Statewide Moose Habitat Project:

Linking Habitat and Nutrition with Population Performance in Shiras Moose

Annual Report 2014

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Background

Currently, Shiras moose (*Alces alces shirasi*) herds in the region (Fig. 1) are exhibiting a wide range of population performance, with some declining, some relatively stable or even increasing despite historic declines, and some too data poor to be certain about the trend (Fig. 2). Regardless of a given herd unit's recruitment trajectory current (2011-2013) recruitment rates range from 40-60 calves per 100 cows in 'older' moose populations (i.e., Jackson, Sublette, Uinta, Bighorn) and 60-80 calves per 100 cows in 'younger' populations (i.e., Snowy Range, North Park, South Park, Flat Tops)(Fig. 2 & 3), suggesting density dependence is playing major role determining population performance (Forsyth and Caley 2006). For the declining herds, potential mechanisms that may affect nutritional carrying capacity and population performance are habitat deterioration due to current and historic overbrowsing (Boertje et al. 2007; McArt et al. 2009), and regional variation in forage quality due to climatic warming and drying (Monteith et al. *In Press*). 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 cannot account for declines elsewhere in Wyoming, Colorado, and Utah. Further, a newly emergent parasite, 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 parasite on the nutritional condition, survival and reproduction of moose.

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

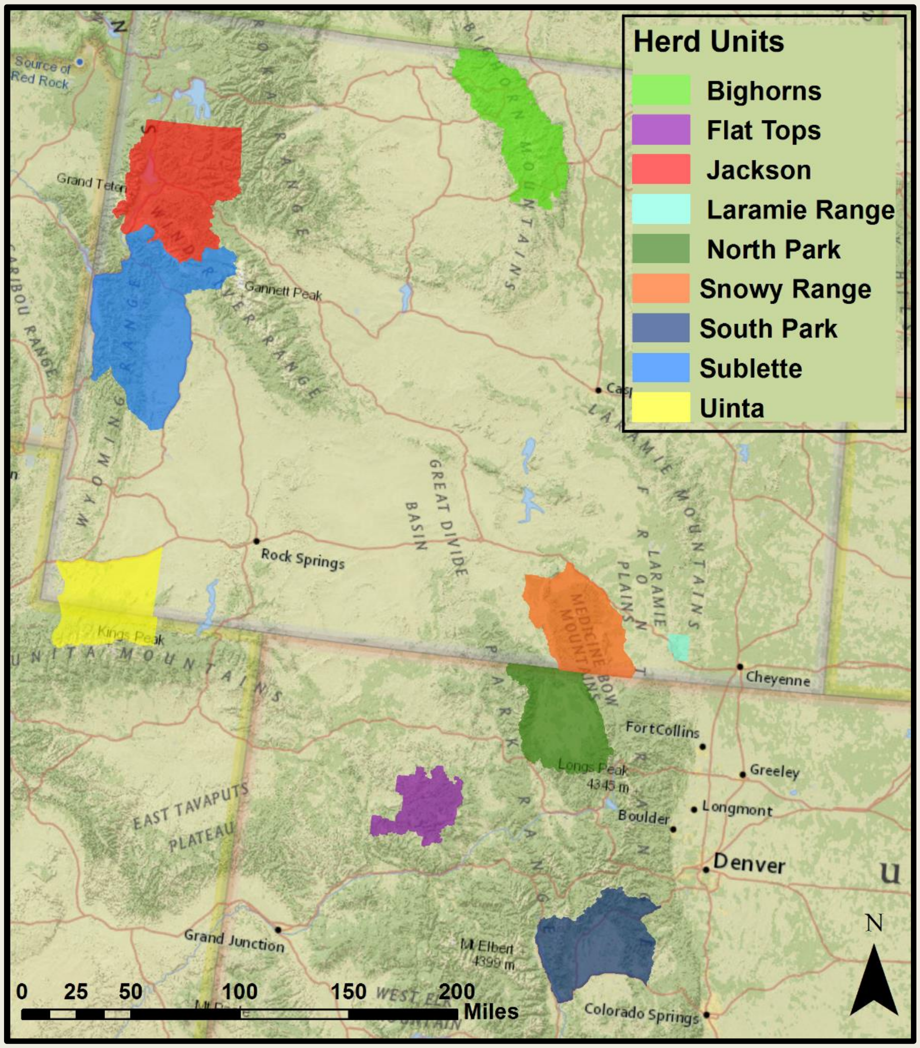


Fig. 1- Map depicting the project study areas.

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 tools from which they can assess a population's proximity to nutritional carrying capacity and adapt management strategies accordingly. Therefore, we have developed the following objectives:

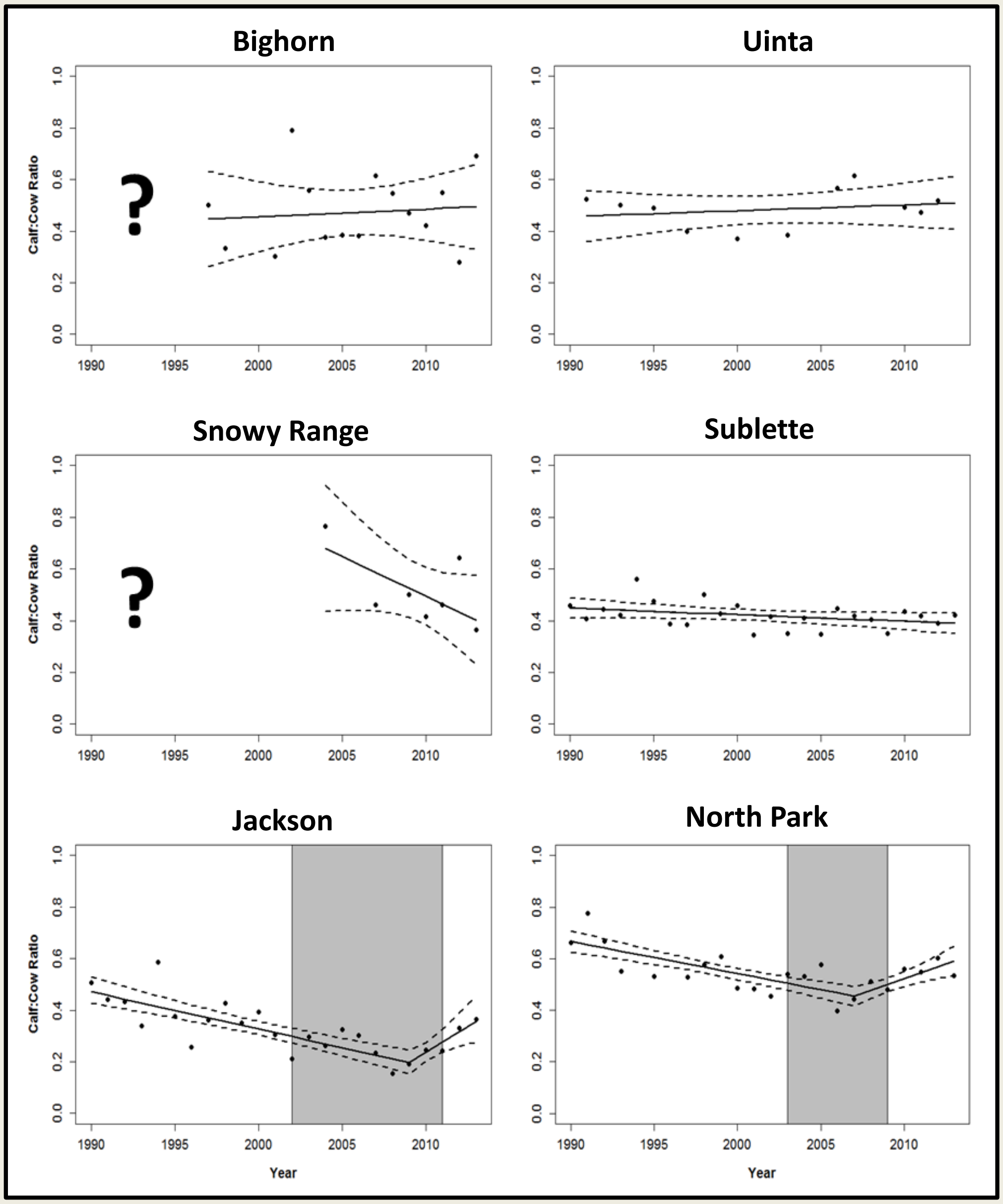
1. Understand the relationship between resource limitation (habitat conditions and drought) and herd productivity.

