

FINAL REPORT - SMM: SMALL GRAND IN AID OF RESEARCH (2022)

Philogeography and genetic conservation of the southern elephant seal (*Mirounga leonina*) at Potter Peninsula, Antarctica: Genetic variation of the breeding and molting colony and gene flow with other colonies.

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Due to the polygyny characteristic of the southern elephant seal (SES), the impact of a male migrant that manages to control a harem for several consecutive reproductive seasons could be clearly reflected in the genetic characteristics of a small or medium-sized colony. Although it is known that members of this species return to their natal site to breed and moult (Hofmeyr 2006, Negrete 2011), there is strong direct evidence that not all individuals show breeding site fidelity during the moulting season, as they often moult closer to their feeding grounds (Bogdanowicz et al. 2013; Oosthuizen et al. 2011).

In this study we determine the genetic variation at 7 microsatellite markers of the SES breeding and moulting at Peninsula Potter (**PP**), 25 de Mayo/King George Island, Antarctica. For this we used 96 samples of SES belonging to the 2007 and 2019 breeding seasons and to the 2020 moulting season. Each season represented by 32 samples.

PCR reactions were carried out at the Laboratorio de Ecología Molecular (CADIC-CONICET) and their products were sent to MacroGen Korea for fragment analysis services. Genotyping was done with the software Peak Scanner v1.0 (Applied Biosystems).

All PCR reagents and laboratory disposable material were obtained thanks to the Society for Marine Mammalogy small grand in aid of research. As well as the fluorescently labeled primers and the fragment analysis services at MacroGen Korea.

The genotyped sizes for each microsatellite, the MgCl₂ concentrations and the annealing temperature are shown in Table 1.

We compared our data to that published in previous studies to determine the genetic relationships between the colony under study and the rest of the world SES population stocks, identifying own and shared alleles to establish gene flow paths (Table 2). These findings are

relevant to understand the role of the **PP** colony in the global population dynamics. We are currently analyzing our data to compare the genetic diversity and parentage relationships between the breeding and molting season to test the level of philopatry in each group (Figure 1).

Final results and conclusion from these analyses will be published as part of Mr. Lanusse's PhD thesis.

