

Connectivity and population structure of blacktip reef sharks, *Carcharhinus melanopterus*, in two islands in Terengganu, Malaysia

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In the last decades sharks and their population dynamics are increasingly studied because of their importance for the ecosystems and their high sensitivity to overfishing and anthropological activities, due to their long gestation period, slow reproducing rate, slow growth, and high level of maternal investment (Dulvy et al., 2014).

In this study we investigate the population structure of *Carcharhinus melanopterus* (Quoy & Gaimard, 1824), an ovoviviparous shark of the family Carcharhinidae, which has an important role in the top-down control in coral reef habitats.

The study area is in two islands on the east coast of Peninsular Malaysia: Pulau Redang (Latitude: 5°48'40"N; Longitude: 103°00'20"E), and Pulau Bidong (Latitude: 5°36'40"N; Longitude: 103°03'30"E), that are in a distance of 13.5 km from each other. The objective of the research is two investigate the genetic and haplotype diversity of this species in this area and to understand its worldwide phylogeography. For this purpose, sharks will be caught from the beach using a rod, a tiny tissue sample from the second dorsal fin (<2 cm²) will be taken and preserved in absolute ethanol, length and weight will be measured using a flexible measuring tape (\pm 0.1 cm) and a weight scale (\pm 0.1 kg) and finally, before the shark will be released, a picture of the dorsal fin will be taken on both side of the animal in order to identify each individual.

DNA will be extracted from the tissue samples using a standard phenol-chloroform extraction. According to Keeney et al. (2003), the polymerase chain reaction (PCR) will be performed to amplify a 811 bp long fragment of mtDNA control regions using the two primers Pro-L (proline tRNA; 5'-AGG GRA AGG AGG GTC AAA CT-3') and 282 (12S rRNA; 5'-AAG GCT AGG ACC AAA CCT-3'; J.C. Patton, unpublished data). Both strands will be sequenced and will be read and checked using the programme ABI Sequence Scanner v1.0. The assembly programme CAP3 will be used to edit and align the forward and reverse sequences.

CLUSTALW as implemented in the software MEGA6 will be used to align the sequences. Haplotype and nucleotide diversity (the indicators used to detect the diversity) will be calculated using ARLEQUIN v.3.5.1 as well as haplotype matrices, haplotype frequency and F_{st} . Sequences and F_{st} obtained, will be compared with previous studies made in Red Sea, Australia and French Polynesia (Vignaud et al., 2014) to determine the world-wide phylogeography of the blacktip reef shark.

Carcharhinus melanopterus has been already described as a sedentary species with a high level of site attachment (Mourier and Planes, 2013). Thus, from this research we expect to observe high level of population structure on a global scale, but a low or inexistent genetic structure in the study area due to two reasons: 1) the proximity of the two islands and 2) the low depth in between the two islands (< 30m) that allow movements among the two areas (gene flow).

The importance of this study is to assess the genetic structure of blacktip reef sharks populations, because low gene flow can induce isolation that can enhance the susceptibility of this species to anthropogenic impacts.

References

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