5-2024

Reinforcements of a Greater Sage-Grouse Population in Utah: Applications for Range-Wide and Local Conservation Translocation Efforts

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Recommended Citation

Chelak, Melissa S., "Reinforcements of a Greater Sage-Grouse Population in Utah: Applications for Range-Wide and Local Conservation Translocation Efforts" (2024). *All Graduate Theses and Dissertations, Fall 2023 to Present*. 122.
https://digitalcommons.usu.edu/etd2023/122

REINFORCEMENTS OF A GREATER SAGE-GROUSE POPULATION IN UTAH: APPLICATIONS FOR RANGE-WIDE AND LOCAL CONSERVATION TRANSLOCATION EFFORTS

by

Melissa S. Chelak

A dissertation submitted in partial fulfillment
of the requirements for the degree

of

DOCTOR OF PHILOSOPHY

in

Ecology

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2024

ABSTRACT

Reinforcements of a Greater Sage-Grouse Population in Utah: Applications for Range-Wide and Local Conservation Translocation Efforts

by

Melissa S. Chelak, Doctor of Philosophy

Utah State University, 2024

Major Professor: Dr. David Stoner
Department: Wildland Resources

In a small, isolated greater sage-grouse (*Centrocercus urophasianus*) population in the Sheeprock Mountain Sage-Grouse Management Area (SGMA) located in Utah's West Desert, peak male lek counts declined from 190 males in 2006 to 23 males in 2015. A collaborative effort across all federal, state, and local partners yielded 146 (40 male, 106 female) sage-grouse captured, marked with either a very-high frequency or global positioning systems (GPS) transmitter, and translocated into the Sheeprock sage-grouse management area between 2016 and 2019, complete with radiotelemetry monitoring during the spring and summers of 2016-2020 translocated individuals in addition to radiotelemetry monitoring of 39 (12 male, 27 female) resident Sheeprock sage-grouse. Coincident management efforts included extensive habitat restoration, predator control, and monitoring off-highway vehicle (OHV) recreation.

To evaluate the movements, habitat selection, demographics, and genetics of this population, I performed a behaviorally segmented, movement-based habitat selection analysis, an integrated population model (IPM) of the Sheeprock SGMA and the translocation source populations, and analyses quantifying allelic richness, allelic frequency, and genetic heterogeneity. Additionally, I evaluated the GPS transmitters' performance to monitor the grouse, which is essential for quantifying and accounting for fix error for GPS-based spatial models. The probability of sage-grouse beginning in the exploratory phase at the time of release was marginally lower for adult females than yearlings. The analysis also suggested that to reduce post-release dispersal, practitioners should prioritize release sites to maximize the restricted state selection in areas closer to mesic habitat, higher elevation, and lower tree cover. The IPM predicted declining populations following translocations due to low recruitment, dictated by low chick survival, and estimated population abundance of 22 individuals (95% CI: 2 – 63) by 2027. However, we also detected an increase in allelic richness and the potential for the increased admixture of the source population genetics in the reinforced population.

(257 pages)

PUBLIC ABSTRACT

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Melissa Chelak

In a small, isolated greater sage-grouse (*Centrocercus urophasianus*) population in the Sheeprock Mountain Sage-Grouse Management Area (SGMA) located in Utah's West Desert, peak male lek counts declined from 190 males in 2006 to 23 males in 2015. A collaborative effort across all federal, state, and local partners yielded 146 (40 male, 106 female) sage-grouse captured, marked with either a very-high frequency or global positioning systems (GPS) transmitter, and translocated into the Sheeprock sage-grouse management area between 2016 and 2019, complete with radiotelemetry monitoring during the spring and summers of 2016-2020 translocated individuals in addition to radiotelemetry monitoring of 39 (12 male, 27 female) resident Sheeprock sage-grouse. Coincident management efforts included extensive habitat restoration, predator control, and monitoring off-highway vehicle (OHV) recreation.

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DEDICATION

To my late maternal grandparents, Jerry C. and Sue Brooks, who attended every concert, race, and academic event in which I participated. Though you both passed away during my sojourn out West, I would not be where I am today without you. Papa B, your academic and running pursuits inspired me to discover my physical and mental limits. Mama B, your support for me and love for all things growing left a definite mark on my character. The haven you both created in the Appalachian foothills of North Carolina was a peaceful place to explore the world and learn about the trees, the creek, and the wildlife therein. It will forever be a formative collection of memories that fuel me. This dissertation is yet another branch on the tree of your legacy. I love you, miss you, and wish you could be here to see me cross another finish line.

To my daughter, Genevieve, who was born during the latter portion of this doctoral process. Though you may not read this (no judgement therein), I hope that this work serves as an example of how, often, we can shape our outcomes despite our beginnings. However, do not use my accomplishments (or those of anyone else) as a shadow to try and match or supersede. *Crées ta propre ombre sur le paysage, ma petite.*

To my spouse and partner, Clint, having been with me since those aforementioned beginnings. Thank you for being a constant by my side throughout it all. This work I have accomplished is as much your blood, sweat, and tears as it is my own. Thank you for letting me explore to discover and achieve that which fulfills me. *Enfin, c'est ton tour de te découvrir.*

ACKNOWLEDGMENTS

I want to thank my current advisor, Dr. David Stoner, for first accepting the invitation to join my committee and then taking on the much more significant role of serving as my doctoral advisor in the final 400 meters of this Ph.D. marathon. I have immensely appreciated your support and encouragement from day one, and I have also enjoyed your ability to take a fairly decent story and project it considerably farther with your knowledge, insight, and perspective. Your honed diction and philosophical demeanor have created many enjoyable conversations.

I also want to thank my committee members who have served to improve my doctoral process. I express my thanks to Dr. Dave Dahlgren, who has continually encouraged me to build a better knowledge of the galliforms we study, especially in viewing them and their landscapes through the lens of a bird dog (specifically, a Lovey one). Dr. Jordan Smith, thank you for serving as my recreation specialist throughout my Ph.D. You helped me to understand that humans are inherently a part of virtually every landscape and to consider them an equal component in wildlife ecology. Dr. Mary Conner, for your analytical expertise and your centered, realistic perspective in both statistics and social aspects in academia. Your view served as a salve for the plight of imposter syndrome. Dr. Michel Kohl, for being a support and friend while you finished your Ph.D., joined our lab as a postdoctoral fellow, and subsequently nailed an assistant professor position at UGA. You've helped me through my comps and through analyses with messy data, and I am highly appreciative you offered to serve on my committee when the need presented itself. Finally, thank you, Dr. Nicki Frey, for "coming in clutch" as the 6th [wo]man at the 11th hour. But also, thank you for your cordiality and continued encouragement during our interactions throughout my Ph.D. and for collaborating with me (and others) on our GPS performance paper.

Additionally, I would like to thank Drs. Michael Guttery and Julie Young. In particular, thank you to Michael for helping me realize the importance of the "Ph" in Ph.D. through your reading recommendations many years ago, and thank you to Julie for recommending "Headstrong- 52 Women Who Changed Science—and the World."

I want to especially thank Dr. Terry Messmer, who funded and laid the foundation for this work to come to fruition. Terry, thank you for offering me the opportunity to obtain a graduate degree on a fantastic, multi-faceted project, sustaining me during hard times, and showing empathy when many other advisors would not have. You were a great mentor in the seven years you were my doctoral advisor, and I have gained an enormous amount of insight into community-based conservation through you.

I would also like to thank numerous collaborators. Drs. Pete Coates (USGS) and Steven Mathews (USGS) for the opportunity to collaborate on range-wide sage-grouse translocations, Dr. Simona Picardi (U of I) for your thorough training and mentoring through behaviorally segmented movement-based habitat selection models, Dr. Kristen Ellis (USGS) for your help in spatial abundance models, and Susan Durham for many hours of aiding me in formulating statistically-rigorous models. Thank you to Dr. Jeff Beck (UWyo), Randy Larsen (BYU), and Brian Maxfield (UDWR) for combining your large GPS datasets to answer some critical questions and, most importantly, for your patience in waiting a few more years than we initially anticipated to finish them.

There have been two incredible mentors I have had the pleasure of learning from through these many years. First, I would like to thank Jason Robinson for your work in creating this Sheeprock sage-grouse translocation project and for all of the hard work you put into ameliorating Utah's upland game program. Thank you also for making time to help trap grouse in the source and Sheeprock populations, run bird dogs to find new leks, and share your finely tuned grouse, dog, hunting, and naturalist knowledge. Second, I would like to thank Dr. Kezia Manlove for sharing your limited time during spurious hallway conversations that always imbued me with a new idea, reinforced direction, or just an all-around better day. Also, thank you for reaching out and lending a much-needed hand following an actual series of unfortunate events.

Throughout these 7.5 years of my doctorate, I've met many dear friends and colleagues, many of which I consider family. Thank you to Dr. Justin Small and Priscilla (and their children) for their continued comradery and support. Thank you to Kade Lazenby for your help with fieldwork, bird dog training, hunting, and many great conversations on conservation translocations. Thank you to Codi Backen for your support and patience through my 2nd field season as a manager and for being a genuinely great friend when you returned to USU to get your Master's. Thank you also to many other great friends: Dr. Stephanie Landry, Lorien Belton, Dr. Lacy Smith, Dr. Rachel Buck, Trevon Strange, Luke McDonald, Brandon Flack, Hailey Wayment, Charles Sandford, Wayne Smith, and Skyler Farnsworth. I could write pages on how each of you has helped me (but, for the sake of brevity, we can have a conversation!). Thank you to a long-time friend, Taylor Schmuki-Chapman (Schmuks), for your continued friendship since our first field season together in the West Desert. To a childhood friend (and chosen family), Kara Wylie, who, through innumerable shared experiences in academic and athletic pursuits, has remained my friend, alongside Clint, for two decades.

Across the five field seasons, thank you to many technicians who helped make this project a success and had patience with me while I was learning (some before I started learning) to improve my skills as a manager (still a work in progress—as it should be): Cassidy Becker (dedicated *two* field seasons), Clint Chelak, Codi Backen, Peter Hasik, Zach David, Nathan Redon, Sam Lau, Shivani Upadhyayula, Abby Stone, Holland Rupp, Jen Edgel, Celeste Silling, Tony Keith, Steven Hall, Zack Petrie, Adam Cupito, and Coburn Blunt. I sincerely thank everyone for their hard work and contributions. Additionally, I thank my furry coworker and companion, Opal, for locating brooding females and their chicks during the summer heat. I've enjoyed working on the sagebrush landscape with you.

Thank you to the countless agency folks who worked on grants and invested many hours improving the Sheeprock SGMA. Thank you to Avery Cook, Robby Edgel, Boyd White, and many others from the UDWR. Thank you to Renee Chi and others involved in the West Desert Area Regional Management local working group. Thank you to those in the BLM, Forest Service, Yamaha LLC, Utah PLPCO, USU PLI, and others who contributed funding to this project.

Thank you to the great landowners who participated in the community-based conservation within this SGMA and allowed us access to their land to track grouse. Thank you to Alan and Elizabeth Mitchel for their support and kindness during my work in the Sheeprocks.

Finally, thank you to my family. Thanks to my mom, Apryll. Thank you to my dad, David Smith, for your support, for taking a sincere interest in my work, and for carrying on a conversation about it when no other family would ask. Thank you to my

Nanna, Carolyn Smith, for always supporting me with a smile and for being okay with letting me explore 2,000 miles away from home. Lastly, thank you to my brother, Daniel Smith, and his wife, Kileen, for your support. To their children, Nova, Luna, and Mars, I hope you can discover what you love and pursue it! I will be there to cheer you on every step of the way.

Melissa Smith Chelak

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CHAPTER 1

INTRODUCTION AND LITERATURE REVIEW

The Deliberate Movement of Animals

Humans have been moving animals for thousands of years whether purposefully for resource management, ornamental or sentimental, or religious reasons or through accidental introductions (Grayson, 2001; Kirch, 2005; Seddon et al., 2012). It has not been until recently within the past 130 years, however, that humans have been deliberately moving them with the intent to establish, re-introduce, or reinforce populations (Seddon et al., 2012). The first documented conservation translocations were performed in 1894 in New Zealand, when kakapo (*Strigops habroptilus*) and kiwi (*Apteryx* spp.) were translocated to prevent their extinction affected by the recently-introduced invasive mammals such as stoats (*Mustela erminea*), rats (*Rattus* spp.), and domestic cats (*Felis catus*) (Miskelly & Powlesland, 2013; Seddon & Armstrong, 2016). From there, managers across North America, Europe, and the world began translocating animals.

In North America, two initial conservation translocations were designed to prevent extinctions: snowy egrets (*Egretta thula*) and American bison (*Bison bison*). In the late 1800's, snowy egret populations were declining across their range (Seddon & Armstrong, 2016). In 1895, Edward McIlhenny created a private island sanctuary off the coast of Louisiana in which to translocate captive-bred egrets (Trefethen, 1975; Seddon & Armstrong, 2016). After propagating a large breeding population of 2100 individuals, egrets were released into the wild to restore a declining native population (Trefethen, 1975; Seddon & Armstrong, 2016). Bison populations were on the verge of extinction due to overharvest of the once-abundant herds across the Midwestern and western United States (Trefethen, 1975; Seddon & Armstrong, 2016). To prevent their imminent extinction, the American Bison Society (ABS) was formed in 1905, and, beginning in 1907, the ABS captured bison from Yellowstone National Park (YNP) and began releasing groups in habitats where populations had been extirpated (Trefethen, 1975; Seddon & Armstrong, 2016).

In Europe, managers employed the first conservation translocations in Switzerland with captive-bred Alpine ibex (*Capra ibex*) in 1911 to prevent the species' extinction in the Alps (Seddon & Armstrong, 2016). Additional conservation translocations were performed again in 1914, though these were listed as unsuccessful due to poaching of naïve animals (Seddon & Armstrong, 2016). Subsequent conservation translocations were initiated with peregrine falcons (*Falco peregrinus*) in North America, North Island saddlebacks (*Philesturnus rufusater*) in New Zealand, and northern goshawks (*Accipiter gentilis*) in the United Kingdom (Seddon & Armstrong, 2016). These are among the first examples of *successful* conservation translocations. Because practitioners and researchers tend to publish successful efforts rather than unsuccessful efforts, there have been fewer published conservation translocation efforts relative to the number of actual attempts to reintroduce, reinforce, or rescue populations (Griffith et al., 1989; Wolf et al., 1996; Fischer & Lindenmayer, 2000).

Conservation Translocations

Reintroduction biology as a science emerged in the late 1980s and the early 1990s. In 1987, the International Union for Conservation of Nature (IUCN) Species

Survival Commission (SSC) released a "Position Statement on the Translocation of Living Organisms," where it outlined guidelines on reintroductions and called for more science on the subject (IUCN 1987). In 1986, Price published his book on the reintroductions of the Arabian oryx (*Oryx leucoryx*) in Oman that included defining and reviewing reintroduction literature. The following year, the Reintroduction Specialist Group (RSG) was formed, and Griffith et al. (1989) published their review of the translocation literature. In the early 1990s, the RSG held their first workshop, the result being the first set of IUCN reintroduction guidelines released in 1998 (IUCN, 1998). The last 20 years have seen a proliferation of science developed around species reintroductions and translocations (Seddon & Armstrong 2016). In 2018, the RSG changed their name to the Conservation Translocation Specialist Group (CTSG; IUCN/SSC CTSG: https://iucn-ctsg.org/).

Because of its relative infancy, there had been little consensus in terminology used in the conservation translocation field. Recently, Ewen et al. (2012), IUCN/SSC (2013), Jachowski et al. (2016a), and Gaywood et al. (2023) defined the terminology, summarized and synthesized the science, and highlighted avenues for progress, though debates are still ongoing (Novak et al., 2021). Imprecision of language is problematic (Fauth et al. 1996), so I will be using terminology from the aforementioned sources to frame my research within the conservation translocation literature (Ewen et al., 2012; IUCN/SSC, 2013; Jachowski et al., 2016a; Gaywood et al., 2023).

Reintroduction biology is a branch within conservation biology defined as the field of study restoring plant and animal populations through conservation translocations (Seddon et al., 2012). Conservation translocations are the broad term used to label the deliberate movement of plants and animals with the intention of benefiting the target species or ecosystem through quantifiable conservation measures (Seddon et al., 2012; IUCN/SSC, 2013). They differ from non-conservation translocations—non-lethal removal of nuisance animals, commercial and recreational translocations, aesthetics, religious purposes, wildlife rehabilitation, and animal rights activism liberations—in their intent: to conserve native wild, free-ranging populations (Seddon et al., 2012). Having now delineated the difference between conservation and non-conservation translocations, I will hereafter use the term "translocation" to refer exclusively to conservation translocations.

Translocations

There are three main types of translocations: reintroductions, reinforcements, and introductions (IUCN/SSC, 2013; Seddon & Armstrong, 2016; Gaywood et al., 2023). Reintroductions of plant and animal populations are defined as translocating and releasing individuals into areas that were once a part of their historic distribution from which they have been extirpated or become extinct in the wild (Seddon et al., 2012b; IUCN/SSC, 2013; Seddon & Armstrong, 2016). Reinforcements, also referred to as augmentations or supplementations, translocate and release plants and animals into existing populations to alleviate decline, inbreeding depression, etc. (Gaywood et al., 2023). In contrast, introductions translocate and release plants or animals into areas outside of the species' historic distribution. These efforts encompass assisted migrations, which involve translocating species into suitable habitat outside of the historic range to address human-induced threats (Seddon et al., 2012; Chauvenet et al., 2013). Ecological replacements involve introducing a species of equal ecological value outside of its own historic range and into the historic range of an extinct species to mimic the ecological role of that species in the ecosystem (Seddon et al., 2012).

Theoretical and Philosophical Basis for Translocations

The branch of science known as *conservation biology* is based on several philosophical foundations. Reiners and Lockwood (2010) proposed a model containing three main branches from which philosophical foundations in ecology—and, as an extension, conservation biology— can be derived: aesthetics, truth, and what is right/known. Aesthetics is delineated into nature, art, and ideas; truth is divided into ethics, politics, and justice; and what is right/known is divided into ontology, epistemology, and metaphysics (Reiners & Lockwood, 2010).

In any decision made within the context of conservation biology, there are underlying principles from which decisions stem (Reiners & Lockwood, 2010). One principle could be based on fairness or a moral right: the species has been extirpated or extinct in the wild, presumably due to anthropogenic influences, and has an inherent right to exist in the wild (Reiners & Lockwood, 2010). For a possible second principle, the selecting party could base a decision on a given species' importance amongst the natural systems they inhabit. A third could stem from the cultural or religious significance of that species.

However, conservation biology and translocation biology are typified by issues of scale. They are framed as historical sciences; researchers and practitioners base their actions upon a historical state of the species, population, ecosystem, etc. (Reiners & Lockwood, 2010; deLaplante et al., 2011). This has led to problems determining the spatio-temporal scale upon which to base the conservation goal because defining the historical state or spatial extent over which the conservation action is to be enacted can often be somewhat arbitrary (deLaplante et al., 2011). This subjectivity has caused skepticism from many philosophers assessing the scientific merit of conservation biology (deLaplante et al., 2011; Price, 2019), and much of the literature within the past two decades has included methods for incorporating systematic review or structured decision making to reduce subjective application of conservation management tools (Pullin & Stewart, 2006; Converse & Armstrong, 2016).

Often, this is characteristic of younger branches of science, relative to more established sciences (i.e. physics, mathematics, etc.), and Pickett et al. (2007) argued against using physics as a comparison upon which to determine the scientific merit of ecology. They argued that there are two differing viewpoints in the philosophy of science, referred to as the old and new scientific philosophies. The old philosophy bases "good science" on the notion of falsifiability; whether a statement made in science is falsifiable or not designates it from pseudoscience (Pickett et al., 2007). The new scientific philosophy paradigm encompasses probability in its tools for legitimizing statements in addition to maintaining a pluralistic view of science and not following the strict inductive chain commonly seen in physics (Pickett et al., 2007). By establishing this distinction, we can then move on to the specific philosophy dealing with translocation biology.

There are several theoretical assumptions and arguments for implementing translocations. In reintroductions, for example, one could argue that the existence of that species has a functional niche they occupy in a given system. Here, I am referring to the Hutchinsonian niche, where the species not only occupies a physical place within an ecosystem but also contributes to the function of that ecosystem and community structure (Hutchinson, 1957; Holt, 2009). Another argument could be that the species forms a portion of an intricate food web, connecting producers and consumers on multiple levels depending on the system they inhabit, and, in their absence, the web function would be inhibited on some continuous scale of effects or create potentially irreversible alternative states (Soulé, 2010; Vander Zanden et al., 2016).

The aforementioned assumptions could also be the case for reinforcements, however, there are also additional theoretical assumptions associated with reinforcing an existing population in the wild. In deciding to reinforce, the managers posit that there are factors inhibiting dispersal and population connectivity such that the population in question is at risk of extirpation due to declining population growth, inbreeding depression, etc. In the case of population dynamics, there is little-to-no emigration or immigration or adequate reproduction and recruitment are somehow inhibited from sustaining the population. This also could relate to source-sink dynamics, where variation in habitat quality may describe population vital rates, in that a certain population may exhibit sink-like characteristics (Dunning et al., 1992; Battin, 2004; Kauffman et al., 2004). These are common justifications for implementing a translocation program.

For introductions—assisted migration and ecological replacements—there are similar niche, food web, demographic, and dispersal bases. In assisted migration, the existing habitat provided for the species in question has become unable to sustain the population due to climate, invasives, etc. (Seddon & Armstrong, 2016). Thus, conservation planners have chosen to assist in translocating them to a novel area of similar characteristics. However, one could argue that the species may have not been present there for more reasons other than a lack of connectivity, in which case, those reasons must be addressed (IUCN/SSC, 2013). In ecological replacements, conservation planners aim to restore ecological functions and food web structure through translocating species theoretically able to replace the functional niche that was lost through the extinction of another species (IUCN/SSC, 2013, Ripple et al., 2014; Seddon & Armstrong, 2016).

Planning Translocations

Upon assessing the theoretical and philosophical reasons to employ conservation translocations, there are a number of considerations to address before committing to reintroducing, reinforcing, or introducing individuals for conservation benefits. The IUCN/SSC (2013) suggests that all translocations be adequately justifiable due to the inherent risks and costs involved. However, one cannot first assess the risks without holistically identifying their partners involved in making the decisions (Riley & Sandström, 2016).

When identifying partners involved in the translocation, one should not only identify the institutional dimensions, (i.e. government agencies, universities, etc.,), but should also consider the social dimensions (i.e. public values, politics, etc.; Dunham et al., 2016). Government wildlife management agencies may collaborate with university scientists to discuss the need for the translocations. Ultimately, however, the public, whether it be local private landowners or citizens in the surrounding area, will play an integral part in the sustaining of the translocations through their support, or lack thereof (Dunham et al., 2016; Riley & Sandström, 2016). Consider all stakeholders—persons who are potentially influenced by or have a “stake” in the translocations— during this phase (Decker et al., 1996). Riley and Sandström (2016) presented a conceptual framework for translocations. They heavily relied on the human dimensions throughout the process and argued that it is imperative to incorporate each party's input into the beginning phases of translocations (Moehrenschlager & Lloyd, 2016; Sampson et al., 2020).

Engaging the public and attempting to develop a comprehensive list of stakeholders will also aid in added funding conservation actions (IUCN/SSC, 2013; Dunham et al., 2016). Funding is not only important to begin the translocations, but also to sustain them throughout the number of years in which they are planned and to allow flexibility for additional years or monitoring needs (Chauvenet et al., 2013). In cases of translocating large carnivores or herbivores, additional funds for restitution of personal property losses, such as livestock or agriculture, should be included as well (Moehrenschlager & Lloyd, 2016). This will aid in mitigating the risks associated with funding translocated species.

The IUCN/SSC (2013) outlined the need for a risk assessment in the beginning phases of translocation. They define risk as "the probability of a risk factor occurring combined with the severity of its impact." There are additional inherent risks involved with most management actions in translocations. the categories of risks that should be addressed, include (1) ecological risks, in which a translocated species could have unexpected impacts on the ecosystem or other species,; (2) the potential for translocated species to spread disease to conspecifics or livestock within the release site and surrounding areas; (3) genetic risks, in which genetic drift has occurred between the translocated species and closely-related subspecies, resulting in potential lower fitness of offspring (more so for species introductions); (4) socio-economic risks, mentioned earlier where species may have impacts on livelihoods or even ecosystem services; (IUCN/SSC, 2013). Lastly, physiological and behavioral risks should also be considered for understanding how stress affects survival, movements, and reproduction of the translocated species (Stamps & Swaisgood, 2007; Dickens et al., 2009; Dickens et al., 2010; Jachowski et al., 2016b).

After assessing risk, it is then important to address the factors contributing to the original decline, extirpation, or extinction of the target species. If the factors, such as habitat loss or fragmentation, invasive predators, etc., have not been addressed or corrected, the translocation would not be justified and is considered unethical (IUCN/SSC, 2013). There are several international and national mandates that require proper justification. For example, the Convention on Biological Diversity requires "Contracting Parties"—those performing the translocations— to rehabilitate and restore degraded ecosystems and promote the recovery of threatened species through the development and implementation of plans or other management strategies (Osborne & Seddon, 2012). While looking at historical versus current needs of the target species, it is equally important to address the future needs and how those intersect with climate forecasting in that area (Osborne & Seddon, 2012).

Once partners and the associated risks involved in the translocations have been identified, researchers must justify translocation efforts through a set of clearly defined objectives. Across most of the translocation literature, this has been one of the least employed steps due to the difficulty of defining realistic and quantifiable objectives (Fischer & Lindenmayer, 2000; Chauvenet et al., 2016). Ultimately, the goal of a translocation is to establish or support a free-ranging, viable population; however, as written, this goal is vague and must be parameterized with measurable factors such as spatio-temporal scale (Seddon, 1999; Fischer & Lindenmayer, 2000, Armstrong & Seddon, 2008; Sutherland et al., 2010; Chauvenet et al., 2013; Chauvenet et al., 2016). Additionally, it is rare that translocation projects do not need further management (i.e. supplemental feeding, additional reinforcements, etc.) following the bulk of the effort (Chauvenet et al., 2013).

The IUCN/SSC (2013) recommended translocation plans explicitly define goals, objectives, and actions. A goal was defined as the ultimate intended result of the translocation in terms of the benefit and time period; an objective specifically outlined how the goal will be realized; and actions were quantifiable statements to carry out objectives that include details of time frame, participants, and accountability (IUCN/SSC, 2013; Brichieri-Colombi & Moehrenschlager, 2016; Chauvenet et al., 2016). Chauvenet et al. (2016) reviewed 129 translocation case studies and reported that only 50% of them had clear indicators of success and that, often, these indicators were not understood to be different than objectives. To remedy this, they recommended applying structured decision making (SDM) to planning translocations, where there is an established theoretical framework upon which to define the problem, formulate objectives, identify alternative actions, predict expected outcomes, and solve the decision problem using trade-offs (Chauvenet et al., 2016; Converse & Armstrong 2016). Incorporating an SDM framework in translocation programs allows researchers to use adaptive management to reassess actions and ensure a methodological way to learn from the process and improve upon it to inform future translocations.

Adaptive management is an iterative process of planning, assessing, and ameliorating methods that aid in addressing uncertainty (McCarthy et al., 2012; Converse & Armstrong, 2016). In translocations, sufficient sample sizes are not present for typical hypothesis testing of methods and often require researchers to learn the most effective methods within the same study (McCarthy et al., 2012). Adaptive management provides a structured framework of a process that researchers can take to address this need; the key features of this framework are: defining the problem by using explicit statements of measurable objectives; utilizing models and predictions to address the question despite uncertainty utilizing available data or inferred data from provided meta-analyses; implementing the method; monitoring the response; updating the uncertainty based on the response data and reviewing methods; and learning from results (McCarthy et al., 2012). Converse and Armstrong (2016) noted that structured decision making was the least utilized strategy in translocations and called for this improvement in future research.

Once goals, objectives, actions, and the SDM framework have been outlined, the specific methods of the translocation can be reviewed. In this step, guided by the best available science and biological knowledge of the species, researchers and stakeholders would define the methods of capture, release, and monitoring and including an exit strategy contingent upon certain factors or outcomes (IUCN/SSC, 2013).

Implementing Translocations & Evaluating Success

Upon completing the planning phase by addressing, identifying, and acquiring the necessary funding, stakeholders, habitat issues—including forecasted climate effects on habitat—, comprehensive risks involved, objectives, and frameworks for structured decision making and adaptive management, an organization can move to implementing the translocations. This is the phase where monitoring, evaluating, reviewing, and learning lead to adaptive management. Post-release monitoring is integral to any translocation and aids in assessing if any of the aforementioned risks occur (Nichols & Armstrong, 2012; Gitzen et al., 2016; Bubac et al., 2019). Utilizing the SDM framework to evaluate and reevaluate translocation efforts to dictate the length and eventual strategies for exiting will lead to the highest probability of success (IUCN/SSC, 2013).

Greater Sage-grouse Populations

Greater sage-grouse (*Centrocercus urophasianus*; sage-grouse) populations have declined across the range due to loss and fragmentation of sagebrush (*Artemisia* spp.) ecosystems (Schroeder et al., 2004; Aldridge et al., 2008; Miller et al., 2011). Concomitantly, the U.S. Fish and Wildlife Service (USFWS) has reviewed the species' status in consideration for protection under the U.S. Endangered Species Act (ESA) several times since 1999 (Stiver, 2011). However, in 2015, the USFWS determined the listing the species for ESA protection was unwarranted and precluded by other species due to the considerable range-wide conservation and research efforts (USFWS, 2015).

Range-wide conservation efforts included several translocations to prevent extirpations in many areas across the distribution from the early 20th century to present (Reese & Connelly, 1997; Stiver, 2011; Baxter et al., 2013; Whiklo & Nicholson, 2015; Bell & George, 2012; Alberta Environmental and Sustainable Resource Development (AESRD), 2013; Balderson, 2017; Duvuvuei et al., 2017; Ebenhoch et al., 2019; Lazenby, 2020; Meyerpeter et al., 2021). Translocation protocols for sage-grouse have remained nearly static since 1997. Reese and Connelly (1997) published a review on all sage-grouse translocation literature and outlined the best methods for translocation.

Protocols leading to increased success outlined within that document included the following suggestions: translocating sage-grouse overnight during the breeding season, releasing them on an active lek the morning of capture, release sites are isolated sagebrush habitat surrounded by non-habitat, and the release sites are located at least 100km from capture areas. Baxter et al. (2013) completed a six-year translocation project in Utah that added additional protocols to increase success: in areas where high predation rates were implicated as a significant factor contributing to the population declines, then predator control was shown to have increased probability of survival; however, predator control can only be considered as a short-term solution (Moehrenschlager & Lloyd, 2016).

Several new methods for translocation protocols have been developed within the last decade of sage-grouse conservation. Thompson et al. (2015) experimented reinforcing a sage-grouse population with captive-reared chicks released into wild surrogate broods and found evidence of success. Captive-reared chicks were adopted 88.7% by wild surrogate broods, and adopted chicks had similar survival rates as native chicks (0.42, 95% CI = 0.33 – 0.52; Thompson et al., 2015). This novel method aided to expand the possibility of protocols that could contribute to improving the translocation of sage-grouse. Schneider et al. (2019) developed a method of artificial insemination for use on pre-nesting female sharp-tailed grouse (*Tympanuchus phasianellus*) translocations in Nevada. Researchers in this publication tested the effectiveness of artificial insemination to aid in reducing the exploratory phase post-release and increase the possibility of nesting within the first breeding season post-translocation, of which a lower probability of reproduction post-release is often present in translocated animals (Dickens et al., 2009; Whiting et al., 2012; Jachowski et al., 2016b; Schneider et al., 2019).

In the translocations performed in the bi-state population located on the border of California and Nevada (2017-present), North Dakota (2017-2021), and Sheeprock Mountain, UT (2016-2019), researchers collaborated on improving range-wide protocols. In 2017 and 2018, we experimented with artificial insemination for pre-nesting sage-grouse females after Schneider et al.'s (2019) protocols (Chelak & Messmer, 2018; Lazenby, 2020). In addition, we developed and employed a "soft" or delayed remote release method at the lek sites to aid in mitigating additional stressors during the release portion of the translocation process (Dickens et al., 2009; Dickens et al., 2010; Lazenby, 2020). In the bi-state and North Dakota populations, beginning in 2017 and 2018, respectively, researchers built upon the methods of Thompson et al. (2015) in translocating wild-caught broods to further increase the probability of first-year translocated females adding to the target population's vital rates in addition to providing an incentive for those females to establish at the release site (Lazenby, 2020; Meyerpeter et al., 2021).

Dissertation Purpose

My dissertation aims to advance the field of translocation biology utilizing sage-grouse as a case study species within a remote, spatially isolated population in central Utah called the Sheeprock Mountain Sage-Grouse Management Area (SGMA). My research was completed as part of a multi-state collaboration with two other sage-grouse translocations in the bi-state and North Dakota. Along with the translocation in central Utah, these three populations represent the western, southern, and eastern edges of the species' current range, and will serve to improve the current knowledge and methods of translocations for sage-grouse range-wide. Using sage-grouse as a case study species, we are contributing to the field of translocation biology by progressing from the descriptive to the inferential phases to aid in predicting how best to reinforce sage-grouse populations.

Study Area

My research is based in the Sheeprock Mountain SGMA in central Utah. Eleven SGMA's were established in Utah in 2013, in which more than 90% of the combined Utah population of sage-grouse resides and represent the highest breeding density areas (Dahlgren et al., 2016; PLPCO, 2019). The Sheeprock Mountain SGMA is located at the eastern edge of the Great Basin and precedes Utah's West Desert (Figure 1-1). It is an area comprised of 611,129 acres located in both Tooele and Juab counties and exhibits a mixed patch framework of land ownership that includes Bureau of Land Management (BLM), U.S. Forest Service (USFS), private, Utah School and Institutional Trust Lands (SITLA), and Utah Department of Wildlife Resources (UDWR). Given the multiple land ownerships, a local working group, the West Desert Adaptive Resource Management (WDARM) group, was established to facilitate frequent dialogue and collaboration amongst all stakeholders on conservation issues related to sage grouse and other sensitive wildlife.

This area is characterized by warm, dry summers and cool winters. The 50-year average maximum summer temperature is 32.4 ˚C in July, and the minimum winter temperature is -10.4 ˚C in January (Figure 1-2). The average annual precipitation is 10.24

inches, with the highest amount being in the spring and fall months (Figure 1-2). Average snowfall is 36.2 inches (Western Regional Climate Center, 2016).

Elevation ranges from 1500 m in the lower valleys to 2950 m at the tallest peak. The lower elevation vegetation is comprised of bulbous bluegrass (*Poa bulbosa*), crested wheatgrass (*Agropyron cristatum*), gray horsebrush (*Tetradymia canescens*), intermediate wheatgrass (*Thinopyrum intermedium*), rubber rabbitbrush (*Ericameria nauseosa*), sandberg bluegrass (*Poa secunda*), Wyoming big sagebrush (*A. tridentata* w*yomingensis*; Robinson, 2007; Robinson & Messmer, 2013). Invasive vegetation located in the lower elevation includes bur buttercup (*Ceratocephata testuculata*), cheatgrass (*Bromus tectorum*), desert madwort (*Alyssum desertorum*), knapweed (*Centaurea* spp.), redstem stork's bill (*Erodium cicutarium*), and tansy mustard (*Descurainia pinnata*; Robinson 2007; Robinson & Messmer 2013). As precipitation increases with elevation, mesic vegetation becomes more prevalent, including aspen (*Populus tremuloides*), antelope bitterbrush (*Purshia tridentata*), blue-eyed Mary (*Collinsia parviflora*), bulbous bluegrass (*Poa bulbosa*), common snowberry (*Symphoricarpos albus*), crested wheatgrass (*Agropyron cristatum*), Douglas rabbitbrush (*Chrysothamnus viscidiflorus*), Great Basin wildrye (*Leymus cinereus*), intermediate wheatgrass (*Thinopyrum intermedium*), juniper (*Juniperus* spp.), mountain big sagebrush (*A. t. vaseyana*), pinyon pine (*Pinus* spp.), and serviceberry (*Amelanchier alnifolia*; Robinson, 2007; Robinson & Messmer, 2013). Higher elevations, along ridgelines, are dominated by black (*A. nova*) and low sagebrush shrubs (*A. arbuscula*; Robinson, 2007; Robinson & Messmer, 2013).

Sage-grouse populations typically oscillate on 9-12-year cycles from peak to peak (Garton et al., 2011). In Utah's populations, between 2006-2015, all eleven SGMA's exhibited gradual declines from the peak around 2006 to trough around 2011; however, when most populations began to increase following the trough, the Sheeprock SGMA continued to decline. In the 2006 breeding season, 190 males were observed across 5 active leks in the SGMA (Robinson, 2007; Robinson & Messmer, 2013), and this declined to 23 males across 3 active leks by year 2015 (UDWR, unpublished data; Figure 1-3).

Given these trends, the stakeholders within the WDARM met and discussed avenues for immediate action to prevent extirpation of the Sheeprock sage-grouse population. Both the WDARM and USU worked to establish the goals, objectives, and actions for this population. The ultimate goal was to prevent population extirpation within the research period between 2016-2020—and beyond this time frame—and assess areas for future habitat improvements, to mitigate loss and fragmentation of remaining habitats. This goal was realized through the following objectives:

1. Employing translocations with males and pre-nesting females for multiple years during the lekking season
2. Estimating the Sheeprock population's demographics; monitoring translocated and resident individuals' survival, movements, reproduction, and habitat selection
3. Estimating the Sheeprock population's genetics for insights into any reduction in genetic heterogeneity
4. Implement habitat management projects designed to improve nesting and brooding habitat and reduce fragmentation
5. Implement predator control

6. Evaluating whether off-highway recreation affects habitat selection

The actions outlined for this translocation project are the following:

1. USU, UDWR, and volunteers translocate 40 marked individuals (30 pre-nesting females and 10 males) per year in the lekking season from two genetically compatible populations in Utah from 2016-2019
2. USU, UDWR, and volunteers mark up to 10 residents (8 females and 2 males) per year from 2016-2019
3. USU measures vital rates of translocated and marked individuals every 2-3 days during the breeding season (lekking, nesting, and brooding from March to August) 2016-2020
4. USU collects genetic samples from all marked individuals and each marked individual's nest to evaluate effects of translocated individuals on resident genetics from 2016-2020
5. Federal and state partners employ habitat restoration projects from 2016-2020 (and after) to reduce habitat fragmentation and loss due to conifer expansion, invasive expansion, and fire
6. USU performs off-highway vehicle recreation needs-based surveys and study area use through GPS loggers 2018-2020
7. Wildlife Services perform predator removal of ravens, red fox, and coyotes to contribute to successful individual, nest, and brood survival from 2016-2020;
8. USU evaluate the movements, habitat selection, and population vital rates from 2016-2020 to assess translocated and resident population status.

