Statewide Moose Habitat Project:

Linking Habitat and Nutrition with Population Performance in Wyoming Moose

Annual Report 2012

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Background & Objectives

The Wyoming Game & Fish Department (WGFD), Wyoming Cooperative Fish and Wildlife Research Unit, and the University of Wyoming initiated the Statewide Moose Habitat Project in June 2011. Currently, Shiras moose (*Alces alces shirasi*) herds in the state (Fig. 1) are exhibiting a wide range of population performance (Fig. 2), with some declining (e.g. Jackson, Snowy Range, North Park, CO) and some relatively stable (e.g. Sublette, Uinta) or increasing (Bighorns). For the declining herds, potential mechanisms that may affect carrying capacity are habitat deterioration due to current and historic overbrowsing (Fig. 3; Boertje *et al.* 2007; McArt *et al.* 2009), and regional variation in forage quality due to climatic warming and drying (Monteith *et al.* in prep) or other disturbances, such as large, intense wildfire (Vartanian 2011) or bark beetle (*Dendroctonus* spp.) outbreaks. Additionally, a new and growing predator community is present in the northwest corner of the state and may prevent higher recruitment rates from being achieved, but these predators can not account for declines elsewhere in Wyoming, Colorado, and Utah. Further, a newly emergent disease, the carotid artery worm (*Elaeophora schneideri*), appears to be prevalent in Wyoming (Henningsen *et al.* 2012). Unfortunately we do not yet understand the impacts of this disease on the nutritional condition and survival of moose.

In combination with the observed range in population performance (Fig. 3), variability of moose habitat (see Vartanian (2011), Monteith *et al.* in prep) in the state represents a timely opportunity to evaluate habitat-performance relationships (i.e. local carrying capacities). Such a statewide habitat evaluation could serve as a benchmark to understand the relationship between moose habitat and population performance and would provide the WGFD with "early warning" metrics to predict where and when declines are likely to occur, and would improve the scientific basis of moose population objectives.

This project aims to both understand the role of habitat and nutrition in recent declines in population performance as well as provide managers with adaptive management tools. Therefore, we have developed the following objectives:

1. Understand the relationship between resource limitation and herd productivity.
2. Establish meaningful browse condition indices for monitoring and management purposes.
3. Explore alternative 'early warning' metrics to preempt declines in herd productivity.

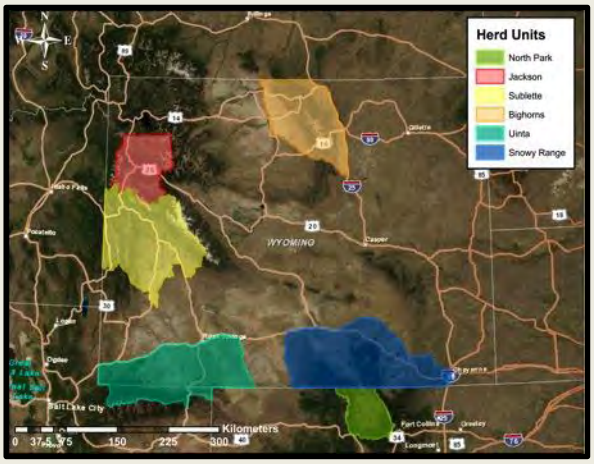


Fig. 1- Map depicting the project study areas.

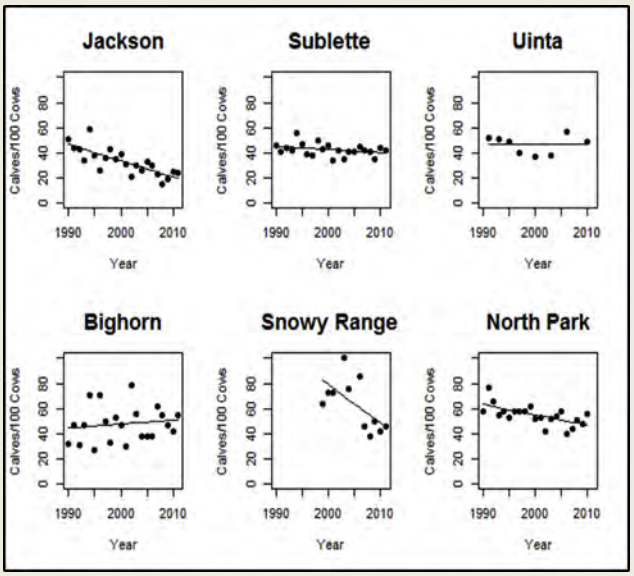


Fig. 2 – Trends in calf-cow ratios from 1990-2011 across our six areas.

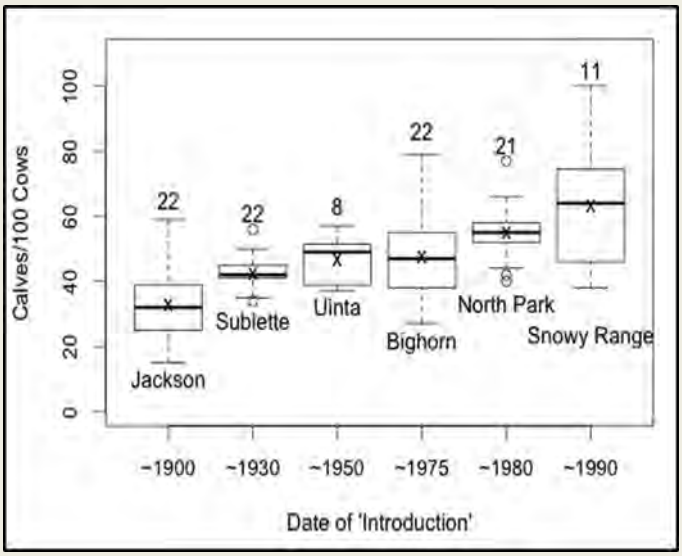


Fig. 3- Variation in recruitment across the six study populations from 1990-2011 with respect to date of introduction (i.e. herd age). Thick horizontal lines represent medians, boxes are upper and lower quartiles, x's equal means, whiskers depict the data range minus outliers (open circles), and numbers above whiskers equal sample size.

Research Design & Methods

Vartanian (2011) concluded that **winter-range** was non-limiting to the Jackson moose population because of the underutilization of 'peripheral' winter-ranges that were previously described as heavily used by Houston (1967). Therefore, we used stratified random sampling across core (red) and peripheral (blue) winter ranges (both ranges defined as areas available to overwintering moose) to characterize the extent of willow browse utilization in each of six study areas. To quantify **winter habitat condition**, we used the WGFD Wildlife Observation System (WOS) moose location dataset and a local convex hull (LoCoH) home-range estimator to calculate core (%50 herd-range; red) and peripheral (%95 herd-range; blue) herd-ranges (Figs. 4, 5 and 6). Only WOS location data collected between January 1 and March 31 from 2000 through 2010 was used in herd-range analyses. Sufficient location data was only available in four herd units: (1) Jackson, (2) Sublette, (3) Uinta, and (4) North Park.

