

Genetic population structures of the blue starfish *Linckia laevigata* and its gastropod ectoparasite *Thyca crystallina*

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<b>First Author</b>	Kochzius, M.; Seidel, C.; Hauschild, J.;
<b>Last Author</b>	Timm, J.
<b>Authors</b>	Kochzius, M; Seidel, C; Hauschild, J; Kirchhoff, S; Mester, P; Meyer-Wachsmuth, I; Nuryanto, A; Timm, J;
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<b>Abstract</b>	Comparative analyses of the genetic population structure of hosts and parasites can be useful to elucidate factors that influence dispersal, because common ecological and evolutionary processes can lead to congruent patterns. We studied the comparative genetic population structure based on partial sequences of the mitochondrial cytochrome oxidase I gene of the blue starfish <i>Linckia laevigata</i> and its gastropod ectoparasite <i>Thyca crystallina</i> in order to elucidate evolutionary processes in the Indo-Malay Archipelago. AMOVA revealed a low fixation index but significant genetic population structure ( $\phi(ST) = 0.03$ ) in <i>L. laevigata</i> , whereas <i>T. crystallina</i> showed panmixing ( $\phi(ST) = 0.005$ ). According to a hierarchical AMOVA, the populations of <i>L. laevigata</i> could be assigned to the following groups: (1) Eastern Indian Ocean, (2) central Indo-Malay Archipelago and (3) Western Pacific. This pattern of a genetic break in <i>L. laevigata</i> between the Indian and Pacific Ocean, congruent to studies on other marine species in the Indo-Malay Archipelago, is likely clue to allopatry caused by Pliocene and Pleistocene glacial sea level low stands.
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<b>Author</b>	Dr AGUS NURYANTO, S.Si, M.Si