Evaluating the success of some of these goals, objectives, and actions is also a portion of this dissertation, though, monitoring the Sheeprock population through lek counts will continue yearly beyond the end of this study.

Dissertation Outline

This dissertation is comprised of three stand-alone research products. In Chapter 2, I compare the functionality and effectiveness of two GPS transmitters most commonly deployed on sage-grouse using data from Utah and Wyoming collected between 2011-2019. Metrics explored include daily fix inefficiency (excluding nesting), the number of 1-day fix gaps, and transmitter loss rates in the field. In addition, I evaluated transmitter functionality during the sage-grouse nesting period: daily nesting fix inefficiency, fix error distance mean and standard deviation (i.e., accuracy and precision), and mean fix error direction. It is critical to evaluate transmitters deployed on wildlife, especially for translocations. Knowing the expected fix error for each transmitter can inform data screening in preparation for analysis to account for fix error bias associated with nesting and non-nesting individuals (Nielson et al., 2009; Patterson et al., 2010; Ranacher et al., 2016). Accurately accounting for known fix errors inherent in GPS data improves the inference at which researchers can understand free-ranging animal individual- and population-level behavior and movement, demographics, predator-prey dynamics, and human-wildlife conflict (Latham et al., 2015).

Chapter 3 utilizes post-release monitoring data of translocated global positioning system (GPS)- marked sage-grouse within the Sheeprock SGMA from 2016-2020 to assess the effects of off-highway vehicle (OHV) recreation traffic estimates, landscape characteristics (e.g., slope or elevation), vegetation cover, roads, etc. on habitat selection of the translocated individuals post-release. Individuals' behavior was separated into exploratory and restricted movements before performing a movement-based habitat selection. This aids in identifying dispersal patterns for translocated individuals based on release-site within the study area, identifying seasonal movements to and from wintering areas, and identifying future release sites within the SGMA if further translocations are planned.

Chapter 4 is a demographic and genetic analysis of the Sheeprock population that uses both metrics to evaluate the success of the translocations within the period studied, 2016-2020, where the translocations were performed in 2016-2019. The demographic portion utilizes an integrated population model (IPM) framework for both the source populations and reinforced population with 18 years of male peak lek count data (2005 – 2022) combined with five years of in-depth population monitoring with marked individuals (2016 – 2020) to estimate before-after impact (BA) population demographic effects on each population. Using these data, we project expected population size of the Sheeprock SGMA population to 2027. We utilize genetic data collected prior to the translocation (2005-2015), and compare it with post translocation samples (2016-2020) to assess changes in genetic diversity resulting from the translocation.

Lastly, Chapter 5 concludes my dissertation and summarizes the lessons learned from this research's findings, and highlights avenues for future research in recommendation for management within the Sheeprock SGMA.

Appendix A includes a note on a case of aspergillosis, a fungus that develops in birds' air sacs that leads to death in wild individuals, found in a female in 2018. This work was published in Western North American Naturalist in November 2020. Appendix

B includes the supplementary information for the statistical methods and results that were not central to the story in Chapter 2 but were relevant for reviewing the validity of the analysis. Appendix C includes the supplementary information for Chapter 3 that provides the specifics involved in measuring and modeling the off-highway vehicle daily count estimates. Appendix D includes the supplementary information for the statistical methods and results that were not central to the story in Chapter 4 but were relevant for reviewing the reproducibility of the analysis.

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Figures

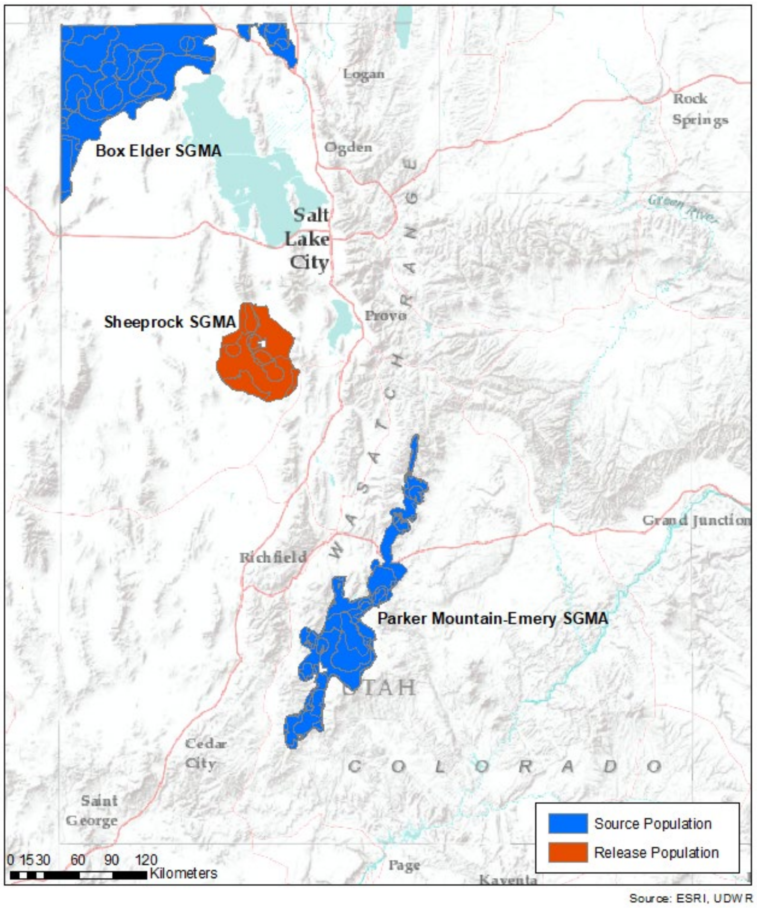

Figure 1-1 The release site population and source populations utilized for the Sheeprock Mountain Sage-Grouse Management Area (SGMA), Utah translocations to reinforce the resident greater sage-grouse (*Centrocercus urophasianus*) population. The sage-grouse were translocated 2016-2019 from both Park Valley, located in the Box Elder SGMA, and Parker Mountain, located in the Parker Mountain-Emery SGMA.

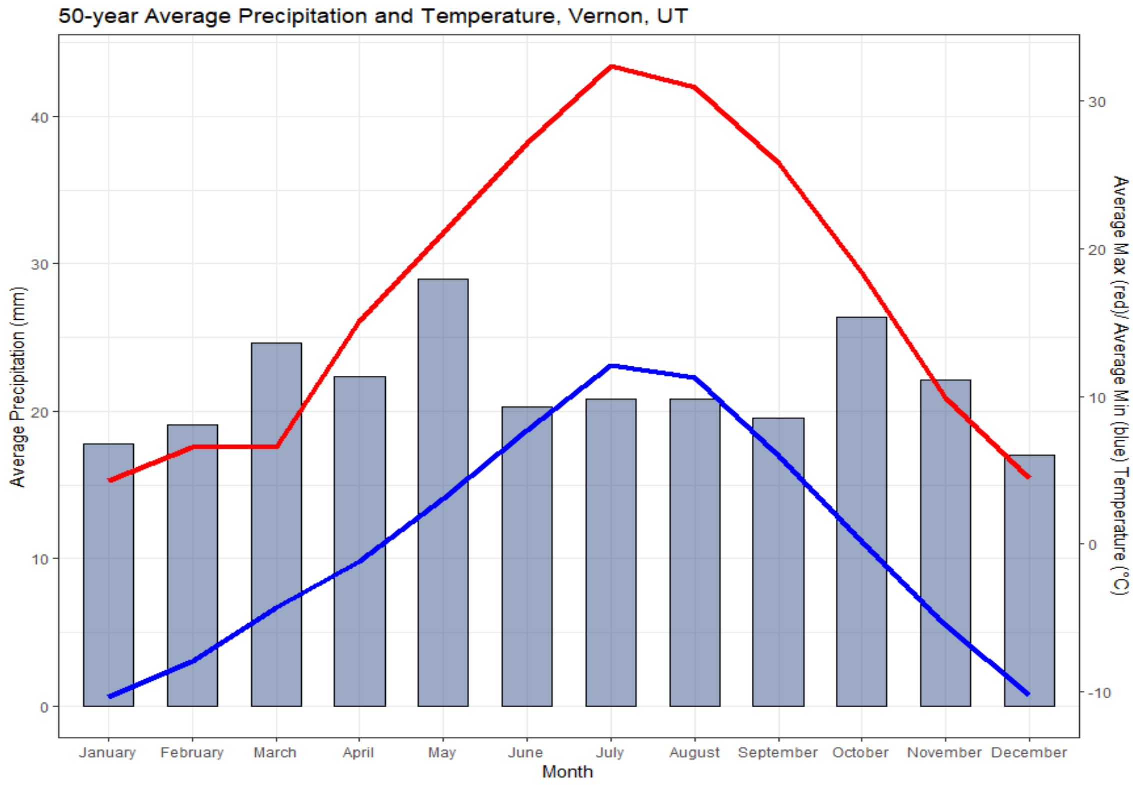

Figure 1-2. The 50-year average minimum (blue) and maximum temperatures (red; degrees Celsius) and average annual precipitation (millimeters) per month for the Sheeprock Mountain Sage-Grouse Management Area as collected by Western Regional Climate Center in Vernon, Utah (Western Regional Climate Center 2016).

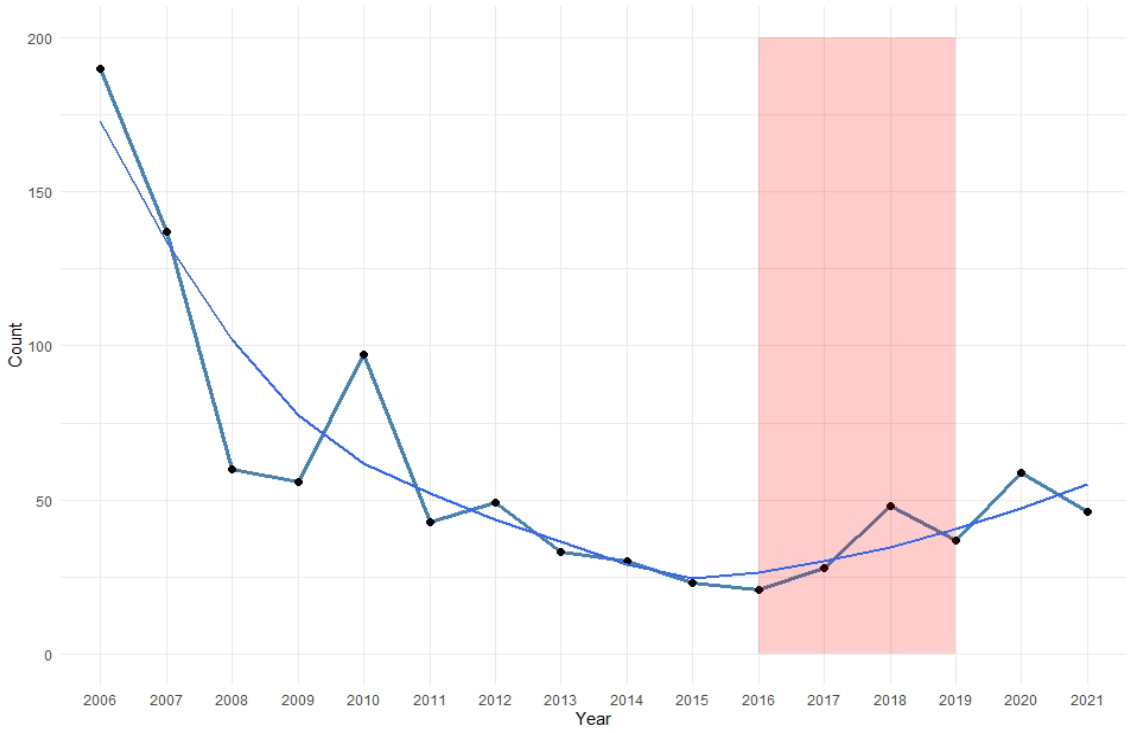

Figure 1-3. Peak male greater sage-grouse (*Centrocercus urophasianus*) lek counts in the Sheeprock Mountain Sage-grouse Management Area from 2006-2021. Translocations (blocked in red) were performed from 2016-2019.

CHAPTER 2

REFURBISHING USED GPS TRANSMITTERS IMPROVES PERFORMANCE FOR SUBSEQUENT DEPLOYMENTS ON GREATER SAGE-GROUSE

ABSTRACT

Global Positioning Systems (GPS) radio transmitters are increasingly used in research across taxa to monitor animal populations. However, transmitters can be susceptible to malfunctions that may result in location errors, data loss, and, thus, potential inferential bias that can have important implications for monitored species. Research using GPS transmitters on greater-sage grouse (*Centrocercus urophasianus;* sage-grouse) has increased precipitously, but few studies have evaluated GPS performance. Because sage-grouse have been subject to intense legal/political scrutiny with consequential economic implications, reliable data acquisition is central to the species' management. I evaluated differences in the performance of two commonly used solar-powered GPS transmitters (Microwave Telemetry, Inc. [MTI], GeoTrak, Inc.) deployed on sage-grouse populations throughout Wyoming from 2011–2017 and Utah from 2013–2019. This investigation of GPS performance included daily fix inefficiency, the number of 1-day fix gaps, and transmitter loss rates in the field. In addition, I evaluated transmitter functionality during the nesting period: daily nesting fix inefficiency, fix error distance mean and standard deviation (i.e., accuracy and precision), and mean fix error direction. New and refurbished MTI transmitters outperformed GeoTrak transmitters in daily fix inefficiency and day gaps during most seasons except for winter. Cumulatively redeployed MTI transmitters did not perform differently than GeoTrak transmitters. Transmitter loss, daily nesting fix inefficiency, and nest fix precision did not vary significantly between the two transmitters. GeoTrak performed better than MTI for nest fix accuracy across all latitudes (40-45°N). The mean error direction to the nest location ranged between 105° and 135° for GeoTrak and between 135° and 155° for MTI. I recommend refurbishing transmitters following deployment to retain higher fix efficiency than cumulatively redeploying transmitters.

KEYWORDS GPS, fix success, solar-powered GPS, greater sage-grouse, *Centrocercus urophasianus*, location error, GPS accuracy, sage-grouse nesting

Fish and wildlife population monitoring has been greatly influenced by the advent of global positioning systems (GPS) technology, especially since the early 2000's. Increased GPS use has primarily been driven by the desire to acquire better knowledge to inform managers and researchers about target species (Frair et al. 2010, Latham et al. 2015). Data acquired from GPS transmitters can reveal fine-scale patterns of space use, behavior, population dynamics, and predator-prey interactions (Kays et al. 2015), while at the same time reducing telemetry bias and improving accuracy and precision beyond that available from unmarked individuals or those marked with very-high frequency (VHF) transmitters. These technological advances have allowed researchers to address new and important questions related to animal behavior that are quickly contributing to changes in management directives and policies (e.g., Wyoming Migration Initiative https://migrationinitiative.org/, Utah Migration Initiative https://wildlifemigration.utah.gov/, Audubon Society's Bird Migration Explorer https://explorer/audubon.org). The decade from 2010 to 2020 witnessed a massive increase in the use of GPS transmitters and has thus been deemed the beginning of the "golden age" of fine-scale data acquisition for fish and wildlife populations (Kays et al. 2015, Hofman et al. 2019).

Growth in GPS transmitter market demand has sparked a diverse array of transmitter production companies, with > 40 globally producing GPS transmitters for animal research (Table B.1, available in Supporting Information). Costs per transmitter range between 1,000 and 5,000 USD, with smaller units costing more due to the increased cost of smaller hardware. Other unforeseen costs can include monthly data fees for data acquisition. These high costs, weighed against the value of the resulting data, make it essential to evaluate variation in GPS data reliability (Hebblewhite and Hayden 2010).

GPS data reliability and consistency dictate the accuracy of movement, habitat selection, and vital rate estimates (Cagnacci et al. 2010, Christin et al. 2015, Kays et al. 2015). Reliability and consistency are quantified through functionality, i.e., the transmitter's ability to record and transfer data as expected (Frair et al. 2010, Camp et al. 2016, Jung et al. 2018). Measures of GPS functionality include unit longevity and two primary sources of error: spatial error and fix error (Frair et al. 2010, Camp et al. 2016). Longevity among GPS units with non-rechargeable batteries is a function of the frequency of scheduled fixes, battery charge capacity, and ambient temperatures. For solar rechargeable units, longevity is determined by the battery capacity and frequency of scheduled fixes, traded off against access to solar radiation. Spatial error, termed "[in]accuracy" or "[im]precision", describes a registered fix that is not representative of an animal's estimated actual or approximate location (Frair et al. 2004, Cagnacci et al. 2010, Williams et al. 2012). Spatial errors can be categorized as minor (10-30 meters) or large (several kilometers or less) and must be removed or corrected before analysis (Frair et al. 2010, Morris and Conner 2017). Fix errors can describe failed location attempts, such as when the GPS transmitter attempted to register a fix and failed (Frair et al. 2010), or spurious fixes produced outside of scheduled fix acquisition times (Thomas et al. 2011).

Internal and external variables can affect GPS transmitter functionality, including longevity and spatial and fix errors. Internal variables include hardware- or software-based issues such as battery charge (Silva et al. 2017), insufficient communication with available satellites (Ranacher et al. 2016), transmitter age (García-Jiménez et al. 2020), and the fix schedule (e.g., Acácio et al. 2022). External variables can include latitude (Jung et al. 2018), vegetation characteristics (e.g., Liu et al. 2018), topography (e.g., Ironside et al. 2017), animal species and behavior (see Hofman et al. 2019), climate (e.g., Schlippe Justicia et al. 2018), season (e.g., Silva et al. 2017), and solar time (e.g., Byrne et al. 2017). Many studies recommend data screening to account for errors associated with these variables (Lewis et al. 2007, Villepique et al. 2008). However, researchers must evaluate their transmitters' performance to inform their data screening process and account for errors.

Between 2007 and 2010, many researchers began using GPS transmitters on greater sage-grouse (*Centrocercus urophasianus*: 'sage-grouse') throughout the western United States and Canada (Stringham 2010, Dzialak et al. 2011, Fedy et al. 2012). Sage-grouse, the largest grouse species in North America, are a sagebrush (*Artemisia* spp.)-obligate galliform regarded as an indicator species of sagebrush ecosystem health (Rowland et al. 2006, Carlisle et al. 2018, Smith et al. 2021). Continuous range-wide population declines (i.e., 80%, Coates et al. 2021) have resulted in multiple Endangered Species Act (ESA) listings since 2002, ultimately leading to large-scale research and collaboration efforts aimed at better understanding sage-grouse ecology and highlighting possible avenues for conservation (Connelly et al. 2011a, Duvall et al. 2017).

These research efforts fitted sage-grouse with GPS transmitters to address critical conservation and management questions (Wann et al. 2019, Kirol et al. 2020). Despite numerous studies using GPS transmitters to monitor sage-grouse populations, researchers have yet to evaluate transmitter performance to the best of my knowledge. Here, I utilize a large dataset compiled from 15 study areas in Utah and Wyoming to assess the functionality of the two most commonly-used 22 g solar-powered GPS-Argos Doppler (GPS) transmitters, one from GeoTrak, Inc. (Model #: GT-22GS-GPS https://www.geotrakinc.com/, Apex, NC, USA) and the other from Microwave Telemetry, Inc (MTI; Model #: PTT-100-22 Argos-GPS https://www.microwavetelemetry.com/, Columbia, MD, USA). Specifically, I compared transmitters regarding daily fix inefficiency, day gaps, and loss rate. I also assessed inefficiency during the nesting period through fix precision and accuracy with known nesting locations.

STUDY AREA

I used data from sage-grouse transmitter studies at 15 study areas (Utah = 13; Wyoming = 2; Table 2-1). Sage-grouse studied in the Bighorn Basin (Table 2-1) were located in Wyoming and a southern portion of Montana, but I refer to these grouse as “Wyoming” for simplicity. For detailed information regarding prevailing climate regimes, elevational bands, and species of sagebrush that dominate these sites, see the references in Table 2-1.

METHODS

Field Sampling

Capture and marking

Grouse in all studies included in this analysis were marked with solar-powered GPS-Argos satellite transmitters mounted on the rump to monitor their space use and vital rates (Bedrosian and Craighead 2007; Figure 2-1). In Utah, researchers from Utah State University (USU) and Brigham Young University (BYU) mounted GPS transmitters on 469 sage-grouse from 2013–2019. In Wyoming, University of Wyoming (UWyo) researchers mounted GPS transmitters on 133 sage-grouse from 2011–2017. Male and female sage-grouse were captured at night near active leks (2100 hr to 0500 hr; Connelly et al. 2003) using all-terrain vehicles, spotlights, and long-handled nets. Sage-grouse were either processed at the capture site and released or brought to nearby processing areas. Processing included aging, sexing, weighing, leg banding, recording capture locations (UTM, 12N, NAD 83), and attaching transmitters. Some MTI GPS transmitters included ultra-high frequency (UHF) capabilities to allow for relocating marked birds in the field, and the GeoTrak GPS transmitters included a 3-g VHF transmitter epoxied to the side of the GPS transmitter. Each GPS transmitter weighed 22 g without harness straps and approximately 33 g with straps included. All sage-grouse were captured and marked per approval from the respective agencies and educational institutions (see Ethics statement).

Scheduled fixes occurred at 00 minutes for all fix schedules. The manufacturer programmed fix schedules between 4 and 10 daily fixes according to specific project objectives and seasons. GPS units from both manufacturers transmitted fixes to the Argos satellite system according to a pre-determined duty cycle that ranged from 3 to 8 days (Table B.2). Before deployment, GeoTrak and MTI manufacturers required that users charge transmitters for 2 and 5 days, respectively, at a 45-degree angle facing south to ensure the most direct sun exposure for battery charging.

Nest sampling

Researchers monitored all instrumented females 2 to 3 times weekly during the nesting season to determine the nest initiation date. Once observers confirmed a female was nesting, they monitored the nest until failure or hatch, after which they registered a GPS coordinate using a handheld GPS unit at the site of the nest. Handheld GPS unit models varied, but I assumed all types had a GPS error < 5 m.

Due to differing vegetation measuring methods between the 3 universities, I only included USU and UWyo vegetation data. Researchers measured nest shrub height (cm) and diameter (cm) for each nest site using line intercept (Canfield 1941, Connelly et al. 2003) to determine average shrub cover and height (cm) across a 15-m radius from the nest site.

Using remotely sensed satellite data, I calculated the average slope, aspect, and roughness within an approximately 18-m radius—determined to best incorporate the 15-m radius for vegetation measurements—around each nest location using the approximately 6-m^2 raster layer (highest zoom level 14 in function the *get_elev_raster()* function in R's *raster* package [Hijmans 2022; R core team 2022], which accesses products from the U.S. Geological Survey's 3D Elevation Program).

Data Screening

I assembled and cleaned raw GPS data according to each fix schedule. I first subset the GPS dataset to eliminate fixes collected in the first 2 or 7 days for resident or translocated birds (i.e., Sheeprock Sage-grouse Management Area translocations), respectively, after the last-known alive location (LAL) or after the analysis cutoff date (0559 UTC on 1 Mar 2019). I censored locations following capture to allow individuals to acclimate to the transmitters and prevent potential bias associated with this period. I visually inspected the data to identify clusters of locations indicating mortalities to assign the LAL. If transmitters went offline with no apparent mortality upon inspection in the field, I assigned the last recorded location as LAL.

I then used a sequence of data cleaning steps to remove unscheduled or outlier data, which I term 1) non-hour, 2) duplicate time, 3) incorrect schedule, and 4) spatial outlier locations. See *Data Screening Steps* in Appendix C for specific details and justification. Additionally, I separated non-nesting and nesting GPS data to avoid underestimating overall functionality simply because functionality among nesting individuals was low due to proximity to high vegetation cover.

Analyses

I modeled all response variables of interest (e.g., daily fix inefficiency, day gaps, etc.) using a top-down approach guided by hypothesized effects to assess model fit (Burnham and Anderson 2002). I selected model combinations from a global model, including additive effects of all covariates, along with up to 3-way interactions between covariates. I assessed correlations among all pairs of covariates using Pearson's correlation coefficients and included covariates with correlations whose absolute values were below

0.6. Highly skewed continuous variables were log-transformed to improve symmetry. For the mixed effects models (all excluding transmitter loss, see below), I considered all candidate models that fell within 7 ΔAICc of the best model to be competitive (Cavanaugh and Neath 2019). All generalized linear mixed-effects models were fit using the *glmmTMB* 1.1.5 package (Brooks et al. 2017) in R 4.2.1 (R core team 2022). I ran linear mixed-effect models in the *lme4* 1.1-30 package (Bates et al. 2015) in R 4.2.1 (R core team 2022). I report covariate results in terms of beta estimates and 95% CIs. I evaluated model fit and assumption violations (including zero-inflation and overdispersion) using randomized quantile residuals generated through the *DHARMa* package (Hartig 2022) in R. If several models yielded similar AICc values and similar *DHARMa* residual plots, I favored the most parsimonious predictor variable combination. If any coefficients were found to have non-significant p-values with 95% confidence intervals (CI) that included zero, I assessed model versions with and without them, comparing their respective AICc values and *DHARMa* plots to determine the best-fit model. Models with zero-inflation were refit using a zero-inflated structure capturing two processes: a process describing whether the device could take any fixes in a given day and a second process describing the number of scheduled fixes that occurred, given that any fixes were possible.

Daily fix inefficiency

I calculated daily fix inefficiency as the proportion of the unsuccessful fixes registered out of the number of scheduled fixes across the window of dates over which the transmitter was deployed and included multiple deployments, if applicable. The device registered all scheduled fixes successfully when there was zero daily fix inefficiency. I modeled inefficiency on the daily scale rather than the single fix scale because I deemed daily fixes the most broadly relevant for modeling sage-grouse location data (e.g., daily survival monitoring).

Daily fix inefficiency was modelled as a zero-inflated binomial generalized linear mixed effects model (GLMER). For the zero-inflation model, I relied on hypothesis-driven notions about what might drive the tendency to exhibit more zeros. I evaluated GPS Company, transmitter deployment status at the beginning of the deployment (new, cumulative (e.g., redeployed), or refurbished), calendar-based meteorological season (Spring = 1 March – 31 May, Summer = 1 June – 31 August, Fall = 1 September – 31 November, Winter = 1 December – Feb 28/29). For the conditional model, I considered GPS company (MTI or GT), transmitter status at the beginning of the deployment (new, cumulative [e.g., redeployed], or refurbished), calendar-based meteorological season (Spring = 1 March – 31 May, Summer = 1 June – 31 August, Fall = 1 September – 31 November, Winter = 1 December –28/29 Feb), cumulative photoperiod summarized over the preceding 7 days (photoperiod), and either deployment length or cumulative deployment length as possible fixed effects in the conditional model. I included random intercepts for bird ID and study area in the conditional model.

Transmitter status was delineated as follows: new, never deployed; cumulative, redeployed without being sent to the manufacturer; and refurbished, sent to the manufacturer for hardware and software updates prior to redeployment. I computed the daily photoperiod using the date, latitude, and longitude in WGS84 for each fix location from the package *meteor* 0.3-4 (Hijmans 2019) in R 4.2.1 (R core team 2022). I calculated the rolling summation of the previous 7-day photoperiod length because the solar-powered battery relies on approximately 3 to 5 days of quality solar exposure and may be affected by previous days' availability rather than the photoperiod length on that specific day, and I added a 2-day buffer. Deployment length was the number of days a transmitter was deployed on one sage-grouse from the capture date to the known/estimated end date. I obtained cumulative deployment length by calculating the total number of days that unit was deployed across multiple individuals. For refurbished units, I reset the cumulative deployment length to zero upon redeployment.

Day gaps

To calculate the number of full 24-hour data gaps, I counted the number of calendar dates in which no location fix was recorded (“day gaps”) per deployment. I modeled the number of day gaps as a GLMER with a log link, containing a random effect for bird ID and log(deployment days) as an offset. I considered GPS Company, transmitter status, the proportion of days spent in low photoperiods, and either deployment length for that individual's deployment or cumulative deployment length as potential fixed effects. Because day gaps are summarized per deployment, I calculated the quantiles of the photoperiod distribution. I reported the percentage of time the transmitter had spent in photoperiods ≤ 25% percentile, considering this a low photoperiod.

Daily nest fix inefficiency

Daily nest fix inefficiency was the proportion of unsuccessful fixes registered out of the number of scheduled fixes between the nest initiation and end dates. I used a zero-inflated binomial GLMER with a random effect for the transmitter serial ID. For the zero-inflated model, I evaluated GPS company, number of days incubating, shrub height or shrub cover, and either the slope or topographic roughness around the nest. For the conditional model, I evaluated GPS company, transmitter status, cumulative photoperiod over the previous 7 days (i.e., 7-day photoperiod), the year the transmitter was manufactured, nest shrub height and diameter (see Nest Sampling), deployment length or cumulative deployment length, number of days nesting, average 10- or 15-meter radius shrub cover and height (see Nest Sampling), and average 18-meter radius slope, aspect, and roughness as fixed effects. To account for differences between university vegetation measuring methods, I considered a categorical "method"(e.g., USU or UWyo) fixed effect to account for any variation between methods. However, it was not significant and thus I removed it.

Fix Error Mean and Standard Deviation

To estimate nest fix error distance mean (i.e., accuracy) and standard deviation (i.e., precision) of transmitters, I calculated the mean and standard deviation of the distance between the known nest location and all registered locational fixes while the focal bird was nesting. I modeled both nest accuracy and nest precision as linear mixed effects models. I log-transformed the fix error mean and square-root transformed the fix error standard deviation. I considered GPS Company, transmitter status, nest location latitude, nest shrub height and diameter, deployment length or cumulative deployment length, number of days nesting, average 10- or 15-m radius shrub cover and height, and average 18-m radius slope, aspect, and roughness as potential fixed effects. I considered Bird ID per study area as a random effect. I performed the same test for university vegetation measurement method outlined above, and method again had no effect.

Transmitter Loss

I assessed transmitter loss as the total number of days a transmitter was active until a loss when it no longer transmitted fixes and was not found in the field upon investigation. Transmitters still deployed on a sage-grouse at the analysis cutoff date (1 Mar 2019) or associated with confirmed sage-grouse mortalities were censored. Sometimes, devices were not recoverable in the field because they no longer transmitted, so I could not consistently identify the cause of device loss and, therefore, did not pursue "cause-specific" loss analyses.

I assessed transmitter loss with a Cox proportional hazards (CoxPH) model (Andersen and Gill 1982) fit using the *survival* 3.4-0 package (Therneau 2022) in R 4.2.1 (R core team 2022). I considered the GPS company, the year the transmitter was new (2011–2018), and either the number of times the transmitter was refurbished or the number of times the transmitter was deployed as potential fixed effects. I considered the manufacturer year because I expected varying performance due to hardware (e.g., battery technology) and software changes between 2011 and 2019. I compared candidate models with Akaike's information criterion adjusted for small samples (AICc). Then I evaluated each model's beta residuals using the *ggcoxdiagnostics* function in the *survminer* 0.4.9 package (Kassambara et al. 2021), Schoenfeld individual tests using *cox.zph* in *survival* 3.4-0, analysis of deviance tables, test statistics, beta estimates, and p-values. If any models yielded similar AICc, I relied on the most parsimonious equation of predictor variables.

RESULTS

Daily Fix Inefficiency

I modeled daily fix inefficiency using 139,899 daily observations across 506 marked sage-grouse between 2011 and 2019. The top model included a zero-inflation formula with an additive effect for season and an interactive effect of GPS company by transmitter status (Table 2-2). Summer (β = 0.41, 95% CI = [0.37, 0.45]) and fall (β = 0.08, 95% CI = [0.02, 0.12]) had higher probabilities of zero-miss-days than spring, though the effect was higher for summer. Winter (β = -0.18, 95% CI = [-0.23, -0.14]) had a lower probability of zero-miss-days. New (β = 0.24, 95% CI = [0.19, 0.29]) and refurbished (β = 0.39, 95% CI = [030, 0.48]) GeoTrak transmitters had a higher probability of zero-miss-days than when cumulatively redeployed. Cumulatively redeployed MTI (β = -0.69, 95% CI = [-0.75, -0.62]) transmitters performed worse than cumulatively redeployed GeoTrak transmitters. New (β = 0.57, 95% CI = [0.52, 0.62]) and refurbished (β = 1.77, 95% CI = [1.69, 1.84]) MTI transmitters exhibited a higher probability of zero-miss-days than cumulatively redeployed GeoTrak transmitters.

The conditional model contained an additive effect for the log of cumulative deployment length, interactive effects for GPS company and season, and a nested random effect for birds per study area (Table 2-2). As the logged cumulative deployment length of the transmitter increased, the daily fix inefficiency increased (β = 0.15; 95% CI = [0.14, 0.17]). GeoTrak transmitters in the summer (β = 0.20; 95% CI = [0.31, 0.39]), fall (β = 0.35; 95% CI = [0.31, 0.39]), and winter (β = 0.46; 95% CI = [0.42, 0.50]) exhibited higher fix inefficiency than during the spring, with winter exhibiting the most considerable effect. MTI transmitters exhibited a lower unsuccessful fix probability than

GeoTrak transmitters (Figure 2-2). This relationship was consistent across all seasons except for winter, when GeoTrak transmitters' spring performance did not differ (Figure 2-2; β_{MTI}= 0.12; 95% CI = [-0.34, 0.41]).

Day Gaps

The day-gap dataset included 139,407 individual transmitter days across 547 deployments between 2011 and 2019. The best-fit model included additive effects for the GPS company, the proportion of days spent in low photoperiods, transmitter status, and the log-transform of cumulative deployment length with a random effect for bird ID (Table 2-2). MTI exhibited 1.5 times fewer day gaps than GeoTrak (95% CI = [-1.84, -1.12]). Every 1-unit increase in the log-transform cumulative deployment length led to 0.5 more day gaps (95% CI = [0.30, 0.70]). Increasing the proportion of time a transmitter had spent in low photoperiods increased the expected day gaps (Figure 2-3). New and refurbished transmitters exhibited fewer day gaps than cumulatively deployed transmitters, which is valid for both GeoTrak and MTI transmitters (Figure 2-3).

Daily Nest Fix Inefficiency

Daily nest fix inefficiency included a dataset of 2,300 nesting days across 84 individual sage-grouse between 2011 and 2018. The best-fit model included a zero-inflation formula with additive effects for GPS company, days nesting, and average shrub height surrounding the nest (Table 2-2). MTI transmitters exhibited an 85% higher probability of exhibiting zero-miss-days during the nesting period than GeoTrak (β = 0.85, 95% CI = [0.47, 1.23]). The probability of transmitters exhibiting zero-miss-days decreased by 6% per 1-day increase in the number of days nesting (95% CI = [-0.08, -0.04]) and 2% per 1-centimeter increase in the average shrub height (95% CI = [-0.03, -0.01]).

The conditional model included an additive effect for the mean topographic roughness surrounding the nest and an interactive effect for transmitter deployment status and deployment length with a random effect for the transmitter ID (Table 2-2). Increases in mean topographic roughness (β = 0.52, 95% CI = [0.34, 0.71]) were associated with more fix misses. New transmitters exhibited a lower probability of missing fixes than cumulatively redeployed transmitters as their respective deployment lengths increased (β = -0.008, 95% CI = [-0.009, -0.006]; Figure 2-4). Refurbished transmitters exhibited a higher probability of missing fixes than cumulatively redeployed transmitters as deployment length increased (β = 0.42, 95% CI = [0.18, 0.66]; Figure 2-4), though this may be a function of the low sample size of refurbished transmitters in this nesting dataset rather than reflecting actual performance. The DHARMa residual plots suggest other relationship(s) in the observed response that I may not be considering (Figure B.1). I plotted this response variable per individual's nesting period to explore nest fix inefficiency further. The best-fit model could not accurately determine a relationship that fully explained this variation (Figure B.2).

Fix Error Mean and Standard Deviation

The model evaluating the mean of the distance from each fix to the nest relied on a dataset of 92 nests for 76 individuals. The best-fit model included fixed effects for GPS company and nest location latitude with a nested random effect for birds per study area (Table 2-2). Both GPS companies' mean fix error decreased as latitude increased (Figure 2-5A). MTI exhibited fix error means farther from the nest site than GeoTrak (β_{MTI}= 0.64, 95% CI = [0.29, 1.00]), and fix error mean decreased as latitude increased (β = -0.19, 95% CI = [-0.26, -0.11]).

The model evaluating the standard deviation of the distance from each fix to the nest relied on the same dataset. The best-fit model included fixed effects of GPS company, days spent on the nest, and latitude, with a random effect for birds per study area (Table 2-2). Standard deviation for the fix error increased proportionally with days spent nesting for both GPS transmitters ($\beta = 0.07$, 95% CI = [0.007, 0.13]; Figure 2-5B). Fix error standard deviation decreased as latitude increased ($\beta = -0.40$, 95% CI = [-0.77, -0.01]). The mean error direction from the reported fix(es) to the nest location ranged between 105° and 135° for GeoTrak and between 135° and 155° for MTI (Figure 2-6).

Transmitter Loss

The transmitter loss analysis used a dataset encompassing 266 transmitters with 40 loss events from 2011 to 2019. The best-fit model was the intercept-only model (Table 2-2). The predicted loss rate across all transmitters' ages remains relatively low through time, with ≤50% hazard of losing transmitters up to ~1300 days (~3.6 years; Figure 2-7).

