Presentation Abstracts

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(Alphabetical by Lead Author)

Comparison of harvest statistics and deer management programs in the eastern and western U.S.

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Deer hunting is America's pastime, and deer are among the most widespread wildlife species. They live everywhere and they impact everyone. They are also the most sought-after game animal with nearly 8 of every 10 hunters identified as a deer hunter. Mule and white-tailed deer harvest statistics and management programs differ in many ways. To compare these programs, we surveyed state wildlife agencies in the contiguous United States in September 2020 and collected data on time spent managing each species, budget allocations, hunting popularity, and population estimate trends for mule deer relative to whitetails. We also collected data on harvest rates, sex ratios, harvest by weapon type, percentage of successful hunters, and bag limits for Eastern and Western deer management programs. We received data from 47 of 48 states (98%). All Western states that provided data reported spending more time and money on managing mule deer than white-tailed deer, and mule deer were hunted more than whitetails in all but one Western state. Mule and white-tailed deer populations were stable or increasing in most states they inhabit. Eastern hunters harvested antlered bucks [1.6 bucks per square mile (PSM)] and antlerless deer (1.6 PSM) at far higher rates than Western hunters (0.2 bucks and <0.01 antlerless deer PSM). Western hunters harvested a higher percentage of deer with a firearm (85%) than Eastern hunters (64%). Hunters from both regions experienced similar success rates (41%), while Eastern hunters enjoyed higher annual buck bag limits (2.3 vs. 1.0 bucks).

Characterization of the prion protein gene in axis deer and implications for susceptibility to chronic wasting disease

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Chronic wasting disease (CWD) affects both native and non-native North American Cervids. The

expanding geographic distribution of CWD and list of affected species is concerning, especially for stakeholders who manage Cervid populations or harvest wild animals. In areas where native and non-native Cervids overlap, the potential for interspecific transmission of CWD is of concern when the CWD susceptibility of the non-native species is unknown. Axis deer (*Axis axis*) occur both in captivity and free-ranging populations in portions of North America but to date, no data exist pertaining to their susceptibility to CWD. Because CWD susceptibility is linked to the amino acid (AA) sequence of the prion protein (PrPC), we obtained DNA sequences of PRNP exon 3, the gene that encodes PrPC, from 133 axis deer to assess potential susceptibility to CWD. We identified and compared AA substitutions in axis deer PrPC to substitutions reported to confer reduced susceptibility in Cervids and compared the axis deer sequence to those of CWD-susceptible species. A single PRNP allele without individual variation was recovered from axis deer, that indicates axis deer PRNP is most similar to North American elk (*Cervus canadensis*) PRNP in both nucleic and translated AA sequence. The AA sequence similarity to elk suggests that axis deer are likely susceptible to CWD, but with a potentially lower susceptibility level than white-tailed deer (*Odocoileus virginianus*). We recommend increased CWD surveillance for axis deer focused on areas where CWD has been detected and axis deer coexist with native North American CWD susceptible species.

Examining green-wave surfing in mule deer populations

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Many ungulate populations follow seasonal migration patterns, residing in low-elevation regions during winter and travelling to high-elevation locations in the summer. Plant phenology also follows elevation gradients, with vegetation at lower elevations undergoing spring green-up earlier in the season. Previous research has demonstrated that, at the individual level, ungulate migration often coincides with this vegetation green-up, a behavior that is hypothesized to allow animals to increase energy uptake by following peak forage quality across the landscape. However, it is still unknown whether these individual level patterns scale up to the population level, and the relative effects of biomass quantity versus quality are still unclear. This project investigated how mule deer (*Odocoileus hemionus*) densities coincide with vegetation green-up across space and time during migration events, and tested the hypothesis that population-level migration is driven by spring vegetation green up. In early 2019, I placed 100 motion-triggered cameras along migration routes in Spanish Fork Canyon in central Utah, which is home to a large migratory mule deer population. Deer-image capture rates provided spatiotemporally explicit estimates of local deer density through the spring season, and were combined with remotely sensed indices of biomass availability and growth. My results indicate that deer spring migration in my study area was driven by both forage quantity and quality, and that the wave of vegetation regrowth advancing from low to high elevation during the spring is closely tracked by a traveling wave of peak deer densities. My study thus provides not only a novel technique to quantify wildlife density dynamics at high spatiotemporal resolution, but also the first demonstration of population-level green-wave surfing.

Risky business: relating risk of direct contact with disease risk

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Chronic wasting disease (CWD) is a fatal, prion disease of cervids that was first detected in Alberta in 2005. Transmission of CWD occurs by direct contact with infected individuals and via contaminated environments. We investigate the seasonal effects of grouping patterns and landscape heterogeneity on direct, pair-wise contacts within and between sex-specific (same or mixed sex) groups of mule deer (*Odocoileus hemionus*) in eastern Alberta. First, we establish criteria based on spatial-temporal movements of collared deer to define sex-specific group membership. Second, we classify whether sex-specific dyads of collared deer are in different groups and model the relative risk of a sex-specific contact occurring in a locale based on landscape characteristics. Third, we relate seasonal predictions of the spatial relative risk of contacts to the risk of deer being CWD-infected in an area based on hunter-harvest, CWD surveillance data. We predict that a harvested male deer being CWD+ is more strongly related to risk of contact with other between-group males than females, whereas the risk of a harvested female deer is most related to within-group contacts between females. Further, we predict that winter contact risk is more related to the risk of deer being CWD+ than summer contact risk across all group and pair types.

Individual-based modelling of chronic wasting disease

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Chronic wasting disease (CWD) is an emerging prion disease in Canada that infects mule deer, white-tail deer, elk, and moose by direct and environmental transmission and is invariably fatal. CWD spread can be promoted at "hotspots" that attract deer, such as those are created intentionally via supplemental feeding or accidentally via grain spills. Hotspots may increase contacts between- and within-groups depending on how many animals use the site and how long individuals spend at the site. An individual-based model was created to investigate the effects of different densities and arrangements of hotspots on contact rates between- and within-groups. The model tracks contacts (when two individuals come within three meters of one another), which are defined as between- or within-group depending on the group membership of the two individuals. Simulations are run in Netlogo on a heterogeneous landscape and include behaviours such as grouping and home ranges. Grouping behaviours and home range are simulated via a biased turning angle distribution. Deer are moved across the landscape model at a two-hour time step based on step-selection movement rules relative to resources and group behaviours. The step-selection function utilizes GIS layers for environmental weights and GPS-collar movement data for calculating step-selection coefficients, as well as turning angle and step length distributions. We present preliminary results of how hotspot density and configuration influence contact rates and the potential for disease transmission.

