A Comparison of Nutritional and Foraging Ecology of Sympatric
Mule and White-tailed Deer

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Mule deer (Odocoileus hemionus) and white-tailed deer (O. virginianus) are the only 2 extant
species in their genus, are similar in morphology and life history, and can hybridize where
sympatric. However, their distributions are segregated across much of their ranges in North
America, with a zone of overlap primarily along the Rocky Mountains from Canada to Mexico
(Fig. 1). Although these deer have been extensively studied in areas of both allopatry and
sympatry, the role of potential differences in their fundamental dietary niche in shaping each
species’ distribution has yet to be explored. Previous studies documented a wide range of
dietary overlap between the species depending on location, but have been unable to determine
whether the extent of dietary overlap reflects differences in dietary or habitat niches because
diet composition was confounded with habitat use in these studies. Therefore, we compared
nutritional ecology of mule and white-tailed deer in a common garden experiment during which
tractable individuals of each species were allowed to feed together in the same habitats across
a wide range of forage conditions in dry conifer forests in northeastern Washington, USA. We
hypothesized that if mule and white-tailed deer truly differ in their fundamental dietary niche, we
would detect differences in their diet composition caused by differences in foraging behavior,
dietary quality, daily intake, or diet selection when they forage in the same space at the same
time. Finally, we predicted that when forage biomass was low, diets of sympatric deer would
overlap more frequently as they were forced to compete for limited resources.

Four female deer of each species were acquired as newborns from eastern Washington and
hand-raised together. From June – August 2016, these animals were placed in 0.5-ha
enclosures across 21 forest stands in areas of northeastern Washington where mule deer and
white-tailed deer co-occur. In each enclosure, we measured biomass of all understory plant
species, measured harvesting rates and diet composition of each deer using bite-count
methods, and estimated daily foraging time using calibrated activity sensors. In addition, we
measured the nutritional quality of each deer’s diet and major forage species found in each site.
We compared foraging parameters between deer species using crossed random effects models
with site and animal as grouping variables. We compared dietary similarity using the Bray-Curtis
non-metric multidimensional scaling method. When living together in the same stands, both
deer foraged for 44% of their day. However, mule deer took larger bites and harvested forage
faster, whereas diets selected by white-tailed deer were more diverse and nutritious. Mule deer
achieved a 20% higher daily digestible energy intake than white-tailed deer. Both species
selected diets of mostly deciduous shrubs and forbs, but across the 119 species of plants
consumed by all deer combined across all sites, estimated similarity of plant species in diets of
mule deer and white-tailed deer was only 48%. Contrary to our expectations, deer diets were
the least similar when the biomass of forages was either very low or very high (Fig. 2). Our
results suggest that mule deer may be able to tolerate forages with more fiber and higher levels
of some secondary metabolites, such as tannins. In addition, the dietary niches of the
Odocoileus species may differ enough that they partition resources both when competing for
limited forage and when food is so abundant they can each specialize. Confirming these
findings requires further studies comparing mechanics of foraging, digestion and detoxification
by deer.
Figure 1: Distribution of extant populations of mule and white-tailed deer in North America.

Figure 2: The relationship between diet dissimilarity and acceptable biomass for mule deer and white-tailed deer across 21 forest stands in dry conifer forests in northeastern Washington from June–August 2016.
A Comparison of White-tailed Deer Harvest Rates on Public Versus Private Land: The Impact of Age and Sex

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The management of age structure and sex ratios in white-tailed deer populations are important objectives for biologists and state managers seeking to improve hunter satisfaction while maintaining appropriate deer densities. The management of public versus private lands is complicated by differences in hunter densities [1], management philosophies [2], and habitat quality. The impact on rates of harvest mortality among different age and sex classes are poorly understood, particularly when harvest regulations do not differ between landownership types. We monitored cause-specific mortality in 66 fawns (~6 months old), 72 subadult males (1 – 2 years old), 57 adult females (≥ 2 years old), and 33 adult males during the hunting season (1 September – 31 January) from 2015 – 2017 in Sussex County, Delaware, USA (Fig. 1). Non-harvest related mortalities (n = 8) and collar failures (n = 12) were right censored from analysis. Overall, rates of harvest related mortality were relatively low in fawns (0.08; SE = 0.03) and adult females (0.07; SE = 0.03), but greater in subadult males (0.36; SE = 0.06) and adult males (0.40; SE = 0.08). We tested for differences in rates of harvest mortality among deer that were exclusively on private land and for deer that utilized public land during the hunting season using a log-rank test. We did not find any difference in rates of harvest between public and private land in fawns, adult females, or adult males. The harvest rates for subadult males however, was greater (P < 0.01) for deer that utilized public land (0.73; SE = 0.08) than for deer that only utilized private land (0.20; SE = 0.06). We observed low rates of harvest for antlerless deer on both public and private lands. Overall rate of harvest was greater in adult males than subadult males, but hunters on public land appeared to select for males regardless of age, while private land hunters restricted harvest primarily to adult males. Rates of harvest mortality among subadult males on private land were comparable to research from properties that actively manage male age structure [3,4], but harvest on public land was similar to research from areas lacking such management [5] and likely limited male age structure within the study area.