DISCUSSION

To answer increasingly complex ecological questions for targeted wildlife species, recent improvements in GPS technologies have allowed researchers and resource managers to acquire fine-resolution spatiotemporal data remotely that ameliorate analytical frameworks and guide real-time management actions. This study evaluated the performance of two GPS transmitters commonly deployed on sage-grouse. Between 2011 and 2019, new and refurbished MTI transmitters functioned better in general fix performance than new and refurbished GeoTrak transmitters, where MTI exhibited lower daily fix inefficiency and fewer day gaps during most seasons except for winter. Cumulatively redeployed MTI transmitters, however, did not perform differently than

GeoTrak transmitters. Additionally, MTI outperformed GeoTrak during the nesting period for daily nest fix inefficiency zero-miss days (i.e., estimated to have a higher probability of days with 100% fix efficiency). However, GeoTrak outperformed MTI in exhibiting a lower fix error distance mean—higher accuracy— from the nest location than MTI. There was no difference in performance between the two companies' transmitters for the transmitter loss, daily nest fix inefficiency conditional model, and nesting precision models. For nest accuracy precision, latitude and days nesting best explained the observed variation. When transmitters are in a fixed location (e.g., the grouse is nesting or dead), the transmitter can be expected to be located in the NW direction from the fix locations reported from GPS data.

Upon retrieval from the field, transmitters returned to the respective manufacturer for refurbishment produced better efficiency in their subsequent deployment than those cumulatively redeployed. This response was evident through the daily fix and expected day gap analyses, where new and refurbished transmitters outperformed cumulatively deployed transmitters. For some GPS manufacturers, refurbishing can cost less than a third of the cost of a new transmitter (Keith LeSage, GeoTrak Inc, personal communication), presenting an economical option for researchers. I found no publications comparing the fix efficiency between new, refurbished, or cumulatively deployed GPS transmitters.

Both transmitters functioned worse during winter than in other seasons. Lower winter performance in solar-powered GPS transmitters is due to a combination of low solar radiation with fewer hours of sunlight and sage-grouse behavior, where they spend more time amongst higher sagebrush canopy cover and often will create burrows in the snow (Connelly et al. 2011b). Canopy or vegetation cover is inversely related to fix error (Frair et al. 2010) because it affects the available open sky (Forin-Wiart et al. 2015). Thus, topography (Ironside et al. 2017), ground (for fossorial/torpor species; McMahon et al. 2017), and buildings (for urban species; Adams et al. 2013) can lower GPS performance. Additionally, researchers typically reduce the number of fixes in winter to conserve battery. However, this may be counter-productive and lead to compounded reduced performance given the lower solar radiation and increased time between fixes (fix interval). Programming transmitters to collect 15-25% more fixes than needed and decreasing the fix interval (Hofman et al. 2019, see Forin-Wiart et al. 2015 on "cold start" and "warm start" GPS information) in all seasons may counteract low rates of fix acquisition (Cain et al. 2005, Forin-Wiart et al. 2015, Jung et al. 2018). To prevent habitat selection bias, researchers provide recommendations on accounting for fix errors, as even 10% of missing locations can lead to poor inference (see Frair et al. 2004, Nielson et al. 2009, Webb et al. 2013, Christin et al. 2015).

Latitude explained much of the variation in performance for some of the nesting analyses. Other research has found differences in GPS performance and latitude, where transmitters on species that inhabited higher latitudes during the summer solstice performed better (Jung et al. 2018). An increasing array of Argos satellites with increasing latitude may explain this relationship, in addition to the increased solar radiation present during the summer months (Christin et al. 2015, Jung et al. 2018). However, Jung et al. (2018) also found that transmitters in high latitudes during the winter months performed worse than those in latitudes closer to the equator due to the lower solar radiation and less-direct sunlight. These results provide additional support for the effects of latitude on functionality.

No significant relationships were observed in the expected hazard rate for transmitter loss. Many sage-grouse studies depend on the reliable longevity and retrieval of GPS transmitters, especially for population vital rates related to female sage-grouse, where some exhibit long lifespans and nest for several years in a row (Connelly et al. 2011a). Transmitter functionality spanning the entire life of the study species is crucial for elucidating valuable information across multi-year studies as this reduces the recapture cost and potential increased stress to the animal (Baker et al. 2013). MTI and GeoTrak state that the expected functionality for these 22-g transmitters is up to three years. Thus, researchers can utilize either transmitter and expect similar retrieval rates from the field.

I could not determine the best predictors to explain the daily nest fix inefficiency variation. This variation might be explained by individual nesting behavior. Some research has noted the variation in yearling incubation behavior compared to adults (Coates and Delahanty 2008), where yearlings spend more time away from their nests. Further exploration of female incubation behavior (e.g., time spent on or off the nest) may be equally informative (Dudko et al. 2019). After exploring age and individual behavior, decreasing the scale at which I evaluate nesting GPS efficiency from daily to individual fix levels may yield further insights. However, this scale might not be biologically informative. Other variables playing a critical role that I did not include are satellite array (Sager-Fradkin et al. 2007, McMahon et al. 2017), temperature (Schlippe

Justicia et al. 2018), and weather (Jung et al. 2018, Schlippe Justicia et al. 2018), and, thus, further exploration of this relationship is needed.

This analysis provides detailed performance assessments of MTI and GeoTrak's 22-gram solar-powered GPS-Argos transmitters deployed on sage-grouse over various environmental conditions in both nesting and non-nesting periods. Researchers studying this species or species under similar environmental conditions could consult manufacturers on battery drain trade-offs with increased fix acquisition for solar-powered transmitters. In addition to exploring other variables related to study species and environment, researchers should perform further testing with transmitters produced after 2019, as some manufacturers have improved hardware and software, and lighter-weight solar-powered transmitters (~ 12g) have become available (e.g., GeoTrak Inc.). Stationary tests as controls for performance should be employed within an experimental design framework simultaneously with real-time telemetry studies on free-ranging study animals to isolate transmitter-related variables from variables related to the environment or deployment on the animal (e.g., behavior, plumage or fur covering solar panel, or antenna orientation when mounted on the animal; Blackie 2010, Byrne et al. 2017). Accurately accounting for known fix errors inherent in GPS data improves the inference at which researchers can understand free-ranging animal individual- and population-level space-use, behavior, demographics, predator-prey dynamics, and human-wildlife conflicts (Latham et al. 2015).

CONSERVATION IMPLICATIONS

Cumulatively redeployed transmitters consistently exhibited the worst performance. Refurbishing transmitters following each deployment will retain higher fix efficiency.

For species of conservation concern, reducing errors in data acquired from GPS transmitters is elevated compared to species of least concern (Vance et al. 2017, Sánchez-Giraldo and Daza 2019). The analytical products derived from data garnered from species of concern are often closely scrutinized (e.g., legal conflicts between governing agencies and private entities, landowners, or special interest groups), and any bias or lowered inference can lead to poor legal or management decisions. Thus, in performing studies on species that may encounter high-profile legal actions, researchers should emphasize incorporating methods to improve expected fix error and reduce inferential bias (Hofman et al. 2019, Acácio et al. 2022). I recommend refurbishing transmitters following each deployment, if possible, to ensure the highest efficiency in these transmitters. Research occurring in higher latitudes should expect better performance in the summer months than in lower latitudes but, conversely, worse performance in the winter months and work with manufacturers to potentially counteract this by increasing fix intervals, if possible.

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TABLES AND FIGURES

Table 2-1. The names and locations of study areas of the data collected from two solar-powered GPS-Argos transmitters manufactured by differing companies (GeoTrak Inc. and Microwave Telemetry Inc.) and used for research on greater sage-grouse (*Centrocercus urophasianus*) between 2011 and 2019.

Study Area		Location (lat, long)	For detailed climate/ topographical information, see:
Utah	West Box Elder SGMA[a]	41.75275°N, -113.663125°W	Sandford et al. 2017
	East Box Elder SGMA	41.98975°N, -112.5617°W	Sandford et al. 2017
	Rich SGMA	41.7412°N, -111.23268°W	Stringham 2010
	Crawford Mountains	41.574225°N, -111.051675°W	Stringham 2010
	Morgan-Summit SGMA	40.95386167°N, -111.5320567°W	Flack 2017
	Sheeprock Mountains SGMA	39.9865°N, -112.44903°W	Robinson and Messmer 2013
	Hamlin Valley SGMA	38.1403°N, -113.9687 °W	Beers and Frey 2022
	Bald Hills SGMA	38.07783°N, -113.0305°W	Beers and Frey 2022
	Panguitch SGMA	37.7325°N, -112.4823°W	Beers and Frey 2022
	Parker Mountain-Emery SGMA	38.346267°N, -111.78883°W	Baxter et al. 2013, Duvuvuei et al. 2017
	Anthro Mountain	39.90212°N, -110.41266°W	Duvuvuei et al. 2017
	Strawberry SGMA	40.15624°N, -111.085°W	Baxter et al. 2013
	Uintah SGMA	40.65332°N, -109.47004°W	Baxter et al. 2013
Wyoming	Jeffrey City	42.585625°N, -108.1088325°W	Smith et al. 2016, Kirol et al. 2020
	Bighorn Basin	44.46825°N, -107.80142°W	Pratt et al. 2017, Pratt & Beck 2019

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[a] SGMA: Sage-grouse Management Area

Table 2-2. Top models for each response variable assessed in evaluating the performance of two GPS company transmitters (GeoTrak Inc. and Microwave Telemetry Inc.) deployed on greater sage-grouse (Centrocercus urophasianus) in Utah and Wyoming between 2011 and 2019. Zero-inflation, if applicable) are included.

Top model equation per response variable
Daily fix inefficiency ~ GPS * season + log(CDL) + (Bird/SA), ZI formula ~ GPS * NCR + season
Day gaps ~ GPS + NCR + PLP + log(CDL) + (Bird) + offset(log(DL))
Daily nest fix inefficiency ~ NCR * DL + MR + (TranID), ZI formula ~ GPS + DN + SH
Log(Fix Error Mean) ~ GPS + NL + (Bird/SA)
Sqrt(Fix Error Standard Deviation) ~ GPS + DN + NL + (Bird/SA)
Transmitter loss ~ 1

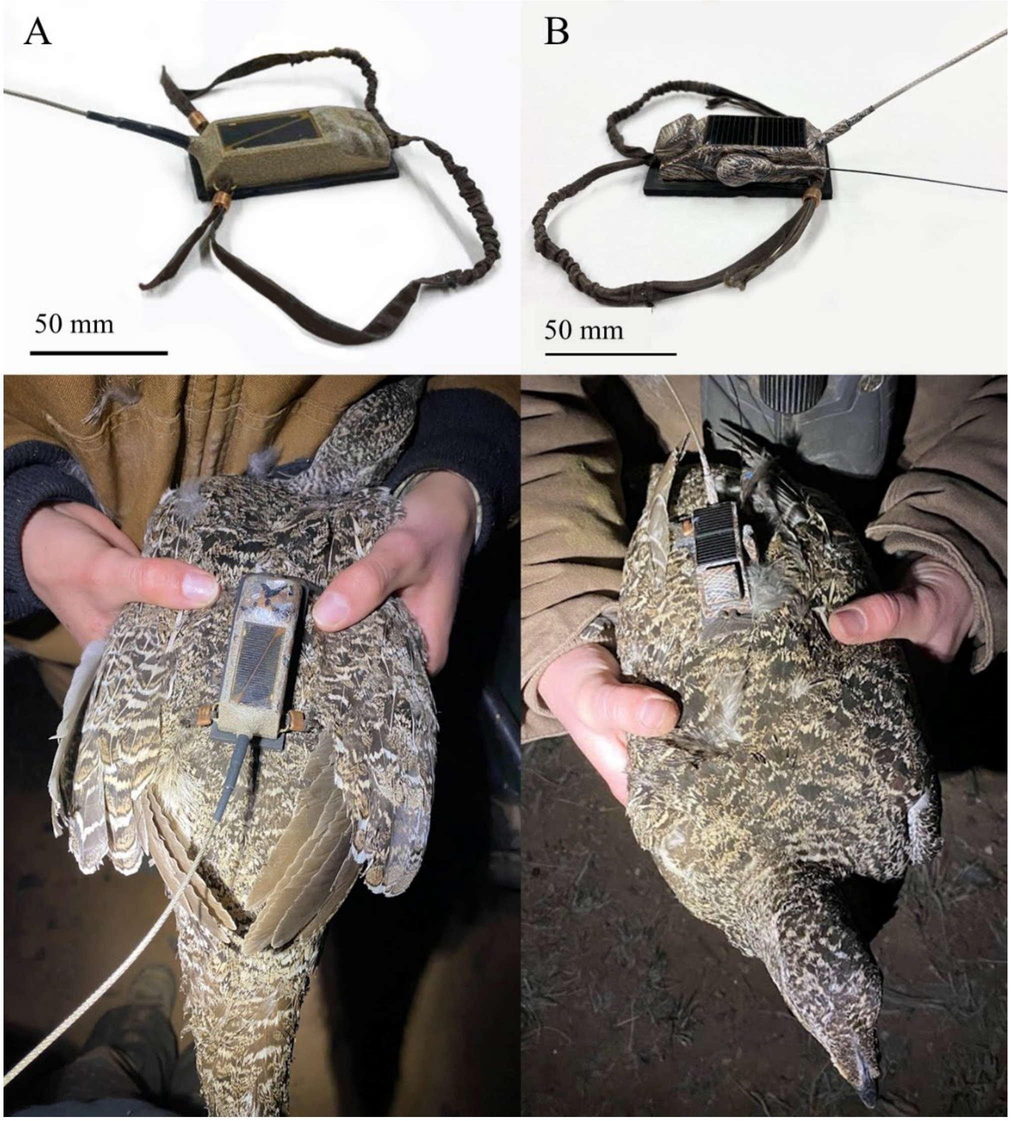

Figure 2-1. Two commonly used solar powered GPS-Argos satellite transmitters made by (A) Microwave Telemetry, Inc. (A) and GeoTrak Inc. (B) with each companies' individual transmitter in the photos located above photos of their deployment on greater sage-grouse in Utah and Wyoming between 2011 and 2019 (photo credit: C. Backen).

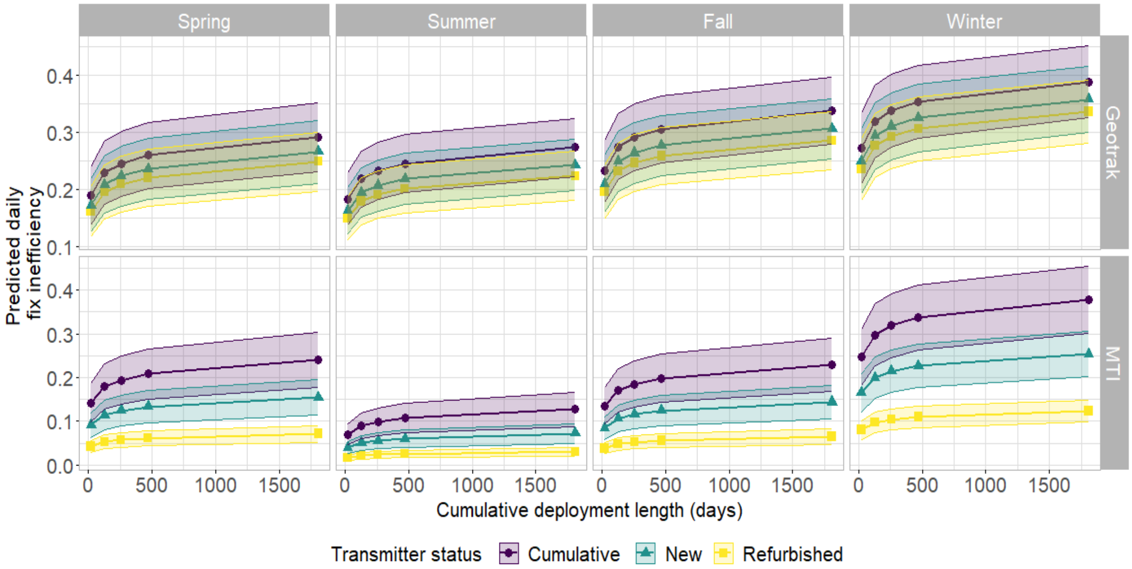

Figure 2-2. Daily fix inefficiency (unsuccessful fixes/scheduled fixes) by season per GPS Company (GeoTrak Inc. and MTI = Microwave Telemetry Inc.) and transmitter deployment status (cumulatively redeployed, new, or refurbished) across the cumulative deployment length (days) for transmitters used on greater sage-grouse in Utah and Wyoming between 2011 and 2019 (n = 506 sage-grouse). Transmitter deployment status: New (never deployed after initially buying from manufacturer), cumulative (redeployed without being sent back to manufacturer), and refurbished (sent to manufacturer for hardware and software updates). For refurbished transmitters, cumulative deployment length was reset to zero.

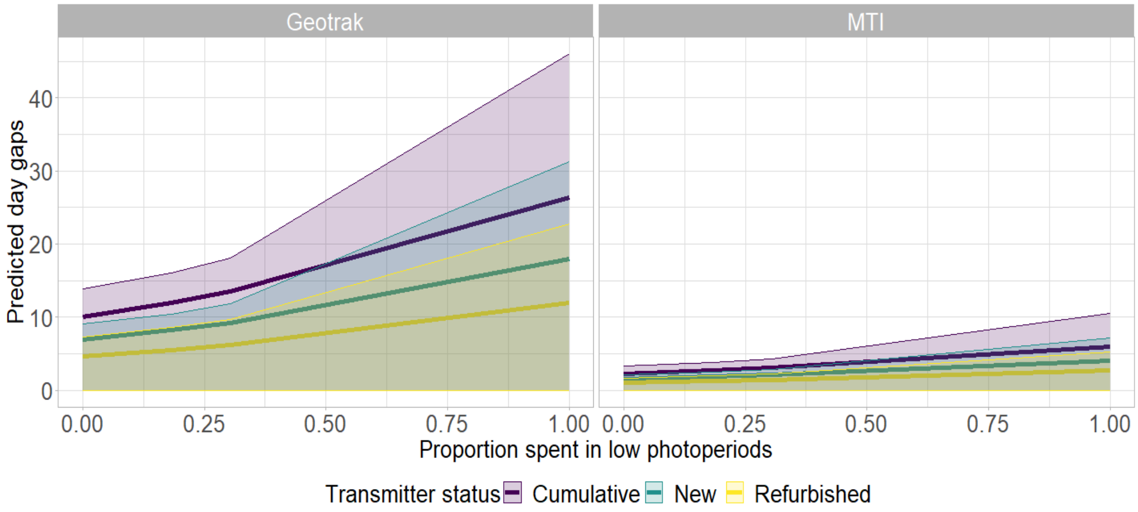

Figure 2-3. Predicted day gaps (full days when the transmitter fails to register any fixes) across the scaled proportion of days the transmitter spends in low photoperiod (≤25th percentile of photoperiod length) per GPS company (GeoTrak Inc. and MTI = Microwave Telemetry Inc.) for transmitters deployed on greater sage-grouse in Utah and Wyoming between 2011 and 2019 (n = 547 transmitter deployments on individual sage-grouse). Transmitter deployment status: New (never deployed after initially buying from manufacturer), cumulative (redeployed without being sent back to manufacturer), and refurbished (sent to manufacturer for hardware and software updates).

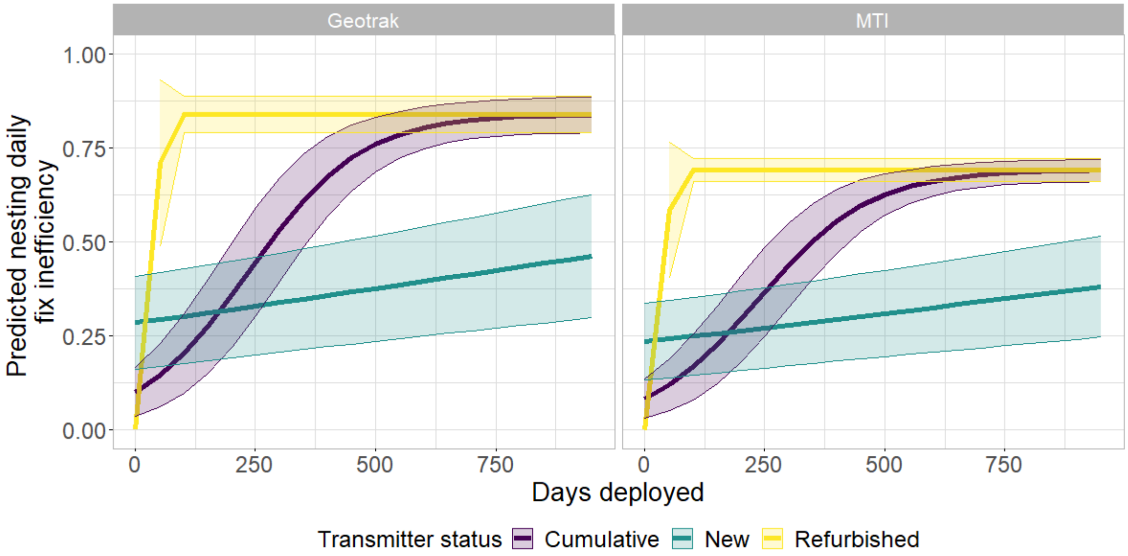

Figure 2-4. Daily nesting fix inefficiency (unsuccessful fixes/scheduled fixes) during the nesting period for nesting individuals by the number of days deployed on the individual the given nesting day (n = 2,300 combined nesting days across 84 individuals) per GPS company (GeoTrak Inc. and MTI = Microwave Telemetry Inc.) for nesting greater sage-grouse (*Centrocercus urophasianus*) in Utah and Wyoming between 2011 and 2018. Transmitter deployment status: New (never deployed after initially buying from manufacturer), cumulative (redeployed without being sent back to manufacturer), and refurbished (sent to manufacturer for hardware and software updates).

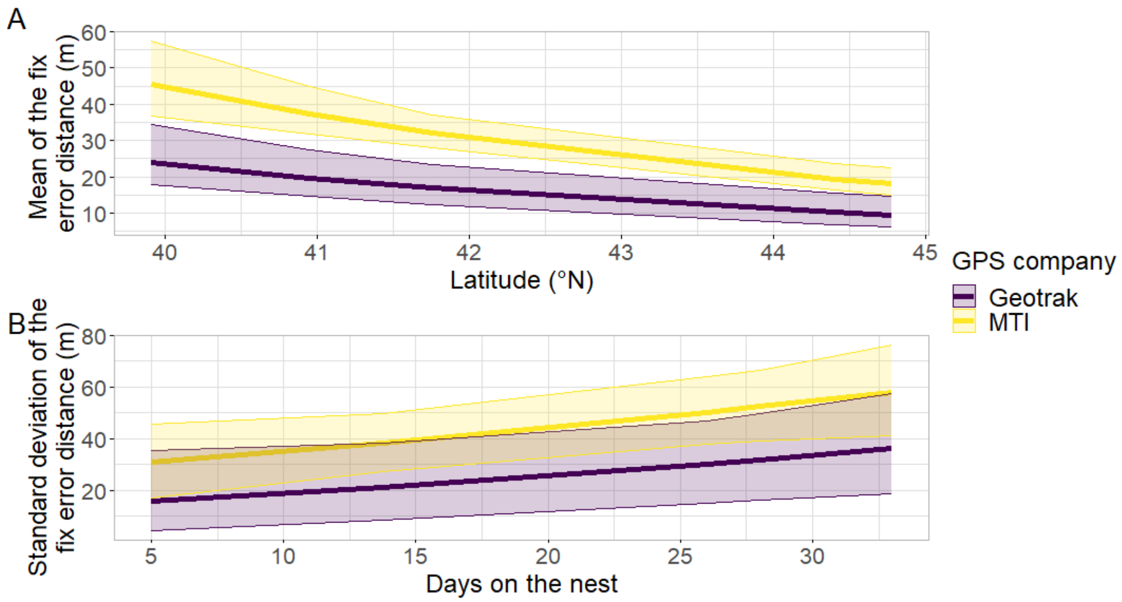

Figure 2-5. Solar GPS transmitter fix error distance for nesting greater sage-grouse (*Centrocercus urophasianus*) in Utah and Wyoming between 2011 and 2018: A) Distance mean: Predicted mean of the nest fix error distance (from the nesting location to the registered fix location) by latitude (°N) per GPS company (GeoTrak Inc. and MTI = Microwave Telemetry Inc.; n = 92 nests), B) Distance standard deviation: Predicted standard deviation of the nest fix error distance by days spent on the nest for each sage-grouse nesting period (n = 92 nests). Both y axes in A and B have been back-transformed (fix error mean was log-transformed, and fix error standard deviation was square-root-transformed).

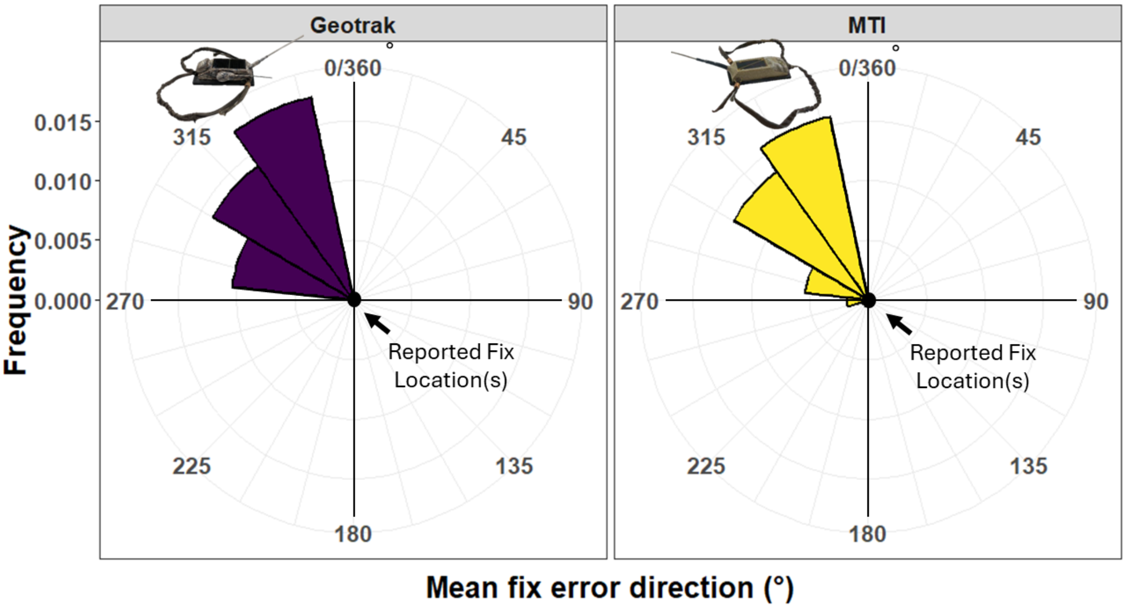

Figure 2-6. Mean fix error direction (in degrees) frequency from the registered fix location (reported point(s) provided by downloading GPS locations from Movebank, movebank.org) to the actual transmitter location on the ground, determined using empirical greater sage-grouse (*Centrocercus urophasianus*) nest location data in Utah and Wyoming between 2011 and 2019 (n= 92). I report the mean nesting fix error direction for each GPS company transmitter type (GeoTrak Inc. purple and MTI = Microwave Telemetry Inc. yellow).

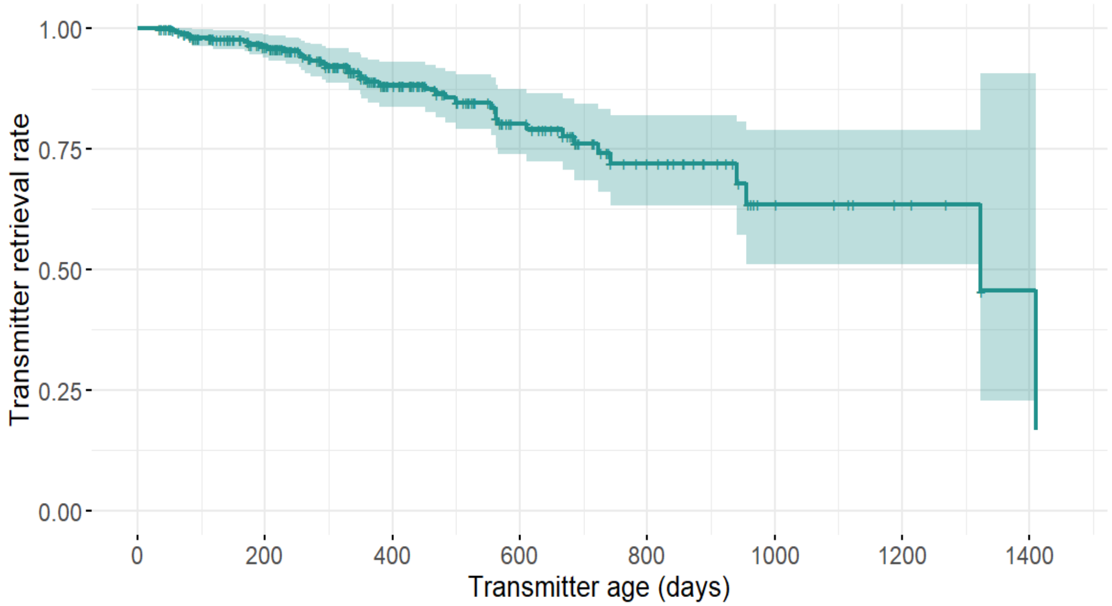

Figure 2-7. Transmitter retrieval rate probability by transmitter deployment age (days) for all transmitters regardless of company (GeoTrak Inc and Microwave Telemetry Inc.) deployed on greater sage-grouse (*Centrocercus urophasianus*) in Utah and Wyoming between 2011 and 2019 (n = 266 transmitters).

CHAPTER 3

ASSESSING POST-RELEASE BEHAVIORAL STATES AND SPACE-USE: A MEANS TO INFORM METHODOLOGICAL IMPROVEMENTS IN CONSERVATION TRANSLOCATIONS

Abstract

Conservation translocations to reinforce declining populations of species are a common management strategy. Although dispersal is an expected behavior observed in wildlife translocations post-release, it can impact the success of translocation efforts if not accounted for during planning or appropriately monitored in the management phases. To reinforce a small, isolated, declining greater sage-grouse (*Centrocercus urophasianus*, sage-grouse) population in the Sheeprock Mountains Sage-grouse Management Area (SGMA) in central Utah, US, practitioners translocated 146 individuals during the springs of 2016-2019 from two source populations in Utah. My objectives were to evaluate post-release dispersal in translocated sage-grouse to inform and refine existing translocation protocols. I monitored the movements of 38 translocated sage-grouse post-release with solar-powered global positioning satellite transmitters from 2016-2020 and segmented movement behavior into two phases: exploration and restricted. I then fit a movement-based habitat selection analysis for each behavioral state to determine the influence of landscape habitat covariates and off-highway vehicle traffic volume on sage-grouse habitat selection. The probability of beginning in the exploratory state at the time of release was marginally lower for adult females than yearling females. The analysis also suggested that to reduce post-release dispersal, practitioners should prioritize release sites to maximize the restricted state selection in areas closer to mesic habitat, higher elevation, and lower tree cover. Practitioners should further evaluate methods to reduce post-release dispersal, such as evaluating temperament traits and testing acclimatization with pre-nesting females if logistical constraints for brood translocations are present.

Keywords behavioral ecology, *Centrocercus urophasianus*, conservation translocations, post-release dispersal, post-release habitat selection, reinforcements

1. Introduction

Closed animal populations experiencing consistent declines rendering them at risk of extirpation or extinction often receive management intervention in the form of conservation translocations (translocations) called reinforcements (Ewen et al., 2023; International Union for the Conservation of Nature/Species Survival Commission (IUCN/SSC), 2013). Despite the global application of translocations, there remain difficulties associated with their success (Berger-Tal et al., 2020; Skikne et al., 2020; Taylor et al., 2017). Translocated individuals' establishment at the release site and the persistence of a viable population typify demographic success metrics (Armstrong and Seddon, 2008; IUCN/SSC, 2013; Robert et al., 2015). Accurately quantifying these metrics is difficult however, due to a host of issues such as inadequate post-release monitoring (Seddon et al., 2014; Wolf et al., 1996), unresolved issues with available suitable habitat (Dunham et al., 2016; Osborne and Seddon, 2012), and post-release dispersal away from the release area (Berger-Tal et al., 2020; Moehrenschlager and Lloyd, 2016; Stamps and Swaisgood, 2007).

Post-release dispersal from the focal release area or population is expected in at minimum a small proportion of translocated individuals; however, such dispersals directly affect translocation success by preventing individuals from contributing demographically or genetically to the targeted population or area (Jachowski et al., 2016; Le Gouar et al., 2012). Dispersal is an energy-intensive, stressful event for individuals under typical life history drivers (e.g., natal or breeding dispersal), but that stress and energy-expenditure are compounded with the events involved in translocations (Dickens et al., 2010; Ewen et al., 2023; Jachowski et al., 2016). Understanding the mechanisms that influence translocated individuals' propensity to disperse away from the release site can aid in mitigating negative behavioral and physiological responses (Bell, 2016; Jachowski et al., 2016). Plausible reasons for dispersal responses are related to individual- or species-level characteristics, where individual-level characteristics are a function of personality traits, physiology, homing behavior, or natal habitat preference induction, and species-level characteristics are a function of age, sex, reproductive status, or sociality (Bell, 2016; Berger-Tal et al., 2020; Jachowski et al., 2016; Le Gouar et al., 2012; Stamps and Swaisgood, 2007). Methods to limit dispersal away from and increase their establishment at the release site focus on accounting for the above characteristics, mitigating stressful release environments, and addressing species' habitat requirements (Bell, 2016; Le Gouar et al., 2012; Tetzlaff et al., 2019). It is important to note of a trade-off, however, where at finer spatial scales within the target release area, individuals must demonstrate some dispersal-like behaviors post-release to acquire knowledge of the novel environment to maximize fitness (Bell, 2016; Berger-Tal et al., 2014).

Post-release, an individual should initially dedicate most of their movement behavior to exploration of the novel area (the exploratory behavioral phase) and, as time progresses, should transition to exploitation of the knowledge formulated from the exploration period (the restricted behavioral phase; Berger-Tal et al., 2014). This behavioral shift has been called post-release behavioral modification, which includes predation avoidance and social interactions in its influence on movement behavior (Bell, 2016; Berger-Tal and Saltz, 2014). Remaining within the release area and exploiting the resources therein is one of the key drivers affecting survival and recruitment into the study area and, therefore, the success of translocations.

Thus, practitioners can monitor behavior and space use to elucidate factors that could both indicate and influence the propensity for dispersal in translocated individuals post-release (Bell, 2016). Initially, practitioners can differentiate their post-release behavior into exploratory and restricted states and evaluate if any translocation factors correlate with either (Picardi et al., 2022). Subsequently, practitioners can then evaluate when individuals exhibit post-release behavioral modification (Bell, 2016; Berger-Tal and Saltz, 2014). Practitioners can also evaluate each behavior's habitat selection (Gelling et al., 2022; Roever et al., 2014; Smith et al., 2018). This process benefits through assuring identification of habitat favorable to the restricted phase (Roever et al., 2014) and aiding practitioners in ameliorating translocation strategies to increase the probability of success (Picardi et al., 2022).

There has been a significant effort in translocating greater sage-grouse (*Centrocercus urophasianus*; sage-grouse), a sagebrush (*Artemesia* spp.)-obligate galliform experiencing persistent range-wide population decline due to habitat fragmentation and loss (Aldridge et al., 2008, Coates et al., 2021; Conover and Roberts, 2016). This decline led to the increased use of translocations to reinforce or reintroduce sage-grouse populations across the range beginning in 1933 (Reese and Connelly, 1997). Reese and Connelly (1997) established methods that would maximize translocation success. Baxter et al. (2013) demonstrated that predator control increased translocated individuals' survival probability. Recent sage-grouse translocation research has focused on further refining the protocols above to increase survival during transit and post-release, increase the probability of first-year reproduction, and reduce post-release movements (Lazenby, 2020; Meyerpeter et al., 2021; Picardi et al., 2022).

Though recent research has shown promise of increased success through translocating sage-grouse broods (Meyerpeter et al., 2021; Picardi et al., 2022), some translocation programs exhibit logistical or habitat-related constraints that preclude their use; therefore, continuing to evaluate translocations using pre-nesting females and males remains relevant. The goal of this research on sage-grouse translocations in the Sheeprocks Mountains, Utah, was primarily to prevent extirpation and secondarily to further improve current sage-grouse translocation protocols by identifying characteristics associated with males and pre-nesting females that established within the release area. Specifically, my objectives were to: 1) identify age classes or sexes that are least likely to exhibit post-release dispersal; 2) quantify the duration of the exploratory phase preceding restricted movements; and 3) differentiate the habitat characteristics selected for by individuals in the exploratory behavioral phase versus the restricted behavioral phase after establishing, whereby aiding in identifying appropriate release habitat for future translocations.

2. Methods

2.1 *Study Area*

a. Focal Population

The Sheeprock Mountain SGMA encompasses 4256.5 km^2 at the eastern edge of Utah's West Desert in the Great Basin (Figure 3-1)**.** The SGMA is characterized by warm, dry summers and cool winters. The 50-year average maximum summer temperature is 32.4˚C in July, and the minimum winter temperature is -10.4˚C in January. The average annual precipitation is 26.01 cm, with the highest in spring and fall, and the average snowfall is 91.95 cm (Western Regional Climate Center, 2016).

Elevation ranges from 1500 m in the lower valleys to 2950 m at the tallest peak. The dominant sagebrush species are Wyoming big sagebrush (*A. tridentata* w*yomingensis*), mountain big sagebrush (*A. t. vaseyana*), and elevations along ridgelines are dominated by black (*A. nova*) and low sagebrush shrubs (*A. arbuscula*). Invasive annual vegetation includes bur buttercup (*Ceratocephata testuculata*), cheatgrass (*Bromus tectorum*), desert madwort (*Alyssum desertorum*), knapweed (*Centaurea* spp.), redstem stork's bill (*Erodium cicutarium*), and tansy mustard (*Descurainia pinnata*).

b. Source Populations

Parker Mountain is located in Utah's Parker Mountain-Emory SGMA on the Colorado Plateau in south-central Utah. It is approximately 200 km from the Sheeprock Mountain SGMA (Figure 3-1) and is characterized by primarily black sagebrush on the ridges and slopes and big sagebrush in the drainages. Elevation ranges from 2,140 m to

3,000 m. The average annual precipitation is 56.7 cm, with the highest in fall, winter, and spring.

Box Elder is located in northwestern Utah in the West Box Elder SGMA, approximately 200 km from the Sheeprock Mountain SGMA (Figure 3-1). It contains predominately big sagebrush and black and low sagebrush. It is on the edge of the Snake River Plain and the Great Basin Desert. Elevation ranges from 1,350 m to 2,950 m, with average annual precipitation ranging from 17.7 cm to 78.3 cm from low to high elevation, respectively.