Trade-offs in forest disturbance management for plant communities and mule deer in northwest Montana

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Land and wildlife managers use disturbance to reset forests to earlier successional stages and improve the quality and quantity of forage available to ungulates. However, management of vegetation communities to increase forage nutrition has implications for other vegetation targets as well. We studied changes in vegetation in three forested areas of Montana, USA during 2017–2019. Specifically, we studied how management of fire and timber harvest affected 3 metrics of vegetative response: forage quality for mule deer (*Odocoileus hemionus*), invasive species biomass, and floristic quality, or native species conservatism. We found differences in all 3 metrics of plant responses that were specific to disturbance type and study area. Increased deer forage quality in disturbed areas suggested that targeted forest management would provide nutritional benefits to mule deer populations in forested areas. Other vegetative responses revealed similar disturbance type- and study area-specific responses. Lastly, we used decision analysis techniques to illustrate trade-offs and overall support for different management actions while also accounting for underlying differences among study areas. Consideration of multiple vegetative responses can help managers balance potential tradeoffs of management alternatives.

Mule deer and anthropogenic change: effects of agricultural encroachment on movement, morphology, and population performance

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Conversion of native rangeland to row-crop farming is accelerating the process of habitat fragmentation in the Southern Great Plains. However, the effects of encroaching agriculture on wildlife are poorly understood. We evaluated how presence of agriculture influenced resource selection and linked habitat use to life metrics of mule deer (*Odocoileus hemionus*) in the Panhandle region of Texas. We collected multi-year movement (via GPS collars) and morphometric measurements from 122 males and 185 females. We assessed mule deer resource selection at different spatio-temporal scales and tested functional responses of agriculture availability towards mule deer use. Cropland only accounted for 3–14% use and we observed greater selection for cropland during winter than summer months. Mule deer exhibited a quadratic functional response, where use of agriculture increased in proportion with availability, then decreased when >20% land cover was cropland. Males that used cropland in summer months relative to those that did not have greater body condition, and therefore endogenous reserves to allocate towards reproduction. Further, female cropland use during gestation increased the probability of lactating in autumn, an indicator of successfully recruiting young. The presence of crops can provide a nutritional subsidy to wildlife, but habitat selection functional responses indicate there is a threshold beyond which cropland is no longer beneficial to mule deer. Understanding the influence of anthropogenic changes on the landscape will help mitigate human-wildlife interactions and aid in adaptive management plans for mule deer in the Great Plains.

Odocoileus rex and the evolution of mule deer

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The earliest ungulates appeared in the fossil record during the Eocene Epoch, 34–56 million years ago (YBP) and gradually evolved into whales and hoofed mammals worldwide. All deer today are descendants of Eurasian deer-like animals that possessed tusks and, eventually, antlers before invading North America through Beringia 5–7 million YBP. The earliest deer in North America are represented by 3 forms that appear nearly simultaneously in the fossil record about 5 million YBP: *Eocoileus*, *Bretzia*, and *Odocoileus*. The divergence of *Odocoileus* between the eastern form (white-tailed deer) and western form (mule/black-tailed deer) occurred sometime in the Pliocene or Pleistocene (1–4 million YBP). Glaciers covered northern North America only as far south as the Canada-U.S. border in the West. All North American deer were south of the glaciers, except perhaps the black-tailed deer as they were trapped in refugia along the coast by alpine glaciers extending down the Cascade Range through the middle of northern California, Oregon, Washington, and southern British Columbia. I will discuss 4 main theories that have been proposed to describe the origin of black-tailed and mule deer and their evolutionary relationship to white-tailed deer. The scenarios are not mutually exclusive, and all are based on different information in an attempt to explain the observed physical or genetic differences. No theory is without serious contradictions and contrary evidence, which reflects the reality of our fragmented understanding of these genetic, behavioral, geographical, and phenotypic relationships.

Harvest management and chronic wasting disease prevalence trends in western mule deer herds

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We analyzed retrospective data on harvest management practices and corresponding chronic wasting disease (CWD) prevalence trends in 36 western US and Canadian mule deer (*Odocoileus hemionus*) management units ("units"). Our analyses employed logistic regression and model selection, exploiting variation in practices within and among jurisdictions to examine relationships between harvest management and apparent prevalence (the proportion of positive animals among those sampled). Despite notable differences in hunting practices among jurisdictions, our meta-analysis of combined data revealed strong evidence that the amount of harvest was related to CWD prevalence trends among adult male mule deer in the 32 units where prevalence at the start of the analysis period was <5%. All competitive models included the number of male deer harvested or number of hunters 1−2 yr prior as an explanatory variable, with increasing harvest leading to lower prevalence among males harvested in the following year. Competitive models also included harvest timing. Although less definitive than the number harvested, median harvest dates falling closer to breeding seasons were associated with lower prevalence in the following year. Our findings suggest harvest—when sufficient and sustained—can be an effective tool for attenuating CWD prevalence in adult male mule deer across western ranges, especially early in the course of an epidemic. Evidence of a broad relationship between the amount of harvest and subsequent changes in CWD prevalence among adult male mule deer provides an empirical basis for undertaking adaptive disease management experimentation aimed at suppressing or curtailing CWD epidemics.

Demographic performance of a large herbivore: effects of winter nutrition and weather

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Variation among demographic rates for a population reflects the allocation of available energy by

individuals to competing life-history strategies. Survival of adult female ungulates is generally high with little variability, whereas survival of young is lower and often highly variable. Weather also may affect population dynamics directly by influencing survival of young or adults, or indirectly through changes in nutritional condition of adult females. We experimentally manipulated forage availability during winter, by supplementing native forage, to a subset of a population of mule deer (*Odocoileus hemionus*) to understand the effects of winter nutrition on survival of adult females and their young born the subsequent summer. We evaluated the effects of winter nutrition, individual-based parameters, and environmental covariates on survival of adult female mule deer from 2013–2018, and neonatal mule deer from 2014–2016. We documented a 26% decrease in annual survival of adult female mule deer in 2017 in response to increased snowpack during the preceding winter. Neonates born to females that receive enhanced nutrition during winter preceding parturition had higher survival to weaning (0.49, SE = 0.12), compared to neonates born to females that did not receive enhanced nutrition (0.29, SE = 0.07). Our results suggested winter nutrition of maternal females may influence juvenile survival and demonstrates the importance of forage quality available to adult females during mid-pregnancy. Although we were unable to detect an effect of winter forage on survival of adults, direct effects of deep winter snow resulted in lower survival of adult females.

