NUCLEAR AND MITOCHONDRIAL DNA EVOLUTION IN ADÉLIE PENGUINS:

STUDIES OF MODERN AND ANCIENT POPULATIONS

A thesis presented in partial fulfillment of the requirements for the degree of **Doctor of Philosophy (PhD)** in **Genetics**

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Teatro mágico - sólo para locos

La entrada cuesta la razón

- Hermann Hesse

ABSTRACT

The Adélie penguin of Antarctica (*Pygoscelis adeliae*) breeds on the Antarctic continent and on offshore islands. Its evolutionary history has been, and its current biology remains, dependent on a range of climate variables. Over geological time, glacial warming and cooling periods have resulted in Adélie penguin populations decreasing and expanding. Therefore, understanding Adélie penguin population dynamics at a genetic level can provide insights into how the species responds to changing climates, one reason why Adélie penguins are an important natural model species. In addition, sub-fossil bone deposits of this species below modern and abandoned colonies provide an excellent source of ancient DNA that can bring a temporal dimension to population studies of the species. In combination, these attributes enable us to address some fundamental questions regarding evolutionary change.

Making use of known mitochondrial DNA mutation rates and current population sizes, a positive and significant correlation between population size and modern mitochondrial control region diversity was detected. This finding supports the use of mitochondrial DNA for population inferences. Effective population sizes of breeding colonies are shown to have increased since the late Pleistocene. To extend current tools available for understanding Adélie penguins, six nuclear intron loci were recovered from a wide range of introns that can be applied to population genetics and phylogenetic studies of penguins. Five introns were used to investigate the persistence of the mitochondrial Antarctic (A) and Ross Sea (RS) lineages. No evidence for the existence of these lineages was found in the nuclear loci sequenced. A signature of historical population expansion, preceding the mitochondrial one, was detected. The utility of four introns in resolving penguin phylogenetic signals was also determined. Non-coding nuclear sequence of one intron were obtained from ancient sub-fossil remains of Adélie penguins using multiplex PCR enrichment, followed by second-generation sequencing of a barcoded library. A shift in haplotype frequencies was detected between ancient and modern intron sequences in Adélie penguins, despite a small sample size. In the future, advancing the current methodologies and extending sampling to additional introns as well as older samples, is likely to provide a new level of understanding of this remarkable species.

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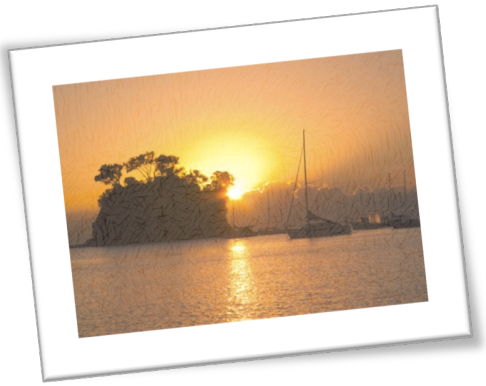

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