# NORTH DAKOTA GREATER SAGE-GROUSE (CENTROCERCUS

### UROPHASIANUS) RECOVERY PROJECT: USING TRANSLOCATION

### TO PREVENT STATE-WIDE EXTIRPATION AND DEVELOP

### **RANGEWIDE PROTOCOLS**

by

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### ABSTRACT

North Dakota Greater Sage-Grouse (Centrocercus urophasianus) Recovery Project: Using

Translocation to Prevent State-wide Extripation and Develop Rangewide Protocols

by

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Greater sage-grouse (*Centrocurcus urophasianus*; hereafter sage-grouse) are the largest grouse species in North America. Sage-grouse occupy 11 western states. The northeastern edge of sage-grouse range extends into North Dakota. Conservation of sagegrouse has been on the forefront of conservation management since the 1990s. In 2015 the USFWS declared sage-grouse were not warranted for listing based on range-wide collaborative efforts. Translocations of sage-grouse are an example of these efforts.

Translocations have been described as the movement and release of animals into a novel and free environment. Translocations can be a viable management tool for wildlife management. There have been more than 7200 sage-grouse translocated during more than 56 translocation events.

We used Resource Selection (RSF) framework to estimate habitat selection on marked sage-grouse during the nesting, brooding, and summer seasons, this combined with the nesting and brooding analysis provides an overview of available and needed resources during the life cycle of sage-grouse. Furthermore, we provide an analysis of past available and current available shrub to illuminate future habitat projects.

We initiated brood translocations in 2018 by capturing and translocating for broods (n=6) with chicks (n= 26). Five of the 6 chicks survived  $\geq$  50 days post hatch (individual apparent chick survival 0.10). Compared to pre-nesting translocated females, translocated broods moved less distance per day. Averaging 11.35 km/day (95% CI 4.91-19.79) for GP males and 6.52 km/day (95% CI 1.56-11.50) for VHF females compared to smaller movements of 0.19 km/day (95% CI 0.0-0.39).

We developed protocols for artificial insemination (AI). Research is ongoing which that will evaluate the success of the inseminations. We found no differences in nest initiation rates between treatment groups (AI, Sham, and No Treatment) ( $\chi^{2}$  = 0.53414, df = 2, P = 0.7656, AI mean = 0.26, SE = 1.20, Sham mean = 0.17, SE 0.67, Control mean = 0.22, SE 0.87). We found no difference in seasonal movement. (F = 1.43, DF = 2.0, 1464.5 P = 0.24, AI mean = 1.27 km/day, SE 0.161 Sham mean = 1.75 km/day SE, 0.200, Control mean = 1.24 km/day, SE 0.115) between treatment groups.

(166 pages)

#### PUBLIC ABSTRACT

North Dakota Greater Sage-Grouse (Centrocercus urophasianus) Recovery Project: Using Translocation to Prevent State-wide Extripation and Develop Rangewide Protocols Kade D. Lazenby

Greater sage-grouse (*Centrocurcus urophasianus*; hereafter sage-grouse) are the largest grouse species in North America. Sage-grouse occupy 11 western states, extending into North Dakota. North Dakota sage-grouse population is part of the Great Plains Management Zone. Conservation of sage-grouse has been on the forefront of conservation management 1990s. In 2015 the USFWS declared sage-grouse were not warranted for listing based on significant management efforts. Translocations of sagegrouse to prevent populations from extirpation are an example of these efforts.

Translocations have been described as movement and release of animals into a novel environment. There have been more than 7200 sage-grouse translocated during more than 56 translocation events.

We used Resource Selection (RSF) framework to estimate marked sage-grouse in their new environment during the nesting, brooding, and summer seasons. With Resource selection analysis we provide the release site locations within our study site with the highest probability of use during the respective seasons. We also provided resource selection analysis during the summer months, this combined with the nesting and brooding analysis provides an overview of available and needed resources during the yearly life cycle of sage-grouse. Furthermore, we provide an analysis of past available shrub and current available shrub to illuminate future habitat projects for sagebrush obligates.

We initiated brood translocations in 2018 by capturing and translocating 6 broods and 26 chicks. Four broods were released successfully, with 5 of the 26 translocated chicks known to survive  $\geq$  50 days post hatch. Additionally, 2 of the 6 brood females were documented surviving through the end of the year. Compared to pre-nesting translocated females, translocated broods moved less distance per day.

We developed protocols for artificial insemination (AI). We disseminated male sage-grouse, and inseminated female sage-grouse with collected semen. Research is ongoing which will evaluate the success of the inseminations that occurred. We were able to compare nest initiation and movement rates for pre-nesting translocated females in each group. Because translocated female sage-grouse placed in novel environments have been documented to have lower reproduction and survival rates, our research provides important evaluations of methods to mitigate known setbacks when translocating grouse.

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Kade Lazenby

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#### CHAPTER 1

#### INTRODUCTION AND LITERATURE REVIEW

#### **Description and General Ecology**

Greater sage-grouse (*Centrocurcus urophasianus*; hereafter sage-grouse) are the largest grouse species in North America (Patterson 1952, Knick and Connelly 2011). Sage-grouse are aptly named, being sagebrush (*Artemesia* spp.) obligates throughout their life-cycle, as well as having a winter diet consisting of high amounts of sagebrush leaves (Connelly et al. 2000). Although male and female sage-grouse have very similar morphological traits with black bellies, yellow eye-combs, pointed tail-feathers, and cryptic coloration, sage-grouse are sexually dimorphic with males having greater body sizes of 65 – 75 cm in length and weighing up to 2.8 kg. Whereas, females range from 50 – 60 cm in overall length and weigh up to 1.58 kg (Connelly et al. 2011). Male sage-grouse have stiff white specialized feathers on the breast and sides of the neck, longer pointed tail-feathers, and large air sacs used in breeding displays, while females are more drab and cryptic (Patterson 1952, Dalke et al. 1963, Schroeder et al. 1999). Sage-grouse, having evolved in sagebrush ecosystems, are a comparatively long-lived (e.g., up to 8-years) gamebird with relatively low productivity (Zablan et al. 2003, Taylor et al. 2012).

Although sage-grouse depend on sagebrush throughout their life history and are considered an obligate species, they use various sagebrush communities during different times of the year (Connelly et al. 2000). Seasonal habitat types have generally been categorized as breeding, late brood-rearing, and winter (Connelly et al. 2011). Breeding habitat includes pre-laying, lekking, nesting, and early brood-rearing (Connelly et al. 2011). Late brood-rearing includes the summer period when herbaceous vegetation starts to desiccate and chicks begin to alter their diet to incorporate more sagebrush (Crawford et al. 2004, Smith et al. 2019). Winter habitat can be generally characterized by lower elevation, higher sagebrush canopy cover (Crawford et al. 2004, Doherty et al. 2008).

#### Distribution

Currently, sage-grouse occupy ~ 670,000 km<sup>2</sup> throughout California, Colorado, Idaho, Montana, Nevada, Oregon, Utah, Washington, Wyoming, South Dakota, North Dakota, Alberta, and Saskatchewan (Knick and Connelly 2011). They currently occupy approximately 56% of their pre-settlement distribution (Schroeder et al. 2004). Sagegrouse have been extirpated from the edges of their historic range, including: Arizona, New Mexico, Nebraska, and British Colombia (Schroeder et al. 2004). Sage-grouse depend on large intact sagebrush communities throughout their life history and have been considered an indicator species for sagebrush ecosystems (Hanser et al. 2011, Copeland et al. 2014).

The northeastern edge of sage-grouse range extends into extreme southwestern North Dakota, where the species only occupies 17% of their historic range within the state's borders (Schroeder et al. 2004, Garton et al. 2011). Sage-grouse have never been widespread in North Dakota and are confined to the southwest portion of the state (Johnson and Knue 1989, McCarthy and Kobriger 2005). Little is known about the habitat use or seasonal movements in North Dakota (Brunson 2007). However, the North Dakota sage-grouse population is contiguous with populations in South Dakota and Montana, being part of the Great Plains Management Zone (McCarthy and Kobriger 2005, Garton et al. 2011, Knick et al. 2011).

#### **Breeding Habitat**

Sage-grouse are a gregarious species, with a polygamous mating strategy, where the majority of females mate with a select few males (Patterson 1952, Connelly et al. 2011). The breeding period begins in March and continues through July and includes prelaying, lekking, nesting, and early brood-rearing activities (Connelly et al. 2000, Crawford et al. 2004, Connelly et al. 2011).

*Pre-laying*—Connelly et al. (2011) defined pre-laying as the 5-week period preceding incubation. Females move into the area of nesting, and consume increasing amounts of forbs (20-50%) as they become available (Barnett and Crawford 1994, Crawford et al. 2004). The forbs selected in this area are high in calcium, phosphorus, and protein (Barnett and Crawford 1994, Connelly et al. 2000). Increased consumption of forbs may increase nest initiation rates, clutch size, and other reproductive rates (Crawford et al. 2004).

*Lekking*— Connelly (2003, et al. 2011) describe a lek as a traditional display area where more than one male sage-grouse has attended for more than one of the last 5 years. Lekking generally begins in mid-March and continues through April into early May (Patterson 1952). Females visit the lek and select a male for copulation prior to laying their clutch (Bradbury et al. 1989). Sage-grouse lek sites are generally small areas (i.e., < a few ha), sparsely vegetated, and often occur on disturbed sites directly adjacent to sagebrush dominated and nesting habitats (Connelly et al. 2000, Crawford et al. 2004, Connelly et al. 2011). Leks can occur in naturally open areas like stream beds ridge tops, or natural grassy openings in sagebrush or openings created by human disturbances such as stock ponds, gravel pits, and burned areas (Schroeder et al. 1999, Connelly et al. 2011). Sage-grouse populations are generally not considered limited by lek habitat. Although a small portion of lek locations within a population can change over time sagegrouse exhibit strong inter-annual fidelity to lek locations (Connelly et al. 2011). For example, Dalke et al. (1963) reported finding a small bird point arrowhead on or near a lek in Idaho suggesting that during pre-European settlement times native peoples may have hunted sage-grouse at lek locations that have maintained active breeding activities up to at least the mid-1900s. Since the mid-1900s, biologists have taken advantage of sage-grouse lekking behavior to locate and regularly count males attending leks during morning surveys. Although the validity of the lek survey method has been criticized, most experts consider male lek counts reliable for population trends (Beck and Braun 1980, Garton et al. 2011, Dahlgren et al. 2016).

Nesting— Female sage-grouse have reportedly nested under a variety of vegetation types including: greasewood (*Sarcobatus vermiculatus*), bitterbrush rabbitbrush, horsebrush, snowberry (*Symphoricarpos spp.*), and basin wildrye (*Leymus cinereus*). Connelly et al. (2000) recommended that nesting habitat should contain 15% – 25% sagebrush canopy cover. Understory in sagebrush habitat includes native grasses and forbs that will provide adequate concealment and forage for hens, nests, and chicks (Holloran et al. 2005, Gibson et al. 2016). Across the range of studied sage-grouse populations, female sage-grouse select nest sites based on habitat covariates such as: sagebrush height, sagebrush density, grass cover, herbaceous cover, and visual obstruction (Connelly et al. 2000, Kolada et al. 2009, Holloran et al. 2005, Aldridge and

Brigham 2002). Although there have been some studies that show sage-grouse demonstrated nest area fidelity, where inter-annual nest sites for individual females are relatively close (i.e., < 1600 m) to each other (Schroeder and Robb 2003, Holloran et al. 2005), there have been other studies that show there may be great distances inter-annually (i.e.,  $\geq$  10km) (Peck et al. 2012. Nest initiation begins when a female deposits the first egg in the nest bowl. Females will then lay an egg about every 1.5 days (Schroeder et al. 1997). Incubation begins after the female lays the final egg and lasts approximately 27 days (Schroeder 1997). In a range-wide synthesis of published studies, Connelly et al. (2011) reported an average of 7.1 eggs per nest and a nest survival rate ranging from 15-85 %.

*Early brood-rearing*— Early brooding occurs during the first 3 weeks post hatch (Hagen et al. 2007). Early brooding habitat is relatively near and very similar in characteristics to nesting habitat (Crawford et al. 2004, Connelly et al. 2011). For these first 3 weeks, broods begin to seek out sagebrush dominated communities with decreasing shrub canopy cover and increasing herbaceous plant and insect abundance which provide high protein and energy supporting rapid chick growth (Schroder et al. 1999, Connelly et al. 2000, Westover et al. 2016). In a meta-analysis provided by Hagen et al. (2007), it was evident that early broods were more often found in areas that had less sagebrush cover, taller and more grass and forb cover.

*Late Brood Rearing*— Although there is some variation due to weather conditions, late brood-rearing occurs July to early September (Connelly et al. 2011). Sage-grouse will continue to use sagebrush dominated habitats throughout the summer and habitat selection is generally characterized with a significant decrease in shrub canopy and an increased availability of herbaceous vegetation (Gregg et al. 1993, Connelly et al. 2011). Although sage-grouse do not require free standing water to survive, they will used free water when available (Connelly et al. 2000). Moreover, these more mesic habitats are selected more often during the late summer, such as irrigated farmlands, wet meadows, or increased elevation, as herbaceous plants and grasses are desiccating and intermittent springs or water sources likely effect the distribution of sagegrouse and broods during the hot months of the year (Patterson 1952, Connelly et al. 2011, Donnelly et al. 2016). The distance covered during late brood-rearing can vary from very little to 82 km or more depending on resource availability (Connelly et al. 2000, Connelly et al. 2011).

#### Wintering Habitat

Sage-grouse winter habitat is dominated by dense sagebrush canopy cover (Connelly et al. 2000, 2011). Sage-grouse use sagebrush for forage and shelter during the winter and can be found on wind-swept ridges, valleys or draws when snow becomes too deep to access sagebrush in other areas (Crawford et al. 2004, Doherty et al. 2008, Holloran et al. 2015). Although winter habitats are generally big sagebrush (A.*tridentata*); silver (A. *cana*), low (A. *arbuscula*), and black (A. *nova*) sagebrush are also used when available (Schroeder et al. 1999, Crawford et al. 2004). Thacker et al. (2012) found in Utah when analyzing winter sage-grouse fecal pellets, that the majority contained only black sagebrush. The preference of one species or subspecies sagebrush to another may be due to selection of protein abundance or against volatile oils (Remington and Braun 1985, Welch et al. 1988).

Winter spatial distribution of sage-grouse can be dependent on sex and on snow depth; with the onset of winter precipitation sage-grouse generally move down in elevation where there is greater exposure to sagebrush above the snow (Patterson 1952, Connelly et al. 2000). Sage-grouse survival in the winter is most often higher than other seasons throughout the year. However, in some years of extreme weather, survival can decrease significantly (Moynahan et al. 2006). Forbs and grass abundance is somewhat irrelevant due to the fact that sage-grouse depend on sagebrush almost exclusively for food and shelter (Patterson 1952, Beck 1977, Connelly et al. 2000, Smith et al. 2016). Sage-grouse congregate in large segregated groups or flocks in the winter (Beck 1977, Smith et al. 2016). Although researchers have seen some fidelity to sage-grouse wintering habitat in Washington and Wyoming, others have reported that sage-grouse do not exhibit fidelity behaviors in other areas (Berry and Eng 1985, Welch et al. 1990, Schroeder et al. 1999, Connelly et al. 2004).

#### **Conservation and Management**

Conservation of greater sage-grouse has been on the forefront in the West since the late 1990s. Sage-grouse were considered a candidate species under the Endangered Species Act (ESA) of 1973, since the early 2000s. The U.S. Fish and Wildlife Service (USFWS) has made three listing decisions. Decisions made in 2005 and 2010 were overturned and in 2015 the USFWS declared sage-grouse were not warranted for listing based on significant range-wide planning, conservation, and collaborative efforts.

Habitat loss and degradation are the most significant risk to sage-grouse across their range (Connelly et al. 2000, 2011, Storch 2007). Habitat has undergone significant changes due to energy development, agriculture, development, climate change, and urbanization (Johnson et al. 2011, Beck et al. 2012, Forbey et al. 2013). Energy development fragments the landscape and habitat, creates roads, and increases traffic. Energy development in North Dakota began in the 1950s when Clarence Iverson discovered petroleum in a wheat field, and has proliferated to the point where North Dakota produces approximately one million barrels of oil a day, second only to the oil production in Texas (ndstudies.gov 2019). Agriculture converts the landscape from the sagebrush mosaic needed to support sage-grouse populations, to monoculture of harvested crops (e.g., cash crops) or grasses needed to produce cattle.

Connelly et al. (2004) reported that breeding populations are declining at a lower rate after 1985; however, populations continue to decline range-wide and will likely continue to decrease (Garton et al. 2015). Despite concern for sage-grouse habitat and management there has been little change in the trajectory of sage-grouse populations (Garton et al. 2015). For many species, populations at the fringe of the range extents are at most risk for population declines (Doherty et al. 2003). Garton et al. (2011) estimated that by 2037 the populations at the eastern extent of sage-grouse range in North and South Dakota will be below a minimum viable population threshold if wildlife managers do not intervene. North Dakota's western landscapes consist of multifaceted systems of wildlife, cattle, energy, and humans, all of which have shown to have ill effects on sage-

grouse habitat and populations (Johnson et al. 2011).

To compound the complicated nature of this system, in the 2000s there was an outbreak of West-Nile Virus (WNV) that negatively impacted sage-grouse populations (Walker and Naugle 2011), this precipitated the rate that these populations were decreasing and further amplified the need for intense management actions. In summary, the North Dakota population is habitat limited, with an increasing risk of less suitable habitat due to environmental changes, such as climate change (Homer et al. 2015, Connelly et al. 2000).

North Dakota's sage-grouse population is at a much higher risk of extirpation and need an intervention to increase recruitment into the population. In cases such as this, translocation projects have been used as a management tool to bolster populations (Reese and Connelly 1997, Baxter et al. 2008). Most sage-grouse translocation efforts to date have not been successful (Reese and Connelly 1997). However, in recent years research has shown that using novel methodology, habitat alterations, and predator management in concert with translocations, can be successful at bolstering sage-grouse populations (Baxter et al. 2008, Gruber-Hadden et al. 2016, Duvuvuei et al. 2017).

#### Translocations

Translocations have been described by the International Union for Conservation of Nature and Natural Resources (IUCN), as the deliberate and meditated movement and the release of captive or wild animals into a novel and free environment (Seddon et al.2012). Translocations are the action that is required to introduce, reintroduce, or augment a population with desired propagules (Seddon et al. 2012). Introductions are the placement of propagules into areas where there are not, and have never contained conspecifics (Jackowski et al. 2016). Reintroductions are the placement of propagules into areas where there are not, currently conspecific, but were historically occupied (IUCN 2013, Destro et al. 2018). Augmentation is the supplementation or restocking of organisms into an existing population of conspecifics (IUCN 2013, Destro et al. 2018). There is no evidence of deliberate introductions of non-domestic animals until the Holocene (~11,000 years before present) (Kirch 2005; Seddon et al. 2012). In the year 1786, George Washington started a progression of introductions when he first had French partridge (Alectoris rural) sent to Mount Vernon, Virginia (Phillips 1928). Shortly thereafter the first introductions of the Ring-necked pheasants (Phasianus lorqualus and P. colchicus) began across North America, along with many other galliformes, with little success (Phillips 1928). One of the more widely known introductions happened when Eugene Schieffelin translocated European Starlings (*Sturnus vulgaris*) into central park New York in 1890, for purely aesthetic objectives (Seddon et al. 2012). In 1881, 100 ring-necked pheasants were introduced from China and the 30 birds that survived the trip were released and quickly established a thriving population in Willamette Valley, Oregon (Phillips 1928, Bump 1951, Banks 1981).

Though some introductions were successful, due to the growing concern by the federal government with the issue off displacement of local flora and fauna an amendment to the Lacey Act of 1900 (sections 241-244) was passed which prohibits the import into the United States (U.S.) of any animal or bird without a permit from the U.S. Secretary of Agriculture. Over 700 wildlife translocations of various species have been documented from 1973 to 1986 ranging from Australia to Hawaii, including many areas

in North America (Griffith et al. 1989, Seddon and Armstrong 2016).

Translocations remain a common wildlife management technique, especially within state wildlife agencies. For example, 254 Black bear (Ursus americanus) were reintroduced into the interior highlands of Arkansas that are now estimated to have a populations of more than 2500 individuals (Smith and Clark 1994). Grey wolf (Canis *lupis*) were extirpated from Yellowstone National Park in 1944 and reintroduced in 1995; today there are around 271 individuals in the greater Yellowstone area (USFWS 2004). Translocations can be a viable management option for increasing genetic diversity (Oyler-McCance and Quinn 2011, Gruber-Hadden et al. 2016, Mussmann et al. 2017), population structure (Davis et al. 2015, Whiteley et al. 2015), or to relocate nuisance wildlife (Miller 2018). However, the primary purpose of translocations has usually been to establish or augment populations (Griffith et al. 1989, Seddon et al. 2007). Although the majority of wildlife introduction, reintroduction, and augmentations have been unsuccessful due to methodology, there have been several studies that have conducted and evaluated translocations and proved them to be a useful management and conservation tool (Kleiman 1989, Seddon et al. 2007, Baxter et al. 2008, Bell 2011, Seddon et al. 2012, IUCN 2013). There have been other studies that have evaluated and modified translocation methodologies to increase the probability of success. Some aspects that have been identified are: the timing of capture and how that may improve reproductive behavior in the target population, method of release and life stage of translocated individuals and how these variables may decrease movement at the release site, and positively affect proximate success in the target populations (Coates and Delehanty 2006, Coates et al. 2006, Mathews et al. 2018).