Figure 1. Deer were captured on a combination of public and private lands (dark gray) in Sussex County, Delaware, USA from 2014 – 2017.
References
A Headache From Our Past? Cranial Abscess Disease And A Legacy Of Translocating White-tailed Deer

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Intracranial abscessation-suppurative meningoencephalitis, commonly referred to as a brain abscess, is a reported cause of natural mortality, particularly for mature, male white-tailed deer (Odocoileus virginianus). Most cases of brain abscesses are associated with infection by the opportunistic bacterium Trueperella pyogenes (formerly Arcanobacterium pyogenes) but little else is known about the disease. We examined 4983 male white-tailed deer across 60 sites throughout Georgia, USA for signs of cranial abscesses, the etiological predecessor of brain abscesses, to model the distribution of the disease across the state and investigate risk factors for the disease. A generalized linear mixed model treating property as a random effect suggested that age was the most important risk factor. Furthermore, vegetation and soil features of each site were not strongly associated with increasing risk of the disease. However, the model suggested that a large amount of variance occurred at the site level.

We speculated the occurrence of this disease to be influenced by virulence of T. pyogenes residing along the skin layer of white-tailed deer in geographically distinct metapopulations. To investigate if the virulence of T. pyogenes was affecting the variation in disease occurrence across sites, we examined the infectious potential of T. pyogenes from the foreheads of apparently healthy male white-tailed deer harvested from a subsample of 28 of 60 sites (Fig. 1). We used Polymerase Chain Reaction (PCR) to determine the presence of seven different virulent determinants. Six of the seven virulence determinants, all of which promote bacterial adhesion to epithelium, were more commonly detected on properties where abscesses were found (p≤0.05; Fig. 2). Our findings suggest differences in pathogenic-potential of T. pyogenes at individual sites may help explain spatial variability of this disease. Incidence of cranial abscess disease in Georgia appears associated with areas restocked with white-tailed deer from a single location in Wisconsin between 1962 and 1963 (Fig.1). Given the spatial distribution of this disease, we speculate these genetic differences in T. pyogenes may have arisen from white-tailed deer restocking efforts, and our observations may be a legacy of an introduced disease manifesting itself generations later.
Figure 1. Location of sites where we quantified the presence of *Truepella pyogenes* and 7 associated virulence determinants from swabs taken from the forehead of hunter-harvested, apparently healthy adult (≥1.5 years old) white-tailed deer. Deer were also examined for the presence cranial abscess disease in Georgia, USA during Fall 2011 and 2012. We considered sites in which an adult (≥1.5 years old) male deer was detected with a cranial abscess to be positive for this disease. Counties colored in red represent locations where historic records demonstrate a) deer from the Sandhill Game Farms in Wisconsin, USA were released and b) and only counties in which records indicate ≥20 deer were released (Blackard 1971). The occurrence of cranial abscess disease seems strongly linked to areas where the predominant restocking source was Wisconsin.

Figure 2. Percent occurrence of virulence determinants of *T. pyogenes* from the forehead of white-tailed deer. Grey colored bars represent the percent occurrence from sites where no cranial abscesses were found (17 unaffected sites; n = 88 samples), whereas black bars represent the percent occurrence from sites where cranial abscesses were found (11 affected
sites; n = 96 samples). Results of a chi-square test suggested significantly higher frequency of virulence determinants at affected sites (p < 0.05), excluding cbpA.
Chronic Wasting Disease (CWD) was discovered in Newton County, Arkansas in February 2016. Not only was CWD identified in a free-ranging white-tailed deer but also in Arkansas’s free-ranging elk herd. Once CWD presence was confirmed, agency staff immediately implemented actions to determine the prevalence and distribution of the disease and to begin discussions on future management. One fundamental aspect of the agency’s response and continued actions is communication with hunters and other constituents. The Arkansas Game and Fish Commission (AGFC) have found that, in regards to communication of CWD management to the public, a measured response is crucial. An agency that relies on hunters to manage the resource and provide valuable funding through hunting license sales must balance discouraging participation by over-messaging any speculated harm of the disease, while avoiding minimization of the science and portraying any sense of complacency. AGFC has attempted complete transparency and open communication to educate hunters and other constituents on what is known about CWD in Arkansas and the value of developing a strong working relationship. The messaging was targeted statewide, incorporated diverse media outlets, and active dialogue, while aiming to consistently build long-term partnerships. The AGFC believes that any attempts to manage CWD without the valuable partnership of Arkansas’s hunters and the various stakeholders would be sure to fail. The presenter will discuss in further detail the various aspects and challenges the agency faces as it continues to manage CWD and the various trials associated with keeping a team approach active and viable.
A New Paradigm for Huemul Conservation