2. Establish indices of browse condition for monitoring and management purposes.

3. Explore alternative 'early warning' metrics derived from simple fecal collections. These metrics include diet composition and quality, nutritional condition and pregnancy.

4. Develop thresholds or guidelines in habitat and nutritional metrics that managers can use to help preempt declines in herd productivity.

Project Expansion in 2014



Upon initiation of the study in 2011 we expected the ‘younger’ (30-70 years) herd units in the eastern part of the study area (Snowy Range, North Park) to be characterized by good browse conditions and high levels of nutritional condition. We found these eastern herd units to be characterized by heavy browsing (often hedging) of their most highly preferred willow species (*Salix planifolia*) and autumn nutritional condition to be similar to those herd units lying to the west. Therefore, we solicited CPW in an attempt to collect data on habitat and nutritional condition of moose in recently established (5-15 years) herd units (South Park and Flat Tops) in central Colorado. These populations are exhibiting high levels of population performance (Calves/100 Cows ≈ 70) and are likely not experiencing habitat limitation. In June 2014 CPW joined the effort and we began willow surveys and fecal collection. Additionally, we began data collection in the Laramie Range, WY, another more recently established population.

Fig. 2 – Trends in calf-cow ratios from 1990-2013 across six of our study areas. Solid lines indicate the slope and direction of the trend while dashed lines indicate the 95% confidence interval for the slope. Years with less than 10 females classified were omitted from the data set. Most data points from Bighorn and Snowy Range classified less than 30 females. Trend lines were established through piecewise regression. Piecewise regression quantifies multiple differing trends in a single data set. Grey polygons represent 90% confidence intervals for detecting the year in which the trend changed. Note that the trend line for Uinta is not statistically significant (P>0.05), meaning the actual slope is likely zero. Herd units accompanied by a “**?**” (Bighorn & Snowy Range) are also not statistically significant and the confidence intervals indicate that the trend is unknown.

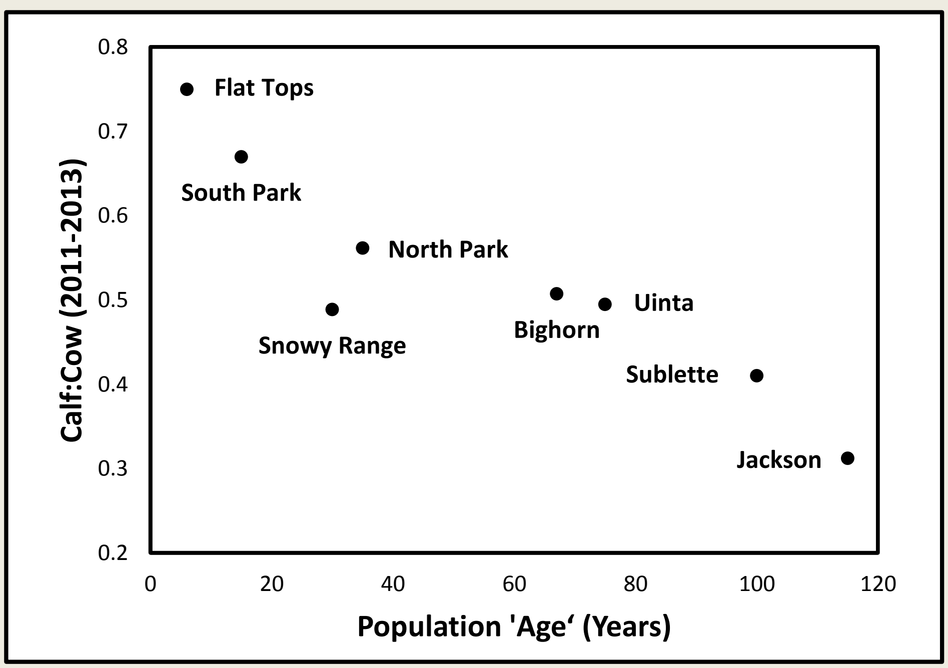


Fig. 3- Relationship between current calf:cow ratios and approximate number of years since colonization of moose into currently defined herd units (Brimeyer and Thomas 2004, CPW unpublished data).

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 moose locations during classification efforts by WGFD and CPW 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 and 5). Location data collected post-hunt from 2000 through 2012 were used in herd-range analyses. When sufficient location data was unavailable (i.e., Laramie Range, South Park, Flat Tops), we mapped the resource selection function of Baigas (2010) across each management unit and considered the75th quantile core-range, and peripheral-range the 50th quantile.