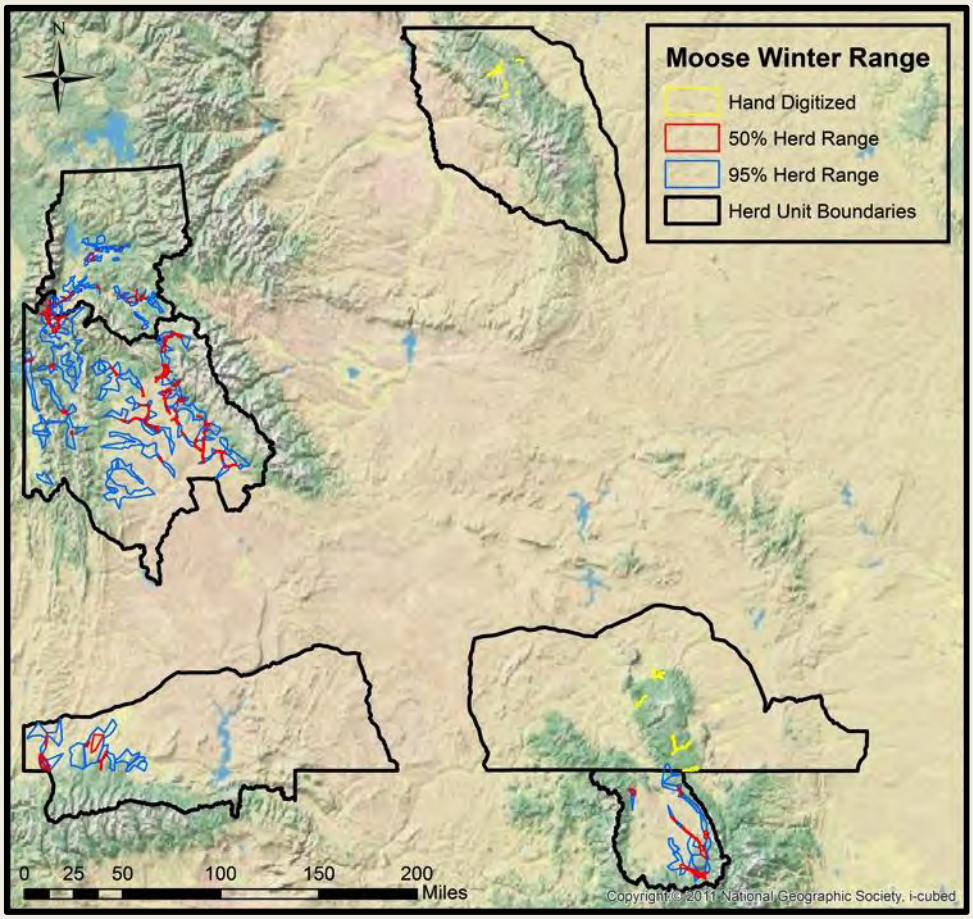


Fig. 4- Distribution of core (50%; red), peripheral (95%; blue), and hand digitized (yellow) moose winter ranges across the six study areas. Note- not all core and peripheral areas displayed here were sampled (see pg. 5 for details).

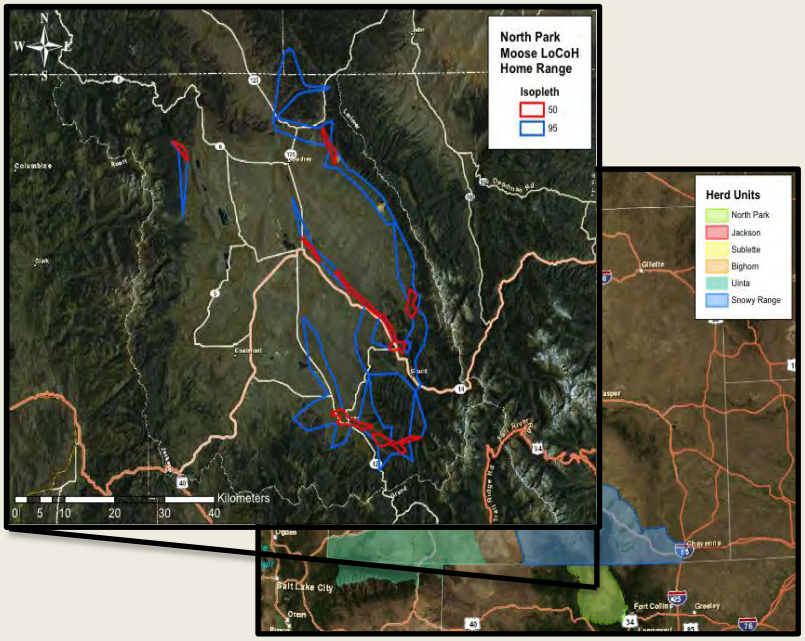


Fig. 5- In each herd unit, such as North Park (shown here), core (red) and peripheral (blue) moose habitat was identified to guide sampling of willow browse conditions and scat (see pg. 5 for details).

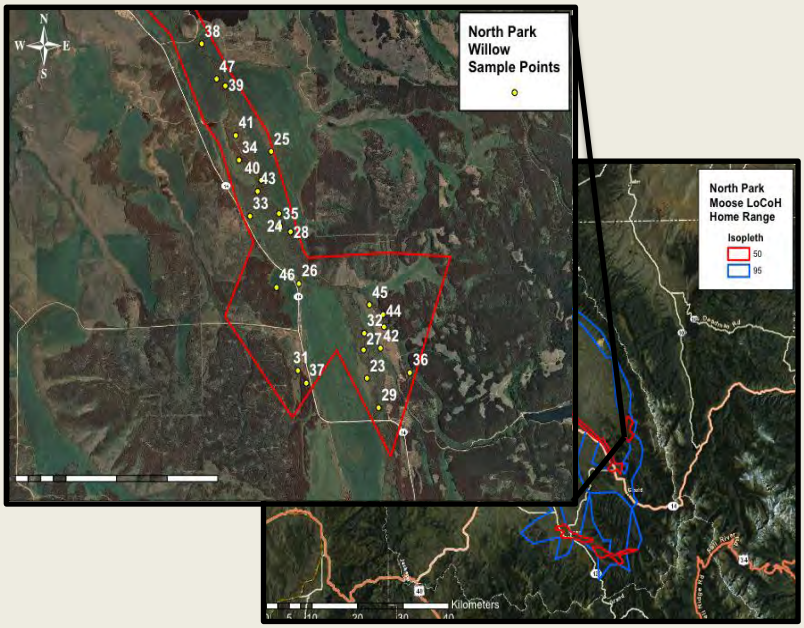


Fig. 6- Within each core and peripheral range, such as North Park's Michigan River (shown here), randomly generated points were drawn in willow habitat to prevent observer bias (see pg. 5 for details).

Adequate location data was unavailable to calculate herd-range polygons in two herd units: (1) Snowy Range and (2) Bighorn. When location data was unavailable to generate core- and peripheral-ranges using a home-range estimator, we developed boundaries comparable to LoCoH herd-ranges by hand-digitizing willow habitat using the National Land Cover Database (NLCD; Figs. 8 and 9). We delineated winter ranges by calculating a probability-of-use surface using the winter resource selection function (RSF) of Baigas (2010; Figs. 7 and 9). The RSF was reclassified into 25% quantiles. The 75-100% (red) quantile area was considered winter core-area, the 50-75% quantile (orange-yellow) was considered peripheral-area, and areas with <50% probability of use (blues or no color) were considered unavailable to moose.