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The Patagonian huemul (*Hippocamelus bisulcus*), an endangered deer native only to Chile and Argentina, has less than 1500 individuals remaining, with an approximate third of these in Argentina. Of the estimated 101 populations left, none on the eastern side of the Andes (Argentina) are expanding, and 60% of these are known to have fewer than 10-15 animals. Although the huemul has been declared a natural monument, and as such receives the highest protection allowed under Argentine law, the conservation strategies of the past three decades have failed as shown by the lack of recovery of any of the approximate 50 subpopulations in Argentina [1]. In this presentation, we will review the history of huemul conservation and the philosophy behind the decline, which determined which strategies were emphasized over the past three decades. Now, recent studies, revealing new perspectives on the situation, are taking the attention away from actual proximate to ultimate causes [2,3,4]. Cattle, for one, have been blamed since 1992 as one of the predominant factors behind the decline of the huemul numbers [5]. Yet, removal of cattle from various areas hasn’t shown any population recovery response of huemul. To the contrary, a cattle removal program in one Argentine national park resulted in a 17.6% decrease of that huemul subpopulation over a 5 yr period, which coincided with a 19.2% decrease in the densities of fecal pellets along established transects [6]. Moreover, cattle ranching has been compatible with a huemul population on a southern Argentine ranch since the early 1990s. Attention needs to be directed towards other diagnoses, especially given other evidence. Live and dead specimens of huemul from the east and west of the Andes consistently reveal clinical signs of osteopathologies in at least six populations and a shortened lifespan (0 adult age of 3.1 in one Argentine population, n=20) [2] that are accompanied by trace mineral deficiencies (i.e., selenium and iodine) in the soils of the upper ranges [7,8] where huemul currently remain year round as resident deer. We will describe how anthropogenic activities resulted in the loss of migrational behavior to historic winter ranges, which ultimately would then be responsible for the current situation. With this knowledge, conservation efforts are now shifting to focus on bringing huemul back to their former ranges, while keeping in mind the basic nutritional requirements for trace minerals. Meanwhile, opinions are polarized in the huemul conservation community today, which seriously hinder progress. As in all paradigm shifts, resistance is expected. We will discuss means to minimize these roadblocks and the progress thus far achieved, including an overview of recent advances in huemul research and conservation efforts in Argentina.

References:


A New Species of Dwarf Deer (Cervidae: Previously in the Genus *Pudu* Gray 1852)?

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The deer from South America have a complex and confusing taxonomy, caused by originally having been based only on morphology. Once genetics were used to elucidate the phylogeny, the trees became scrambled: while some problems were resolved, more questions were added. It can be said that the lack of resolution was in part due to the large number of species included in the analyses while at most a single gene or few samples from a species was used. Recent publications disentangle the problem a little but still doubts remain. The last publication by Gutiérrez et al. [1] fills up several blanks thanks to a larger sample size used, but leaves areas still unresolved, such as "How far apart are some species from others in the taxonomic tree?", a question that needs sampling using other genes to be properly answered. One of the main unresolved areas is the taxonomy of the "Pudu" species as currently known, with the two species considered to be nested in totally separate genera-related branches with the northern species being basal to at least 6 different other genera.

"Pudu species"
The genus *Pudu*, as currently known, includes two species, the northern pudu (*Pudu mephistophiles*) from the Andean forests of Colombia, Ecuador and Peru, and the southern pudu (*Pudu puda*), from the Patagonian forests of Argentina and Chile. "*Pudu* mephistophiles", as recognized today, has its distribution split in two geographically allopatric populations. The northern population of *P. mephistophiles* distributes throughout the southern two-thirds of the central Andes of Colombia to the northern tip of the Peruvian Andes, close to 5°14'S. The second population, cut off from the first one, occurs along the northern and central part of the eastern Peruvian Andes, east of the Marañón, from 5°42’30"S to 11°15’S. The gap between the two populations is caused by the Huancabamba Depression, a barrier of low elevation and drier environments along the Huancabamba and Marañón Rivers. Here I suggest a new "Pudu" taxon based on the geographically allopatric "*Pudu* mephistophiles" population that had never been analyzed taxonomically, not even morphologically. This separated population had already been mentioned as deserving a morphological analysis back in 1969.

The "new taxon" proposed here is distributed along the montane forests of the eastern Andean Cordillera on the central Peruvian Andes. Differences in morphology, geographic distribution, including ecological niche preferred, and probably genetics (process pending) render this allopatric population as a different species from the northern one. The collected and studied specimens come from 1800 to 3500masl in Peru, mainly from the cloud forest, as opposed to 2800-4500masl reports for Ecuador, mainly in highland Páramo [2]. A test comparing BW and ZB measures for each of the three taxa separates the eastern montane Peruvian population from the other two species (Figure 1). Its skull length of 148.2 mm (full adult female), based on the only skull with the pre-maxilla not broken, added to the ZB and BW data in a PCA puts the species skull closer to *puda* than *mephistophiles* (Figure 2), besides the different physical appearance of the skull among the three taxa.

