Genetic diversity of Spotted-tailed quolls (*Dasyurus maculatus*) at 11 microsatellite loci

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The Spotted-tailed quoll (*Dasyurus maculatus*) is an endangered species found in eastern Australia. There are concerns surrounding the genetic diversity of this species due to continuously small population sizes over generations. Greater genetic diversity in a population can lower the probability of extinction in the case of an epidemic and/or major catastrophe, along with providing greater variation for natural selection to work upon. In this study, the genetic diversity of five populations (Cathedral, Glen Innes, Kunderang, Petroi, and Tabletop) of Spottedtailed quolls was determined. This was done through DNA extraction, optimal primer annealing temperature determination, and subsequent polymerase chain reactions (PCR) run for each DNA sample at 12 microsatellite loci. All loci were found not to be in linkage disequilibrium, and 11 out of 12 loci were found to be in Hardy-Weinberg Equilibrium. The average number of alleles was highest in the Tabletop population (6.4±0.49 alleles) and lowest in the Kunderang population (3.6±0.28 alleles). The rarefied allelic richness ranged from 3.2±1.6 (Glen Innes) to 3.6±0.28 (Kunderang). There were a fairly low number of private alleles in all populations. Glen Innes was the only sampled meta-population with an inbreeding coefficient greater than zero. The pairwise F_{ST} estimates for five different pairs of the populations all differed significantly from zero. This research may advise future quoll management and relocation sites in order to increase genetic diversity.