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

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Marine protected areas (MPAs) are important not only to protect endangered species but also as a tool to recover the surrounding areas and enhance resilience. One important aspect is the dispersal and connectivity among populations, which provides new recruits for other MPAs and adjacent areas. Therefore, the study of connectivity of different species from different locations is important (Yasuda et. al., 2012), Linckia laevigata is an abundant species that can be found in the Indo-Pacific region. It has a long pelagic larval duration (PLD), which is between 20 and 28 days. That means that the distance of dispersal is large and therefore gene flow is high (Williams et.al., 1996). Hence, it is expected to observe a lack of population structure in the different areas, in other words, high connectivity. However, it is not only gene flow that influences the dispersal capability, there are also other factors such as physical, geographic, climatic and historical that affect the recruitment of individuals in different populations. The objective of this study is to investigate the genetic diversity and the connectivity of L. laevigata among different regions of Indonesia and Cebu (Phillippines). For this study 150 samples were taken at 10 localities to compare them by using microsatellites markers. Previous studies showed a low differentiation between blue starfish populations, but they were divided in two clear groups: 1) Indian Ocean and 2) Pacific Ocean. This is because of the sealevel fluctuations in the Pliocene and Pleistocene exposing the continental shelves acting as a barrier between the two oceans (Crandall et. al., 2008; Kochzius et al., 2009).

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