This "new taxon" is characterized by a dark orange reddish body, sometimes with a narrow yellowish tinge on the lateral and front neck, dark brown head and legs, small white inner ears, and fawn colored underside. Overall, species currently allocated to the genus *Pudu* are distinguished from other Cervidae primarily by their very small overall size, a trait shared with a couple of species currently allocated to the genus Mazama, by the small size of their extremities, and the coalition of the cuboid-navicular bone and the medial and external cuneiform tarsal bones in a single element, a characteristic also present in the Asian cervids.
Muntiacus and Elaphodus. Additionally, cervical vertebrae in what were these 3 “Pudu” dwarf species are very short, as opposed to the relatively longer length in most deer species’ vertebrae. This and the longer legs give the “Mazama” dwarf species an appearance of being more proportionate. I evaluated discrete and mensural morphological characters to compare the two allopatric northern populations, to define the status of the Peruvian population of the northern pudu, and will overlay this information on the molecular genetic evidence. The number of specimens available for the Peruvian population is still small, and additional specimens are needed to help elucidate the evolutionary history of this new dwarf deer.

References

Figure 1. BW vs ZB (Green: puda, maroon: mephistophiles, orange: new taxon)

Figure 2. PCA including skul TL, ZB and BW (yellowish: puda, maroon: mephistophiles, orange spot: new taxon)
A Synopsis of an 8 Year Evaluation of a Population of Mule Deer (*Odocoileus hemionus*) on the Mojave National Preserve, California USA.

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The changing climate will likely have strong effects on arid environments as a result of increased temperatures, increasing frequency and intensity of droughts, and less consistent pulses of rainfall [1]. Understanding the link between the environment and population performance of species occupying these environments will continue to increase in importance as climatic shifts occur within these natural ecosystems. We captured and radio-collared 198 adult female and 110 juvenile mule deer (*Odocoileus hemionus*) from 2008 – 2016 throughout 3 study sites on the Mojave National Preserve, California USA. We evaluated how environmental conditions and habitat characteristics affected seasonal resource selection, adult survival, and juvenile recruitment. We also sought to test how the access to perennial, manmade water sources affected adult body condition and reproductive output. Lastly, we then focused on the reproductive timeframe of adult females and assessed parturition site selection and tradeoffs associated with the reproductive timeframes. Adult mule deer exhibited smaller home ranges in the study site with a higher density of permanent water sources (95% KDE= 1005ha versus 1610ha and 1960ha) and selected areas closer to water sources regardless of season and site (P=<0.001) [2]. Additionally, adult survival varied annually and was affected by life history stage (reproductive time period) and drought conditions (Palmer Drought Severity Index; β=0.65 95% CI= 0.15 – 1.15). Precipitation events occurring in mid- to late-pregnancy (January – April) leading to spring green-up (β = 0.52 95% CI= 0.27 – 0.77) and neonate structural size (β =0.33 95% CI= 0.10 – 0.56) had the strongest positive effect on juvenile survival and recruitment [3]. We did not detect an effect of permanent water access on body condition (P=0.555), but did identify a positive, effect of total accumulation of precipitation from the previous year (P= <0.001). The top model for probability of producing twins did not contain an effect of study area but suggested a positive influence of body condition (β = 0.45 95% CI= -0.08 – 0.99). Females chose parturition sites closer to permanent water sources, at higher elevations, further from roads, and with higher amounts of shrub cover relative to what was available on the landscape. Lastly, we evaluated resource and habitat selection of females during 3 reproductive time periods; pre-parturition, provisioning young, and post juvenile mortality using a novel means of evaluating resource selection with GPS data [4]. We found that females selected areas more rugged while provisioning young compared to pre-parturition and post- juvenile mortality (Relative Importance=1 versus 0.62 and 0.54 respectively) potentially indicating anti-predation risk behavior. We also observed selection for higher amounts of NDVI (Normalized Difference in Vegetation Index) as the reproductive timeframes progressed suggesting increased nutritional requirements after provisioning nutrients to young (Relative Importance= 0.05, 0.30, and 0.34 respectively). The results from this robust evaluation of mule deer occupying a harsh, arid environment will aid in the management and conservation of these populations moving forward. Furthermore, understanding the link between environmental patterns and population performance has vast implications for comprehending how our natural ecosystems will react to the expected shifts in climate throughout our natural world.
References
A novel method to estimate spatio-temporal deer abundance dynamics by a Bayesian integrated population model

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Estimation of deer abundance and its spatio-temporal dynamics are essential for population of management of deer species. There are many methods to estimate wildlife abundance. However, it is difficult to obtain sufficient data to estimate wildlife abundance by classical estimation ways because of budget limitations. It is necessary to develop a model that can integrate various but fragmented data to estimate spatio-temporal deer abundance dynamics. The objective of this study is to develop a model to estimate spatio-temporal abundance dynamics of sika deer (Cervus nippon). I used monitoring data of sika deer that were obtained in Yamanashi Prefecture, central Japan. The monitoring data included three type of deer abundance indices, the number of hunted and culled deer, and landscape characteristics. The three indices were seen deer per unit effort (SPUE) obtained from hunters’ reports, pellet group density, and block count survey. As the landscape characteristics, the percentages of evergreen forests, deciduous forests, and artificial grasslands were obtained. The number of hunted and culled deer was available from 2005 to 2015. The period and sampling area of three deer abundance indices differed. I constructed a Bayesian integrated population model for these data. In the model, I assumed that the latent spatio-temporal deer abundance correlated with three deer abundance indices, deer abundance decreased by hunting and culling but increase by population growth rate of each location that was affected by the difference of carrying capacity of each location. The carrying capacity of each location was assumed to be determined from landscape characteristics. The developed model could estimate deer abundance by 5 km square unit from 2005 to 2015. The carrying capacity of each location was enhanced by the higher percentages of deciduous forests and artificial grasslands. The result indicated that the increase of food availability provided suitable habitat for sika deer. The increase of deer abundance was regulated by hunting, culling, and density-dependence that was determined from the relationship between deer abundance and carrying capacity.