Effects of spatial and temporal mismatch in monitoring programs

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Deer, elk, and other game management programs rely on multiple data streams to make inference to population dynamics. Harvest regulations and population objectives are influenced by those data. Often monitoring programs and harvest seasons cover only a portion of the population of interest. In addition, animals move throughout the year such that the animals observed in on location many differ by season. Mismatch of monitoring data to populations of interest can result in unreliable population inference. We demonstrate how mismatched data and populations influence results from integrated population models. We further show how temporal and spatial mismatch become particularly challenging for linking harvest to populations. Our results emphasize the need to consider the biological population scale when designing monitoring programs and when developing harvest regulations. The results are widely applicable to deer and elk, but also extend beyond those species.

Nutritional-landscape models link habitat use to condition of mule deer

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In heterogeneous landscapes, large herbivores employ plastic behavioral strategies to buffer themselves against negative effects of environmental variation on fitness. Yet, the mechanisms by which individual responses to such variation scale up to influence population performance remain uncertain. We combined fine-scale data on forage biomass and quality with movement data and measures of somatic energy reserves to determine whether variation in use or selection of the nutritional landscape predicted early-winter body condition of mule deer (*Odocoileus hemionus*). At the population level, mule deer exhibited stronger selection for high forage biomass at the landscape scale than at the home-range scale, and during summer than during spring. Use of the nutritional landscape varied among individual deer and had important consequences for early-winter condition. Females that consistently used vegetation communities that provided high biomass of preferred forage plants throughout spring and summer entered winter in better condition than females that used those vegetation communities less frequently. In contrast, selection (i.e., use relative to availability) of the nutritional landscape by individual deer was not significantly related to early-winter condition at either the landscape or home-range scales. Our results highlight the value of using mechanistic, nutritional approaches to understand the potential fitness consequences of individual variation in behavior.

Migrational behavior and its influence on survival during a short distance migration

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Stopover use has been demonstrated among many species of migrating taxa. Stopover behavior during migration is characterized by a slower rate of movement as well as less directionality to movement that is associated with foraging behavior. Stopover sites are critical locations within the migration route that may positively influence survival. The Pacific Deer Herd is a migratory population of deer consisting of mule deer (*Odocoileus hemionus*) in the Eldorado National Forest located on the western slope of the Sierra Nevada Mountains, California. We hypothesize that stopover use will influence survival of a migratory ungulate population. Collar data was analyzed using the Brownian Bridge Movement Model (BBMM). The collar data shows a mean migration distance of 31 km and BBMM estimated that 58% of deer used stopovers. Patterns of mortality were also assessed. Survival comparisons were made based on an individual either occupying summer or winter home range. We found that 5 of the 12 observed mortalities occurred during migration, and there were no observed mortality events at stopover sites.

Stopover behavior has been assessed in ungulate migrations of 160 km or more. Our data shows stopover behavior is important in a short distance migration (31 km). We examined patterns of mortality during migration and found higher survival at stopover sites when compared to the rest of the migration route. This migratory population shows high fidelity to stopover locations and migration routes. It is important for managers to be able to identify these locations as areas of high conservational status.

Balancing CWD risk and public expectations: an experiment in a mule deer special management area in western Montana

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In 2017, Chronic Wasting Disease (CWD) was detected in wild Montana cervids and has since spread throughout the state. CWD has not yet been detected in Administrative Region 2, home to Hunting District (HD) 270. HD270 is a mule deer Special Management Area (SMA; managed for the harvest of older-age-class bucks) with the lowest draw odds for a deer permit within Montana. Deer densities in HD270 have decreased by 50% over the last 20 years, yet buck:doe ratios remain high (45:100), increasing the risk of CWD spread in the area. Public resistance to reducing those ratios presents a challenge to managers who wish to reduce CWD transmission risk while maintaining the availability of older-age-class bucks. Montana Fish, Wildlife, and Park's CWD Action Plan does not provide for differential management responses within SMAs if CWD is detected. Beginning in the 2020 hunting season, we offered an additional buck permit that limits hunters to the harvest of deer with ≤3 antler points on one side, with a mandatory post-harvest inspection and tooth extraction for cementum annuli aging. We expected hunters would harvest older bucks with poor or declining antler quality that hunters with the unrestricted permit would not choose to harvest, but still represent an age class with a higher likelihood of transmitting CWD. In the first year, 12 of 15 permits were filled, with a mean age of 6 years (range 3–9), similar to the mean age of bucks harvested with the unrestricted permit. Although these 15 additional permits are unlikely to substantially alter buck:doe ratios, we hope to evaluate their utility for expanded implementation if warranted in future seasons.

Pilot: a toolkit for survey design

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Random sampling serves as the foundation of all statistical analyses and as such is fundamental to wildlife management. Unfortunately, this step is often overlooked or too onerous to carry out. We created an interactive web-based tool that attempts to make the experience of creating a wildlife survey that incorporates random sampling a simple and intuitive task. In addition, an open-source R package is available for users familiar with programming. The genesis of the idea came from conversations with wildlife managers and seeing how difficult it can be to design a statistically rigorous survey. While it is

true that many software packages provide some of the functionality needed to design a survey, users typically have to switch between GIS, Excel, R, or other programs before arriving at a final product. These gyrations increase the likelihood of errors and generally make it more difficult to be efficient. The tools we built provide a single source for all the necessary functionality. In addition, users have the flexibility to create purely random samples, stratified samples and even create spatially balanced designs. In developing the package, we considered various types of surveys such as camera traps, aerial surveys, transect and quadrat based, and collar deployments. The advantages of using random sampling become obvious when data are confronted with a model. Monitoring programs become resilient to landscape changes and animal movements while estimates prove less biased and measures of uncertainty more reasonable. Given the open-source nature of this project we encourage others to contribute to the development of the package.

