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.

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

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.

RESULTS

Genetic Diversity

No. haplotypes (mainland/island) 39
No. variable sites 9
Gene diversity mainland/island 0.88 ± 0.05/0.88 ± 0.04
% nucleotide diversity (%) mainland/island 12.7 ± 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.

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.

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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