Compared to other estimation ways, a Bayesian integrated population model had advantages as: 1) the model could incorporate various but not-systematically obtained monitoring data, 2) the model could consider the latent and unobservable population dynamics of target species, and 3) the model could discriminate the stochastic error and observation error. If other type of data about vital rate of sika deer from capture-recapture, GPS tracking, or camera-trapping are obtained, the model can be easily expanded to estimate such vital rate by incorporating these data. Furthermore, the information about spatio-temporal abundance dynamics will contribute the development of hunting and culling program of target species.
Deer vocalizations have been shown to be extremely varied and conspicuous in their frequency and temporal parameters, especially in rutting calls of Old World male polygynous deer. These calls also convey important information about the size and quality of the caller through their pitch and formant parameters which is used by other males and females in their evaluation and mate choice [1]. In contrast, little is known about vocalizations in New World Odocoileine deer. The males produce courtship grunts, they produce snorts instead of barks in alarm situations and females and fawns have calls that seem similar to those in Old World deer. Only a few spectrograms have been published on vocalizations in the white-tailed deer, Odocoileus virginianus, in North America [2]. A few recordings of moose (Alces alces) and reindeer (Rangifer tarandus) have also been done. Male mating calls have also been used to make a phylogeny of 11 representatives of the family Cervidae [3]. However, in these studies, Neotropical deer are not included.

Neotropical deer comprise 6 genera and at least 17 species [4]. The most speciose genus is Mazama, the brocket deer, currently with 10 species accepted. M. americana, the largest species, probably includes several cryptic species. All brocket deer are very similar morphologically and it is difficult to distinguish between species of similar size. They are solitary, territorial and live in regions of dense cover.

The objective of this study was to record the vocalizations and analyze the pitch parameters of individuals of Neotropical species available, especially Mazama in order to characterize them and to see 1) whether there are reliable differences among species that could be used taxonomically 2) possible functions 3) whether there are individual differences that would permit individual identification.

Recordings were made at the Horco Molle Experimental Reserve in Tucuman, Argentina, and at the Deer Research and Conservation Center, FCAV, UNESP, Jaboticabal, SP, Brazil. Deer recorded included the red brocket Mazama americana (5 males, 4 females), the brown or grey brocket M. gouazoubira (4 males, 3 females, 1 fawn), the Amazonian brown brocket M. nemorivaga (3 males), the Brazilian dwarf brocket M. nana (1 male), the white tailed deer Odocoileus virginianus (1 male), taruka Hippocamellus antisensis (1 male) and swamp deer Blastocerus dichotomus (1 male). Captive deer were allowed to interact with humans (in the case of hand-raised deer) or with a female deer. Adult male deer vocalized as they showed sexual behavior (courtship licking, mounting attempts). Some females vocalized with a male or when they heard humans. Recordings were made with a digital recorder and shotgun microphone and analyzed with the programs Audacity and Praat 5.1.37 DSP. The Sound Edit menu was used to determine fundamental frequency F0 (pitch) and duration parameters. Pitch parameters analyzed included F0 Mean, Maximum, Minimum, and the frequency at the beginning, middle and end in each call. Vocalizations of 3 species of Mazama, in which various individuals were recorded, were analyzed statistically with a linear hierarchical model, using
species, sex and age as fixed variables and individual, call and recording year as random variables.

All vocalizations were short duration, low intensity bleats, usually produced repeatedly with an interval of one to 30 sec or more. Some individuals produced bouts with from 3 to 18 bleats with intervals of < 1 sec. Durations of bleats ranged from 0.05 to 0.3 sec, with some exceptions (one female). Frequencies ranged from 100Hz for *O. virginianus* to 300-400Hz in other species and up to 600Hz in the fawn. There was great variation in parameters between calls and individuals. Frequency parameters were not related to body size. The statistical analysis of 3 brocket deer species showed considerable overlap among species and significant individual variation in all cases (p<0.001). There were no differences between sexes. Among the males, *M. nemorivaga* had durations significantly longer (p=0.012) than the other two species, while all the frequency parameters were significantly higher (p=0.011-0.017) in *M. americana* than in the other two species. There are significant differences with age in *M. gouazoubira*.

There are differences in species in the acoustic parameters of their bleats, but these differences are not great enough to distinguish reliably among species. Individual differences are striking, but the significance of this is not clear in solitary species where mate choice is limited and reproductive barriers not well developed [5, 6]. Also, under the conditions of these recordings, only a minority of the individuals vocalize. Males seem to vocalize when they are sexually aroused and courting a female and the female could possibly be stimulated by the males’ calls. Some females of *M. americana* vocalized when they were with males, but it seemed to be in rejection of the males’ advances. Females of *M. gouazoubira* and *M. nemorivaga* were not observed to vocalize in the presence of males. Most female brown brocket vocalizations were observed in juveniles and may be a retention of infantile behavior, since all fawns vocalize. No mothers with fawns were available for recording in these experiments, so the characteristics of these calls are not known.