Habitat selection by partially migratory mule deer in northwest Montana

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Ungulate behavior is often characterized as a balancing of selection for forage and avoidance of predation risk. Within partially migratory ungulate populations, this balancing occurs across multiple spatial scales, potentially resulting in different exposure to costs and benefits between migrants and residents. We assessed how availability and selection of forage and risk from wolves (*Canis lupus*) and mountain lions (*Puma concolor*) varied between summer ranges of migrant and resident mule deer (*Odocoileus hemionus*) in 3 study areas in western Montana, USA, during summers 2017–2019 using 2nd and 3rd order resource selection functions (RSFs). We hypothesized that migration and residency would pose contrasting availability of forage and risk at the summer range-scale, driving alternate finer scale selection patterns of each strategy. In one study area, residents faced lower forage and higher risk than migrants, but residents compensated for this disadvantage through stronger selection of forage and avoidance of risk at finer scales. In the other two study areas, migrants faced lower forage and higher risk than residents and did not compensate through stronger selection for beneficial resources, suggesting partial migration may persist in populations even when exposure to forage and predation risk appears unequal between strategies. The majority of mule deer in our study system were migratory, though the benefits of migration were unclear. Therefore, improving forage conditions in areas with high relative probability of home range selection by migrants could yield the greatest benefits for mule deer populations.

Analysis of a gamete recognition protein called zonadhesin

reveals unique insight into the hybridization of deer species in North America

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Natural hybridization between two North American deer species, mule deer (*Odocoileus hemionus)* and white-tailed deer (*O. virginianus*), is known to occur across a vast geographic expanse ranging from western Canada to northern Mexico. This widely distributed and dynamic multi-species system presents an opportunity to examine introgressive hybridization across populations in the United States (hybridization levels: 24% in the Trans-Pecos Region of Texas, 13% in the Texas Panhandle, 44% in the Pacific Northwest). The *Odocoileus* hybrid zones offer an excellent model to assess gamete specificity, considering egg and sperm from two different species are able to overcome post-mating isolation barriers and allow for a hybridization event. In this study, we examine zonadhesin (ZAN), a multi-domain, transmembrane, sperm protein that is crucial in species-specific binding of the spermatozoa with the zona pellucida of the egg prior to fertilization. ZAN is the only mammalian protein which shows species specificity across multiple mammal species and may act as a potential post-mating isolation mechanism that can prevent (or allow) interbreeding between two closely related species. If the ZAN pathway fails and no longer serves as a barrier for reproductive isolation, then presumably the sperm cell of one species can recognize the egg cell of the other species, allowing fertilization to occur. Examining the mechanism of deer hybridization in populations across the U.S. will reveal hybridization-based issues related to hunting and conservation of these cervid species.

Forage quality and quantity in migratory and resident mule deer summer ranges

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The quality and quantity of forage available to reproductive female ungulates during the summer can

influence body condition and lactation, ultimately influencing herd production. We examined differences in forage quality and quantity between migratory (n = 19) and resident (n = 17) summer home ranges for a population of mule deer (*Odocoileus hemionus*) in the John Day Basin of NE Oregon, USA. During 2018, we collected vegetation measurements 3 times throughout the summer (mid-May, mid-June, mid-July) to determine changes in dry-matter digestibility (DMD; %) at three different phenological stages (emergent, mature, and cured) for three forage classes (grass, shrub, forbs), as well as biomass and cover data. Migratory deer had access to overall higher quality forage at higher elevation summer ranges. Forbs had the highest forage quality on both summer ranges. Forage quality declined across the entire study area as moisture declined and vegetation senesced. Shrub forage quality was higher (DMD = 54.1%) on resident ranges than migratory ranges (49.7%; p = 0.001). Grasses had higher biomass (26.1 Mg/ha) and cover (50.1 %), than forbs (19.2 Mg/ha; 34.7% cover) or shrubs (20.6 Mg/ha; 6.7% cover) across the entire summer range. Overall, migratory deer had access to higher quality forage throughout the summer, yet resident deer had access to higher quality shrub browse. This trade-off in forage availability may partially explain the persistence of a partially migratory population as a bet-hedging strategy on a landscape where low moisture availability, and episodic drought and disturbance create variable foraging conditions.

Idaho's success: winter and migration habitat improvements with SO3362

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Idaho Department of Fish and Game (IDFG) and partners have studied Idaho's big game winter ranges and migrations for decades. Through funding and prioritization spurred by Secretarial Order 3362 (SO3362), an energized and directed plan was established. This Idaho State Action Plan brought more partners and funding to the table to better focus actions that enhance habitat for big game. The plan created a coordinator position co-supervised by Mule Deer Foundation and IDFG with funding support from National Fish and Wildlife Foundation. These actions have resulted in large-scale habitat and migration route improvements for migratory big game and other wildlife species in Idaho. This presentation will highlight some of the successful projects in Idaho made possible by SO3362, including innovative wildlife fencing in the Lemhi Valley, woven-wire fence removal in select hot spots, and large-scale aerial cheatgrass treatments. "Success without duplication is merely future failure in disguise" –Randy Gage.

Post capture mortality in eastern Sierra mule deer populations

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Wildlife capture is a major facet of agency conservation work, but it comes with risks of injury and death to captured animals. Agencies conducting captures should consider self-assessment of capture-related mortalities, not only to evaluate potential bias to survival data, but also in the interest of improving animal welfare. It is important to evaluate local data because mortality rates vary by population and capture method. Between 2014–2021 the California Department of Fish and Wildlife captured 1041 mule deer (*Odocoileus hemionus*) by helicopter net-gun across six herds along the eastern slopes of the Sierra Nevada. Direct mortality from capture was 1.25%, and mortality within two and four weeks of capture was 4.5% and 7.4% respectively. However, natural mortality in the deer populations of the eastern Sierra during the late winter likely causes overestimation of capture-related mortalities occurring during the same time. We used Kaplan-Meier to evaluate weekly survival within each herd during this capture window to compare survival rates of deer captured during the current year versus those captured in previous years. We hypothesized that newly captured deer would exhibit lower survival rates for the first two weeks after capture. We also evaluated capture-related variables to look for predictors of mortality and found that severe injuries and extreme behaviors were associated with decreased survival within 2 weeks of capture.