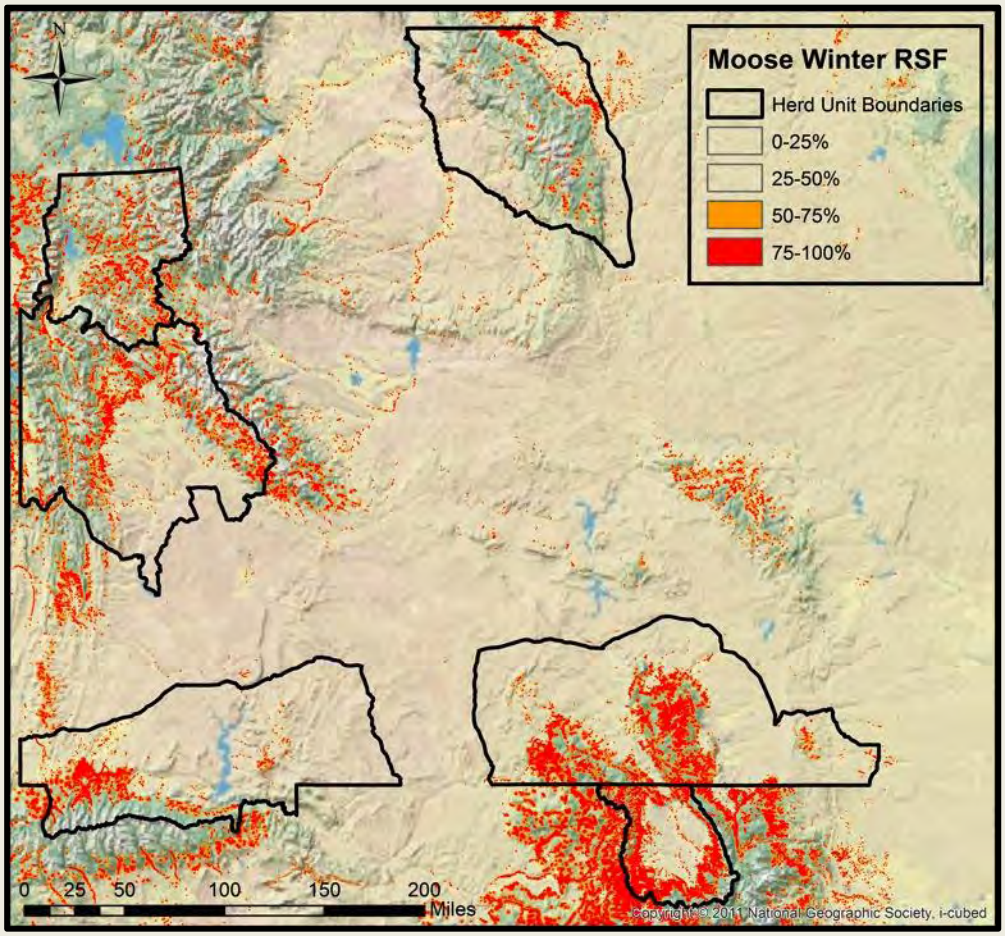


Fig. 7- Resource selection function (RSF) of Baigas *et al.* 2010 applied to Wyoming, northern Colorado, and northern Utah.

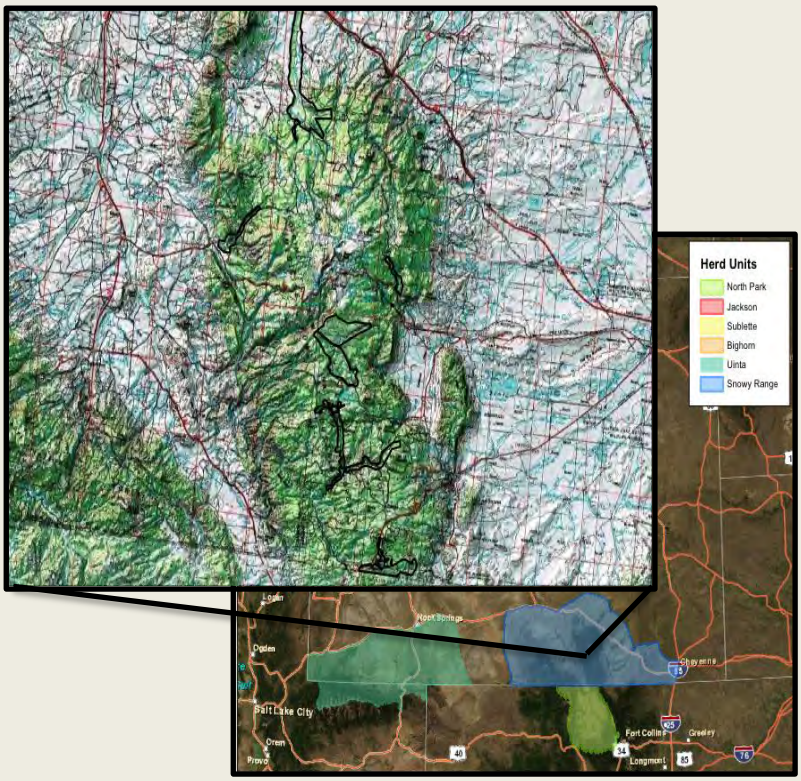


Fig. 8- In some cases, such as the Snowy Range (shown here), we had to hand digitize willow habitat in order to guide our field sampling.

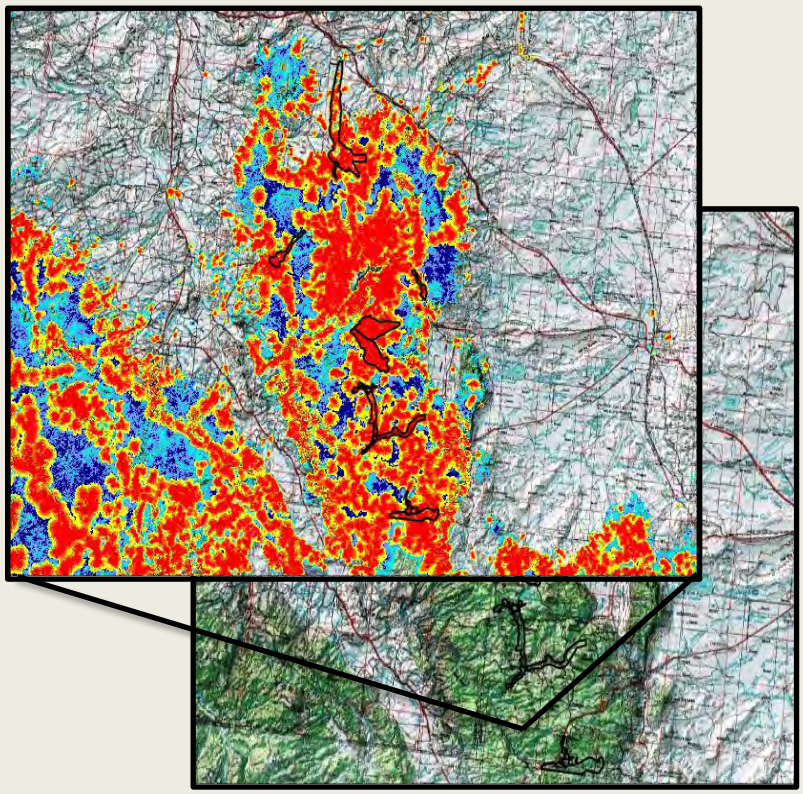


Fig. 9- To determine whether a given willow patch fell with a core or peripheral area, we used a probability of use according to the RSF of Baigas *et al*. (2010) to guide our categorization.