This study confirms again that, between species, F0 is not related to body size. Two of the larger species (*M. americana*, *H. antisensis*) had the highest frequencies, while there was considerable overlap among the other species of *Mazama*, despite considerable size differences between *M. nana* and the other two.

**References**

Adult Female Survival and Population Dynamics of White-tailed Deer in Louisiana, USA

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Recent studies on white-tailed deer (*Odocoileus virginianus*) neonates in the southeastern U.S. have indicated that rates of survival have declined in some areas. Vital rates, including adult female survival, fecundity, and neonate survival, can have varying effects on population growth, and few studies have used field-based vital rates to conduct sensitivity analyses or model deer population trajectories under potential changes in survival rates. Restoration of large carnivores, such as the Louisiana black bear (*Ursus americanus luteolus*), may contribute to decreased survival rates, and managers are interested in the long-term effect of restoration efforts on the sustainability of deer populations. During 2013-15, we radiocollared and monitored 70 mature (≥2.5 years) and 21 yearlings (1.5-year-old) female deer on Tensas River National Wildlife Refuge, Louisiana, USA (TRNWR). Annual survival averaged 0.815 (95% CI = 0.734-0.904) for mature females and 0.857 (95% CI = 0.720-1.00) for yearling females. Using observed values of neonate survival, female survival, and fecundity data from TRNWR, we estimated an increasing population trajectory ($\lambda = 1.043$). We modeled low, medium and high values for these parameters and determined that survival of mature females was the most elastic vital rate. For potential harvest intensity scenarios, we projected the population for 10 years using observed vital rates. Projections for 0% ($\lambda = 1.126$) and 10% hunting mortality ($\lambda = 1.041$) predicted increasing populations, whereas 20% ($\lambda = 0.959$) and 30% hunting mortality ($\lambda = 0.878$) resulted in population declines. Reductions in neonate survival led to population declines ($\lambda = 0.950$), but elimination of female harvest offset declines ($\lambda = 1.037$). Our results suggest that deer populations on TRNWR are sustainable under current harvest guidelines. If neonate survival decreases, reductions in female harvest or predator populations may be necessary. Therefore, managers will need to balance public perception and acceptance, economics, and population dynamics when assessing potential management strategies.
Analysis of Allelic Variation in Prion Protein Gene of Texas Mule Deer

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Chronic Wasting Disease (CWD) was discovered in North American cervids in 1980 and has become a major management concern in recent decades. Chronic wasting disease was detected in Texas mule deer (*Odocoileus hemionus*) in 2012, most likely spread to Texas from New Mexico via natural movements of mule deer in the Hueco Mountains. Management has focused on containment of the disease as the most realistic and economically viable option. There is no cure or evidence of resistance to CWD, but mutations in the prion protein (*PrP*) gene affect susceptibility, incubation time, and the ability to detect the disease. We amplified and sequenced the *PrP* gene from tissue samples collected at CWD check stations in the Trans-Pecos and Panhandle regions of Texas during 2012-2015. We observed both synonymous and nonsynonymous mutations in the *PrP* gene, including six not previously reported in cervids. Twenty deer phenotypically identified as mule deer had nucleotide substitutions at codon 96, mutations originally identified in the white-tailed deer (*O. virginianus*) *PrP* gene. Seven mule deer had mutations at codon 225, resulting in an amino acid substitution associated with CWD prevalence and progression in Colorado and Wyoming populations. Our preliminary results reveal a diverse set of *PrP* alleles in Texas mule deer, due to past hybridization and backcrossing with white-tailed deer, as well as novel nonsynonymous mutations, with unknown significance. Genetic variation in the *PrP* gene has implications for detection of CWD and future management decisions throughout the state aimed at controlling the spread of the disease.
Animal-indicated nutritional carrying capacity: a nutritional approach to assessing the capacity for population growth

