Mapping marine park coverage and detecting cryptic populations of sea snakes using eDNA

Dr Jenna Crowe-Riddell^{1,2}, Amelia Rose Pointon², Mathew Campbell³, Katrina West⁴, Arne Rasmussen⁵, Shaun P. Collin¹, Morten Allentoft³, Dr Vinay Udyawer⁶, Dr Kate L. Sanders², Nicole E. White³

¹La Trobe University, Bundoora, Australia, ²University of Adelaide, North Terrace, Australia, ³Trace and Environmental DNA Laboratory, Curtin University, , Australia, ⁴CSIRO Australian National Fish Collection, National Research Collections Australia, Hobart, Australia, ⁵The Royal Danish Academy of Fine Arts, School of Architecture, Design and Conservation, Copenhagen, Denmark, ⁶The Australian Institute of Marine Sciences, Darwin, Australia

Western Australia is a global hotspot for sea snake diversity with a total of 20 species including six endemics. However, two critically-endangered sea snakes were thought to have gone extinct during rapid population crashes at offshore Marine Protected Areas (MPAs) such as Ashmore Reef. Incredibly, these vulnerable species have been recently rediscovered in unprotected coastal and deeper waters in Western Australia. eDNA presents a further opportunity to non-invasively monitor and identify populations of vulnerable species across large geographical distances. However, there are many challenges to overcome before eDNA can become a reliable tool for monitoring marine reptiles. Two major issues are: 1) the assumed lower cell shedding rate of sea snake (cf. fish), which is thought to reduce the total eDNA that can be detected from non-invasive sampling, and 2) how to adequately sample the fragmented distribution of sea snakes within Australia's vast network of MPAs. To improve eDNA detection of sea snakes, we are developing a metabarcoding eDNA protocol from seawater collected from enclosed habitats within Exmouth Gulf, with the view of expanding to open water habitats along the Western Australian coastline. To understand cell-shedding rate in sea snakes, we have collected seawater from sea snakes in captivity to quantify the concentration of eDNA using quantitative PCR. By using complementary eDNA methods, we aim to map the distribution of Australian sea snakes across MPAs and improve detection rates for marine reptiles that have large geographic ranges.