Seddon et al. (2007) estimated that 30% of more recent translocations are avian, some of which have been used to manage grouse populations, specifically sharp-tailed grouse (Typanuchus phasisianellus), prairie-chickens (Typanuchus cupido), and sagegrouse (Snyder et al. 1999, Coates et al. 2006, Baxter et al. 2008, Stonehouse et al. 2015). There have been more than 7200 sage-grouse translocated during more than 56 translocation events in the last century (Reese and Connelly 1997). Sage-grouse translocations have occurred in many states including: New Mexico, Oregon, Montana, Wyoming, Utah, Colorado, Idaho, Washington, and British Colombia (Reese and Connelly 1997, Stonehouse et al. 2015). The first of these translocation events started in 1933 when Allred (1946) began trapping in Wyoming to reintroduce sage-grouse into New Mexico (Reese and Connelly 1997). By 1969, 326 sage-grouse were translocated from four states into New Mexico (Reese and Connelly 1997). The last reported sagegrouse sighting in New Mexico was June 1989. Although Hamertom and Hamerstrom (1961) stated that these reintroductions were successful, this populations failed to persist (Hamerstrom and Hamerstrom 1961, Reese and Connelly 1997).

There have been few sage-grouse translocation projects that have been intensely monitored and many efforts have provided little to no information to our collective knowledge (Connelly and Braun 1993, Musil et al. 1993, Reese and Connelly 1997, Snyder et al. 1999, Seddon and Armstrong 2016). The few documented studies indicate that recruitment of a large number of translocated individuals, either directly via survival or indirectly via reproductive success, is needed over a several consecutive years and monitoring is needed during short and long term assessments of success (Snyder et al. 1999, Seddon et al. 2007, Baxter et al. 2008, Bell 2011, Seddon et al.2016, Baxter et al. 2013). However, most efforts have been plagued with low rates of survival, recruitment, and reproduction of translocated individuals (Snyder et al. 1999, Seddon and Armstrong 2016).

Translocation of sage-grouse is continually becoming more popular and as previously occupied habitats are restored, translocation into these areas as reintroductions or augmentations has the potential to restore sage-grouse populations (Wolf et al.1996, Knick and Connelly 2011). Baxter et al. (2008) translocated sage-grouse into Strawberry Valley, Utah, from larger populations throughout the state and is one of the first sagegrouse translocation efforts which documented successfully meeting their objectives to reverse declining population trends. While Baxter et al. (2008) success can be attributed to many factors such as pre-translocation monitoring and planning, habitat assessments, predator removal, and public awareness; the primary factors underlying their success were likely: 1) the total number of females translocated, 2) the number of consecutive years of augmentation, and 3) the increase in genetic diversity of haplotypes within the population (Oyler-McCance et al. 2005, Dunken 2014).

#### **Study Area Description**

Our study areas occurred in two locations (Fig. 1.1). The Augmented study area (i.e., where birds were moved to) was located in Bowman and Slope counties in southwestern North Dakota (46.050780, -104.028600). This area was on the eastern fringe of the Great Plains Sage-Grouse Management Zone (SMZ) (Garton et al. 2011). The source population (i.e., were the birds came from) was the Stewart Creek Area in south-central Wyoming (42.068902,-107.611964). The Stewart Creek Area is within the

Wyoming Basin SMZ (Garton et al. 2011).

North Dakota's sage-grouse population was very closely tied to populations in Montana and South Dakota (Garton et al. 2011). The North Dakota study area supported a small population of sage-grouse that had severe declines in the last decade or more (Johnson and Knue 1989, Smith et al. 2004, Robinson 2014). For this project we planned on having release locations occur on at least one of three historical lek sites in North Dakota (Robinson 2014). A more specific description of the North Dakota study site is from Camp Crook road out of Marmarth, ND proceed south to Camp Crook, SD. From Camp Crook northwest on Tie Creek road to highway seven; north on highway seven to Baker, MT. In Baker, MT take highway 12 southeast to Camp Crook road in Marmarth ND.

The topography in North Dakota was unglaciated rolling prairie with buttes and intermittent streams. Annual precipitation was 36.9 cm with a majority during the months of May and June. Average temperatures are 12.7°C and -0.8°C (US Climate Data, October 16, 2018). The vegetation in this area was transitional between shrub-steppe and shortgrass prairie. Habitat consisted of a mixture of shrubs with an understory of perennial and annual forbs and grasses, as well as large areas of open grasslands (Johnson and Larson 1999). Within shrub-steppe communities, shrub species included silver sagebrush (*A. cana*), Big sagebrush (*A.tridentata*), western snowberry (*Syphocarpus occidentalis*), rubber rabbit brush (*Chrysothamnus nauseosus*), and greasewood (Johnson and Larson 1999). The dominant grasses consisted of Kentucky blue grass (*Poa pratensis*), western wheatgrass (*Pascopyrum smithii*), Japanese brome (*Bromus japonicas*), needle and thread (*Stipa comada*), and June grass (*Koeleria macrantha*).

Prevalent forbs were common yarrow (*Achillea millefollium*), common dandelion (*Taraxacum officinale*), and textile onion (*Allim textile*) (Johnson and Larson 1999).

Landownership within our study site was a mixture of private and publicly owned lands. The public properties were primarily under the management of the Bureau of Land Management (BLM), although some national grasslands, managed by the U.S. Forest Service (USFS), occurred in the northern parts of this study area. The primary land-use on the study site was livestock grazing and energy extraction. Livestock, primarily cattle, stocking rates in Bowman County were 4-10 acers per animal unit per month (AUM). In some areas livestock was rotated through grazing pastures seasonally, although some year-round grazing occurred (Brunson 2007). Average oil and gas well spatial distribution was one well for every 63 hectares within the North Dakota portion of the study site (dmr.nd.gov).

Wyoming Basin SMZ is part of one of the largest intact sagebrush ecosystems in the world (Connelly et al. 2004). Our source population study site was located in Carbon and Sweetwater counties in south central Wyoming. Elevation ranges from 1520 to 2080 m Annual precipitation was 23.47 cm with a majority during the months of May and June. Average annual temperatures were 13°C and -1.5°C (US Climate Data, October 16, 2018). The ownership of land was a checkerboard of Private, State, and BLM. Domestic sheep and cattle grazing were the dominant land use. Sagebrush (*Artemisia spp.*) dominated the landscape at this site; Wyoming big sagebrush (*A. tridentata wyomingensis*) and mountain big sagebrush (*A. t. vaseyana*) were the most common. Black Sagebrush (*A. nova*) and dwarf sagebrush were found on exposed ridges. Other common shrub species at this site included: antelope bitterbrush (*Purshia tridentata*), common snowberry, chokecherry (*Prunus virginiana*), alderleaf mountain mahogany (*Cercocarpus montanus*), rabbitbrush , greasewood, saskatoon serviceberry (*Amelanchier alnifolia*), and spiny hopsage (*Grayia spinosa*). Isolated stands of juniper (*Juniperus spp.*) and quaking aspen (*Populus tremuloides*) were found at the higher elevations on north facing hillsides

#### **Objectives**

We plan to model our project after Baxter et al. (2008), including pre-project habitat assessment and planning (Robinson 2014), monitoring of the source and translocated populations following augmentation and other management actions. We will evaluate success based on survival, integration, recruitment, and population persistence (Baxter et al. 2008, Baxter et al. 2013). We will use an adaptive management approach to rehabilitating the North Dakota sage-grouse population by remaining flexible and learning as we go (Franklin et al. 2007). Although Moynahan et al. (2006) have shown that translocations can be more productive in the spring during lekking, recently others have shown some success translocating sage-grouse hens with their chicks after successfully nesting within the source population (Peter Coates, USGS, Personal communication). We hypothesize that our translocation efforts, both spring and brooding period, will increase site fidelity and individual recruitment. We will attempt to evaluate and improve brood translocation techniques as this is a fairly novel undertaking within gamebird research. We plan on having our source population monitored with  $\geq 20$  female sage-grouse in the Stewart Creek area near Rawlins, Wyoming. We planned to translocate 40 females and 20 males during the spring of 2017 to the North Dakota

population. In 2018, we planned to translocate 20 females and 20 males during the spring. In 2018, we will also capture, radio-mark, and release an additional 20 females within the source population and recapture and translocate them with their chicks if they successfully hatch and produce a brood.

In Chapter 2, we will incorporate a Resource Selection Function (RSF) provided by North Dakota Game and Fish (NDGF) (Robinson 2014) to guide our translocation release sites. The RSF provided by NDGF may be outdated, but is the best available data at this time. In Chapter 2 we will provide an updated Resource Selection Analysis based on data collected in North Dakota and separated by season i.e., breeding, summer, and winter based on the ecology of sage-grouse. We will use this RSF to provide recommendations to guide future management, including: spring translocations, brood locations, and habitat alteration sites.

In Chapter 3 we will show how we have attempted to mitigate for low reproductive rates by translocating broods as a single unit during early brooding period. We will provide the methods we used, information on our learning process, and results, including recommendations for future methods and descriptive statistics based on our translocations.

In Chapter 4 we will show another way that we have attempted to mitigate for low reproductive rates by administering artificial insemination during spring translocations. We have provided methods, study design and brief outcome regarding artificial insemination; we tested this process during spring translocations as an attempt to promote nest initiation, recruitment, and discourage movement post-translocation.

In Chapter 5, we have included key findings in our project, and attributes

accredited to successful past translocation projects that we also included in North Dakota translocations. In conclusion we included some thoughts about future research possibilities regarding translocation placement, artificial insemination, and brood translocations.

In appendix A, we have provided a summary table of all translocated Greater sage-grouse and their vital rates and statistics

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#### **FIGURES**

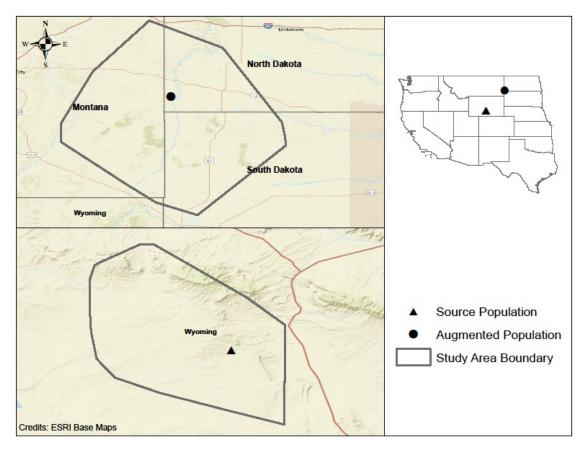


Figure 1.1. North Dakota translocation project study site locations. Our study areas occurred in 2 locations; i.e., the augmented population and the source population. The augmented population study area (i.e., where birds were moved to), was located in Bowman and Slope counties in southwestern North Dakota (46.050780, -104.028600), our augmented population area can be described as a polygon beginning at Camp Crook road out of Marmarth, ND, proceed south to Camp Crook, SD, northwest on Tie Creek road to highway 7.North on highway 7 to Baker, MT, and lastly highway 12 southeast back to Camp Crook road in Marmarth North Dakota. The source population (i.e., were the birds came from) occupied the Stewart Creek Area in south-central Wyoming (42.068902,-107.611964). Source population area can be described as a polygon beginning at US-287 and Mineral Excavation Road (24.30 Km from Rawlins Wyoming) proceed northwest to Wamsutter- Crooks Gap Road, north to Jeffery City, then southeast to Muddy Gap on Highway 789 to highway 220 and south to the intersection of Mineral Excavation Road. The North Dakota translocation study sites are defined by minimum convex polygons based on geographical locations of monitored Greater sage-grouse (Centrocercus urophasianus) in 2017-2018. Minimum convex polygons were created using 10594 locations in North Dakota and 9971 locations at the Wyoming study area.

## CHAPTER 2

# USING HABITAT SELECTION TO GUIDE RELEASE LOCATIONS OF TRANSLOCATED SAGE-GROUSE<sup>1</sup>

## ABSTRACT

Human-altered landscapes have led to large-scale changes in rangelands and wildlife populations which require efficient and effective conservation strategies. These changes have been facilitated by increased human populations, roads, energy development, etc. Sage-grouse (Centrocercus urophasianus; hereafter sage-grouse) are a widespread sagebrush (Artemisia spp.) obligate species that have been declining across their range since the mid-1900s. Population declines have been extremely evident on the north eastern edge of their distribution, such as North Dakota. Habitat has been highly altered in this region. Managers have determined that there is an increased need for innovative management techniques, including translocations, for the North Dakota sagegrouse population. Translocations have become a common tool for wildlife management. Although there is a vast amount of literature that outlines how to locate, capture, relocate, and introduce sage-grouse into novel and historical environments, there has been little research that used quantitative habitat evaluations, such as resource selection functions (RSFs), to provide guidance for choosing the best release sites. We provide an example of using locations from radio-marked sage-grouse previously released in the study area in an RSF framework to guide for future release sites in North Dakota. We also compared spatial data, provided by Rangeland Analysis Platform (www.rangelands.app), of shrub

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canopy cover from the late 1980s to current data to assess changes in sagebrush cover over time. We found that habitat selection was closely tied to sagebrush cover and mesic habitat, and that shrub cover decreased from 1987 to 2018, resulting in an increased selection of the remaining sagebrush cover within the study area. We provided mapping to guide managers for future translocations release locations and habitat improvement projects.

Alteration of land use accompanied European settlement of the West. Human development in this region facilitated significant changes resulting in an increased risk of losing important ecosystem processes (West 1983, Whisenant 1989, Berquist et al. 2007). Wildlife populations, especially obligate species dependent on a singular ecosystem type, have been particularly at risk because of these changes. Thus, there remains an increased need to facilitate proactive conservation actions to help maintain functioning ecosystems. Translocations of wildlife are one of the examples of a conservation action that can help maintain populations and distributions of species (Wilson 1988, Griffith et al. 1989).

Translocations of wildlife have been described by the International Union for Conservation of Nature (IUCN) as the deliberate and meditated movement and release of captive or wild animals into novel and free environments (Seddon et al. 2012). Over 700 wildlife translocations of various species have been documented from 1973 to 1986 across the globe extending from Australia to Hawaii, including North America (Griffith et al. 1989, Seddon et al. 2012). Translocations may include several objectives, singularly or combined, such as: augmentation of declining populations, removal of nuisance animals, reintroduction of an extirpated species, establishment of a non-endemic species, and increasing genetic diversity (Smith and Clark 1994, Oyler-McCance and Quinn 2011, Gruber-Hadden et al. 2016, Mussmann et al. 2017, Miller 2018). The objectives of most past translocations have been to re-establish or augment extirpated or declining wildlife populations (Griffith et al. 1989, Seddon et al. 2007, Seddon et al. 2012, Jackowski et al. 2016).

Although there has been documentation of successful translocations, many have been plagued with uncertainty and failure due to poor planning, low number of translocated individuals, and lack of essential resources (Armstrong and Craig 1995, Armstrong et al. 1999, Seddon et al. 2007, Seddon et al. 2012). Incorporating pre-project planning, habitat assessments, health risk assessments, appropriate source population, and campaigning for community support can increase the probability of success (Kleiman 1989). These attributes were exemplified when Kleiman (1989) translocated bison (*Bos Bison*) in Wichita, Oklahoma and during Baxter et al.'s (2008) successful translocation and augmentation of a greater sage-grouse (*Centrocercus urophasianus*; hereafter sagegrouse) population in Strawberry Valley, Utah.

Sage-grouse are a sagebrush obligate species that currently occupies 11 states and two Canadian provinces (Schroeder et al. 2004). Since the mid-1900s, it has been estimated that many sage-grouse populations have decreased by more than 33% and currently the species occupies ~ 56% of their historical distribution (Aldrich 1963, Connelly and Braun 1997, Connelly et al. 2011, Schroder et al. 2004). Translocations have been used to manage sage-grouse populations since 1933 when Allred (1946) translocated sage-grouse into New Mexico. Since then translocations have occurred in seven western states (Reese and Connelly 1997). Reportedly, > 7200 sage-grouse have been translocated during > 56 translocation events in the last century (Reese and Connelly 1997, Snyder et al. 1999, Coates et al. 2006). However, only a small portion of translocation efforts have used scientific study designs, and most were not monitored sufficiently post-release, and therefore provided little to no scientific information (Musil et al. 1993, Reese and Connelly 1997, Snyder et al. 1999). An evaluation of past translocations indicated that a population-level recruitment of a large number of grouse, either directly via survival of translocated individuals or indirectly via reproductive success of translocated birds, is needed over a several-year period to achieve translocation project objectives; i.e., deem the effort successful (Seddon et al. 2007, Baxter et al. 2008, Snyder et al. 1999, Seddon et al. 2012, Baxter et al. 2013). Reese and Connelly (1997) and Baxter et al. (2013) reported several environmental factors that correspond with success for translocated sage-grouse including capture locations, release location attributes, and timing of release. These attributes, however, were based on observational data from the respective studies and did not come from a robust quantitative assessment. The possibility of releasing birds into ecological traps (e.g., sink habitat) could be costly and severely impact project success and the perception of wildlife managers by the public (Schlaepfer et al. 2002, Jachowski et al. 2016). Baxter et al. (2008) recommended that translocations be implemented before a population declines to a level where it could be at risk of stochastic events leading to extirpation. North Dakota's sage-grouse population in the extreme southwest corner of the state was an example of a declining population at risk of extirpation.

North Dakota's sage-grouse population occurred on the northeastern edge of the species' range-wide distribution (Stiver et al. 2006, Garton et al. 2011). Historically, sage-grouse have been documented in North Dakota where sagebrush (*Artemesia* spp.)

occurs, which is the extreme southwest portion of the state (Johnson and Knue 1989, Smith et al. 2004). North Dakota's sage-grouse have always been contiguous with much larger populations in southeastern Montana. Although male lek counts historically numbered in the hundreds, North Dakota's relatively small sage-grouse population experienced consistent declines from the early 1970's until the mid-2000s. However, following a West Nile virus outbreak in the mid to late 2000s (Walker and Naugle 2011) the population declined precipitously, and by 2016 biologists counted a total of 15 males across 6 active leks within North Dakota. Although this population represents only a small portion of sage-grouse range-wide, the extirpation of sage-grouse from North Dakota would be detrimental to state and range-wide conservation objectives (Robinson 2014). In order to address these concerns, we captured and translocated sage-grouse from a source population in south-central Wyoming to North Dakota in 2017 and 2018.

Our primary objective herein was to determine the best release locations for future translocations of sage-grouse into North Dakota by implementing resource selection functions (RSF) using translocated sage-grouse locations to examine habitat selection based on seasonal and spatial variation. Secondarily, we also examined the difference in shrub cover from 1987 to 2018 based on data provided by Rangeland Analysis Platform (RAP) to better understand changes to sagebrush habitat in our study area. We hypothesized 1) that sage-grouse selection would be closely tied to sagebrush cover and mesic habitat, and 2) that shrub cover decreased from 1987 to 2018.

#### **STUDY AREA**

Our study area occurred in two distinct locations (Fig. 2.1); i.e., the augmented

population and the source population. The augmented population study area (i.e., where birds were moved to), was in southwestern North Dakota (46.050780, -104.028600), this area was part of the Great Plains Sage-Grouse Management Zone (SMZ) (Stiver et al. 2006, Garton et al. 2011). More specifically, our augmented population area can be described as a boundary beginning at Camp Crook road out of Marmarth, ND, proceed south to Camp Crook, SD, northwest on Tie Creek road to highway 7. North on highway 7 to Baker, MT, and lastly highway 12 southeast back to Camp Crook road in Marmarth ND. The source population (i.e., were the birds came from) occupied the Stewart Creek area in south central Wyoming (42.068902, -107.611964). The Stewart Creek area was part of the Wyoming Basin SMZ (Garton et al. 2011). More specifically, our source population area can be described as a boundary beginning at US-287 and Mineral Excavation Road (24.30 km from Rawlins Wyoming) proceed northwest to Wamsutter-Crooks Gap Road, north to Jeffery City, then southeast to Muddy Gap on Highway 789 to highway 220 and south to complete the boundary at the intersection of Mineral Excavation Road.

The Great Plains SMZ consisted of populations, adjacent to North Dakota's sagegrouse population, in southeastern Montana and northwest South Dakota (Stiver et al. 2006, Garton et al. 2011). Elevation ranged from 900 – 1,052 m. Annual precipitation was 36.9 cm with a majority during the months of May and June. Average annual temperatures were 12.7° C and -0.8° C (US Climate Data, 16 Oct 2018). This study site was a mixture of private, BLM, and state land. Primary land use was energy development, row crop agriculture, and livestock grazing. The landscape included gravel roads, oil pads, and power lines throughout the area. Vegetation in this area was on the edge of the shrub-steppe and shortgrass prairie bio-regions. A patch-work of shrub-steppe habitats included a mixture of shrub species, often dominated by sagebrush, with an understory of perennial and annual forbs and grasses, as well as vast areas of open grasslands (Johnson and Larson 1999). Within shrub-steppe communities, shrub species included silver sagebrush (*A. cana*), big sagebrush (*A.tridentata*), western snowberry (*Syphocarpus occidentalis*), rubber rabbit brush (*Chrysothamnus nauseosus*), and greasewood (*Sarcobatus vermiculatus*) (Johnson and Larson 1999). The dominant grasses consisted of Kentucky blue grass (*Poa pratensis*), western wheatgrass (*Pascopyrum smithii*), Japanese brome (*Bromus japonicas*), needle and thread (*Stipa comada*), and June grass (*Koeleria macrantha*). Prevalent forbs were common yarrow (*Achillea millefollium*), common dandelion (*Taraxacum officinale*), and textile onion (*Allim textile*) (Johnson and Larson 1999).