2.2 *Capture and Translocations*

Practitioners followed previously established translocation guidelines for pre-nesting females and males outlined by Reese and Connelly (1997) and Baxter et al. (2008) with the addition of novel protocols for pre-nesting females and males outlined by Lazenby (2020). During the breeding seasons of 2016-2019, practitioners translocated 146 grouse (106 females and 40 males; approximately 30 females and 10 males per year) from genetically compatible sage-grouse populations located in Box Elder and PM. Utah State University IACUC protocol #2560 reviewed and approved all protocols.

Practitioners captured sage-grouse at night using all-terrain vehicles, spotlights, and long-handled nets near active leks (2100hr to 200hr; Connelly et al., 2003), and practitioners either processed individuals upon capture or at a nearby processing area before departing the source site. For this analysis, I used 48 (9 male, 39 female; Table 1) individuals marked with a solar-powered GPS transmitter following (Bedrosian and Craighaid, 2007). Practitioners fit each bird with a leg band (females: size 14, males: size

16). Processing also included recording the age, capture location (UTM, 12N, NAD 83), leg band ID, sex, and weight.

In 2016, practitioners placed translocated sage-grouse in individual cardboard boxes (30 cm x 23 cm x 30 cm) for release at the study site. Beginning in 2017, practitioners placed translocated birds in wooden release boxes equipped with a long pulley rope attached to a hinged front panel, allowing researchers to open it remotely. Practitioners transported individuals overnight via truck to the study site (0100 hr to 0600 hr) and placed the release boxes within 200 m to active lek sites. After scanning for predators, practitioners released them at sunrise facing lek sites.

2.3 *Field Monitoring*

I monitored all GPS-marked individuals from capture to mortality or transmitter loss. GPS transmitter data were uploaded remotely to the Argos System and accessed through Movebank (movebank.org) at the end of each duty cycle. Units were programmed to record four to six locations daily across four seasons, coinciding with sage-grouse lekking, nesting, brooding, and late fall through winter (Appendix C). The transmitters were programmed each fix to record the date, time, location, elevation, and speed. I determined mortality for the GPS transmitters using indicators of several fixes at the exact location or a last fix with no other fixes registered thereafter. After detecting mortality, observers located the transmitter or death site in the field and determined the cause of death, if possible.

2.4 *Off-highway vehicle recreation*

Practitioners gathered daily traffic count data on unpaved roads from TRAFx vehicle counters (TRAFx Research Ltd., Canmore, Alberta, Canada) placed by the BLM at sites adjacent to roads throughout the study area to monitor recreational traffic (see Figure C.1). TRAFx counters use a magnetometer to detect passing vehicles, which includes passenger vehicles and off-highway vehicles. There were ten traffic counters in 2016, and four additional counters were placed in 2017.

I used daily count data from 2016-2020 to estimate daily traffic by recreationalists in the study area. In accounting for overdispersion, I modeled daily traffic counts with a negative binomial linear model using *glm.nb* in the *MASS* package (v7.3-55; Venables and Ripley, 2002). Covariates included in this model were: season, defined as spring (February – April), summer (May – July), fall (August- October), and winter (November-January); weekend (0/1); state or federal holiday (including big and upland game hunt start and end dates; 0/1); road width (m); and an interaction for weekend and holiday (see Fig. C.2 for predicted vehicle traffic counts across covariates).

2.5 *Sage-grouse GPS Data Processing*

I performed data processing for GPS location data and analysis in R Version 4.1.2 (R Core Team, 2022). I removed steps corresponding to movement rates of zero (i.e., no movement) and fixes before translocation release times and outside the plausible study timeline. In addition, I removed mortality data from the location data, where field-confirmed mortalities guided the cut-off date. In instances where observers could not confirm mortality in the field, I visually explored data for consistent step lengths of zero at the end of movement steps.

2.6 *Data Analysis*

a. Behavioral Segmentation

To format the data for the analyses, I removed individuals that had fewer than 20 steps, fit a continuous-time movement model (Fleming et al., 2017) to regularize tracks at a 6-hour resolution, and removed interpolated locations on days where no actual data were available (Picardi et al., 2022). I used a discrete-time hidden Markov model (HMM) to segment movement tracks of 38 translocated individuals from 2016-2020 into homogeneous behavioral phases (McClintock and Michelot, 2018). I used the time series of step lengths and turning angles in the HMM to discriminate between two hidden states: restricted movements and exploratory movements. The HMM estimates each track's initial state probability (probability of beginning in either state) and transition state probabilities (probability of transitioning from one state to another). I modeled step length as a gamma distribution and turning angles as a Von Mises distribution (McClintock and Michelot, 2018). I defined initial parameter values via visual exploration of the raw data (for the step lengths) and based on conceptual expectations (for the turning angles) as follows: for the restricted movement state, a mean step length of 117.5 m and a standard deviation of 54.5 m and mean turning angle of π and concentration of 0.1 (indicating that animals are likely to take turns in any direction), and for the exploratory movement state, a mean step length of 10 km and standard deviation of 5 km and a mean turning angle of 0.001 and a concentration of 0.99 (indicating that the animals are most likely to move linearly). I modeled initial state probabilities as a function of age, sex, and translocation month and the transition probabilities as a function of days since translocation release. I used the Viterbi algorithm to assign behavioral states to individuals' steps (Zucchini et al., 2017), and I fit the HMM in R using the package *momentuHMM* (McClintock and Michelot, 2018).

b. Landscape Covariates

Based on previous literature and my knowledge of the system, I attributed both used and available steps with a set of environmental covariates representing relevant predictors for sage-grouse habitat selection. The covariates included annual herbaceous cover, distance to habitat restoration projects, distance to mesic areas, distance to roads, elevation, perennial herbaceous cover, road density, sagebrush cover, slope, tree cover, and interaction for distance to roads with temporally based traffic count estimates matched according to the day of the corresponding movement of the bird (i.e., if the step fell on a weekend, season, and holiday). I standardized all landscape covariates to a 30 m by 30 m resolution.

For tree and annual herbaceous cover, I used data from the Rangeland Analysis Platform (RAP) vegetation classification system provided on Rangeland.App (https://rangelands.app/). Because annual herbaceous and tree cover were most likely to change significantly between years, given the extensive conifer removal treatments as well as the favorable conditions of the Great Basin to cheatgrass (Boyte et al. 2016), I used these annually varying layers within the RAP data for annual herbaceous and tree cover layers ranging from 2016-2020.

I used data from the 2016 National Land Cover Database (NLCD; https://www.usgs.gov/centers/eros/science/national-land-cover-database) for sagebrush and perennial grass cover. The NLCD is available through the U.S. Geological Survey (USGS) Earth Resources Observations and Science (EROS) Center. The NLCD has mapped sagebrush cover across its distribution and an herbaceous cover layer, which includes both annual and perennial herbaceous plants. I subtracted the 2016 annual herbaceous RAP layer from the NLCD herbaceous cover layer using ArcGIS® software by ESRI to calculate the percent perennial herbaceous cover layer.

I acquired data on mesic areas from the Sage-Grouse Initiative website (https://map.sagegrouseinitiative.com) and calculated distance from mesic areas using Euclidean distance in ArcGIS® software by ESRI. I acquired aspect, slope, and elevation from digital elevation maps from the Utah Geospatial Resource Center (UGRC; https://gis.utah.gov/), and calculated them using ArcGIS® software by ESRI.

I downloaded road data for the state of Utah from the UGRC (https://gis.utah.gov/). Distance from roads was calculated using Euclidean distance, and road density was calculated using a line density function in ArcGIS® software by ESRI.

Utah's Watershed Restoration Initiative (https://wri.utah.gov/) had treated 470 km^2 (11%) by 2020 in efforts to restore sage-grouse habitat in the Sheeprock SGMA. Treatments included removing conifer stands to increase sagebrush availability or enhancing mesic habitat (Pilliod et al., 2018; Rondeau et al., 2023; Sandford et al., 2017). Shapefile data of restoration projects completed between 2016 and 2020 were acquired from WRI's website. I created a distance-to-WRI project raster layer by calculating Euclidean distance in ArcGIS® software by ESRI.

c. Integrated Step Selection Analysis

I completed an integrated step selection analysis (iSSA; Avgar et al., 2016) to analyze behavioral state-dependent habitat selection (Picardi et al., 2022). I fit models for each behavioral state and season combination, as defined above.

I removed combinations of individuals with fewer than 30 steps per season. I logged the distance variables and centered and scaled all continuous variables to improve covariate symmetry and ensure model convergence. I assessed correlations among all pairs of covariates using Pearson's correlation coefficients and included covariates with correlations whose absolute values were below 0.6. In addition to the landscape covariates, I included step length, log of step length, and cosine of turning angle to account for the underlying movement process (Avgar et al., 2016). I compared each used step against 100 available steps, stratified those steps in the iSSA model, and included the stratum as a covariate. I fit the iSSA using the *fit_issf* function within the *amt* package in R (Signer et al., 2019). Parameter estimates in output from the iSSA provide individual-level values of log-relative selection strength (log-RSS; Avgar et al., 2017), which quantify the strength of selection (if positive) or avoidance (if negative) for a 1-unit increase in the covariate value. After fitting the iSSA model using an all-combination approach, I compared model fit with and without the interaction of distance to roads and traffic count. The iSSA function *fit_issf* uses a conditional logit regression model from package *survival* (Therneau, 2023), so I determined the best-fit model as exhibiting lower concordances (Therneau and Atkinson, 2023), higher R^2, and lower AIC values. Following the iSSA model selection, I ran an inverse-variance weighted regression to explore the inference from the individual-based models at the population level as a function of behavioral state and season (Picardi et al., 2022). I obtained mean parameter estimates of log-RSS at the population level and calculated the 95% confidence intervals using bootstrapping (n = 1000). To view the interaction between distance to roads and traffic volume, I used the 25th, 50th, and 75th percentiles for traffic counts to categorize them as low, medium, and high.

3. **Results**

3.1 *Behavioral Segmentation*

After filtering individuals using the above methods, 38 individuals with 31,619 steps were included in the translocated dataset. These individuals included 13 adult females, 20 yearling females, three adult males, and two females of unrecorded age. Individuals were tracked for an average of 246 days, ranging from 9 to 755. There were 34 confirmed mortalities, and observers inferred four mortalities based on location data and field notes, though the transmitters were not recovered. The average number of days post-release that these mortalities occurred was 223.92, ranging from 4 – 814.

The mean step length distribution for restricted individuals was 177.42 m (95% CI = 174.33, 180.51) with a standard deviation of 172.28 m (95% CI = 168.50, 176.05). The exploratory step length distribution mean was 1276.52 m (95% CI = 1231.09, 1321.95) with a standard deviation of 1546.37 (95% CI = 1489.87, 1602.87). The mean turning angle distribution for the restricted state was 0.021 (95% CI = -0.051, 0.092) with a concentration of 0.265 (95% CI = 0.246, 0.285). The mean turning angle distribution for the exploratory state was 0.059 (95% CI = -0.009, 0.127) with a concentration of 0.530 (95% CI = 0.491, 0.569).

For the exploratory state, initial state probability estimates were: for adult females translocated in March <0.001 (95% CI = NA) and April <0.001 (95% CI = NA); yearling females translocated in March 0.529 (95% CI = 0.147, 0.879), April 0.279 (95% CI = <0.001, 0.673), and May 0.998 (95% CI = <0.001, 1.00); and adult males translocated in

March <0.001 (95% CI = <0.001, 0.994) and April <0.001 (95% CI = <0.001, 0.981; Figure 3-2). The average duration of the initial exploratory phase was eight days (IQR 1-5 days; Figure 3-3). The initial restricted phase's average duration was 22 days (IQR 18-28 days; Figure 3-3). At 200 days post-release, the probability at each step of transitioning from exploratory to restricted was 0.068 (95% CI = 0.060, 0.077) and 0.020 (95% CI = 0.018, 0.022) for switching from restricted to exploratory.

3.2 *Integrated Step Selection Analysis*

After filtering records, the iSSA included 37 individuals (4M/33F) with 32,541 used steps. The seasonal models for individuals exhibiting the restricted behavioral state included distance to mesic areas, elevation, perennial herbaceous cover, and tree cover (Figure 3-4). In spring, translocated individuals in the restricted state selected for areas closer to mesic habitat (β = -0.12, 95% CI = -0.24, -0.002). In the summer, they selected higher elevations (β = 0.71, 95% CI = 0.12, 1.29). In the fall, they selected areas closer to mesic areas (β = -0.13, 95% CI = -0.20, -0.17), higher elevation (β = 0.61, 95% CI = 0.03, 1.20), and lower tree cover (β = -0.27, 95% CI = -0.46, -0.08).

Seasonal models for individuals exhibiting the exploratory state included annual herbaceous cover, distance to mesic areas, distance to WRI projects, elevation, road density, sagebrush cover, and tree cover (Figure 3-4). In the spring, individuals in the exploratory state selected for marginally lower annual herbaceous cover (β = -0.08, 95% CI = -0.15, -0.01), higher elevation (β = 0.44, 95% CI = 0.25, 0.63), higher road density (β = 0.31, 95% CI = 0.18, 0.45), and lower tree cover (β = -0.48, 95% CI = -0.63, -0.33). In the summer, they selected higher elevation (β = 0.41, 95% CI = 0.15, 0.66) and lower tree cover (β = -0.23, 95% CI = -0.40, -0.07). In the fall, they selected areas with marginally higher annual herbaceous cover (β = 0.14, 95% CI = 0.002, 0.28). In the winter, they selected areas marginally farther from roads (β = 0.01, 95% CI = 0.001, 0.03), closer to areas with WRI projects (β = -0.14, 95% CI = -0.259, -0.02), higher road densities (β = 0.40, 95% CI = 0.122, 0.68), lower sagebrush cover (β = -0.13, 95% CI = -0.235, -0.02), and lower tree cover (β = -0.45, 95% CI = -0.76, -0.14).

The distance to roads intersected with traffic volume was also included in the exploratory behavioral state model (Figure 3-5). In all seasons, they did not select differing distances to roads coinciding with changes in traffic volume.

4. **Discussion**

Translocations are inherently interdisciplinary. Evaluating post-release movements and space use proves most effective when intersecting behavioral ecology, population ecology, and conservation biology (Berger-Tal and Saltz, 2016; Ewen et al., 2023). Understanding the variables that lead to the successful establishment of translocated individuals post-release and their differential habitat selection compared to exploratory individuals is integral for improving translocation programs (Bell, 2016; Picardi et al., 2022). This study provides another example of incorporating behavior-based dispersal (Ebrahimi et al., 2015) and habitat selection analyses into translocation programs (Berigan et al., 2024; Picardi et al., 2022). As others have, I suggest this as a standard for evaluating movement and space use within translocation projects (Jachowski et al., 2016; Kemink and Kesler, 2013; Roever et al., 2014) monitoring GPS-marked individuals where results are incorporated best within a structured decision-making framework (Converse and Armstrong, 2016; Ewen et al., 2023). These results enhanced the understanding of sage-grouse responses to translocation and informed avenues for improvement of translocation protocols. These results suggest there may be a difference in post-release dispersal between adult pre-nesting females and yearling females, as adults were marginally less likely to engage in exploratory behavior immediately after release than yearlings by 25 or 50%, depending on the month translocated. Moreover, these findings indicate sage-grouse translocated in the Sheeprocks Mountains spent an average of 8 days in the exploratory phase and did exhibit differential post-release behavioral habitat selection; the patterns I observed suggest that sage-grouse translocated during the spring and summer should be released at sites closer to mesic areas with higher elevation and low tree density. Where low post-release dispersal and habitat selection that maximizes fitness is paramount in translocation programs' success, these results present some plausible methods to contribute to that success. Further evaluation of behavioral-state-dependent habitat selection should include ties to survival and reproduction, as dispersal, especially hyper-dispersal (Bilby and Mosby, 2024), is typically inversely related to translocated individuals' demographic contributions to the focal population (Le Gouar et al., 2012; Stamps and Swaisgood, 2007). I provide suggestions for incorporating these results into planning or updating translocation strategies.

Age-based differential dispersal post-release has also been reported in other translocation projects across taxa (Garnier et al., 2021; Hammond et al., 2022; Heezik et al., 2009; Muriel et al. 2016). To minimize and account for age-based differences in post-release behavior, practitioners should review physiological and behavioral differences between age classes of their study species if such information is available (Jachowski et al., 2016). Typically, sage-grouse translocations have observed yearling females exhibiting more extensive home ranges than adult females (Baxter et al., 2008; Duvuvuei, 2013). Home range data may be linearly related to dispersal distance in some translocated animals (Bowman et al., 2002), but this may depend on the time scale when the movement data are tested (i.e., data must be tested on the same temporal scale and may differ between exploratory and restricted phases). The propensity for yearling females to disperse farther post-release than adult females is related to biological differences in younger grouse age classes as they develop, where juvenile sage-grouse females (the age from brood separation to the first breeding season) disperse farther than males from the natal area to the breeding area (i.e., natal dispersal; Dunn and Braun, 1985; Thompson, 2012). Because this phenomenon has yet to be sufficiently reported in the sage-grouse translocation literature, I am hesitant to recommend selecting adult females preferentially to yearlings; more research must be published on this, preferably in an experimental framework. Due to the logistical difficulty of capturing sage-grouse in some study areas, this might also result in sufficiently increased effort. To minimize age-based dispersal post-release, some translocations across taxa have used release pens at the release site for a "soft release" (Darymple and Bellis, 2023; IUCN/SSC, 2013; Jachowski et al., 2016). More recently, this has been performed in sage-grouse with brood translocations (Lazenby, 2020; Meyerpeter et al., 2021; Picardi et al., 2022) but, to my knowledge, has not been tested pre-nesting female or male translocations since Musil (1989; Reese and Connelly, 1997).

The temporal duration of the exploratory phase varies throughout the translocation literature across taxa, ranging from several days to several months (Berger-Tal and Saltz, 2014; Berigan et al., 2024; Hinderle et al., 2015; McNicol et al., 2020).

Generally, practitioners aim to prevent extensive lengths of time for exploration due to elevated risk, but this also serves as an essential period for individuals learning about the novel environment (Bell, 2016; Bonte et al., 2012, Le Gouar et al. 2012). The mean duration of individuals beginning in the exploratory phase for this project was 8 days, with two outliers exhibiting 38 and 90 days. Across the sage-grouse translocation literature, other projects have reported averages of 20 days (Lazenby et al., 2021), 3 weeks (Balderson, 2017), and 4-6 weeks (Musil, 1993), but this last project did not incorporate GPS-marked individuals. In contrast, brooding females and their chicks exhibited no exploratory period (Picardi et al., 2022), emphasizing the need to select suitable release sites. Some research has evaluated differing durations of time spent in release acclimatization pens to reduce the time and energy spent dispersing post-release (Moehrenschlager and Lloyd, 2016). Managers must compare risk-to-benefit trade-offs of lower dispersal with decreased survival experienced as time held in the acclimatization pen increases (Devineau et al., 2011; Moehrenschlager and Lloyd, 2016; Ruzicka et al., 2024).

The availability of suitable habitat (provides the basic biotic and abiotic needs per life stage per season; Day et al., 2019; IUCN/SSC, 2013) highly influences post-release behavior at all steps in the post-release learning process for newly translocated individuals (e.g., at the release site, within the study area, and surrounding the study area; Attum and Cutshall, 2015; Parlato and Armstrong, 2013). Ideally, animals should choose the habitat patch that optimizes fitness (MacArthur and Pianka, 1966; Matthiopoulos et al., 2015); under compounded stressors derived from changes in the environment (i.e., translocations), the same animals may be prone to selecting ecological traps, areas of habitat that appear beneficial but are detrimental to fitness (Heinrichs et al., 2018; Madlinger, 2012; Robertson and Hutto, 2006). I observed differential habitat selection between individuals in the exploratory and restricted phases. Throughout the year, individuals in the exploratory phase were more prone to select higher annual herbaceous cover, higher road density, and lower sagebrush cover, which are correlated with lower survival in sage-grouse (Brussee et al., 2022; Connelly et al, 2011; Pratt and Beck, 2021). Habitat characteristics selected for by individuals in the restricted phase (areas closer to mesic habitat, higher elevation, lower tree cover) were consistent with other sage-grouse literature on spring and summer habitat across the species' range and in Utah populations (Connelly et al., 2011; Dahlgren et al., 2019; Picardi et al., 2020). Because the restricted phase is the desired result for translocated individuals post-release, these general habitat characteristics should be targeted when planning future sage-grouse translocations, especially within the Sheeprock Mountain SGMA. Understanding the connection between post-release dispersal, habitat selection, and survival and reproduction is essential, so assessing each step's associated fitness would be critical to evaluating each behavioral state's differential energetic effects (Matthiopoulos et al., 2015; Monk et al., 2020). Differences in vital rates between the two behavioral states would further emphasize the need to reduce post-release dispersal (Bell, 2016; Day et al., 2019; May et al., 2016).

Much of the recent translocation literature emphasizes that translocation programs should be framed as making decisions under uncertainty and iteratively moving through the planning, implementing, and modeling phases of the translocation actions (Converse and Armstrong, 2016; Ewen et al. 2023). Beginning with the first year of translocations, practitioners should assess behaviorally differentiated habitat selection within species distribution models (Eyre et al., 2022; Osborne and Seddon, 2012), species utilization models (Day et al., 2019), or spatial source-sink dynamic models (Heinrichs et al., 2018). Within the iterative structured decision framework, this would help assess release sites for subsequent years and glean insights into yearly changes in habitat selection and fitness in connection with management strategies (Ewen et al., 2023). Brood translocations for sage-grouse offer promising results in reducing dispersal and maximizing fitness (Lazenby, 2020; Meyerpeter et al., 2021; Picardi et al., 2022), and release sites by broods should be guided by modeled habitat suitability (Eyre et al., 2022; Osborne and Seddon, 2012) that include climate change (Bellis et al., 2020). If practitioners are unable to employ brood translocations, the addition of behavioral screening temperament traits (Jachowski et al., 2016; May et al., 2016) for pre-nesting females during capture, transit, and release in connection with post-release habitat selection and fitness offers further avenues to assessing the role of behavior in post-release movements and space-use. Employ caution with behavioral screening that restricts temperament traits, as individual variation could have important population-level benefits (May et al., 2016; Réale et al., 2007). Additionally, practitioners could explore acclimatization release pens for translocating pre-nesting females and their role in post-release dispersal and fitness (Jachowski et al., 2016). However, extensive planning would need to be involved in experimentally testing group size, release pen dimensions, locations near conspecifics (actively lek sites), and length of time spent in the pen prior to release (Ewen et al., 2023; Jachowski et al., 2016). The methods involved in using acclimatization release pens are highly dependent upon species characteristics and have had mixed results for avian taxa (Le Gouar et al., 2012; Moehrenschlager and Lloyd, 2016; Ruzicka et al., 2024); for landscape-level species, holding individuals short-term (e.g., 1-5 days) would theoretically provide the best benefit. Researchers should continue to assess behavioral responses post-release to improve the outcome of their translocation programs and employ a structured decision framework facilitate adaptive management during the execution of translocation efforts rather than post-hoc evaluations (Chauvenet et al., 2016, Converse and Armstrong, 2016; Ewen et al. 2023).

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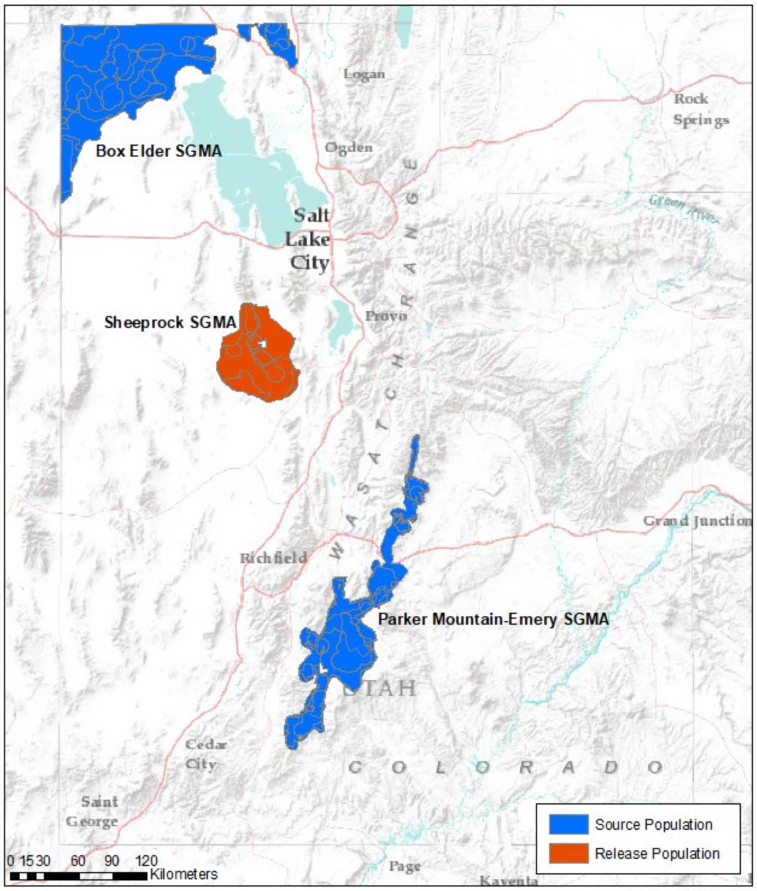
Tables and Figures

Table 3-1. Number of greater sage-grouse (*Centrocercus urophasianus*) fitted with rump-mounted solar-powered global positioning system (GPS) transmitters translocated into the Sheeprock Sage-Grouse Management Area from 2016-2019, Utah, US.

Year	Male	Female	Total
2016	4	8	12
2017	2	12	14
2018	2	12	14
2019	1	7	8
Total	9	39	48



Source: ESRI, UDWR

Figure 3-1. The release site and location of source populations for greater sage-grouse (*Centrocercus urophasianus*) translocated to the Sheeprock Sage-Grouse Management Area (SGMA; orange) to reinforce resident populations. Sage-grouse were translocated 2016-2019 from either Park Valley, located in the Box Elder SGMA, and Parker Mountain, located in the Parker Mountain-Emery SGMA, Utah, US.

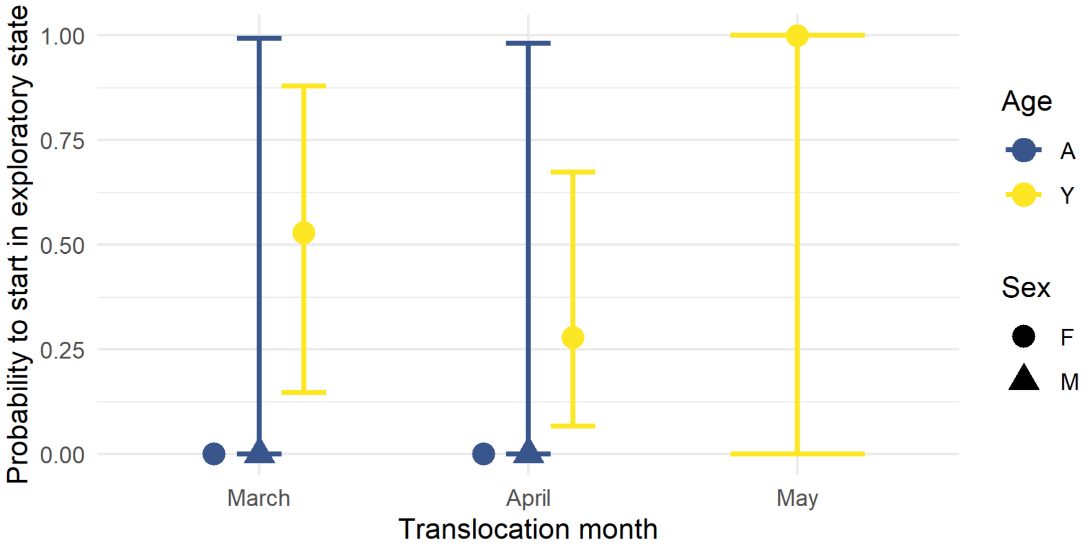


Figure 3-2. Initial state probabilities (estimated via a Hidden Markov Model) showing the propensity of greater sage-grouse (Centrocercus urophasianus) translocated to begin in the exploratory state (defined by long step lengths and low turning angles) immediately post-release. Sage-grouse were translocated between 2016-2019 into the Sheeprock Mountain Sage-Grouse Management Area, Utah, US, during the lekking season, from March to May. Adults (A) are in blue, yearlings (Y) in yellow; the circles indicate females (F), the triangles indicate males (M).

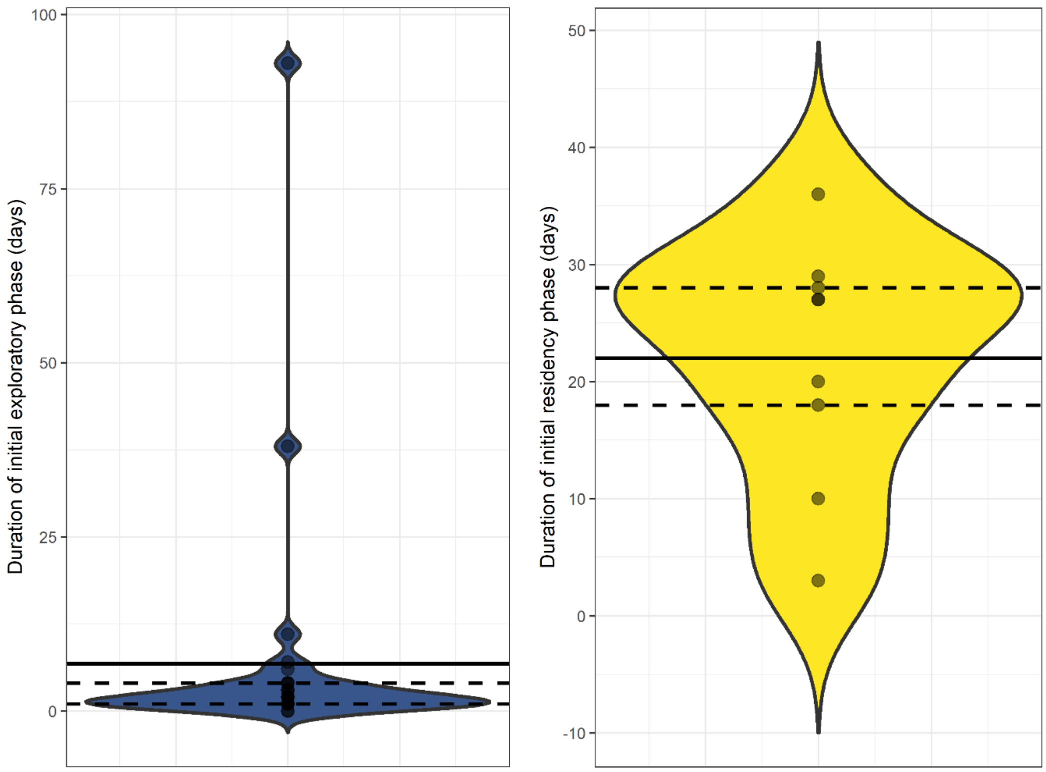


Figure 3-3. Distributions of the duration (in days post-release) of initial exploratory phase (left; defined by long step lengths and low turning angles) and the initial residency phase (right; defined by short step lengths and high turning angles) for translocated greater sage-grouse (*Centrocercus urophasianus*) in the Sheeprock Sage-Grouse Management Area, Utah, US, from 2016-2019. The exploratory phase was, on average, a short duration, with the mean less than 10 days. The mean of the initial residency phase duration is 22 days.

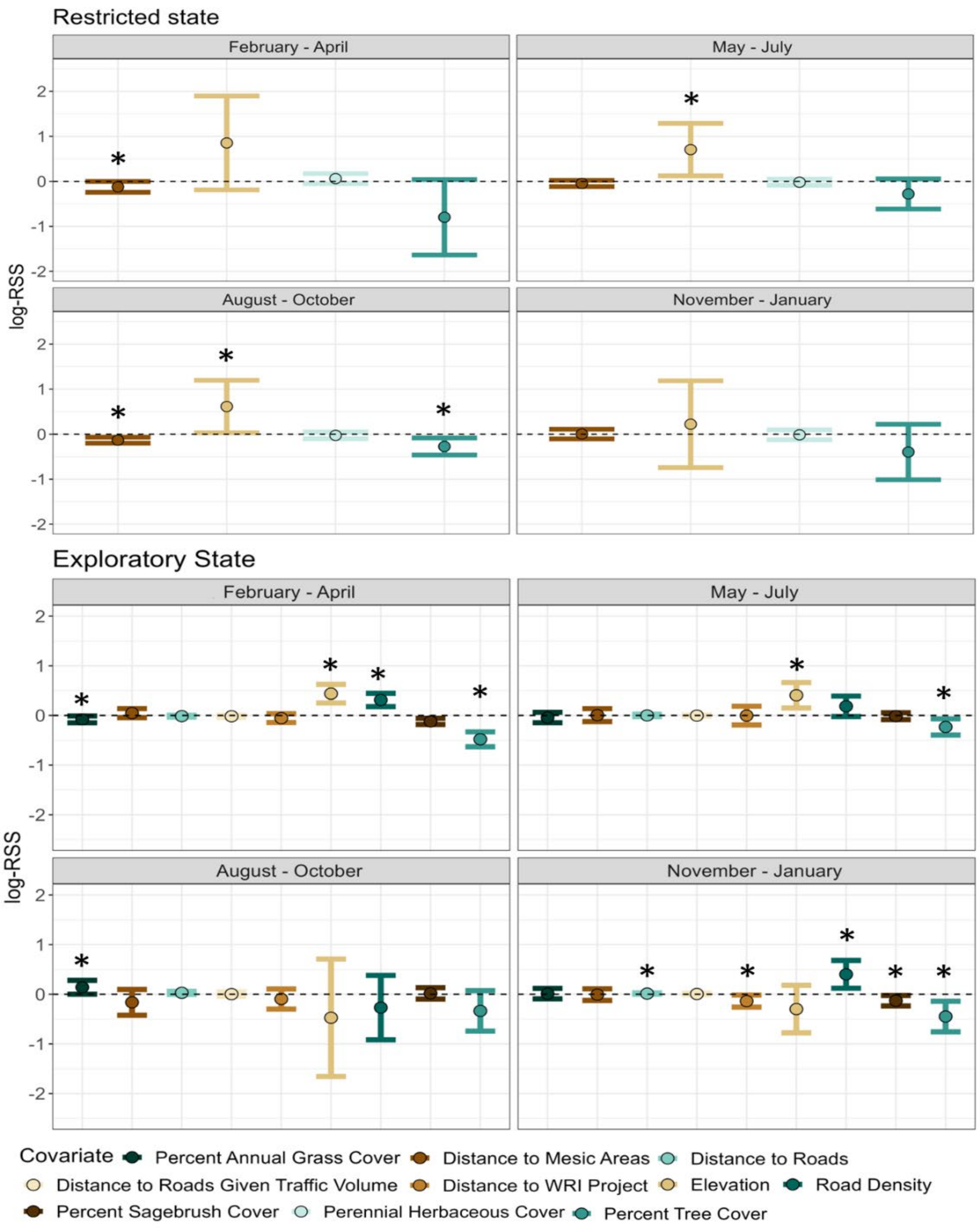


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Figure 3-4. Seasonal log-relative selection strength for greater sage-grouse (Centrocercus urophasianus) translocated from 2016-2019 into the Sheeprock Sage-Grouse Management Area, Utah, US. Post-release, individual behavior was delineated as either restricted (defined by short step lengths and high turning angles) or exploratory (defined by long step lengths and low turning angles) behavioral states, estimated via Integrated Step Selection Analysis.

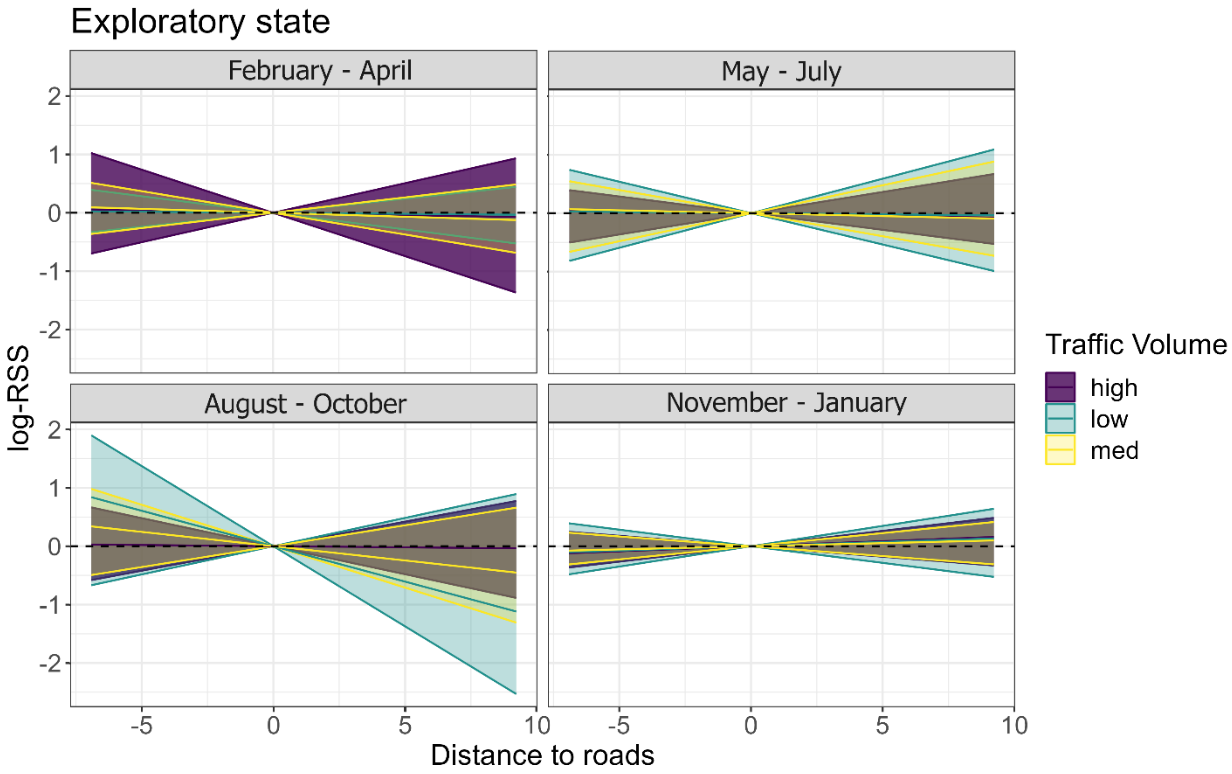

Figure 3-5. Population-level log-relative selection strength for distance to roads as a function of traffic volume by translocated greater sage-grouse (*Centrocercus urophasianus*) exhibiting the exploratory behavioral state (defined by long step lengths and low turning angles) between 2016-2019 in the Sheeprock Sage-Grouse Management Area, Utah, US. Estimated via Integrated Step Selection Analysis.

