Connectivity of sea cucumber populations on Indonesian coral reefs

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Increasing industrialisation causes anthropogenic climate change, sedimentation and other changes of environmental conditions influencing coastal marine habitats (Wild *et al.*, 2011). Combined with overexploitation this may lead to depletion of populations and eventually local extinctions. This influences the resilience of the whole ecosystem against disturbances.

The recovery of an ecosystem from disturbance is enhanced by high genetic diversity, which gives species the potential to adapt to changing environmental conditions (Hughes *et al.*, 2003; Ehlers *et al.*, 2008). Exchange between populations is necessary to maintain genetic diversity. Therefore, this project aims at studying the genetic connectivity of populations. Specifically, genetic diversities, population structures and dynamics of a minimum of 20 specimens of different sea cucumbers will be investigated at different sites in Indonesia, including the Spermonde Archipelago (South West Sulawesi). Around 20 different species of holothurians are fished and the most valuable ones have been heavily exploited, leading to a serious depletion of stocks (Kinch *et al.*, 2008). Because of their limited mobility and slow mode of reproduction, as well as low recruitment rates, they are easily targeted and overexploited (Uthicke & Benzie 2000, Uthicke *et al.*, 2004), making it necessary to get background data for a sustainable management of these little investigated but ecologically and economically important marine animals.

We will apply the mitochondrial cytochrome oxidase I (COI) sequence, which is applicable to many holothurian species (Uthicke *et al.*, 2010), and/ or nuclear microsatellites to investigate the genetic population structure of sea cucumbers. Since overexploitation might lead to very low abundances and local extinctions, the choice of the model species depends on the results of initial surveys. So far, *Holothuria nobilis* and *Stichopus chloronotus* are the most promising candidates.

Knowledge on the genetic diversity and connectivity to other conspecific populations allows assessing the state of the studied ecosystems and estimating the resilience of disturbed and/ or exploited populations. Management and conservation strategies such as the design and management of MPA networks could be improved on the basis of this information.

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