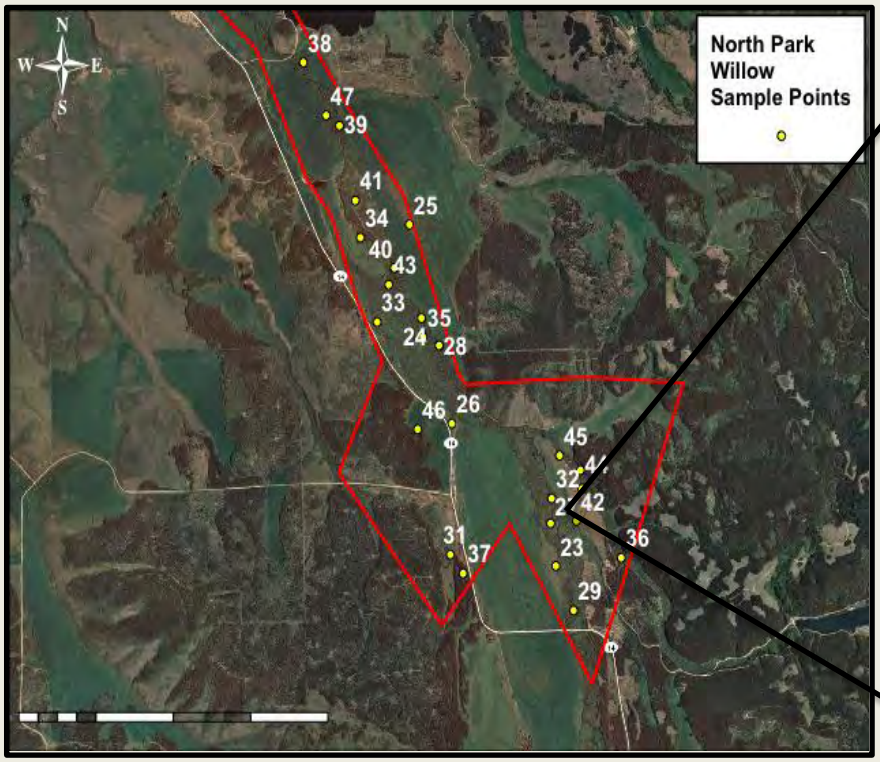


Fig. 10- Map depicting randomly generated sample sites in willow habitat along the Michigan River, Jackson County, CO.

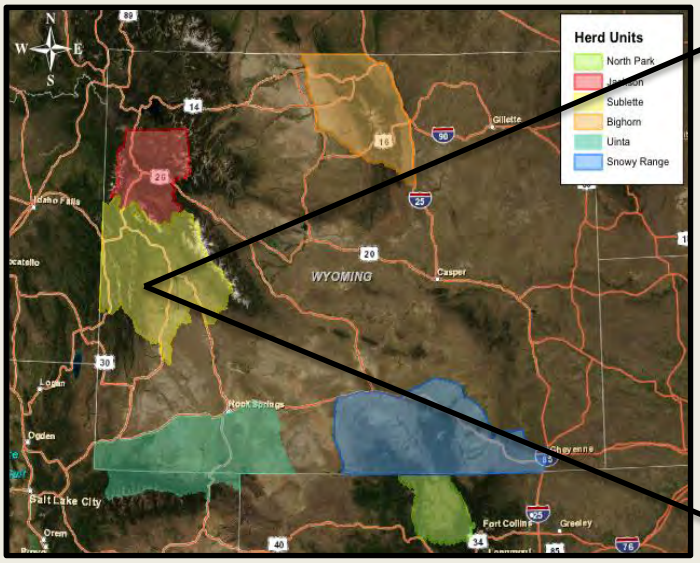
Fig. 11- Technician**,** Allie Hunter, takes an LD reading along Spread Creek, Teton County, WY.

Within core and peripheral ranges we plotted random points with a minimum of 200m spacing between points using the generate random points tool in ArcGIS (Fig. 10; ESRI 2011; analysis tools). Using the NLCD we calculated sampling weights by determining the proportional amount of willow habitat in each polygon (i.e. drainage) per herd unit using the tabulate area tool in ArcGIS (ESRI 2011; spatial analyst tools); meaning drainages with relatively greater amounts of willow received greater number of sampling points. Financial and logistical constraints determined that 30 live-dead (LD; measure of willow condition; Keigley and Fager 2006) transects could be accomplished per herd unit. Therefore, we multiplied the proportion of willow (i.e. sampling weight) in each of the six drainages per herd unit by 30 to calculated the final number of transects per drainage. Final sample sites were chosen in the sequential order that they were generated in GIS. However, in some cases a lack of land owner permissions or accessibility via snowmobile and snowshoes inhibited us from sampling in exact sequential order.

At each of 188 (when time permitted we completed additional transects) sampling points across the six study areas we completed LD transects (Fig. 11). According to previously established protocols (see Keigley and Fager 2006; Vartanian 2011; Smith et al. 2011) 20 willow plants of the most preferred species (planeleaf willow (*Salix planifolia* in the eastern herds, Booth's willow (*Salix boothii*) in the western herds, and Drummond's willow (*Salix drummondiana*) when present in Uinta) were measured along a random bearing every 20m starting at a given sampling point. LD, leader length, and percent browse were recorded at each plant.

To assess **winter diet** (i.e. foraging behaviors) and identify important **winter forages**, we collected scat samples along LD transects when present (Fig. 12) according to a sterile protocol developed to eliminate cross contamination, and we only collected scats that appeared to be fresh and were determined to have originated from an adult moose according to morphometrics (i.e. size). Using molecular techniques we will group scat piles by individual and determine sex prior to diet analysis (via microhistology) and **pregnancy** analyses (via hormones; progestagens; Monfort et al.1993; Cain et al. 2012), and potentially assess nutritional state (nourished vs. malnourished) via additional hormone (triiodothyronine (T3)) assays (Wasser et al. 2010). Progestagen and T3 thresholds will be validated using scats collected during the Jackson and Sublette moose studies in combination with serum-based pregnancy specific protein B and ultrasonography.

Fig. 12- Scats found along North Horse Creek, Sublette County, WY.



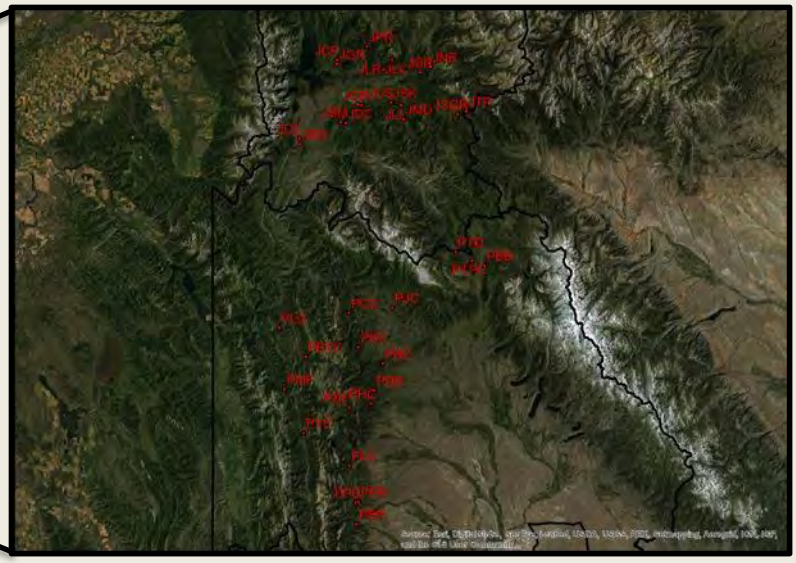


Fig. 13- Map depicting randomly generated sample sites across different habitats where summer scats were sampled in Sublette and Teton Counties, WY.