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Density dependence is an essential component for understanding the ecology of many species, especially $K$-selected large mammals. Misunderstandings, however, abound from failing to recognize that density dependence is both a life-history characteristic of a species, and a functioning attribute of populations. Despite methodological advances, interactions among predation, climate, and density dependence continue to obscure factors ultimately responsible for regulating population growth. Through long-term, individual-based monitoring of demography and nutritional condition, my colleagues and I have revealed the importance of nutrition for understanding life-history characteristics and population regulation of large herbivores. Nutritional condition is a product of an individual’s environment because it integrates nutrient intake and demands, which are a function of habitat, density dependence, and reproduction. Nutritional reserves are preferentially used to support survival and secondly to support reproduction in long-lived herbivores, thereby creating important links from habitat to nutrition to population dynamics. Nutritional condition in turn, can indicates the relative position of a population to its annual food supply (i.e., nutritional carrying capacity), and can yield a practical measure of the potential for population growth. Furthermore, nutrition illuminates the consequences of mortality, because it ultimately determines the baseline potential for survival and recruitment of young—mortality up to this baseline is imminent and irrespective of the proximal cause. In summary, coupling nutritional ecology with life-history theory provides a fruitful avenue to understand the capacity of landscapes to support population growth and the role of other extrinsic factors in population regulation.
Aerial surveys are a practical method for estimating wildlife population densities. However, methods to account for imperfect detection using aerial surveys are limited and not always practical for wildlife managers. Distance sampling is a well-established method for obtaining abundance and density estimates, while accounting for imperfect detection, and has been applied to aerial surveys. N-mixture models are a new analytic tool that have recently been applied to wildlife population estimation. N-mixture models explicitly estimate detection probability and abundance yet have not been applied to aerial surveys of terrestrial free-ranging wildlife. While these methods are fundamentally analogous, there are important conceptual and statistical differences. Application of both methods to real data for simultaneous comparison have been rare and there are no direct comparisons of the relative efficacy of each with real data. Our objectives were to: 1) compare detection and abundance parameters estimated from N-mixture models and distance sampling methods and 2) to test the sensitivity of the spatial unit size inherent in the study design to the N-mixture approach. We evaluated the N-mixture model and distance sampling analytical approaches with data collected from surveys for white-tailed deer ("Odocoileus virginianus") conducted during the winter via fixed-wing aircraft. Estimates from both modeling approaches were similar, but N-mixture models provided abundance estimates with greater precision. We found that aerial surveys using N-mixture binomial models are a practical tool for estimating abundance of a free-ranging wildlife population. Further, we found the selected spatial unit size in the N-mixture model had a significant effect on abundance and detection probability estimates, and their associated variance. These results suggest that managers and researchers evaluate the spatial unit used for these models prior to survey implementation. N-mixture models may provide an improved approach to estimate populations from aerial surveys in the future.
Most ungulate studies focus on forage-predation interactions, but parasites can be as important in some situations.\(^1\) Parasites can have significant impacts on body condition,\(^2\) reproduction,\(^1\) and longevity in ungulates,\(^3\) but the interaction between migration and parasite levels is not well understood, especially for environmentally transmitted parasites in partially migratory ungulates. Parasite exposure may differ on summer ranges of migratory herd segments for several reasons: (1) early migration from a highly contaminated winter range may provide an “escape” during spring peak infectious period, (2) differences in forage quality on summer ranges may alter susceptibility to parasite infection due to improved body condition, (3) differences in either quality habitat configuration or use of predator refuges may concentrate hosts and increase subsequent transmission, (4) summer ranges may differ in secondary host habitat, or (5) parasite exposure from other ungulate species may differ. This project addresses the above hypotheses in a partially migratory elk (\textit{Cervus elaphus}) herd that winters at the Ya Ha Tinda (YHT), AB, bordering Banff National Park (BNP). The YHT elk herd has been experiencing a population decline and a shift in summer migration from westward into BNP to eastward onto industrial lands along the Red Deer river. Results from a 2017 field season show average intensity of giant liver fluke (\textit{Fascioloides magna}) infection was 0.78 eggs/g for western migrants, 2.12 eggs/g for residents, and 5.29 eggs/g for eastern migrants. There were significant differences between fluke prevalence in migrant segments during the summer (\(P<0.0001\)) and overall (\(P<0.0001\)) but not in the spring (\(P=0.41\)) and fall (\(P=0.25\)). \textit{F. magna} infection was significantly higher in the eastern migrants than both residents and western migrants but not between residents and western migrants. My study will address changing dynamics among migrant segments and contribute to understanding the trade-offs between forage, predation, and parasite dynamics of a shifting migration strategy.

References
The supplementary feeding of ungulates, which is widespread across North America and Europe, typically seeks to improve individual and population performance, compensate for the loss of habitat, and improve hunting opportunities [1]. However, despite its prevalence as a management strategy, this practice can have significant impacts on individual movement and space-use patterns [2]. We aimed at evaluating the behavioral and spatial response of European roe deer (Capreolus capreolus) to spatiotemporal dynamics in supplementary feeding management. To address this question, we captured and tagged nine individual roe deer with GPS collars in an area with supplementary feeding (Eastern Italian Alps). We monitored the availability of food at the feeding stations on a weekly basis from January to May to obtain a temporal classification of feeding site management into two states: active (available feed) or inactive (unavailable). We examined each individual's space-use patterns in relation to temporally dynamic food availability at intensively attended, focal feeding sites. We computed three metrics of space-use in subsequent alternate periods of food provisioning at focal feeding sites: home range size (95% multiple convex polygon, MCP), and spatial overlap and centroid distance between subsequent home range cores (50% MCP). Furthermore, we investigated the periodicity of movement recursions towards feeding sites using spectral analysis. For each existing feeding site, we generated a presence-absence (P/A) time series using a 50 m buffer. Individual feeding site time series were then aggregated based on management status to obtain both active and inactive feeding site P/A time series. We conducted two Fourier analyses on active and inactive time series to assess landscape-level response to management, and a wavelet analysis on focal feeding site time series to evaluate temporal patterns in periodicity [3]. The home range size was unaffected by feeding site management (active: mean = 46.78 ha, CI = 18.01 - 71.55; inactive: mean = 45.70 ha, CI = 32.67 - 58.73; paired t test: t = -0.10, df = 8, p-value = 0.92, n = 9). However, management influenced the location of the home range core: successive home range cores barely overlapped (mean = 20%, CI = 0 - 42%) and were relatively distant (mean = 284 m, CI = 145 - 422 m). Roe deer recursions showed a consistently clear peak at 24-h periodicity for active feeding sites, whereas this characteristic circadian signal was weak or absent for inactive sites (Fig. 1). In addition, disruptions of recursions towards focal feeding sites were consistently observed following supplementary feed depletion (Fig. 2). Our results suggest that roe deer shift space-use in response to spatiotemporal dynamics in supplemental resource availability. Specifically, we found a reallocation of movement and home range cores towards active feeding sites, and a temporary decline in movement recursions towards inactive sites. These findings are concordant with previous studies demonstrating a
high plasticity in feeding site use of the European roe deer [4], as well as space-use implications of supplemental feeding [5].

