Molecular approaches define the interactions and impacts of Tasmania's native, introduced and invasive marsupials.

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Abstract

Diversification of new species is driven by genome evolution, which is influenced by demographic processes such as gene flow, genetic drift and geographic isolation. These processes do not act alone but work together. Modern molecular technologies mean that we now have unparalleled power to monitor the role that humans may play in species introductions and understand the ecological processes affecting both introduced and native species. Here I have used a range of molecular and statistical techniques to study the ecological impacts of three separate invasion events involving Tasmania and how these invasions impact the genomes of invaders and the diet and interactions of the native conspecifics.

Firstly, I used historical records, genetic data and Bayesian analysis to uncover the provenance of a once thought native marsupial in Tasmania, Australia. This species, the sugar glider (*Petaurus breviceps*), has recently been found to prey upon an endangered parrot and knowledge of the alien provenance of this marsupial predator will allow managers to correct legislation dealing with its current protection in the state. Secondly, I used genotype-by-sequencing to reveal population structure of an introduced marsupial in Hawkes Bay, New Zealand. Multiple introductions of the common brushtail possum (*Trichosurus vulpecula*) from mainland Australia & Tasmania into the area have generated a novel genetic form and here I show how the current population structure aligns closely with the introduction histories of the area. This reveals that the introduced Hawkes Bay population is not a single interbreeding population but at least four sub-populations in a relatively small geographic area. Thirdly, I identified two informative molecular barcode markers for the identification of Diprotodontia in Tasmania from unknown DNA sequences. My research highlights the need for a localised DNA reference database to be developed for successful identification of unknown sequences in metabarcoding studies. I showed that uncharacterised intraspecific genetic variation can increase the failure rate of species ID. Thus, I identified the *16sMam* and *12sV5* markers which give the highest assignment to species level for mainland Australian and Tasmanian Diprotodontia species in DNA metabarcoding studies, when used in combination. Lastly, I used high throughput sequencing of predator scats to look at predator and prey interactions across time and space, in the north of Tasmania. This ecosystem is changing with an incursion of disease affecting the apex predator, Tasmanian devil (*Sarcophilus harrisii*), and so it provides a unique opportunity to study ecosystem changes using non-invasive sampling techniques. My research showed the proportion of scats

detected for each predator significantly changed across space, with devil scat detections increasing in an area where the population is thought to be decreasing. There is a high amount of dietary overlap between the introduced predator, feral cat (*Felis catus*), and the smaller *Dasyurus spp.* found in Tasmania. Any interaction between devils and cats is not a competitive one, with a significant difference being found between the two species diets. There was no detectable difference in prey species diversity for cats or quolls when devils were found within the same survey unit.

My research highlights the need for a thorough understanding of both invasive and native species molecular evolution and the ecological processes which have affected the individual populations and may have influenced their genetics. Local genetic knowledge will allow more effective and efficient management protocols to be developed and deployed because we are able to understand the biological mechanics of introduced species at a deeper level.

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