Our source population study site was in Carbon and Sweetwater counties in south central Wyoming. Elevation ranged from 1,520 – 2,080 m. Annual precipitation was 23.47 cm with a majority during the months of May and June. Average annual temperatures were 13° C and -1.5° C (US Climate Data, 16 Oct 2018). Ownership was a mixture of private, state, and BLM. Managed livestock grazing, in the form of domestic sheep and cattle was the dominant land use. During this research feral horses occurred in this area and were numerous, which can impact sage-grouse (Beever and Aldridge 2011). Much of unnatural disturbance was caused by gravel or four-wheel drive roads. Sagebrush communities dominated the vast majority of this study area. Wyoming big sagebrush (*A. tridentata wyomingensis*) and mountain big sagebrush (*A. t. vaseyana*) were the most common. Black sagebrush (*A. nova*) and dwarf sagebrush (*A. arbuscula*)

were found on exposed ridges. Other common shrub species at this site included: antelope bitterbrush (*Purshia tridentata*), Common snowberry (*Symphoricarpos albus*), chokecherry (*Prunus virginiana*), alderleaf mountain mahogany (*Cercocarpus montanus*), rabbitbrush (*Chrysothamnus* and *Ericameria* spp.), greasewood, saskatoon serviceberry (*Amelanchier alnifolia*), and spiny hopsage (*Grayia spinosa*). Isolated stands of juniper (*Juniperus* spp.) and quaking aspen (*Populus tremuloides*) were found at the higher elevations on north facing hillsides

#### **METHODS**

## **Capture and Marking**

We trapped sage-grouse at night on all-terrain vehicles (ATVs) with the aid of a spotlight and dip-net (Giesen et al. 1982, Wakkinen et al. 1992, Connelly 2003). Upon capture, every sage-grouse was fitted with aluminum leg band, weighed, sexed, aged and evaluated for general health (Patterson 1952, Eng 1955, Braun and Schroeder 2015). Morphometries were documented for each bird including: body mass, wing length, tarsus length, and culmen length (USGS 2018). Post-capture, female sage-grouse were fitted with either rump-mounted solar-powered GeoTrak (Apex North Carolina, USA) Global Positioning System-Platform Transmitter Terminal (GPS-PTT; hereafter GPS) transmitters (22g) with a 3.5 g VHF radio (Holohil Systems, Ltd., Ontario, Canada) epoxied to the side of the GPS transmitter, or Advanced Telemetry Systems (Isanti, MN, and Holohil Systems, Ltd., Ontario, Canada) very high frequency (VHF) necklace style transmitters (22 g).

We also captured and marked another group of female sage-grouse that were

immediately released back into the source population. We attached 22 g ATS necklacestyle VHF transmitters or the same rump-mounted GPS transmitters and a leg band as described above. The purpose of this effort was to monitor the source population and provide the potential to translocate broods (i.e., adult female and chicks) of females that successfully hatched within the source population in 2018. Using nocturnal spotlight methods described above, we recaptured previously marked females and their chicks in June and July 2018. To increase our sample size of translocated broods, we also captured and radio-marked brooding females and their chicks that had not been previously captured. Chicks were marked with a 1.3 g ATS, VHF backpack radio transmitter using the suture method (Burkepile et al. 2002, Dahlgren et al. 2010). Following handling procedures after capture, the brood female and chicks were placed in the translocationrelease box for transport and then were released in North Dakota.

We monitored all radio-marked female sage-grouse either remotely via ARGOSenabled downloads) or with ground telemetry using VHF signals. We only used ground telemetry to approach within a few meters of marked females to verify nest initiation and nest success. Marked brood females with chicks were monitored remotely until retrapping and translocation of the entire brood.

Veterinarians from Wyoming Game and Fish Department and North Dakota Game and Fish Department attended all spring translocations and a local veterinarian attended the brood captures. Veterinarians examined the general health of all translocated sage-grouse and obtained blood and cheek swab samples from translocated sage-grouse for disease testing. Colorado State University Veterinary Diagnostic Laboratory tested for Mycoplasma, and Michigan State Veterinary Laboratory tested for Salmonella and Mycobacterium Avium, and Wyoming State Veterinary Laboratory tested for Avian Influenza. An agreement with North Dakota State Board of Animal Health indicated that translocated grouse could be released in North Dakota as quickly as possible prior to researchers receiving disease testing results to avoid holding the birds for an inordinate amount of time, with the caveat that if any results came back positive then those individual sage-grouse would be immediately tracked down via telemetry and euthanized.

#### **Translocation and Release Methods**

Sage-grouse were translocated either in a fixed wing aircraft provided by North Dakota Game and Fish (NDGF) or a covered truck to the release locations within the augmented population. Prior to release, each spring translocated bird was transferred into individual compartments within a manufactured release box fixed with a remote door opener to enable a soft release (Rodgers 1992). On the morning of release, we placed all spring translocated sage-grouse near predetermined lek site, set up silhouette decoys, and used Fox pro NX4s (FOXPRO Inc.14 Fox Hollow Drive - Lewistown, PA) to transmit pre-recorded sage-grouse lekking sounds, in an attempt to decrease post-release stress and movements (Snyder et al. 1999, Coats et al. 2006, Baxter et al. 2008). All translocated broods were transported via truck using a specially made brood box ( $\sim 8$ hours), released into acclimation pens (~30 to 45 min), and then released into nearby habitat (see Chapter 3). Brood augmentation sites were also distributed close to historic lek sites near initial spring translocations. When considering release locations, we also considered brooding areas where endemic broods had been detected and the availability of sagebrush and mesic habitat (Dahlgren et. al. 2010, Connelly et. al. 2011). All capture

and handling procedures were approved by The Utah State University Institutional Animal Care and Use Committee (IACUC; permit #2729).

## **Data Collection**

All sage-grouse were monitored intensely during the nesting and brooding seasons (April -August) to identify nesting and brooding activity. GPS locations were downloaded remotely via ARGOS-enabled downloads (http://www.argos-system.org/) from transmitters that were programed with 4 seasons, which were: March - May, May -June, June - October, and October - March. Each season provided up to 6 locations per day. We also used ground telemetry for VHF signals and approached within a few meters of marked females to verify nest initiation, nest success, brooding activity, or mortality. Females marked with VHF transmitters were located weekly or as often as possible with handheld Communication Specialist R1000 receivers (Communication Specialist Inc. 426 West Taft Avenue, Orange, Ca.), and Yagi antennae. We located all nesting and brooding females at least once per week. Nests were considered successful if  $\geq 1$  egg hatched. We completed nocturnal spotlight brood checks at roost locations 20, 30, and 50 days post hatch (Dahlgren et al. 2010). We also used pointing dogs to locate broods if we were unable to locate broods at night for broods greater than 30 days post hatch, or if the VHF transmitter failed on GPS transmitters (Dahlgren et al. 2010). We classified a brood as successful if  $\geq 1$  chick was present  $\geq 50$  days post-hatch.

#### **Resource Selection Analysis Methods**

*Landscape Variables.*— Landscape variables were selected based on biological significance to sage-grouse habitat use. We categorized variables into topographic,

biological, and anthropogenic factors (Connelly et al. 2000, Connelly et al. 2011; Table 2.1). Topographic variables included elevation, slope, ruggedness (Riley et al. 1999), and aspect. These variables were derived from 30-m DEM (<https://viewer.nationalmap.gov/advanced-viewer> accessed 1 October 2018). Biological factors included linear water (e.g., rivers, streams) (US Census < https://tigerweb.geo.census.gov/tigerweb/> accessed 1 October 2018) mesic habitat, and percent shrub canopy cover from Rangeland Analysis Platform (RAP; <https://rangelands.app/> accessed 11 June 2019). Anthropogenic variables included, state and federal roads from US census database

(<https://tigerweb.geo.census.gov/tigerweb/> accessed 1 October 2018).

We estimated distance metrics for roads, water, and mesic variables with the Euclidean Distance tool in ArcMap 10.3 (ESRI, Redlands, CA; Knick and Connelly 2011, Wisdom et al. 2011, Dinkins et al. 2014, Sandford et al. 2017). In addition, because sage-grouse have demonstrated selection of landscape features at different spatial scales across seasons (Connelly et al. 2011, Fedy et al. 2014), we evaluated log-transformed ruggedness and shrub canopy cover using a circular moving window (focal statistics neighborhood analysis in ArcGIS<sup>TM</sup>). The size of the moving window was controlled by a variable radius chosen to represent daily movement patterns, measured by the average minimum, mean, and maximum movements from all individuals during nesting & brood-rearing (r = 60, 331, and 887 m, respectively), and separately during summer (r = 111, 767, and 3,005 m, respectively). Due to the wide range of movements during summer, we considered an additional radius length (r = 1,503 m) that represented half the maximum movement. To accommodate inter-annual variability, we used percent shrub canopy

cover obtained from RAP, with data estimated annually for 1987, 2005-09, and 2017-18. We associated the percent shrub canopy cover data with the respective years throughout our study site.

For point and linear features (center of mesic area, water bodies or streams, roads, and pseudo-lek release locations), we calculated exponential decay functions,  $exp(-d/\alpha)$ , to accommodate declining effect sizes with increasing distance (Nielson et al. 2009, Coates et al. 2016), where *d* represented distance to the feature, and  $\alpha$  was specified as either the mean distance value at all used locations, or 6.4 km (e.g., Green et al. 2017), whichever was smaller.

We tested for correlation using Pearson's correlation test with an r > +/- 0.7threshold for location data (Hosmer et al. 2013). We removed slope, due to its collinear relationship with ruggedness and elevation; the latter variables were retained due to their importance to sage-grouse habitat selection patterns in other regions (e.g., Coates et al. 2016, 2020). No other significant correlations occurred among the variables we considered.

*Nesting.*— To increase our sample size, we combined our 2017 and 2018 nest location data with nest location data acquired during the 2005-2009 nesting seasons recorded within our same augmentation study area (Brunson 2007). We created a study area boundary by using location data with the Raster Calculator Tool in ArcMap 10.3 (ESRI, Redlands, CA). Then, we created a database of used and available points within the study area using a random sampling approach, where 5 random points were generated for each used point to create a second order RSF (Johnson et al. 2006). After combining used and available locations with habitat predictors, we standardized predictors ( $\mu = 0$ , sd

= 1) so that all were scaled similarly and coefficients were more comparable among variables occurring in models.

We estimated a nest resource selection function (RSF) using a generalized linear model with a binomial link function in a Bayesian modeling framework. The nest model was initially estimated as follows with g(x) estimated for  $\iota^{\text{th}}$  location where  $\beta_0$  is the mean intercept, *n* are covariates with fixed regression coefficient  $\beta_n$ 

$$g(x) = \beta_0 + \beta_1 x_{1\iota} + \beta_2 x_{2\iota} + \dots + \beta_n x_{n\iota} + \varepsilon$$

The observations followed a Bernoulli distribution, where y=1 indicated a nest location and y=0 indicated a random background location. To estimate the RSF from this model,  $\widehat{w}(x)$ , we discarded the intercept and calculated the exponential function

$$\widehat{w}(x) = \exp(\beta_1 x_{1\iota} + \beta_2 x_{2\iota} + \dots + \beta_n x_{n\iota})$$

(Johnson et al. 2006, McDonald 2013). To obtain a final RSF for habitat mapping, we performed a 2-stage modeling process, where an appropriate spatial scale was determined for shrub cover and ruggedness during the first stage, and the model was refit to the selected spatial scales in the second stage. We selected the most informative spatial scale for these two variables using Bayesian latent indicator scale selection (BLISS; Stuber et al. 2017), which employs a reversible-jump MCMC sampling algorithm to estimate probabilities for each specified spatial scale being the most important predictor of habitat selection among those considered. We then used only the scale with the highest probability in the final RSF model.

We fit these models on  $\sim 2/3$  of the dataset (e.g. training data), randomly selecting and holding out  $\sim 1/3$  of the data for validation (testing data). To validate the model with the testing data, we used calibration plots described in Johnson et al. (2006) and Fieberg et al. (2018) to compare the true number of observations to predicted numbers of locations occurring within 10 quantile bins from $\widehat{w}(x)$ . We report the slope and  $R^2$  of a linear regression model fit to the calibration plot (Johnson et al. 2006), as well as the Spearman correlation, to determine how well the model predicted habitat selection patterns for individuals that were not included in the model-fitting process. If results were not satisfactory, we generated used-habitat calibration (UHC) plots (Fieberg et al. 2018) for predictors in the model to determine the need for non-linear functions or interactions. If this was the case, we first fit quadratic terms to the most influential predictor and measured improvement based on the calibration statistics (e.g. improved correlation,  $R^2$ , and slope coefficient near 1.0 (Johnson et al. 2006). If necessary, we continued this procedure with additional predictors until correlation and  $R^2$  were > 0.75 and slope was between 0.8 and 1.2.

All models were fit using JAGS 4.2.0 (Plummer 2003), implemented within R (R Core Development Team 2019, version 3.6.1) using '*rjags*' (Plummer 2016) and '*jagsUI*' (Kellner 2019). To protect against potentially overfitting the model to small effective sample sizes (i.e., number of used locations), we implemented *L*-1 regularization (Tibshirani et al. 2012) by specifying Lasso (i.e., Laplace, or double-exponential) prior distributions for each predictor variable in the full model, with an uninformative hyperprior specified for the tuning parameter  $\lambda$  (Park and Casella 2008, Hooten and Hobbs 2015). We ran three chains of 30,000 MCMC iterations, following a burn-in of 15,000, and thinned by selecting every 5<sup>th</sup> sample to posterior distributions of parameter estimates. We examined chains and calculated Gelman-Rubin statistics ( $\hat{r} < 1.05$ ) to verify convergence of all parameters. Brooding.— We created a location database that included all brooding female sage-grouse that provided  $\geq 5$  locations in 2017 - 2018. We selected 1 brood location per day, per individual, in the event that multiple locations were gathered in the same day. We used similar methods as for the nest model to develop our data and run analyses, generating 5 random points per used location, and withholding ~ 1/3 of the broods as a validation dataset. An exception was that individual was treated as a random effect, to account for repeated locations gathered from the same sampling unit over time. The brood model was calculated as follows with g(x) estimated for location  $t^{\text{th}}$  individual jwhere  $\beta_0$  is the mean intercept,  $x_{1...n}$  are covariates with fixed regression coefficient  $\beta_n$ , and  $\gamma_{0j}$  is a random intercept for individual j.

$$g(x) = \beta_0 + \beta_1 x_{1\iota j} + \beta_2 x_{2\iota j} + \cdots + \beta_n x_{n\iota j} + \gamma_{0j}$$

We discarded the intercepts and calculated the exponential RSF following the same formulation for  $\widehat{w}(x)$  as was done for the nest model, this time fit to the brood location data. All other procedures followed those of the nest model.

Summer.— All GPS marked female sage-grouse locations from 2017 - 2018 were combined into an inclusive database. We then created a subset that included all nonreproductive female sage-grouse from June through October. We deleted any individual that did not provide at least 10 independent locations. We randomly selected one location per day, per individual to avoid spatial dependence between locations collected close to each in space and time. Locations occurring on separate days were considered independent. The summer model was calculated as follows with g(x) estimated for location  $i^{\text{th}}$  individual j where  $\beta_0$  is the mean intercept, n are covariates with fixed regression coefficient  $\beta_n$ , and  $\gamma_{0j}$  is the random intercept for individual *j*.

$$g(x) = \beta_0 + \beta_1 x_{1ij} + \beta_2 x_{2ij} + \dots + \beta_n x_{nij} + \gamma_{0j}$$

We discarded the intercepts and calculated the exponential RSF following the same formulation for  $\widehat{w}(x)$  as was done for the nest and brood models, this time fit to the GPS location data. All other procedures followed those of the previous models. Shrub Canopy Cover Change.— After modeling each season we exported the results from the respective seasons into ArcGIS, and then used the Raster Calculator tool in ArcMap 10.3 (ESRI, Redlands, CA) for further analysis of the data. We first calculated logistic RSF models to predict relative probability of selection across the study region for each season using the 2018 shrub raster layer, smoothed at the selected spatial scale indicated by the analyses. Then we performed the same calculation using the 1987 percent shrub canopy raster layer provided by RAP, and also smoothed at the selected spatial scale for each life stage. We used the 1987 shrub layer based on information found on the North Dakota Geology database that shows little new oil development in the study area after 1987 (https://www.dmr.nd.gov/ndgs). We then subtracted the smoothed 1987 RAP shrub layer from the smoothed 2018 RAP shrub layer to create a layer that would represent the change in shrub canopy cover in our study area at the same spatial scale as analyses. Then we subtracted the coinciding 1987 RSF model from the 2018 RSF model for each season, respectively. The results demonstrate how habitat availability has changed with changing shrub canopy cover over 30 years within our study area.

## RESULTS

We translocated 158 sage-grouse (n = 60 female, n = 6 brood female, n = 26

chicks), during lekking season (March – April) and brooding season (May-July) of 2017 and 2018, from the source population site to southwest North Dakota. During the 2017 spring breeding season, n = 40 female sage-grouse were translocated. In the spring of 2018, n = 20 female sage-grouse were translocated to North Dakota. During the 2018 brooding season we translocated n = 6 brood females and n = 26 chicks.

#### Nesting

We used locations from n = 17 nests in 2005, and n = 27 in 2007 from previous research. From our efforts we documented nest locations for n = 8 in 2017, and n = 9 in 2018. Our total nests were n = 61. Our nest model included elevation, roughness, aspect, distance to roads, distance to water, distance to mesic, distance to translocation release site, and percent shrub canopy cover. Shrub canopy cover and roughness both had greatest support for inclusion in this model when measured within an 887 m radius circular moving window (Table 2.2). Non-linear functions and/or quadratic terms were deemed unnecessary based on satisfactory results from used-habitat calibration plots (Fig. 2.3). Nesting females selected nesting habitat close to the translocation release site, with lower topographic roughness and greater shrub cover relative to available locations (Table 2.3, Fig. 2.3). The model predicted validation data adequately (nest locations withheld from analysis; r = 0.92,  $R^2 = 0.87$ ,  $\beta = 0.90$ ).

## Brooding

We monitored n = 6 broods produced by spring translocated females and we translocated an additional n = 6 broods that were included in analyses. Our brood model included elevation, roughness, aspect, distance to roads, distance to water, distance to

mesic, distance to translocation release site, and percent shrub canopy cover. Shrub canopy cover and roughness had greatest support for inclusion in this model when measured within an 887 m radius circular moving window (Table 2.5). Non-linear functions and/or quadratic terms were again deemed unnecessary based on results from used-habitat calibration plots (Fig. 2.5). Relative to available locations, brooding female sage-grouse in our augmented study area selected for areas farther from roads and mesic habitats, in closer proximity to release sites, with lower topographic roughness and greater shrub canopy cover (Table 2.4; Fig. 2.5). Sage-grouse displayed little to no selection regarding other geographic variables. The model predicted validation data adequately (nest locations withheld from analysis; r = 0.80,  $R^2 = 0.83$ ,  $\beta = 1.00$ ).

#### **Summer Non-breeding**

We monitored n = 32 female sage-grouse that were marked with GPS transmitters during 2017 and 2018. Our top model for summer included elevation, roughness, aspect, distance to roads, distance to water, distance to mesic, percent shrub canopy cover. We also included a quadratic term for percent shrub canopy cover, to calibrate the model based on a non-linear relationship between habitat used and shrub cover, which improved the calibration plots (Fig. 2.7). Shrub canopy cover had greatest support for inclusion in this model when measured within a 1,503 m radius circular moving window, whereas roughness was most supported using a 767 m radius (Table 2.6). Our RSF model indicated selection relative to availability for lower relative elevations near mesic areas but further from open water sources and roads. In contrast to nesting and brooding periods, we observed little influence of translocation release sites. Shrub cover was selected at intermediate shrub canopies (quadratic effect). The model predicted validation data adequately (nest locations withheld from analysis; r = 0.80,  $R^2 = 0.79$ ,  $\beta = 1.12$ ).

## Shrub Canopy Cover Change

Percent shrub canopy cover decreased by  $\sim 2\%$  in areas of southwest ND between 1987 and 2018. This change had substantial influence on the composition and extent of available habitat for all three seasons (Fig. 2.14).

#### DISCUSSION

We employed multiple RSF analyses to better understand habitat selection and availability in southwest North Dakota. We provided information for selecting release locations for translocated sage-grouse to give them the highest probability of success. We found substantial seasonal variation in habitat selection regarding shrub canopy cover, elevation, topographic roughness, distance to water, distance to roads, and mesic habitat variables.

Although Connelly et al. (2000; 2011) outlined what is needed for sage-grouse habitat and Wolfe et al. (1996) outlined the actions needed for successful translocation release, there remained a need to connect habitat needs with potential release locations. We provide managers with information needed to guide the selection of future release sites with the highest relative probability of selection by sage-grouse. We determined that the primary components determining sage-grouse selection of habitat in southwest North Dakota were similar to previous literature and included: percent shrub canopy, proximity to roads, proximity to water, topographic roughness, and mesic habitat. In addition, breeding sage-grouse selection (nesting and brood rearing) was influenced by proximity to release locations, but not for non-breeding sage-grouse.

Sage-grouse require sagebrush for their entire life history, including nesting activity (Connelly et al. 2011). It was necessary to include previously studied nests in increase the sample size, therefore, we used point locations from nest of endemic sagegrouse in a previous study as well as translocated sage-grouse from Wyoming. We used RAP percent shrub canopy cover data to represent sagebrush cover in southwest North Dakota. Hagen et al. (2007) confirmed previous estimates by Connelly et al. (2000) of 15 -25 % sagebrush cover for optimum sage-grouse nesting habitat. Kaczor et al. (2011) stated that nesting sage-grouse used higher amounts of sagebrush canopy cover compared to random sites in a nearby study area in South Dakota. Similar to Brunson (2007), we determined that horizontal cover was an important predictor for highly selected nesting habitat. For nesting habitat, we observed general selection patterns for increased shrub cover at a relatively coarse spatial scale (r = 887 m). In addition, areas of lower topographic roughness were selected. Female brooding sage-grouse in North Dakota during the 2017 - 2018 seasons selected for ~ 9% sagebrush cover near mesic habitat. Sage-grouse in North Dakota also showed higher avoidance for roads during the broodrearing and summer seasons, much like other studies (Hagen et al. 2007, Fedy et al. 2014).

We found that during summer, non-breeding sage-grouse avoided roads and waterways, similar to findings in Fedy et al. (2014). Although translocations have not generally occurred in the summer, our results for brooding and non-brooding habitat selection during the summer provide important information for future translocation planning. Land-use change, and climate change have altered many habitats, including the sage-grouse habitat in North Dakota (Larrucea and Brussard 2008). The availability of sagebrush, as indicated by overall shrub cover, declined substantially in southwest North Dakota. Because shrub cover was one of the strongest influences on sage-grouse habitat selection across all seasons, the loss of sagebrush may be a critical issue for the sage-grouse population in southwest North Dakota. Sagebrush loss was likely most significant for breeding activities (nesting and brood-rearing) where we found high selection for increased shrub cover. However, non-breeding summer habitat use patterns were driven more by selection for intermediate shrub cover and at a broader spatial scale.

