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Long-Range Paternal Gene Flow in the Southern Elephant Seal

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Female philopatry and male dispersal are thought to be typical of mammalian species, although detecting genetic dispersal events remains difficult. Like many mammals, the southern elephant seal (*Mirounga leonina*) shows greater population structure for mtDNA than for nuclear DNA markers (*1–3*) and one possible interpretation is greater male- than female-mediated gene flow. However, the different effective population sizes for these markers limit the strength of this interpretation. Here, we show evidence for male-mediated genetic dispersal over a geographic range of about 8000 km (from one extreme of the species range to the other), indicating current gene flow between populations that show fixed differences and reciprocal monophyly for mtDNA markers and significant differentiation for some nuclear markers (ESUs) (*4*).

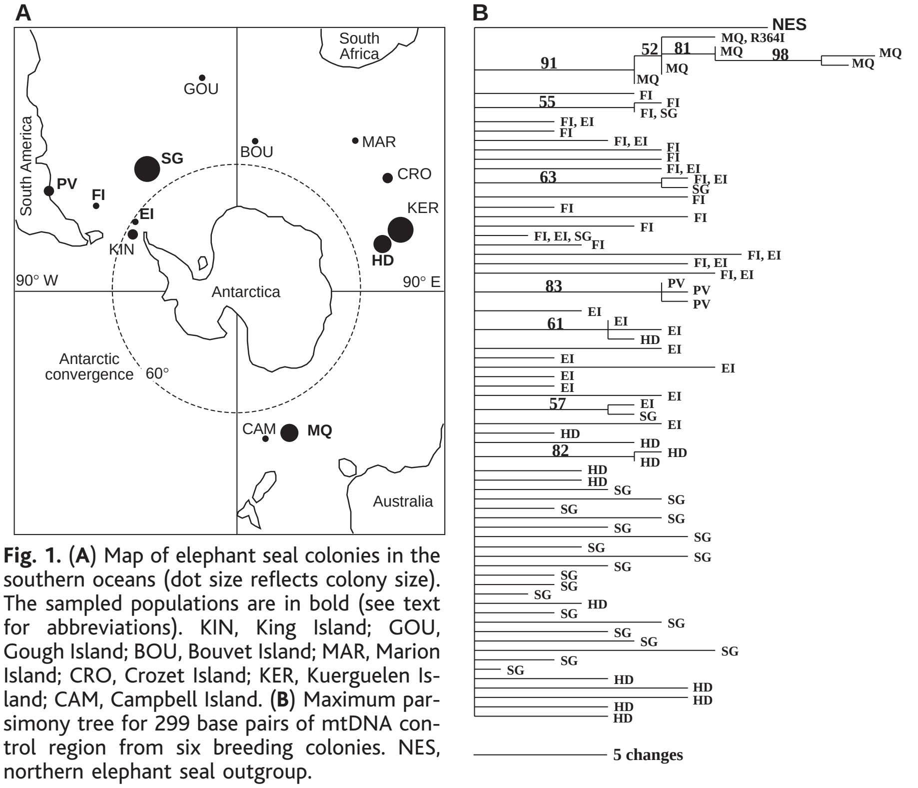

Fig. 1. (**A**) Map of elephant seal colonies in the southern oceans (dot size reflects colony size). The sampled populations are in bold (see text for abbreviations). KIN, King Island; GOU, Gough Island; BOU, Bouvet Island; MAR, Marion Island; CRO, Crozet Island; KER, Kuergeulen Island; CAM, Campbell Island. (**B**) Maximum parsimony tree for 299 base pairs of mtDNA control region from six breeding colonies. NES, northern elephant seal outgroup.

The southern elephant seal has a circum-Antarctic distribution (Fig. 1A). We sequenced the HVR1 segment of the mtDNA control region from 57 seals from the Falkland Islands (FI, 27 females and 30 reproductive males) and 30 seals from Elephant Island [EI, 15 females and 15 males; for accession numbers and methods, see (*5*)] and compared these with published sequences (*1– 3*) from South Georgia (SG; $N = 28$), Peninsula Valdez, Argentina (PV; $N = 32$), Heard Island (HD; $N = 13$), and Macquarie Island (MQ; $N = 6$). This includes all major and several minor breeding colonies. The resulting phylogeny (Fig. 1B) shows little structure, apart from well-supported lineages for MQ and PV. The MQ lineage is further defined by two fixed differences. The haplotype of one male from FI (R364I) matches a unique haplotype within the MQ lineage, and all other samples ($N = 127$) from FI, SG, HD, and EI have haplotypes that are within a separate, interspersed, poorly defined lineage. The most parsimonious interpretation is that R364I was born on MQ. A stepping-stone effect is possible but much less likely, because the six MQ haplotypes would need to be present at a combined-frequency of less than 1.8% among the other samples to have gone undetected (95% confidence for a binomial probability of zero). Given known patterns of female philopatry and fecundity (*1–3*), it is unlikely that this matriline has become established anywhere but MQ. Assessment of matrilineal population structure showed strong differentiation between MQ and all other populations (F_{ST} estimates from 0.45 to 0.92; $P \leq 0.002$), but less structure among the other islands ($F_{ST} = 0.05 – 0.22$; n.s. and $P \leq 0.01$).

Nuclear markers showed less structure. Two loci (*Mhc-DQA* and *ALD-A*) (*1*) showed no significant heterogeneity among SG, HD, and MQ, although MQ was significantly differentiated from the other five populations at two pentanucleotide microsatellite loci [amplified simultaneously, located within the β-*Globin* complex; $G \geq 30$, $P \leq 0.004$; based on 263 FI and 46 EI samples from this study and 31 to 37 samples (*1*) from PV, SG, HD, and MQ]. Nuclear DNA data also supported our interpretation of R364I as an immigrant to FI. On the basis of five di-nucleotide microsatellite loci (not available for MQ), we could exclude (*6*) PV, FI, SG, and EI as the likely natal populations for R364I ($P < 0.05$).

R364I bred on FI in 1996, gaining control of a harem and successfully fathering at least 19 offspring [paternal inference from nine microsatellite DNA loci (*1–3*, *7*); average probability of a correct paternal match was 0.999; see (*5*, *8*)]. Excursions from breeding grounds of up to 5200 km have been documented for the southern elephant seal (*9*), but there are no other records of long-distance genetic dispersal. Our data suggest significant gene flow between distant populations, despite extensive mtDNA differentiation, illustrating the potential homogenizing effect that even rare dispersal events could have for species with polygamous mating systems.

References and Notes

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10. We thank R. Slade for providing MQ and HD DNA samples.

Supporting Online Material
www.sciencemag.org/cgi/content/full/299/5607/676/DC1
Materials and Methods
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