Comparing the fundamental nutritional niches of mule and white-tailed deer

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Congeneric species often share ecological niche space resulting in competitive interactions that either limit co-occurrence or lead to niche partitioning. We propose that differences in fundamental nutritional niches are a potential mechanism that could explain overlapping distribution patterns of congenerics. We directly compared the fundamental nutritional niches of mule (*Odocoileus hemionus*) and white-tailed deer (*O. virginianus*) that occur in sympatry and allopatry in similar realized ecological niches across their ranges in North America. Nutritional niches of mule and white-tailed deer were quantified using in vivo digestion and intake tolerance trials with six diets ranging in content of fiber, protein, and plant secondary metabolites (PSMs) using tractable deer raised under identical conditions in captivity. We found that compared to white-tailed deer, mule deer had higher fiber, energy, and dry matter digestibility, produced glucuronic acid (a byproduct of PSM detoxification) at a slower rate when consuming the monoterpene ⍺-pinene, and required 54% less digestible protein and 21% less digestible energy intake per day to maintain body mass and nitrogen balance. The mule deers' enhanced

physiological abilities to cope with low-quality, chemically defended forages relative to white-tailed deer might minimize potential competitive interactions in shared landscapes and provide a modest advantage to mule deer in habitats dominated by low-quality forages.

Comparing fecal DNA mark-recapture to mark-resight for estimating mule deer abundance on winter range in the eastern Sierra Nevada

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Monitoring big game populations is vital for making well-informed management and conservation decisions. In the eastern Sierra Nevada, the Round Valley mule deer (*Odocoileus hemionus*) herd is monitored using traditional mark-resight methods on winter range. Although mark-resight methods work well for estimating population abundance, animal capture for marking is expensive, invasive, and can be dangerous for animals and researchers. These drawbacks motivated us to evaluate fecal DNA-based mark-recapture, a non-invasive method for estimating population abundance. This method has been successful for estimating abundance in areas where it is difficult to use resighting methods but has not been evaluated on winter ranges where traditional methods work well. Our primary goal was to compare precision and cost of fecal DNA mark-recapture surveys to aerial mark-resight surveys for estimating population abundance. We used closed-capture models to estimate population abundance (N) and precision (CV), which we compared to estimates from concurrent aerial mark-resight surveys in 2019 and 2020. The economic analysis will evaluate whether fecal DNA mark-recapture has potential as a cost-effective and non-invasive method for estimating population abundance. Additionally, results from this study aim to advance the management and conservation of big game species by providing recommendations for long term monitoring of mule deer and other migratory ungulates.

Quantifying the impacts and assessing the permeability of a divided four-lane highway on migratory mule deer

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Increased human development and expansion has led to an ever-growing transportation network, which has created a variety of direct and indirect ecological impacts to wildlife. Wildlife crossing structures have become an increasingly popular mitigation strategy and a fundamental component of wildlife conservation throughout the United States. The study area for this project is a 14 km section of US Highway 395 in Mono County, California, where the California Department of Transportation has found a disproportionally high number of deer-vehicle-collisions (DVC's) and has identified it as the highest priority for implementation of wildlife crossing structures. This 4-lane section of highway bisects the migration corridors mule deer (*Odocoileus hemionus*) that annually move between winter and summer range. The main goal of this study is to use a multiple data source approach to identify mule deer crossing locations within the project area and make recommendations for placement of crossing structures. Specifically, we will use standardized roadside carcass counts that record all mule deer involved in DVCs to create a heatmap, which will identify DVC hotspots in the project area. We will also use GPS location data from collared mule deer in herds that migrate across US 395 in the project area to create a habitat-selection-function (HSF) model. From this, we will delineate crossing areas and identify environmental covariates that influence highway crossings. Finally, we will extrapolate from the HSF model to identify likely highway crossings for other mule deer herds that migrate across US 395 in the rest of Mono County.

Implication of prion disease across geographic populations: a case study examining wild North American deer

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Spongiform encephalopathies are caused by the misfolding of a common prion protein (PrPC) into an infectious conformation (PrPSc). Various prion amino acid polymorphisms are associated with three categories of spongiform encephalopathy: 1) familial, where disease alleles are inherited, 2) sporadic, in which mutations arise spontaneously, and 3) transmissible, where the prion disease is infectious among mammalian organisms. Chronic wasting disease (CWD) is the only transmissible prion disease documented in free-ranging and captive animals, specifically Cervids (deer species). Our hypothesis is that geographically-based genetic variation, arising in part from historical inter-species hybrid formation

and intentional translocations and movements, affects susceptibility to CWD. The aims of this research are to establish a PrP allele database, determine if PrP allele distribution is consistent with mitochondrial haplotype (cytochrome b) distribution and inferred hybridization history, and predict whether deer species in different geographic regions will vary in susceptibility to CWD. While transmission to humans has not been documented, the Centers for Disease Control and Prevention recommends testing any deer harvested in areas reported with CWD before consumption. Several known codon variants affect susceptibility to prion misfolding, some that spontaneously result in disease and others that can confer resistance (*Odocoileus virginianus*, white-tailed deer: Q95H, G96S, A116G; *O. hemionus*, mule deer: S225F). This is the first exploratory study to examine the PRNP exon 3 in North American deer species. To date, we have found the amino acid substitutions Q95H and G96S (confers reduced susceptibility to CWD) in populations of white-tailed located in New York, South Carolina, and Texas. Further, populations of mule deer in California and Alaska do not differ from other mule deer where CWD has been detected, indicating that mule deer populations in western states potentially have the same susceptibility to CWD.

Genetic diversity and connectivity of tule elk herds in Northern California's Interior Coast Range

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The tule elk (*Cervus canadensis nannodes*)—a subspecies endemic to California—was nearly driven to extinction in the late 19th century and has subsequently experienced multiple genetic bottlenecks. Active management, including reintroductions and augmentations, has facilitated population recovery; today tule elk number near 6,000 animals across 22 recognized herds. These herds exist in a metapopulation, with distinct groups separated by unoccupied intervening habitat, which can lead to increased population structure and rapid loss of genetic diversity in the absence of genetic exchange. Yet genetic status and connectivity among adjacent populations at the local scale is not well understood. We used 19 microsatellites and a sex marker to obtain baseline data on effective population sizes and gene flow of 4 such populations that were reestablished in the early- and late-20th century. Bayesian clustering suggested 5 discrete genetic clusters occurred corresponding to four primary populations and two subpopulations within the oldest herd. Genetic effective population sizes ranged from 15 (95% CI 10–22) to 51 (32–88). Evidence of gene flow among most populations was lacking, except for unidirectional gene flow to one population founded by emigrants of the other 30 years prior, and bidirectional gene flow between subpopulations within the oldest herd. We hypothesize that social cohesion, more so than landscape features, explained observed population structure. Understanding genetic status at the local scale is useful for guiding and improving management, including targeted translocations to maximize genetic benefits and creation of redefined harvest units to align quotas with biologically representative population dynamics.

