Genetic variation and population structure in southern elephant seals *Mirounga leonina* at Marion Island

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The southern elephant seal (SES), *Mirounga leonina*, was intensively harvested during the late 18th and early 19th century, though never reduced to the levels seen for the northern species (*Mirounga angustirostris*). Although a number of putative populations occurring within the species' circumpolar distribution in the southern oceans have been genetically characterised, no data were previously available for the Marion Island population. This study integrates Marion Island into the broader database by genetically profiling 68 individuals with 7 microsatellite DNA loci and a single mitochondrial DNA (mtDNA) locus corresponding to HVRI. These data were then combined with existing genotypes from Argentina, Macquarie, South Georgia, Elephant Island and Sea Lion Island breeding colonies, permitting inter-population level comparisons. Genetic variation was high for both microsatellite and mtDNA loci at Marion Island, consistent with levels previously reported for the other populations, with the exception of Peninsula Valdés (Argentina) where diversity levels are low. Marion Island was significantly differentiated from each of the other breeding colonies included in the study based on F_{ST} analyses for both microsatellite and mtDNA data. The magnitude of these values was somewhat higher than those previously reported between South Georgia, Sea Lion Island and Elephant Island, but considerably less than the distances reported between either Peninsula Valdes or Macquarie Island in comparison with the rest (including Marion Island). These data are consistent with the earlier interpretation that most putative island populations show moderate levels of differentiation not directly related to geographic distance, while the mainland population in Argentina and the island population at Macquarie stand out as highly differentiated from the rest.