

Genetic diversity in a moulting colony of southern elephant seals in comparison with breeding colonies

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Supplement. Additional information

Parentage analysis in Cervus

Parentage analysis was performed using a maximum-likelihood approach implemented in Cervus 3.0 (Marshall et al. 1998, Kalinowski et al. 2007). We simulated 10 000 offspring based on the allele frequencies in the study population to determine the level of confidence in the assigned parentages. We allowed for 50% of mothers and 75% of fathers to be unsampled. This was justified by greater site fidelity of males than females, inferred from behavioural and genetic data (Lewis et al. 1996, Hoelzel et al. 2001, Fabiani et al. 2006). Only adult individuals were considered as candidate parents, and all sampled individuals were included as candidate offspring (because adult offspring may use the same moulting sites as their parents). Parentage assignment was accepted if it had no more than one mismatching locus and was assigned at the strict (95%) confidence level. The putative mother–offspring pairs were checked for consistency of mtDNA haplotypes. Besides assigning a mother or a father separately, we also performed a parent pair analysis, but none of the sampled individuals was assigned both parents at either the strict or relaxed confidence level.

Cervus estimated the mean polymorphic information content at 0.5525. the probability of false parentage assignment was 0.025 for a single parent and 0.00001 for a parent pair. The probability of a false assignment of individuals as full siblings was 0.0002. The probability of identity (i.e. the probability that 2 different individuals would have identical genotypes) was 9.68×10^{-10} .

Only 2 of 24 putative mother–offspring pairs assigned by Cervus, with either strict (95%) or relaxed (80%) confidence, had matching mtDNA haplotypes and age class (adult/pup) consistent with the mother–offspring relationship. To make sure that the discrepancy of mtDNA haplotypes in the remaining 22 pairs was not caused by any kind of laboratory errors (e.g. mislabelling the samples), we randomly selected 4 putative mother–offspring pairs and repeated mtDNA sequencing for them. In each case, we obtained the same mtDNA haplotypes as in the first analysis, mismatched between the putative mothers and offspring. This allowed us to exclude the mother–offspring relationship for these pairs.

Among all parent–offspring pairs from Cervus, assigned with or without confidence, there were 175 mother–offspring pairs and 218 father–offspring pairs with no mismatching loci, as

well as 48 mother–offspring pairs and 79 father–offspring pairs with one mismatching locus. Although the lack of mismatches alone (especially assigned without confidence) does not necessarily mean that 2 individuals form a parent–offspring pair, it makes it likely that they are related. This way Cervus may be used to identify close relatives other than parent–offspring. In the KGI moulting colony, only 9 individuals were assigned no relatives, i.e. did not have any putative parent assigned with or without confidence. Among them, there were 2 putative immigrants, M1 and M2.

Breeding dispersal of southern elephant seals between colonies

Despite breeding site fidelity, several cases of breeding dispersal between colonies were observed based on tagging or satellite data, and are listed below:

- A breeding female dispersed from Iles Crozet to Marion Island (Bester 1989)
- Two females from Marion Island bred at Iles Crozet (Guinet et al. 1992)
- 18 females from Possession Island (Iles Crozet) were found present 33 times during breeding seasons at Marion Island, with pupping confirmed in 27 cases (Oosthuizen et al. 2011)
- Six adult males from Possession Island were found present 16 times during breeding seasons at Marion Island, and three males successfully gained a harem holder status in 11 instances; one male from Possession Island controlled harems at Marion Island for six consecutive breeding seasons, and during this period 196 females (7.6% of all breeding females) were present/passed through harems under his control (Oosthuizen et al. 2011)
- Two males from Marion Island hauled out for breeding at Iles Kerguelen, and one of them returned to Marion Island for moulting (Oosthuizen et al. 2011)
- Two males from Marion Island hauled out for breeding at Iles Crozet, and one of them returned to Marion Island for moulting (Oosthuizen et al. 2011)
- An adult male from Marion Island was observed at Gaugh Island during a breeding season (Reisinger & Bester 2010).

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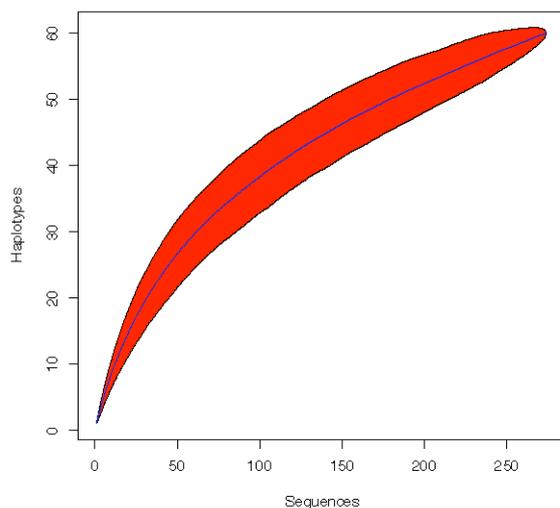
Table S1. List of mtDNA haplotypes found in the King George Island southern elephant seal moulting colony and the number of individuals carrying each haplotype (N), as well as a reference to a study where a given haplotype was published for the first time