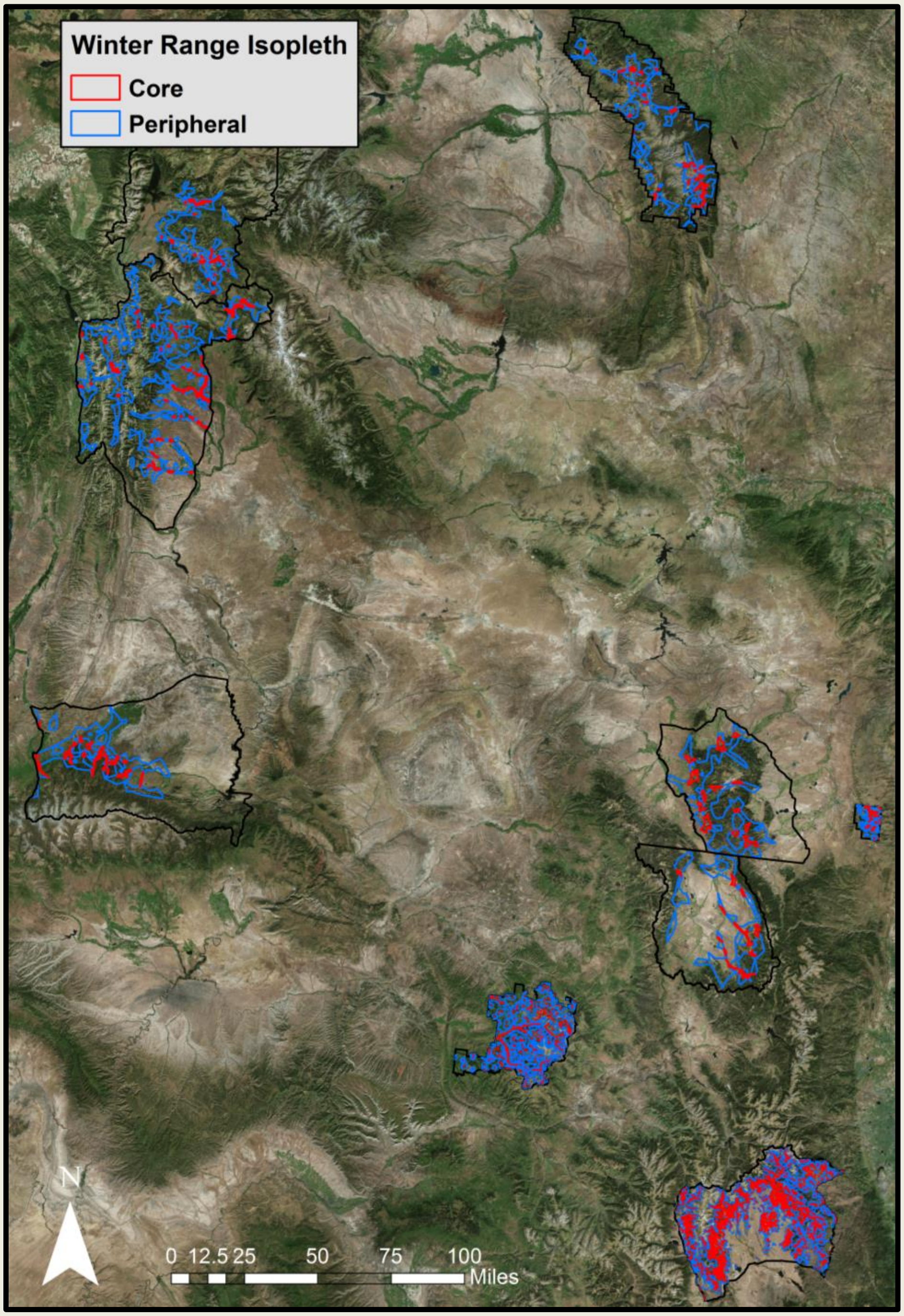
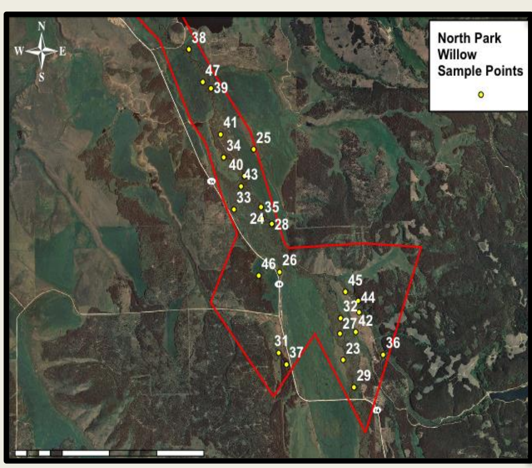
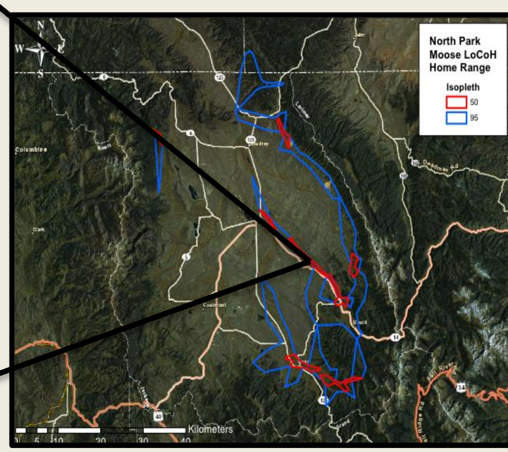


Fig. 4- Distribution of core (red) and peripheral (blue) moose winter ranges across the six study areas. Note- not all core and peripheral areas displayed here were sampled (see pg. 4 for details).





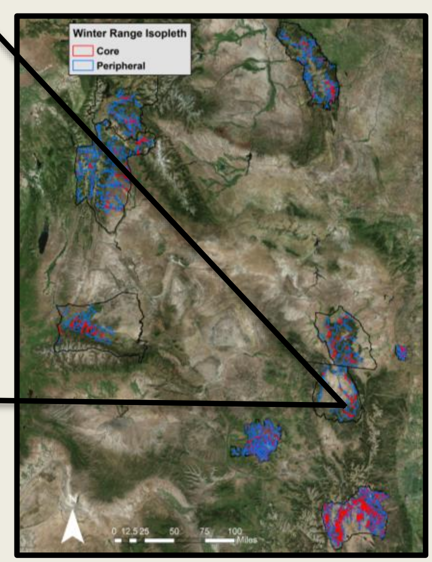


Fig. 5- Within each core and peripheral range, such as North Park’s Michigan River (shown here), randomly generated points were drawn in willow habitat to prevent observer bias (see pg. 5 for details).

