

Progress Report STP 2017-024 (FY 2016-2017)

**Genetic assessment of a reintroduced population
of brushtail possum (*Trichosurus vulpecula*) at
Matuwa (Lorna Glen)**

Animal Science

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Genetic assessment of a reintroduced population of brushtail possum (*Trichosurus vulpecula*) at Matuwa (Lorna Glen)

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This study focused on a declining population of south-western Brush-tailed Possums (*Trichosurus vulpecula hypoleucus*) to assess genetic variability and inform future management strategies. Between 2007 – 2009 a total of ninety-five individuals of *T. v. hypoleucus* were translocated from four extant populations within Western Australia to the Matuwa Kurrara Kurrara Indigenous Protected Area in central Western Australia. The latest monitoring survey at Matuwa in 2015 indicated the minimum number of animals known to be alive as 25, though capture-recapture analysis estimated that the total population size may be up to 50 animals. The reasons for this decline are unknown. Mortality of reintroduced radio-collared individuals was largely undetermined but there were no records of individuals being predated by cats. However, during trap monitoring of reintroduced possums, many individuals were considered to be under-weight suggesting the possibility of resource limitation in the period soon after translocation. In addition, this current small population may now be vulnerable to effects of reduced genetic variation and inbreeding.

This study investigated whether a lack of genetic diversity or presence of inbreeding could be contributing factors in the decline of the translocated population at Matuwa. Genetic diversity and inbreeding in the Matuwa population was compared to the original source populations to detect whether there has been a loss of diversity or increase in inbreeding. A population viability model was constructed for *T. v. hypoleucus* at Matuwa to investigate factors important for the long-term persistence of the translocated population.

Tissue samples from 146 animals were analysed using 13 microsatellite loci. Inbreeding was lower and heterozygosity was higher in the translocated Matuwa population than two source populations studied, highlighting the benefits of promoting outbreeding through the use of multiple source populations in translocations. However, allelic richness at Matuwa is low suggesting the impact of population bottlenecks on genetic diversity, which was supported by significant tests for genetic bottlenecks. Despite the genetic health of the population being stronger than predicted, this population is still threatened due to environmental factors. Population viability analysis suggests it is facing further declines within the next 10-15 years without future management of the site. Several management strategies are suggested including population supplementation and provision of artificial nest boxes. A manuscript has been prepared for submission to a peer-reviewed journal.