CHAPTER 4

LOW CHICK SURVIVAL BUT POSITIVE ALLELIC RICHNESS FOLLOWING CONSERVATION TRANSLOCATIONS PROVIDES SHORT-TERM INSIGHTS INTO SAGE-GROUSE REINFORCEMENTS

Abstract

In the Anthropocene, large-scale habitat loss dictates the decline of many species, leading to global species extirpation or extinction combatted by a plethora of conservation intervention tools. Conservation translocations (translocations; e.g., reintroductions, introductions, and reinforcements) are one tool consistently deployed to slow the increased rate of species loss. Translocations often have mixed success and can be evaluated using demographic or genetic modeling, although it is less common to model both to ascertain translocation outcomes. Greater sage-grouse (sage-grouse; *Centrocercus urophasianus*) are among these species experiencing unprecedented declines, which have been slowed by intense range-wide management interventions, including translocations. I used an integrated population model (IPM) to describe the effects of sage-grouse reinforcements performed in Utah from two source populations to a reinforced population between 2016 and 2019. I used 18 years (2005-2022) of peak male lek count data for both the source populations and reinforced population, combined with five years of in-depth demographic monitoring from radio-marked individuals (2016 – 2020) to estimate before-after-impact (BA) effects of the translocation on each population's demography. Additionally, I used microsatellite data to evaluate the effects of the translocations on genetic variation and population admixture from feathers collected from 2005 to 2015 (prior to translocations) and 2017 to 2020 (post-translocation initiation). The IPM predicted declining populations following translocations due to low chick survival, and estimated population abundance of 35 (95% credible interval: 17 – 59) individuals in 2022 and 22 individuals (2 – 63) by 2027. However, I also detected an increase in allelic richness and the potential for the increased admixture of the source population genetics in the reinforced population. I demonstrate that genetic and integrated population models can provide a more comprehensive view of translocation efficacy. Although short-term genetic data can be informative, long-term monitoring is still required to understand the success of translocation objectives.

Keywords: conservation translocations; reinforcements; integrated population model; conservation genetics; greater sage-grouse

Introduction

The Anthropocene is marked by the pervasive, large-scale loss and degradation of wildlife habitats in the wake of human activities, habitat fragmentation, and land-use change (Dirzo *et al*., 2014). Wildlife populations are driven by fluctuations in vital rates stemming from interannual variation in the relative rates of additions (births and immigration) and losses (deaths and emigration; Anderson *et al*., 1982). One of the demographic consequences of habitat fragmentation has been the reduction or outright loss of migration and dispersal, which increases the extirpation and extinction risks to which habitat specialists are particularly susceptible. Often, this leaves small populations increasingly vulnerable to demographic, environmental, and genetic stochasticity (Caughley, 1994) that can have compounding effects on vital rates in a continual negative trend known as the extinction vortex (Gilpin & Soulé, 1986; Fagan & Holmes, 2006). Under these circumstances, conservation interventions may influence vital rates for at-risk species or populations (Young *et al*., 2005; Dirzo et al., 2014; Horne *et al*., 2020). Interventions can include: predator, competitor, or invasive species management (Moehrenschlager & Lloyd, 2016; Fulbright *et al*., 2020); disease management (Silk *et al*., 2019); habitat restoration to improve species' abiotic and biotic needs (IUCN/SSC, 2013); installation of structures to promote connectivity (e.g., wildlife crossings; Hess & Fischer, 2001; Bissonette & Adair, 2008; Liu *et al*., 2018); or physically moving individuals, a practice known as conservation translocations (hereafter, translocations; IUCN/SSC, 2013; Jachowski *et al*., 2016; Gaywood *et al*., 2023).

All of these management actions are designed to ameliorate survival and demographic connectivity indirectly, but translocations can serve as a temporary proxy for lost population components through direct, successive releases of individuals over a calculated timespan (Ewen *et al*., 2012; Jachowski *et al*., 2016; Gaywood *et al*., 2023). There are three forms in which translocations are applied: reintroductions, releasing individuals into previously occupied habitats; introductions, releasing individuals into suitable habitat outside of their known historic distribution; or reinforcements, releasing individuals into extant populations that are small, closed, declining, or genetically inbred (IUCN/SSC, 2013). The goal of translocations is to establish a viable, self-sustaining population in which little or no further management interventions are needed (Seddon, 1999; Fischer & Lindenmayer, 2000; Chauvenet *et al*., 2016; Morris *et al*., 2021).

Demographic modeling (e.g., mathematical modeling, forward simulation, and inferential modeling) is one of the principal ways to evaluate a translocation program's success (Armstrong & Reynolds, 2012; Converse & Armstrong, 2016). Demographic modeling can be used to determine the age class, sex, group size, and the total number of translocated individuals to remove from the source and release into the reinforced population. Furthermore, demographic modeling can be used to quantify the population-level effects of removing individuals from the source populations and releasing individuals into the reinforced population or area by projecting the trajectory of either population forward in time (Armstrong & Reynolds, 2012; Converse & Armstrong, 2016; Mitchell *et al*., 2022).

In addition to evaluating demographic metrics for translocations, genetic metrics can provide valuable information on genetic diversity, which can be measured by assessing genetic heterozygosity, allelic richness, and allelic frequency (Frankham *et al*., 2010; Biebach *et al*., 2016; Neaves *et al*., 2023). In large populations, rare alleles have a higher probability of occurring, which strengthens the inherent ability of that population to adapt in the long term (Biebach *et al*., 2016). Higher genetic variation in a population increases the adaptive potential of that population, which has important implications for persistence (Frankham *et al*., 2010; Allendorf *et al*., 2013; Biebach *et al*., 2016). Thus, a lower level of allelic richness can affect the population's ability to respond and adapt to environmental and demographic stochastic in a phenomenon known as the "small population paradigm" (Caughley, 1994; Frankham *et al*., 2010; Horne *et al*., 2020). Therefore, it can be important for practitioners and researchers involved in translocation programs to evaluate demographic and genetic components when analyzing translocation outcomes (Robert *et al*., 2007; Manlick *et al*., 2017).

Translocation projects are inherently multi-faceted and require multiple metrics to assess true rather than perceived success (Robert *et al*., 2007; Brichieri-Colombi & Moehrenschlager, 2016). Evaluating demographic and genetic metrics can provide more insight into translocation success than evaluating either alone (Lande, 1988; Robert *et al*., 2007; Manlick *et al*., 2017). Researchers can measure gene flow among populations and population structure in translocation programs intended to improve population connectivity and dispersal (Thompson, 2012) or quantify genetic variability and parentage analyses to assess the reproduction of translocated individuals (Manlick *et al*., 2017). Robert *et al*. (2007) summarized ways previous research had integrated genetics and demographics to evaluate possible reasons for extinction and assessed translocation release strategies (i.e., how many individuals over what period and when). Monitoring genetic and demographic markers in both the reinforced and the source population(s) is essential (Jamieson & Lacy, 2012; Converse & Armstrong, 2016). Removing individuals from the source population to reinforce another population has similar implications to harvest management, and in resource-limited years, removing a certain number of individuals from a population could act as an additive effect on mortality (Dimond & Armstrong, 2007; Mitchell *et al*., 2022). Genetically, determining an appropriate source population involves assessing that population's genetic structure to prevent genetic divergence or outbreeding depression (Frankham *et al*., 2011; Groombridge *et al*., 2012; Jamieson & Lacy, 2012).

In greater sage-grouse (*Centrocercus urophasianus*; sage-grouse), an avian sagebrush (*Artemesia* spp.) obligate declining across its range primarily due to habitat loss, translocations have been utilized to prevent extirpations beginning in the early 20th century with mixed results (Reese & Connelly, 1997). Reese and Connelly (1997) estimated only 5% of sage-grouse translocation projects had successful outcomes and established translocation methods to increase the probability of translocation success.

Only one of the 11 sage-grouse translocation projects reported since 1997 estimated the effects of translocation-associated removals on the source populations (Meyerpeter, 2020; Table 4-1). Only two of the 11 projects evaluated genetic effects alongside demographic outcomes (Thompson, 2012; Dunken, 2014; Table 4-1). Thus, sage-grouse managers need more information on translocations' aggregate genetic and demographic consequences on both source and reinforced populations. The sage-grouse population in the Sheeprock Mountain (SR) Sage-Grouse Management Area (SGMA) in central Utah is a closed population (Robinson & Messmer, 2013), having experienced no immigration or emigration following European settlement and anthropogenic development around these areas between the mid-1800s to mid-1900s (Beck *et al*., 2003). The population peaked over the monitoring period at 190 lekking males in 2006 (Robinson, 2007; Robinson & Messmer, 2013); however, it began to decline in 2007 and reached an estimated low of 23 lekking males in 2015 (Figure 4-1). As a result, researchers and managers translocated male and pre-nesting female sage-grouse into the SR SGMA from two source populations between 2016 and 2019. The primary goal of this intervention was to prevent population extirpation in the immediate term and, ideally, improve population demographic performance in the future. In this paper, I assessed the short-term success of this primary goal by: 1) estimating population parameters and abundance during the monitored study period and projected to 2027 for the SR SGMA via an integrated population model (IPM); 2) estimating potential effects of removing founder individuals from the two source populations; and 3) estimating allelic frequency, allelic richness, heterozygosity, inbreeding statistic, and the genetic structure of the SR SGMA population in comparison to the source populations and SR SGMA prior to translocations.

Materials and Methods

Study Areas

Reinforced Population

The SR SGMA is located at the eastern edge of the Great Basin in Utah's West Desert (Figure 4-2). It is an area comprised of 2473 km^2 overlapping Tooele and Juab counties and exhibits a mixed patch framework of land ownership that includes Bureau of Land Management (BLM), U.S. Forest Service (USFS), private, Utah School and Institutional Trust Lands (SITLA), and Utah Department of Wildlife Resources (UDWR). Given the multiple land ownerships, a local working group, the West Desert Adaptive Resource Management (WDARM) group, was established to facilitate frequent dialogue and collaboration amongst all stakeholders on conservation issues.

This area is characterized by warm, dry summers and cool winters. The 50-year average maximum summer temperature is 32.4˚C in July, and the minimum winter temperature is -10.4˚C in January (Western Regional Climate Center, 2016). The average annual precipitation is 26.01 cm, with the highest accumulation in spring and fall. The average snowfall is 91.95 cm.

Elevation ranges from 1500 m in the lower valleys to 2950 m at the tallest peaks. The lower elevation vegetation includes bulbous bluegrass (*Poa bulbosa),* crested wheatgrass (*Agropyron cristatum*), gray horsebrush (*Tetramydia canescens*), rubber rabbitbrush (*Ericameria nauseosa*), sandberg bluegrass (*Poa secunda*), Wyoming big sagebrush (*A. tridentata* spp *wyomingensis*; Robinson, 2007; Robinson & Messmer, 2013). Invasive vegetation located in the lower elevation includes bur buttercup (*Ceratocephata testuculata*), cheatgrass (*Bromus tectorum*), knapweed (*Centaurea* spp.), and tansy mustard (*Descurainia pinnata*). As elevation increases, native shrubs and trees, including antelope bitterbrush (*Purshia tridentata*), aspen (*Populus tremuloides*), common snowberry (*Symphoricarpos albus*), Douglas rabbitbrush (*Chrysothamnus viscidiflorus*), juniper (*Juniperus* spp.), mountain big sagebrush (*A. t. vaseyana*), pinyon pine (*Pinus* spp.), and serviceberry (*Amelanchier alnifolia*) become more prevalent. Higher-elevation ridgelines are dominated by black (*A. nova*) and low (*A. arbuscula*) sagebrush shrubs.

Source Populations

The project relied on two source populations: Parker Mountain and West Box Elder. Both source populations were greater than 50 km away from the reinforced population (Reese & Connelly, 1997; Oyler-McCance, Taylor, & Quinn, 2005). Parker Mountain (PM; Figure 4-2) is part of Utah's Parker Mountain-Emery SGMA located in south-central Utah and contains one of the largest sage-grouse populations in the state. It is situated on the Colorado Plateau and is characterized primarily by black sagebrush (*A. nova*) on the ridges and slopes and big sagebrush (*A. tridentata*) in the drainages (Baxter, Flinders, & Mitchell, 2008). Elevation ranges from 2140 m to 3000 m (Chi, 2004; Baxter *et al*., 2008). Average annual precipitation is 56.7 cm, receiving the highest precipitation in fall, winter, and spring, which is characteristic of cold deserts (Dulfon, 2016).

West Box Elder (WBE; Figure 4-2) is located in northwestern Utah in the western portion of the Box Elder SGMA. It contains predominately big sagebrush, black sagebrush, and low sagebrush, similar to the SR SGMA (Sandford *et al*., 2017). WBE is located on the boundary between the Snake River plain and the Great Basin Desert.

Elevation ranges from 1350 m to 2950 m, with average annual precipitation ranging from 17.7 cm to 78.3 cm across that elevational gradient (Sandford *et al*., 2017).

Capture and Translocations

During the spring breeding seasons from 2016 to 2020, researchers captured 39 (12 male/27 female) resident sage-grouse in the SR population. Between 2016 and 2019, 146 (40 male/106 female) translocated sage-grouse were captured from the PM and WBE source populations and released into the SR population. Additionally, 91 WBE population individuals (10 male/ 81 female) were captured and monitored from 2016 to 2019. All sage-grouse were captured at night using all-terrain vehicles, spotlights, and long-handled nets near active leks (2100hr to 200hr; Connelly, Reese, & Schroeder, 2003). Sage-grouse were randomly marked with either an 18 g necklace-style very-high-frequency (VHF) radio transmitter (Advanced Telemetry systems, Insanti, MN, USA) or a rump-mounted, solar-powered global positioning system (GPS) transmitter (Microwave Telemetry, Inc., Columbia, MD, USA, and GeoTrak, Inc., Apex, NC, USA; Bedrosian & Craighead, 2007). Individual data collection included aging, sexing, weighing, marking with a 14-16 leg band for females and males, respectively, collecting a feather sample for genetic analyses, and recording the capture location (UTM, 12N, NAD 83).

Feathers from resident and translocated sage-grouse were collected either 1) as clean feathers lost incidentally during capture or 2) removing feathers from the breast in the absence of clean incidental feathers on the ground following capture. I placed all feather samples in paper envelopes, sealed them, and labeled them with the date, sex, collector's name, bird ID, and capture location. I stored the envelopes in desiccant and placed them in the freezer for tissue preservation.

Following capture, SR and WBE resident sage-grouse were processed and immediately released at the capture site. However, translocated individuals were either processed upon capture or brought to a central location adjacent to capture sites and processed before departing the source populations. There was no active radiomarked monitoring study between 2016-2020 in PM. Between 2016 and 2019, researchers marked 142 translocated sage-grouse with transmitters, but 4 of the translocated sage-grouse were unmarked due to transmitters falling off in transit or immediately following release.

The translocations followed capture and release guidelines outlined by Reese and Connelly (1997) and Baxter *et al*. (2008), with a few exceptions. For the translocation release in 2016, researchers and practitioners placed sage-grouse in individual cardboard boxes (30 cm x 23 cm x 30 cm) containing pine shavings for transport and release at the study site. Beginning in 2017, I modified my translocation protocols to align with two concomitant sage-grouse translocation studies range-wide. Following this modification, I used wooden remote-release boxes to translocate sage-grouse. The wooden remote-release boxes contained five separate compartments with padded walls and pine shavings. Transport was overnight by pickup truck to the study site (0100 hr to 0600 hr) to release at sunrise within the same night of capture. At the release site, the remote release boxes were placed within 200 m of active lek sites, and grouse were released at sunrise facing the lek, with researchers operating the remote release from the vehicle to facilitate a lower-stress release environment (Baxter *et al*., 2008; Dickens, Delehanty, & Romero, 2010). Individuals were released after scanning the immediate area for predators.

Field Monitoring

Survival and space use of male and female translocated and resident sage-grouse were monitored weekly from capture, between March and April until August, and intermittently throughout the fall and winter for VHF-marked individuals. The GPS transmitters remotely registered four to six sage-grouse locations each day during the five-day duty cycle, with schedules varying according to four seasons that coincided with sage-grouse lekking (March 1 [0100hr, 0700-0800, 1300, 1700-1800]), nesting (May 1 [0100-0700-0800, 1300, 1800-1900]), brooding (June 16 [0000, 0200, 0700, 1300, 1600, 2000]), and late fall seasons (October 1 [0000, 0800, 1600, 2000]). Transmitters registered each fix location's date, time, elevation, and speed. I determined mortality for the GPS transmitters by monitoring the data for several consecutive fixes in the same location. After I detected a mortality, I located the transmitter and determined the cause of death, if possible.

Lek counts were conducted in the spring according to the procedures outlined in the UDWR protocol. I performed lek counts between March 20 and May 7 each year. On a given morning, counts occur three to five times within a period of 30 minutes before to 90 minutes after sunrise. Observers recorded the maximum number of males and females that visited the lek during that period (the male count is used for the lek count). To record whether translocated males and females visited the lek, the observer used radio telemetry equipment to listen for the translocated males' frequencies. I excluded radio-marked translocated males if released in the same season to prevent bias from that year's population estimates.

For female sage-grouse during the nesting season (late March through early June) in SR and WBE, all were located two to three times per week to determine the nest initiation date. I confirmed a nest by visually observing a female on a nest without causing her to flush or through triangulation three times in one area within 10 meters. Following confirmation, I monitored the nest two to three times a week from 30 to 50 meters away to determine if the female's signal was still in the direction of the confirmed nest; if I did not detect a signal around the triangulated point, the observer approached the nest while listening for the signal and determined whether the female was still nesting. If a nest failed (e.g., depredated or abandoned), I attempted to identify the cause for failure and monitored that female two to three times a week to document re-nesting attempts. Once the eggs hatched after 26-28 days of incubation, I estimated the clutch size by counting the number of eggshells after the female left the nest.

I monitored broods visually three times per week until the brood reached 50 days post-hatch, at this point, a brood was classified as successful if at least one chick was present with the female. In 2016 and 2017 in the SR population, 50-day brood surveys were conducted during the day with observers flushing the hen and walking in increasing concentric circles to count the number of other females and chicks present (Dahlgren *et al.*, 2010b). From 2018-2020 in the SR population and 2016-2019 in the WBE population, pointing dogs were used to point the hens and, while the observer walked increasing concentric circles, the bird dog would pursue scent and point any other females or chicks detected (Dahlgren *et al.*, 2010b). Chicks were not individually radio-marked in the SR population, but chicks were radio-marked with VHF transmitters in

WBE from 2018-2019 to monitor brood admixture and chick survival (Dahlgren *et al.*, 2010a; Small, 2021).

For all males and non-nesting and broodless females, I monitored them one to two times per week through mid-August. During the fall and winter, I monitored GPS-marked sage-grouse remotely. I monitored VHF-marked individuals intermittently in the fall and through one fixed-wing aircraft flight in the winters of 2016 and 2017.

All research activities were performed per Utah State University IACUC protocol #2560 (SR translocation project) and #2322 (WBE monitoring project) and associated UDWR protocols.

Genetic Sample Preparation

Genetic material was extracted from feathers gathered from the breast of translocated and resident birds at capture. Using data from previous studies, I included 14 SR, 112 PM, and 29 WBE feather samples previously genotyped before translocation between 2005 and 2015. Using feathers collected between 2017-2020, I included 32 SR resident feather samples collected from individuals for the post-translocation evaluation. The bases of the calamus from feathers were cut into approximately 2-5cm pieces. DNA was extracted using the DNeasy Blood & Tissue kit (Qiagen, Inc.) and the user-developed protocol (Oyler-McCance & St. John, 2010; Fike *et al.*, 2015). This protocol was modified to incubate samples for at least 8 hours to maximize the process of tissue lysis. The DNA sample was then eluted in 100 µL of Buffer AE (Qiagen, Inc.).

Microsatellite Fragment Analysis

There were 16 highly polymorphic microsatellite loci used (BG6 (Piertney & Höglund, 2001): SGMS06.4, SGMS06.6, SGMS06.8, MSP11, MSP18 (Oyler-McCance & St.

John, 2010); SG21, SG28, SG29, SG36, SG39 (Fike *et al*., 2015); SGCA5, SGCA11, SGCTAT1 (Taylor, Oyler-McCance, & Quinn, 2003); TUT3, and TUT4 (Segelbacher *et al*., 2000). Sex was determined by amplifying a region of the CDH gene using the primers 1237L and 1272H (Kahn *et al*., 1998). The primers for two loci were redesigned by T. Cross (University of Waterloo, pers. comm.) for better performance (SGCA5F: CGGACAGGTACATCCTGGAA, SGCA5R: GGGAAAAGATGTCAGAATCTACAAA, SGCA11F: GCAGTAAAGAAAATTTGGAAGCA, SGCA11R: TCTTGAACTGATGTTGGATTTG). Amplifications were performed in four ten µL multiplexed PCRs using the 2x Qiagen Multiplex PCR Master Mix (Qiagen) following the manufacturer's protocol. The loci were grouped based on their annealing temperature, size, and primer label. Multiplexes were comprised of the following loci: Set 1—MSP18, SGMS06.4, SGCA5, BG6 and the sexing locus; Set 2—TUT3, SGCA11, MSP11, SGMS06.6, SGMS06.8, and SGCTAT1; Set 3—SG28, SG36, and SG39; Set 4— SG21, SG29, and TUT4. All PCRs consisted of 2 µL of template DNA, 1 mL primer mix, 5 mL 2x Master Mix, and 2 mL water. Amplification conditions for multiplex sets were as follows: 95 oC for 15 min, then 94 oC for 30 sec, annealing temperature (55 oC: sets 1 and 2, 60 oC: sets 3 and 4) for 1.5 min, 72 oC for 1 min for 40 cycles, then 60 oC for 45 min. PCR products were combined with GeneScan LIZ 600 internal lane size standard. Each multiplex PCR was run separately on an AB3500 Genetic Analyzer (Applied Biosystems). Allele sizes were determined for each locus using GENEMAPPER v5software (Applied Biosystems). All feather samples were amplified and genotyped twice to verify allele classifications.

Data Analysis

Integrated Population Model

The integrated population model (IPM) combined 18 years (2005-2022) of annual male sage-grouse peak lek counts from the reinforced population, SR, and the two source populations, WBE and PM, with individual-level demographic data on survival of resident and translocated males and females, nest survival, and brood (chick) survival from the SR and WBE populations from 2016 to 2020. My objective was to understand the effect the translocations had on the finite rate of population change, λ, and the apparent abundance of both the reinforced population and the source populations following the removal of translocated individuals (Dimond & Armstrong, 2007; Mitchell *et al*., 2022). I modeled these data similarly to Meyerpeter (2020), using models developed initially by Mathews *et al*. (2018).

Survival and recruitment were the two fundamental vital rates included in the IPM. The recruitment model accounted for real-world uncertainty associated with nest propensity, clutch size, nest survival, egg hatchability, chick survival, and juvenile survival (Dowd & Meyer, 2003). Below, I describe the components of the survival and recruitment models, including their associated likelihood. All prior distributions are in Appendix D. Each equation utilizes i, j, and k subscripts to signify age, site, and year, respectively.

Survival model:

I used a shared-frailty model to estimate monthly survival probabilities of yearlings and adults for both male and female translocated and resident individuals in the reinforced SR population and WBE monitored population (Halstead *et al*., 2012). The equation below describes the monthly unit hazard ($UH_{survival,ijk}$), intercept (α_i), fixed effect of sage-grouse age class ($\beta_i * x_{ijk}$), and nested random effects for year (κ_k), site (γ_j), and site*year (ζ_{jk}). I then calculated the annual (12-month, $t = 12$) cumulative survival (CH) as a derived quantity by summing UH across months. The hazard function then relates to survival (S) in the equation below and provides the overall survival estimate per group (Halstead *et al*., 2012; Severson *et al*., 2019).

Equation for monthly unit hazard shared-frailty model:

$$UH_{survival,ijk} = exp\ (\alpha_i + \beta_i x_{ijk} + \kappa_k + \gamma_j + \zeta_{jk})$$

Cumulative hazard survival model:

$$CH_{ijk} = \sum_{k=1}^{k=12} UH_{ijk}$$

Survival parameter model:

$$S_{ijk} = e^{-CH_{ijk}}$$

Recruitment model:

Recruitment was performed for both age classes in the SR (with resident and translocated recruitment combined due to sample size of the former) and WBE population. Recruitment was a function of first and second nest propensity ($np1$ and $np2$), clutch size for first and second nests ($cl1$ and $cl1$), nest survival for first and second nests ($ns1$ and $ns2$), egg hatchability (h), chick survival (cs), and juvenile survival (js). Due to inherent bias in estimating first nest propensity, informative priors were based on vital rate estimates from Taylor *et al*. (2012; $np1_{i=adult} = 0.96, 95\%\ \text{CI} = [0.94, 0.97]; np1_{i=yearling} = 0.89, 95\%\ \text{CI} = [0.87, 0.91]$). I then modeled the informative priors as beta distributions with alpha and beta parameters (Meyerpeter, 2020). The first component in the recruitment (R_{ijk}) equation represents first nest initiations. The second component represents any re-nesting initiations from the individuals included in the first component after failing the first nest initiations. Below is the equation for recruitment:

Recruitment equation:

$$R_{ijk} = \left(ns1_{ijk} \times np1_{ik} \times cl1_{ijk} \times h_{ijk} \times cs_{ijk} \times js\right)$$
$$+ ((1 - ns1_{ijk}) \times np2_{i} \times cl2_{ijk} \times ns2_{ijk} \times h_{ijk} \times cs_{ijk} \times js)$$

Nest propensity

First nest propensity:

$$np1_{i=adult} \sim Beta(97,5)$$
$$np1_{i=yearling} \sim Beta(90,12)$$

Sage-grouse may re-nest if they fail their first nesting attempt, although some populations have lower probabilities of re-nesting than others (Connelly *et al.*, 2011). Thus, I modeled the second nest propensity as a binomial distribution with $p_{np2,ij}$ as the proportion of failed nests per age class and site and $n_{np2,ij}$ representing the number of attempted re-nests for each age class and site. I modeled $p_{np2,ij}$ using a logit link and a linear combination of covariates (α and $\beta_i x_{ijk}$), where all regression coefficients were assigned weakly informative (N(0,0.1)) priors to improve the efficiency of model convergence.

Logistic model for second nest propensity:

$$y_{np2,i} \sim Binomial(p_{np2,ij}, n_{np2,ij})$$

$$logit(p_{np2,ij}) = \alpha + \beta_i x_{ijk}$$

Clutch Size

Clutch size ($y_{cl,ijk}$) was modeled using Poisson distributions with rate parameters ($\mu_{cl,ijk}$) that varied as a log-linear function of age ($\beta_i x_{ijk}$), site, year, and nest attempt ($x_{n,ijk}$).

Log-linear model for expected clutch size:

$$y_{cl,ijk} \sim Poisson(\mu_{cl,ijk})$$

$$log(\mu_{cl,ijk}) \sim \alpha + \beta_i x_{ijk} + \beta_n x_{n,ijk} + \kappa_k + \gamma_j + \zeta_{jk}$$

Nest Survival

I used a second shared-frailty model to model nest survival for both first and second nests ($ns1$ and $ns2$) and included both fixed effects for age and nesting attempt (n). Nest survival was modeled at a daily timescale and calculated as the cumulative hazard of nest survival as a derived quantity. To account for random variation associated with individuals nesting across multiple years, I included the hierarchical effect v_v, see Appendix D.

Nesting unit hazard shared-frailty model:

$$UH_{nest,ijk} = exp\ (\alpha + \beta_i x_{ijk} + \beta_n x_{n,ijk} + v_v + \kappa_k + \gamma_j + \zeta_{jk})$$

Hatchability

Hatchability was modeled similarly to second nest propensity, where the egg hatchability (h) in a nest is captured through a binomial distribution with number of hatched eggs ($n_{h,ijk}$) being the number of successes out of the total clutch size ($p_{h,ijk}$). The hatchability model also included hierarchical effects for year and site.

Logit-link linear model for hatchability:

$$y_{h,ijk} \sim Binomial(p_{h,ijk}, n_{h,ijk})$$

$$logit(p_{h,ijk}) = \alpha + \beta_i x_{ijk} + \kappa_k + \gamma_j + \zeta_{jk}$$

Chick survival

Chick survival (cs) was modeled as a binomial distribution with the number of success being the number of chicks present with a given female at the end of the 50-day brood monitoring period ($p_{cs,ijk}$) and the number of trials being the number of hatched eggs in that given female's successful nest ($n_{cs,ijk}$). I modeled the probability of chick survival using a logit-link linear function with hierarchical effects for site and year, and an additional fixed effect capturing density-dependence ($\beta_{dd} x_{dd,ijk}$) based on the previous years' chick abundance (taking the log of that previous year's chick abundance).

Logit-link linear model for chick survival:

$$y_{cs,ijk} \sim Binomial(p_{cs,ijk}, n_{cs,ijk})$$

$$logit(p_{cs,ijk}) = \alpha + \beta_i x_{ijk} + \beta_{dd} x_{dd,ijk} + \kappa_k + \gamma_j + \zeta_{jk}$$

$$\sigma_\zeta \sim Uniform(0,5)$$

Juvenile survival

Because I did not monitor broods past 50 days post-hatch and only have intermittent monitoring for VHF-marked individuals, I could not obtain accurate empirical survival data for juveniles (defined as the age class between brood dispersal at the end of August and until the first spring, when they are considered yearlings). I therefore utilized informative priors exactly from Taylor *et al*. (2012) to inform the juvenile survival estimates and assigned these estimates to a beta distribution.

$$js \sim Beta(100{,}34)$$

Estimating $\hat{N}$ *and* $\hat{\lambda}$*:*

Apparent abundance ($\hat{N}_{app,j}$) is the sum of the recruited and surviving individuals ($\hat{N}_{ijk}$) and the newly translocated or removed individuals ($\pm\hat{N}_{trans,ijk}$). To estimate apparent abundance, I modified the total estimated population size by either subtracting (from the source populations) or adding (from the reinforced population) the precise number of individuals translocated.

$$\hat{N}_{app,j} = \hat{N}_{ijk} \pm \hat{N}_{trans,ijk}$$

After calculating apparent abundance, I calculated the estimated total abundance ($\hat{N}_{tot,j}$) in the following equation by incorporating sightability (v), the probability of a male being present on a lek but not observed (Coates *et al*., 2019); lek attendance (φ); lek detection (o), the probability of a lek being detected; and sex ratio (ω), based on estimates from Guttery *et al*. (2013). For the source and reinforced populations, I projected population abundance for five years (up to 2027).

Total population estimate:

$$\hat{N}_{tot,j} = \frac{\hat{N}_{app,j} + (\hat{N}_{app,j} * \omega)}{v * \varphi * o}$$

Prior distributions and values:

$$v \sim Beta(61.29{,}9.98)$$

$$\omega \sim Normal(1.458,0.099)$$

$$o = 0.95$$

$$v = 0.84$$

I then calculated estimates of $\hat{\lambda}$ by dividing the estimated total abundance for each year ($\hat{N}_{totk+1,j}$) by the previous years' total abundance ($\hat{N}_{totk,j}$), shown in the equation below.

Finite rate of growth ($\hat{\lambda}$) estimate:

$$\hat{\lambda}_j = \frac{\hat{N}_{totk+1,j}}{\hat{N}_{totk,j}}$$

BA Parameters

I used a BA ratio ($\hat{R}_{BA}$) of the $\hat{\lambda}$ posterior distributions to estimate the translocation treatment effect that was modified from Connor *et al*. (2016), where $\hat{R}_{ibefore}$ equates to the ratio of the impact (i) sites before the reinforcement, and $\hat{R}_{iafter}$ corresponds to the ratio after reinforcements were initiated (Meyerpeter, 2020; Coates *et al*., 2021). Ratio scores above or below 1 indicate a positive or negative effect, respectively.

BA ratio equation:

$$\hat{R}_{BA} = \frac{\hat{R}_{ibefore}}{\hat{R}_{iafter}}$$

I also employed the use of Chevalier, Russell, & Knape (2019)'s control-impact (CI)-divergence and CI-contribution metrics, which further aid in interpreting BA results

(Meyerpeter, 2020). CI-divergence quantifies how large the similarities are in the impact (i) and control (c) sites before (b) and after (a) the reinforcement, and CI-contribution quantifies how much the treatment impacted the impact site. Below are the calculations, where μ represents the mean of the response variables across years.

$$CI - divergence = |\mu_{ia} - \mu_{ca}| - |\mu_{ib} - \mu_{cb}|$$

$$CI - contribution = |\mu_{ia} - \mu_{ib}| - |\mu_{ca} - \mu_{cb}|$$

Model posteriors were generated by running 3 MCMC chains for 50,000 iterations following a burn-in period of 10,000 iterations and thinning each chain by a factor of 10. I assessed model convergence based on visual examination of MCMC mixing and based on the Gelman-Rubin diagnostic, R. Specifically, if the upper bound of the 95% credible interval on R was lower than 1.1, the MCMC chain was assumed to have converged to its stationary distribution (Gelman 2014). Models were fit using the package *rjags* (Plummer, 2022) in R 4.2.1 (R core team, 2022).

Genetic Analyses

I calculated the number of microsatellite alleles per locus, mean number of alleles per population (N_a), observed and expected heterozygosity (H_o/H_e), inbreeding statistic (F_{st}), and deviations from Hardy-Weinberg equilibrium using GenAlEx (Oyler-McCance *et al.*, 2022). Allelic richness (AR) was corrected for differences in sample size using the program FSTAT. I also conducted a principal coordinate analysis (PCoA) in GenAlEx to understand the genetic distance of each individual sampled to assess how the genetic samples compared visually and whether there were clear groupings (based on population) of samples (Dunken, 2014; Oyler-McCance *et al.*, 2022).

The population structure of the source and reinforced population before and after reinforcements was assessed using the Bayesian clustering program STRUCTURE version 2.3.4 (Prichard *et al*., 2000). Individuals were grouped into genetic clusters according to model-based clustering analysis. I first separated the source populations according to the number of unique genetic clusters (K: 1-5) estimated by conducting 20 runs of each K with 200,000 MCMC iterations with 100,000 burn-ins with admixture, correlated allele frequencies, and uninformative priors (Pritchard *et al*., 2000). I then further analyzed them using STRUCTURE HARVESTER to determine K using "second-order rate of change in log-likelihood for each K" (Earl & vonHoldt, 2012). Once the source and SR pre-translocation populations were genetically separated, I added SR post-translocation initiation data to observe the samples' clustering.

Results

Integrated Population Model

Survival and Recruitment

Because only the SR (from 2016 – 2020) and WBE (from 2016 – 2019) had active monitoring simultaneously, I have only included these populations in the estimates for survival and recruitment (Figure 4-3, Figure 4-4, Table 4-2). Figures 4-3 and 4-4 illustrate the estimates for the survival and recruitment of yearlings from 2016-2020, except for translocated individuals in Figure 4-3, which were translocated from 2016-2019. Survival for both yearlings and adults in the SR population was estimated to be higher than for the WBE population; however, recruitment for both age classes was higher in WBE, with recruitment from adults being significantly higher.

Table 4-2 illustrates the estimates for clutch size, nest survival, hatchability, and chick survival for yearlings and adults for the SR (from 2016 – 2020) and WBE (from 2016 – 2019) populations. The overall clutch size was estimated per population. Mean clutch sizes were 6.37 (95% CI 5.39 – 7.47 for SR yearlings and 5.64 – 7.18 for SR adults) in the SR population and 6.46 (95% CI 5.24 – 7.82 for WBE yearlings and 5.75 – 7.22 for WBE adults) in the WBE population. Both SR and WBE have high hatchability rates, where means vary between 95 and 99% hatchability in all years, except for 2017 in WBE when hatchability rates were 87% (95% CI 55.19 – 99.43) for yearlings and 72.49% (95% CI 60.92 – 82.72) for adults. Nest survival was lower overall in WBE across most years, with mean estimates between 20 – 35% for yearlings and 54 – 68 % for adults, whereas mean nest survival in the SR population ranged between 29 – 45% for yearlings and 63 – 74 % for adults. Chick survival, however, was higher in WBE, where mean chick survival ranged from 23 – 39% for yearlings and 29 – 40% for adults. The SR mean chick survival estimates ranged between 15 – 27% for both yearlings and adults.

Total population estimates and Lambda

Figure 4-5 shows the total estimated abundance for all three populations from 2005-2027, where PM had an estimated 1080 (884 – 1364) individuals in 2022 and is estimated to have 806 (626 – 1039) individuals in 2027; WBE was estimated to have 790(568 – 1065) individuals in 2022 and is estimated to have 766 (67 – 2350) individuals in 2027; and the SR population (Figure 4-6) was estimated to have 35 (17 – 59) individuals in 2022 and is estimated to have 22 (2 – 63) individuals in 2027. For lambda, Figure 4-7 illustrates the estimates for all three populations.

BA ratio

The BA ratio for the SR site was estimated to be 1.05 (0.98 – 1.11), for WBE 0.96 (0.89 - 1.05), and pooled for both SR and WBE sites 0.96 (0.86 – 1.05). There was relatively no or small positive effect of the translocations on the SR population and slight evidence for a possible adverse effect of removing individuals from WBE. Due to only having lek counts, I could not estimate this for PM.

CI-divergence/contribution

CI-divergence for the SR site was estimated to be -0.05 (-0.09 – 0.004), for the WBE site 0.02 (-0.01 – 0.09), and for both SR and WBE sites pooled, it was 0.02 (-0.02 – 0.12). CI-contribution for the SR site was estimated to be -0.01 (-0.04 – 0.04), for the WBE site 0.01 (-0.03 – 0.09), and for SR and for SR and WBE pooled, it was 0.02 (-0.01 – 0.12). I did not estimate this for PM, as mentioned above.