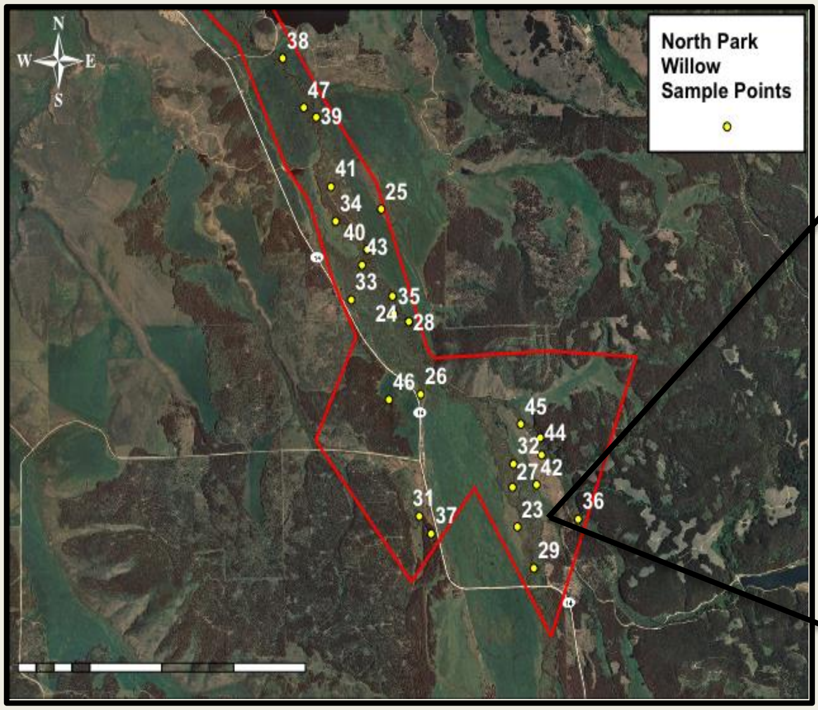


Fig. 6- Map depicting randomly generated sample sites in willow habitat along the Michigan River, Jackson County, CO.

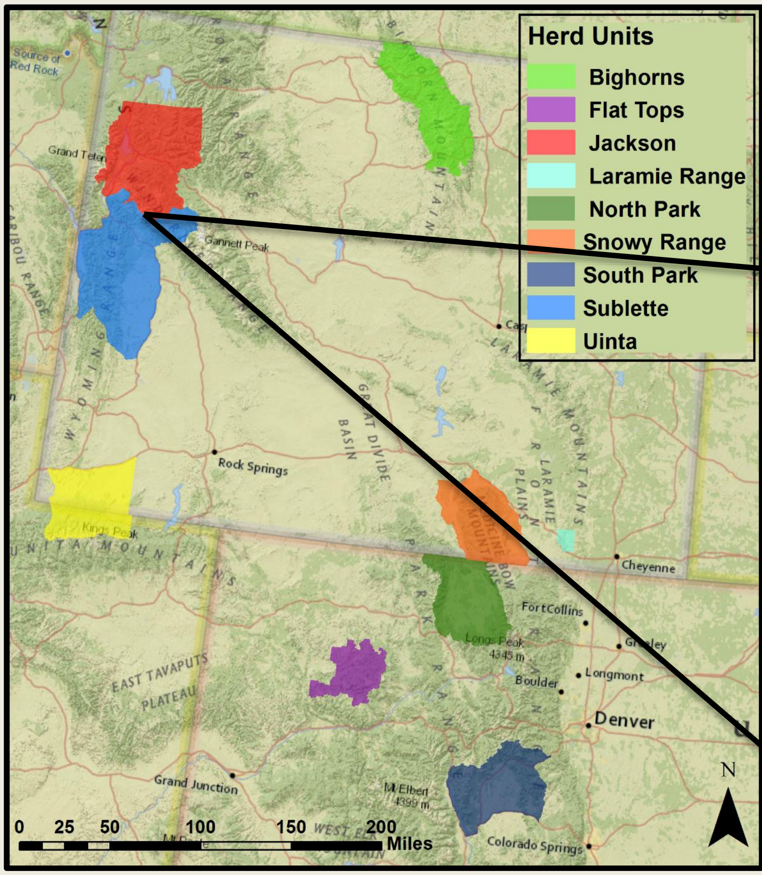
Fig. 7- Example of planeleaf willow transect in Flat Tops, Rio Blanco County, CO

Within core and peripheral ranges we plotted random points with a minimum of 200m spacing between points using a generalized random tessellation stratified (GRTS; Stevens and Olsen 2004) sample generator (R; Sdraw package) to develop a spatially-balanced random sample across the two strata. 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. In 2012 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. In 2013 we increased our sample by adding 5-10 transects per herd unit as time permitted. During summer of 2014 we completed approximately 30 LD transects in the South Park and Flat Tops herd units. 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 inhibited us from sampling in exact sequential order.

We completed LD transects at each randomly selected sampling point across the six study areas (Fig. 6 and 7). 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) were measured along a random bearing every 10m starting at each sampling point. LD, leader length of the dominant apical meristem, percent browse, percent decadence, and plant height were recorded at each plant.

To assess **winter diet** (i.e. foraging behaviors) and identify important **winter forages**, we collected fecal samples opportunistically and along LD transects (Fig. 7) according to a sterile protocol developed to eliminate cross contamination. We only collected fecal samples that appeared to be fresh and were determined to have originated from an adult moose according to size. Using molecular techniques we will group fecal piles by individual and determine sex prior to diet and **pregnancy** analyses (via progestagen analysis; Monfort et al.1993), and potentially assess nutritional state via additional hormone (triiodothyronine (T3) and glucocorticoid (GC)) assays (Wasser et al. 2000, 2010). Progestagen, T3 and GC thresholds will be validated using feces, blood samples and ultrasonography data collected during captures associated with the Sublette and Uinta moose studies.

Fig. 8- Scats found along North Horse Creek, Sublette County, WY.



We collected moose scats along each transect when present (see figs. 10 and 11) using a sterile protocol. Currently, we are extracting DNA from scats (see pg. 6) to determine individuality and sex prior to diet (qPCR) and forage quality (fecal nitrogen and fecal neutral detergent fiber) analyses.