To characterize the range of **diets** (i.e. foraging behavior) and the **quality of forages** used by moose on **summer ranges**, we once again employed a stratified random sampling design. Due to the widely-reported preference for riparian and upland shrub forage amongst moose inhabiting montane regions of North America (Renecker and Schwartz 2007), we chose two strata consisting of: (1) willow habitat, and (2) all other upland habitat types (i.e. deciduous forest, coniferous forest, mixed deciduous and coniferous forest, shrub-scrub, grassland-herbaceous, and emergent herbaceous wetlands) as defined by the NLCD. We used a generalized random tessellation stratified (GRTS; Stevens and Olsen 2004) sample generator (R; spsurveyGUI package) to develop a spatially-balanced random sample across the two strata (Fig. 13). To ensure that our scat-dog teams found as many fecal samples as possible, we restricted our search effort across strata to the top 25% quantile (summer core area) of Baigas *et al*. (2010) summer RSF model. Logistical and financial constraints determined that 20 transects (10 willow, 10 upland) per herd unit (i.e. n=120) could be completed within a single season. We chose sampling points in sequential order from which they were drawn until 10 samples from each strata were established using the following criteria: (1) < 1500m from a drivable road due to the limited distance in which a working dog can travel on any given day, (2) the willow patch must have been ≥ 2000m in Euclidean length, and (3) the upland patch was within a logistically feasible proximity (daily travel distance) to another sampling point (willow or upland) whereby we could complete two transects per day. Each transect started at, or intersected with, the sampling point.

We collected moose scats along each transect when present (see figs. 14 and 15) using a sterile protocol. Currently, we are extracting DNA from scats (see pg. 7) to determine individuality prior to diet analysis via microhistology.

Fig. 14- Map illustrating a scat transect (5-6 km each) in willow habitat. Kilgore Creek, Sublette County, WY.

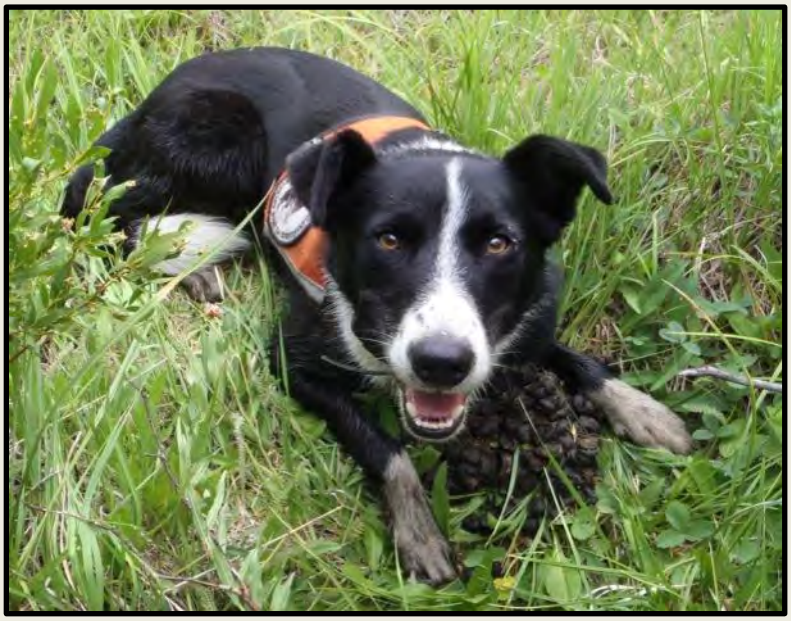
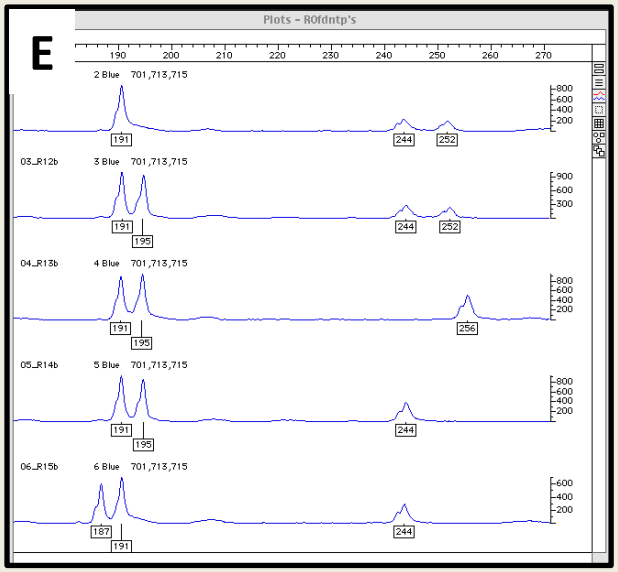


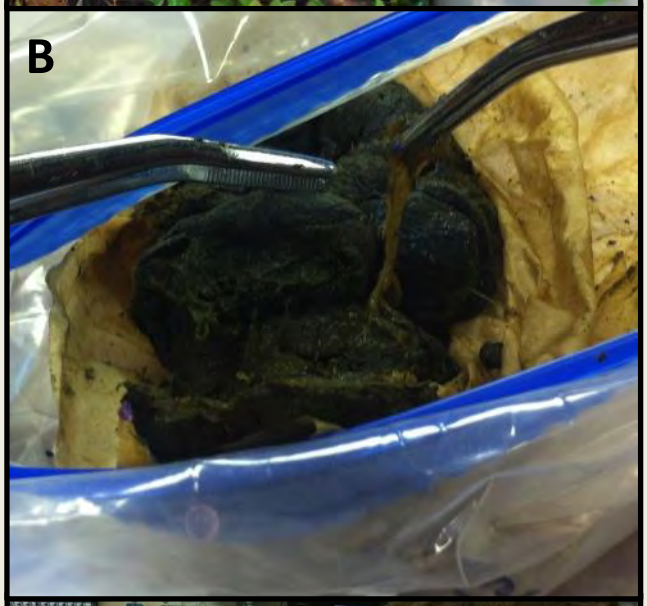
Fig. 15- Orbee the detection dog is very proud of his find (mostly he just wants his reward; a short game of fetch with a ball).

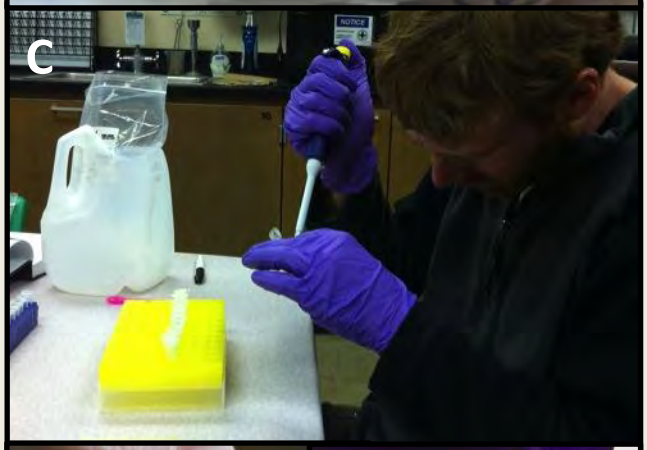
Only ‘fresh’ (i.e. typically <1 week old) scats were collected along each transect. When a fresh scat was identified, approximate age, GPS location, and habitat information was collected. The scat was then wrapped in non-bleached filter paper (coffee filters) and placed inside a plastic freezer bag on a bed of silica desiccant (photo A). The desiccant removed moisture from the scat during the day while we were in the field to help reduce bacterial action which degrades genetic material. Scats were placed in a portable battery/propane-powered freezer immediately upon returning to the campsite; followed by a cryofreezer once returning to the University of Wyoming.