Genetics

Table 4-3 illustrates the results for N_a, H_o/H_e, F_{st}, and AR. The metric, N_a, increased in the SR population after translocations were initiated, where the average was 5.80 (SE 0.428) in the SR population before and was 7.27 (SE 0.722) after, and AR also increased from 5.64 to 6.98. The H_o/H_e did not change following the translocations in the monitored period: H_o was 0.729 (SE 0.035) and H_e was 0.69 (SE 0.031) before the translocations, and H_o was 0.70 (SE 0.040) and H_e was 0.68 (SE 0.035) after translocations. The F_{st} demonstrated a possible reduction in inbreeding depression following translocations (SR before -0.061 [SE 0.029] and SR after -0.030 [0.020]), where negative values signify an excess of heterozygotes, and positive values signify a deficit of heterozygotes (Oyler-McCance *et al.*, 2022).

The PCoA plot (Figure 4-8) shows three separate clusters corresponding to each population's genetics (PM, WBE, and SR before/after), along with some areas of overlap. The STRUCTURE analysis identified 3 genetic clusters, where the SR, PM, and WBE populations were all recognized as distinct (Figure 4-9). Following the identification of these three populations, adding the samples from the SR population following the initiated translocations illustrated the potential for the incorporation of the PM and WBE genetics for several samples, with minimal incorporation in many.

Discussion

Incorporating genetic and demographic monitoring in conservation translocation programs can provide deeper insights into the population-level effects of translocations (Robert *et al*., 2007; Bouzat *et al*., 2009; Thompson, 2012; Manlick *et al.,* 2017). I used a two-step approach wherein I evaluated both demographics using an IPM and genetics, using allelic diversity to evaluate the population status in the short-term following reinforcements. The IPM results highlighted the probability of the SR population's decline through 2027; however, the genetic results provide additional insight into the potential improvement of the SR population's evolutionary potential as a result of the reinforcements (Frankham *et al*., 2010; Keller *et al*., 2012). The increased allelic richness resulting from the reinforcements observed during 2017-2020 indicates a possibility of further improvement as alleles from translocated individuals propagate through the population. This population had begun to show evidence for genetic inbreeding (Table 4-3; Keller *et al*., 2012), and continued monitoring would provide insight into whether these translocations prevented, halted, or slowed inbreeding depression in the SR population.

The evolutionary potential of a population is measured through its heterozygosity, the number of effective alleles, and the population's allelic richness (Frankham *et al*., 2010; Allendorf *et al*., 2013; Keller *et al*., 2012). However, while heterozygosity takes several generations to be affected, allelic richness is more sensitive to changes from generation to generation (Allendorf *et al*., 2013; Keller *et al*., 2012). The Na and AR improved during the sampling period, whereas I did not detect a significant change in Ho/He, as expected (Table 4-3). This improvement in Na and AR signals the incorporation of new alleles that could buffer the population from environmental stochasticity (Keller *et al*., 2012). Other translocation studies have illustrated positive (Bouzat *et al*., 2009; Dunken, 2014; White *et al*., 2018), neutral or minimal (Manlick *et al*., 2017), and negative (Jamieson, 2011; Tollington *et al*., 2013) outcomes of translocations on their respective populations of interest, with some reporting both positive (Hogg *et al*., 2020) and negative (Furlan *et al*., 2020) genetic consequences on the source populations. However, I did not assess the genetic effects of removal on the source populations. This remains a potential direction for future work that should be incorporated into the population-level effects of removing individuals from the source populations (Mitchell *et al*., 2022).

Genetic sampling can often be more cost-effective in the effort needed to obtain samples and can allow researchers to gain demographic insight into populations (Tollington *et al*., 2013; Neaves *et al*., 2023), but, where available, robust demographic models, such as the IPM used in this analysis, can utilize data from several different sources and, often, aid in incorporating incomplete datasets (Schaub & Abadi, 2011; Duarte *et al*., 2017; Zipkin & Saunders, 2018). They also provide translocation programs with the tools to simultaneously estimate the source and reinforced populations' demographics and can be effectively incorporated into adaptive management strategies for informing future translocations (Duarte *et al*., 2017; Riecke *et al*., 2019).

Through utilizing the IPM, I found that removing individuals from the WBE source population may have contributed to its decline in population growth. However, sage-grouse populations typically oscillate on 6-13-year cycles (Garton *et al*., 2011; Dahlgren *et al*., 2016; Coates *et al*., 2018), and Utah's sage-grouse populations were on the decline during the SR translocations. Lek counts strongly influence the IPM estimate for total population abundance; thus, whether removing the translocated individuals increased the decline in the WBE population abundance is up for debate. This result still contributes to a growing body of translocation literature that includes this effect in evaluating translocation management actions (Dimond & Armstrong, 2007; Meyerpeter, 2020; Mitchell *et al*., 2022). Meyerpeter (2020) found positive effects on the reinforced populations when translocating broods in both ND and the bi-state population and additionally found no effects on any of their respective source populations. In juxtaposing the methods of translocating >100 pre-nesting females versus less than 30 broods (Meyerpeter, 2020; Lazenby, 2020), this novel technique of translocating female sage-grouse with their chicks may prove more beneficial for both the reinforced and the source populations.

The low recruitment rates observed in the SR population were dictated chiefly by low chick survival. If unabated, the SR population is likely to decline below 30 individuals by 2027. Low chick survival has also been observed on the periphery of their species range in Alberta (12% survival; Aldridge & Boyce, 2007) and North and South

Dakota (6-17% survival; Herman-Brunson, 2007; Kaczor, 2008). In a previous study from PM, prior estimates of chick survival were 47.5% (95% CI: 37.5 – 56.6%; Guttery *et al*., 2013). Dahlgren, Messmer, & Koons (2010) reported chick survival estimates from 2005- 2006 in PM with around a 50% probability of survival to 42 days post-hatch. For translocated individuals in Strawberry Valley in UT, apparent chick survival percentages were 47.2% and 58.1% for first- and second-year translocated females' broods 50 days post-hatch in 2005-2006 (Baxter *et al*., 2008). In the Anthro Mountain, UT translocations, resident and second-year translocated females within the reinforced population exhibited 62% (95% CI = 46-79%) brood success, and first-year translocated females' brood success was 38% (95% CI = 12-63%; Duvuvuei *et al*., 2017). However, these publications evaluate their chick survival using different methodological and analytical techniques. Thus, the only more closely comparable study is Meyerpeter (2020), though the methods for field monitoring were somewhat different. Chick survival appears to be low in the reinforced population of SR, which is likely a major causal factor in recent population declines.

In the sage-grouse literature, chick survival is dictated by access to adequate mesic habitat within the sagebrush community, which provides forbs and invertebrates (Connelly *et al*., 2000; Dahlgren, Chi, & Messmer, 2006; Connelly *et al*., 2011). In sagebrush landscapes altered by disturbance, sagebrush community variables (e.g., available mesic areas, forbs, invertebrates) are more susceptible to environmental stochasticity (Chambers *et al*., 2014). Caudill *et al*. (2014) found that brood success was tied to April moisture availability. The physiological condition of the female, dictated by the availability of forbs (Barnett & Crawford, 1994), before nest initiation may also influence chick survival post-hatch (Blomberg *et al*., 2014).

In the SR population, stakeholders have committed numerous resources to prevent population extirpation, as it would have critical state and federal jurisdictional management implications. Most notably, in 2015, agencies began conducting habitat restoration projects aimed at improving brood-rearing habitat, including removing conifers and installing beaver dam analogs to increase the availability of mesic habitat (Pyke, 2011; Pollock *et al*., 2014). Across the range, research has documented the population-level benefits of these habitat restorations (Sandford *et al*., 2017; Severson *et al*., 2017; Olsen *et al*., 2021). However, though soil water availability could benefit treated areas within the first year depending on the treatment (Roundy *et al*., 2014), there is a notable time-lag in demographic and habitat selection patterns observed prior to the habitat restoration treatment could be seen for some years post initiation of habitat restoration, with increasing probability of population-level benefits as time since treatment increases (Harju *et al*., 2010; Sandford *et al*., 2017; Severson et al., 2017; Olsen *et al*., 2021).

The IUCN/SSC (2013) and other translocation literature (Bubac *et al*., 2019; Berger-Tal, Blumstein, & Swaisgood, 2020; Dalrymple & Bellis, 2023) have recommended that researchers and stakeholders employing translocations wait to move individuals into the reinforced population until the habitat is suitable, primarily if the original reasons for decline had not been fully addressed. Nonetheless, stakeholders may opt to employ translocations before or concurrently with restoration projects to prevent the effects of factors related to the small population paradigm leading to the extinction vortex (Caughley, 1994; Gilpin & Soulé, 1986; Fagan & Holmes, 2006). In the SR, managers may consider additional habitat improvement to improve chick survival.

Because many of the population-level effects mentioned above (heterozygosity, recruitment, and habitat restoration) have documented time-lag effects, this reintroduction project needs continued population monitoring. Continued monitoring is characteristic of translocations, where long-term monitoring is needed to assess management effects and success (quantifiable success; Armstrong, Parlato, & Ewen, 2022). Thus, long-term monitoring is highly recommended by the IUCN/SSC group (IUCN/SSC, 2013). Temporal extent is an essential component in monitoring the outcome of translocations, and populations should be reevaluated at 5, 10, and even 20 years following initial efforts dependent upon the species' life history (Sutherland *et al.*, 2010).

If the state and federal agencies managing this population aim to prevent its extirpation, I recommend continued monitoring and habitat restoration aimed at improving brood-rearing habitat, in addition to incorporating brood translocations (Lazenby, 2020; Meyerpeter *et al.*, 2021). However, due to the location of the population and its potential to experience further effects of climate change, I recommend performing species distribution models that incorporate estimates for changes in precipitation and temperatures to understand the potential of this area to be suitable for further releases of sage-grouse (Bellis *et al.*, 2020); species distribution models would also serve to inform future releases of brood females with their chicks, which have low dispersal probabilities post-release (Picardi *et al.*, 2022), emphasizing the need to release these individuals in the most suitable habitat.

Additionally, given the genetic analyses from Oyler-McCance *et al*. (2022), showing the genetic relatedness of sage-grouse populations across their range, I do not recommend removing broods or pre-nesting females from WBE to reinforce the SR population without updated demographic analyses and simulations. The demographic results indicate the potential negative effect the translocations may have had on removing individuals. Sage-grouse populations across UT have also shown notable decreases beginning in 2021 (UDWR, personal communication), and modeling the potential removal of broods in these populations should also be considered.

Conclusions

Demographic models applied to conservation translocation studies can provide researchers and practitioners with detailed information on population vital rates. This information provides insight into population-level processes of translocation programs that can identify a direction in which to apply their management actions to increase the probability of their success. In this study, chick survival was identified as a critical component in constraining population growth in the SR SGMA, and translocating pre-nesting males and females did not overcome the negative effects associated with low chick survival.

Short-term genetic data can be informative and provide additional insights into monitored translocated populations. Long-term data from continued monitoring are still essential for gaining information on evolutionary potential (Neaves *et al*., 2023).

Closed populations receiving reinforcements and other management actions may see temporary positive trends during these conservation actions, but they often require long-term continual interventions to prevent extirpation. Formal exit strategies should be defined at the inception of translocation projects (IUCN/SSC, 2013; Dalrymple & Bellis, 2023); I recommend that stakeholders involved in this project reconvene and determine the point in which they will no longer put additional resources into this population.

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Tables and Figures

Table 4-1. Greater sage-grouse (Centrocercus urophasianus) conservation translocations performed since Reese and Connelly (1997). Literature review performed 2023.

Translocation Population	Translocation Type	Years of Translocations	Source Populations	Metrics Evaluated	Associated Literature
Strawberry Valley, UT	Reinforcement: pre-nesting females	2003-2008	Parker Mountain, UT, Diamond Mountain, UT, Box Elder, UT	Translocation methods, vital rates, predator control, genetics	Hennefer 2007†, Baxter 2007†, Baxter et al. 2008*, Baxter et al. 2009*, Baxter et al. 2013*, Dunken 2014†
Yakima Training Center, WA	Reinforcement: pre-nesting females, post-nesting females, males	2004-2006; 2014-2016	2004: Elko & Humbolt County, NV; 2005-2006: Hart Mountain, OR; 2014: South ID; 2015: Idaho; 2016: Nevada	Movements, vital rates	Schroeder et al. 2014‡, Schroeder et al. 2016‡, Ebenhoch et al. 2019*, Schroeder et al. 2014‡, Schroeder et al. 2016‡,
Cold Springs, CO & Axial Basin, CO	Reinforcement: chicks	2005-2007	Axial Basin, CO, Cold Springs Mountain, CO, North Moffat, CO	Movements, vital rates, genetics, captive-rearing chicks	Thompson 2012†, Thompson et al. 2015*
Clear Lake National Wildlife Refuge, CA	Reinforcement: pre-nesting females	2005-2010	2005-2006, 2009: Hart Mountain, OR; 2007-2008, 2010: Wall Canyon, NV	Vital rates	Bell 2011†, Bell and George 2012*
Yakima Nation, WA	Reintroduction: pre-nesting females, post-nesting females, males	2006-2007; 2013-2014	2006: Hart Mountain, OR, Wind River Indian Reservation; 2007: Hart Mountain; 2013-2014: Nevada	Vital rates (apparent)	Schroeder et al. 2014‡, Schroeder et al. 2016‡, Schroeder et al. 2014‡, Schroeder et al. 2016‡,
Swanson Lake, Lincoln County/Crab Creek Management Unit, WA	Reintroduction: pre-nesting females, post-nesting females, males	2008-2015	2008: Hart Mountain; 2009: North of Plush, OR; 2010-2011: Southern OR (one near McDermitt, NV and the other near Vale, OR); 2012: Hart Moutain and Steens Mountain, OR; 2013: NW of Plush, OR; 2014: NW of Plush, OR and Beatys Butte, OR; 2015: NW of Plush, OR and So of Beatys Butte, OR	Habitat selection, vital rates, predator management	Schroeder et al. 2014‡, Schroeder et al. 2016‡, Schroeder et al. 2014‡, Schroeder et al. 2016‡,
Anthro Mountain, UT	Reinforcement: pre-nesting females	2009-2010	Parker Mountain, UT	Vital rates, movements, habitat use	Gruber 2012†, Duvuvuei 2013†, Gruber-Hadden et al. 2016*, Duvuvuei et al. 2017*
Alberta	Reinforcement: pre-nesting females, males	2011-2012; 2016; 2019	Valley County, MT, Phillips County, MT	Translocation methods, vital rates, movements, habitat selection, Spatially-explicit individual based model, source-sink dynamics	Whiklo and Nicholson 2015‡, Balderson 2017†, Heinrichs et al. 2018*, Spilker et al. 2021‡
Sheeprock Mountain Sage-grouse Management Area, UT	Reinforcement: pre-nesting females, males	2016-2019	Parker Mountain, UT, Box Elder, UT	Vital rates (apparent), movements, Translocation methods	Chelak and Messmer 2016‡, Chelak and Messmer 2017‡, Chelak and Messmer 2018‡, Chelak and Messmer 2019‡, Chelak and Messmer 2021‡
North Dakota	Reinforcement: pre-nesting females, post-nesting females, broods, males	2017-2020	Stewart Creek, WY	Translocation methods, vital rates, movements, habitat selection,	Lazenby 2020†, Meyerpeter 2020†, Lazenby et al. 2021*, Meyerpeter et al. 2021*, Picardi et al. 2021*
Parker Meadows, CA/NV (bi-state)	Reinforcement: pre-nesting females, post-nesting females, broods, males	2017-2021	Bodie Hills, CA/NV	Translocation methods, vital rates, movements	Bi-State Accomplishment Report 2022‡, Meyerpeter 2020†, Meyerpeter et al. 2021*

Footnote: grey literature‡, thesis/dissertation†, peer-review*

Table 4-2. Greater sage-grouse (*Centrocercus urophasianus*) vital rates (clutch size, nest survival, hatchability, and chick survival) input into the recruitment (R) equation for both the Sheeprock Mountain Sage-grouse Management Area (SGMA; pooled resident and translocated individuals) population and the West Box Elder SGMA (source) populations, Sheeprock Mountain SGMA translocation study, Utah, USA, 2016-2020. Data from the Parker Mountain SGMA (source) population was not included, as there was no active monitoring project during this period.

Population		Clutch Size (cl1)	Nest Survival (n1)	Hatchability (h)	Chick Survival (cs)
		mean (95% CI)	***mean (95% CI)***	***mean (95% CI)***	***mean (95% CI)***
Sheeprock Mt.	2016				
	Yearlings	6.37 (5.39 - 7.47)	29.36 (3.81 - 57.44)	99.44 (97.15 - 99.99)	18.93 (9.85 - 31.46)
	Adults	6.37 (5.64 - 7.18)	63.67 (39.60 - 83.39)	98.67 (96.06 - 99.80)	19.14 (11.12 - 28.73)
	2017				
	Yearlings	6.37 (5.39 - 7.47)	45.29 (18.52 - 75.23)	95.28 (82.05 - 99.83)	25.70 (15.21 - 40.19)
	Adults	6.37 (5.64 - 7.18)	74.98 (55.14 - 91.36)	89.05 (79.48 - 95.76)	26.04 (17.18 - 36.26)
	2018				
	Yearlings	6.37 (5.39 - 7.47)	39.49 (17.48 - 63.97)	99.67 (98.37 - 99.95)	27.33 (18.24 - 38.43)
	Adults	6.37 (5.64 - 7.18)	71.62 (53.04 - 87.43)	99.13 (97.10 - 99.95)	27.79 (19.86 - 36.25)
	2019				
	Yearlings	6.37 (5.39 - 7.47)	38.26 (16.89 - 62.34)	99.82 (99.10 - 99.99)	15.31 (8.87 - 24.30)
	Adults	6.37 (5.64 - 7.18)	70.88 (53.17 - 86.52)	99.53 (98.36 - 99.97)	15.57 (9.89 - 22.35)
	2020				
	Yearlings	6.37 (5.39 - 7.47)	31.48 (6.33 - 59.21)	98.56 (93.97 - 99.96)	23.38 (12.97 - 35.87)
	Adults	6.37 (5.64 - 7.18)	65.40 (40.21 - 85.16)	95.93 (88.22 - 99.49)	23.84 (13.91 - 35.63)
W. Box Elder	2016				
	Yearlings	6.46 (5.24 - 7.82)	20.02 (1.69 - 43.98)	98.23 (91.47 - 99.96)	28.98 (16.55 - 44.51)
	Adults	6.46 (5.75 - 7.22)	54.94 (31.34 - 74.68)	96.19 (91.25 - 99.08)	29.34 (19.62 - 39.70)
	2017				
	Yearlings	6.46 (5.24 - 7.82)	35.18 (12.12 - 64.19)	87.19 (55.19 - 99.43)	37.73 (24.48 - 54.54)
	Adults	6.46 (5.75 - 7.22)	68.61 (51.15 - 86.85)	72.49 (60.92 - 82.72)	38.27 (28.07 - 49.32)
	2018				
	Yearlings	6.46 (5.24 - 7.82)	29.13 (8.70 - 54.65)	98.91 (94.32 - 99.99)	39.90 (26.91 - 55.50)
	Adults	6.46 (5.75 - 7.22)	64.10 (44.85 - 82.17)	97.31 (91.20 - 99.82)	40.52 (29.35 - 52.27)
	2019				
	Yearlings	6.46 (5.24 - 7.82)	27.84 (9.31 - 49.94)	99.42 (97.10 - 99.99)	24.18 (14.39 - 37.07)
	Adults	6.46 (5.75 - 7.22)	63.35 (46.15 - 79.20)	98.58 (95.71 - 99.90)	24.55 (16.59 - 33.26)

Table 4-3. Sample size, average alleles per loci, observed and expected heterozygosity, inbreeding statistic, and allelic richness for the two greater sage-grouse (Centrocercus urophasianus) source populations (Parker Mountain and West Box Elder Sage-grouse Management Areas SGMA) and the reinforced population (Sheeprock Mountain SGMA) prior to initiation of reinforcements (2012) and after (2016-2020).

Population		Sample Size (n)	Number of Alleles (Na)	Number of Effective Alleles (Ne)	Observed Heterozygosity (Ho)	Expected Heterozygosity (He)	Inbreeding Statistic (F)	Allelic Richness
Sheeprocks Before	Mean	14	5.800	3.611	0.729	0.690	-0.061	5.64
	SE	0	0.428	0.289	0.035	0.031	0.029	
Parker Mountain	Mean	112.6	7.600	3.686	0.705	0.698	-0.005	7.99
	SE	0.821	0.722	0.300	0.035	0.029	0.018	
W. Box Elder	Mean	29.533	9.267	5.972	0.810	0.815	0.005	6.25
	SE	0.533	0.686	0.519	0.018	0.014	0.020	
Sheeprocks After	Mean	32.933	7.267	3.607	0.697	0.676	-0.030	6.98
	SE	0.067	0.492	0.366	0.040	0.035	0.020	

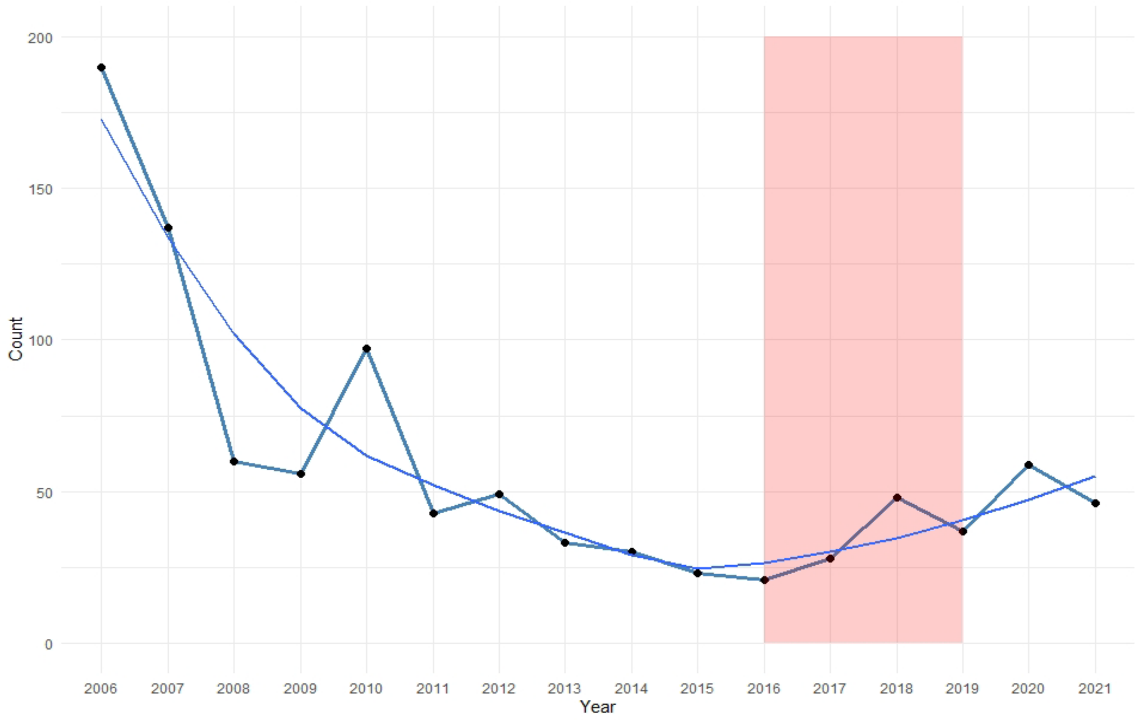
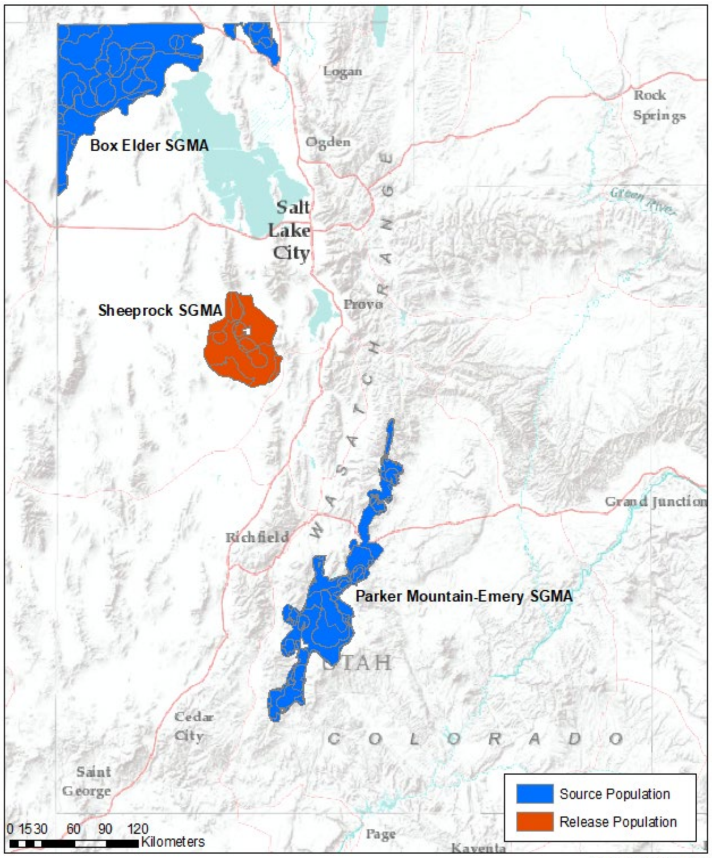


Figure 4-1. Peak male greater sage-grouse (*Centrocercus urophasianus*) lek counts in the Sheeprock Mountain Sage-grouse Management Area, Utah, USA, 2006-2021. Translocations (blocked in red) were performed from 2016-2019.



Source: ESRI, UDWR

Figure 4-2. The release site and location of source populations for greater sage-grouse (*Centrocercus urophasianus*) translocated to the Sheeprock Mountain Sage-Grouse Management Area (SGMA) to reinforce the resident population. Sage-grouse were translocated 2016-2019 from both the West Box Elder SGMA, and Parker Mountain, located in the Parker Mountain-Emery SGMA.

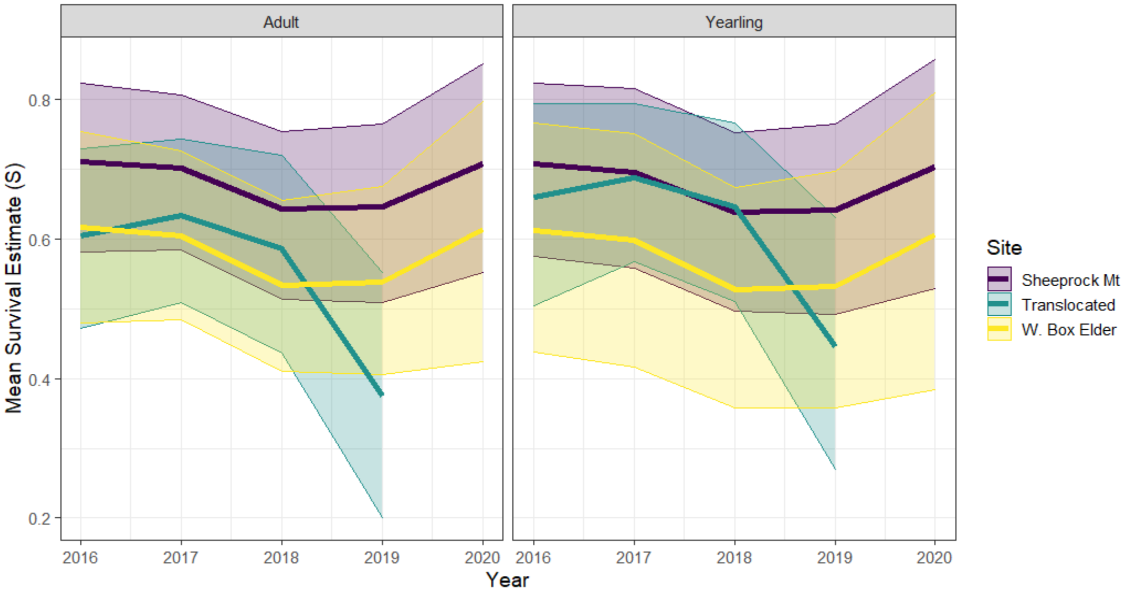


Figure 4-3. Mean survival estimates (S) with 95% credible intervals from 2016-2019 for translocated (blue) greater sage-grouse (*Centrocercus urophasianus*) individuals and 2016-2020 for the Sheeprock Mountain (reinforced; purple) and West Box Elder (source; yellow) Sage-Grouse Management Area populations, Utah USA. Data from the Parker Mountain SGMA (source) population was not included, as there was no active monitoring project during this period.

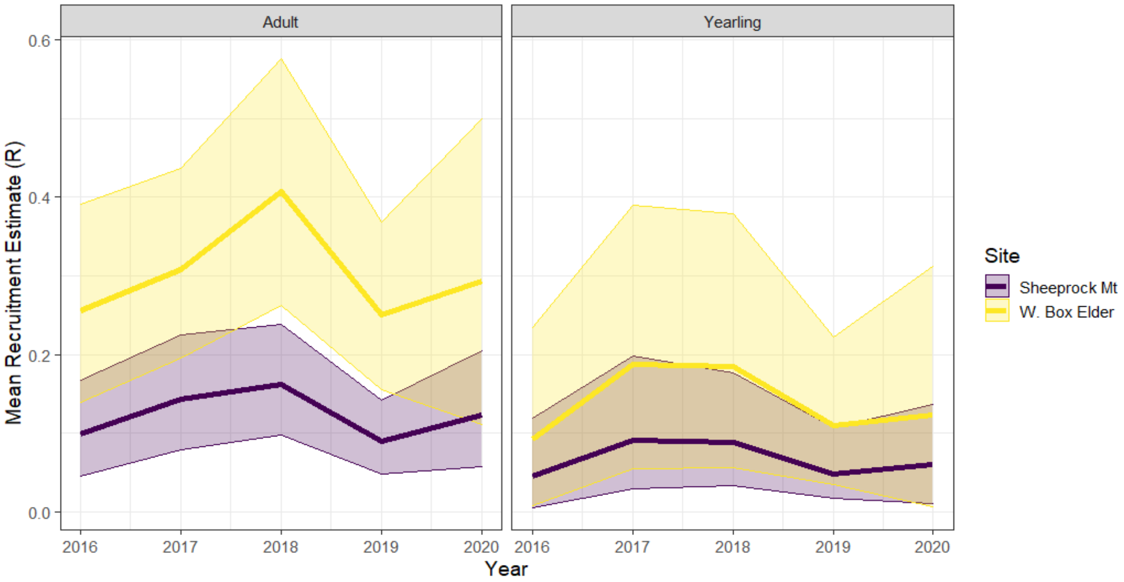


Figure 4-4. Mean recruitment estimate (R) from 2016-2020 with 95% credible intervals for the Sheeprock Mountain (pooled resident and translocated; purple) and West Box Elder (source; yellow) Sage-Grouse Management Areas (SGMA) greater sage-grouse (*Centrocercus urophasianus*) populations. Data from the Parker Mountain SGMA (source) population was not included, as there was no active monitoring project during this period.

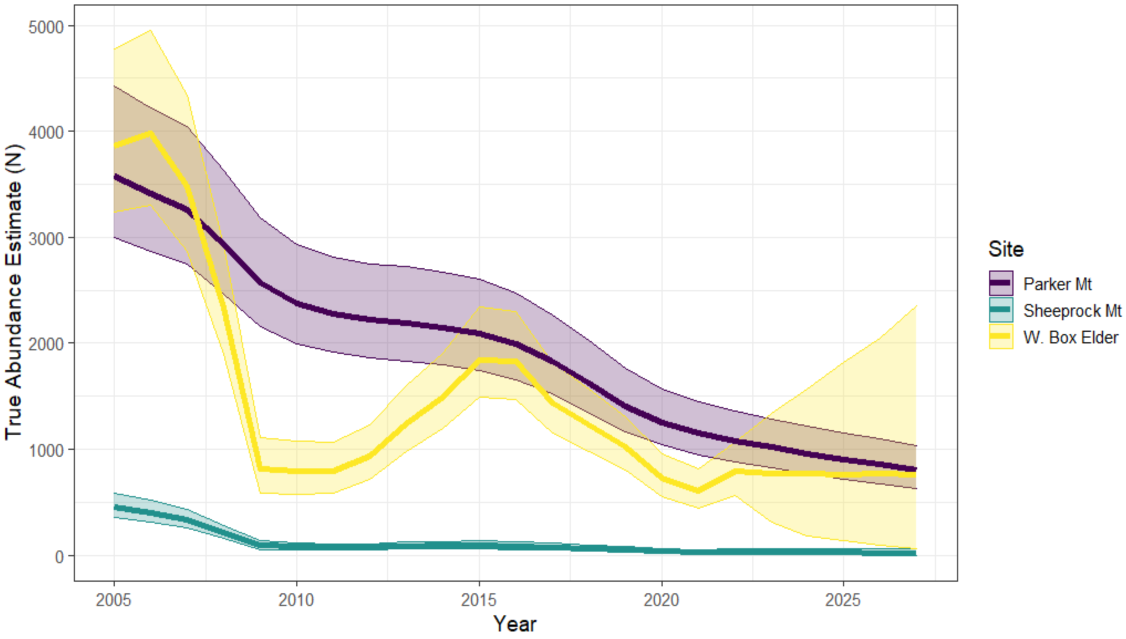


Figure 4-5. Greater sage-grouse (*Centrocercus urophasianus*) abundance estimates (N) 2005-2027 with 95% credible intervals for the reinforced Sheeprock Mountain Sage-Grouse Management Area (SGMA) population (blue) and the source populations, Parker Mountain (purple) and West Box Elder (yellow) SGMAs, Utah, USA.

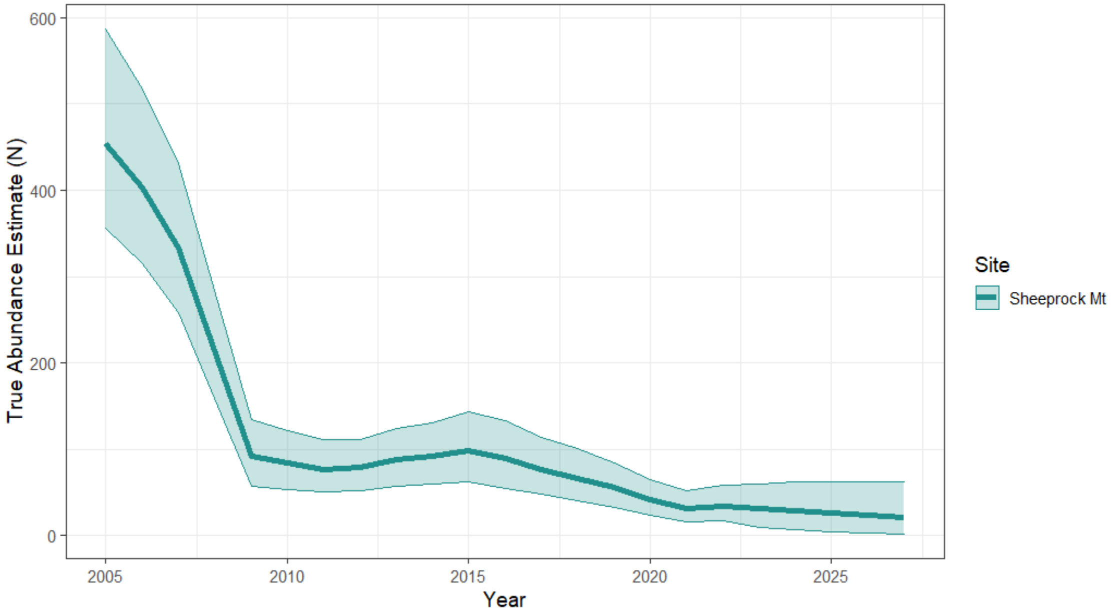


Figure 4-6. Greater sage-grouse (Centrocercus urophasianus) abundance estimates (N) 2005-2027 with 95% credible intervals for the reinforced Sheeprock Mountain Sage-Grouse Management Area population, Utah, USA.

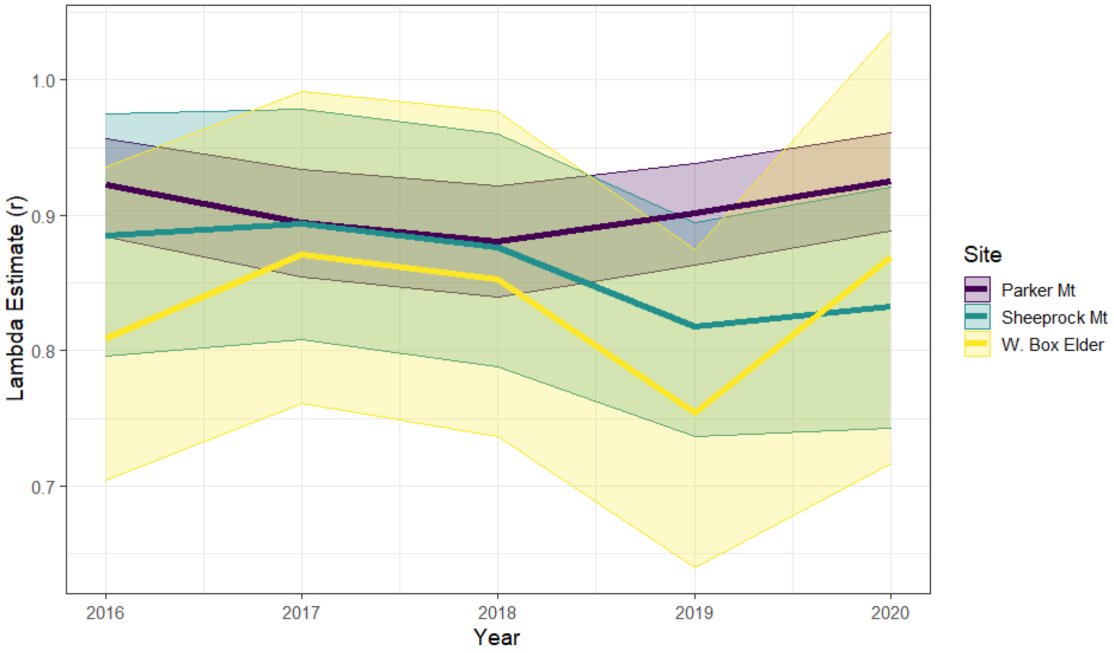


Figure 4-7. Greater sage-grouse (*Centrocercus urophasianus*) lambda estimates (r) with 95% credible intervals for the reinforced Sheeprock Mountain Sage-Grouse Management Area (SGMA) population (blue) and the source populations, Parker Mountain (purple) and West Box Elder (yellow) SGMAs, 2016-2020, Utah, USA.

