Summary
I was recently awarded a $3.000 travel grant from NCCARF to spend four months at the Human Cancer Research group at the Sanger Centre, Wellcome Trust, Cambridge, UK. During my visit I sequenced complete mitochondrial genomes from 500 contemporary Tasmanian devil samples. The results will shed light on the impact of Devil Facial Tumour Disease (DFTD) on genetic diversity of the species. The devil has low genetic diversity (Jones et al., 2004; Siddle et al., 2007), facilitating the spread of DFTD. Since DFTD's emergence in 1996 it has led to an overall population decline of 85% (McCallum et al., 2009). The continuous reduction in population size is expected to further deplete genetic variation within the devil. This can lead to inbreeding depression, loss of adaptation potential, and possibly extinction of the species (Frankham, 2005).

Major findings and outcome of collaboration
In my time collaborating with Dr. Liz Murchison we sequenced complete mitogenomes from 500 Tasmanian devils. The samples were taken from seven devil populations, between 1999 and 2009, representing the species current geographic range. We extracted DNA and amplified it using Whole Genome Amplification to ensure there would be plenty of DNA for current and future laboratory work. Each mitogenome was sequenced in 23 fragments using ABI Capillary Sequencing machines. While at the Sanger Institute I received first class guidance on laboratory technologies. In particular, I learned how to use laboratory robots and gained skills in the use of bioinformatics tools for the assembly of DNA fragments. Currently, I am assembling the mitogenomes, re-sequencing fragments of low quality, and will shortly start my analysis. During my stay I met many scientists working in the field of genomics and population genetics. I will continue to collaborate with Human Cancer Research group and Dr. Liz Murchison on this and future projects.

Significance to adapting and protecting Australia's terrestrial biodiversity
The mitochondrial data generated during my visit at the Sanger Institute, along with the mitochondrial data from ancient samples (~15.000 years) and contemporary nuclear data, provide a comprehensive understanding of the historic and contemporary changes in the genetic diversity of the Tasmanian devil. These will be invaluable for future management of the species, because the information can be applied to better manage both captive insurance and wild populations. The information can be applied by: (i) selecting individuals for insurance populations by assuring the largest amount of genetic diversity is represented; (ii) identification of geographic or genetic lineages that raise an immune response or may be resistant to DFTD, (iii) selection of individuals for reintroduction based on their genotype. Knowledge on how the devil has previously coped with changes in genetic diversity can be used to predict how captive insurance and wild populations will respond to future decreases in genetic diversity caused by population size reductions or DFTD.

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