Management of multiple migration routes for mule deer and elk across Idaho

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Seasonal migration routes used by elk and mule deer in Idaho, sustain these populations by providing viable movement paths to more productive summer forage necessary for recruitment and survivorship. There is an increasing interest in the conservation of ungulate seasonal migrations across the inter-mountain western US and these conservation efforts can co-benefit several other natural resource management goals and objectives. IDFG has assessed scores of seasonal migration route for mule deer and elk throughout Idaho and adjoining summer ranges via migration mapping routines that centers these routes based on winter herd sites and available location data. One challenge to conserving seasonal migration routes is that the distance these ungulates move (e.g., 10–100 mi), near always include several different land-stewardships, meaning that conservation will always require multiple stake holders and thus several management paradigms. Further complementing and complicating the diversity of stewardship, lager regional scale analyses often contain multiple species and several winter herds using sections of migration routes and summer range sympatrically. These spatially emergent properties of shared migratory routes and summer ranges present challenges to management since working across species and multiple winter herds since management guidance and methods are not as developed. In this talk, we attempt to prioritize mule deer and elk migration routes prioritized by the number of individuals, number of species, number of winter herds, and fiscal gains based on harvests that directly use specific migration route to sustain their life histories.

Using nutritional indices, population estimates, and harvest data to manage elk on a large private ranch in northeastern New Mexico

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Since 2009, Vermejo Park Ranch has used a landscape management approach to managing elk (*Cervus canadensis*) and other ungulates on its property. The overall goal is to manage all ungulates to what the ranch can support during an average dry year. This is particularly important since climate data suggests the southwestern United States will become drier and hotter in the future. Beginning in 2011, range data in the form of forage production and precipitation data were collected to establish forage availability for land carrying capacity. Historical elk survey data were used to develop a population model for the VPR elk herd. This model is updated annually based on annual helicopter survey data and harvest data. The model revealed an extremely high elk population and an elk populations reduction occurred from 2010–2016. As a result of this management approach, VPR has seen habitat improvements along riparian areas and aspen regeneration. Herd health is monitored via nutritional and trophy quality indices in the form of field dressed body weight, pregnancy rates, and antler scores. The results and findings are

shared and discussed with state biologists and neighboring landowners to maintain a healthy and viable elk population in the region.

Long-term (1870–2010) retrospective evaluation of forage resources for elk in north-central Idaho

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Disturbance and subsequent succession greatly influence forage quality and quantity may influence dynamics of ungulate populations. Long-term, landscape-level changes in forage resources for wild ungulates have rarely been reported despite compelling evidence that nutritional resources during summer may disproportionately affect productivity of ungulates. Therefore, we developed equations to estimate forage quality and quantity as a function of stand age in the major vegetation communities across 5 elk (*Cervus canadensis*) management zones in north-central Idaho. Using digital records of wildfire and forest management boundaries, we assigned, at 5-year intervals, forage quality and quantity estimates for each pixel from 1870–2015. We then reconstructed spatial-temporal patterns of forage quality and quantity and provided nutritionally explicit estimates of summer-range carrying capacity primarily as a function of disturbance and succession. In the late 1800s, >95% of our study area, predominantly forests in mid- to late seral stages, supported inadequate or marginally adequate forage resources for meeting nutritional requirements of lactating elk during summer. Substantial forest disturbance and concomitant elevated forage abundance occurred in the early to mid-1900s followed by low levels of disturbance and gradual declines in forage that continued into the early 2000s, although this pattern varied across our study area. Changes in nutritional carrying capacity varied up to 10-fold in response to wildfire and logging and were more related to forage abundance than quality. Existence and performance of elk and other wildlife may have depended on these periodic wildfire events in the region's forested areas for thousands of years.

Assessing the impacts of the recovering Mexican wolf population on elk behavior

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Predators change prey behavior, demographics, and movements. These changes have the potential to decrease the fitness of prey through a reduction in foraging time, increased stress levels, and use of lower quality habitat. Although the magnitude of these indirect effects are still debated, if strong enough, they can reduce birth rates and decrease neonate survival. Prey have the ability to reduce the indirect effects of predators through behavioral changes, such as increased vigilance. This study aims to quantify the effects of the Mexican gray wolf (*Canis lupis baileyi*) reintroduction to Arizona and New Mexico on elk (*Cervus canadensis*) behavior. We captured adult female elk across a gradient of wolf densities and fitted them with GPS collars. We captured a subset of calves from collared females and monitored their survival via VHF/GPS to determine maternal status. Lastly, we conducted behavioral observations to investigate the effect wolves have on elk behavior by using a predation risk metric derived from Mexican wolf spatial and temporal use of the landscape. We also investigated the interaction between the risk of predation with offspring presence/absence across three time periods relevant to maternal investment (i.e., pre-parturition, limited mobility, and social mobility) on elk behavior. The results from our preliminary Bayesian hierarchical analysis are pending but are expected to be completed for the presentation.

The role of supplemental feeding on winter elk aggregation and methods for assessing disease risk

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In Wyoming, supplemental feeding of elk during winter occurs on 22 feedgrounds, including the National Elk Refuge, and concern that feeding increases elk aggregation and thus the potential for disease spread has been rising. However, the comparison of feeding to other factors, including abiotic drivers of aggregation, such as snow levels has been underexplored. We assessed daily joint space use of elk and modeled contact rates as a function of abiotic weather-related effects and biotic effects such as supplemental feeding and hunting pressure. Daily contact rates of elk were 2.6 times larger when feeding occurred on the Refuge but was also regulated by snow cover and hunting pressure. The framework we present supports the evaluation of temporally varying management actions that influence aggregation broadly and can be easily implemented to answer questions about disease transmission, human-wildlife conflict, and inter-species competition. To further support future assessments and management of ungulate populations and wildlife more broadly we developed 'wildagg' an R package designed to streamline estimating, summarizing, and visualizing wildlife aggregation metrics using location information like GPS collar data.