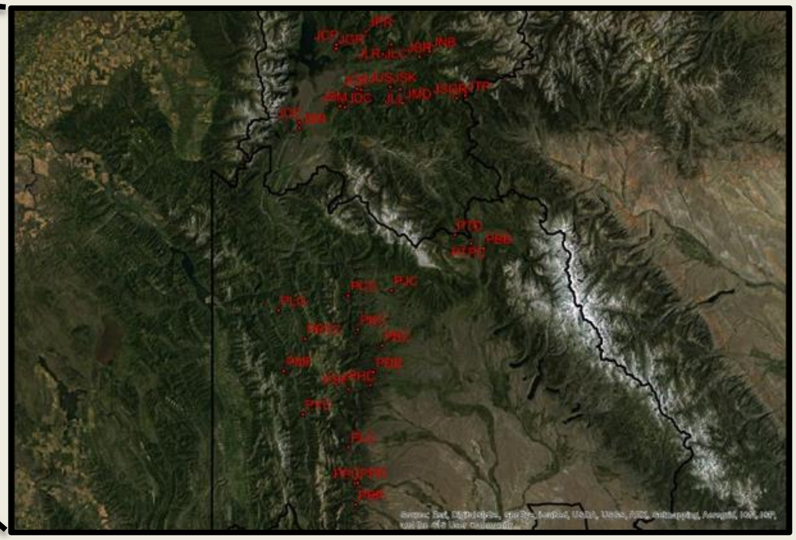


Fig. 9- Map depicting randomly generated sample sites across different habitats where summer fecal samples were sampled in Sublette and Teton Counties, WY.

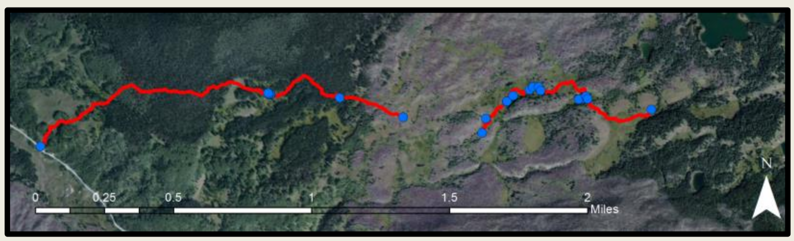


Fig. 10- Map illustrating a fecal transects (red; 5-6 km each) and fecal samples collected (blue) in both willow and upland habitat. Fish Creek, Rio Blanco County, CO.

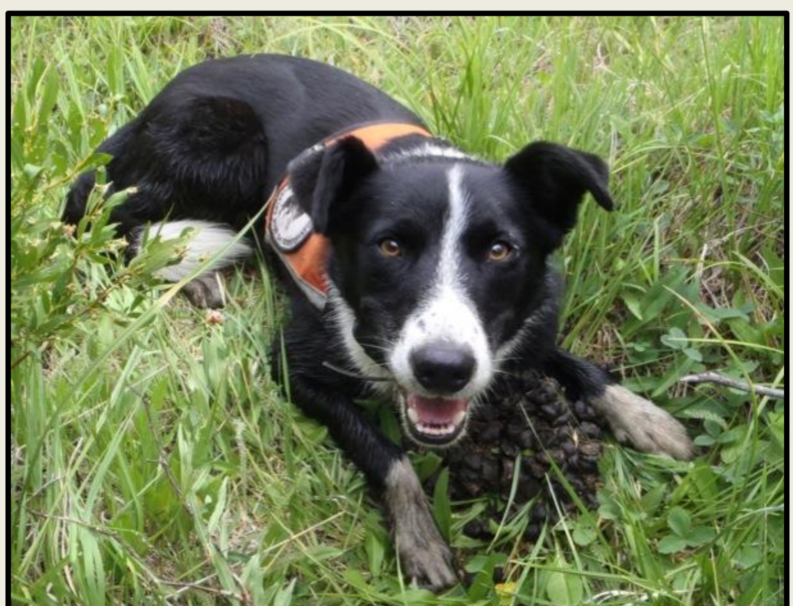


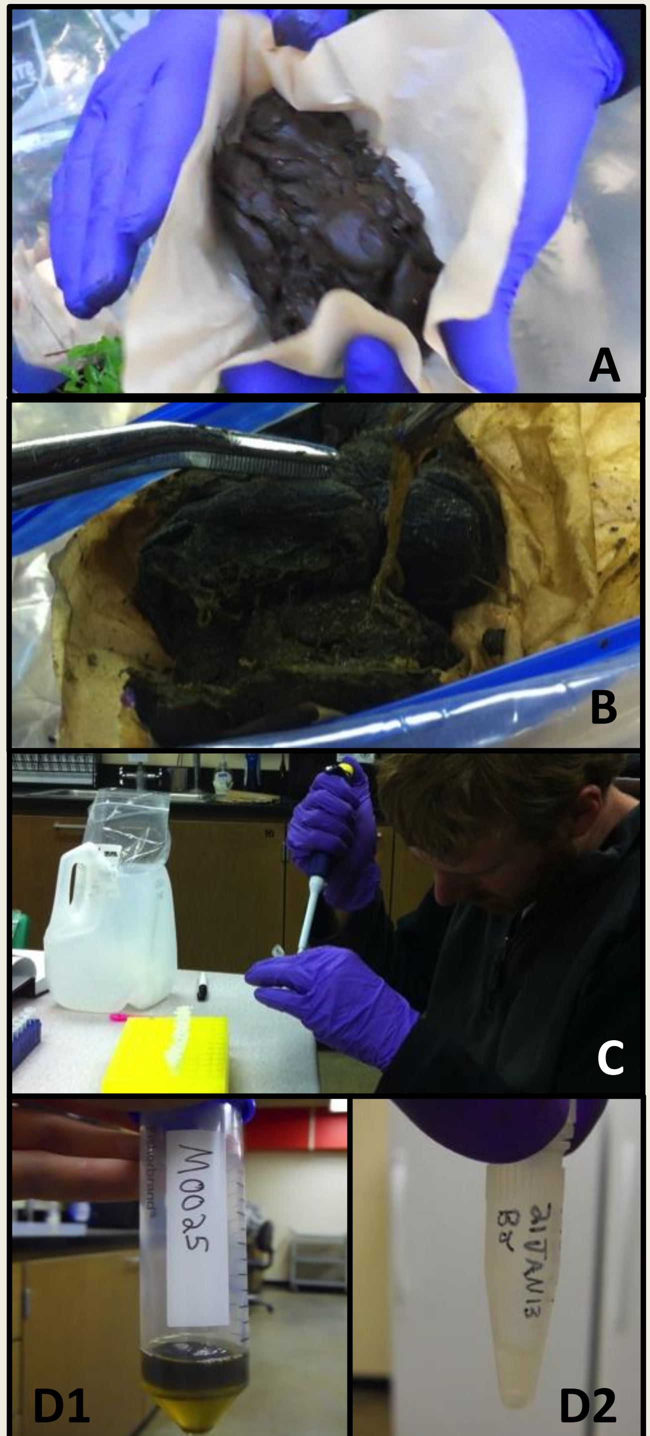
Fig. 11- Orbee the detection dog is very proud of his find (mostly he just wants his reward; a short game of fetch with a ball).