The loss of shrub canopy cover in North Dakota can be attributed to multiple factors including: conversion to row-crop agriculture, improper livestock grazing, climate change, energy development, exurban expansion, and an increase in roads (Knick and Connelly 2011). Roads are associated with many anthropogenic features all of which have potential to impact sage-grouse populations (Johnson et al. 2011). Oil and gas exploration require roads during construction and maintenance. Electric transmission and distribution lines are needed to provide power to development and structures. Tall structures have also been described as a deterrent to sage-grouse during various stages of their life history (Dinkins et al. 2014, Hovick et al. 2014, Gibson et al. 2018, Kohl et al. 2019). Roads are created when power lines are constructed to place the poles and wires that lead to oil wells and refineries. Kohl et al. (2019) were unable to isolate the effects of power lines from the effects of roads on sage-grouse habitat selection in Utah. As technology advances there is an increasing probability of future energy development that may disrupt habitat and cause sage-grouse to abandon leks and surrounding habitat (Johnson et al. 2011). Notably, sage-grouse have continued to occupy areas where sagebrush cover has been conserved over time within our study area. Increased efforts to conserve the remaining sagebrush cover and to restore sagebrush communities within our study area are likely key to future persistence of sage-grouse within North Dakota.

## **Management Implications**

One of the most daunting challenges associated with increasing the probability of translocation success is knowing the best placement of release sites. We have attempted to address these challenges by providing information that aids in selecting release sites based on how translocated sage-grouse used their novel environment. We understand that the selection of resources are directly tied to the release site locations that are chosen by researchers or managers and other augmented populations may provide different outcomes. We recommend that spring translocation release sites are in or adjacent to areas with high sagebrush cover ( $\geq 9$  %). In addition, we also recommend that brood translocations are released adjacent to areas with mesic habitat that provide resources for chicks, and all release sites should be located 1-3 km away from roads. As future development is planned within our study area there should be consideration regarding the negative impact on shrub cover and mesic habitat. We also recommend that sagebrush restoration projects be implemented in areas that are adjacent to existing shrub and mesic habitat, with priority given to locations 1 - 3 km away from roads. Finally, we recommend reclamation of any landscape features, such as unnecessary roads and structures, back to sagebrush cover whenever feasible.

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# **TABLES AND FIGURES**

Table 2.1. Landscape variables that were selected based on biological significance to sage-grouse habitat use. We categorized into topographic, biological, and anthropogenic factors. Topographic variables included elevation, slope, ruggedness, and aspect. These variables were derived from 30m digital elevation model. Biological factors included rivers streams, springs, mesic, and shrub cover from Rangeland Analysis Platform. Anthropogenic variables include, state and federal roads from US census database, and oil well/pad locations from North Dakota Geological Survey.

Variable	Туре	Resolution	Category	Description
elev	Continuou s	30m	Topographic	Extracted from 30m DEM
aspect	Continuou s	30m	Topographic	Extracted from 30m DEM
slope	Continuou s	30m	Topographic	Extracted from 30m DEM
dist_Road	Continuou s	30m	Anthropogeni c	USCensus
dist_water	Continuou s	30m	Biological	USCensus
dist_mesi c	Continuou s	30m	Biological	Polygons layers provided by Sage-grouse Initiative
dist_well	Continuou s	30m	Anthropogeni c	ND/MT Energy
shrub	Continuou s	30m	Biological	percent shrub cover provided for years of interest provided
				by Rangeland Assessment Platform

Table 2.2. Nesting scale selection parameters. Parameters indicate support for varying neighborhood radius sizes for characterization of shrub cover and topographic roughness in a resource selection model of greater sage-grouse nests (Centrocercus urophasianus) within the North Dakota study area.

Scale selection	Probability	
Shrub cover (r=60)		0.27
Shrub cover (r=331)		0.252
Shrub cover (r=887)		0.478
Roughness (r=60)		0.065
Roughness (r=331)		0.068
Roughness (r=887)		0.867

Table 2.3. Nesting Posterior distribution coefficient estimates. Estimates from a resource selection model of greater sage-grouse nests (*Centrocercus urophasianus*) contrasted with random available locations within the North Dakota study area. Nest locations were collected during 2005-2008 and 2017-2018

Parameter	Label	Mean	SD	q2.5	q50	q97.5	f	Rhat
				-		-		
b0	Intercept	-2.11	0.257	0.2635	-2.1	1.636	1	1.001
beta[1]	Aspect	0.035	0.175	-0.314	0.029	0.391	0.575	1
		-			-			
beta[2]	Elevation	0.133	0.221	-0.626	0.108	0.257	0.722	1.001
	Proximity to	-			-			
beta[3]	water	0.092	0.185	-0.498	0.074	0.245	0.679	1
	Proximity to							
beta[4]	mesic	0.065	0.179	-0.279	0.053	0.441	0.638	1
1 ( [6]	D · · · / / 1	-	0 175	0.422	-	0.205	0 (01	1
beta[5]	Proximity to road	0.048	0.175	-0.423	0.039	0.295	0.601	1
hata[6]	Proximity to release location	1.309	0.255	0.84	1.297	1.844	1	1
beta[6]	Shrub cover	1.309	0.233	0.64	1.297	1.044	1	1
beta[7]	(r=887 m)	0.235	0.213	-0.136	0.221	0.684	0.878	1
	Roughness		0.215	0.150	0.221	-0.00	0.070	1
beta[8]	(r=887  m)	0.577	0.267	-1.121	0.567	0.072	0.991	1

Table 2.4. Brooding Greater sage-grouse (*Centrocercus urophasianus*)scale selection parameters. Parameters indicate support for varying neighborhood radius sizes for characterization of shrub cover and topographic roughness in a resource selection model of greater sage-grouse broods within the North Dakota study area.

Scale selection	Probability
Shrub cover (r=60)	0.15
Shrub cover (r=331)	0.399
Shrub cover (r=887)	0.451
Roughness (r=60)	0
Roughness (r=331)	0.126
Roughness (r=887)	0.874

Parameter	Label	Mean	SD	q2.5	q50	q97.5	f	Rhat
		-		-	-	-		
b0	Intercept	2.285	0.663	3.438	2.241	1.457	0.998	1.076
				-				
beta[1]	Aspect	0.216	0.175	0.096	0.207	0.579	0.902	1
				-				
beta[2]	Elevation	0.16	0.206	0.207	0.14	0.603	0.775	1
	Proximity to	-		-	-			
beta[3]	water	0.083	0.161	0.422	0.073	0.218	0.693	1
	Proximity to	-		-	-			
beta[4]	mesic	0.141	0.171	0.493	0.133	0.182	0.799	1
	Proximity to	-		-	-	-		
beta[5]	road	0.734	0.2	1.143	0.728	0.356	1	1
	Proximity to							
	release							
beta[6]	location	0.395	0.179	0.066	0.387	0.769	0.994	1
	Shrub cover			-				
beta[7]	(r=887 m)	0.388	0.24	0.028	0.374	0.89	0.96	1
	Roughness	-		-	-	-		
beta[8]	(r=887 m)	1.001	0.247	1.497	0.993	0.544	1	1

Table 2.5. Brooding Greater sage-grouse (*Centrocercus urophasianus*) posterior distribution coefficient estimates. Estimates from a resource selection model of greater sage-grouse broods contrasted with random available locations within the North Dakota study area. Brood locations were collected during 2017-2018.

Table 2.6. Summer scale selection parameters. Parameters indicate support for varying neighborhood radius sizes for characterization of shrub cover and topographic roughness in a resource selection model of greater sage-grouse summer locations (*Centrocercus urophasianus*) within the North Dakota study area.

Scale selection	Probability
Shrub cover (r=111)	<0.001
Shrub cover (r=767)	<0.001
Shrub cover (r=1503)	>0.999
Shrub cover (r=3005)	<0.001
Roughness (r=111)	<0.001
Roughness (r=767)	>0.999
Roughness (r=1503)	<0.001
Roughness (r=3005)	<0.001

North Dakota study area. Summer locations were collected during 2017-2018.								
Parameter	Label	Mean	SD	q2.5	q50	q97.5	f	Rhat
		-		-	-	-		
b0	Intercept	1.854	0.211	2.307	1.843	1.453	1	1
				-				
beta[1]	Aspect	0.064	0.051	0.033	0.064	0.164	0.893	1
				-		-		
beta[2]	Elevation	-0.49	0.068	0.623	-0.49	0.357	1	1
	Proximity to	-			-	-		
beta[3]	water	0.597	0.057	-0.71	0.596	0.488	1	1.001
1 . 547	Proximity to	0.000	0.051	0.105	0.000	0.000		
beta[4]	mesic	0.206	0.051	0.107	0.206	0.306	1	1
1. et a [ <b>6</b> ]	Proximity to	-	0.054	-	-	0.56	1	1
beta[5]	road	0.664	0.054	0.772	0.664	-0.56	1	1
hata[6]	Proximity to release location	0.066	0.047	0.027	0.066	0.158	0.922	1
beta[6]	Shrub cover	0.000	0.047	0.027	0.000	0.138	0.922	1
beta[7]	(r=1503  m)	1.311	0.108	1.103	1.31	1.522	1	1
oeta[/]	Roughness	1.511	0.100	-	-	-	1	1
beta[8]	(r=767  m)	-0.92	0.064	1.049	0.918	0.796	1	1.001
0000[0]	Shrub cover -	0.02	0.00.	110 15	019 10	01720	-	11001
	quadratic	-		-	-	-		
beta[9]	(r=1503 m)	0.715	0.069	0.853	0.714	0.584	1	1

Table 2.7. Summer Greater sage-grouse (*Centrocercus urophasianus*) posterior distribution coefficient estimates. Estimates from a resource selection model of greater sage-grouse summer locations contrasted with random available locations within the North Dakota study area. Summer locations were collected during 2017-2018.

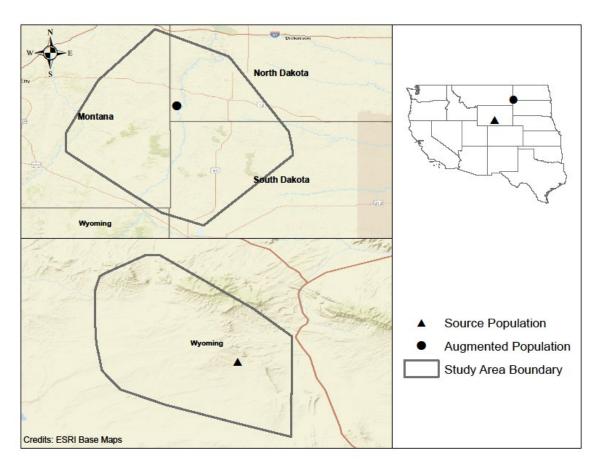


Figure 2.1. North Dakota translocation project study site locations. Our two study areas included the augmented population (i.e., where birds were moved to) located in Bowman and Slope Counties in southwestern North Dakota (46.050780, -104.028600) and the source population (i.e., where birds were taken from) located in the Stewart Creek Area in south-central Wyoming (42.068902, -107.611964). Our two study sites were defined by minimum convex polygons, 10,594 locations in North Dakota and 9,971 locations at the Wyoming study area, based on radio-marked greater sage-grouse (*Centrocercus urophasianus*) locations, 2017-2018.

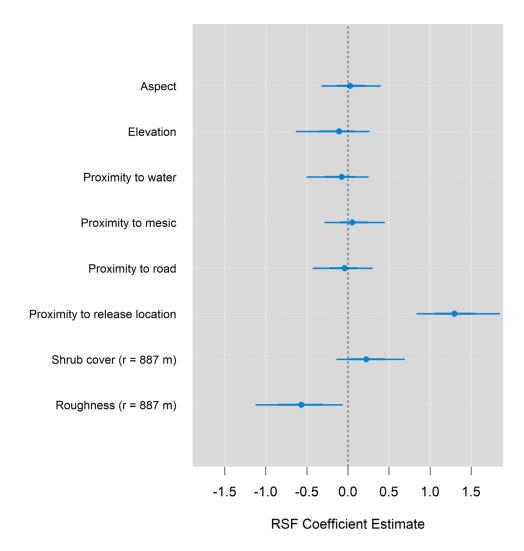
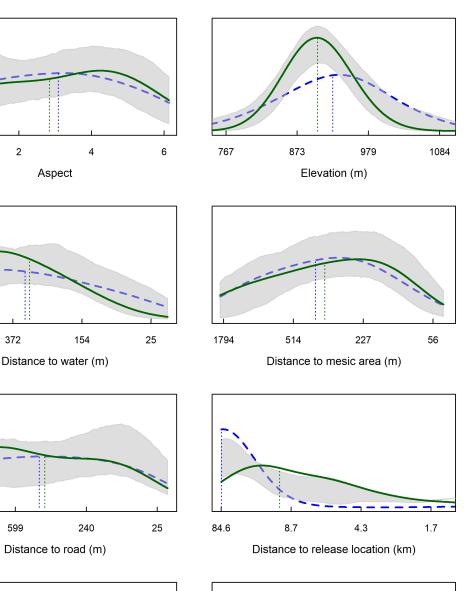


Figure 2.2. Nesting Resource selection parameters and error. Proximity to release location is the highest predictor determining the locations of Greater sage-grouse *(Centrocercus urophasianus)* during nesting season in southwest North Dakota.



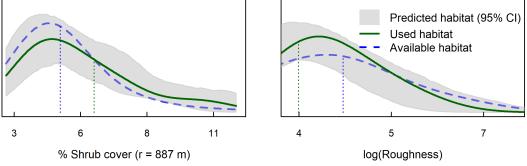


Figure 2.3. Sage-grouse (Centrocercus urophasianus) nesting season habitat parameters and probability of use.

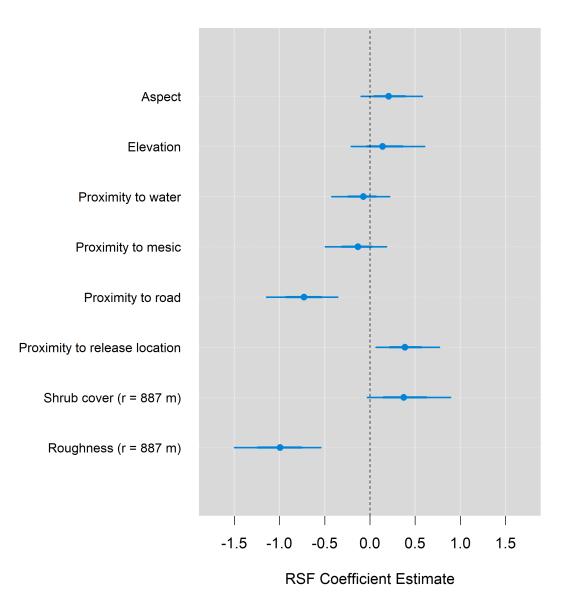


Figure 2.4. Brooding Resource selection parameters and error. Proximity to release location and shrub cover are the highest predictor determining the locations of Greater sage-grouse (*Centrocercus urophasianus*) during brooding season in southwest North Dakota.

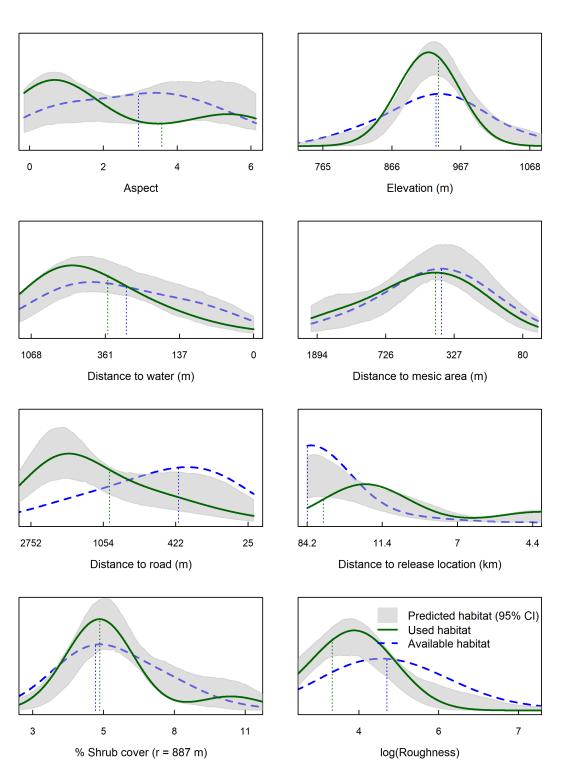


Figure 2.5. Sage-grouse (*Centrocercus urophasianus*) Brooding season habitat parameters and probability of use.

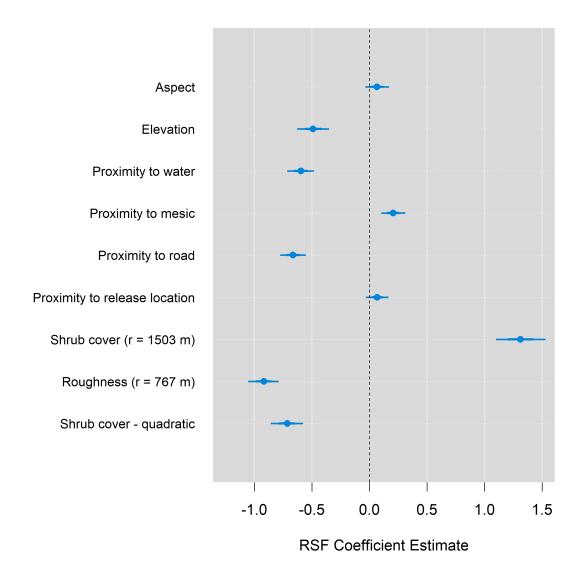


Figure 2.6. Summer non-breeding Resource selection parameters and error. Shrub cover is the highest predictor determining the locations of Greater sage-grouse (*Centrocercus urophasianus*) for non-breeding female sage-grouse in southwest North Dakota.

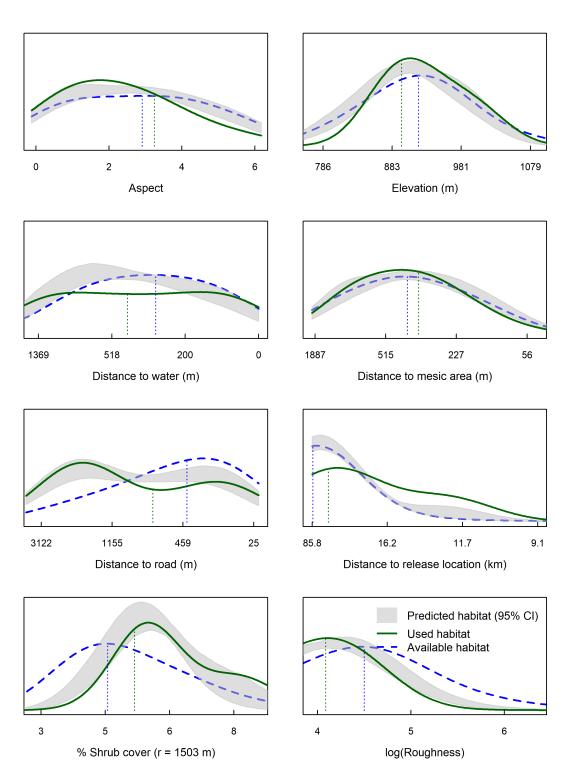
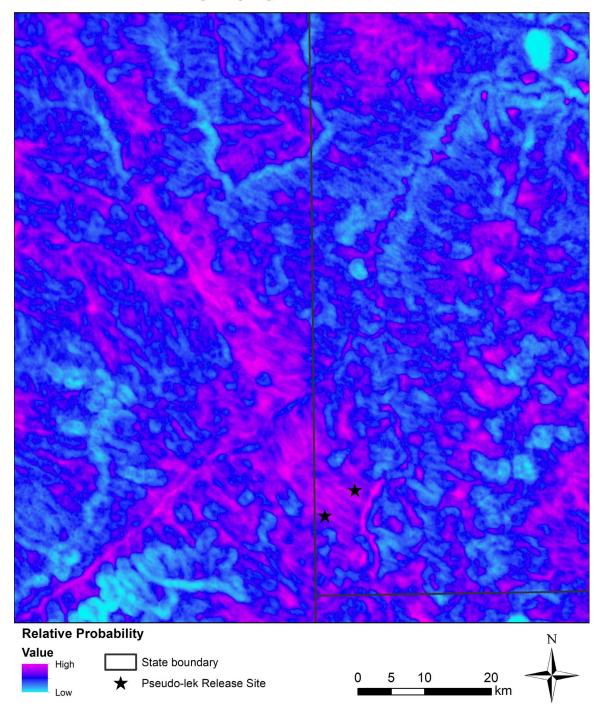


Figure 2.7. Female non-breeding Sage-grouse (*Centrocercus urophasianus*) habitat parameters and probability of use during the summer months.



Nesting sage-grouse RSF, 1987-2018

Figure 2.8. Nesting resource selection of sage-grouse (*Centrocercus urophasianus*) from 1987-2018 in southwest North Dakota. Areas in high (red) locations have greater probability of selection compared to low (blue) areas.

