

Connectivity of *Amphiprion akallopisos* (Skunk Clownfish) in the coral reefs of Zanzibar

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Coral reefs form an important and diverse environment for many different marine species. Fish, algae and many invertebrates, such as crustaceans and sponges, inhabit these patchy ecosystems. Over the past few decades, environmental and human induced factors, such as pollution and global warming, have severely decreased the global coral reef quality and quantity. Healthy coral reefs are declining, with already 30 % completely deteriorated or even vanished worldwide. The reefs are also heavily overexploited by economic activities like fisheries and tourism. This poses a great threat to the future of these highly diverse ecosystems and all the organisms that inhabit them. Certain protective measures have already been developed, mainly in the form of Marine Protected Areas (MPAs) which attempt to restrict human impact. These no-take zones or other forms of MPAs should help maintaining the biodiversity of the coral reefs by protecting certain reef-species that are vulnerable to fishing or otherwise suffer from human impact. However, in order to construct effective MPA networks, it is important to space these areas correctly. This could be achieved by having a greater understanding of gene flow among populations. In this study, the connectivity between populations of *Amphiprion akallopisos* in six coral reefs at the West coast of Unguja Island (Zanzibar), situated in the Western Indian Ocean, will be investigated with the use of several microsatellite loci as genetic markers. *A. akallopisos* is a poor swimmer and cannot migrate out of its natal reef. Its dispersal therefore depends on a short pelagic larval stage. These larvae cannot usually bridge very large distances. Recently, it was demonstrated that there is highly limited connectivity between the populations of *A. akallopisos* in the Western and Eastern Indian Ocean. On a smaller scale however, like the coral reefs of Zanzibar, it is more likely that connectivity will be higher.

There is only one MPA at the whole west Coast of the Island of Unguja (Chumbe Coral Park). As a baseline, to be able to preserve the full extent of genetic diversity around Unguja Island, this MPA should therefore be connected with other reefs through historic gene flow and genetic breaks should be absent. We use microsatellite markers because these loci of repetitive DNA are often highly polymorphic and abundant in the genome of most organisms. Because of the generally high mutation-rate of these markers, it is possible to estimate the genetic distance between populations or individuals and thus assess gene flow between them even if genetic differentiation is small. From each of the six reefs, 24 small tissue samples of *A. akallopisos* were collected in the form of fin clips while scuba-diving and preserved in 96% ethanol. After incubation of every sample, DNA extraction will be performed using an extraction kit provided by QIAGEN. These DNA-extracts will be amplified using multiplex PCR with four different fluorescent labels, applied to two sets of eight primers each. Length analysis will be performed on these loci and this data will be used in population genetic analysis using Genalex, Arlequin, and Structure.

The aim of our study is to establish whether the reefs along the West coast of Unguja are one panmictic meta-population or if a genetic break is present on such a short geographic scale. This will provide baseline information on the design of MPAs near Unguja that will later be complemented by parentage analysis and self-recruitment estimation to establish the effectiveness of current MPA design on a shorter timescale. Understanding connectivity among these reefs and how the pelagic larvae disperse, will result in a better spacing of MPAs and therefore a better protection and management of these endangered coral reefs