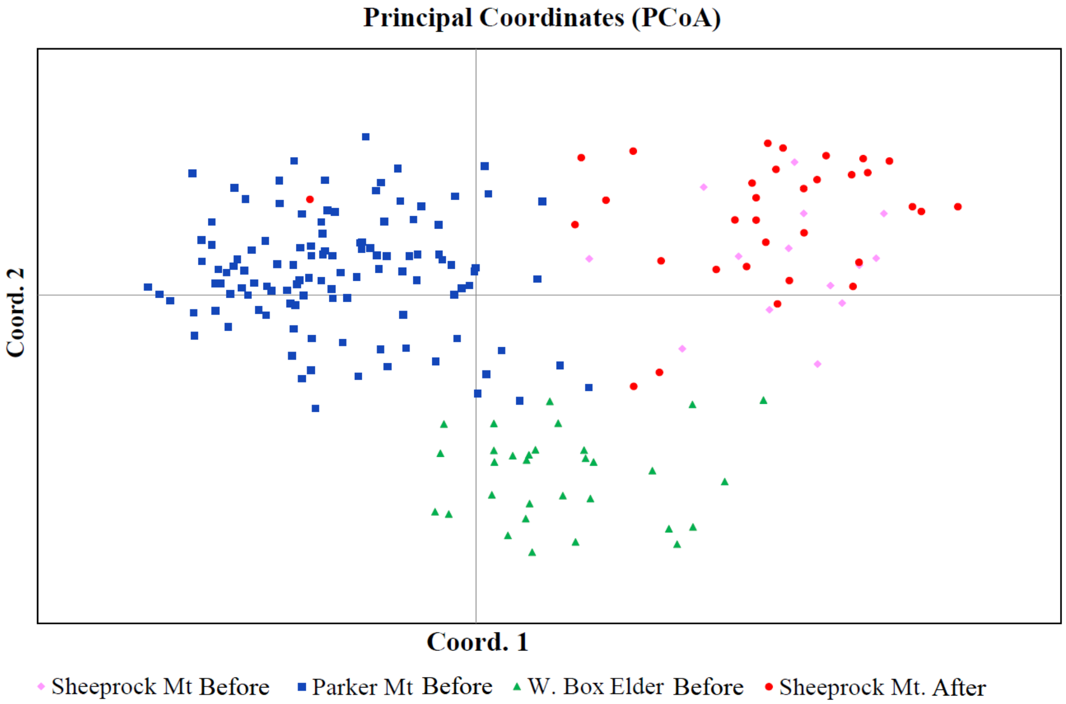


Figure 4-8. Principle coordinates analysis for clustering genetic samples taken from greater sage-grouse (*Centrocercus urophasianus*) populations in Sheeprock Mountain Sage-Grouse Management Area (SGMA; reinforced), West Box Elder SGMA, and Parker Mountain SGMA's (source populations) prior to initiating translocations and the Sheeprock SGMA samples post-initiation of reinforcements from the source populations, 2015-2020, Utah USA.

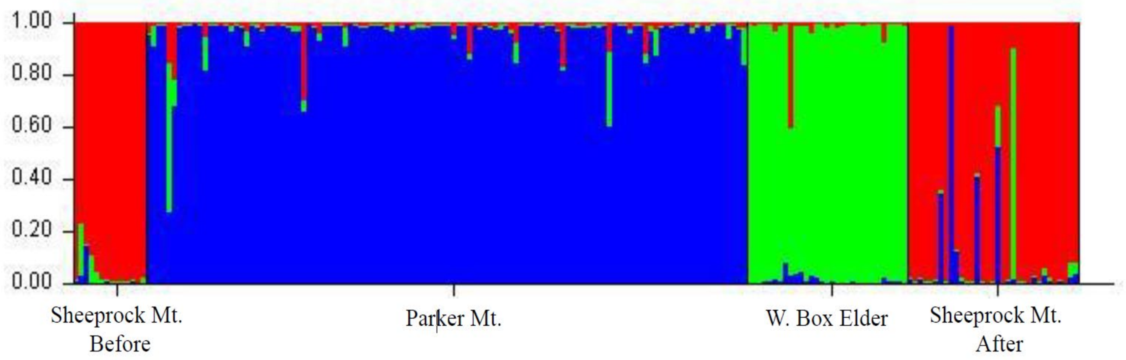


Figure 4-9. Greater sage-grouse (*Centrocercus urophasianus*) population clustering from K = 3 populations in a STRUCTURE analysis. The reinforced population, Sheeprock Mountain Sage-Grouse Management Area (blue; SGMA), prior to translocations (red, far left) is juxtaposed with its source populations, Parker Mountain (blue) and West Box Elder (green) SGMAs, and the Sheeprock SGMA post translocations (red, far right), Utah, USA.

CHAPTER 5

CONCLUSIONS AND LESSONS LEARNED

What We Accomplished

When small, isolated populations have declined and indicate the lost ability to recruit lower age classes and replace enough individuals lost to mortality or emigration, practitioners may intervene by conducting conservation translocations (Seddon et al., 2012). The science of conservation translocations (translocations) has progressed considerably since its official establishment in the 1980s (Price, 1986; IUCN/SSC, 1987). Since that time, researchers and practitioners have ameliorated the iterative process involved in the planning, methodology, and monitoring of translocated animal and plant populations (Ewen et al., 2012; Armstrong 2015; Jachowski et al., 2016; Gaywood et al., 2023). Nevertheless, there continues to be much to learn about the specific details of each species' life history and how it influences translocation success. A prime example of this is the greater sage-grouse (*Centrocercus urophasianus*; sage-grouse). Despite 90 years of translocation experience, researchers still need to determine the most effective methods of successfully buffering isolated sage-grouse populations from extirpation (Reese & Connelly, 1997).

In this dissertation, I have shown some examples of evaluating sage-grouse reinforcements in a small, isolated population in the Sheeprock Mountain Sage-Grouse Management Area (SGMA) located in Utah's West Desert. This population experienced a decline from 190 lekking males in 2006 to 23 lekking males in 2015. A collaborative effort across all federal, state, and local partners yielded 146 (40 male, 106 female) sage-grouse captured, marked, and translocated into the Sheeprock sage-grouse management area between 2016 and 2019, complete with radiotelemetry monitoring during the spring and summers of 2016-2020 (Table 5-1). Coincident management efforts included extensive habitat restoration, predator control, and monitoring off-highway vehicle recreation. In Table 5-2, I have compiled a summary of the management actions and analyses we performed, what conclusions we came to understand, and some next steps in this restoration effort.

As a result of collaborations with other western states, we have advanced the knowledge of how both recipient and source sage-grouse populations respond to translocations. Population reinforcements were performed in the Bi-State area of California and Nevada (bi-state) from 2017-present and in southwestern North Dakota from 2017-2021 (Lazenby, 2020; Meyerpeter et al., 2021). In 2017 and 2018, we experimented with artificial insemination for pre-nesting sage-grouse females after Schneider et al.'s (2019) protocols (Chelak and Messmer, 2018; Lazenby, 2020). In addition, we developed and employed a "softer" or delayed remote release method at the lek sites to mitigate additional stressors during release (Dickens et al., 2009; Dickens et al., 2010; Lazenby, 2020). In the bi-state and North Dakota populations, beginning in 2017 and 2018, respectively, researchers built upon the methods of Thompson et al. (2015) in translocating wild-caught broods to increase the probability that first-year translocated females would contribute to the target population's vital rates (Lazenby, 2020; Meyerpeter et al., 2021).

In chapter one, I used data from sage-grouse marked between 2011 and 2019 from populations in Utah and Wyoming. I compared and evaluated the performance of the two most commonly used GPS transmitters for sage-grouse, 22-gram solar-powered GPS-Argos transmitters manufactured by Microwave Telemetry (MTI) and GeoTrak (GT). Metrics explored daily fix inefficiency, the number of 1-day fix gaps, and transmitter loss rates in the field. In addition, I evaluated transmitter functionality during the nesting period: daily nesting fix inefficiency, fix error distance mean and standard deviation (i.e., accuracy and precision), and mean fix error direction. Knowing the expected fix error for each transmitter can inform data screening in preparation for analysis to account for fix error bias associated with nesting and non-nesting individuals and subsequent habitat selection models (Nielson et al., 2009; Patterson et al., 2010; Ranacher et al., 2016). Accurately accounting for known fix errors inherent in GPS data improves the inference by which researchers can understand free-ranging animal individual- and population-level behavior and movement, demographics, predator-prey dynamics, and human-wildlife conflict (Latham et al., 2015). New and refurbished MTI transmitters outperformed GeoTrak transmitters in daily fix inefficiency and day gaps during most seasons except for winter. Cumulatively redeployed MTI transmitters did not perform differently than GeoTrak transmitters. Transmitter loss, daily nesting fix inefficiency, and nest fix precision did not vary significantly between the two transmitters. GeoTrak performed better than MTI for nest fix accuracy across all latitudes (40-45°N). The mean error direction to the nest location ranged between 105° and 135° for GeoTrak and between 135° and 155° for MTI.

For chapter two, I assessed behaviorally segmented, movement-based habitat selection for translocated GPS-marked sage-grouse released into the Sheeprock SGMA. I then utilized post-release monitoring data from 2016-2020 to assess the effects of off-highway vehicle (OHV) recreation traffic estimates, landscape vegetation cover, roads density, etc., on movement-based habitat selection of the translocated individuals post-release. Individual behavior phases were separated into exploration and establishment before performing the movement-based habitat selection. The probability of beginning in the exploratory phase at the time of release was marginally lower for adult females compared to yearlings. The analysis also suggested that to reduce post-release dispersal, practitioners should prioritize release sites to maximize the restricted state selection in areas closer to mesic habitat, higher elevation, and lower tree cover. Understanding the variables that lead to the successful establishment of translocated individuals post-release and their differential habitat selection compared to exploratory individuals is integral for improving translocation programs (Bell, 2016; Picardi et al., 2022).

Additionally, I performed demographic and genetic analyses of the Sheeprock population to evaluate the success of translocations during the study period, 2016-2020. The demographic portion utilizes an integrated population model (IPM) before-after impact (BA) framework for both the source and reinforced populations with 17 years of male lek count data (2005 – 2022) and five years of in-depth monitoring of marked individuals (2016 – 2020) to estimate demographic effects on each population. Using these data, we estimated the population size of the Sheeprock SGMA population to 2027. We utilized genetic data collected before the translocation (2005-2015) and compared it with post-translocation samples (2016-2020) to assess changes in genetic diversity resulting from the translocation, which would indicate the translocated individuals' genetics being incorporated into the reinforced population. The IPM predicted declining populations following translocations due to low recruitment, dictated by low chick survival, and estimated a population abundance of 22 individuals (95% CI: 2 – 63) by 2027. However, we also detected an increase in allelic richness and the potential for the increased admixture of the source population genetics in the reinforced population.

I also monitored disease. Appendix A includes a note on a case of aspergillosis, a fungal infection that develops in birds' air sacs that leads to death in wild individuals, found in a female in 2018. I hypothesized that the *Aspergillus* spp. spores were propagated either in mesic nesting conditions or in residual damp mulch piles created from sagebrush (*Artemisia* spp.) habitat restoration projects and infected the individual within several days of inhaling the spores.

What We Learned

Study Preparation and Design

Sage-grouse translocations lie within the broader branch of translocation science, which has yielded updates in study design since this project began in early 2016 (Jachowski et al., 2016; Runge et al., 2020; Gaywood et al. 2023). Namely, much new literature has been published on structured decision-making frameworks for translocation design (Converse et al., 2013; Canessa et al., 2016). Because of the need for high efficacy when dealing with translocations (e.g., dealing with critically endangered species), there is little room for error, and, thus, a typical experimental design is not always possible with translocations for these species (Armstrong et al., 2007, Morandini & Koprowski, 2023). Structured decision-making provides a basis by which translocation practitioners can compare alternative methods and learn from them with statistical backing (Converse & Armstrong, 2016).

Translocations come with high monetary and temporal costs that often render them unsustainable long-term for many of the agencies that initiated them (Gitzen et al., 2016; Hayward & Slotow, 2016). Often, only a few years of costly mark-recapture monitoring (e.g., multiple technicians following radio-marked birds on the ground for months or years) are sustainable (Gitzen et al., 2016). Building one or several low-cost monitoring methods (e.g., distance sampling, camera trap arrays, etc.) within a study design framework can be sustained for many years post-translocation after monitoring marked individuals and can provide vital information with less relative investment (Gitzen et al., 2016; Novak et al., 2021). In our project, lek counts had been performed by UDWR since the 1950s, so we have long-term, low-cost population size information; however, because brood survival is often the bottleneck for declining sage-grouse populations (Connelly et al., 2011), a low-cost measure of annual brood production would be valuable for long-term population monitoring. Though some research has shown that brood counts are correlated with the following year's male lek counts (Dahlgren et al., 2016), a measure of brood abundance in a declining population could aid in anticipating the following year's lek counts and also provide a measure of response following habitat restoration projects aimed at promoting brood-rearing habitat. Performing the low-effort monitoring in concert with mark-recapture monitoring would also enable correlations of the low-effort population monitoring to trends following the end of the in-depth monitoring period utilizing IPMs, which allow for synthesizing multiple data types (Zipkin & Saunders, 2018).

Methodological

Remote release boxes with multiple compartments and a large door attached to a pulley system seem less stressful than releasing individuals from cardboard boxes, with researchers actively opening boxes, creating a loud, stressful release environment for the birds (Dickens et al., 2009; Dickens et al., 2010). In the first year (2016) we used cardboard boxes, we did not have any individuals attend leks or begin lekking right away, and all individuals flew immediately from the boxes; in subsequent years, using the remote release boxes, we did record individuals walking out of the boxes and did have at least one male in both 2018 and 2019 that lekked upon release. Walking or lekking, instead of flying and quickly leaving the release site, are behavioral indicators for lower stress and should correspond to lower post-release mortality (Dickens et al., 2009; Dickens et al., 2010).

During 2019 translocations we had limited access to source population leks because the increased snowpack caused us to delay translocations into late April and early May (Table 5-1). Of the birds caught during that effort, 18.75% (n =16) of females laid an egg in the transport boxes; females exhibited higher mortality during transit (18.75%, n = 16), and higher mortality and dispersal following release (Chapter 2, Figure 2-10). Rather than performing translocations under higher stress, we should not translocate sage-grouse from source populations in Utah after 2-3 weeks following peak male attendance, which lags the peak female lek attendance (Connelly et al. 2011). Further studies could confirm this threshold.

We collaborated with the bi-state and ND translocations to look at artificially inseminating pre-nesting females and continued using pre-nesting females while both ND and the bi-state employed brood translocations. Artificial insemination was not successful in preventing dispersal away from the release site or increasing the nest initiation rate for pre-nesting translocated females. I combined my data with those from ND's translocation data in Lazenby (2020), and we found no significant difference between the control, SHAM (only the avian semen buffer solution), or artificial insemination (viable semen combined with the semen buffer solution) groups. Instead, brood translocations are more effective at preventing dispersal and overcoming the lowered nesting propensity in the first year following translocations that would typically be present (Meyerpeter, 2020; Picardi et al., 2022).

Monitoring

Chick survival (to 50 days post-hatch) is the life stage is the most vulnerable to mortality and the demographic bottleneck in the Sheeprock population. Though this is typical for sage-grouse, the Sheeprock population exhibited low and variable chick survival relative to other sage grouse populations (Connelly et al., 2011). Post-hatch, chick diets consist of mostly insects and gradually transition to mostly forbs (Dahlgren et al., 2015). In late June through August, water (available on the landscape in mesic habitat) is the limiting factor in the Sheeprock SGMA, a typical characteristic of cold-desert sagebrush landscapes in the Great Basin (Coates et al., 2018). During this same time in the season, the raptor migration is beginning, leaving chicks more vulnerable as available mesic resources are limiting. Many of the Utah Watershed Restoration Initiative (WRI) projects applied in the Sheeprock SGMA, beginning in 2015 and continuing to fall 2022, were aimed at improving brood-rearing habitat that would promote forb and insect production, which are critical for chick development and survival. Brood-rearing habitat restoration projects should be placed adjacent to nesting habitat to limit the distance that a female needs to move her brood post-hatch, which is riskier and equates to lower brood survival (Gibson et al., 2017; Prochazka et al., 2017). The bulk of the WRI projects have been mainly pinyon-juniper (conifer) removal and installation of beaver dam analogs. The restoration ecology literature indicates lag effects of up to ten years in sagebrush ecosystems (Harju et al., 2010; Williams et al., 2019; Olsen et al., 2021). Thus, continued monitoring of chick survival will be critical for evaluating watershed-level effects of these treatments.

Reinforcements designed around genetic restoration also exhibit time lag effects (Frankham et al., 2010; Biebach et al., 2016). Male sage-grouse live an average of 2-3 years, and females live between 3-6 years, with many females nesting several years in a row (Schroeder et al., 2020). Male sage-grouse typically become dominant males when they are adults, at least in their second lekking season post-hatch, with greater body mass (Gibson & Bradbury, 1985). In translocations utilizing pre-nesting females, females exhibit lower nesting propensity in the first-year post-release (Baxter et al., 2008; Gruber-Hadden et al., 2016; Duvuvuei et al., 2017; Ebenhoch et al., 2019), which increases the time to wait for integration of translocated individuals into the reinforced population. Therefore, you would need to translocate enough pre-nesting females to survive past the first-year translocations (Baxter et al., 2013), survive into the following breeding season and raise a successful brood, and potentially detect an effect of that surviving progeny's genetics being incorporated into the third breeding season post-translocation. From the analyses outlined in Chapter 3, we saw some positive effects that the four years of reinforcements helped improve allelic richness, which indicates improving population genetic variation (Frankham et al., 2010). We did not see a statistical difference in observed heterozygosity pre- and post-translocations, but this metric takes longer to change than allelic richness (Frankham et al., 2010; Biebach et al., 2016; Neaves et al., 2023). Continued monitoring of population genetics, therefore, would aid in the long-term genetic effects of the reinforcements (Biebach et al., 2016; Neaves et al., 2023).

Next Steps

I would recommend the following steps, in order of priority, for further monitoring and continued analysis of extant data:

1. Practitioners develop an updated Sheeprock SGMA management plan that incorporates management strategies for this sage-grouse population informed by structured decision making that includes an exit strategy (e.g., no further interventions)
2. Conduct a minimum viable population analysis for the Sheeprock SGMA
3. Establish randomly placed brood count transects similar to those performed annually on Parker Mountain, but only use 1-2 volunteers since the Sheeprock SGMA is a small, vulnerable population with extensive visitor recreation
4. Establish low-cost genetic monitoring by collecting feathers during the lekking season
5. Perform a habitat priority removal analysis to determine where the Sheeprock SGMA could benefit most from further habitat restoration projects (beaver dam analogs, conifer removal, etc.)
6. If further translocations are planned, employ brood translocations after completing the following steps:

1. Evaluating mesic habitat improvements from 2016 to the present using changes in normalized difference vegetation index (NDVI)
2. Building a species distribution model that would identify release sites
3. Establish a low-cost monitoring method for tracking translocated broods and estimating brood abundance across the SGMA

Conservation Translocation Resources

Below are some relevant and helpful resources for reviewing conservation translocation literature:

- ***Groups:***
    - The International Union for the Conservation of Nature (IUCN)/ Species Survival Commission (SSC) Conservation Translocation Specialist Group (CTSG)- world-wide group of researchers and practitioners involved in translocating plants and animals: https://iucn-ctsg.org/
- ***IUCN Reintroduction/Translocation Guidelines:***
    - IUCN Position on the Translocation of Living Organisms (1987)
    - IUCN Guidelines for Re-Introductions (1998)
    - IUCN Guidelines for Reintroductions and Other Conservation Translocations (2013)
- ***Books:***
    - Reintroduction Biology: Integrating Science and Management (2012), eds: J.G. Ewen, D.P. Armstrong, K.A. Parker, and P.J. Seddon

- Advances in Reintroduction Biology of Australian and New Zealand Fauna (2015), eds: D.P. Armstrong, M. Hayward, D. Moro, and P.J. Seddon
- Reintroduction of Fish and Wildlife Populations (2016), eds: D.S. Jachowski, J.J. Millspaugh, P.L. Angermeier, and R. Slotow
- Structured Decision Making (2020), eds: M.C. Runge, S.J. Converse, J.E. Lyons, and D.R. Smith
- Conservation Translocations (2023), eds: M.J. Gaywood, J.G. Ewen, P.M. Hollingsworth, A. Moehrenschlager

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Tables

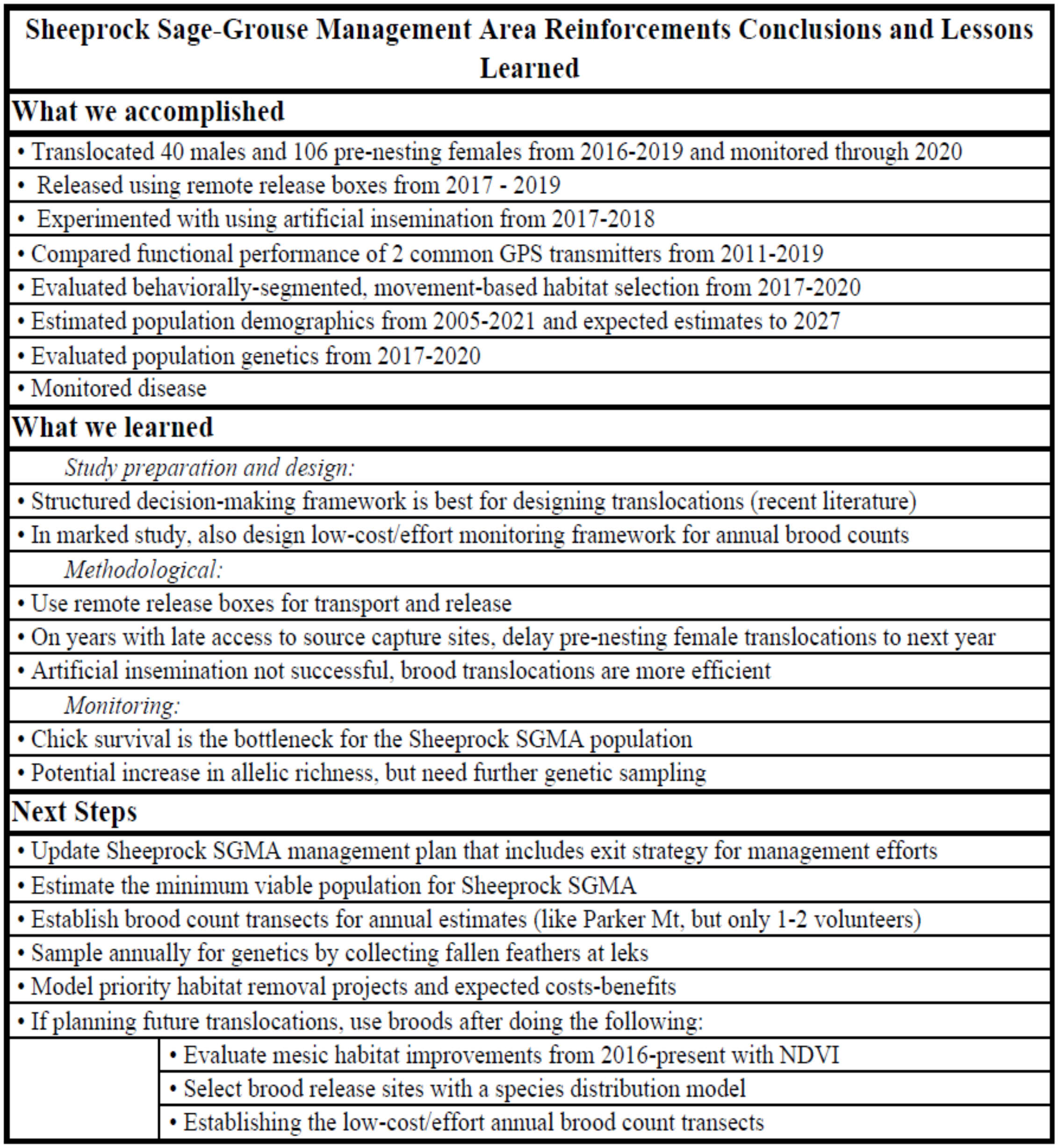
Table 5-1: A summary of the greater sage-grouse (Centrocercus urophasianus) translocation efforts in the Sheeprock Sage-Grouse Management Area in central Utah. This table includes information on the translocation dates for each source population and how many individuals were removed from that source, the number and cause of mortalities, and behavior that not recorded elsewhere in this dissertation but remains relevant. Though not often included in translocation papers, this information is still important to assess any potential factors that may contribute to increased stress, such as translocating sage-grouse later in the lekking season and the increased mortalities and eggs laid by females in transit.

Translocation Year	Translocation Dates	Transport/ Release Method	Total Male/ Female by Source Popn	Mortalities in Transit Male/Female	Mortality causes	Number Females that laid eggs in boxes	Males Observed Lekking Post-release
2016	March 9- Box Elder April 8- Parker Mt	Individual cardboard boxes	8 M/ 11 F - Box Elder 2 M/ 19 F - Parker Mt	1 M/ 0 F	broken wing	0	0
2017	April 6- Parker Mt April 15- Box Elder	5-compartment remote release box	6 M/ 25 F - Parker Mt 4 M/ 5 F - Box Elder	0 M/ 1 F	capture-related injury	0	0
2018	March 20- Parker Mt March 24- Box Elder April 6- Box Elder	5-compartment remote release box	7 M/ 21 F- Parker Mt 3 M/ 9 F- Box Elder	0 M/ 1 F	capture myopathy	0	≥ 1†
2019	April 24-25, May 2- Parker Mt	5-compartment remote release box	10 M/ 16 F- Parker Mt	0 M/ 3 F	2 blunt force head trauma, 1 capture myopathy*	3	≥ 1†

*During necropsies, 2 of these hens were found to be gravid

† Insufficient data recorded for some translocation releases, so there may have been lower detection of these observations

Table 5-2: A summary of the conclusions and lessons learned from the reinforcement translocations that we performed with greater sage-grouse (*Centrocercus urophasianus*) from 2016-2019 and monitored to 2020 in the Sheeprock Sage-Grouse Management Area, Utah.



Sheeprock Sage-Grouse Management Area Reinforcements Conclusions and Lessons Learned	
What we accomplished	
• Translocated 40 males and 106 pre-nesting females from 2016-2019 and monitored through 2020	
• Released using remote release boxes from 2017 - 2019	
• Experimented with using artificial insemination from 2017-2018	
• Compared functional performance of 2 common GPS transmitters from 2011-2019	
• Evaluated behaviorally-segmented, movement-based habitat selection from 2017-2020	
• Estimated population demographics from 2005-2021 and expected estimates to 2027	
• Evaluated population genetics from 2017-2020	
• Monitored disease	
What we learned	
Study preparation and design:	
• Structured decision-making framework is best for designing translocations (recent literature)	
• In marked study, also design low-cost/effort monitoring framework for annual brood counts	
Methodological:	
• Use remote release boxes for transport and release	
• On years with late access to source capture sites, delay pre-nesting female translocations to next year	
• Artificial insemination not successful, brood translocations are more efficient	
Monitoring:	
• Chick survival is the bottleneck for the Sheeprock SGMA population	
• Potential increase in allelic richness, but need further genetic sampling	
Next Steps	
• Update Sheeprock SGMA management plan that includes exit strategy for management efforts	
• Estimate the minimum viable population for Sheeprock SGMA	
• Establish brood count transects for annual estimates (like Parker Mt, but only 1-2 volunteers)	
• Sample annually for genetics by collecting fallen feathers at leks	
• Model priority habitat removal projects and expected costs-benefits	
• If planning future translocations, use broods after doing the following:	
	• Evaluate mesic habitat improvements from 2016-present with NDVI
	• Select brood release sites with a species distribution model
	• Establishing the low-cost/effort annual brood count transects

APPENDICES

APPENDIX A

Aspergillosis in an augmented greater sage-grouse (*Centrocercus urophasianus*) population in central Utah: a case report[1]

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[1] Chelak, M. S., A. A. Cook, D. D. Frame, and T. A. Messmer. 2020. Aspergillosis in an augmented greater sage-grouse (Centrocercus urophasianus) population in Utah: A case report. WNAN 80: 547-550.

ABSTRACT

We present the first known case of aspergillosis found in a wild, augmented greater sage-grouse (*Centrocercus urophasianus*) population. This case was not directly associated with the sage-grouse translocations and is the first documented in wild sage-grouse populations since the mid-1900s. Aspergillosis is a fungal infection of the lungs caused by an inoculation of *Aspergillus* spp. spores. Wild birds that are infected by the pathogen's spores die from the resulting infection. We hypothesize that the *Aspergillus* spp. spores were propagated either in mesic nesting conditions or in residual damp mulch piles created from sagebrush (*Artemisia* spp.) habitat restoration projects and infected the individual within several days of inhaling the spores. This case may have conservation implications for small, augmented, or reintroduced avian populations, especially those of conservation concern where concurrent habitat restoration projects and other conservation actions may create conditions conducive to the propagation of *Aspergillus* spp. spores and enhance the risk of sage-grouse inoculation.

NOTE

In May 2018, we recovered the intact carcass of an adult female greater sage-grouse (*Centrocercus urophasianus*; sage-grouse) marked with a radio-transmitter that had been translocated in March 2017 from the south-central Utah to the Sheeprock Mountain Sage-Grouse Management Area (SGMA) as part of an augmentation program to prevent extirpation. At the time we recovered the carcass, we could not confirm that the female was nesting. However, based on her localized movements detected via radio-telemetry, she may have initiated a nest that had failed earlier in the season. The recovered carcass was necropsied by Utah Veterinary Diagnostic Laboratory personnel

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[1] Chelak, M. S., A. A. Cook, D. D. Frame, and T. A. Messmer. 2020. Aspergillosis in an augmented greater sage-grouse (Centrocercus urophasianus) population in Utah: A case report. WNAN 80: 547-550.

(UDVL; Spanish Fork, UT), and the necropsy revealed that the female died from aspergillosis, a fungal infection of the lungs caused by an inoculation of *Aspergillus* spp. spores.

According to the nature of the gross and histological examinations, UDVL personnel concluded that the infection was caused by a recent inhalation of a significant quantity of *Aspergillus* spp. spores in spring 2018. Their examination revealed multiple spherical granulomatous lesions within the left lung and thoracic air sacs, suggestive of subacute aspergillosis. This diagnosis was substantiated upon subsequent culture and histologic examination of the lesions (Figures 1 A & B). Cestodiasis, a severe tapeworm intestinal infestation, was also detected.

Disease occurrences in wild sage-grouse populations are cause for concern because of documented range-wide population declines (Schroeder et al. 2004). In 2003, the discovery of the West Nile Virus (WNV; *Flavivirus*), spread by mosquitoes (*Culex* spp.) in sage-grouse, increased range-wide conservation concerns about the impacts of disease on declining populations in increasingly anthropogenic and fragmented landscapes (Walker and Naugle 2011). Unlike WNV, *Aspergillus* spp. spores are not spread by an active vector, so there is a low risk of the pathogen to contribute to extirpation or population declines (MacPhee and Greenwood 2013). However, if environmental factors in areas inhabited by small, isolated sage-grouse populations create conditions for the pathogen to propagate, the circumstances contributing to potential outbreaks should be evaluated (Tell et al. 2019).

The documented declines in sage-grouse populations and their distribution as a result of the loss and fragmentation of sagebrush (*Artemisia* spp.) ecosystems (Schroeder

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[1] Chelak, M. S., A. A. Cook, D. D. Frame, and T. A. Messmer. 2020. Aspergillosis in an augmented greater sage-grouse (Centrocercus urophasianus) population in Utah: A case report. WNAN 80: 547-550.

et al. 2004) resulted in the U.S. Fish and Wildlife Service (USFWS) reviewing the species' protection status under the U.S. Endangered Species Act (USFWS 2015; ESA). Because of the species' conservation status, range-wide research and conservation efforts have included the capture and radio-marking of thousands of sage-grouse within the last two decades as well as efforts to augment declining populations through translocations to prevent extirpations in many areas (Stiver 2011). These range-wide efforts were cited in the USFWS in the decision not to provide sage-grouse ESA protection (USFWS 2015).

Despite this plethora of research and conservation activity, this case is the first documented occurrence of aspergillosis in a wild sage-grouse since Patterson (1952), who reported a nesting sage-grouse mortality that he attributed to aspergillosis in a wild population in Wyoming. This case is also the only documented in a wild, augmented sage-grouse population further supporting that aspergillosis is not common in sage-grouse (Christiansen and Tate 2011). In captive-bred populations, Oesterle et al. (2005) reported one incident of aspergillosis in a population of sage-grouse and noted the high-stress environment where there was heightened aggression among the captive-bred individuals. Similarly, aspergillosis has also been reported in wild Gunnison sage-grouse (*C. minimus*) captured and released into captive-breeding facilities (Apa and Wiechman 2015). However, the source of the infection was attributed to fungal spores propagated in the dusty conditions of the captive-breeding facilities (Apa and Weichman 2015).

Aspergillosis occurring in wild populations is infectious and non-contagious, but leads to mortality of the infected individual because it cannot be treated (Tell 2005, Beernaert et al. 2010). In wild avian species, it is most commonly found in waterfowl, raptors, upland game birds, and corvids (Friend 1999, Tell 2005, Kornillowicz-Kowalska

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and Kitowski 2013, Tell et al. 2019). It occurs in concentrations of plant and keratinous material and propagates between 30-45˚C (Kornillowicz-Kowalska and Kitowski 2013).

In many areas in the United States, woody plant expansion is displacing native shrublands and grasslands, which has led to habitat restoration projects to remove the target species (Miller et al. 2017). Western rangelands specifically are facing the onset of conifer expansion into sagebrush habitat, and managers are working to mitigate that impact by removing conifers through mastication—grinding down trees where they stand— as well as other methods (Sandford et al. 2017). The remaining mulch is then left in place to decompose adding new keratinous material to the landscape. High residual concentrations of mulch, associated with widespread conifer mastication, in combination with mesic seasonal micro-climate conditions associated with sage-grouse nests, could facilitate conditions favorable *Aspergillus* spp. growth and spore propagation (Kornillowicz-Kowalska and Kitowski 2013).

In domestic turkeys, an *A. fumigatus* intra-air sac infection causes lesions similar to those found in the recovered female sage-grouse carcass within 72 h post-exposure (Kunkle and Rimler 1996). This observation led us to believe the female was exposed to the fungal spores in 2018 and not directly connected to the translocations of 2017. However, the immunosuppressive stressors of the 2017 capture, transport, and release associated with the translocation (Dickens et al. 2010, Parker et al. 2012, Jachowski et al. 2016), in addition to the stressors of the 2018 breeding season and concurrent cestodiasis, likely contributed to a decreased ability of the female to suppress an overwhelming inoculation of fungal spores (Redig et al. 1980, Alley et al. 1999, Tell 2005, Beernaert et al. 2010, Kornillowicz-Kowalska and Kitowski 2013).

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Although we only detected aspergillosis in one radio-marked individual, further research should examine if the mulch piles created from conifer removal projects or the plant and keratinous material in sage-grouse nests could propagate *Aspergillus* spp. spores. This research should be conducted in seasonally mesic environments common in spring, when breeding and nesting facilitate higher stress conditions, and where habitat restoration projects may provide novel substrates conducive to the fungus. As climate change shapes and alters weather patterns across landscapes, it is likely that some sagebrush habitats also will experience increased spring soil moisture (Palmquist et al 2016), which may create favorable conditions for the propagation of *Aspergillus* spp. spores and increase avian species inoculation risks (Kornillowicz-Kowalska and Kitowski 2013).

As previous literature has suggested with WNV and other diseases (Christiansen and Tate 2011), we recommend continued monitoring of sage-grouse populations for disease, and that any individuals' carcasses or remains containing air sacs and lungs be sent for necropsy. In areas receiving augmentations, reintroductions, or other conservation translocations, adequate post-release monitoring is integral for not only movements and demographics, but also for disease (IUCN/SSC 2013, Muths and McCallum 2016).

ACKNOWLEDGEMENTS

We thank the numerous landowners providing access to their lands and the Utah Division of Wildlife Resources, Bureau of Land Management, U.S. Forest Service, Utah Public Lands Policy Coordinating Office, and Yamaha Outdoor Access Initiative for their

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support. We also thank the several technicians and volunteers who have helped with the translocations and field work.

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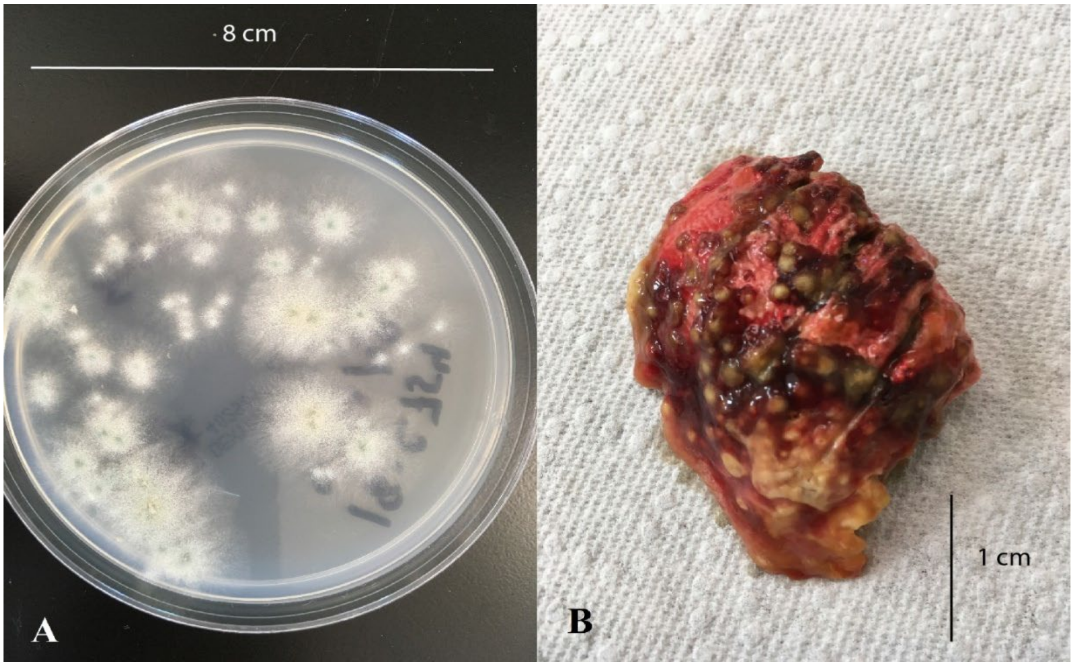

Figure A-1. Aspergillus spp. culture (A) taken from a 2018 sample of the lung (B) of an infected female Greater Sage-Grouse (Centrocercus urophasianus; sage-grouse), which was an individual translocated into the study area in 2017 as part of an effort to augment the resident sage-grouse population, Sheeprock Sage-Grouse Management Area, Utah, USA.