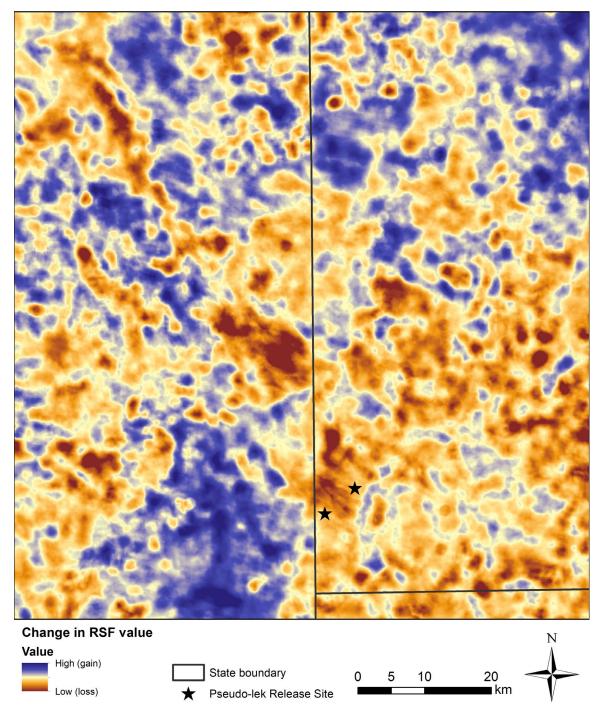
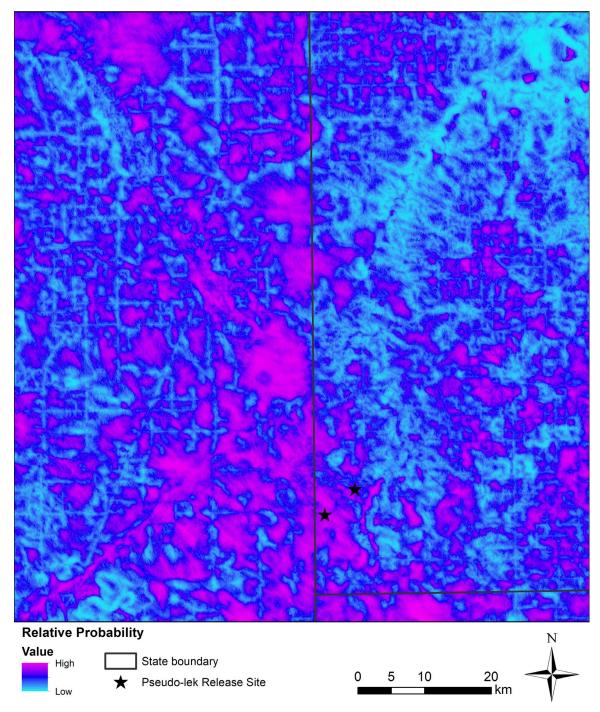


Figure 2.9. Change in sage-grouse (*Centrocercus urophasianus*) nesting habitat from 1987-2018 in southwest North Dakota. Areas in high (Blue) locations displayed a gain in sagebrush habitat, areas in red exhibited a loss is sagebrush habitat.

Change in Nest Habitat, 1987-2018



Brooding sage-grouse RSF, 1987-2018

Figure 2.10. Brooding resource selection of sage-grouse (*Centrocercus urophasianus*) from 1987- 2018 in southwest North Dakota. Areas in high (red) locations have greater probability of selection compared to low (blue) areas.

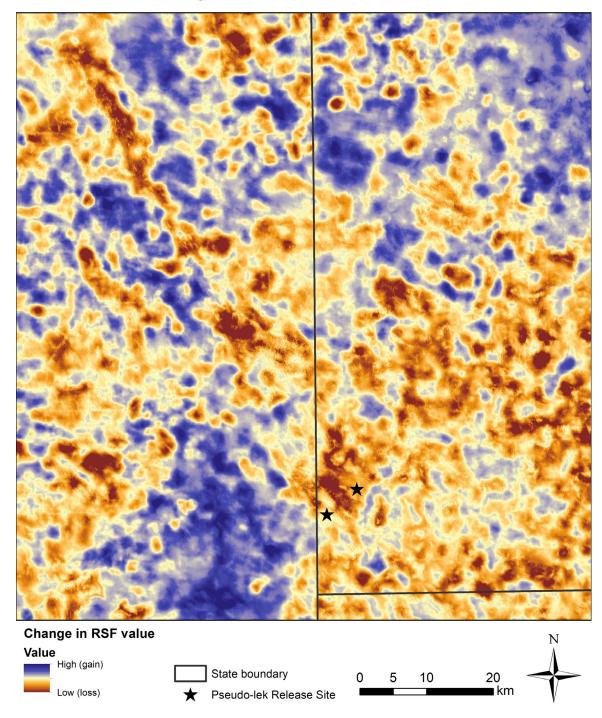
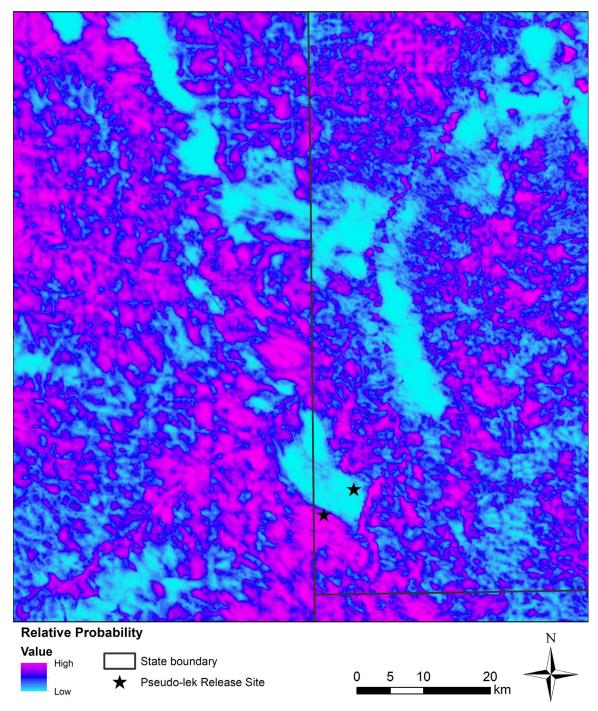


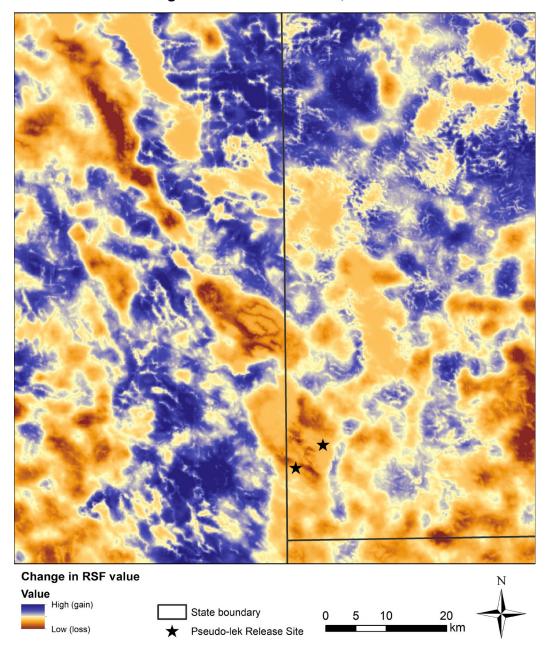
Figure 2.11. Change in sage-grouse (*Centrocercus urophasianus*) Brooding habitat from 1987-2018 in southwest North Dakota. Areas in high (Blue) locations displayed a gain in sagebrush habitat, areas in red exhibited a loss is sagebrush habitat during the brooding period.

Change in Brood Habitat, 1987-2018



Summer sage-grouse RSF, 1987-2018

Figure 2.12. Summer non-breedig female sage-grouse (*Centrocercus urophasianus*) resource selection of from 1987- 2018 in southwest North Dakota. Areas in high (red) locations have greater probability of selection compared to low (blue) areas.



Change in Summer Habitat, 1987-2018

Figure 2.13. Change in summer non-breeding female sage-grouse (*Centrocercus urophasianus*) habitat from 1987- 2018 in southwest North Dakota. Areas in high (Blue) locations displayed a gain in sagebrush habitat, areas in red exhibited a loss is sagebrush habitat during the summer non-breeding season.

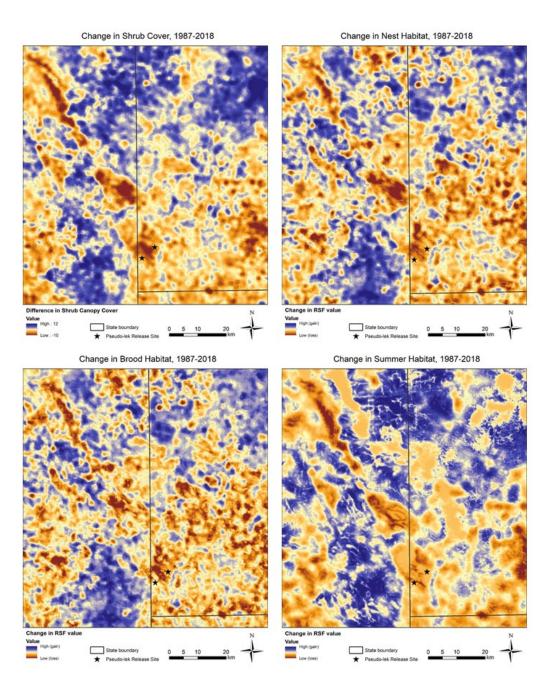


Figure 2.14. Change in shrub cover from 1987-2018, and difference in habitat during nesting, brooding, and summer seasons. Red shows a loss of habitat and blue displays a gain of habitat yellow indicated that there is no change detected.

#### CHAPTER 3

# DEVELOPING NOVEL METHODS FOR TRANSLOCATING GREATER SAGE-GROUSE BROODS

# ABSTRACT

Greater sage-grouse (*Centrocercus urophasianus*; hereafter sage-grouse) are an obligate species inhabiting sagebrush (Artemesia spp.) ecosystems in western North America. In general, sage-grouse populations have been declining since the turn of the mid-1900s and continue to decline range-wide. Many factors, such as habitat loss and degradation, disease, and climate change have had negative effects on populations, specifically populations at the outer extents of the species distribution, including the small population in North Dakota. To compound declining numbers, in the mid-2000s there was an outbreak of West-Nile Virus (WNV) in western North Dakota that caused an abrupt population decline, potentially below a viable level. Conservation concern over the species as whole and specifically this population led to discussions about augmenting North Dakota's sage-grouse population through translocations. We have taken an adaptive approach, including this pilot study, to augment this population via translocations. In addition to other methods, we implemented novel techniques to translocate brood females with their chicks from a source population in south-central Wyoming. We initiated brood translocations in June and July of 2018 by capturing and translocating six broods. During the brooding season of 2018 we translocated 6 brood females and 26 chicks from central Wyoming to southwest North Dakota. Each grouse, females and chicks, were radio-marked prior to transport and release. No chicks or brood

females died during transport. Two of our first 3 broods had difficulties leaving the release pen, resulting in one complete brood failure. After making adjustments to our release pen design the last 3 broods were successfully released without incident. Brood success (i.e.,  $\geq 1$  chick surviving  $\geq 50$  days) occurred for 2 of the 6 translocated broods, with 5 of the 26 translocated chicks surviving  $\geq 50$  days post hatch. Additionally, 2 of the 6 brood females survived through the end of the calendar year. Compared to pre-nesting translocated females, translocated broods moved considerably less distance per day and had relatively higher reproductive success. Brood translocations may offer an alternative to pre-nesting female translocations during the lekking period, with lower numbers of reproductive females being removed from the source population and potentially higher reproductive success rates during the first year of translocation.

#### **INTRODUCTION**

Greater sage-grouse (*Centrocercus urophasianus*; hereafter sage-grouse) are sagebrush (*Artemesia* spp.) ecosystem obligates and the largest native grouse species in North America (Patterson, 1952, Autenrieth 1981, Knick and Connelly 2011). Currently, sage-grouse occupy ~670,000 km<sup>2</sup>, approximately 56% of their pre-European settlement distribution (Schroeder et al. 2004, Knick and Connelly 2011). Population extirpations have been most prevalent at the outer extents of their range-wide distribution (Schroeder et al. 2004). Although some areas continue to support robust and stable populations, since the mid-1900s many sage-grouse populations have, and are projected to, decline throughout the species' range (Garton et al. 2011). Due to the loss and degradation of sagebrush ecosystems and declining populations trends, sage-grouse were identified as a candidate species by the U.S. Fish and Wildlife Service (USFWS) under the Endangered Species Act (ESA) of 1973, with ESA listing decisions in 2005 and 2010 that were later overturned (USFWS 2010). In 2015, the USFWS determined sage-grouse were not warranted for ESA listing due to an unparalleled conservation effort between private, state, and federal partners. However, over the past decade or more some sage-grouse populations have continued to decline (Crawford et al. 2004, Garton et al. 2011).

In many areas sage-grouse habitat has undergone significant changes due to energy development, agriculture conversion, climate change, invasive plants and associated wildfire, and urbanization (Knick and Connelly 2011). Extreme southwestern North Dakota is on the very northeastern edge of sage-grouse distribution (Schroeder et al. 2004). Being located at the outer extent of the species' range, sage-grouse populations in North and South Dakota are inherently habitat limited and sagebrush communities therein, have generally degraded over time (Connelly et al. 2011, Garton et al. 2011, Miller et al. 2011, Forbey et al. 2013). Although sage-grouse have never been widespread in North Dakota, they currently occupy  $\sim 17\%$  of their historical range within the state (Johnson and Knue1989, Schroeder et al. 2004, Garton et al. 2011, McCarthy and Kobriger 2005). Anthropogenic land use and development have impacted sage-grouse in this area, similar to other parts of the species' range (Johnson et al. 2011). To compound the issue, an outbreak of West-Nile Virus (WNV) occurred in the mid-2000s exacerbating population declines in the region (Walker and Naugle 2011), thus, amplifying the need for significant management intervention. Garton et al. (2011) projected Dakotas' populations will drop below minimum viable thresholds by 2037 if significant management actions, such as habitat restoration and translocations, are not

implemented.

Translocations have been defined by the International Union for Conservation of Nature (IUCN), as the deliberate and meditated movement and release of captive or wild animals into a novel and free environment (Seddon 2012). Translocation is the method used in introductions, reintroductions, or augmentations of a population with desired propagules (Seddon et al. 2016). Introductions are the placement of propagules into areas where there are not, and have never contained conspecifics (Jackowski et al. 2016). Reintroductions are the placement of propagules into areas where there are not currently conspecific, but occupied the area historically (Destro et al. 2018). Augmentation is the supplementation of propagules into an existing population of conspecifics (Destro et al. 2018). Translocations may be a viable management strategy to address population declines and augment existing populations. Over 700 wildlife translocations have been documented since 1973 (Griffith et al. 1989, Reese and Connelly 1997, Seddon and Armstrong 2016). Notably,  $\geq$  7200 sage-grouse have been translocated during  $\geq$  56 translocation events in the last century (Griffith et al. 1989, Reese and Connelly 1997, Seddon and Armstrong 2016). Scientific literature has shown a low success rate for translocations of gamebirds (Griffith et al. 1989, Jachowski et al. 2016).

In recent years, there have been relatively few gamebird augmentation projects, including sage-grouse projects, that have provided intensive monitoring and evaluation of impacts to augmented populations, and to date no studies have assessed potential impacts to source populations (Seddon et al. 2016). Some of the most intensively monitored and successful augmentations of sage-grouse have occurred in Utah, providing key findings for future projects (Baxter et al. 2008, 2009, 2013, Gruber-Hadden et al. 2016, Duvuvuei

et al. 2017). Success of these sage-grouse augmentations cab most likely be attributed to several factors, including but not limited to: pre-translocation monitoring and planning, the large number of translocated birds/year, the number of consecutive years of translocations (i.e., > 4 years), habitat assessments, predator management, genetic improvements, and public awareness (Seddon and Armstrong 2012). In recent years, sage-grouse reintroductions and augmentations have increased and will almost certainly be important for future management options as degraded sagebrush habitat is restored (Wolf et al. 1996, Knick and Connelly 2011). Large movements, lower survival, reduced reproductive success, and lack of fidelity to novel environments have been the most significant issues facing the probability of success for the restoration of augmented grouse populations during the spring breeding season; i.e., pre-nesting period (Musil et al.1993, Coates and Delehanty 2006, Coates et al. 2006). Although Moynahan et al. (2006) reported little success translocating any time other than early spring, to our knowledge no published research has assessed the translocation of brooding females with their chicks.

We initiated brood translocations in June and July of 2018 by capturing and translocating females with their chicks (Franklin et al. 2007). We implemented an adaptive approach to augmenting the North Dakota sage-grouse population with brood females and their chicks from a source population in south-central Wyoming. Our objectives were to: 1) report initial methods, 2) describe subsequent refinement of those methods, 3) report results of this pilot study, and 4) describe our observations and how they might be used to guide future brood translocations for sage-grouse and other galliformes. We hypothesize that translocated brood females will experience higher reproductive success rates i.e., successful copulation, nest initiation, clutch size, and nest success by remaining in their source population during these critical early reproductive phases compared to females translocated during the pre-nesting period. Brood females will not experience the stress of adapting to a novel environment until post-hatch during early chick development, a phase when the brood female's behavior (e.g., movement, fidelity, etc.) is naturally restricted. Therefore, we hypothesize that translocated brood females with their chicks have less movement post-release compared to females translocated pre-nesting. We also anticipate that placing a brooding female with chicks into a novel environment will increase the likelihood of both the female and her chicks developing fidelity to the area of release, although this cannot be assessed herein, but will be considered in future years.

# **STUDY AREA**

Our study areas occurred in 2 locations (Fig. 3.1); i.e., the augmented population and the source population. Translocated population study area (i.e., where birds were moved to), was located in in southwestern North Dakota (46.050780, -104.028600), this area is part of the Great Plains Sage-Grouse Management Zone (SMZ) (Stiver et al. 2006, Garton et al. 2011). More specifically, our augmented population area can be described as a polygon beginning at Camp Crook road out of Marmarth, ND, proceed south to Camp Crook, SD, northwest on Tie Creek road to highway 7.North on highway 7 to Baker, MT, and lastly highway 12 southeast back to Camp Crook road in Marmarth ND. The source population (i.e., were the birds came from) occupied the Stewart Creek Area in southcentral Wyoming (42.068902,-107.611964). The Stewart Creek Area is part of the Wyoming Basin SMZ (Garton et al. 2011). More specifically, our source population area can be described as a polygon beginning at US-287 and Mineral Excavation Road (24.30 Km from Rawlins Wyoming) proceed northwest to Wamsutter- Crooks Gap Road, north to Jeffery City, then southeast to Muddy Gap on Highway 789 to highway 220 and south to complete the polygon at the intersection of Mineral Excavation Road.

The Great Plains SMZ is closely tied to populations in extreme southeast Montana and northwest South Dakota (Stiver et al. 2006, Garton et al. 2011). The topography within the North Dakota study site was unglaciated rolling prairie with buttes and intermittent streams. Elevation ranges from 900 —1,052 m. Annual precipitation was 36.9 cm with a majority during the months of May and June. Average annual temperatures are 12.7° C and -0.8° C (max = 42.2° C, min = -34.9° C; US Climate Data, 16 Oct 2018). This study site was a mosaic of private, BLM, and state land. Primary land use was energy development, row crop agriculture, and livestock grazing. The landscape was fragmented by gravel roads, oil pads, and power lines. Vegetation in this area was transitional between shrub-steppe and shortgrass prairie. There was a mixture of shrubs with an understory of perennial and annual forbs and grasses, as well as large areas of open grasslands (Johnson and Larson 1999). Within shrub-steppe communities, shrub species included silver sagebrush (A. cana), big sagebrush (A.tridentata), western snowberry (Syphocarpus occidentalis), rubber rabbit brush (Chrysothamnus nauseosus), and greasewood (Sarcobatus vermiculatus) (Johnson and Larson 1999). The dominant grasses consisted of kentucky blue grass (*Poa pratensis*), western wheatgrass (Pascopyrum smithii), japanese brome (Bromus japonicas), needle and thread (Stipa comada), and june grass (Koeleria macrantha). Prevalent forbs were common yarrow

(*Achillea millefollium*), common dandelion (*Taraxacum officinale*), and textile onion (*Allim textile*) (Johnson and Larson 1999).

Our source population study site was located in Carbon and Sweetwater counties in south central Wyoming. Elevation ranges from 1,520 to 2,080 m. Annual precipitation was 23.47 cm with a majority during the months of May and June. Average annual temperatures were 13° C and -1.5° C (max = 35.6° C, min = -26° C; US Climate Data, 16 Oct 2018). Ownership was a mosaic of Private, State, and BLM. Managed livestock grazing, in the form of domestic sheep and cattle were the dominant land use. During this research our Wyoming study site also had numerous feral horses that were relatively unmanaged and which can impact sage-grouse (Beever and Aldridge 2011). The majority of all fragmentation was caused by gravel or four wheel drive roads. Sagebrush (Artemisia spp.) dominated the landscape at this site. Wyoming big sagebrush (A. tridentata wyomingensis) and mountain big sagebrush (A. t. vasevana) were the most common. Black sagebrush (A. nova) and dwarf sagebrush (A. arbuscula) were found on exposed ridges. Other common shrub species at this site included: antelope bitterbrush (Purshia tridentata), Common snowberry (Symphoricarpos albus), chokecherry (Prunus virginiana), alderleaf mountain mahogany (Cercocarpus montanus), rabbitbrush (Chrysothamnus and Ericameria spp.), greasewood, saskatoon serviceberry (Amelanchier alnifolia), and spiny hopsage (Gravia spinosa). Isolated stands of juniper (Juniperus spp.) and quaking aspen (*Populus tremuloides*) were found at the higher elevations on north facing hillsides.

#### **METHODS**

## Female and Brood Capture and Radio-Marking

We trapped all female sage-grouse intended for spring and brood translocations in April of 2018 during lekking activities, at night using all-terrain vehicles (ATVs) with the aid of a spotlight and dip-net (Giesen et al. 1982, Wakkinen et al. 1992, Connelly et al. 2003). Upon capture, females were fitted with an aluminum leg band, weighed, sexed, aged and evaluated for general health (Patterson 1952, Eng 1955, Braun and Schroeder 2015). Morphometric measurements were documented for each female including: body mass, wing length, tarsus length, and culmen length (USGS 2018). Post-capture, birds were fitted with either rump-mounted, solar-powered Geotrak (GeoTrak Inc., 2521 Schieffelin Rd, Apex, NC, USA) global positioning system-platform transmitter terminal (GPS-PTT) 22 g transmitters with a 3.5 g glue-on VHF radio for ground tracking, or an Advanced Telemetry Systems (ATS) (Advanced Telemetry Systems, 470 First avenue NW, Isanti, MN, and Holohil Systems, Ltd., 112 John Cavanaugh Drive, Carp, Ontario, Canada) very high frequency (VHF) necklace-style transmitter (22 g). After capture and processing all translocated sage-grouse were transported and released at the North Dakota study site. Translocated sage-grouse were driven in a covered truck or transported to the release sites in a fixed wing aircraft provided by North Dakota Game and Fish (NDGF). Prior to release, each bird was transferred into a constructed box with individual compartments and remote opening door to enable a soft release (Rodgers 1992). The morning of release we placed all birds near lek site, planted decoys, and used up to two Fox pro NX4s (FOXPRO Inc.14 Fox Hollow Drive - Lewistown, PA) to transmit lekking

sounds, as an attempt to decrease post release movements (Coates et al. 2006; Snyder et al. 1999; Baxter et al. 2008). We also marked another group of female sage-grouse with a 22 g ATS necklace-style VHF transmitter and a leg band for monitoring the source population. Following capture protocols, all females left in the source population for source monitoring and brood translocations were immediately released back into the source population and these females became our primary source of brooding females for potential translocation if their nest successfully hatched. We monitored radio-marked female sage-grouse either remotely via ARGOS-enabled downloads (http://www.argos-system.org/), or with ground telemetry using VHF signals. We only used ground telemetry to approach within a few meters of marked females to verify nest initiation and nest success. Marked brood females with chicks were monitored remotely until re-trapping for translocation of the entire brood.

