Genetic diversity and population genetic structure in the South American sea lion (*Otaria flavescens*)

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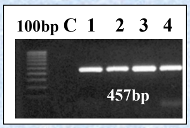
INTRODUCTION

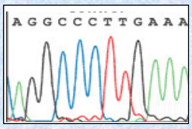
- The South American sea lion (*Otaria flavescens*) was severely exploited for body parts in Argentina and the Falkland Islands, causing sharp declines of 90-93%.
- Population genetic theory predicts smaller populations lose genetic variation at a faster rate due to the amplified effects of drift.
- Fisheries interactions, extreme polygyny and slow population growth rate were also hypothesized to slow recovery and limit variation.
- Genetic consequences of the decline and effect of sustained small island population size on genetic diversity were examined.
- Limited gene flow and strong geographic structuring between the mainland and island were also predicted due to female philopatry, divergent foraging niches and isolation by distance.

METHODS

Phenol-chloroform DNA extraction in 39 Argentine and Falkland Islands samples.



PCR amplification from 5' ^{mt}tRNA^{thr} end of control region to the middle of the central conserved domain.



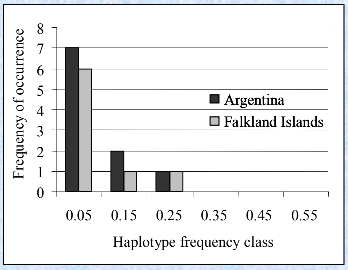
Direct sequencing of the 5' end. Sequence alignment in ClustalX.

RESULTS

Genetic Diversity

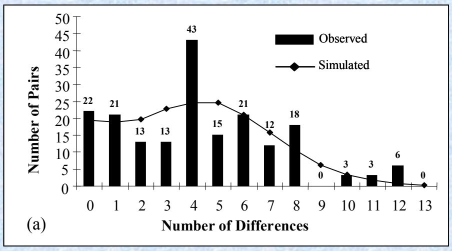
No. haplotypes (mainland/island)	No. variable sites (%)	Gene diversity mainland/island	% nucleotide diversity (π) mainland/island
18 (10/8)	24 (5.62)	0.88 ± 0.05 / 0.88 ± 0.04	1.2 / 0.77

Indices of genetic diversity. Executed in Arlequin ver2. Locations did not share haplotypes. Genetic diversity is high, however nucleotide diversity indicates an island effect.

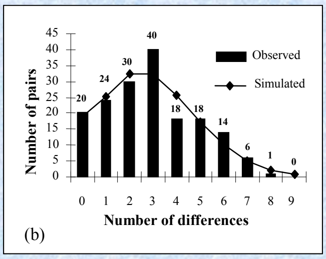


Control region haplotype distributions. The L-shaped distribution represents a high number of low frequency haplotypes in both locations. This indicates the presence of many rare alleles in the gene pool.

Demographic Structure

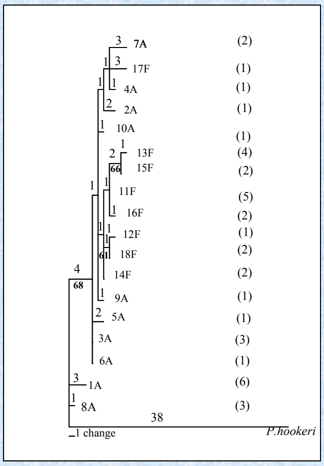


Mismatch distributions in Argentina (a) and the Falkland Islands (b). α = 0.010 and is based on 1000 replicates. Argentina exhibits a rugged multimodal distribution, inferring a stable genetic structure over time.

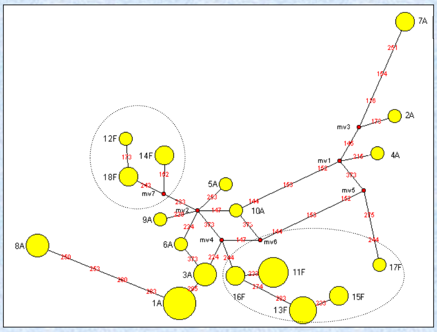


The Falkland Islands however exhibit a unimodal distribution, illustrating that it has undergone an ancient population expansion.

Genetic Structure



50% majority-rule consensus maximum parsimony tree. Bootstrap values above 50% are indicated in bold below branches. Numbers above branches indicate the number of parsimonious steps assigned to each haplotype. Fifteen sites were parsimony-informative. Numbers in brackets indicate the number of individuals in the dataset with that haplotype. A and F refer to Argentina and the Falkland Islands respectively. Neighbour-joining and maximum likelihood trees were analogous. The tree exhibits weak patterning. Argentine sequences are both at the tips and basal positions. Two small Falkland matrilineages are apparent at its centre. Executed in PAUP ver4.0b10.



Phylogeographic network of mtDNA haplotype sequences. Haplotypes are represented by the yellow circles. Their size corresponds to their relative frequency in the dataset. Red numbers along the connecting lines between haplotypes indicate the position of mutations in the sequence alignment. Intermediate nodes (mv1-7) represent inferred intermediate haplotypes not present in the dataset. The Falkland Islands haplotypes are circled. Executed in NETWORK ver3.1.1.1.

CONCLUSIONS

- Contrary to predictions, a high level of diversity and weak geographic structuring were found.
- The magnitude and duration of the decline, and lag in recovery until recent times were insufficient to cause dangerous levels of genetic erosion.
- Mismatch distributions indicate the Falkland Islands acted as an ice-age refuge from ice-covered Patagonia, producing migrations and mixing of populations.
- Subsequent seasonal, historical gene flow to warmer Patagonian waters are supported by hunting data, also explaining structure and diversity levels.
- Increasing fisheries interactions and illegal trading are threatening these populations. Results support their classification as a single, genetically diverse management unit for conservation.

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