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APPENDIX B

Supplementary Material for Chapter 2

Data Screening Steps: Non-hour locations are recorded on the hour accounting for the transmission window (Microwave Telemetry, Inc. [MTI]: 2 minutes, GeoTrak, Inc. [GT]: 4 minutes). The transmission window encompasses the total time the GPS transmitter is powered on and attempts to obtain a location fix. To account for any movement in the internal PTT clock, we included any location that occurred one minute prior to the scheduled fix. We excluded all locations from the dataset that did not fall between 59 – 02 for MTI and 59 – 04 for GT.

We next removed all duplicate locations from the dataset by identifying and excluding any location that fell within the same 3- (MTI) or 5- (GT) minute window for an individual. We retained the first recorded location when any duplicates occurred.

Next, we removed any locations that did not occur on a scheduled hour for that programming schedule. Relocation schedules were programmed such that they attempted to obtain a GPS fix at a predetermined local time using an offset (e.g., -6 hours) from UTC that does not account for Daylight Savings Time. The determination of a UTC offset differed by companies, however.

For GT units, clients determined a desired offset (e.g., -6 hours UTC) for their study area, and all units were programmed accordingly. For MTI units, the spatial location of the previous GPS location of the PTT determines the local time (solar time) from the longitude of the last fix recorded at the next scheduled fix. The longitude boundaries PTTs use do not always coincide precisely with the political time zones. Thus, the offset and, as a result, relocation schedule fluctuated throughout the deployment period for any units deployed on grouse that moved across a longitudinal boundary. Because spatial outlier data will influence these offsets, we maintained outlier locations at this stage to properly account for offset schedules. Once we determined the correct offset for all units, we censored all locations that did not occur on a scheduled hour.

Lastly, we developed a suite of movement parameters that had the potential to identify spatial outliers while maintaining sage-grouse movement behaviors. This step was necessary because, upon visual inspection of the data, transmitters utilizing the Argos satellite array appeared to transmit a larger proportion of extreme spatial outliers (e.g., UT bird recording a location in Canada) than GPS transmitters that operate using other satellite arrays (e.g., Iridium). Many of these outliers were likely due to signal noise during transmission that resulted in an incorrect recording of a binary digit (0 or 1). Digits could be incorrectly recorded at any level of the decimal degree coordinates resulting in wide-ranging error possibilities (meters to kilometers). Thus, this prevents the simple exclusion of only large-scale spatial outliers because the outlier is as likely to be large (e.g., 2,000 km) as small (e.g., 400 m).

Furthermore, because some sage-grouse in our study populations demonstrated migratory behaviors (Connelly et al. 2011), it required that we exclude spatial outliers while maintaining large-scale migratory movements. Thus, we removed spatial outliers using a combination of four movement parameters including: 1) travel speed (m/sec), 2) location divergence, 3) sequential step-length behaviors, and 4) tortuosity. Movement parameters, including step length and tortuosity, were calculated using the *adehabitatLT* (Calenge 2006) in R 4.0.0 (R core team 2020).

We calculated travel speed by dividing step length (meters) by time (seconds) between subsequent fixes. Location divergence was the average distance between location i and the average location of the two preceding ($i - 1$, $i - 2$) and two succeeding locations ($i + 1$, $i + 2$). To calculate sequential step-length behaviors that identified spatial outliers, we subtracted the absolute difference in the current step length (Euclidean distance in meters between $i - 1$ and i) and the preceding step length ($i - 2$ and $i - 1$) from 1. The result provided an inverse measure such that large step lengths followed by another large step length were estimated as higher values than a large step length followed by a small step length. Lastly, we estimated tortuosity as the relative angle between the current and preceding steps.

For each movement parameter, we assayed varying thresholds (from 60th to 95th percentile by increments of 5) for where the distribution fell and identified the upper 85th percentile of the distribution. We removed any location that fell above those upper percentiles for all four movement parameters. Upon visual inspection, this threshold provided a reasonable trade-off between liberal and conservative removals of spatial outliers.

Table B-1. Table summarizing the number of companies within countries that produced GPS transmitters for tracking wildlife in 2023.

Country	Number of GPS Companies
Australia	3
Canada	2
Czech Republic	1
Germany	3
India	1
Italy	1
Kenya	1
Lithuania	1
Mexico	1
Netherlands	1
New Zealand	3
Norway	1
Poland	2
Romania	1
South Africa	5
Spain	1
UK	2
USA	12
Total	**42**

Table B-2. The differing fix acquisition schedules of fix intervals for a 22-g Microwave Telemetry Inc. and 22-g GeoTrak Inc. model of solar-powered GPS-Argos satellite transmitters deployed on greater sage-grouse from 2011–2019 in Utah and Wyoming by Utah State University, Brigham Young University, and University of Wyoming.

Yearly Fix Intervals (month change)	Number of Daily Fixes (ordered by scheduled season)	Duty Cycle Transmission (days)
1 (no change)	4	7 or 8
2 (Mar, Nov)	5, 4	8
3 (Mar, May, Nov)	8, 9, 6	3 or 5
4 (Mar, May, Jun, Oct)	6, 6, 6, 4	5 , 7, or 8
4 (Mar, May, Aug, Nov)	4 or 5, 6 or 8, 5, 4	3
5 (Mar, May, July, Sept, Oct)	8, 10, 9, 8, 7	3

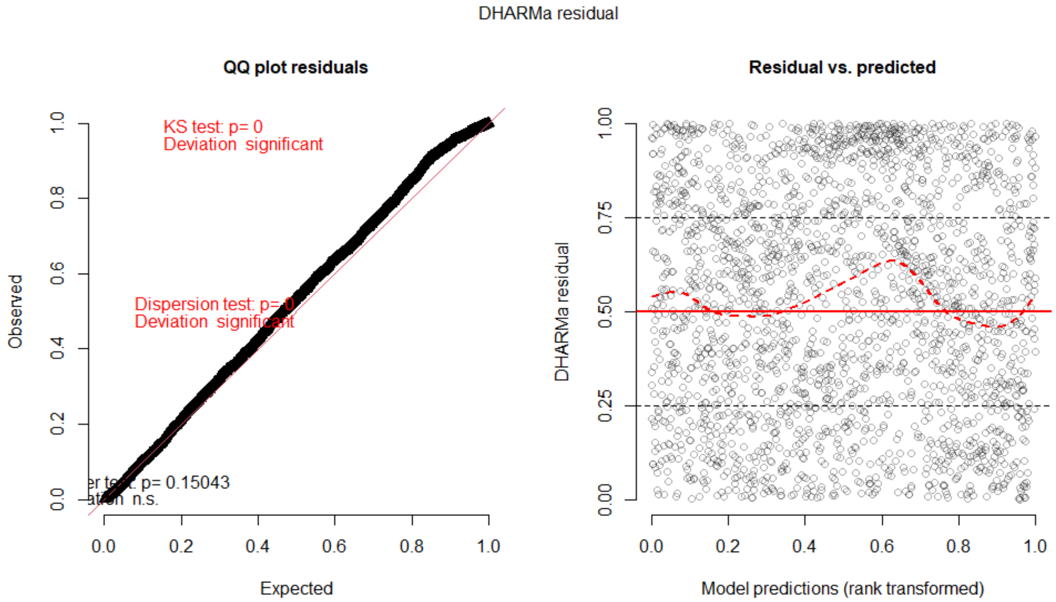

Figure B-1. *DHARMa* residual plots for the best-fit model for daily nest fix inefficiency (DNFI) for two solar-powered GPS-Argos satellite transmitters (GeoTrak Inc. and MTI = Microwave Telemetry Inc.) deployed on greater sage-grouse (*Centrocercus urophasianus*) from 2011–2019 in Utah and Wyoming by Utah State University, Brigham Young University, and University of Wyoming (n = 2,300 nesting days for 84 individuals).

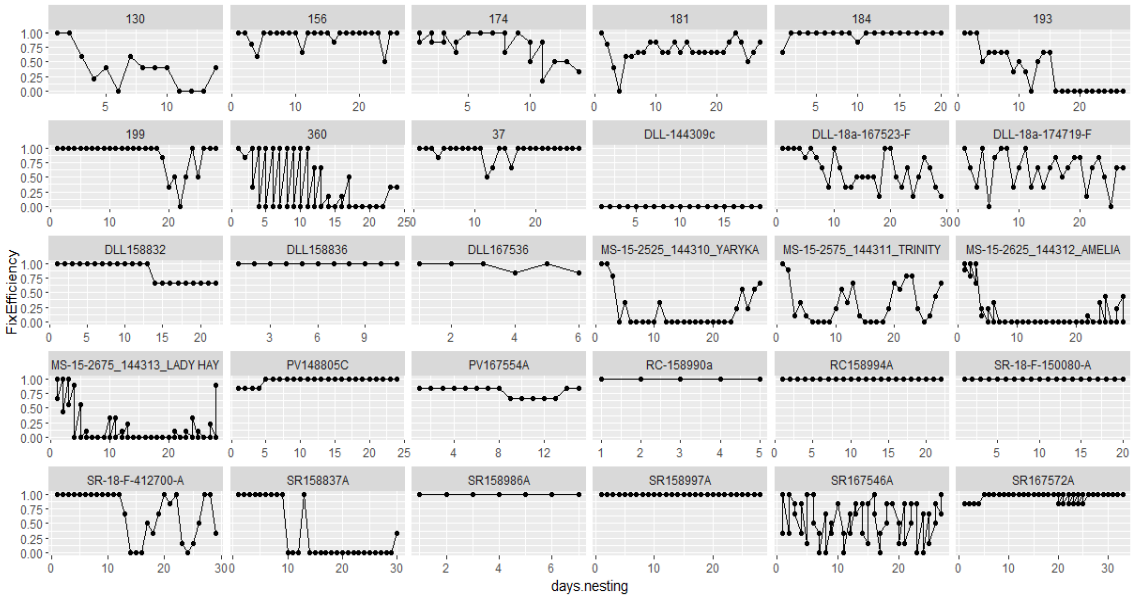

Figure B-2. Individual variation for daily nest fix inefficiency for 22-gram solar-powered GPS-Argos satellite transmitters (one manufactured by Microwave Telemetry Inc., and the other by GeoTrak Inc) deployed on n = 30 female greater sage-grouse (*Centrocercus urophasianus*) during the nesting periods observed between 2011 and 2019 in Utah and Wyoming.

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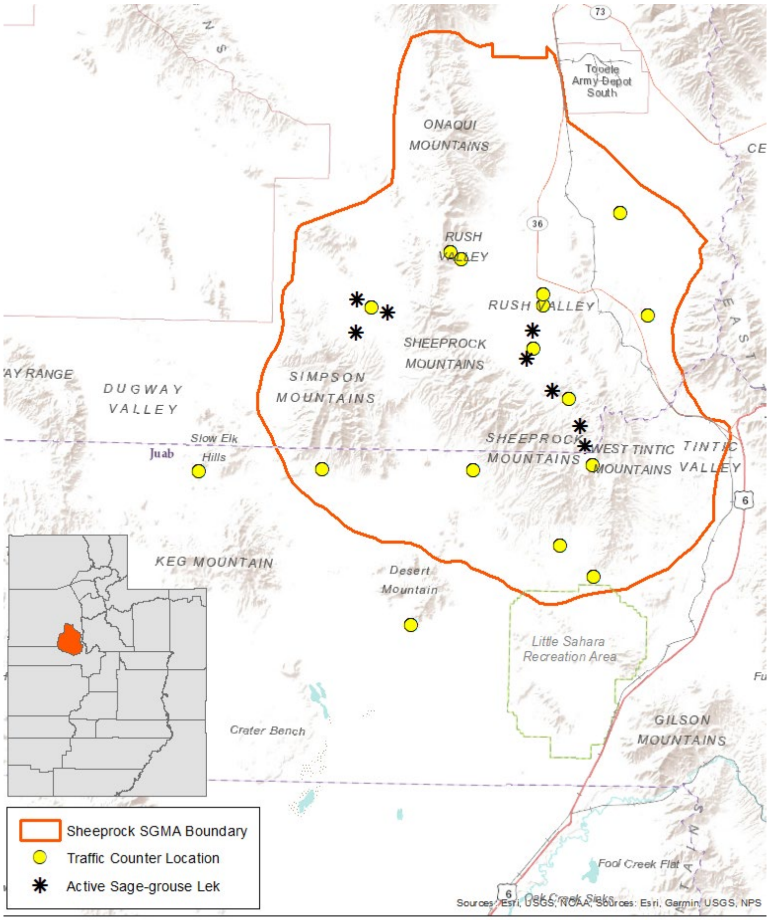
APPENDIX C

Supplementary Material for Chapter 3

GPS transmitter duty cycle information

March 1 (0100hr, 0700-0800, 1300, 1700-1800), May 1 (0100-0700-0800, 1300, 1800-1900), June 16 (0000, 0200, 0700, 1300, 1600, 2000), and October 1 (0000, 0800, 1600, 2000).

Off-highway vehicle traffic volume



Source: Esri, USGS, UDWR, BLM

Figure C-1. Off-highway vehicle TRAFx (TRAFx Research Ltd., Canmore, Alberta, Canada) counter locations between 2016-2020 to collect daily traffic counts in the Sheeprock Sage-grouse Management Area (SGMA), Utah, US. Asterisks show active sage-grouse display sites.

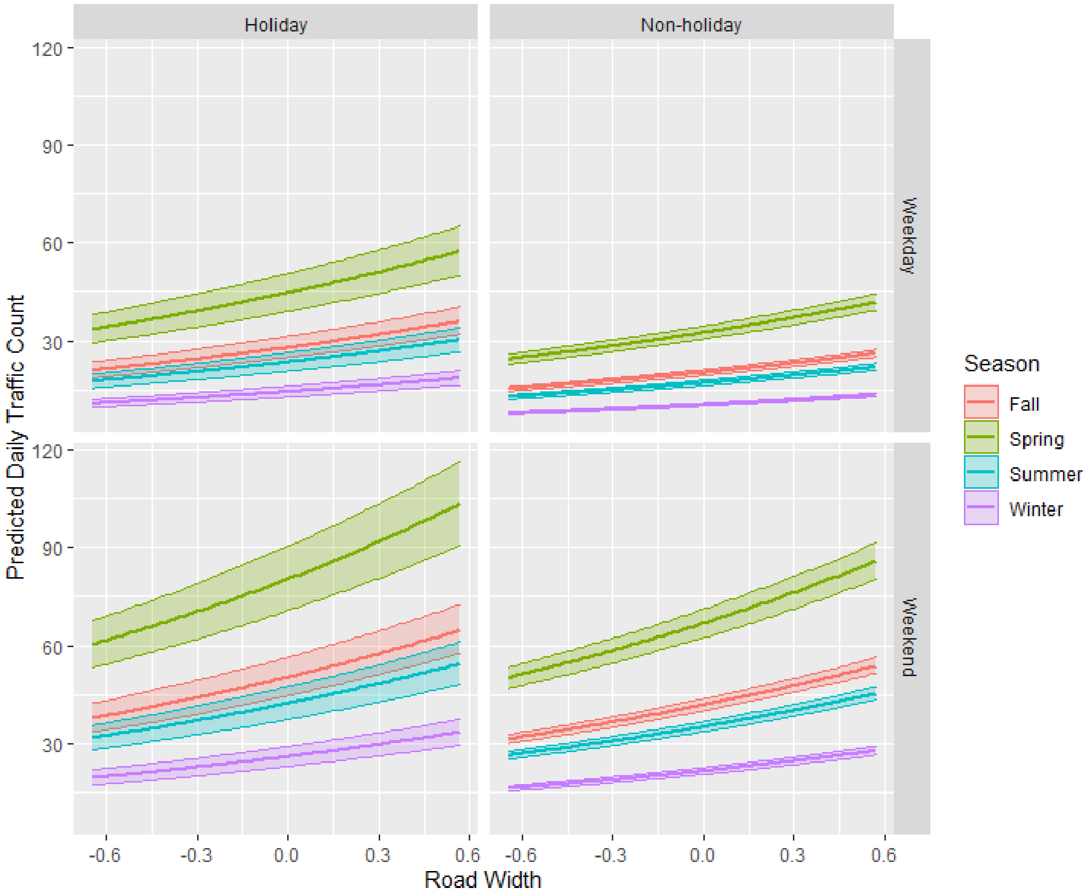


Figure C-2. Predicted daily traffic counts estimated via negative binomial generalized linear model on data collected in the Sheeprock Sage-grouse Management Area, Utah, US, between 2016-2020.

APPENDIX D

Supplementary Material for Chapter 4

Equation for monthly unit hazard shared-frailty model:

$$UH_{survival,ijk} = \exp\left(\alpha_i + \beta_i x_{ijk} + \kappa_k + \gamma_j + \zeta_{jk} \right)$$

Prior distributions:

$$\alpha_i \sim Uniform(-20,0)$$

$$\beta_i \sim Normal(\mu_i = 0, 100)$$

$$\kappa_k \sim Normal(\mu_k = 0, \sigma_k^2)$$

$$\gamma_j \sim Normal(\mu_\gamma = 0, \sigma_\gamma^2)$$

$$\zeta_{jk} \sim Normal(\mu_\zeta = 0, \sigma_\zeta^2)$$

$$\sigma_k \sim Uniform(0, 5)$$

$$\sigma_\gamma \sim Uniform(0, 5)$$

$$\sigma_\zeta \sim Uniform(0, 5)$$

Cumulative hazard survival model:

$$CH_{ijk} = \sum_{k=1}^{k=12} UH_{ijk}$$

Survival parameter model:

$$S_{ijk} = e^{-CH_{ijk}}$$

Recruitment equation:

$$R_{ijk} = \left(np1_{ik} \times\ cl1_{ijk} \times\ ns1_{ijk} \times\ h_{ijk} \times cs_{ijk} \times js\right)$$
$$+ (1 - ns1_{ijk} \times np2_{i} \times cl2_{ijk} \times ns2_{ijk} \times h_{ijk} \times cs_{ijk} \times js)$$

Nest propensity:

First nest propensity:

$$np1_{i=adult} \sim Beta(97, 5)$$

$$np1_{i=yearling} \sim Beta(90, 12)$$

Second nest propensity:

Logit-link linear model for second nest propensity:

$$y_{np2,i} \sim Binomial(p_{np2,ij}, n_{np2,ij})$$

$$logit\left(p_{np2,ij}\right) = \ \alpha + \ \beta_{i}\mathrm{x}_{ijk}$$

Prior distributions:

$$\alpha \sim \mathrm{Normal}(0, 100)$$

$$\beta_{i} \sim Normal(0, 100)$$

Log-linear model for expected clutch size:

$$y_{cl,ijk} \sim Poisson(\mu_{cl,ijk})$$

$$\log\left(\mu_{cl,ijk}\right) \sim \alpha + \ \beta_{i}\mathrm{x}_{ijk} + \ \beta_{n}\mathrm{x}_{n,ijk} + \kappa_{k} + \gamma_{j} + \ \zeta_{jk}$$

Prior distributions:

$$\alpha \sim Normal(0, 100)$$

$$\beta_{i} \sim Normal(\mu_{i} = 0, 100)$$

$$\beta_{n} \sim Normal(\mu_{n} = 0, 100)$$

$$\kappa_k \sim Normal(\mu_k = 0, \sigma_k^2)$$

$$\gamma_j \sim Normal(\mu_\gamma = 0, \sigma_\gamma^2)$$

$$\zeta_{jk} \sim Normal(\mu_\zeta = 0,\ \sigma_\zeta^2)$$

$$\sigma_{\ k} \sim Uniform(0, 5)$$

$$\sigma_{\ \gamma} \sim Uniform(0, 5)$$

$$\sigma_{\ \zeta} \sim Uniform(0, 5)$$

Nesting unit hazard shared-frailty model:

$$UH_{nest,ijk} = \exp\,(\alpha + \beta_i x_{ijk} + \beta_n x_{n,ijk} + v_v + \kappa_k + \gamma_j + \zeta_{jk})$$

Prior distributions:

$$\alpha \sim Normal(0, 100)$$

$$\beta_i \sim Normal(\mu_i = 0, 100)$$

$$\beta_n \sim Normal(\mu_n = 0, 100)$$

$$v_v \sim Normal(\mu_v = 0, \sigma_v^2)$$

$$\kappa_k \sim Normal(\mu_k = 0, \sigma_k^2)$$

$$\gamma_j \sim Normal(\mu_\gamma = 0, \sigma_\gamma^2)$$

$$\zeta_{jk} \sim Normal(\mu_\zeta = 0,\ \sigma_\zeta^2)$$

$$\sigma_{\ v} \sim Uniform(0, 5)$$

$$\sigma_{\ k} \sim Uniform(0, 5)$$

$$\sigma_{\gamma} \sim Uniform(0, 5)$$

$$\sigma_{\zeta} \sim Uniform(0, 5)$$

Logit-link linear model for hatchability:

$$y_{h,ijk} \sim Binomial(p_{h,ijk}, n_{h,ijk})$$

$$logit(p_{h,ijk}) = \alpha + \beta_i x_{ijk} + \kappa_k + \gamma_j + \zeta_{jk}$$

Prior distributions:

$$\alpha \sim \mathrm{Normal}(0, 100)$$

$$\beta_i \sim Normal(0, 100)$$

$$\kappa_k \sim Normal(\mu_k = 0, \sigma_k^2)$$

$$\gamma_j \sim Normal(\mu_\gamma = 0, \sigma_\gamma^2)$$

$$\zeta_{jk} \sim Normal(\mu_\zeta = 0, \sigma_\zeta^2)$$

$$\sigma_{k} \sim Uniform(0, 5)$$

$$\sigma_{\gamma} \sim Uniform(0, 5)$$

$$\sigma_{\zeta} \sim Uniform(0, 5)$$

Logit-link linear model for chick survival:

$$y_{cs,ijk} \sim Binomial(p_{cs,ijk}, n_{cs,ijk})$$

$$logit(p_{cs,ijk}) = \alpha + \beta_i x_{ijk} + \beta_{dd} x_{dd,ijk} + \kappa_k + \gamma_j + \zeta_{jk}$$

Prior distributions:

$$\alpha \sim \mathrm{Normal}(0, 100)$$

$$\beta_i \sim Normal(0, 100)$$

$$\beta_{dd} \sim Normal(0, 100)$$

$$\kappa_k \sim Normal(\mu_k = 0, \sigma_k^2)$$

$$\gamma_j \sim Normal(\mu_\gamma = 0, \sigma_\gamma^2)$$

$$\zeta_{jk} \sim Normal(\mu_\zeta = 0,\ \sigma_\zeta^2)$$

$$\sigma_{\ k} \sim Uniform(0, 5)$$

$$\sigma_{\ \gamma} \sim Uniform(0, 5)$$

$$\sigma_{\ \zeta} \sim Uniform(0, 5)$$

Juvenile survival model

$$js \sim Beta(100, 34)$$

Total population estimate:

$$\widehat{N}_{tot,j} = \frac{\widehat{N}_{app,j} + (\widehat{N}_{app,j} *\ \omega)}{v *\ \varphi * o}$$

Prior distributions & values:

$$v \sim Beta\ (61.29, 9.98)$$

$$\omega \sim Normal(1.458, 0.099)$$

$$o = 0.95$$

$$v = 0.84$$

Finite rate of growth ($\hat{\lambda}$) estimate:

$$\hat{\lambda}_j = \frac{\hat{N}_{tot\ k+1,j}}{\hat{N}_{tot\ k,j}}$$

Extirpation probability equation:

$$P(Extirp)_j = \frac{\#\ of\ samples\ where\ \hat{N}_{app,j} < 2}{total\ number\ of\ samples}$$

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Areas of Concentration: Ecology, GIS, Ornithology

PUBLICATIONS

M.R. Carver, S.L. Petersen, **M.S. Chelak**, R.T. Larsen, B.R. McMillan, D.L. Eggett, L. Allphin, and T.A. Messmer. 2022. Non-native ungulate impacts on greater sage-grouse late brood-rearing habitat in the Great Basin, USA. Human Wildlife Interactions 16 (2): 262-279 **2022**

M.S. Chelak, A.A. Cook, D.D. Frame, and T.A. Messmer. 2020. Aspergillosis in an augmented greater sage-grouse (Centrocercus urophasianus) population in central Utah: a case report. Western North American Naturalist 80 (4): 547-550 **2020**

Kade D. Lazenby, **Melissa Chelak**, Steven R. Matthews, David K. Dahlgren, and Peter S. Coates. 2020. Developing Artificial Insemination Methods for Translocated Female Greater Sage-Grouse (Centrocercus urophasianus). Pp 121-146 In Kade D. Lazenby. 2020. North Dakota Greater Sage-Grouse (Centrocercus urophasianus) Recovery Project: Using Translocation to Prevent State-Wide Extirpation and Develop Rangewide Protocols. Thesis. Utah State University. https://digitalcommons.usu.edu/etd/7774/ **2020**

M.S. Chelak, M.T. Kohl, J.R. Small, A.C. Pratt, K.T. Smith, J. L. Beck, C.R. Backen, M.B. Flack, H.P. Wayment, J.A. Wood, R. Howell, T. Strange, L.

McDonald, S.N. Frey, R.T. Larsen, B.A. Maxfield, D.K. Dahlgren, T.A. Messmer, and D.C. Stoner. *Refurbishing used GPS transmitters improves performance for subsequent deployments on greater sage-grouse* ***In Prep***

M.S. Chelak, S.R. Mathews-Sanchez, K.D. Lazenby, J.R. Small, C.R. Backen, L.R. McDonald, T.D. Strange, P.S. Coates, D.K. Dahlgren, T.A. Messmer, and D.C. Stoner. *Low chick survival but increased allelic richness provide more insights into sage-grouse reinforcements.* ***In Prep***

M.S. Chelak, S. Picardi, K.D. Lazenby, L.R. McDonald, M.T. Kohl, C.R. Backen, T.D. Strange, D.K. Dahlgren, T.A. Messmer, and D.C. Stoner. *Assessing post-release behavioral states and space-use: A means to inform methodological improvements in conservation translocations* ***In Prep***

UNIVERSITY EXTENSION PRODUCTS

Chelak, Melissa; Justin Small; and David Dahlgren. 2020. North American Forest Grouse Harvest Regulations. USU Extension Fact Sheet. Paper 2143. https://digitalcommons.usu.edu/extension_curall/2143/ **2020**

Kohl, Michel; Melissa Chelak; and Terry Messmer. 2019. Greater Sage-grouse Translocations: The Science Behind Utah's Conservation Policy. USU Extension Fact Sheet. Paper 1953. https://digitalcommons.usu.edu/extension_curall/1953 **2019**

REPORTS & GREY LITERATURE

Chelak, Melissa. 2023. Grouse chasing and bear conflicts: Ideas for grouse research & hunting with dogs in bear country. Grouse News Issue 66. **2023**

M.S. Chelak and T.A. Messmer. 2021. 2020 Annual Report & 2021 Research Update: Population Dynamics and Seasonal Movements of Translocated and Resident Greater Sage-Grouse (*Centrocercus urophasianus*), Sheeprock Sage-Grouse Management Area. Annual Report, Jack H. Berryman Institute, Utah State University, Logan, Utah. **2021**

M.S. Chelak and T.A. Messmer. Population dynamics and seasonal movements of translocated and resident greater sage-grouse (Centrocercus urophasianus), Sheeprock Sage-grouse Management Area. 2019 Annual Report. Utah State University. **2019**

M.S. Chelak and T.A. Messmer. Population dynamics and seasonal movements of translocated and resident greater sage-grouse (Centrocercus urophasianus), Sheeprock Sage-grouse Management Area. 2018 Annual Report. Utah State University. **2019**

J.W. Smith, B. Muhlestein, **M.S. Chelak**, L. Belton, and T.A. Messmer. Sheeprock Mountains Visitor Use Report. 2018. Institute of Outdoor Recreation and Tourism, Utah State University. **2018**

M.S. Chelak and T.A. Messmer. Population dynamics and seasonal movements of translocated and resident greater sage-grouse (Centrocercus urophasianus), Sheeprock Sage-grouse Management Area. 2017 Annual Report. Utah State University. **2017**

M.S. Chelak and T.A. Messmer. Population dynamics and seasonal movements of translocated and resident greater sage-grouse (Centrocercus urophasianus), Sheeprock Sage-grouse Management Area. 2016 Annual Report. Utah State University. **2016**

GRANTS AND SCHOLARSHIPS

Wayne Sandfort Student Travel Grant, $250, TWS Central Mts & Plains Section	**Nov 2022**
USU Wildland Resources Department Travel Grant, $300, Utah State University	**Nov 2022**
USU QNCR Travel Grant, $300, Utah State University	**Nov 2022**
USU Public Lands Initiative, $60000, Utah State University (PI Terry Messmer, M. Chelak named student)	**Jun 2021**
USU Wildland Resources Department Travel Grant, $300, Utah State University	**Oct 2019**
USU QNCR Travel Grant, $300, Utah State University	**Oct 2019**
USU Ecology Center Travel Grant, $300, Utah State University	**Oct 2019**
Ecology Center Research Award, $5000, Utah State University	**Jan 2017**
The Wildlife Society Scholarship, $1000, Utah Chapter of The Wildlife Society	**Jan 2017**

RESEARCH EXPERIENCE

Research Assistant/Data Analyst, Utah State University **Sep 23-Mar 24**

Functioning as a postdoctoral fellow. Mule deer seasonal home ranges and implications for disease transmission; Brownian bridges; networks; urban vs non-urban deer dynamics. Mentor: Dr. Kezia Manlove

Graduate Research Assistant- Utah State University **Jan 16-Mar 24**
Greater Sage-grouse reinforcements, integrated Step Selection, and Off-highway vehicle effects on Greater Sage-grouse Ecology

TEACHING EXPERIENCE

ATV Safety Training and Introduction **Apr 2023**
Utah State University, Logan, UT, *Training*
Co-led a 1-day training on ATV safety and introductory operations to a group of 11 people

Teaching Assistant: *Plant and Animal Populations* **2018**
Utah State University, Logan, UT*, Undergraduate Course*
Assisted instructor in teaching lab on basics of plant and animal population ecology and coding in R, including population growth, life histories, single and multi-species interactions, and metapopulations. Developed code in R for lab topics and a special topic on a sage-grouse case study

Teaching Assistant- Brigham Young University
***Introduction to Soil Science* lab*,* undergraduate level** **2011-2012, 2014-2015**
Aided instructors in teaching soil science concepts and performing laboratory test procedures, met with students upon request, developed weekly quizzes, and graded written and online work, including final exam papers

Teaching Assistant- Brigham Young University
***Rangeland Vegetation Measurements*, undergraduate level** **2014**
Assisted instructors in preparing materials for class lab assignments, teaching students on methods of vegetation measurements and analyses, graded all work and exams.

PROFESSIONAL EXPERIENCE

Interim Facilitator- WDARM Local Working Group May 2023-present
Voluntarily served as the interim facilitator for the UT West Desert Adaptive Resource Management local working group beginning in fall 2023. Coordinated meetings for local working group and initiated update of Utah West Desert sage-grouse management strategy using structured decision making.

Scientific Advisor- WDARM Local Working Group 2016-2024
Served as the scientific advisor for the UT West Desert Adaptive Resource Management local working group. Presented research and advised local agencies on greater sage-grouse ecology in the area.

Lab Assistant- BYU Environmental Analytical Lab 2014-2015

Worked in BYU's Environmental Analytical Lab performing analyses on soil, water, plants, and biosolids. Sample preparation, analyses and sending results. Trained new lab assistants on common analyses and instrument setup

Research Field Technician- Fish Springs National Wildlife Refuge, UT 2012-2013
Wetland vegetation mapping on the refuge for field-truthing remote sensing data, Wetland vegetation species identification, Compiled and compared peak bird count information for national and refuge surveys on common waterfowl species for a 30-year period

Research Field Technician- Brigham Young University, UT 2012
Aided in field data collection on a snowy plover project on the Fish Springs Wildlife Refuge and the Dugway Proving Grounds; nesting behavior, nest site selection, and occupancy of snowy plover on Fish Springs and Dugway.

Research Assistant- Brigham Young University, UT 2011-2012
Worked independently under the direction of a graduate student using the dissolved organic carbon (DOC) method preparing soil samples to be analyzed; Prepared and centrifuged soil samples to be run on the nitrate and ammonium methods

WORKSHOPS, FIELD TRIPS, & SYMPOSIA

Designing Effective Avian Translocations
The Wildlife Society, 2022, Spokane, WA *Symposium*
Designed and led symposium along with co-organizers Drs. Simona Picardi, Pete Coates, Steven Mathews, and David Dahlgren for the TWS meeting that incorporated researchers from across the US

Connecting and preparing diverse early-career scientists in resolving complex wildlife problems
The Wildlife Society, 2020, Louisville, KY *Workshop*
(*accepted & planned but canceled due to COVID-19*)
Designed workshop for the 2020 TWS meeting that incorporated a diverse group of early-career scientists in understanding the feral animal wildlife issue, brainstormed and presented ideas for resolving some of the issues involved, and connected them with top researchers/managers who deal with the various feral animal issues (feral equids, felines, and swine)

Great Basin Ecology: The Evolving Saga of Humans, Sage-grouse, and Wild Horses
Ecological Society of America 2020, SLC, UT *Field Trip*
(*accepted & planned, but canceled Due to COVID-19*)
Designed a field trip in the west desert of Utah for the 2020 ESA meeting that planned to tour the eastern-most portion of the Great Basin and review its ecology, including invasive annuals, free-roaming equids, sagebrush ecology, and recreation

POSTERS AND PRESENTATIONS

P.S. Coates*, **M.S. Chelak**. Synthesizing “Designing Effective Avian Translocations” for direct application. The Wildlife Society 2022, Spokane, WA. *Presentation in Designing Effective Avian Translocations symposium*.

M.S. Chelak*. Incorporating climate change aspects into translocation design: A literature review and helpful resources. The Wildlife Society 2022, Spokane, WA. *Presentation in Designing Effective Avian Translocations symposium*.

M.S. Chelak*, S. Picardi, and T.A. Messmer. Evaluating habitat-related and anthropogenic drivers of post-release movements for translocated greater sage-grouse in the Sheeprock Mountains of central Utah, Logan, UT. *Presentation.*

M.S. Chelak*, S. Picardi, and T.A. Messmer. Evaluating drivers of post-release movements for translocated greater sage-grouse in the Sheeprock Mountains of central Utah. Utah Chapter of the Wildlife Society 2022, Virtual, UT. *Presentation*.

M.S. Chelak*, J.R. Small, and D.K. Dahlgren. Forest Grouse Hunting Regulations in North America. Prairie Grouse Technical Council 2019, Bartlesville, OK. *Poster*.

M.S. Chelak*, M.T. Kohl, J.R. Small, H. Wayment, W. Smith, N. Frey, B. Maxfield, R. Larsen, and T.A. Messmer. Functionality and Effectiveness of Two Solar-Powered GPS Transmitters Fitted on Greater Sage-Grouse in Utah. The Wildlife Society 2019, Reno, NV. *Presentation*.

M.S. Chelak*, K.D. Lazenby*, M.B. Meyerpeter, S.R. Mathews, M.T. Kohl, D.K. Dahlgren, P.S. Coates, M. Ricca, D. Delehanty, and T.A. Messmer. Updating the Knowledge and Protocols of Greater Sage-Grouse Translocations Range-Wide from Reese & Connelly (1997). The Wildlife Society 2019, Reno, NV. *Poster.*

M.S. Chelak* and T. Messmer. Five Important Considerations for Sage-Grouse Translocations: A Case Study from Utah’s West Desert. Utah All Hands-All Lands Summit 2019, Salt Lake City, UT. *Presentation.*

M.S. Chelak and T. Messmer*. Five Important Considerations for Sage-Grouse Translocations: A Case Study from Utah’s West Desert. Utah Chapter of the Wildlife Society 2019, Springdale, UT. *Presentation.*

M.S. Chelak* and T. Messmer. Greater Sage-grouse use of habitat restoration projects located within the Sheeprock Sage-grouse Management Area. Utah Chapter of the Wildlife Society 2018, Vernal, UT. *Presentation.*

M.S. Chelak*, B. Muhlestein*, J. Smith and T. Messmer. Greater sage-grouse (Centrocercus urophasianus) habitat selection in response to off-highway vehicle recreation in the Sheeprock Mountains, Utah, USA. Restoring the West Conference 2018, Logan, UT. *Poster.*

* indicates presenting author(s)

JOURNAL MANUSCRIPT REVIEWER

The Journal of Wildlife Management
Human-Wildlife Conflicts
Wildlife Society Bulletin

Ecosphere

MEMBERSHIPS

American Association for the Advancement of Science
The Wildlife Society
Utah Chapter of the Wildlife Society
Wilson Ornithological Society
American Ornithological Society
Ecological Society of America
The Society for Conservation Biology
Galliformes Specialist Group
Jack H. Berryman Institute

VOLUNTEER EXPERIENCE

Grouse News "Bird Dogs in Research" Highlight	2019-present
After-school elementary class presentation: Wildlife conflicts, UT	2020
Dusky Grouse Capture and Brood Vegetation Surveys, NV	2019
Black bear mitigation translocation, Escalante, UT	2019
Burrowing Owl Capture and Banding, Tooele, UT	2016-2018
Black-tailed Jackrabbit Surveys, Dugway Proving Grounds, UT	2018
Passerine Banding, University of Utah, Salt Lake City, UT	2017
Dusky and Ruffed Grouse Breeding surveys, Logan, UT	2017
Christmas Bird Count, Audubon Society, Provo, UT	2016
Raptor Education, Great Basin Wildlife Rescue, Springville, UT	2015
Small Mammal Trapping, Brigham Young University, Provo, UT	2012

LANGUAGES

English – native language
French – speak fluently and read/write with professional proficiency