# Identification, distribution and diet of Tasmanian predators inferred by scat DNA

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**ABSTRACT**

Species interactions within an ecosystem can appear in many ways and because of this variety, changes to one species can have cascading effects on other species or the environment. The outcomes of these interactions can be direct or indirect and happen at the intra or inter-specific level and studying them in more depth can provide greater understanding of network functions in a geographic area. Organism interactions in an ecological community are often difficult to measure and study because of the multitude of processes happening simultaneously. Nonetheless, DNA-based techniques are available to explore some of the interactions occurring in nature.

In this thesis, I focus on the Tasmanian faunal intreactions. This provides a real-life example of an ecosystem that has been subjected to considerable change in its faunal assemblage in the past century owing mainly to invasive species (Chapter 1).

I investigate the identity, the distribution and the vertebrate diet of mammal predators in Tasmania: *Sarcophilus harrisii* (Tasmanian devil), *Dasyurus viverrinus* (eastern quoll), *Dasyurus maculatus* (spotted-tailed quoll), *Felis catus* (feral cat) and *Canis lupus familiaris* (dog). I aim to explore predator dynamics that evolved among them such as the effect of invasive species through direct predation, competition or niche utilisation.

The need to identify, detect and monitor species can be achieved by analysing the DNA left by species in the environment. This provides a non-invasive technique to explore interactions among a cryptic, rare and threatened assemblage of species. By extracting eDNA (environmental DNA) from trace samples, sequencing and correctly identifying the species it belongs to, I can obtain a wide range of information without the need to directly interfering with the multitude of species under study. The limiting factors of dealing with DNA can be overcome with new technologies and the costs are less extravagant than a few decades ago.

Scats (i.e. faeces) provide a valuable source of eDNA and genetic information that they contain can persist for up to a few months in the environment, even when subjected to weather. This provides information about multiple predators and prey that can be discriminated in the laboratory, as well, as scats are a mixture of species DNA. Scats, combined with GPS localisations, provide single tools to evaluate interactions about predators relating to their environment, other predators and their prey. Because our target species, the predators in Tasmania, are relatively big in size, finding their faecal material in the landscape is relatively simple and DNA extraction has been made easier with the development of specialised kits.

I was able to develop a mini-barcode on the 12S rRNA mitochondrial gene region to identify the six large to medium-sized carnivores of Australia from scats (chapter 2). I used bioinformatics to develop the best primers from a range of sequences included in a reference DNA database. The amplification success of the mini-barcode was assessed using known tissue samples and tested in the laboratory for its sensitivity using a serial dilution of tissue samples from the Tasmanian predator species. To examine its sensitivity further, I applied the mini-barcode to DNA extracted from known captive animal scats collected in 2011 and correct identification was recorded for all successfully sequenced portions of DNA.

This barcode was applied on *ca*. 1500 field-collected scats to model predator distribution in Tasmania (chapter 3) using several species distribution modeling methods. My data suggested that dogs did not influence the distribution of any species but were negatively influenced by devils. The devils and cats influenced negatively the distribution of each other and both influenced negatively the distribution of eastern quolls. Devils were mainly restricted to rainforests and eucalypt forests and woodlands, and cat scats were found mainly in non-eucalypt forests and woodlands. No habitat preference could be determined for quolls

or dogs, and spotted-tailed quolls were removed from the study, owing to the small sample size.

Finally, I identified the vertebrate prey intake from more than 170 Tasmanian predator scats by applying two mitochondrial barcodes, 12SV5 and 16SMam and conclude on a vertebrate diet for Tasmanian devil, eastern and spotted-tailed quoll, cat and dog (chapter 4). I found that cats have a wide diet which includes small to medium-sized vertebrates, compared to the other predators in this study while devils had a more specific diet, feeding mainly on five native prey taxa. The two quolls could not be discriminated with these two barcodes, but applying the mini-barcode developed in Chapter 2, amplifying a different short region from the 12S rRNA gene, on the scats identified as "quoll" (genus level only), I could distinguish them at species level. They had similar restricted diet feeding mainly on possums, pademelons and wallabies and separated their diet by size with the eastern quoll predating on smaller prey in general. Finally, dogs were also feeding on native wildlife such as half of their diet consisted of native mammals and half was livestock/dog food. Overall, I detected between nine (for quolls) and 31 (for cats) different prey items per predator with a total of 44 prey taxa identified within 176 scats and showed the value of using scat metabarcoding for future detection and/or monitoring surveys.

I determined that using scats, considerable information about identity, distribution and diet was obtained by retrieving DNA from trace samples enabling the detection of interactions among species relating to their environments. Tools are now available to detect possibly rare Tasmanian species without going into the trouble of trapping or observing them directly and enabling management solutions to be developed based on the type of information gathered with them.

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