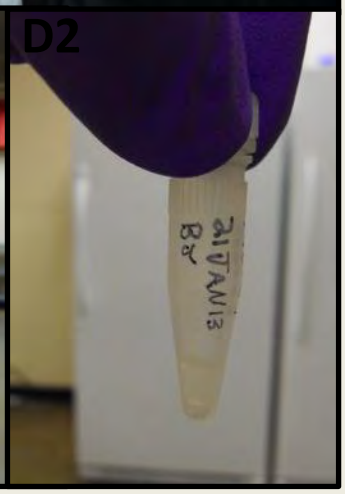
Most of the DNA in moose feces is found in a ‘mucusy membrane’ on the outside of the ‘pellets’ where intestinal cells are sloughed off as the pellets move through the intestinal track. We collect portions of this ‘mucusy membrane’ (photo B) and place in vials with a substance that breaks down cell walls to release the genetic material (photo D1). We used a modified ‘ungulate’ DNA extraction protocol tailored specifically for moose scat in combination with Qiagen- QIAamp DNA stool mini kits© to obtain purified DNA products (photo D2).

Through a series of chemical reactions (photo C) we duplicate the DNA many times over and characterize eight specific portions of the genome that allow us to ‘fingerprint’ the sample so that we can tell which individual the scat came from (photo E; example from river otter; credit Dr. Merav Ben-David). For example, photo E depicts five distinct individuals identified by variation in ‘peaks’ across specific portions of the genome. We also look for a specific area on the Y-chromosome (only found in males) to determine the sex of the individual. Finally, species identification is determined by analyzing a specific portion of the mitochondrial DNA. This process is extremely similar to that used by criminal forensic scientists and has been streamlined so that individual, sex, and species identifications can be assessed simultaneously.





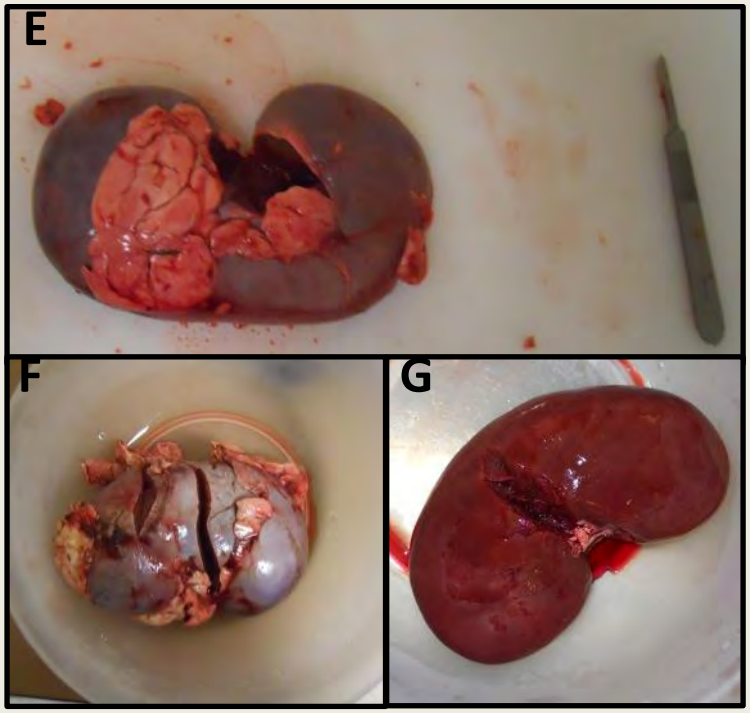


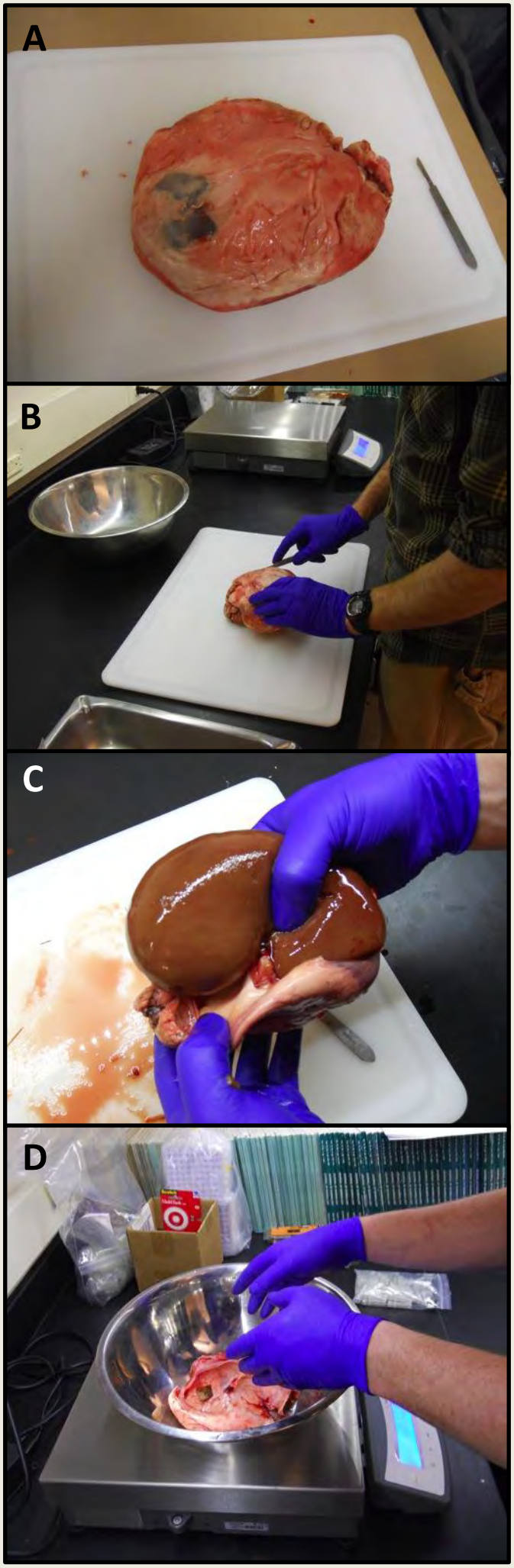


To understand how winter habitat condition and quality, and summer forage quality affect the **nutritional condition** of moose, we are measuring autumn kidney fat. The amount of fat found attached to the kidney is a good predictor of total body fat in moose (Stephenson *et al*. 1998). We collaborated with the WGFD and the Colorado Division of Parks and Wildlife (CDPW) to solicit hunters to collect kidneys from their harvested moose. With each kidney hunters and WGFD and CDPW biologists noted sex, age, location of harvest (hunt area and drainage or GPS location), antler size (if any), and parasite information.