Using nocturnal spotlight methods described above, we recaptured brooding females with their chicks in June and July 2018. Although, we began with a goal of recapturing and translocating broods at 10 days post hatch, we decided to follow a more logistically efficient approach. If we had more than one brood that would be close to ten days post hatch we decided to relocate multiple broods at the same time. Due to unforeseen circumstances described below, following the recapture and translocation of our previously radio-marked sample of brood females, and using the same methods described above, we located, captured, radio-marked, and translocated brood females with their chicks that were not previously captured and radio-marked in the spring. For all translocated broods, all chicks were marked with a 1.0 g ATS, VHF backpack radio transmitter using the suture method (Burkepile et al. 2002, Dahlgren et al. 2010). We

estimated chick ages by either calculating the hatch date from nest initiation or by measurements of the primary flight feathers and under-tail covert feathers using tables provided by Wallestad (1975). A translocation-release box (described below, Fig. 3.2) was taken into the field during nocturnal captures. For most brood captures, an ATV and spotlight were used to locate and capture the brood. Upon successful capture a technician would be notified and drive a truck out to the capture location with the translocationrelease box. Following handling procedures after capture, the brood female and chicks were placed in the translocation-release box until released in North Dakota.

A local veterinarian attended nocturnal captures and examined the general health of the brood female and chicks. The veterinarian also took saliva cheek swab and blood samples from brood females for disease testing. To avoid too much risk to the chicks from extended handling and blood loss, disease testing was not completed for chicks. We tested all brood female as part of a requirement of the North Dakota State Board of Animal Health. We had all samples tested for Mycoplasma, Salmonella, Mycobacterium avium, and Avian Influenza submitted for testing prior to any translocated grouse being released in North Dakota. There was an agreement with North Dakota State Board of Animal Health that stated, translocated grouse could be released as quickly as possible prior to researchers receiving disease testing results to avoid holding the birds for an inordinate amount of time, but with the caveat that if any results came back positive then the brood female and her chicks would be immediately tracked down and euthanized.

#### **Brood Translocation**

After broods were captured, we placed all brood females and chicks in a

fabricated translocation-release box. Translocation-release boxes were constructed using 1.27 cm (0.5 inch) plywood, and measured 33.02 cm (13 inch) x 33.02 cm (13 inch) x 66.04 cm (26 inch) (Fig. 3.2). A removable divider separated the brood female and chicks to prevent trampling of chicks during transport. The release door on the translocationrelease box was located in the chicks' compartment, ensuring that as the brood female was released she would walk past her chicks once the divider was removed and release door opened. In the chick compartment we installed a standard sized 10 watt Repticare® rock heater (item number RH1), 0.231 (1cup) non-skid stainless steel dish, and indoor outdoor cordless LaCrosse Technology® thermometer. We used gorilla epoxy® to attach the food dish and heat rock to the floor. We used zip ties to attach the thermometer sensor through holes drilled into the side of the transport box approximately two-thirds up, to provide the most accurate temperature readings. We provided 60 g of cantaloupe to both the brood female and chicks for hydration, we cut the melon provided to the chicks in 3, 20 g pieces and left the brood females in one large piece. Mealworms were also provided to the chicks for nutrition (Table 3.1). Meal worm and melon consumption was estimated by measuring melon before and again after release had been carried out. We gathered the remaining melon and assessed how much had been consumed in 5 categories: none (no visible sign of consumption), light (visible sign but little melon was absent), moderate (visible sign that about half of the melon had been consumed), and heavy (more than half of the melon had been consumed). Mealworm consumption was assessed in the same fashion as melon except we were able to count individual worms that had not been eaten by chicks. During travel the heat rock was plugged into a Cyberpower 175W power inverter and then into the 12v outlet in the vehicle. The digital display of the thermometer was monitored to ensure that the chick compartment maintained a constant temperature of 26.7—35° C (80.6—95° F) (Deaton et al. 1996).

## **Brood Release**

Brood release sites were distributed close to the 3 historic lek sites where initial spring augmentations occurred (Robinson 2014). When considering release locations, we also considered brooding areas frequented by endemic broods and the availability of sagebrush and mesic habitat for brooding females and chicks (Dahlgren et. al. 2010, Connelly et. al. 2011). Prior to capture, we constructed acclimation release pens at predetermined release sites. Two blinds were set up to conceal observers on each side of the pen. Originally, our pens were based on plans provided by USGS in previous Parker meadows California brood translocations (P. S. Coates, USGS, personal communication) they were 4.877 m (16 ft) in diameter with 60.96 cm (24 inch) doors (Fig. 3.3). Concrete stakes were pounded into the ground and then zip ties used to secure the chicken wire. The top of the enclosure was 0.953 cm (0.375 inch) scène stretched over the chicken wire and secured with zip ties. The door was 45.72 x 60.96 cm (18 x 24 inch), constructed out of 1.91 cm (0.75 inch) black iron pipe and fittings with chicken wire attached with tiewire and zip ties. The door was remotely opened using a rope and hinged on a concrete stake driven into the ground. The translocation-release box was placed on the outside edge of the pen with the sides of the pen terminating at opposing corners of the box (Fig. 3.3). Due to unforeseen challenges of this design, after 3 released broods we redesigned our acclimation release pens. Our revised acclimation release pen was 1.22 m (4 ft) wide by 2.44 m (8 ft) long 1.91 cm (0.75 inch) poly vinyl chloride (PVC), and 45.72 cm (18

inch) tall. Chicken wire was zip tied to 4 sides forming the walls. The entire 2.44 m (8-ft) side of the pen could be opened, allowing for more congruity of brood members upon release (Fig. 3.4). We used sod stakes and concrete stakes at each corner and when needed to secure the pen to the ground. At each corner of the side that opened, we installed drift fences, each at a widening angle from the other forming a V-shape. Drift fences were made out of 25.4 x 15.24 m (10 inch x 50 ft) chicken wire and aimed to guide all brood members together into nearby habitat with relatively high sagebrush cover. Drift fences were installed by pounding concrete stakes into the ground and zip tying chicken wire to stakes.

After the brood left the acclimation release pen, we attempted to locate each brood daily to determine the location and apparent survival of the brood female and each chick. If we could not detect one or more chicks in a brood, we systematically searched between the previous day's location and current location until the signal was detected and the chick(s) located (Burkepile et al. 2002, Dahlgren et al. 2010). In some rare cases if we were unable to locate a chick via ground telemetry we used fixed-wing aerial telemetry to locate missing chicks. If the brood female demonstrated large movements without returning, we assumed she was not brooding chicks (Berry and Eng 1985). Recruitment (i.e., brood success) was defined as  $\geq 1$  chick within the brood surviving  $\geq 50$  days. We obtained a permit from The Institutional Animal Care and Use Committee (IACUC) (permit #2729) at Utah State University for all capture and handling procedures.

### RESULTS

Of n = 20 GPS radio-marked female sage-grouse trapped during the spring of

2018 for future translocation following a successful nest, n = 17 initiated nests, of which 6 nests successfully hatched, and 2 broods (11 chicks) survived long enough for recapture and translocation. An additional 2 broods from our source population sample were subsequently recaptured and translocated. The final 2 broods were unmarked females with chicks located with nocturnal trapping during the brooding period. Therefore, in 2018, we translocated and released 6 broods and 26 chicks (Table 3.1). All 6 brood females and 26 chicks were successfully released from the translocation-release box into the acclimation release pen, and all but 4 chicks successfully left the release pen. One chick was injured during transport within the translocation-release box. Of the 22 chicks that successfully exited the release pen, 3 died outside the release pen, but still at the release site due to separation from the brood female and subsequent exposure. Thus, 19 chicks successfully joined the augmented population. We experienced issues with our second and third brood releases, likely due to release pen design flaws causing the separation of one or more chicks from the brood female. The release pen was redesigned for our fourth, fifth, and sixth brood releases. All broods were released within 13 hours of capture at the Wyoming study site.

#### **Individual Broods**

*Brood 1.*— This brood was released using our original acclimation release pen design on 04 June 2018 at 15:20 (Fig. 3.3). The female was a GPS radio-marked brood female captured in April of 2018 and released into the source population to be translocated if her nesting attempt was successful. The brood female was moved with 6 chicks that were 7-days post-hatch at the time of recapture. The chicks consumed a moderate amount of cantaloupe and 2/7 mealworms. After leaving the transport release box, within 17-min all chicks and the brood female had exited the acclimation pen. Two of the 6 chicks went missing 3 days after translocation and release. One of the chick's transmitter was located 4 days after it went missing and no remains were found. This chick was assumed dead. The other missing chick was never located and had an unknown fate. Five days post release, the remaining 4 chicks were killed, likely all during the same predation event.

*Brood 2.*— This brood was released using the original acclimation release pen design on 07 June 2018 at 14:15 (Fig. 3.3). The brood female was a source population female marked with VHF necklace-style transmitter. The brood female and 5 chicks were translocated 3 days post-hatch. The chicks did not consume any of the cantaloupe or mealworms. Shortly after the female and all five chicks exited the transport release box into the acclimation release pen, one chick went just outside the acclimation release pen and was separated from its brood mates and the brood female. This seemed to cause the brood female distress. The brood female and the other chicks remained in the pen for 105 min while the first chick was on the opposite side of the fence. When observers returned after dark the brood female and 4 chicks were still in the acclimation pen and the first chick was just outside on the other side of the netting. The next morning all 5 chicks were found dead, likely to exposure and the brood female was not present. Within a few days, the brood female was found with other resident adult sage-grouse.

*Brood 3.*— This brood was released using the original acclimation release pen design on 07 June 2018 at 17:30 (Fig. 3.3). The brood female was a source population female, marked with a necklace-style VHF radio, and had 5 chicks that were translocated

15 days post-hatch. During transport, the chicks consumed a moderate amount of cantaloupe and 1/7 mealworms. Following departure from the transport release box, the brood female and chicks remained in the acclimation pen for more than 2 hours. Two chicks were first to leave the pen and they ended up together on one side of the release pen. During this time a rainstorm developed. The brood female remained in the acclimation pen with the other 3 chicks until dark, at which time observers left the release site with the gate open. The next morning the brood female and 3 chicks, which stayed with her in the release pen after dark, were located together outside the release pen, but nearby. The 2 chicks that left first and became separated were found dead, likely due to exposure, near their last known location. One of the 3 remaining chicks died 6 days post release of unknown causes. The chick was largely intact, but with a scraped leg. One of the 2 remaining chicks died 28 days post release, the cause of death is unknown. We located the transmitter  $\geq$  4 days postmortem and the body was heavily decayed. The remaining chick was recruited into the population having survived more than 50 days post hatch. This was the last brood released using the original release pen design. Our experiences with broods 2 and 3 caused us to redesign our acclimation release pen.

*Brood 4.*— This brood was released from the revised acclimation release pen on 29 June 2018 at 11:25 (Fig. 3.4). The brood female was captured and marked with a GPS in April, 2018, at that time she was designated a brood female. After her first nest was depredated within the source population area, she began a second nest which successfully hatched. She had 1 chick with her when she was recaptured 8 days post-hatch of her second nest. The single chick consumed a light amount of cantaloupe and 5/7 mealworms. The brood female and her chick left the acclimation release pen 46 min after

the transport release box was opened. The chick went missing the following day after release and was never detected again. The brood female was located on the other side of the study site with resident adult sage-grouse two days post release.

Brood 5.— This brood was released from the revised acclimation release pen on 07 July 2018 at 06:20 (Fig. 3.4). The brood female was captured as an unmarked individual during the brooding season within the source population. She had 6 chicks that were estimated at 29 days post-hatch. The chicks consumed a heavy amount of cantaloupe and 7/7 mealworms. The brood female and chicks left the acclimation pen 36 min after the translocation-release box was opened. One chick was injured during capture, transport, or release and died 1 day post release near the release site. One chick was depredated, seemingly by a mammalian predator, 4 days post release. One chick and the brood female were killed, presumably by a raptor, 9 days post release. The remaining 3 chicks amalgamated (i.e., mixed with another brood) into a resident unmarked female's brood for the remainder of the brooding season. In the meantime, we received the disease testing report, which reported that the brood female tested positive for avian tuberculosis. If she had been alive, we would have been required to euthanize her. Although three chicks were found alive at this time having survived to 47 days post hatch, we were required, as per our agreement with the North Dakota State Board of Animal Health, to dispatch all 3 chicks due to the positive results of the brood female for avian tuberculosis. After testing each chick postmortem, none tested positive for avian tuberculosis.

*Brood 6.*— This brood was released from the revised acclimation release pen on 11 July 2018 at 13:05 (Fig. 3.4). The brood female was unmarked when captured within the source population during the brood season with three chicks, estimated at 35 days

post-hatch. The chicks consumed a moderate amount of cantaloupe and 7/7 mealworms. The brood female and chicks left the acclimation pen 63 minutes after the brood tranport box was opened. The brood female was killed near the release site 1 day post release. All 3 chicks amalgamated into our Brood-5, which had formed a brood crèche with a resident unmarked brood female and her chicks near the release site. Although all transmitters were tested before attachment and translocation, it seemed that 2 transmitters from brood 6 failed post deployment. The third chick with a working transmitter survived  $\geq$  50 days and was monitored along with Brood-5 following Brood-6 female's death. Moreover, when we located this chick  $\geq$  50 days, we detected two other chicks the same size (i.e., indicative of the same age) that flushed from the same location, which likely was the other two chicks from Brood-6, though a definitive detection was not made.

In summary, after translocating 6 brood females and 26 chicks. Two chicks were observed alive 50 days post hatch (individual chick apparent survival = 0.07) and 2 of the 6 brood females survived to at least 31 December 2018 (Table 3.1). If we assumed the 3 chicks from Brood-5 that were euthanized at 47 days would have survived to 50 days and the 2 chicks from Brood-6 remained alive with malfunctioning transmitters, then our apparent brood success would have been 0.50, and 7 total chicks (individual chick apparent survival = 0.26) would have been recruited into the population.

*Movement and Reproductive Success Comparison.*—Our spring translocated females exhibited relatively large movements for the first 30 days post release, averaging 11.35 km/day (95% CL 4.91-19.79) for GPS females and 6.52 km/day (95% CI 1.56-11.50) for VHF females compared to much smaller movements of 0.19 km/day (95% CI 0.0-0.39) for our translocated brood females for their first 30 days post release (Appendix A, Table 3.2).

#### DISCUSSION

We successfully developed brood translocation methods during this pilot study and a concurrent study in California, within the Bi-State sage-grouse population, which may aid future translocation studies and management efforts. We were able to develop and adapt our methods by adjusting equipment and procedures to allow for the safe capture, transportation, and release of sage-grouse broods into the augmented population. Our novel developments included: 1) translocation-release boxes for both the brood female and her chicks, which included a removable divider, melon for hydration, meal worms for nutrition, a heat source to maintain chick body temperatures, and a digital thermometer to monitor ambient temperature inside the brood compartment, 2) an acclimation release pen with an entire side that could be opened and drift fencing guiding the immediate movements of the released brood as one group into nearby sagebrush habitat and providing a successful transition from the translocation-release box to full release into the augmented population.

We caution that repeated use of a release location may be detrimental when translocating broods. We placed our acclimation release pens in two separate locations and released all broods from one or the other. We observed avian predators that seemed to key into our release sites and witnessed a predation event occur for one of our translocated broods. By repeatedly releasing broods from the same locations we may have inadvertently contributed to an increased risk of predation for our translocated broods (Dinkins et al. 2012, Guttery 2011). As much as is logistically feasible, we recommend future brood translocations regularly relocate release pens within suitable habitat.

Although sage-grouse chicks are precocial, they depend on the brood female for thermoregulation, modeling behavior, and direction to habitat and food resources (Visser and Ricklefs 1995, Dahlgren et al. 2010). Because we separated chicks from their brood female and transport occurred over many hours, we felt it was prudent to provide hydration, food, and heat to the chicks. While it is likely that, during transport and separation from the brood female, younger chicks experienced a higher risk of negative impact (i.e., thermoregulation, dehydration, and starvation) our older chicks seemed to take more advantage of the resources provided them compared to younger chicks. However, regardless of age none of our translocated chicks died during transport.

Although our pilot study included relatively small sample sizes, the apparent survival and reproductive rates of our translocated brood females were similar or higher than our pre-nesting translocated females and those of other studies (Appendix A; Baxter et al. 2009). Although adult female survival has been shown to be the most important contributor to population growth, of the multiple vital rates that contribute specifically to reproductive success, chick survival and brood success have been shown to have the largest contribution to sage-grouse population growth rates (Taylor et al. 2012, Dahlgren et al. 2016). Incorporation of adults and recruitment of their young into the augmented population has been the ultimate goal of translocations in wildlife management (Baxter et al. 2009). Duvuvuei et al. (2017) reported that female sage-grouse translocated prenesting has a very low probability of nest and brood success. However, they also reported a more than three-fold increase in the probability of success when isolating the brooding period. Although nest initiation and nest success have almost always been reportedly lower for translocated pre-nesting females compared to residents, these same females, if their nest was successful, have had similar brood success compared to resident and females translocated in previous years (Baxter et al. 2009, Musil et al. 1993, Duvuvuei et al. 2017). Our results from this limited pilot study suggests that the probability of reproductive success for translocated females (i.e., recruitment of chicks) may be increased using brood translocations.

Although more research is needed, translocating a female post-hatch with her chicks may avoid the risks associated with facing a novel environment during the nest initiation, nest incubation, and early brooding periods. Compared to females translocated pre-nesting, our brooding females showed considerably less post-translocation movement 30 days post release (Table 3.2). This result is important because larger movements have been reported as one of the primary causes of mortality (Prochazka et al. 2017), which may explain why past translocation studies with larger movements failed (Musil et al. 1993, Fedy et al. 2012). We believe that chick age mattered when conducting brood translocations. The age of our translocated broods ranged from 3-35 days post-hatch. We concluded that the risk of exposure was too high for chicks < 7 days old. Although we found it easier to capture broods when chicks were younger, older chicks have reportedly been more homoeothermic (Visser and Ricklefs 1995), efficient at foraging (Anderson and Alisauskas 2001), and better equipped to evade predators (Potts 1986). Sage-grouse chick survival has been shown to be lowest during the first week or two post-hatch, but then stabilizes thereafter until fledging (Gregg 2006, Dahlgren et al. 2010). However, we observed substantially more struggle and stress in older chicks ( $\sim \ge 30$  days post-hatch)

during processing and translocation and younger chicks seemed to recover faster following handling and transport. Until further research and the results from this and a concurrent study in the Bi-State population can be completed, we recommend that chicks are  $\geq 7$  and  $\leq 28$  days old when translocating a brood.

Brood amalgamation behavior (i.e., when a chick is no longer brooded by its natal mother, but by a non-natal female; also referred to as brood mixing, brood hopping, and/or alloparental care) may be an important consideration for brood translocations and sage-grouse population dynamics in general. Brood mixing is potentially a common phenomenon in sage-grouse and other gallinaceous species (Nastase and Sherry 1997, Faircloth et al. 2005, Wong et al. 2009, Dahlgren et al. 2010, Guttery et al. 2013). In both cases of brood mixing in our study, the radio-marked brood female died prior to chick fledging and radio-marked chicks were assimilated into other broods with non-natal females, one resident and one radio-marked/translocated, within 48 hours of brood female mortality. Similarly, while monitoring radio-marked sage-grouse chicks, Dahlgren et al. (2010) reported that in all cases of natal brood female mortality, chicks amalgamated into other broods within 48-hours. Brood mixing may provide a mitigating buffer for chick survival when a brooding female dies. The probability of brood mixing may be related to the availability of other broods, such as the concentration and density of sage-grouse near mesic habitat during the brooding period (Dahlgren et al. 2010). However, we documented brood mixing within North Dakota's augmented population with extremely low grouse abundance overall.

Nest success of sage-grouse varies annually (Taylor et al. 2012) and in 2018 the success of our radio-marked females, both source and potential brood translocation, was

relatively low. This was likely due to extreme spring weather in the form of heavy precipitation events. With such low nest success, our potential sample of radio-marked brood females became limited. Because of this, we captured and translocated two radio-marked source population brood females with their chicks. To further bolster our sample size, during the brooding period we located, trapped, radio-marked, and translocated previously unmarked broods for translocation was relatively efficient and we experienced little difficulty, even though they had much older chicks ( $\geq$  29 days) than our radio-marked brood females earlier in the brooding period. By capturing aforementioned unmarked broods we learned that as chicks increased in age they seemed more susceptible to stress and struggled more vigorously during processing and transport.

Brood translocations may provide a novel alternative to traditional spring translocation of female sage-grouse. Our results suggest that brood translocation has potentially significant advantages over translocations of pre-nesting females. Past gamebird, and especially sage-grouse, translocations have used relatively large numbers of females during the pre-nesting period, which have consistently shown relatively low productivity within that breeding season. Brood translocations may involve comparatively much lower numbers of reproductively viable females while maintaining or even increasing rates of reproductive success within the augmented population during the year of release. Reproductive success during the translocation year could be especially important because recent research has indicated that reproductive success of the offspring of translocated grouse contribute most to the increase and recovery of the augmented population, thus, the ultimate success of translocation efforts (P. S. Coates, USGS, personal communication). Moreover, although to date no studies have been published showing impacts of translocations on source populations of sage-grouse, or any other galliformes, because of the influence and contribution of adult female survival to sage-grouse population stability, the lower number of reproductively viable females removed from the source population most likely reduces the probability of negative impacts to said source population. Although our results were encouraging and we believe the novel methods we developed could be useful for future translocation efforts. Because of our limited sample size we strongly recommend further assessment of the methodologies used herein and the effects of brood translocations on both augmented and source populations.

