

# Genetic population structure of *Seriatopora hystrix* in the Indo-Malay Archipelago

Heynderickx Hanneloor, Rosa Van der Ven, Puspita Sutrisno and Marc Kochzius

Marine Biology, Departement Biologie, Vrije Universiteit Brussel, Pleinlaan 2, 1050 Brussels, Belgium  
E-mail: [hanneloor.heynderickx@vub.ac.be](mailto:hanneloor.heynderickx@vub.ac.be)

Tropical coral reefs are among the most biologically diverse and dynamic ecosystems of the world and are known to provide economically valuable and vital ecosystem services such as fisheries and coastal protection. As reefs provide habitat, spawning and nursery grounds for many important marine species, ongoing degradation and loss of these reefs can result in local extinctions of marine species. In the last couple of years reefs underwent massive declines in both health and abundance due to increasing anthropogenically induced environmental changes. Acidification, climate change, destructive fishing and pollution for example can lower the corals' capacity for adaptation and survival, eventually resulting in the decline of these coral ecosystems. The need for coral reef protection is high and could be aided by the implementation of marine protected areas (MPA's) which may increase coral reef resilience to environmental changes. A profound knowledge on genetic population structure and hence connectivity of these complex coral reef structures would provide necessary evidence to support such implementations.

In 2012 and 2013 *Seriatopora hystrix*, a hermatypic scleractinian coral, was sampled from 13 sample sites in the Indo-Malay Archipelago. Eight sample sites were in the Spermonde Archipelago off the southwest coast of Sulawesi, while the remaining five sites are from Pulau Seribu, off Jakarta in Java. Genetic structure analysis, supplemented with geographic and oceanographic data, will be used to assess population connectivity patterns within and between these two regions. For this, 12 DNA microsatellite markers specifically designed for *S. hystrix* were selected from literature. Genetic population structures will be analysed with computer programs, such as GeneMarker (v. 2.6.0), FSTAT, and STRUCTURE (v. 2.3) by calculating F-statistics and using model based clustering methods.

Previous research by our group found that *Acropora tenuis*, a broadcast spawning coral associated with long dispersal distances, had high connectivity and low level genetic structuring in the Spermonde Archipelago. *Seriatopora hystrix* is a brooding coral mostly associated with short dispersal distances. Hence, for *S. hystrix*, we would expect low connectivity and a high level of population structure.

Due to the presence of a historical geographical barrier in the Java Sea and the fact that *S. hystrix* is a brooding coral we expect allelic compositions to be different between the two sites. In addition, the presence of four different geographical zones in the Spermonde Archipelago also leads to a higher expected level of genetic structuring within these sample sites. In contrast, the sample sites from Pulau Seribu are very closely located to each other, which can provide more detailed information on the dispersal distance. Overall, the results that will be provided by this study will give us a better insight into the connectivity and dispersal patterns of this species.

Keywords: population genetics; *Seriatopora hystrix*; Indo-Malay Archipelago; microsatellite markers