Kidneys were gathered by regional WGFD and CDPW personnel and delivered to the University of Wyoming where we measured kidney fat levels according to the long-standing method of Riney (1955). Briefly, the kidney fat method requires an undisturbed kidney (photo A; identification of disturbed kidneys described below), trimming of excess fat to standardize the area of fat measured (photo B), removal of the fat and perirenal (kidney) membrane (photo C), and a weight measurement of both the kidney and the kidney fat (photo D).

While processing each kidney, we noted whether or not the kidney and its fat appeared to be disturbed. Because some hunters are unfamiliar with moose anatomy and the exact location of the kidneys, they sometimes cut through visceral fat too quickly and end up cutting into the kidney fat (photo E) and even the kidney itself (photo F); and sometimes hunters even mistakenly removed all of the kidney fat (photo G). We omitted all samples from the final dataset that showed evidence of the fat being disturbed.





Preliminary Results

All results constitute preliminary summaries, not final statistical analyses, and should be interpreted with caution. Additionally, the data presented here only reflects autumn nutrition of moose and winter habitat condition (i.e. quantity of forage). Because winter habitat condition is only one of many factors that may influence autumn nutritional condition in moose (Parker *et al*. 2009), these trends may be strengthened or weakened once winter and summer diet and forage quality are included in the dataset. In fact, due to metabolic demands, summer forage quality is often considered to be more important to overall nutritional condition and pregnancy rates than winter forage condition or quality (Cook *et al*. 2004). It is also important to note that we only present nutritional condition data associated with male moose. The current and past (i.e. 1-2 years prior) reproductive history of all harvested female moose from which we received kidneys was unknown. The energetic demands associated with gestation, lactation, and calf rearing are important factors in determining autumn nutritional condition, and therefore likelihood of pregnancy, in ungulates (Parker *et al.* 2009). Consequently, we chose to use males as our indicator of nutritional condition at the population level because they are not influenced by as many factors as females. Even though males do not represent the reproductive portion of the population, and therefore have less influence of population performance, their nutrition condition remains an excellent indicator of habitat quality (Parker *et al*. 2009).

We found that nutritional condition was significantly different between the six herd units (Fig. 16; ANCOVA: P=0.027; see fig. 3 for description of symbols; note small sample size in Jackson). Willow condition according to the LD index was also significantly different amongst herd units (Fig. 17; ANOVA: P=<0.001). Interestingly, in 2008 Baigas reported to the WGFD even lower LD values for plane leaf willow. Also, we found that LD values for plane leaf willow and Booth's willow differed (T-test: P=<0.001). However, at this point we are unsure whether this is a result of differences between herd units or simply a difference in moose preference relative to the willow specie's availability. And lastly, browse intensity was strongly different between herd units (Fig. 18; ANOVA: P=<0.001).

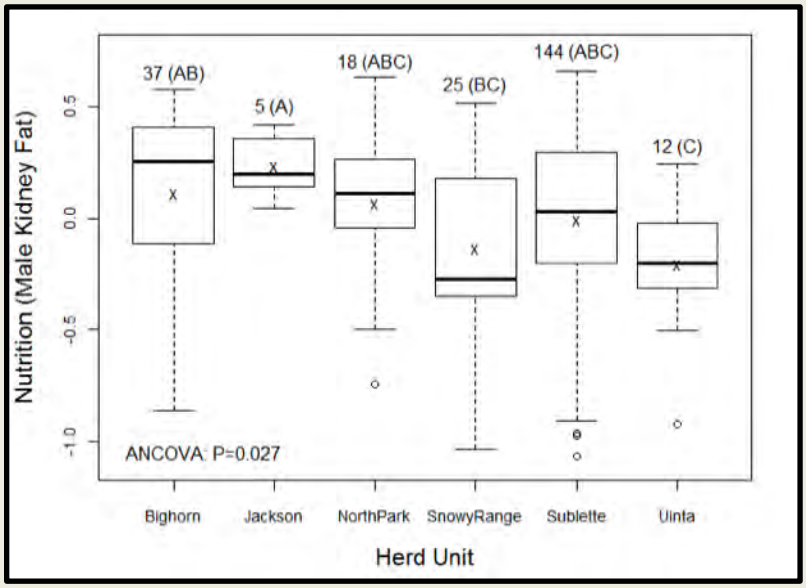


Fig. 16- Variation in male nutritional condition. Herd units with the same letters are statistically similar.

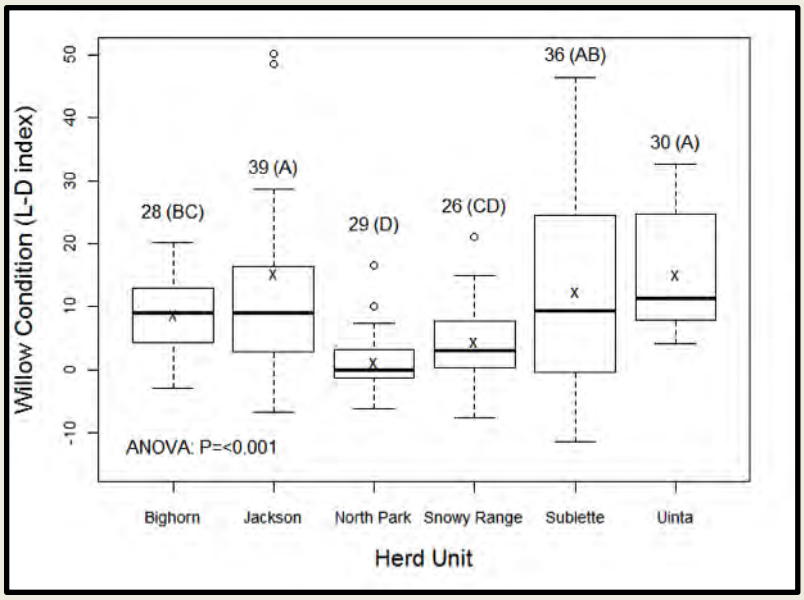


Fig. 17- Variation in willow condition. Herd units with the same letters are statistically similar.

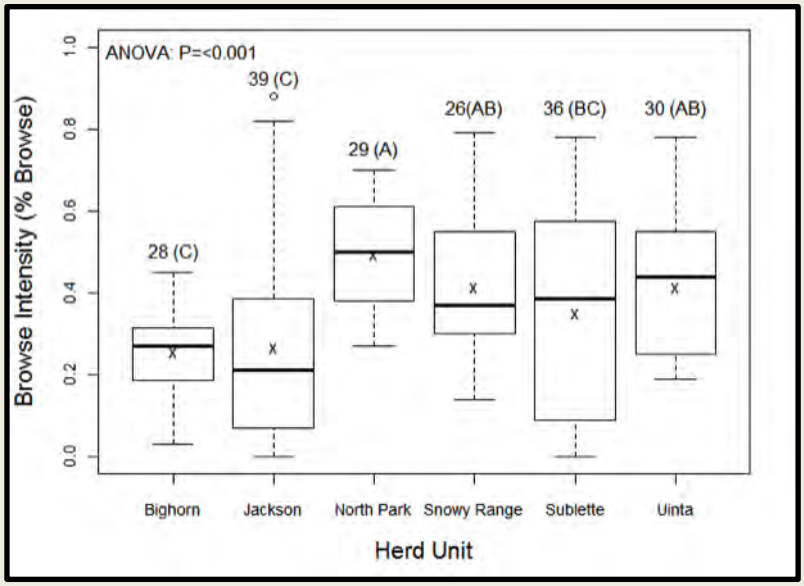


Fig. 18- Variation in willow browse intensity. Herd units with the same letters are statistically similar.

