

Oral presentation

Pre-doc level

Cryptic diversity and limited connectivity in two commercially important octopus species

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Due to the increasing global market demand for cephalopods many traditional octopus fisheries in the Indian Ocean have expanded very fast in the past decades while shifting their focus from local and inland markets to international export. Just as in other regions worldwide, landings of these octopus fisheries are decreasing and concern over sustainability is raised. While octopus farming might be an option for the future, to date, octopus production relies completely on wild fisheries, with many communities having few alternatives to marine resource extraction. To maintain the sustainability of these socio-economic important fisheries, management actions must be taken, such as the establishment of Marine Protected Areas (MPAs). Connectivity among populations through larval dispersal is a crucial factor, which should be taken into account when designing MPA networks, since it influences population genetic structure, as well as the ability to persist and recover from stressors, like overfishing. In order to obtain baseline data for management plans, the present study investigated (1) diversity of Octopodidae in the Western Indian Ocean (WIO) and (2) connectivity and genetic structure among populations of two commercially important species: *Octopus cyanea* and *O. vulgaris*.

Arm tips of 275 octopus individuals were collected on landing sites and markets, at 15 different sites in Madagascar, Tanzania and Kenya. DNA was extracted and a fragment of the mitochondrial cytochrome C oxidase subunit 1 (COI) gene was amplified and sequenced. In addition, 41 COI sequences of *O. vulgaris* from South Africa, Brazil, Amsterdam Island, Tristan da Cunha, Senegal and Galicia were retrieved from online databases to be included in this study.

DNA barcoding revealed the presence of five different species in our collected tissue samples from the WIO, with first records for *Octopus oliveri* and *Callistoctopus luteus* in this part of the Indian Ocean. For *O. cyanea* (n = 229, 563 bp), 22 haplotypes were found, forming a single haplogroup, with one dominant haplotype present at all sites. Analysis of molecular variance (AMOVA) revealed a shallow but significant genetic population structure among all sites ($\varphi_{ST} = 0.025$, $p = 0.02$), with significant differentiation among: (1) Kanamai (Kenya), (2) southern Kenya, Tanzania, North and West Madagascar, (3) Southwest Madagascar and (4) East Madagascar ($\varphi_{CT} = 0.035$, $p = 0.017$). For *O. vulgaris* (n = 71, 482 bp), 15 haplotypes were identified, forming three haplogroups. A significant genetic population structure was found among all sites ($\varphi_{ST} = 0.82$, $p \leq 0.01$). Based on pairwise φ_{ST} -values and hierarchical AMOVAs, populations of *O. vulgaris* could be grouped as follows: (1) Brazil, (2) Madagascar and (3) all other sites. A significant increase in genetic distance with increasing geographic distance was found ($Z = 232443,81$ $r = 0.36$, $p = 0.039$). These results indicate that for *O. cyanea* four regions should be considered as separate management units in the WIO. The very divergent haplogroups in *O. vulgaris* from Brazil and Madagascar might be evolving towards speciation and therefore should be considered as separate species in FAO statistics.

Keywords: Marine Protected Area; population genetics; Gene flow; Mitochondrial DNA; COI