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We know everything about tammars don't we? Intraspecific differentiation of tammar wallaby populations in South and Western Australia

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Gould Seminar Room (Room 235) Gould building, 116 Daley Road, ANU



The tammar wallaby (*Macropus eugenii*) is one of the most intensively studied of all marsupials and was the first Australasian marsupial species to have its genome sequenced. However, comparatively little is known about the amount of genetic differentiation amongst the morphologically distinct allopatric populations of tammars found in Western (WA) and South Australia (SA).

We have compared autosomal and Y linked microsatellite genotypes, as well as sequence data from the mitochondrial DNA (mtDNA) control region in tammar wallabies from Kangaroo Island (SA), mainland south-west WA, Garden Island (WA), Middle Island (WA), North Twin Peaks Island (WA), the Abrolhos Islands (WA) and the introduced population in New Zealand. Levels of diversity at autosomal microsatellite loci were high in the mainland and the Kangaroo Island populations but significantly reduced in other island populations. Autosomal and Y linked microsatellite loci revealed a pattern of significant differentiation amongst populations, especially between SA and WA. Multiple divergent

mtDNA haplotypes were identified in both SA and WA populations. The mtDNA of tammars from SA and WA shows reciprocal monophyly and are highly divergent, with levels of sequence divergence more typical of different species. Within WA tammars, island populations each have unique clusters of highly related mtDNA haplotypes and each is most closely related to different WA mainland haplotypes. Y linked microsatellite haplotypes show a similar pattern of divergence although levels of diversity are lower.

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