Sea. In view of this, we examined the genetic population structure of two invertebrate species: the blue sea star (*Linckia laevigata*) and the boring clam (*Tridacna crocea*) from seven localities across Malaysia, including Pulau Layang-Layang in the Spratly Islands. Additional samples of *L. laevigata* were obtained from the Davao Gulf, the Philippines. The analyses were based on partial mitochondrial cytochrome oxidase I sequences of *L. laevigata* and *T. crocea*. Populations of *L. laevigata* and *T. crocea* showed departure from neutrality, indicating selection or population expansion. However, a mismatch analysis suggested population expansion. Lack of genetic population structure in *L. laevigata* ( $\Phi_{ST} = -0.001$ ,  $P = 0.399$ ) implies high connectivity among the sampled reef sites. There was subtle genetic structuring in populations of *T. crocea* ( $\Phi_{ST} = 0.032$ ,  $P = 0.009$ ), but AMOVA did not detect any structure in the a priori groupings. The genetic population structure and scale in connectivity are most likely attributed to the life history traits of the sea star and giant clam species, and also to the geological history and seasonal current patterns of the region.