Genetic mixing in conservation translocations recovers diversity of a keystone threatened species, Bettongia lesueur

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Australian mammals have undergone unprecedented declines, with nearly one third of the endemic fauna considered extinct and many terrestrial mammals remaining highly threatened due to predation and competition with introduced species. A keystone burrowing mammal, the boodie (Bettongia lesueur), was extirpated from the Australian mainland in the 1960s and is now found on just three Western Australian islands. Conservation translocations have been undertaken to reintroduce the species to feral-free mainland and island safe havens to boost species numbers and insure against future population loss. Here, we used reduced representation sequencing (ddRADseq) to assess the current genetic health of remnant and reintroduced boodie populations, including measures of genomic diversity, structure, and relatedness within and amongst populations. In addition, we used exon-capture data from historical mainland museum specimens and a subset of contemporary samples to assess pre-decline diversity and determine the impact that population founder source (whether multiple or single) has had on genomic diversity relative to this baseline. Natural island populations exhibited strong genetic structure allowing clear visualisation of translocation history. Populations founded by animals from multiple sources showed significantly higher genomic diversity than natural and single-source translocation populations, and we show that mixing the most divergent populations successfully restored heterozygosity close to levels observed in pre-decline mainland samples. A strategy of genetic mixing has led to successful conservation outcomes for the species in restoring genetic diversity and should be more broadly considered as a strategy in reintroductions.