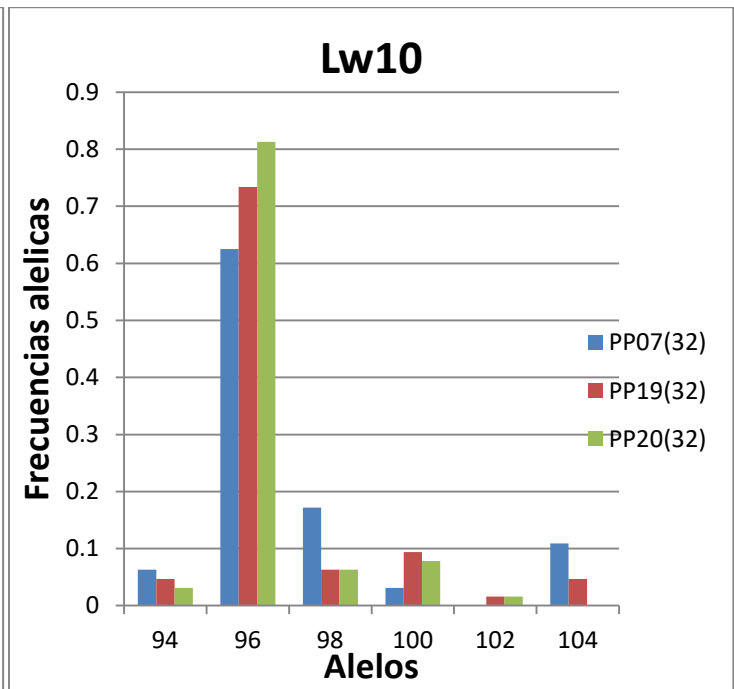
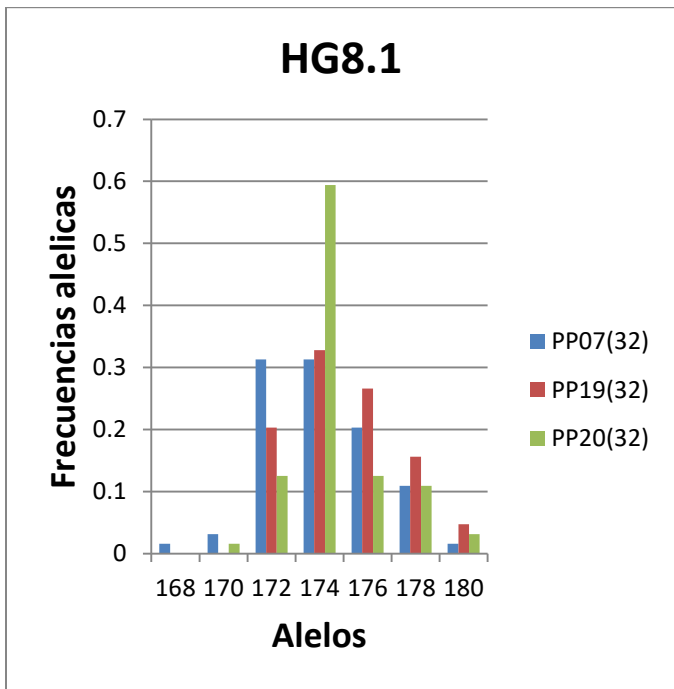
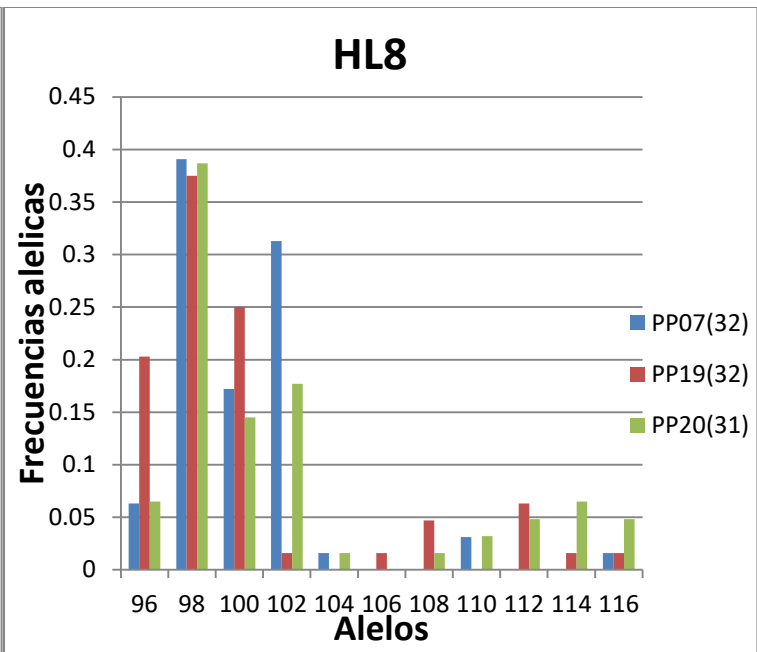
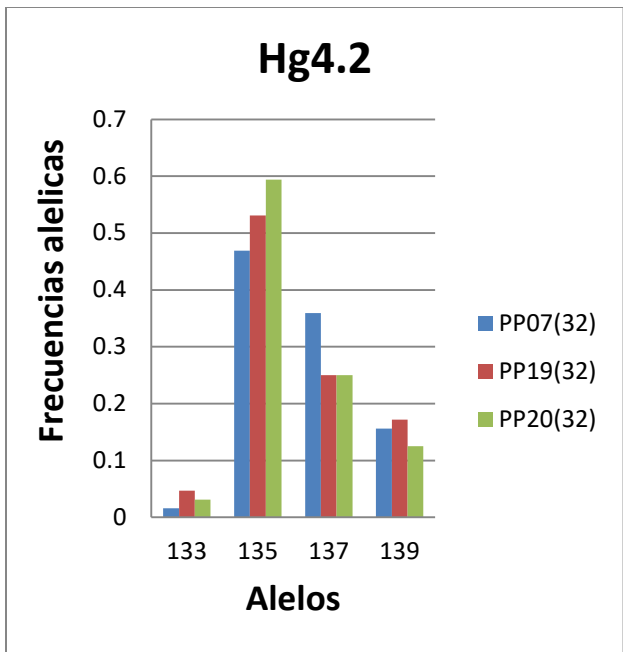
Locus	Size(pb)	Fluorochrome	Genotype d size(pb)	[MgCl2]	T° anne aling (C°)	T° real (C°)	Source
Hg4.2	133-139	FAM	133-139	1.5 mM	56	58	Allen et al. 1995
HI8	96-112	HEX	96-116	2 mM	51	52	Davis et al. 2002
Hg8.1	168-180	HEX	168-180	1.5 mM	54	58	Allen et al. 1995
Lw10	94-104	FAM	94-104	2 mM	60	52	Davis et al. 2002
Lw20	112-132	HEX	114-142	2 mM	60	56	Davis et al. 2002
Hg3.6	78-100	FAM	78-100	1.5 mM	56	54	Allen et al. 1995
M11a	138-150	FAM	138-150	2 mM	51	52	Hoelzel et al. 1999

Table 1. List of amplified microsatellites. The name of each locus; the size of the amplified fragment according to Allen et al. (1995), Hoelzel et al. (1999) and Davis et al. (2002); the fluorochrome with which each microsatellite was labeled; the size of the genotyped fragment (bp); the annealing temperatures according to the works of Allen et al. (1995), Hoelzel et al. (1999) and Davis et al. (2002); and the temperatures used for this study are detailed.

