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Sandhill dunnarts (*Sminthopsis psammophila*) show little differentiation between populations from South Australia and Western Australia.

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The sandhill dunnart (SHD; *Sminthopsis psammophila*) is a small insectivorous marsupial that is sparsely distributed in arid and semi-arid habitat in southern Australia (Menkhorst and Knight 2001; Churchill 2001a). Populations are known to occur in the Great Victoria Desert and also on Eyre Peninsula in South Australia, although it is uncertain whether this distribution is separated because they are highly fragmented or elusive - having only ever been recorded from eight locations. The species is currently listed as "Endangered" under the *Environment Protection and Biodiversity Conservation Act 1999*, recent work (Churchill 2001a) supported a downgrading of status to "Vulnerable" after new populations were found in previously recorded habitat range where they had been thought to be extinct. However, the current extent of the range of the SHD is still uncertain and even after concerted effort it has not been found in the Northern Territory since the type specimen was caught there near Lake Amadeus in 1894 (Churchill 2001a).

Prior to recent and extensive ecological survey work (Churchill 2001b) very little was known about the biology of the SHD. Churchill's study investigated many aspects of the ecology of the SHD including habitat requirements, distribution, home ranges, diet, and reproduction. Churchill's work did not, however, investigate the genetic differences amongst populations of SHDs. We used partial control region sequence to investigate the degree of genetic variation across the sampling range. The samples that were analysed represent nearly all the available DNA/tissue samples of this species.

In total we sequenced 15 individuals, 11 from South Australia (5 from Middleback, Eyre Peninsula, 1 from Pine Hill, Eyre Peninsula, 4 from near Ooldea and 1 from near Maralinga) and 4 from Western Australia (Mulga Rock, Great Victoria Desert).

Combined, these individuals constitute all the samples that were available at this time. Approximately 354 bp of the 5' end of the Dloop was amplified and sequenced, and analysed following procedures described in Alacs *et al*. (2003). Initially the broadly specific Fumagalli *et al*. (1997) control region primers were used (L15999M and H16498), however sequencing was difficult with these primers for at least half of the samples and so we also used sminthopsis primers (M20 and M119) from Blacket *et al*. (1999). We sequenced one *Sminthopsis douglasi* (01-432) individual as an outgroup for the analyses.

There were six SHD haplotypes (amongst samples from Mulga Rocks and Eyre Peninsula), two from Mulga Rock and four from Eyre Peninsula. There was substantial sequence divergence between *Sm*. *douglasi* and the SHD haplotypes, ranging from 24.5%-27.2%. However, there was no strong distinction between the two geographic areas sampled for SHD. Sequence divergence among the Mulga Rock haplotypes was only 0.6%, among the Eyre Peninsula haplotypes ranged from 0.7%-3.6%, and between Mulga Rock and Eyre Peninsula 0.9%-4.6%.

- number of haplotypes found
- Kimura 2-parameter distances
- NJ and MP

Although more extensive studies should be carried out (for example using nuclear markers such as microsatellites), this information will be important for establishing rational conservation policies and to assess the value of these populations as conservation resources.

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