

STATEMENT OF GRANT PURPOSE

Tanya Lama, Spain, Ecology

Genetic monitoring of Iberian lynx (*Lynx pardinus*) populations in Spain

Background: The Earth is experiencing unprecedented biodiversity loss on a global scale. This human-induced “sixth mass extinction” event has already erased over 300 mammal species and, with them, more than 2.5 billion years of unique evolutionary history. And yet, it’s not too late -- the efficacy of conservation measures is rapidly increasing due to global coordination and science-based management. Captive breeding programs have become critical for the conservation of many threatened species, and have played a major role in the recovery of the California condor (*G. californianus*), whooping crane (*G. americana*), and black-footed ferret (*M. nigripes*). They act as a safeguard in case disaster strikes wild populations, and serve as a source for reintroductions. Captive populations also establish a reservoir for critically important genetic diversity – the raw material of evolution that allows populations to adapt to changing environmental conditions. Its preservation is essential to the resiliency of small, isolated populations which are often genetically eroded and exhibit: i) loss of genetic diversity ii) accumulation of inbreeding iii) incidence of genetic disease and iv) compromised reproductive success and survival. Therefore, management strategies for at-risk species are based on maximizing genetic diversity, while minimizing relatedness among individuals.

The Iberian lynx (*L. pardinus*) experienced a steep decline during the second half of the 20th century due to habitat loss and reduced availability of its primary prey species, the European rabbit (*O. cuniculus*). By 2002, less than 100 individuals remained, constrained to two isolated populations in Doñana National Park and Cardena Andújar. On the verge of extinction, the species was classified as Critically Endangered (IUCN), and is recognized as the most endangered felid in the world. Spain’s Iberian lynx recovery initiative has been recognized as one of the most advanced programs in the world. The program integrates captive breeding, reintroduction, and on-the-ground habitat management, expanding the global population seven-fold since its inception in 2003. However, the genetic health of the captive breeding population and the wild populations it has supported needs to be evaluated. To date, just 36 microsatellite markers have provided the scientific basis for programmatic decisions. Recent methodological advances in DNA sequencing have generated new *genomic* tools and data types. This change of scale from few loci to thousands, or even whole genome sequences enables more robust population-level assessments and higher accuracy in the execution of routine tasks such as identifying optimal breeding pairs, estimating relatedness, and selecting suitable candidates for reintroduction.

Objective: Our objective is to evaluate the genetic composition and pedigree of the captive breeding population and wild populations in Doñana National Park and Cardena Andújar using the latest analytical tools and technologies available in genomics.

Methods: I’ve established a working relationships with lynx expert, Dr. Jose Antonio Godoy, a pioneer in wildlife research at the Doñana Biological Station in Seville, Spain. Dr. Godoy has demonstrated commitment to training excellent researchers in ecology and conservation. The proposed project is a collaborative effort, which builds on knowledge, resources, and data accumulated from past projects. Available genomic resources include a reference genome for Iberian lynx, an extensive dataset of whole genome sequences, and customized panels of genome-wide molecular markers called SNPs (single nucleotide polymorphisms). The wild population will be assessed through genetic characterization of non-invasively collected samples (e.g. scat, hair) using optimized SNP panels. Samples (N=50 from each territory) will be

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collected by trained field technicians over 10-day periods in Doñana National Park and Cardena Andújar. Permits will be acquired prior to departure by Dr. Godoy. Scats will be identified by morphology and presence signs (e.g. tracks). Samples will be stored in 15mL tubes with silica desiccant and scat location recorded by GPS. The captive population will be assessed through genetic characterization of blood samples collected during standard veterinary assessments. Genomic DNA will be extracted from all samples and subject to species, sex, and individual identification assays. The unique genetic signature of each sample will allow us to identify the individual, their parents, siblings, and other close relatives, resulting in precise pedigrees. These pedigrees will capture the history of each population, provide estimates of demographic and genetic parameters, characterize existing genetic diversity, and serve as the basis of future management strategies. The genetic management of the captive population will also include selection of new wild-born breeding pairs and design of an optimal cross-breeding scheme.

Timeline: I have obtained candidacy by completing my coursework, qualifying exams and proposal defense at the University of Massachusetts Amherst. I plan to begin my Fulbright project in September 2020. Upon arrival, I will participate in non-invasive sample collection, extract DNA from all samples and begin running species, sex, and individual identification assays. Upon departure in May 2021, I will continue analyzing data, and preparing publications with Dr. Godoy from my home institution.

Qualifications: I am uniquely qualified to participate in this ambitious effort at the direction of Dr. Godoy and the skills gained through this Fulbright will contribute meaningfully to my research. My doctoral work focuses on the development of genomic resources and genetic assessments that inform timely and effective recovery plans for at-risk populations of Canada lynx (*L. canadensis*), a federally protected sister-species of the Iberian lynx. I have proven expertise in genomics, developing a chromosomal-level reference genome for Canada lynx -- the highest quality genomic resource available for any wildcat species. The skills gained from Dr. Godoy's mentorship will be used in the development of a 7-year monitoring program employed in several US states, particularly Maine. If granted a Fulbright, I look forward to contributing to and benefiting from the intellectual and cultural resources at the Doñana Biological Station.

Significance: Non-invasively collected samples have been used for genetic and demographic monitoring of other carnivores. However, there are few applications in the context of captive breeding and reintroduction programs, and **none** at the level of intensity proposed in this project. This work will facilitate cultural and academic exchange between two institutions (Doñana Biological Station and UMass). We anticipate that this work will be highly impactful in at least two dimensions. Firstly, the scientific impact and visibility of this project is likely to be high, because of the high profile of the species and its critical conservation concern, and of the increasing popularity of genomic research. Second, this project has an important applied impact, to the extent that the methodology, application and results will contribute to species conservation of both Iberian lynx and Canada lynx and likely other threatened species (e.g. the Scottish wildcat *F.s. silvestris*).