GENOMIC INSIGHTS INTO ENDANGERED OCELOT (*LEOPARDUS PARDALIS*) POPULATIONS TO INFORM SPECIES RECOVERY

A Thesis

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ABSTRACT

Genomic Insights into Endangered Ocelot (*Leopardus pardalis*)
Populations to Inform Species Recovery

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With habitat and species loss occurring at unprecedented rates, conservation action is needed to preserve threatened and endangered populations. Habitat loss and fragmentation isolate populations, which can result in increased susceptibility to stochastic events such as severe weather or disease. Small populations are also vulnerable to loss of genetic diversity due to genetic drift and inbreeding, both of which can reduce fitness. Reintroduction can increase genetic diversity and mitigate impacts of environmental stochasticity for target species. However, the genetic provenance of stock animals used in reintroductions can have lasting effects and needs careful consideration. Ocelots (*Leopardus pardalis*) are a target species for reintroduction in the United States, given that there are likely fewer than 100 individuals remaining in two isolated populations in South Texas. Reintroduction efforts have begun, with the official ground breaking of the ex-situ breeding center in 2024. To maximize the success of ex-situ breeding and reintroduction efforts, I: 1) assessed genetic diversity and inbreeding of wild ocelots and 2) analyzed genetic divergence between wild and zoo-sourced ocelots to inform the selection of ex-situ breeding candidates. Using whole genome sequencing, I found that wild ocelots had significantly lower nucleotide diversity (Ranch: 0.0017, Refuge: 0.0018, Generic:

0.0032, Brazilian: 0.0033) and higher inbreeding (wild: 43.23-50.67% genome in run of homozygosity, zoo-based: 1.13-3.57% genome in run of homozygosity) than zoo-based ocelots. In addition, I identified evidence of dispersal (n=5) and gene flow (n=2 first-generation offspring) between the wild South Texas populations. These are the first dispersers documented between populations since at least 1991. The offspring of dispersers had higher genetic diversity than either parental population, which demonstrates how gene flow can ameliorate the loss of genetic diversity, even among inbred populations. I evaluated the potential of zoo-based stocks (Brazilian and Generic) for the ex-situ breeding in reference to genetic diversity as well as genetic distance and divergence from wild South Texas stocks. Brazilian ocelots had the highest genetic diversity, with > 32,000 private alleles, while Generic ocelots had > 14,000 private alleles, and were less genetically divergent from wild ocelots. Overall, zoo-based stocks had higher greater nucleotide diversity and fewer ROH than wild stocks. Either stock would be suitable for ex-situ breeding, but consideration of individual variation in the selection of founding individuals is necessary, as ROH ranged from 0% to > 15% of the genome. This research is the first to show gene flow between wild ocelot populations in the United States and adds to the growing literature on ex-situ breeding considerations to inform species reintroductions, ultimately providing critical information to support ocelot reintroduction and recovery.

DEDICATION

This thesis is dedicated to my parents. Starting from when we moved to Montana so that I could grow up surrounded by nature, my parents have always fostered and supported my love for wildlife. I am incredibly lucky that my life has been so surrounded by the animals I love, from watching elk in our yard to raising fox kits for rehabilitation. All of these experiences have had and will have a lasting impact on my life. Pam and Dave, you have set the foundation for my love of animals and science, and for that I am eternally grateful. Your continuous love and support for my work and passions has allowed me to reach all of my dreams and I truly would not be where I am today without your support.

I am also, at heart, a cat lover, and this dedication wouldn’t be complete without my two cats Orion and Jupiter. The constant companionship from them proved to be the best way to de-stress after a long day, and for that they are a part of this thesis as well.

I love you all dearly and thank you for your unwavering support and companionship.

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I thank my committee chair, Dr. Petracca, for taking a chance on me and this project and allowing me to sculpt it into my dream master's. I appreciate your trust and willingness to work with me to create not only something that I am passionate about, but has the chance to improve ocelot conservation. Thank you for your continued support and guidance throughout my time in South Texas.

I thank my committee members, Drs. DeYoung, Martin, and Reeves, for their time, work, and support throughout the course of this research. Dr. DeYoung was instrumental in helping me to understand genetics, and setting the foundation for everything I have learned through the course of this thesis. Dr. Matt Smith and Michael Barret in the last year of my thesis were also instrumental in helping me to decipher code, and providing a safe space for me to bounce around ideas.

I express thanks to all of the collaborators on this project. This work would not have been possible without the continued support from the United States Fish and Wildlife Service, Laguna Atascosa National Wildlife Refuge, the Center for Conservation and Research of Endangered Wildlife, and the East Foundation. The collaboration of all of these organizations allowed for the acquisition and analysis of both wild and zoo-based ocelot blood samples. The inclusion of photographic identification of ocelots from Laguna Atascosa National Wildlife Refuge was only possible due to the efforts of Refuge staff, volunteers, and biologists, notably Andy Grunwald, Brandon Jones, and Laura de la Garza. The long photographic capture history of individuals would not have been possible without all of the hours spent cataloging and identifying individuals, and for that I am extremely grateful.

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Contributors

This work was supervised by a thesis committee consisting of Drs. Lisanne Petracca, Randy DeYoung, and Alynn Martin of the Department of Range and Wildlife Management, Texas A&M University – Kingsville, and Dr. Ashley Reeves of the East Foundation.

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All other work conducted for the thesis was completed by the student independently.

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CHAPTER 1. Genomic effects of rare gene flow between inbred populations of ocelots (*Leopardus pardalis*) in the United States

INTRODUCTION[1]

Loss of habitat connectivity due to rapid urbanization imperils wildlife populations (Taylor et al. 1993, Elmqvist et al. 2015). Populations isolated by habitat loss and fragmentation are more vulnerable to extirpation via stochastic events (Willoughby et al. 2015). As a result, the expanding urban footprint has led to species range contractions and, in some cases, species extinctions. Intact mammal species assemblages are present in only 24% of the world's ecosystems (Ripple et al. 2014, Wolf and Ripple 2017). Overall, the global loss of genetically and ecologically distinct populations has demonstrated the importance and need for genetic management in the conservation of wildlife populations (Lacy 1997).

Population history and demographic factors have significant effects on the amount of genetic diversity in a population. The number of breeding individuals and degree of gene flow directly influence the amount of genetic variation present (Mayr 1954). Thus, small populations are disproportionately impacted by the random differences in survival and reproduction of individuals, termed genetic drift, which can result in the loss of genetic variation and accumulation of deleterious alleles (Wright 1931). Additionally, genetic diversity tends to be lower in populations at the edge of their range, in contrast to those at the core (Antonovics 1976, Brussard 1984, Hardie and Hutchings 2010). This is known as the central-marginal hypothesis, and occurs because those populations tend to be historically smaller and more susceptible to stochastic events and geographic isolation (Antonovics 1976, Hardie and Hutchings 2010).

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[1] This thesis is written in the style of the Journal of Wildlife Management