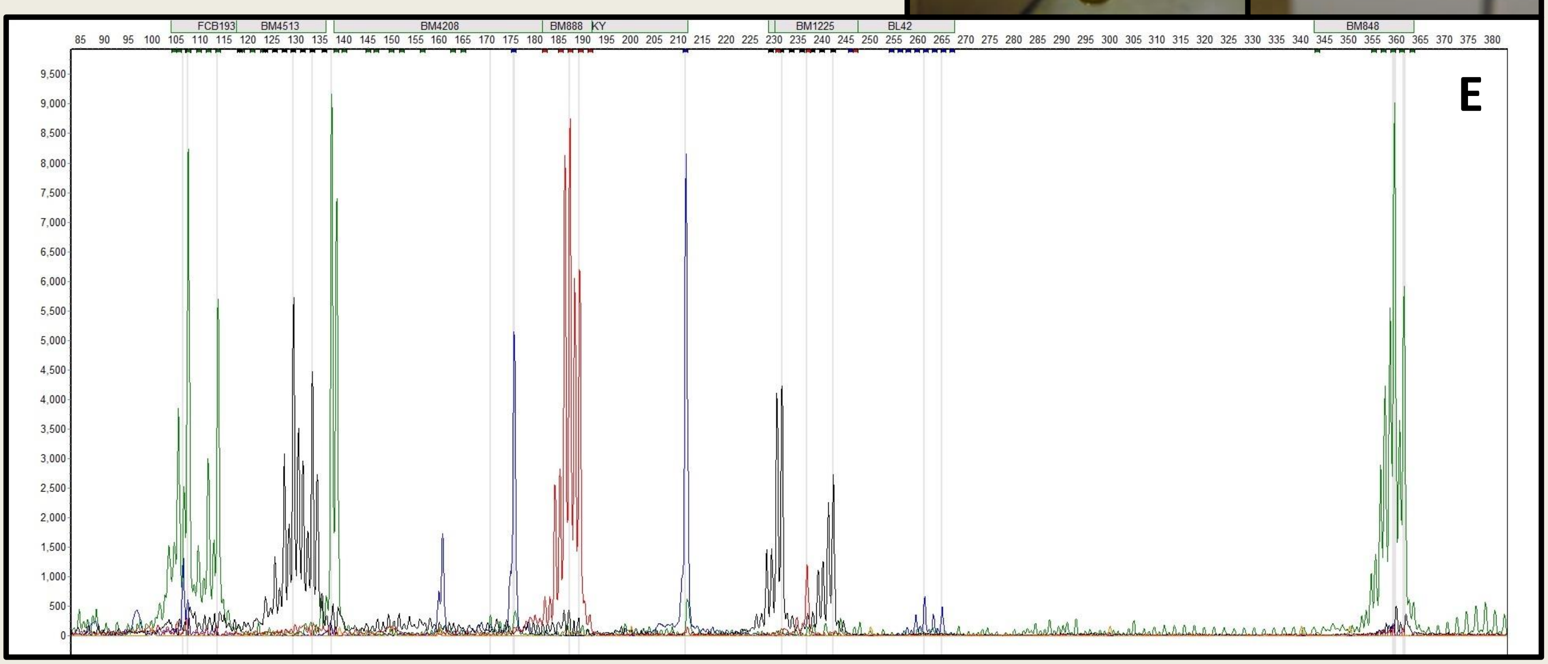
To characterize the range of **diets** (i.e. foraging behavior) and the **quality of forages** used by moose on **summer ranges**, we once again employed a stratified random sampling design. Due to the widely-reported preference for riparian and upland shrub forage amongst moose inhabiting montane regions of North America (e.g., 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 again used a generalized random tessellation stratified sample generator to develop a spatially-balanced random sample across the two strata (Fig. 9). To ensure that our 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 the Baigas *et al*. (2010) summer RSF model. Logistical and financial constraints determined that 20 transects (10 willow, 10 upland) per herd unit 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 $\geq$ 2000m in Euclidean length, and (3) the patches were within a logistically feasible proximity (daily travel distance) to another sampling point whereby we could complete two transects per day. Each transect started at, or intersected with, the sampling point (Fig. 10).

Only ‘fresh’ (i.e. typically <1 week old) scats were collected along each transect (Fig. 10). 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).

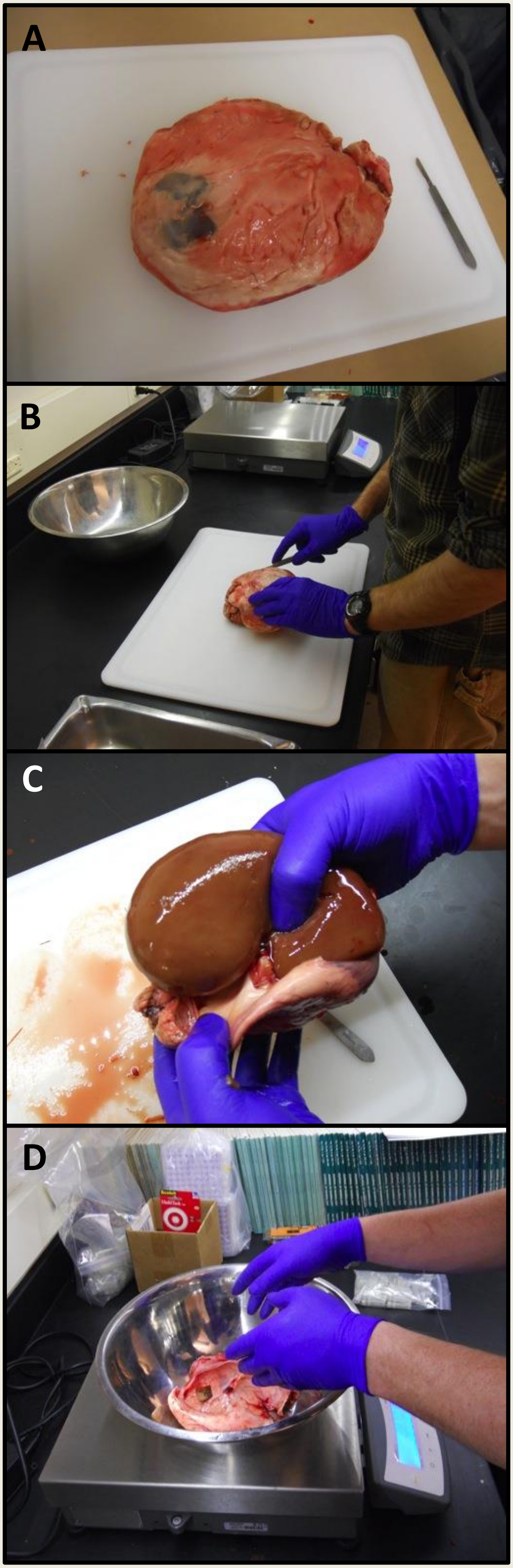
Through a series of chemical reactions (photo C) we duplicate the DNA many times over and characterize nine specific portions of the genome that allow us to ‘fingerprint’ the sample so that we can identify which individual the scat came from and its sex (photo E). For example, photo E depicts nine microsatellite loci, represented by black, green, red and blue ‘peaks’, amplified from one individual moose tissue sample. The two tall blue peaks near the middle of the graph represent genetic products associated with the X and Y chromosomes; meaning this individual is a male. This process is extremely similar to that used by criminal forensic scientists and has been streamlined so that individual and sex identifications can be assessed simultaneously. We repeat this process 2-3 times for each of 1022 fecal samples we have collected and use computer software to match the samples to individual moose.