Table 2. A summary of microsatellite polymorphism in five SES populations.

Locus		PP	SLI	EI	PV	SG	MI	MQ
Lw20	N ind.	63	78	46	48	48	48	48
	n allele (Ar)	11(10.342)	11(10.127)	10(9.327)	8(7.898)	10(9.539)	13(12.174)	9(8.625)
	Fsi	0.090	-0.037	0.041	0.179	0.130	0.023	-0.003
	Ho	0.778	0.859	0.783	0.625	0.729	0.854	0.833
	He	0.854	0.828	0.816	0.759	0.837	0.874	0.830
Hg4.2	N ind.	64	80	46	48	48	48	48
	n allele (Ar)	4(3.932)	5(4.338)	4(3.674)	4(3.646)	6(5.902)	4(3.958)	3(3.000)
	Fsi	0.015	-0.081	0.070	0.000	0.038	0.038	-0.029
	Ho	0.625	0.650	0.565	0.437	0.687	0.625	0.646
	He	0.634	0.601	0.607	0.437	0.714	0.649	0.628
Hg3.6	N ind.	64	80	46	48	48	48	48
	n allele (Ar)	12(10.210)	11(10.337)	11(10.352)	9(8.353)	11(10.342)	9(8.507)	6(5.953)
	Fsi	-0.061	-0.059	-0.011	0.015	-0.008	-0.001	0.133
	Ho	0.891	0.875	0.848	0.708	0.833	0.812	0.646
	He	0.840	0.827	0.839	0.719	0.827	0.812	0.744
HI8	N ind.	64	77	46	48	48	48	47
	n allele (Ar)	11(8.724)	10(8.053)	9(7.875)	9(8.272)	10(8.953)	10(8.583)	10(9.391)
	Fsi	-0.038	0.014	0.027	0.045	-0.011	0.035	-0.056
	Ho	0.797	0.740	0.609	0.708	0.708	0.792	0.830
	He	0.768	0.751	0.626	0.741	0.701	0.820	0.787
Hg8.10	N ind.	64	80	46	48	48	48	48
	n allele (Ar)	7(6.153)	10(7.495)	6(5.642)	6(5.872)	5(4.986)	6(5.632)	5(4.944)
	Fsi	0.038	-0.030	0.001	-0.023	0.076	0.109	-0.142
	Ho	0.734	0.637	0.739	0.750	0.646	0.625	0.667
	He	0.763	0.619	0.740	0.733	0.698	0.701	0.584
Lw10	N ind.	64	75	46	48	48	48	48
	n allele (Ar)	6(5.471)	6(4.998)	4(3.987)	5(4.986)	5(4.943)	5(4.599)	3(2.877)
	Fsi	0.060	-0.082	0.019	-0.070	-0.087	-0.159	0.035
	Ho	0.484	0.533	0.304	0.625	0.500	0.417	0.375
	He	0.515	0.493	0.310	0.584	0.460	0.360	0.389
M11a	N ind.	64	77	46	48	32	48	47
	n allele (Ar)	7(6.484)	7(6.033)	6(5.895)	6(5.644)	5(5.000)	7(6.835)	6(5.658)
	Fsi	0.103	-0.066	-0.174	-0.050	0.035	-0.107	-0.077
	Ho	0.734	0.818	0.913	0.708	0.774	0.854	0.787
	He	0.818	0.768	0.779	0.675	0.802	0.773	0.732

N ind.: number of individuals; n allele: total no of alleles; Ar: allelic richness; FSI:Wright's inbreeding coefficient; HO: observed heterozygosity, HE: expected heterozygosity. EI: Elephant Island, SLI: Sea Lion Island, MI: Marion Island, SG: South Georgia, PV: Peninsula Valdés, PP: Potter Peninsula. Data from the other colonies are from Corrigan et al. 2016. Raw data was kindly provided by Professor Rus Hoelzel.



