

# Genetic study of the Sandy Point koala population

Summary, October 2018



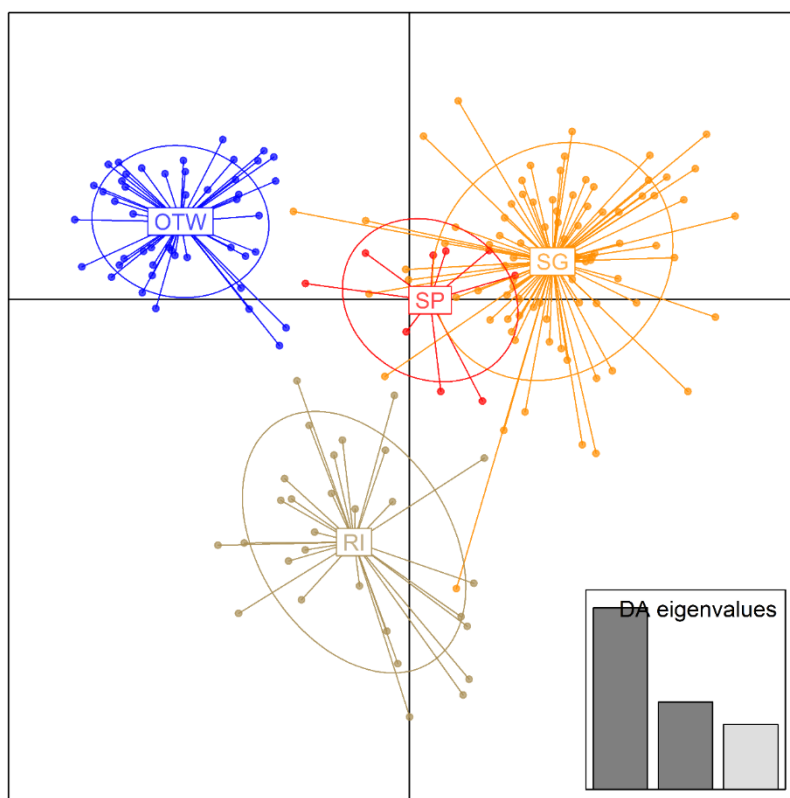
## EXECUTIVE SUMMARY

This report presents the findings of a study into the Sandy Point koala population using genetic data and DNA isolated from sampled koala scats. The study was initiated and funded by the Sandy Point Community Koala Action Group (SPCKAG).

The SPCKAG carried out a koala survey of the Sandy Point area during March 2018 and collected 22 scat samples for genetic analysis. A total of 20 scat samples provided reliable data for analysis from which 11 individual koalas (6 females and 4 males) were detected.

Bacterial infection with *Chlamydia pecorum* was not detected in any of the 11 individuals while koala retrovirus (KoRV-A) was detected in 4 individuals (36%). The rate of KoRV-A detected at Sandy Point is slightly higher but statistically similar to the average rate of KoRV-A infection within the greater South Gippsland<sup>1</sup> koala population (27%).

Genetic data from the Sandy Point koala population were compared to koalas sampled in South Gippsland, Cape Otway (translocated from French Island) and Raymond Island (translocated from Phillip Island). Genetic comparisons of these populations revealed that the Sandy Point koala population is a remnant of the larger South Gippsland koala population, rather than from French or Phillip Island.



**Figure 3** Genetic structure of the Sandy Point koala population in comparison to the South Gippsland, Cape Otway and Raymond Island koala populations (SP: Sandy Point, SG: South Gippsland, RI: Raymond Island, OTW: Cape Otway)

Genetic diversity in the Sandy Point koala population was significantly lower than koalas sampled from South Gippsland, Cape Otway or Raymond Island. The low level of genetic

<sup>1</sup> The South Gippsland koala population includes and is equivalent to the Strzelecki Ranges koala population

diversity in the Sandy Point koala population is likely driven by its isolation and consequent lack of recent koala migration into the area, followed by successful breeding (gene flow). Inbreeding may or may not currently play a role in the population's low diversity and warrants further investigation. Questions such as whether the high incidence of sarcoptic mange in the population is related to the population's low level of genetic diversity also remain to be answered.

Continuing to improve and extend koala habitat to support the local koala population will be important for the future preservation of this koala population. The low level of genetic diversity present in Sandy Point koalas makes this population susceptible to future stochastic events (e.g. novel disease and/or changes in climate and the environment, which could, for example, influence the suitability and/or availability of food sources). Potential strategies to increase the population's genetic diversity and adaptability requires further investigation and assessment of risk.



**Figure 1** Koala scat sampling locations collected in and around Sandy Point. Sample numbers correspond to sample identification (ScatID) provided in Appendix Table A1.