Amplifying DNA from dugong skulls, what will it yield for future applications?

McCarthy Morgan[1], Kochzius Marc[1], Seddon Jennifer[2] and Lanyon Janet[3]

[1] Marine Biology, Ecology and Biodiversity, Vrije Universiteit Brussel (VUB), Marine Biology, Ecology and Biodiversity, Vrije Universiteit Brussel (VUB), Pleinlaan 2, 1050 Brussel, Belgium
E-mail: m.l.mccarthy@uqconnect.edu.au
[2] The University of Queensland, School of Veterinary Science, The University of Queensland, School of Veterinary Science, Gatton, Queensland 4343, Australia
[3] The University of Queensland, School of Biological Sciences, The University of Queensland, School of Biological Sciences, St. Lucia, Queensland 4072, Australia

The use of ancient DNA (aDNA), including DNA extracted from museum samples has been an instrumental tool in the study of historical ecology. Sequencing nuclear DNA for microsatellites and mitochondrial DNA (mtDNA) provides information on genetic diversity and estimates of historical populations, giving our modern calculations perspective. The nature of using museum samples is that DNA degrades overtime and that extraction, sequencing and amplification is inhibited by sequence fragmentation. As the densest bone in the mammalian body, the periotic bone of the petrous portion of the temporal lobe is reported to yield the least degraded DNA. Dentine from human teeth and enamel from elephant tusks have both yielded aDNA as well. This study tests the amplification of microsatellite loci and mitochondrial control regions in DNA extracted from periotic, cheek teeth and permanent incisors (tusks) of dugongs to determine the best portion of the skull to use when extracting DNA from museum samples. This study will determine a best practice for obtaining the least fragmented DNA in dugong skulls. Such data can be used to calculate a historical effective population size and compare it with contemporary estimation methods based on shark-netting bycatch hind casting models in Queensland, Australia. Hence, its results will lay the framework to investigate whether a decline in dugong populations from extreme storm events and a government sponsored shark-netting program from the 1960s is reflected as a loss in present day genetic diversity when compared with present day DNA samples. The findings of this study on the ability to extract degraded DNA from different portions of a dugong skull will provide a tool in conservation genetics for dugongs in Australia and has the potential to provide a standard for *Sirenia* skull DNA extraction in future studies.

Keywords: dugong; ancient DNA; population genetics; dugong dugon; Queensland