

Diversity and hybridisation estimates in Antarctic and Subantarctic fur seals from Marion Island based on mitochondrial and microsatellite DNA markers

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The mitochondrial DNA (mtDNA) control region and 5 microsatellite loci were used to assess genetic variability and the extent of hybridization between the two fur seals (*Arctocephalus tropicalis* and *A. gazella*) that occur on Marion Island. Both species were harvested during the 18th and 19th centuries, leading to a reduction in population size and the extinction of *A. gazella* at some localities. Whilst both species have recovered and are increasing in size¹, it is not clear to what extent sealing has affected genetic variation, although a more pronounced effect would be expected for *A. gazella*, given the more intensive harvesting of this species². The current study confirmed this hypothesis and revealed that *A. gazella* had nucleotide diversity of 2.9 % whilst for *A. tropicalis* it was 4.2 %, across the HRVI region sequenced. For microsatellite DNA, genetic variation in *A. tropicalis* was higher than in *A. gazella* in terms of the total number of alleles detected and the level of heterozygosity ($H_E=0.875/H_O=0.845$, mean number of alleles=13.6) and ($H_E=0.799/H_O=0.781$, mean number of alleles=13), respectively. Diversity in both species is among the highest recorded in pinnipeds, and suggests that sealing did not overly affect the levels of genetic variation in these species³. The level of hybridization between these species was low at Marion Island with only one hybrid being detected among the 134 animals that were genetically characterized. This corresponds to 0.75 %, but may be an underestimate as the samples used in this study were primarily collected from sites where the two species do not co-occur. Future studies focusing on sites where they occur sympatrically, may yield higher estimates

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