Lessons learned from initial surveillance for treponeme-associated hoof disease in elk in California

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In April 2020, pathologists confirmed the first cases of treponeme-associated hoof disease (TAHD) in two Roosevelt elk (*Cervus canadensis roosevelti*) from northwestern California prompting design and implementation of a statewide surveillance program for TAHD. From July 2020 through June 2021, we worked with local biologists, hunters, federally recognized tribes, public land management agencies, and private landowners to collect hooves and document observations from hunter-harvested elk, opportunistic mortalities, and animals with signs of TAHD to determine distribution of the disease among three subspecies of elk across California. To estimate prevalence and improve overall herd health, we removed 33 visibly lame elk from the herd in which TAHD was initially detected and performed diagnostic testing and full necropsies. In total we visually inspected hooves from >360 elk for abnormalities suggestive of TAHD, using a 4-point scale to grade lesion severity. To confirm treponemes in association with suspect lesions, we removed wedge biopsies from the interdigital space of hooves for microscopic examination. Results of initial surveillance suggest high TAHD prevalence in the herd of initial detection with sporadic evidence of TAHD elsewhere. These efforts have improved our understanding of TAHD in elk in California and will inform adaptive management strategies, future surveillance, and research on this emerging disease.

Bull elk survival, vulnerability, and antler size in a partially migratory population

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Migration is a behavioral strategy used to access resources or avoid predation in spatially and temporally heterogenous landscapes. On the eastern slopes of the Rocky Mountains, elk migrate to higher elevation summer ranges to access higher forage quality and avoid predation risk. Thus, the decision to migrate has both individual and population level consequences. Antler growth and development is driven primarily by age and forage quality. Thus, if migratory animals can gain access to higher quality forage and avoid predation, migratory males will have higher fitness than residents. However, migration often results in transboundary populations being exposed to different levels of harvest as they move across the landscape. Our goal was to investigate these potential drivers of male elk survival and antler size in a transboundary, partially migratory population in a multi-carnivore system. We collared 75 bull elk in 2018–2020 for a total of 105 elk-years (mean = 35 collars/year). Male elk survival and antler size was

largely a function of age. Human harvest was the primary cause of mortality(n = 33) with wolf predation having little effect on survival (n = 2). Antler-point-restrictions resulted in low annual survival rates for male elk over 4 years of age (S = 0.42). While migration itself did not enhance antler size or survival, we found a negative effect of increasing forage biomass (and hence decreasing forage quality) on antler size. These advancements highlight the importance of correctly specifying management units while advancing our understanding of how vulnerability to natural and human predation risk affects male elk age structure and antler size.

Using hunter submitted antler measurements to estimate age of elk in Nevada

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Understanding age structure in wild ungulate populations is an important component of harvest management, particularly for state wildlife agencies with age-based harvest objectives. Cementum aging of extracted teeth continues to be the gold standard for accurately estimating age for many large-bodied terrestrial mammals. Nonetheless, extraction and processing of teeth can require significant investment of resources depending on agency needs. Techniques to estimate age of ungulates without teeth would be advantageous to wildlife agencies and personnel tasked with their collection. The Nevada Department of Wildlife (NDOW) has intermittently requested incisor teeth from elk (*Cervus canadensis*) hunters since 2001. We evaluated relationships between age and hunter submitted antler measurements to determine if a detectable relationship existed between age and antler growth exhibited by elk in Nevada. We found length of main beam to be a reasonable predictor of elk age up-to about 7 years when the slope of the curve, depicting length of main beam and age, flattened, and eventually decreased due to senescence. Beginning in 2015, NDOW formally adopted harvest objectives for antler length as a substitute for cementum aging. Comparisons of current age structure to historical trends indicates passive estimation of age, using antler characteristics, is effective for managing age structure of elk herds in Nevada.

Factors influencing predictions of understory vegetation biomass from visual cover estimates

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Accurately estimating forage biomass is essential for understanding the nutritional value of vegetation communities for wild herbivores like deer and elk. However, clipping, drying, and weighing vegetation by species requires substantial labor which may restrict the size and number of plots that can be sampled over a large geographical area. Therefore, visual estimates of plant cover and cover-biomass equations (e.g., double-sampling techniques) have been used for a variety of applications. However, sampling

strategy and environmental covariates have rarely been considered when developing cover-biomass equations. We estimated biomass from plant cover and evaluated environmental and sampling factors that could affect the cover-biomass relationship using 3,404 cover-biomass pairs measured in the Clearwater River Basin in North-central Idaho. Our study demonstrated that when carefully applied, double sampling techniques can streamline field sampling while providing cover-biomass conversion equations with moderate – high predictive ability (pseudo R2 from 0.25–0.99). We recommend using a Gamma family GLM, collecting > 20 cover-biomass pairs spanning a wide range of plant cover (1 to >50%) for each plant species and accounting for environmental factors (e.g., canopy cover and season) through interaction terms. Clipping vegetation on supplemental, targeted plots may be needed to provide adequate range in plant cover. Careful classification of plant species into plant structure groups can reduce the number of equations, but species-specific equations for plant species that are abundant, large, and most relevant to project objectives should be developed. Training is important to reduce observer bias and improve consistency, but may not alleviate inconsistencies among studies.

Assessing the effects of fire severity on elk forage quality and quantity in west-central Montana

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As large-scale and high severity fires continue to increase in frequency, understanding the impact of fire severity on nutritional resources for elk (*Cervus canadensis*) will be imperative for future management. Fire severity plays a key role in the amount of vegetation removed and the plant species that regenerate postfire, potentially altering the nutritional landscape and habitat available to wildlife including elk. We are developing nutrition models to evaluate how fire severity impacts elk summer forage quality (measured as kcal of digestible energy per gram of forage) and quantity (measured as grams of forage biomass per m^2) in mesic and dry mixed-conifer forests in years two and three after a large-scale wildfire in west-central Montana. To estimate forage quality and quantity, our field methods required intensive sampling to determine elk diets using DNA metabarcoding techniques and sampling vegetation plots across a gradient of fire severities and forest types. Field sampling was combined with remotely sensed data, and linear models were used to predict forage quality as a function of spatial covariates. Initial analysis shows that fire increased forage quality in both mesic and dry mixed-conifer forests regardless of fire severity in years two and three postfire. Forage quantity analysis is underway. We expect results from this work will be broadly applicable to western landscapes impacted by wildfire, and to elk management throughout the central Rocky Mountain region.

