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Site-fidelity, movement ranges and abundance of southern right whales in the Antarctic Indo region inferred from genetic tagging

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Genetic markers ('tags') were employed to identify individual southern right whales in order to assess their site-fidelity, sex-specific ranges and abundance in the Antarctic Indo region (i.e., between 80°-135°E and south of 60°S). In total, 157 biopsy samples were collected as skin biopsies from free-ranging whales during fourteen summer surveys. The DNA was extracted from each biopsy sample and genotyped at fourteen microsatellite loci, sequenced for 430 nucleotides of the mtDNA control region, and the sex determined by the presence of a Y-chromosome specific locus. The overall probability of identity (the probability that two unrelated individuals from the same panmictic population have identical multi-locus genotypes) was estimated at 1.95×10^{-14} . After removal of biopsies with identical multi-locus genotypes sampled during the same sighting, the total sample size used for estimating abundance was reduced to a total of 153. Eight 'mark-recapture' incidences were detected (four males and four females). Individual matching by multi-locus genotypes was supported by mtDNA, sex determination, and in two cases where pictures were available, by photo-identification. These eight re-captures suggested that individual whales tended to return to the same location in the Antarctic in subsequent years. The average longitudinal dispersal ranges were 13°06' longitude and 7°15' longitude in males and females, respectively. The time span between the 'mark' and the 'recapture' ranged from 3-13 years with an average at 7.3 years. The abundance was estimated using the Cormack-Jolly-Seber model implemented in MARK, which is an open population model based on surveys conducted on three or more occasions. The estimate of abundance was at 1,619 (95% CI: 868-3,151) individuals, similar to the most recent (2007/08) sighting survey abundance estimate at 1,557 (95% CI: 871-2,783) individuals using the Line Transect Method in the same area.