We further summarize the data using the means (x's) from figures 16-18 to assess the general relationships between winter forage condition, nutritional condition, and population performance (i.e. recruitment rates). Figure 19 indicates a weak positive relationship between winter willow condition according to the LD index and autumn nutritional condition. Figure 20 reveals that a browse intensity measure may be a better indicator of winter-range constraints on autumn nutritional condition. Finally, figure 21 suggests that male nutritional condition in autumn is likely a good indicator of local population performance. Being able to partially identify factors influencing population performance using winter willow condition alone is an encouraging result. We suspect that we will be able to make strong linkages between habitat and population performance in most herd units once we assess summer and winter forage quality.

Future Work

We continue to work towards achieving our objectives in 2013 and suspect to complete the project during the summer of 2014. We are making daily progress with DNA extractions and a second round of winter scat collections to supplement our 2012 efforts. During summer 2013 we plan to sample forages for nutrient analysis and collect additional summer scats. We will finalize our field efforts in autumn 2013 with another round of winter-range condition sampling (i.e. LD transects).

Once the project is complete, we will produce comprehensive reports for state and federal agencies, provide presentations and materials for the general public, and publish our results in peer-reviewed scientific journals.

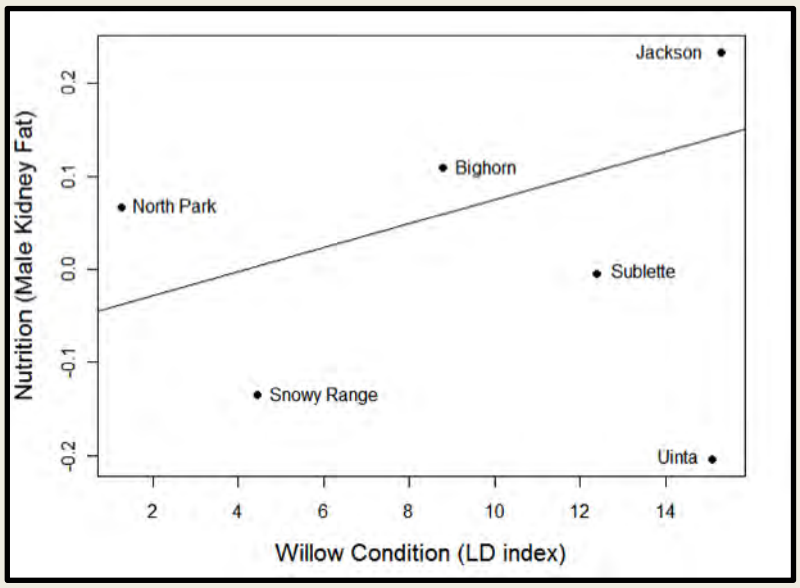


Fig. 19- General relationship between willow condition and nutritional condition of moose.

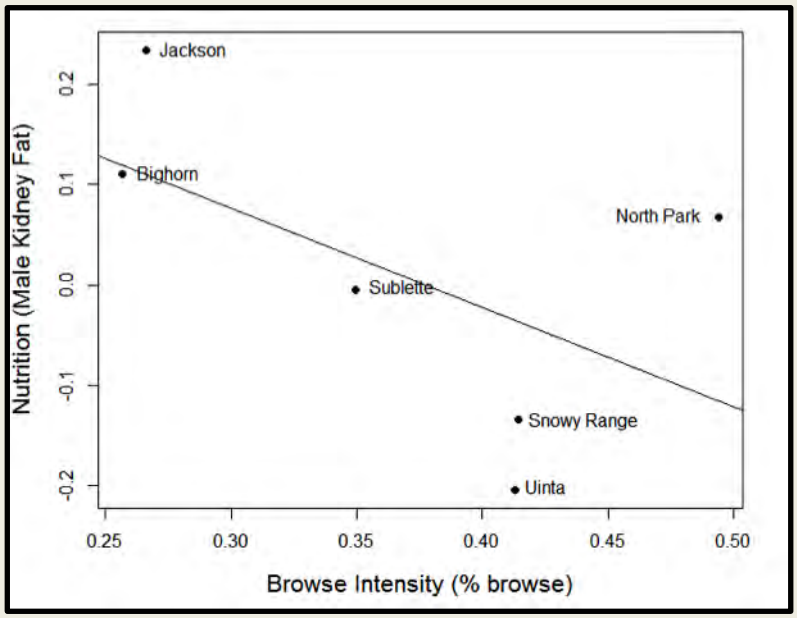


Fig. 20- General relationship between willow browse intensity and nutritional condition of moose.

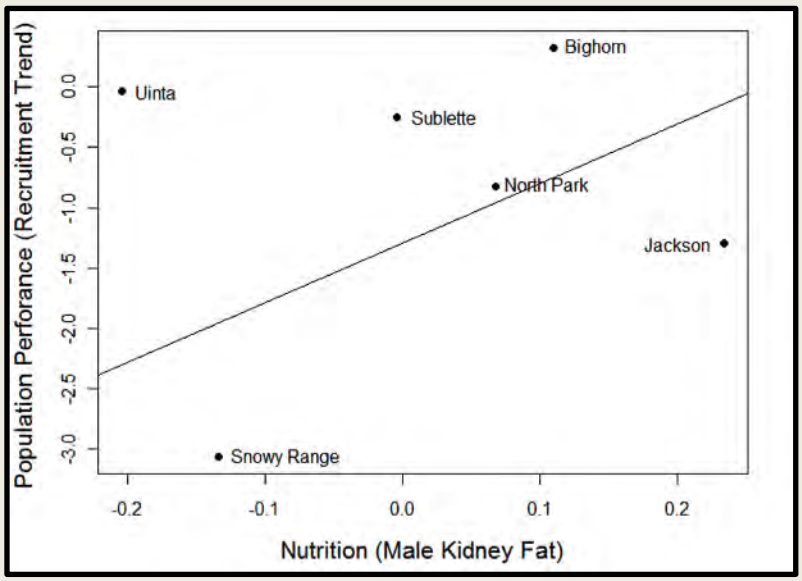


Fig. 21- General relationship between moose nutritional condition and population performance.

Acknowledgements

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Doug Brimeyer
Tim Fuchs
Terry Creekmore
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Ben Wise
Jill Randall
Bert Jellison
Steve Kilpatrick
Bob Lanka
Grant Frost
And many others!

CDPW
Jeff Yost
Josh Dilley
Jeremiah Rummel

USFS
Meg McElveen (RNF)
Diedre Witsen (BTNF)
Kerry Murphy (BTNF)
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USFWS
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Lizzy Berkly (AWR)
Eric Cole (NER)

UWYO
Dr. Shannon Albeke
Dr. Melanie Murphy

Goheen Lab
Ali Hussein
Carol Ng'weno

Kauffman Lab
Jenny Jones
Arthur Middleton
Janess Vartanian

Working Dogs for Conservation Fund
Aimee Hurt
Ngaio Richards
Alice Whitelaw
Orbee (dog)
Wicket (dog)

Field Technicians
Holly Abercrombie
Phillip Damm
Allie Hunter
Lizza Protas
Lyn Snoddy

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