

Connectivity of *Amphiprion akallopisos* (skunk anemonefish) in the Western Indian Ocean using microsatellite markers

Van Nieuwenhove Annelore, Filip Huyghe and Marc Kochzius

Marine Biology, Vrije Universiteit Brussel, Pleinlaan 2, 1050 Brussels, Belgium

E-mail: annelore18.vn@gmail.com

Like many coral reef fishes, *Amphiprion akallopisos* (skunk anemonefish) is very popular in the pet and aquarium hobbyist trade. A rapid increase in demand for aquarium species has resulted in an overexploitation of wild populations and consequent destruction of coral reefs. To protect this species and manage the vulnerable marine ecosystems they are associated with, networks of marine protected areas (MPAs) are necessary. An important factor which should be taken into account when designing MPA networks is connectivity among populations through larval dispersal. Connectivity can be determined using genetic markers such as mitochondrial DNA and microsatellites. Microsatellites - also known as short tandem repeats (STRs) or simple sequence repeats (SSRs) - are very well suited for population genetic studies, because they are often hypervariable in length due to high mutation rates, and ubiquitous in the non-coding DNA of most organisms. Because they are so fast evolving, they are better suited to reveal recent barriers to gene flow among populations than many other genetic markers. In this study, the population genetic structure of the skunk anemonefish in the Western Indian Ocean (WIO) will be determined in order to investigate connectivity among populations, by using microsatellites as genetic markers. Samples from three different populations from the east and west coast of Madagascar will be analysed and compared with each other and with samples from Kenya, Tanzania and Mozambique at the African mainland. Small pieces of fin tissue of 124 individuals of *A. akallopisos* were collected at 6 different sites in the WIO and were preserved in 96 % ethanol right after diving. In the coming months, a genetic analysis of all 124 samples will be conducted, using multiplex PCR with four different fluorescent labels applied to two sets of eight microsatellite markers. Parallel with this study, the same samples will be analysed using mitochondrial Control Region sequences. The aim is to provide an answer to the following questions: is a genetic break present between the populations of Madagascar and the African mainland? Is there gene flow between the east and west coast of Madagascar? Are the results comparable when using mitochondrial DNA, a generally slower evolving genetic marker? The results of this study will contribute to the conservation and management of coral reefs and its inhabitants.