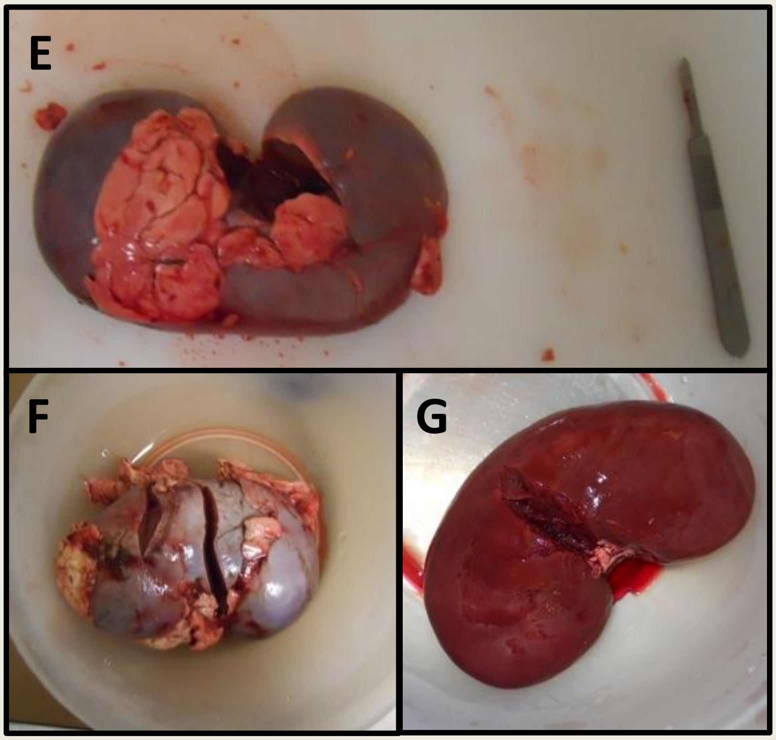




To understand how winter habitat condition and quality, and summer diet and forage quality affect the **nutritional condition** of moose, we are measuring autumn kidney fat. The amount of fat found attached to the kidney is a good predictor of total body fat in moose (Stephenson *et al*. 1998). We collaborated with the WGFD, Colorado Parks and Wildlife (CPW) and the Utah Division of Wildlife Resources (UDWR) to solicit hunters to collect kidneys from harvested moose. With each kidney, hunters and WGFD, CPW and UDWR 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, CPW and UDWR 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 perineal 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 or the visceral cavity 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 available 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 quantity and 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 (Monteith et al. 2014), and therefore likelihood of pregnancy, in ungulates. 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 nutritional condition remains an excellent indicator of habitat quality (Parker *et al*. 2009).

During 2011-2013 we analyzed 544 undisturbed kidneys for nutritional condition assessment. Nutritional condition varied amongst the six herd units of interest (Fig. 12). We also received numerous kidneys from the Lincoln herd unit, so we include those data in figure 12. Although hunter harvested samples are vulnerable to inconsistencies amongst hunters, year to year measures of kidney fat within herd units did not differ (Fig. 12), providing us with confidence that this approach to collecting nutritional data is reliable. Kidney fat was positively related to trends in calves/100 cows censured between 1990 and 2013 (Fig. 13). With the exception of Jackson, kidney fat was also positively related to the mean number of calves/100 cows observed between 2011 and 2013 (Fig. 14).

We completed 435 LD transects, representing 7659 individual willow plants measured from 2012-2014. The condition of planeleaf and Booth's willow was positively related to autumn nutritional condition (kidney fat; Fig. 15). The linkages between willow condition, autumn

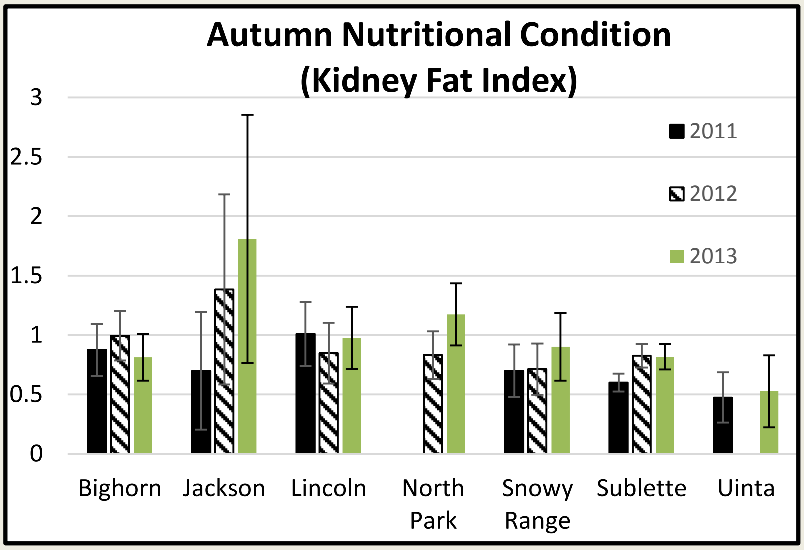


Fig. 12- Variation in male nutritional condition amongst herd units and years.