Haplotype	N	Reference
KGI1	2	Present study, GenBank accession number: JX847037
KGI2	1	Present study, JX847038
KGI3	6	Present study, JX847039
KGI6	1	Present study, JX847040
KGI7	1	Present study, JX847041
KGI8	1	Present study, JX847042
KGI9	4	Present study, JX847043
KGI11	6	Present study, JX847044
KGI12	4	Present study, JX847045
KGI16	5	Present study, JX847046
KGI19	1	Present study, JX847047
KGI22	1	Present study, JX847048
KGI23	2	Present study, JX847049
KGI25	2	Present study, JX847050
KGI26	1	Present study, JX847051
KGI28	1	Present study, JX847052
KGI30	6	Present study, JX847053
KGI32	1	Present study, JX847054
KGI33	2	Present study, JX847055
KGI35	1	Present study, JX847056
KGI38	1	Present study, JX847058
KGI43	1	Present study, JX847057
KGI44	1	Present study, JX847059
KGI46	1	Present study, JX847060
KGI47	2	Present study, JX847061
S12	1	Hoelzel et al. (1993)
SG1	6	Slade et al. (1998)
SG2	2	Slade et al. (1998)
SG4	35	Slade et al. (1998)
SG5	2	Slade et al. (1998)
HD6	3	Slade et al. (1998)
MI	1	L. F. Chauke, A. D. S. Bastos, M. N. Bester unpubl. data, DQ267952
SESEI1	1	Fabiani et al. (2003)
SESEI2	6	Fabiani et al. (2003)
SESEI3	2	Fabiani et al. (2003)
SESEI4	11	Fabiani et al. (2003)
SESEI5	6	Fabiani et al. (2003)
SESEI6	3	Fabiani et al. (2003)
SESEI7	3	Fabiani et al. (2003)
SESEI8	1	Fabiani et al. (2003)
SESEI9	1	Fabiani et al. (2003)
SESEI10	8	Fabiani et al. (2003)
SESEI11	6	Fabiani et al. (2003)
SESEI12	3	Fabiani et al. (2003)
SESFI1	20	Fabiani et al. (2003)
SESFI2	8	Fabiani et al. (2003)
SESFI3	14	Fabiani et al. (2003)
SESFI4	4	Fabiani et al. (2003)
SESFI5	18	Fabiani et al. (2003)
SESFI6	1	Fabiani et al. (2003)
SESFI7	1	Fabiani et al. (2003)
SESFI8	7	Fabiani et al. (2003)
SESFI9	2	Fabiani et al. (2003)
SESFI11	1	Fabiani et al. (2003)
SESFI12	16	Fabiani et al. (2003)
SESFI13	10	Fabiani et al. (2003)
SESFI14	4	Fabiani et al. (2003)
SESFI15	13	Fabiani et al. (2003)

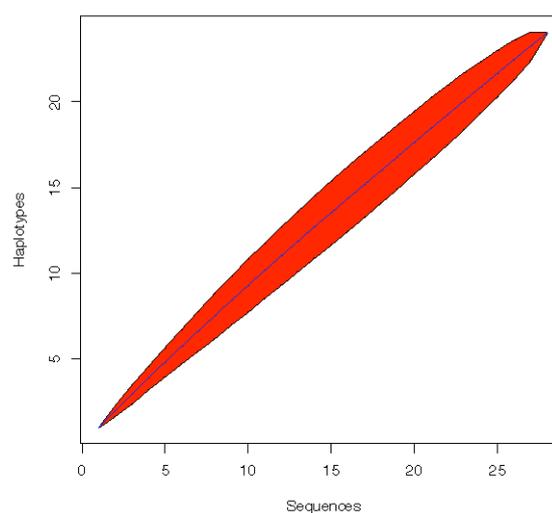
Table S2. Genetic diversity at microsatellite loci in 3 temporal groups of southern elephant seals from the King George Island population sampled in different moulting seasons. N : number of samples, N_a : mean number of alleles at microsatellite loci, H_O and H_E : expected and observed heterozygosity; F_{IS} : inbreeding coefficient. Standard errors for each estimate are shown in parentheses

Season	N	N_a	H_O	H_E	F_{IS}
2002/2003	28	5.167 (0.767)	0.547 (0.082)	0.567 (0.072)	0.022 (0.063)
2003/2004	35	5.417 (0.839)	0.578 (0.074)	0.584 (0.072)	-0.005 (0.030)
2005/2006	76	6.583 (0.900)	0.541 (0.071)	0.597 (0.067)	0.119 (0.043)