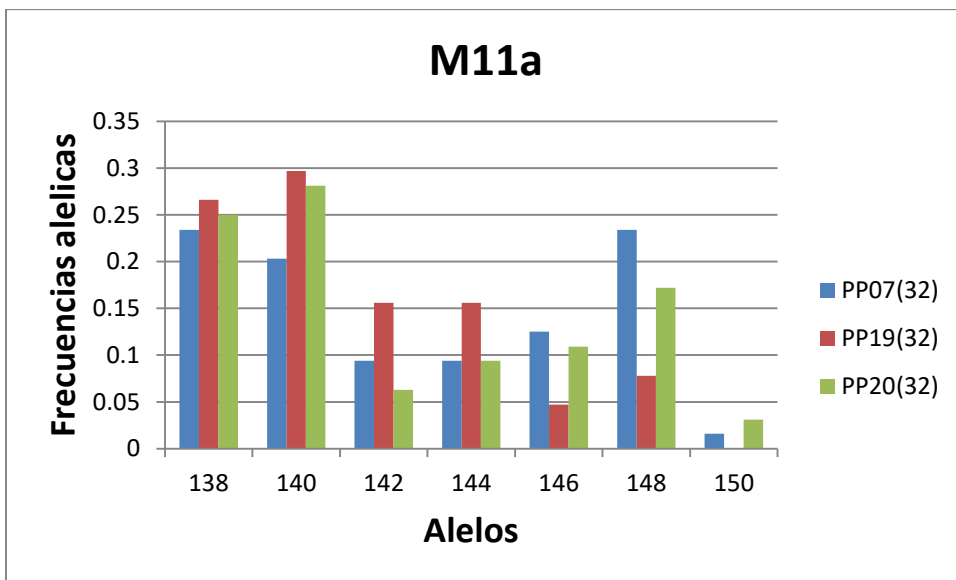
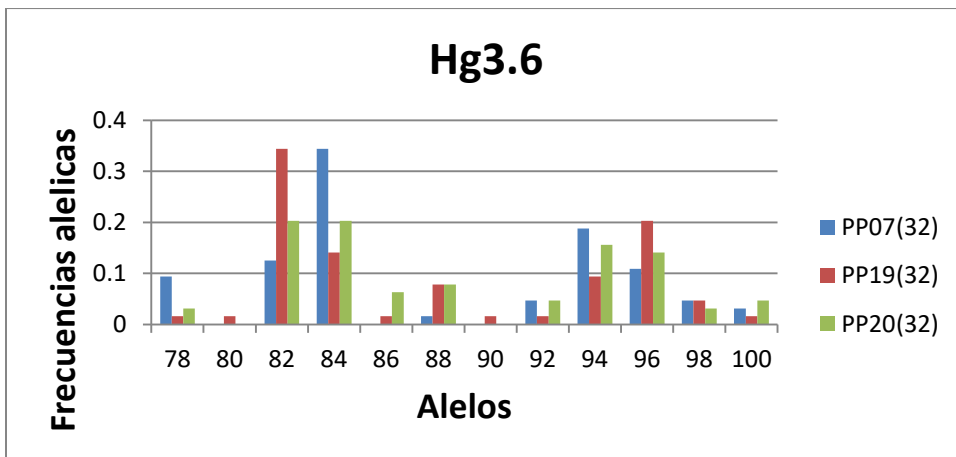
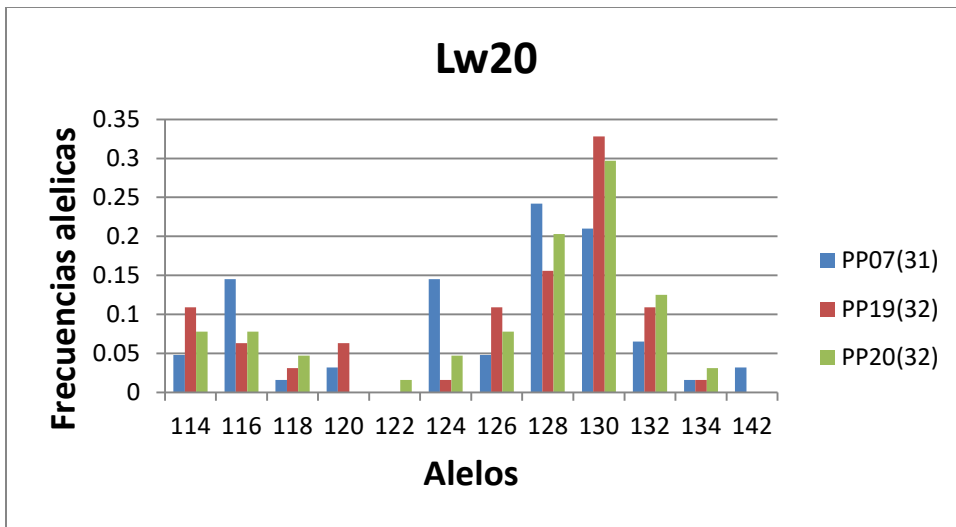


Figure 1. Microsatellite allelic frequencies plotted for each group. PP07:Breeding 2007, PP19:Breeding 2019, PP20:Moult 2020.

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