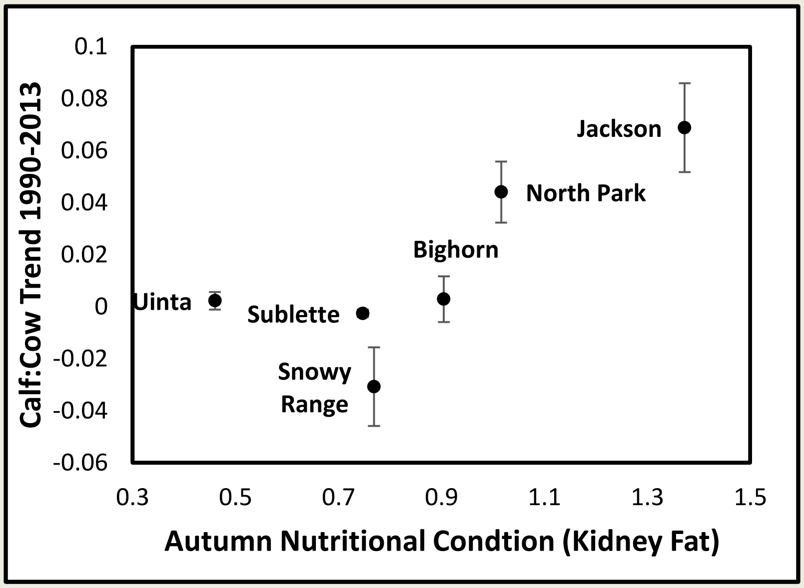


Fig. 13- Relationship between autumn nutritional condition and trends in calves/100 cows from 1990-2013 (see Fig. 2).

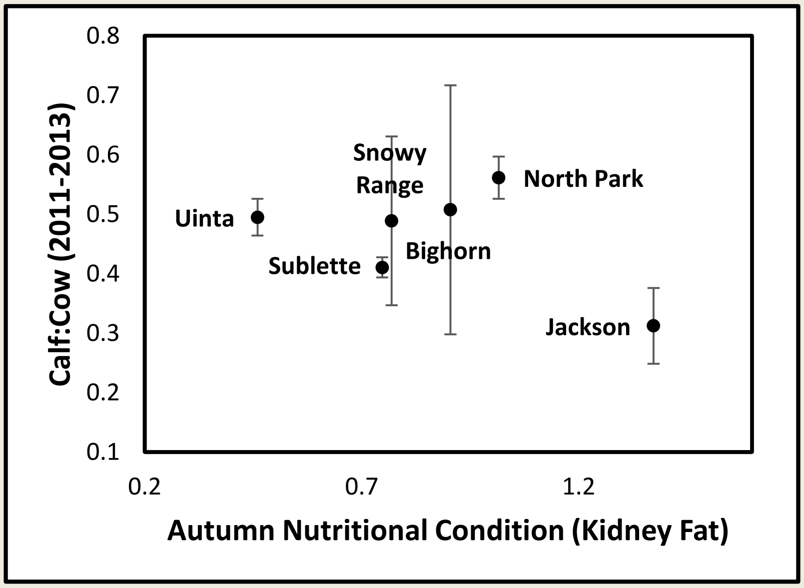


Fig. 14- Relationship between autumn nutritional condition and mean number of calves/100 cows from 2011-2013.

nutritional condition and herd performance indicate that resource limitation is likely contributing to the declines in productivity observed across the region. The ability to observe relationships between winter-range willow condition and population performance, and autumn nutritional condition and population performance using simple summary statistics is an encouraging result. We suspect that we will be able to make strong linkages between habitat, nutritional condition and population performance once we assess drought conditions, summer and winter forage selection and quality, spring nutritional condition, and herd unit pregnancy rates.

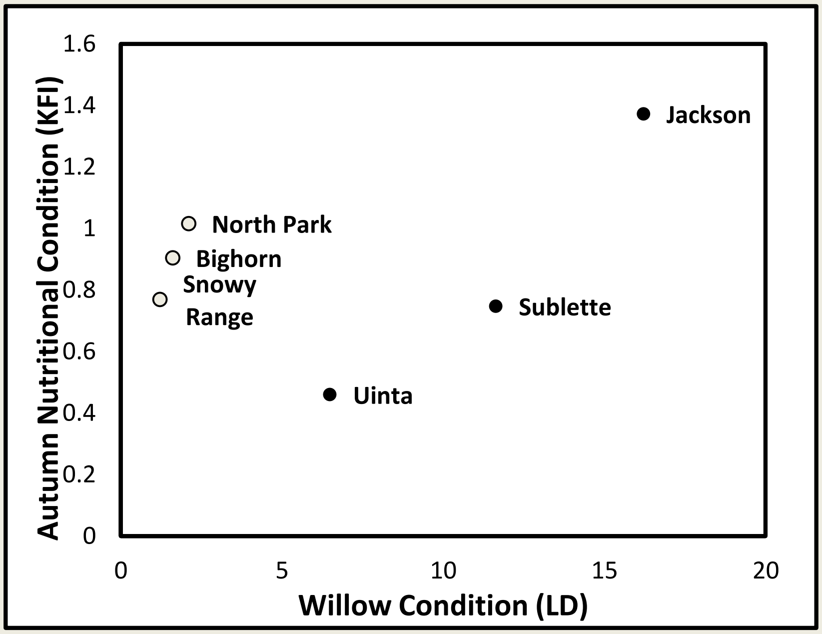


Fig. 15- Relationship between willow condition and nutritional condition of moose. Nutritional condition responds differently to planeleaf willow (open circles) versus Booth's willow (closed circles) condition.

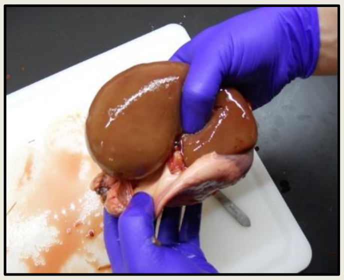
Current and Future Work

We continue to work towards achieving our objective of linking habitat and nutrition to population performance (Fig. 16), and suspect to complete the project during early winter 2016. We are making daily progress with additional DNA extractions and genotype analysis. In 2014 we completed willow condition surveys and summer scat collections in South Park, Flat Tops and the Laramie Range. We are currently conducting winter scat collections at these three new units. Additionally, we began organizing kidney collection with CPW for the 2015 hunting season, which will represent the finalization of our field efforts. During spring 2015 we plan to complete genetic analyses of >1200 fecal samples and obtain finalized diet composition, diet quality, pregnancy and spring nutritional condition data sets. Once data production is completed, we will produce comprehensive reports for our state and federal agencies, provide presentations and materials for the general public, and publish our results in peer-reviewed scientific journals.

Habitat

Diet

Nutrition



Performance

Fig. 16- General conceptual model depicting the linkages between habitat condition, diet quality and composition, and nutritional condition to population performance in Shiras moose. Once we able to quantify how these factors influence population performance, we will be able to provide managers with tools that will allow them to understand the proximity in which their population is to carrying capacity, and hence adapt management strategies accordingly.

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Monteith Lab
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Lyn Snoddy
Clint Atkinson
Thomas Day
Tina Helseth
Mark Baran
Caitlin Danies
Daniel Greenwood
Britt Britto
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