

# Connectivity of the coral *Acropora tenuis* in the Spermonde Archipelago

Demierbe Thibaud, Rosa Maria van der Ven, Puspitaningasih Sutrisno and Marc Kochzius

Department of Marine Biology  
Vrije Universiteit Brussel, Pleinlaan 2, B-1050 Brussels, Belgium  
E-mail: [tdemierb@vub.ac.be](mailto:tdemierb@vub.ac.be)

Coral reefs are the marine ecosystem with the highest biodiversity of marine species. Hermatypic corals are important ecosystem engineers, providing the three-dimensional structure of the habitat. The distribution of coral reefs is patchy at local scale (among islands) and large scale (across oceans). Since the adults of coral reef taxa are sedentary, connectivity among populations is only possible by dispersal of planktonic early life history stages. Due to anthropogenic impacts coral reefs are declining on a global scale and marine protected areas (MPAs) are an important tool for their conservation. However, due to the patchy nature of the habitat MPAs should be arranged in networks that ensure connectivity among them. This will safeguard resilience of these metapopulations by providing new recruits for re-colonisation of disturbed areas.

Insight in the ecology and population dynamics can be used to develop management and restoration strategies. This study will investigate connectivity of the broadcasting hermatypic coral *Acropora tenuis* on two different spatial scales. Connectivity on a local scale will be investigated in Spermonde Archipelago (Indonesia) with a maximum distance among populations of about 80km. A large scale analysis across the Indian Ocean will be conducted between populations from Indonesia and populations from East Africa. The genetic population structure will be investigated by utilising microsatellites. Analysis is based on length polymorphism in Single Sequence Repeats (SSR) of non-coding DNA regions that show a high mutation rate. Sixteen microsatellite markers were selected from literature and are tested for polymorphism. The selected markers will be used in a multiplex PCR and the length of the amplicons will be measured by capillary electrophoresis. DNA fragment length data will be scored with the software Genemarker and analysed with the programmes Genealex, FSTAT and STRUCTURE (cluster analysis). The statistical analysis of the length data will allow us to measure gene flow and to estimate connectivity.