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## **TABLES AND FIGURES**

Table 3.1. Greater sage-grouse brood translocation summary statistics from central Wyoming to southwest North Dakota in 2018. Bird ID is the identification number of each brood. Number of Chicks is the number of chicks with the female at the time of translocation. Number of Chicks Surviving  $\geq 50$  days is the number of chicks still on the landscape  $\geq 50$  days post hatch. Apparent Individual Chick Survival is the proportion of chicks that survived  $\geq 50$  days post hatch. Brood Survival is the Average apparent survival. Melon consumed is the categorical amount of melon (cantaloupe) consumed by each brood. Melon consumption was estimated by measuring 60g of melon dividing it into 3 20g pieces and placing it in the dish in the chick side of the translocation-release box. After release had been carried out we gathered the remaining melon and assessed how much had been consumed, none (no visible sign of consumption), light (visible sign but little melon was absent), moderate (visible sign that about half of the melon had been consumed), and heavy (more than half of the melon had been consumed). Mealworms consumed was assessed in the same fashion as melon except we were able to count individual worms that had not been eaten by chicks.

		Number of	Apparen			
		Chicks	t			Mealwor
	Numb	Survivin	Individu	Brood	Mellon	ms
Bird	er of	$g \ge 50$	al Chick	Surviv	Consume	Consume
ID	Chicks	days *	Survival	al	d	d
B1	6	0	0.00	0.00	Moderat e	2/7
B2	5	0	0.00	0.00	None	0/7
В3	5	1	0.20	1.00	Moderat e	1/7
B4	1	0	0.00	0.00	Light	5/7
B5	6	3	0.50	1.00	Heavy	7/7
B6	3	1	0.33	1.00	Moderat e	7/7
Tota l	26	5	0.19	0.50	NA	NA

\*We included the 3 chicks from B5 that were dispatched at 48 days in the alive at  $\geq$ 50 days column because of the high probability that they would have been successful if we had not been required to dispatch them due to the brood female testing positive for avian TB.

Table 3.2. Movement of spring translocated and brood translocated Greater sage-grouse in southwest North Dakota in 2018. We report mean distance in km per day, which was calculated from the first 30 days of raw movement data. All points were converted into UTMs and the distance was calculated for one location each day per female sage-grouse. We calculated the date post release by converting all dates into Julian dates and subtracting each date from the date of release. For this table we only used 30 days post release, from the larger movement data located in Appendix B, due to the limited amount of brood data. We separated transmitter type because the sampling in the GPS is at a finer scale than the VHF. We did not separate the brood transmitter types because we located each brood once a day.

Transmitter Type	Number of individuals	Mean (km)	Standard Error
VHF	6	6.53	1.94
GPS	16	11.35	3.02
Brood	5	0.19	0.07

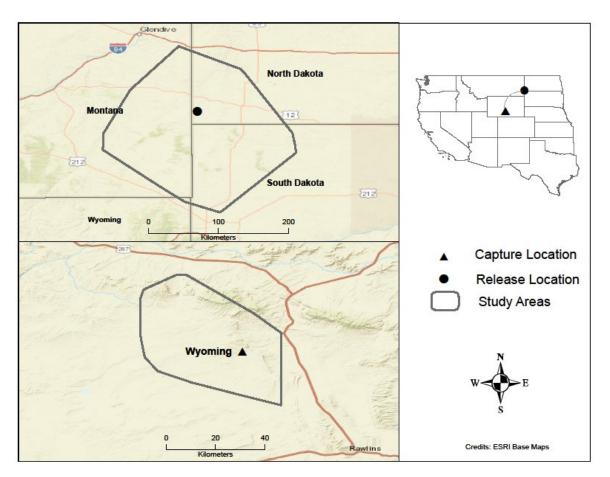


Figure 3.1. Our two study areas included the augmented population (i.e., where birds were moved to) located in Bowman and Slope Counties in southwestern North Dakota (46.050780, -104.028600) and the source population (i.e., where birds were taken from) located in the Stewart Creek Area in south-central Wyoming (42.068902,-107.611964). Our two study sites were defined by minimum convex polygons, 10,594 locations in North Dakota and 9,971 locations at the Wyoming study area, based on radio-marked greater sage-grouse (*Centrocercus urophasianus*) locations, 2017-2018.



Figure 3.2. Translocation-Release Box Box  $33.02 \times 33.02 \times 66.04 \text{ cm} (13 \times 13 \times 26 \text{ inch} dimensions), constructed out of 1.27 cm (1/2 inch) plywood and included two equally sized compartments separated by a removable divider. The rear compartment was for the brood female, in which we placed a small (0.23 l) stainless steel food dish with ~ 20 g of cantaoupe for hydration. The front compartment was for the chicks in which we placed an electric heat rock, a small (0.23 l) food dish with cantaoupe and mealworms, and an inside/outside digital display thermometer to monitor the temperature inside the chick compartment durring translocation. We drilled two holes and attached the thermometer sensor with a ziptie ~ 21.59 cm (8.5 inch) from the inside bottom .We cut out separate openings with vertically sliding removable doors in each compartment We chose the sliding doors as apposed to hinged doors to prevent injuring birds trying to escape when shutting. The release door was a counter levered piece of wood that was 33.02 x 55.88 cm (13 x 22 inch) and connected with a piano hinge. On the bottom and center 2.54 cm (1 inch) from the bottom we installed a 1.90 cm (0.75 inch) eye screw to attach a rope$ 



Figure 3.3. First of two acclimation release pens. After 3 brood translocations we modified this design (see Fig. 3.4). This pen is ~4.88 m (16 ft) in diameter with 25.4cm (10 inch) chicken wire stretched over concrete stakes around the outside edge. We installed 0.953cm (.375 inch) scène over the top and zip tied to the chicken wire. The door is made of black steel pipe and fittings  $45.72 \times 60.96$  cm (18x24 inch). The door hinged on a concreate stake, and was remotely opened with a rope. Top left photo displays the first of 2 acclimation pens set up on the study site prior to release. Top right image displays a close up view of the door and attachment of rope for release on the first acclimation pen. The bottom photo displays the placement of the transport box on the outside of the first acclimation pen.



Figure 3.4. Second of two acclimation pens, this pen is constructed of 1.91cm (0.75 inch) poly vinyl chloride (PVC) pipe. The dimensions are: 1.22 x 2.44m (4 x 8 ft.) long by 25.4cm (10 inch) tall. The corners were placed over concreate stakes. Sod stakes were placed throughout anchoring it to the ground. There was chicken wire on the sides and top. The transport box was placed on the outside back edge opposite of the acclimation pen release door. The acclimation pen release door was first designed out of PVC, but there was too much flex in the pipe. We attached lumber with wire and zip ties to increase the integrity, the door was opened remotely by pulling a rope that was tied to the counter leaver and ran to a ground blind that was placed at the rear of the acclimation pen to conceal the people facilitating the release. There are two drift fences installed by securing 25.4cm (10 inch) tall chicken wire to concrete stakes for ~15.24m (50 ft.) from the corners of the acclimation pen into the desired habitat. Top left image is the view from behind the release pen. This displays the use of 2 ropes to release the brood (e.g., one rope on the transport box, and one on the acclimation pen doors).this image also displays the location of the transport box on the acclimation pen. Top right image displays the release door that is the full length of the acclimation pen. This image also displays the front of the transport box with latches to secure the door shut and handles for carrying. Image on the bottom left displays the placement of the blind to the acclimation pen and the placement of the drift fences. Bottom right image displays the acclimation pen that is free standing, before the transport box is attached. This image also displays a closer view of the acclimation pen release door with lumber attached with wire and zip ties to increase the strength.

#### **CHAPTER 4**

# DEVELOPING ARTIFICIAL INSEMENATION METHODS FOR TRANSLOCATED FEMALE GREATER SAGE-GROUSE (CENTROCERCUS UROPHASIANUS)<sup>2</sup>

## ABSTRACT

Translocations are described by the International Union for Conservation of Nature as the deliberate and meditated movement and the release of captive or wild animals into a novel and free environment. Translocations have been implemented in North America since 1786. Translocations have proven to facilitate many objectives including: augmentation of declining populations, removal of nuisance animals, reintroduction of a species into an area where they have been extirpated, and to increase genetic variability. The objectives of many recent translocations have been to manage game bird species including greater sage-grouse (Centrocercus urophasianus; hereafter sage-grouse) populations. Sage-grouse populations have been declining since the turn of the century and continue to decline range-wide. Many environmental factors, such as habitat loss, habitat degradation, land-use change, disease, and climate change have led to negative effects on sage-grouse populations, specifically populations at the eastern extent of the species distribution. We have taken an adaptive management approach to augmenting this population via translocations. In addition to other methods, we have implemented artificial insemination (AI). The objectives of this study were to: 1) develop protocols for semen extraction from male sage-grouse and insemination of females, 2) assess if individuals that received an AI treatment demonstrated higher nest initiation

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rates and lower dispersal distances following release into the novel environment within the augmented population. We obtained semen for AI during 2017 and 2018 by capturing male sage-grouse on leks. Semen was collected via the massage method, which has been used with success in other grouse species. An assessment of semen volume and spermatozoa density was made and samples were buffered according to quality and then inserted into the female; i.e., AI sample. Sham females were inseminated with a bufferonly solution, and control females were not inseminated. We tested differences in treatment groups using a chi squared analysis to test differences in nest initiation and a ttest to assess difference in movement. When comparing experimental groups, we found no differences in nest initiation rates or movements. Our inability to detect differences could have been influenced by our low sample sizes and further evaluations are needed. However, we were able to develop working protocols for semen extraction and insemination procedures.

## **INTRODUCTION**

Translocations of wildlife have been described by the International Union for Conservation of Nature (IUCN) as the deliberate and meditated movement and release of captive or wild animals into a novel and free environment (Seddon et al. 2012). Translocations have been a worldwide wildlife management practice, including many cases in North America (Phillips 1928, Griffith et al.1989, Seddon 2012, Seddon and Armstrong 2016). Following the 1969 amendment to the Lacey Act of 1900 (sections 241-244), there have been over 700 wildlife translocations of various species documented (Griffith et al. 1989, Seddon 2007). Translocations may include several objectives, singularly or combined, such as: augmentation of declining populations, removal of nuisance animals, reintroduction of a species into an area where they have been extirpated, establishment of a species in an area where they are non-endemic, and increasing genetic diversity (Smith and Clark 1994, Oyler-McCance and Quinn 2011, Gruber-Hadden et al. 2016, Mussmann et al. 2017, Miller 2018). The majority of past translocations have been to re-establish or augment struggling wildlife populations (Griffith et al. 1989, Seddon 2007). Although the majority have been unsuccessful, there have been several studies that have evaluated translocations and provided information that may increase the probability of success and ensure translocation can be a useful management and conservation tool (Kleiman 1989, Seddon et al. 2007, Baxter et al. 2008, Bell 2011, Seddon 2012). Seddon et al. (2007) estimated that 30% of more recent translocations have been completed with avian species, with special emphasis on Galliformes.

In particular, translocations have been used to manage greater sage-grouse (*Centrocercus urophasianus*; hereafter sage-grouse) populations (Reese and Connelly 1997, Baxter et al. 2008, Stonehouse et al. 2015). More than 7,200 sage-grouse have been translocated during more than 56 events in the last century (Reese and Connelly 1997). Success or failure of translocations has generally been evaluated by reproductive success within the year of release and following years in terms of nest initiation, nest success, brood success, or lek attendance (Baxter et al. 2008). Most sage-grouse translocations have relocated female sage-grouse during the spring pre-nesting period, and have been plagued with low survival rates, low reproductive success, and ultimately little recruitment into the augmented population (Snyder et al. 1999, Seddon and Armstrong 2016). The primary causes of low success rates has been due to large post-release movements and low nest initiation rates of translocated females, resulting in translocated individuals dispersing to undesirable locations and/or experiencing high mortality rates (Duvuvuei et. al. 2017, Prochazka et al. 2017).

Artificial insemination (AI) has been used in wildlife management to maximize genetic retention and increase fecundity in isolated wild and captive populations (Pukazhenthi and Wildt 2004). Success in the reintroduction of the black footed ferret (*Mustela nigripes*), the recovery of the peregrine falcon (*Falco peregrinus*), and goshawk (*Accipiter gentilis*) populations used AI to increase the probability of reproductive success (Berry 1972, Howard et al. 2003). As an example from Tetraonids, Stirling and Roberts (1967) experienced success when enlisting AI protocols in captive dusky grouse (*Dendragapus Obscurus*) populations in British Columbia, and Mathews et al. (2018) tested the efficacy of AI in Columbian sharp-tailed grouse in Idaho.

Our primary objectives were to: 1) develop protocols for semen extraction from male sage-grouse and artificial insemination of females, and 2) assess if individuals that received an AI treatment demonstrated higher nest initiation rates and lower dispersal distances following release into the novel environment within the augmented population. We hypothesized that following translocation and release, individual female sage-grouse receiving AI would show an increase in nest initiation rates, and shorter movement distances.

## **STUDY AREA**

Our research was part of a larger collaborative multi-state effort which

implemented AI on translocated female sage-grouse in two other augmented populations, three total including this study, in other portions of sage-grouse range. The information presented herein will only address the study sites involving translocations from Wyoming to North Dakota during 2017 and 2018. Our study areas occurred in 2 locations, the augmented and source populations (Fig. 4.1).

The augmented study area (i.e., where birds were moved to), was located in Bowman and Slope counties in extreme southwestern North Dakota (46.050780, -104.028600). The augmented study area was on the eastern edge of the Great Plains Sage-Grouse Management Zone (SMZ) (Stiver et al. 2007, Garton et al. 2011). More specifically, our augmented population area can be described as an areas bound by Camp Crook road out of Marmarth, ND, proceed south to Camp Crook, SD, northwest on Tie Creek road to highway 7. Proceed north on highway 7 to Baker, MT, and lastly highway 12 southeast back to Camp Crook road in Marmarth ND.

The Great Plains SMZ was closely tied to populations in extreme southeast Montana and northwest South Dakota (Stiver et al. 2006, Garton et al. 2011). The topography within the North Dakota study site was unglaciated rolling prairie with buttes and intermittent streams. Elevation ranged from 900–1,052 m. Annual precipitation was 36.9 cm with a majority during the months of May and June. Average annual temperatures were 12.7° C and -0.8° C (max = 42.2° C, min = -34.9° C; US Climate Data, 16 Oct 2018). This study site was a mosaic of private, BLM, and state land. Primary land use was energy development, row crop agriculture, and livestock grazing. The landscape was fragmented by gravel roads, oil pads, and power lines. Vegetation in this area was transitional between shrub-steppe and shortgrass prairie. There was a mixture of shrubs with an understory of perennial and annual forbs and grasses, as well as large areas of open grasslands (Johnson and Larson 1999). Within shrub-steppe communities, shrub species included silver sagebrush (*A. cana*), big sagebrush (*A.tridentata*), western snowberry (*Syphocarpus occidentalis*), rubber rabbit brush (*Chrysothamnus nauseosus*), and greasewood (*Sarcobatus vermiculatus*) (Johnson and Larson 1999). The dominant grasses consisted of Kentucky blue grass (*Poa pratensis*), western wheatgrass (*Pascopyrum smithii*), Japanese brome (*Bromus japonicas*), needle and thread (*Stipa comada*), and June grass (*Koeleria macrantha*). Prevalent forbs were common yarrow (*Achillea millefollium*), common dandelion (*Taraxacum officinale*), and textile onion (*Allim textile*) (Johnson and Larson 1999).

The source population (i.e., were the birds came from) occupied the Stewart Creek area in south-central Wyoming (42.068902,-107.611964). The Stewart Creek Area was part of the Wyoming Basin SMZ (Stiver et al. 2007, Garton et al. 2011). More specifically, our source population area can be described as an area bound by US-287 and Mineral Excavation Road (24.30 km from Rawlins Wyoming) proceed northwest to Wamsutter-Crooks Gap Road, north to Jeffery City, then southeast to Muddy Gap on Highway 789 to highway 220 and south to complete the boundary at the intersection of Mineral Excavation Road.

Wyoming Basin SMZ encompassed one of the largest intact sagebrush ecosystems in the world (Connelly et al. 2004). Our source population study site was located in Carbon and Sweetwater counties in south central Wyoming. Elevation ranged from 1,520–2,080 m. Annual precipitation was 23.47 cm with a majority during the months of May and June. Average annual temperatures were  $13^{\circ}$  C and  $-1.5^{\circ}$  C (max =

35.6° C, min = -26° C; US Climate Data, 16 Oct 2018). Landownership was a checkerboard of Private, State, and BLM. Managed livestock grazing in the form of domestic sheep and cattle were the dominant land uses. During this research our Wyoming study site also had numerous feral horses that were relatively unmanaged and can impact sage-grouse (Beever and Aldridge 2011). The area had many graded gravel or four wheel drive two-track roads. Sagebrush (Artemisia spp.) dominated the landscape at this site. Wyoming big sagebrush (A. tridentata wyomingensis) and mountain big sagebrush (A. t. vaseyana) were the most common. Black sagebrush (A. nova) and dwarf sagebrush (A. arbuscula) were found on exposed ridges. Other common shrub species at this site included: antelope bitterbrush (Purshia tridentata), common snowberry (Symphoricarpos albus), chokecherry (Prunus virginiana), alderleaf mountain mahogany (Cercocarpus montanus), rabbitbrush (Chrysothamnus and Ericameria spp.), greasewood, saskatoon serviceberry (Amelanchier alnifolia), and spiny hopsage (Gravia spinosa). Isolated stands of juniper (Juniperus spp.) and quaking aspen (Populus tremuloides) were found at the higher elevations on north facing hillsides.

#### Methods

## **Capture and Marking**

We trapped all sage-grouse at night using all-terrain vehicles (ATVs) with the aid of a spotlight and dip-net (Giesen et al. 1982, Wakkinen et al.1992, Connelly 2003). Upon capture, all individuals were placed in a cardboard box and transported to a central location to be processed. All grouse were fitted with aluminum leg bands, weighed, sexed, aged, and evaluated for general health (Patterson 1952, Eng 1955, Braun and Schroeder 2015). Morphometric measurements were documented for each female and translocated males including: body mass, wing length, tarsus length, and culmen length (USGS 2018). Post-capture, females were fitted with either rump-mounted solar-powered (Geotrak Inc., Apex, NC, USA) global positioning system-platform transmitter terminal (GPS-PTT) 22 g transmitters with 3.5 g glue-on very high frequency (VHF) radios for ground tracking,( Advanced Telemetry Systems, Isanti, MN, USA and Holohil Systems, Ltd., Ontario, Canada) or a VHF necklace style transmitters (22g). Males used as semen donors were held in a cardboard box until processing. At that point, males were aged, sexed, and banded prior to semen collection. After semen was collected, all males were released at their respective lek sites.

A team of veterinarians and assistants from Wyoming Game and Fish Department and North Dakota Game and Fish Department attended all spring translocation events. Veterinarians examined the general health of all translocated sage-grouse. They also took samples from all translocated sage-grouse for disease testing. Samples were taken in the form of saliva cheek swabs and blood samples. Colorado State University Veterinary Diagnostic Laboratory tested for Mycoplasma, Michigan State Veterinary Laboratory tested for Salmonella and Mycobacterium Avium, and Wyoming State Veterinary Laboratory tested for Avian Influenza. There was an agreement with the North Dakota State Board of Animal Health that translocated grouse could be released as quickly as possible prior to researchers receiving disease testing results to avoid holding the birds for an inordinate amount of time, but with the caveat that if any disease test results came back positive then the individual sage-grouse would be immediately tracked down using radio telemetry and euthanized.

#### **Artificial Insemination Procedures**

Semen Collection. — Semen was collected from male sage-grouse as soon as possible and then individuals were released back to their respective leks. After a male was removed from the cardboard box, processed, and banded, we designated a handler and a collector. The handler held the male in an upright position with the bird's head covered. For most males, we used a modified leather falconry hood to help keep the bird calm during handling (Fig. 4.2). If feces were on or around the cloaca the collector cleaned the area with a tissue to prevent contamination of the semen sample. For the first portion of semen collection we focused on the left testes, as it was larger and tended to produce greater number of spermatozoa. The collector would then place their index finger and thumb of one hand on the opposing sides of the cloaca, and their other hand on the bird's rump just behind the tail bulbs.

In a rhythmic motion as gently as possible, the collector would gently massage the bird's cloaca, rump, and abdomen simultaneously. The collector's hand that was massaging the cloaca would then move from the bird's epididymis down to the deferent duct and seminal vesicles moving directly towards the cloaca. While massaging, gentle pinching motions would be used to pull the semen towards the cloaca. Concurrent with the abdominal massage, the collector's other hand would gently rub the bird's rump while moving the other hand down the bird's back towards the cloaca. The collector started below the tail, adjacent to the hips and massaged down over the tail bulbs. As the collector moved over the tail bulbs they would shift the tail back and forth one direction per stroke at least 3 times while gently massaging with both hands for 30 seconds (Burrows and Quinn1935). Immediately following the massage, the collector would

gently evert the cloaca by pinching the outer edges. The everted cloaca would force the ejaculate to excrete along the non-intermittent phallus. Ejaculate was then collected with fire polished micro-capillary tubes (50  $\mu$ l). The tubes were filled via capillary action by placing one tube directly below the semen. At times it was necessary to use multiple micro-capillary tubes to collect all the available semen. Micro-capillary tubes were only filled from one end (Fig. 4.3).

