

Genetic population structure of the blue starfish (*Linckia laevigata*) in the Indo-Malay Archipelago based on microsatellites

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Population genetics is the study of naturally occurring genetic differences or polymorphism among organisms (Hartl, 2000). It can be approached by several genetic markers, such as allozymes, mitochondrial DNA (mtDNA) and microsatellites. Microsatellites are tandem repeats of 1-6 nucleotides found at high frequency in the nuclear genomes of most taxa (Selkoe & Toonen, 2006).

The blue starfish (*Linckia laevigata*) is a common benthic animal associated with coral reefs in the Indo-West Pacific. This species lives in shallow waters, lagoons, reefs flats and is distributed from western Indian Ocean to southeastern Polynesia (Clark & Rowe, 1971; Yamaguchi, 1977).

A previous study on the population genetic structure of *Linckia laevigata* in the Indo-Malay Archipelago based on sequences of the mitochondrial cytochrome oxidase subunit I gene (COI) revealed a genetic break between the Indian and Pacific Oceans, but panmixing on most parts of the archipelago (Kochzius *et al.*, 2009) The objectives of the current study are: (1) the characterisation of the genetic variability based on microsatellites, (2) to assess the genetic population structure of *L. laevigata* in the Indo-Malay Archipelago and (3) to compare the results to the previous study based on COI.

Tissue samples of *L. laevigata* were collected at 30 sites across the Indo-Malay Archipelago. Extraction was done with the Chelex method (Walsh *et al.*, 1991) and a multiplex PCR will be carried as described by Yasuda *et al.* (2012).

References

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