IMPLICATIONS OF POTENTIAL DISEASE TRANSMISSION PATHWAYS TO ENDANGERED OCELOTS (*LEOPARDUS PARDALIS*) IN SOUTH TEXAS

A Thesis

by

ALEXANDRIA HIOTT

PREVIEW

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ABSTRACT

Implications of Potential Disease Transmission Pathways to Endangered Ocelots in South Texas

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Alexandria Hiott, B.S. Forest Resources

University of Georgia, Athens

Co-Chair of Advisory Committee: Drs. Lisanne Petracca and Alynn Martin

Disease introduced to wildlife populations through movement of animals, especially of domestic species, has the potential for population-level impacts. Small, isolated populations are at greater risk of interspecific disease transmission, otherwise called a spillover event, due to naïve immune responses and small population sizes. Such spillover events can lead to restricted ability for populations to recover from disease-related losses and potentially reduced fitness due to inbreeding. Understanding disease dynamics and spillover pathways within populations of concern is important for informing management and establishing protocols to safeguard against future spillover events and protect vulnerable populations. This thesis had two main objectives: (1) understand how spatial interactions between sympatric felid species, ocelots (*Leopardus pardalis*) and bobcats *(Lynx rufus*), affect potential disease transmission risk in South Texas, USA, and (2) test three felid species, including the above and mountain lion (*Puma concolor*), for exposure to a disease with potential for spillover from avian hosts, also in South Texas, USA. For the first objective, I used integrated step selection and contact network analyses to understand potential disease transmission pathways between federally endangered ocelots and the more common bobcats. Ocelots persist in the United States in two spatially distinct populations and are associated with Tamaulipan thornscrub. Conversely, bobcats are generalists

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that utilize a wide range of landscape types. Interactions were highest between individuals of different sexes of the same species, followed by male-male intraspecific interactions. While ocelots and bobcats showed positive selection for complexity in vegetation structure and NDVI (a proxy for vegetation density), there was stronger positive selection for vegetation density in ocelots. In addition, interspecific contacts were most likely with greater proportional cover over 0.5 m ($\beta = 0.94$, SE = 0.12) and lower vegetation density ($\beta = -0.20$, SE = 0.06). For my second objective, I screened the three native Texas felid species (ocelots, bobcats, and mountain lions) for highly pathogenic avian influenza (HPAI). HPAI is a disease linked to numerous carnivore deaths after spillover events from the typical avian host. Ocelots and bobcats, in particular, persist in coastal environments along the Central Flyway with migrating and wintering waterfowl and other avian species. One male bobcat tested positive to HPAI H5N1 antibodies at capture. This individual was still alive at the conclusion of this study, 3.5 months after initial capture, suggesting that this individual was exposed to the disease but then recovered. There is still a growing need for research on HPAI in carnivores, as it has demonstrated high lethality in several carnivore species. To promote ocelot conservation and potential disease mitigation, managers should seek to promote areas of high understory density, as this could allow for ocelots to spatially partition from bobcats more effectively. This research provides a greater understanding of disease dynamics among sympatric felid species in this system and can ultimately inform management decisions and reintroduction efforts for ocelots.

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DEDICATION

This thesis is dedicated to my parents and sister. I know your love always follows me as I have chased my dreams around the country. Thank you for always supporting me. This is also for the little girl at the Fernbank Museum of Natural History identifying a red-tailed hawk from her stroller — look at how far we have come.

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I would like to thank my committee chairs, Drs. Lisanne Petracca and Alynn Martin, for allowing me to take on this work. You both have allowed me to grow and foster the skills I have wanted and not stood in the way of me pushing forward with my own ideas for what this project could be. Thank you both for helping me readjust when needed and encouraging me towards my goals.

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Contributors

This thesis was supervised by a thesis committee consisting of Drs. Lisanne Petracca, Alynn Martin, and Clayton Hilton of the Department of Range and Wildlife Management, Texas A&M University – Kingsville, Dr. Ashley Reeves of the East Foundation, and Dr. Mason Fidino of the Lincoln Park Zoo.

Data analyzed for this thesis were collected in partnership with the Caesar Kleberg Wildlife Research Institute and the East Foundation.

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

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CHAPTER 1. USING ANIMAL MOVEMENT MODELS AND CONTACT NETWORKS TO UNDERSTAND POTENTIAL SPILLOVER ROUTES BETWEEN TWO SYMPATRIC FELID SPECIES

INTRODUCTION

Interactions within and among species are a driving force of many ecological processes (Svanbäck et al., 2007, Mutshinda et al., 2009, Singer et al., 2013). These interactions can be conspecific (e.g., social interactions, parent-offspring, courtship events [Elbroch and Quigley, 2017]) or interspecific (e.g., predation events, resource competition [Neumann and Pinter-Wollman, 2022]). Interactions can result in animals coming into contact directly (e.g., mating, aggression, kleptoparasitism) or indirectly, where animals spatially overlap but temporally avoid each other to prevent direct encounters (Caro and Stoner, 2002). When animals are in proximity with one another for brief or extended periods of time, termed a "contact" (Manlove et al., 2022), pathogens may be transmitted from one individual to another. Disease introductions from a spillover—the transmission of a pathogen from an infected individual, population, or species to another—can impact population dynamics (Monk et al., 2022) and even cause population extirpations (Besser et al., 2021). With changing global paradigms through climate change, globalization, and urbanization wildlife populations are at an increased risk to the spillover of disease from conspecific or interspecific interactions (Baker et al., 2000).

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Understanding multi-species spatiotemporal landscape use, such as space sharing and overlap among species, is key to identifying where interspecific interactions may occur and can help inform conservation planning (Webber et al., 2023). This information has implications for disease transmission pathways (Craft, 2015) and prediction of disease spread to new environments (Merkle et al., 2017), and could be used to potentially safeguard an at-risk population from exposure. Recent advancements in movement modeling approaches and global positioning systems (GPS) technology have allowed for the coupling of animal movement and resource selection in movement models (Avgar et al., 2016) and the handling and collection of higher resolution data, permitting a better understanding of potential disease transmission pathways (Wall et al., 2014, Kirby et al., 2017).

Integrated step selection analysis (iSSA) is a modeling paradigm that simultaneously estimates animal movement and selection (Avgar et al., 2016). This framework employs the "used-available" framework at the step level, the distance between two consecutive GPS points, and allows for inference about movement and selection jointly, rather than considering these processes to be operating independently (Avgar et al., 2016). In addition, outputs from iSSA models can be used for simulations, allowing researchers to predict hypothetical movements given parameters related to temporal and spatial states (Signer et al., 2024). This integration of both habitat selection and movement can permit a better understanding of potential disease spread on the landscape, as well how spatial phenotypes can impact contact rates (Webber et al., 2023).

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Animal movement from GPS collars can be used to model real and simulated movement paths, as well as frequency of contacts between individuals. These contacts can be modeled in a contact network analysis, which uses network theory to create interaction networks, with nodes representing individuals and edges representing the connections between these nodes (Craft, 2015). Networks are constructed from recorded contacts between individuals, as defined by a system-appropriate spatial proximity within a set time interval (Craft, 2015, Eames et al., 2014). These contacts are collated to generate a network of interactions, where edge weights reflect the strength of associations between individuals and can be used to evaluate potential disease

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