Semen Analysis. — Before dissemination we measured various amounts of water with a pipette and used a ruler to estimate volume. We recorded the size of pipette and volumes to provide information regarding the amount of semen extender needed for storage and the upcoming AI procedure. After semen was collected, we inspected all samples for contaminates. If any samples were found to be contaminated with fecal matter or uric acid they were discarded. We measured the volume of semen using a micropipette in a micro-capillary tube. We then used a microscope to visually assess all samples for semen motility and density. When microscopes were not in use we would place hand warmers (HotHands®, Kobayashi Healthcare Europe Ltd, Chiswick, London) to warm the stage, an attempt to increase the spermatozoa motility during the next assessment. We then categorized the samples for spermatozoa density and motility (Fig. 4.2). We used a categorical estimation for spermatozoa with 1 = 1 to 20, 2 = 21 to 100, 3 = 101 to 200,  $4 \ge 201$  spermatozoa/visual field, and motility 0 = no movement, 1 = slow, 2 = sedate, 3 = steady pace, 4 = extremely rapid. We then used a micro capillary bulb to transfer all the ejaculate of an individual male into a single Eppendorf tube. To preserve the semen we added Lago 6 hour Avian Semen Extender (Hygieia Biological Laboratories Inc., Woodland, CA, USA), at different proportions depending on the

spermatozoa count according to 0-1 spermatozoa count = 1:0.5  $\mu$ l semen extender, 2–3 spermatozoa count = 1:1  $\mu$ l semen extender, 4 spermatozoa count = 1:2  $\mu$ l semen extender, exceptional spermatozoa count = 1:3  $\mu$ l semen extender. When motility classification was in the higher categories we increased the semen extender proportionately.

*Insemination.* — We randomly assigned all female sage-grouse into experimental groups of AI, sham, or control. Females in the control group were inspected for health, blood and saliva samples taken for disease testing, equipped with a transmitter, then returned to their transport box until transferred to the release box at the release site in North Dakota. Sham and AI treatment groups received the same techniques, except only semen extender was given to sham females. Similar to males (above), a modified falconry hood sized for females was used to calm females after they were removed from the cardboard box and during treatment (Fig. 4.2). Prior to removing sham and AI females from their cardboard boxes, we prepared a needle sheath and syringe filled with buffered semen or semen extender only, respectively. For AI females, all semen was used within 8 hours of collection.

We then designated a handler and an administrator. The handler kept the female sage-grouse in a dorsal recumbent position, with the head slightly elevated. The handler also kept constant support of the bird's head throughout the procedure to ensure that the bird did not have labored breathing or undue stress. The administrator then used a nasal speculum to gently open the female's cloaca, being diligent to keep the area clean. It was necessary to be careful not to cause irritation while opening the cloaca and finding the vaginal opening. The vaginal opening was located on the left of the midline within the urodeum, and appeared as a small pink protrusion on the inside wall of the cloaca. The administrator would then insert the needle sheath carefully into the vagina (0.5–1 cm) and slowly press the plunger (Fig. 4.4). We were carful not to apply too much pressure to the tip of the needle sheath and plunger, or the semen (AI) or semen extender solution (sham) would be forced back along the outside of the needle and exit the vagina. Following treatment, the administrator would then slowly remove the nasal speculum. To complete the procedure, the handler would turn the female's head toward the floor with the tail pointing upwards and the administrator would twitch the female's tail back and forth at least 3 times.

*Field Monitoring.*— Female sage-grouse were monitored either remotely via ARGOS-enabled GPS-PTT downloads (http://www.argos-system.org/), or with ground telemetry using VHF signals. We only used ground telemetry to approach within a few meters of marked females to avoid disturbance to nesting or brooding activities. We used VHF signals to triangulate general locations, verify nest initiation, nest success, or mortality. Females marked with VHF transmitters were located weekly or as often as possible with handheld R1000 receivers (Communication Specialist Inc., Orange, CA, USA) and Yagi antennae or by fixed-wing aircraft with telemetry equipment. We located all nesting and brooding females with VHF at least once per week. Nests were considered successful if one or more eggs hatched.

#### **DATA AND ANALYSIS**

We completed chi-square analyses to evaluate if there were any differences in nest initiation during the year of release and a t-test to asses movement within the first 30 days post-release by treatment group. Thirty days post release was approximately the average time for spring translocated females to settle into their new environment. When we calculated the distance traveled per day for GPS-PTT marked females, we used only one location per day. We used all locations from necklace-style VHF marked females translocated in the spring because frequency of locating each individual varied, but was always more than one day between locations. Although we report movement distances for VHF-marked females, only GPS-PTT marked females were compared with each other in the analysis because the temporal resolution of locations was similar (i.e., once per day). These distances may not be exact because as only a proportion of locations they are likely underestimations of actual movement, however they likely provide a valid comparison.

## RESULTS

We trapped and translocated n = 60 female sage-grouse. We translocated n = 40in spring of 2017 and n = 20 in spring of 2018. We performed AI on n = 17 and n = 6, sham on n = 10 and n = 8, assigned no treatment to n = 13 and n = 6 female sage-grouse in 2017 and 2018, respectively. We collected semen from n = 18 and n = 9 male sagegrouse in 2017 and 2018, respectively. During the semen collection process, we found that the massage method consistently produced semen. We also found that massaging while gently pinching the deferent duct was the best way to pull the semen towards the cloaca. Of note, this technique often had to be repeated 3—4 times before a sample could be obtained. Of all translocated females, AI (n = 6), sham (n = 3), and control (n = 4) females initiated nests the year of translocation. Successful nests occurred for 3 of 6 AI nests, 0 out of 3 sham nests, and 2 out of 4 control nests. There were n = 89 eggs throughout 2017 and 2018 nesting seasons. There were n =36 eggs that belonged to AI females, 24 in 2017, 12 in the 2018 season. Sham females had n = 22 eggs in the 2017, 2018 nesting seasons, 10 in 2017, 12 in the 2018 season. The control group females had n = 21 eggs throughout the study, 9 in 2017, 12 in 2018. Successful hatch rates for individual eggs were AI n = 10, 7 in 2017, 3 in 2018. There were n = 7 eggs that belonged to control hens that hatched, 6 in 2017 and one in 2018 (Appendix A). We found no differences in nest initiation rates ( $\chi^2$  = 0.53414, df = 2, P = 0.7656, AI mean = 0.26, SE = 1.20, sham mean = 0.17, SE 0.67, control mean = 0.22, SE 0.87) between treatment groups. We also found no difference in movement between treatment groups utilizing a one way t-test. We did not assume equal variance (F = 1.43, DF = 2.0, 1464.5 P = 0.24, AI mean = 1.27 km/day, SE 0.161 sham mean = 1.75 km/day SE, 0.200, control mean = 1.24 km/day, SE 0.115) between treatment groups.

### **DISCUSSION AND CONCLUSIONS**

We developed protocols for semen extraction from male sage-grouse. We inseminated female sage-grouse within the AI treatment group with said semen. Further research is ongoing which will evaluate the success of the inseminations that occurred. However, we were able to compare nest initiation and movement rates for pre-nesting translocated females assigned AI, sham, or no treatment for our study. Because translocated female sage-grouse placed in novel habitat have been documented to have lower reproduction and survival rates, our research provides important evaluations of methods to mitigate known setbacks when translocating female grouse (Reese and Connelly 1997, Baxter et al. 2008, Taylor et al. 2012, Duvuvuei et al. 2017).

Although we found no differences within our analyses for treatment type affecting nest initiation or dispersal distances post-release, our work provides an important first step into evaluating methods to improve translocations for sage-grouse, and possibly other gallinaceous species. Moreover, our relatively low sample sizes likely impacted our ability to detect differences. Because resident females tend to have higher reproductive success, specifically nest initiation, and much smaller movements during the pre-nesting period than translocated females, research similar to ours may be critical for guiding translocation protocols for future conservation efforts of sage-grouse and other species (Schroeder et al. 1999, Duvuvuei et al. 2017).

Greater distances between the source and augmented populations, and landscape features within the augmented population area that limit movements of translocated individuals have been suggested as important factors for successful sage-grouse translocation efforts in past studies (Baxter et al. 2008, Gruber-Haden et al. 2016). Our release site in North Dakota was over 500 km from the source population in Wyoming, a much greater distance than most sage-grouse translocation efforts (Schroeder et al. 1999, Gruber-Haden et al. 2016, Duvuvuei et al. 2017). However, the release site lacked geomorphic barriers that might have precluded large dispersal distances post-release in other studies (Reese and Connelly 1997, Gruber-Haden et al. 2016). This may explain, at least in part, the large dispersal distances our translocated pre-nesting females moved post-release.

Although we did not compare and evaluate specific methodologies for semen collection and AI procedures, we did gain valuable experience through trial and error during collection from males and insemination of females. We found that expedience and caution needed to be exercised when pinching the cloaca and during the use of the nasal speculum, both procedures can cause discomfort and could potentially cause infection, damage to reproductive organs, or death. Schneider et al. (2019) concluded that the amount of time spent disseminating the male was negatively correlated with the viability of the sample. We found that a good spermatozoa sample appeared to be clear, transparent, and in some cases have a white tint. Accurate estimates of spermatozoa density and motility have been essential for artificial insemination (Christensen et al. 2004). We acknowledge that there may be a need for more intense semen analysis prior to insemination to increase the likelihood of performing successful AI. We encourage further development and assessment of procedures and protocols for evaluating semen samples.

Additional research with larger sample sizes and more in-depth analyses may help illuminate the usefulness of AI as a method for increasing the probability of success for future translocation efforts. We are currently collaborating others and combining data from concurrent studies, which will include larger combined sample sizes and more indepth analysis of movement and habitat selection of translocated females, as well as genetic analyses of eggshell membranes, feathers, and blood of translocated females to evaluate paternity and the overall efficacy of AI. Although we found interesting results indicating little differences between our treatment groups, there may yet be potential for AI to improve the probability of translocation success. Our overall conclusion is that sample sizes reported herein were likely insufficient for conducting a full assessment of AI as a method. At this time, further research is needed before making reliable conclusions concerning AI's usefulness for translocation efforts.

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## **FIGURES**

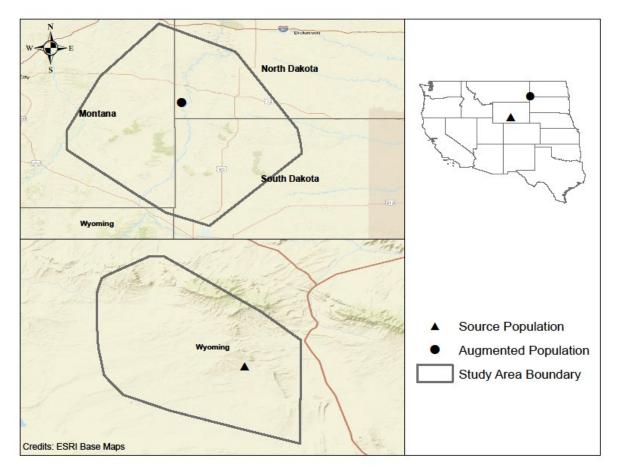


Figure 4.1. North Dakota translocation project study site locations. The translocation of greater sage-grouse (*Centrocercus urophasianus*) included the augmented population (i.e., where grouse were moved to) located in Bowman and Slope Counties in southwestern North Dakota (46.050780, -104.028600) and the source population (i.e., where grouse were taken from) located in the Stewart Creek Area in south-central Wyoming (42.068902,-107.611964). Our two study sites were defined by minimum convex polygons based on radio-marked sage-grouse with 10,594 translocated locations and 9,971 resident locations in North Dakota and Wyoming, respectively, 2017-2018.



Figure 4.2. A modified falconry hood placed on a male sage-grouse (*Centrocercus urophasianus*), and portable laboratory. Hood is to help keep the bird calm during handling. Researchers in the background were analyzing collected semen prior to insemination of a female sage-grouse. Photo credit: Noppadol Paothong.



Figure 4.3. Greater sage-grouse (*Centrocercus urophasianus*) ejaculate being collected with fire polished micro-capillary tubes (50  $\mu$ l). When necessary multiple micro-capillary tubes were used to collect all the available semen. This photograph was taken immediately following the massage method where the collector everted the cloaca by gently pinching the outer edges and forcing the ejaculate to excrete along the non-intermittent phallus. Photo credit: Noppadol Paothong.



Figure 4.4. Insemination of female Greater sage-grouse Greater Sage-grouse (*Centrocercus urophasianus*) prior to translocation to North Dakota, 2017. The administrator would carefully insert the needle sheath attached to a syringe into the vagina approximately 0.5–1cm deep and slowly press the plunger being careful to not apply too much pressure, ensuring the semen (AI) or semen extender solution (sham) would not be forced back along the outside of the needle sheath and exit the vagina. Photo credit: Noppadol Paothong.

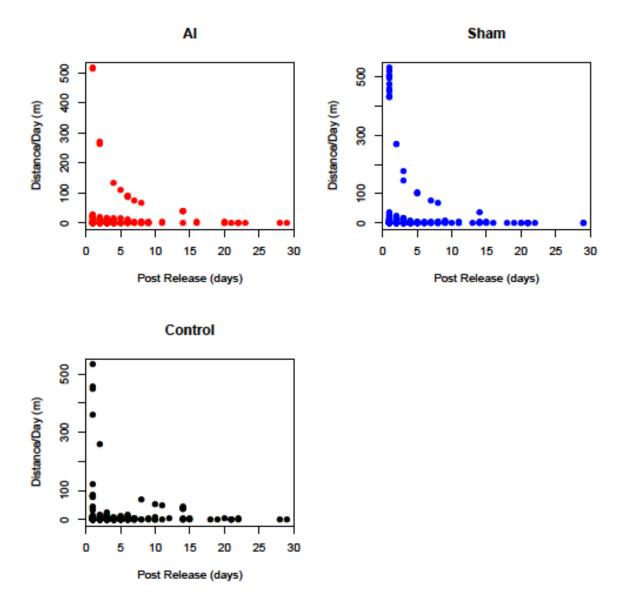


Figure 4.5. Female Greater sage-grouse (*Centrocercus urophasianus*) movements post translocation to southwest North Dakota in 2017 - 2018. These data represent 30 days post release. These data also display the consistency between treatment groups as well as the tendency to settle around 30 days post release.

## CHAPTER 5

### CONCLUSIONS

This project was a collaborative effort that involved U.S. Geological Survey (USGS) Western Ecological Research Center, North Dakota Game and Fish Department, Wyoming Game and Fish Department, and Utah State University. The overall translocation methods in this project were modeled after Baxter et al. (2008, 2013). The North Dakota Game and Fish Department provided the bulk of funding, conducted preproject planning, and their biologists joined in trapping and monitoring of translocated grouse during and after translocations. Wyoming Game and Fish Department also provided funding, in-kind support, and helped with trapping efforts. USGS provided key oversight, data management, and personnel field time.

We monitored the source and translocated populations in 2017 and 2018. Throughout the project we have taken an adaptive management approach (Allen and Garmestani 2015). We first implemented spring translocation protocols (Reese and Connelly 1997) with Rodgers (1992) release methodology. We then utilized and assessed artificial insemination as means to decrease post-translocation movement, and increase propensity to nest. Furthermore, in 2018 we introduced brood translocations (Chapter 3). We provided resource selection function of the nesting, brooding, and summer nonreproductive sage-grouse to better inform any future translocations in this area (Chapter 2).

#### **Review, Recommendations, and Conclusions**

Chapter 2.— We created a resource selection function (RSF) during nesting,

brooding, and summer non-reproductive seasons. Our primary objective therein was to determine the best release locations for future translocations of sage-grouse into North Dakota. We used translocated sage-grouse locations to examine habitat selection based on seasonal and spatial variation. Secondarily, we also examined the difference in shrub cover from 1987 to 2018 based on data provided by Rangeland Analysis Platform (RAP) to better understand changes to sagebrush habitat in our study area. We hypothesized 1) that sage-grouse selection would be closely tied to sagebrush cover and mesic habitat, and 2) that shrub cover decreased from 1987 to 2018.

All three samples (i.e., nesting, brooding, and non-brooding) of radio-marked grouse showed variation in selection. Nesting females selected nesting habitat with the highest percentage of shrub canopy cover closer to mesic sites, open water, and farther away from roads. The relationship to roads was not linear and the highest probability distance from roads that sage-grouse started to select for was ~200 m. Aspect, slope, and elevation all had weak interactions within our model. Brooding female sage-grouse in our augmented study area selected for areas farther from roads and mesic habitats. We detected that ~ 9 % shrub canopy cover is the amount of cover that brooding female sage-grouse selected for, and as canopy cover increased above 9 % the selection began to decrease. Sage-grouse displayed little to no selection regarding other geographic variables. In the summer non-breeding sage-grouse displayed selection closer to northern aspect, with less than 10% slope, and lower elevation throughout the summer. Sage-grouse began to select for habitat ~ 700 m away from open water sources.

Percent shrub canopy (i.e., sagebrush) cover decreased from 1987 – 2018. We found that in the nesting period as shrub canopy cover decreased there was a proportional

increase in selection for shrub canopy cover. We found that during the brooding period there was a decrease in shrub canopy cover from 1987 – 2018, and sage-grouse selection for shrub cover also decreased. Similar to the brooding season, in the summer season for non-breeding grouse we found that with a decrease in shrub canopy cover from 1987 – 2018 sage-grouse selection also decreased.

*Chapter 3.*— We introduced brood translocations as an alternative to spring translocations. This was first initiated by USGS in other study areas. We translocated 6 brood females and 26 chicks as brood units. To quantify the efficacy of brood translocations we looked at chick recruitment, movement, and survival. We observed lower movements in the brood translocations compared to the spring translocations. We added improvements to the translocation-release box and the acclimation pen design. Notably, a smaller acclimation pen with a larger opening was preferred in contrast to a larger pen with a small door. We also found that releasing the broods in the same locations each time may cause avian predators to key in on release sites. We suggest that further consideration of chick age when translocated is needed. However, based on our preliminary data we suggested that between 7-14 days post hatch may be the most advantageous time for translocations. Although there are still many variables that need to be tested and improved upon, we strongly suggest that brood translocations may be a valid way to increase the probability of success for future translocations.

*Chapter 4.*— We introduced artificial insemination (AI) methods, using methods designed by Mathews et al. (2018). We performed AI on n = 23 sage-grouse with the hypotheses that we could increase nest initiation and decrease post translocation movements. When we compared all treatment groups (AI, sham, and control) we saw

little difference in distance traveled per day or the propensity to nest between the treatment groups. However, our data will be combined with two other concurrent studies in Utah and California. We have not received the genetic analysis to determine the efficacy of AI on parentage from blood, feather, and shell samples. AI is a novel and innovative procedure, with some manipulation AI may be a way to increase genetic variability without creating additional negative impacts on the source population. In addition to our work, we suggest that the AI procedure be tested for efficacy in a stable population.

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APPENDIX

			2017	2018 Comments
		AI Females		
		Placebo Females	10	
		Control Females	13	
Spring	BL.	Adult Males		18
		Yearling Males		
		Total Males	21	
		Total Females	40	20
	Brood 1 (pre-tag)			
Translocated	5	Chicks ( age = weeks)		
Sage-Grouse	Brood 2 (source)	Chicks (#)		
		Chicks ( age = weeks)		0.43 3 days
	Brood 3 (source)	Chicks (#)		
		Chicks ( age = weeks)		2.14 15 days
		Chicks (#)	NA	5
Brooding	ding brood 4 (pre-tag)	Chicks ( age = weeks)		1.14 8 days
		Chicks (#)		
	(IIIIODIIA) C DODIG	Chicks ( age = weeks)	NA	4.14 30 days
	Ducod C (Doudom)	Chicks (#)	NA	
		Chicks ( age = weeks)	NA	5 35 days
		Chicks (#)		
		Total Number of Chicks	NA	26
		Total Number of Brood Females	NA	9
Female	Females that initiated a nest Translocation Year	nslocation Year	8/40(0.2%) 9/20(25%)	9/20(25%)
Female	Females that initiated a nest Post-Translocation Year	t-Translocation Year	NA	NA 4/40(10%)
Succes	Successful Nests from Translocated Females	ed Females (proportion)	3/8(38%)	3/20(15%)
Female	Females that Survived Nesting season	ason	20/40(50%)	26/60(43.3%)
Female	Females that Survived Brooding season	season		~
Female	Females that Survived to next breeding season	eeding season	5/40(12.5%)	3/60(5%) This may underepresent VHF, because there has been no 2019 data collection
Al fem	AI females that initiated a nest ()		5/8(62%)	1/5(20%) based on the 5 nests innitiated by 2018 translocations
Placeb	Placebo females that initiated a nest ()	nest ()	1/8(12%)	2/5(40%)
Contro	Control females that initiated a nest ()	lest ()	2/8(25%)	2/5(40%)
total n	total nest innitiation		∞	01
innitati	innitation following year		ΝA	Ω
Males Survival	Males survived first summer post translocat	t translocation	8/20(40%)	9/20(45%)
	Males survived to next breeding season	season	4/20(20%)	5/20(25%) December is the last data we have
Al nest	Al nests - % of eggs that hatched		7/24(50%)	3/12(25%)
Placeb	Placebo nests - % of eggs that hatched	tched	0/10(0%)	0/12(0%) 2018, n=12
Contro	Control nests - % of eggs that hatched	tched	(%99)6/9	1/12(8%) 1, 2017 unsuccessful nest had an unknown clutch size 2018,n=13
Total %	Total % hatched		18/33(55%) 12/55(22%)	12/55(22%)
	Brood 1 (pre-tag)	Survival >= 50 Days (Y/N)	AN	
	Brood 2 (source)	Survival >= 50 Days (Y/N)	NA	N
	Brood 3 (source)	Survival >= 50 Days (Y/N)		
	Brood 4 (pre-tag)	Survival >= 50 Days (Y/N)		N
	Brood 5 (random)	Survival >= 50 Days (Y/N)		
	Brood 6 (random)	Survival >= 50 Days (Y/N)	NA	
		Total Number of Chicks that Survived >= 50 days		5
Numbe	Number of VHF Female (Non-Brood) Locations	ood) Locations	170	191
Numbe	Number of GPS Female (Non-Brood) Locations	ood) Locations	6367	3142
Numbe	Number of Male VHF Locations		95	272
Locations Numbe	Number of VHF Brood Locations		45	55
Numbe	Number of GPS Brood Locations		202	55
Numbe	er of Males in ND or within	Number of Males in ND or within 15 miles of the border end of Summer	4	2
Nimhe	ar of Females in ND or with	Number of Females in ND or within 15 miles of the horder end of summer	Ľ	۲.

# APPENDIX A SUMMARY TABLE

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