King George Island



South Georgia



Peninsula Valdes

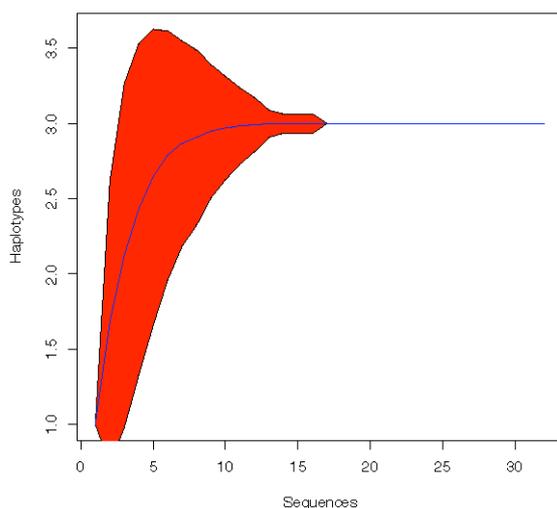


Fig. S1. Rarefaction curves illustrating the rate of increase in haplotype number with increasing sample size for 3 southern elephant seal colonies. The 95% confidence intervals are marked in red

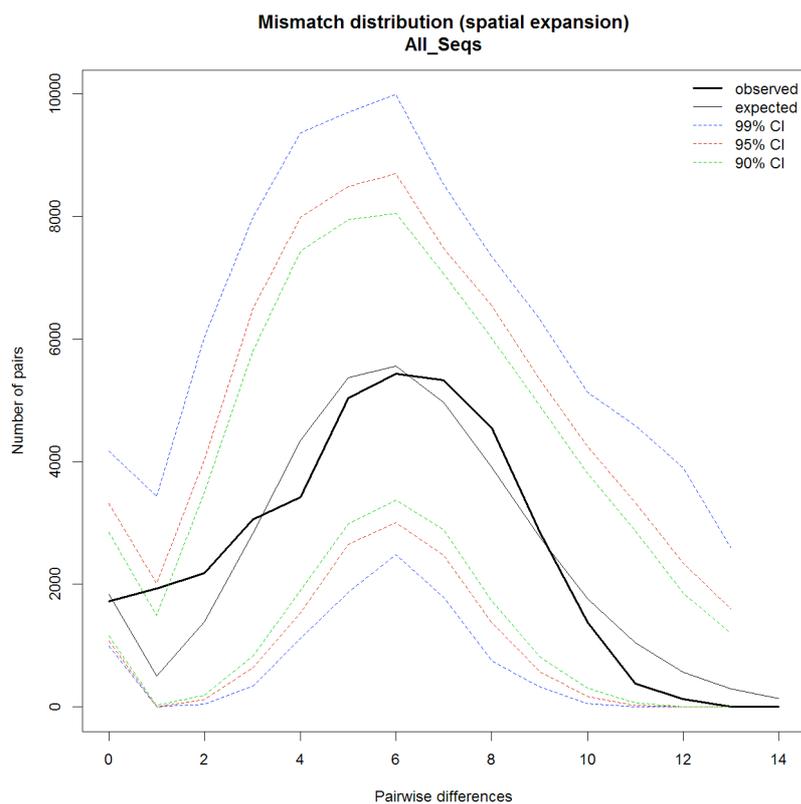
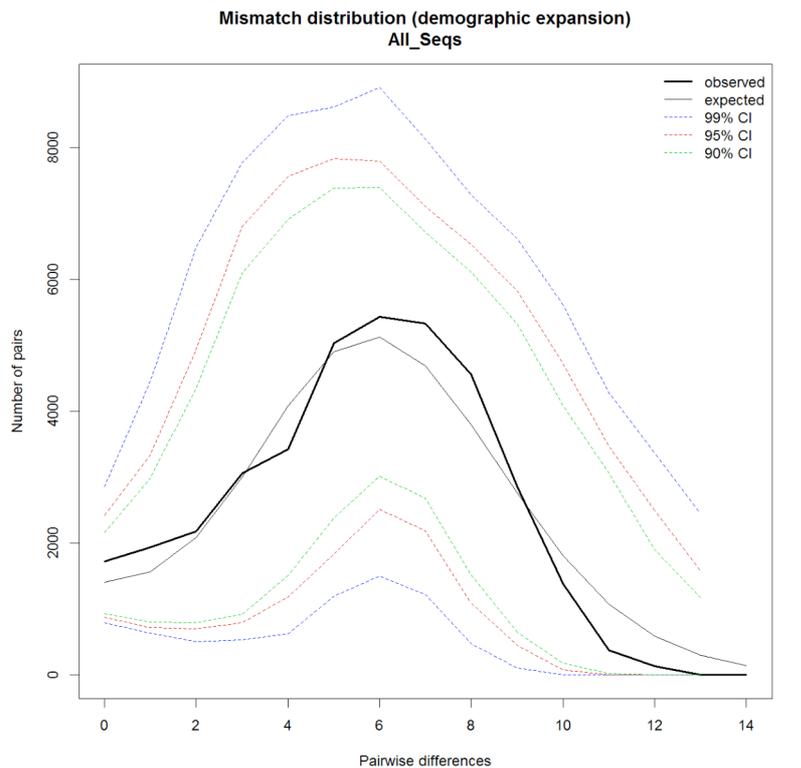


Fig. S2. Observed versus expected mismatch distribution for King George Island southern elephant seal mtDNA haplotypes, assuming either a demographic or a spatial expansion model