Influence of Mexican wolves on elk resource selection

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Predation is a primary limiting factor for prey and in addition to direct impacts (killing of prey), it establishes risk, which indirectly influences prey resource selection strategies. Our objective was to determine the influence Mexican gray wolves (*Canis lupus baileyi*) have on resource selection and spatio-temporal predator avoidance strategies of elk (*Cervus canadensis*). We captured 854 adult female elk over three years and fitted them with Iridium-GPS collars in the Apache-Sitgreaves, Gila, and Cibola National Forests in eastern Arizona and western New Mexico. GPS collar data was also collected on individual wolves (n ~ 77) in collaboration with the U.S. Fish and Wildlife Service. A step-selection function for elk was assessed in relation to habitat attributes, climatic conditions, and diel activity patterns across areas of varying wolf densities to understand the extent the re-establishment of wolves' influences elk populations. Multiple measures of predation risk were examined in relation to elk resource selection, including an index of wolf presence—a function of wolf resource selection, utilization distribution, and pack size—as well as density of wolf-killed elk, openness, and predicted risky areas, modeled from attributes of known wolf-killed elk sites. We assessed if elk are using human refugia or areas of low wolf utilization as low-wolf risk "islands" to mitigate predation pressure and also investigated if elk are altering when they select resources to utilize riskier places at less risky times. The analysis of data is currently in progress, so preliminary results are pending.

Behavioural disparity in a partially migratory elk herd on a sympatric winter range

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Sociality incurs costs and benefits for group-living animals, resulting in behavioural trade-offs, such as dominance, that may drive patterns of association among group members. We examined interaction patterns among elk in the partially migratory Ya Ha Tinda (YHT) elk herd (*Cervus canadensis*) in Alberta following three migratory tactics (residents; eastern migrants; western migrants). Because familiarity may influence dominance and thus group interactions, we predicted that familiarity would be higher within versus among migrant tactics, and thus 1) spatial overlap will be lower among versus within tactics, and 2) rates of interaction and aggression will differ among tactics. At the home range scale, we used GPS telemetry data to document home range overlap of collared female elk on the sympatric range during the winters of 2015–2018. We determined the volume of intersection (VI) of 95% utilization distributions (UD) during the winter between all tactics (resident-resident, resident-eastern, resident-western). Mean overlap was high (0.78 ± 0.013 SE) among all pair types, though resident-eastern overlap was higher (P < 0.005) than resident-western overlap (P < 0.005) compared to average resident-resident VI. At the individual level, we evaluated dominance from direct observations of conspecific interactions during winters 2019–2020 relative to migrant tactic, age, density, and time of year. Preliminary results suggest differences in aggression rates among migrant tactics, but similar rates of

interaction overall (range 0.0031± 0.0005–0.0035 ± 0.0004 interactions/min.). We discuss the differences in dominance among migratory tactics and the effect of this on forage acquisition and predation risk.

Environmental factors influencing forage digestible protein and digestible energy during 6 years of landscape restoration in New Mexico

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Due to historical land use and fire suppression, forests in northern New Mexico are at abnormally high risk for catastrophic wildfires. In response, a coalition of agencies under a USDA Collaborative Forest Landscape Restoration Project began restoring 210,000 acres in the Jemez Mountains via forest thinning and prescribed fire. As part of these restoration efforts, we are monitoring the responses of collared Rocky Mountain elk (*Cervus canadensis*) and mule deer (*Odocoileus hemionus*) relative to changes in forage quality. From 2013–2018, we collected data from 200 vegetation plots (60–70 monthly in summer and seasonally; 130–140 annually in summer) stratified within 6 dominant stand types. Within each plot, we established a 200 m transect and measured herbaceous and shrub biomass, soil moisture, and collected forage nutrition (crude protein, tannins, etc.) and soil quality (pH, nitrates, etc.) samples. We used ANOVAs and GLM stepwise regressions to determine the effects of restoration efforts, wildfires, environmental factors (elevation, aspect, etc.), and soil characteristics on forage quality. Overall forage quality varied (P < 0.05) among stand types, treatment types, and treatment ages. Regression models suggested that season, stand type, northness, and soil moisture consistently influence digestible protein and energy, while other factors varied in significance. Forage protein was higher in aspen and oak stands and following wildfire, while forage digestible energy was higher following most restoration methods within 1–5 years. These results are crucial to evaluating the success of the restoration efforts while providing a rare long-term perspective of forage for ecologically and economically valuable species.

Surveillance for an emergent hoof disease in elk in the U.S. Pacific West supplemented by metagenomic analysis

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A novel hoof disease of elk (*Cervus elaphus*) emerged in southwestern Washington in 2008 and was subsequently diagnosed in northwestern Oregon in 2014. The disease, currently referred to as treponeme-associated hoof disease (TAHD), is characterized by a range of lesions from mild erosions to severe ulcers with overgrown or sloughed hoof capsules that exhibit characteristic histologic lesions. We conducted intensified surveillance in 2018-2020 by opportunistically obtaining 158 cases from four Pacific West states. We detected TAHD for the first time in Idaho and northern California, as well as in multiple counties in Washington and Oregon where it was previously not reported. Using a subset of 29 cases, we evaluated 16S rRNA amplicon sequencing as a supplemental tool that could be applied in TAHD surveillance and to better understand the etiology of this presumed polybacterial disease. Operational taxonomic units of the family Spirochaetaceae were identified in 10/12 histologically diagnosed TAHD-positive cases and 2/10 TAHD-negative cases. Phlya Spirochaetae ($P < 0.008$), Fusobacteria ($P < 0.006$), and Tenericutes ($P < 0.01$) were significantly overrepresented in samples from TAHD-positive feet when compared with TAHD-negative feet. A unique spirochete, PT19, was detected in 14/16 samples from the 12 elk in which spirochetes were detected by 16S and from at least one elk collected from each of the four states. Given the unexpectedly broad disease distribution, further surveillance is required to determine the full geographic extent of TAHD and 16S may contribute as a diagnostic screening tool or for confirmation of histologically diagnosed cases.