

## GENOMIC TOOLS AND SPECIES CONSERVATION – THE PLIGHT OF THE TASMANIAN DEVIL

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The Tasmanian devil is under threat of extinction as a result of a transmissible infectious facial cancer first identified in 1996. In May 2008 Australia’s largest remaining carnivorous marsupial (after the extinction of the Thylacine in 1936), was added to the endangered list. In the same year the “Tasmanian Devil Genome Project” was established as a critical contribution to facilitate the National effort to save an Australian icon. Lack of genetic diversity has been coined the key factor preventing recognition of the devils immune response to this contagious cancer. In this study we have utilized the Roche GS-FLX and Titanium 454 next generation sequencing technology to generate 4-fold coverage of two Tasmanian devil genomes. We establish the extent of both mitochondrial and nuclear diversity and present a new concept we term **DiversiTyping (DT)**. DT is a high-throughput workflow, which utilizes the advantages of the long-read next generation sequencing capability to rapidly generate candidate genome-wide single nucleotide polymorphisms (SNPs), along with high-throughput genotyping technologies. Following SNP validation and allele determination, an informative species-specific DT array is generated. This information can then be rapidly implemented to determine not only the extent of genetic diversity within the population, but also facilitate insurance population selection.