**Figure 1.** Typical Fourier power spectrum for the presence/absence time series in landscape-level active (a) or inactive (b) feeding sites. The 1% and 5% significant thresholds are shown respectively as blue and red dashed lines. These thresholds were obtained by bootstrapping. The raw periodograms were smoothed using a modified Daniell smoother.

![Typical Fourier power spectrum](image)

**Figure 2.** Typical wavelet power spectrum for a presence/absence time series at a focal feeding site. The colors ranges from low power value (weak periodicity, blue) to high power value (strong periodicity, red). The availability of supplemental feed was constant except for a period of about two weeks in February-March (limits: vertical black lines 1 and 2).

Horizontal dashed white lines represent characteristic periods of biological interest: 12 h, 24 h and 7 days. The areas of statistical significance at 5% levels are delineated by a solid black line contour. The "cone of influence", shown as a transparent mask in the margins, indicates time-periodicity domain where spectrum values are unreliable due to edge effects.

![Typical wavelet power spectrum](image)


Benefits of a Bottom-Up Approach to Understanding Disease Dynamics and Management in Deer: Studying Behavior to Test Mechanistic Hypotheses

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Wildlife managers are often concerned whether disease transmission is density-dependent (DD, force of infection proportional to the density of infective animals [I]) or frequency-dependent (FD, force of infection proportional to the fraction of hosts that are infective [I/N]). DD transmission ensures that disease will not deterministically drive its host to extinction, and allows the possibility of eliminating disease by holding host density below a threshold level. In contrast, diseases with FD transmission could eradicate their hosts and are much harder to control by culling or other population reductions. Empirical studies comparing measured values of force of infection to I and I/N in wildlife populations often point to transmission dynamics intermediate between DD and FD. However, I and I/N change in parallel early in an epizootic, which greatly hampers the ability of researchers to reliably distinguish DD and FD dynamics using this “top-down” approach because inconclusive results are likely even if disease dynamics are strictly DD or FD. Our research has focused on an alternative “bottom-up” approach that combines behavioral data with modeling to formulate mechanistic hypotheses for how specific behavioral patterns could alter disease dynamics, and then testing those hypotheses with focused empirical studies. Using data from long-term studies of white-tailed deer (Odocoileus virginianus) social behavior and movement, we built a spatially explicit individual-based simulation and observed that the disease dynamics that emerged in the model were primarily density dependent. However, that modeling exercise pointed to an information gap regarding how deer respond to loss of social group (either due to disease or management activities). Another simulation model confirmed that that a strong "need" to be social after group loss (i.e., remnant animals always join other groups) could generate FD transmission. A controlled experimental test showed that adult does responded very little to group removal, but young deer (ca. 9 months) expanded and shifted their home ranges, which could enhance opportunities for between-group disease transmission. These findings encourage caution when interpreting tests of DD vs. FD early in an epizootic, and point to the benefits of focused behavioral study aimed at testing specific mechanistic hypotheses.
Benzimidazole Resistance in a Farmed Red Deer Herd and in Red Deer, Roe Deer and Sheep Populations grazing in the nearby Area

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The anthelmintic resistance of gastrointestinal nematodes is one of the most important economic risk factors in grazing ruminant systems, all over the world [1]. Underdosing (i.e. a subtherapeutic dose rate) is one of the most important factors contributing to the development of AR [2]. In this study, we aimed to determine the presence of BZ resistance in the generalist worm, *Haemonchus contortus* in a microregion, where the resources partly shared by sheep, free-ranging red and roe deer and in a farmed red deer herd (Fig. 1). In this survey, we used a RFLP-PCR method [3]; and the nomenclature of genotype and allele frequency, we followed detailed by Pierce [4], and their proportions were determined with 95% confidence interval (CI95%). For comparison of genotypes and alleles in the ruminant populations, the chi-square test was performed with Bonferroni correction using R statistical software i386 3.3.0 version.

**Figure 1** Localization of collected *H. contortus* worms from different hosts in S-W Hungary (dots: sheep; triangle: roe deer; star: red deer; quadrant: farmed red deer)

We examined altogether 240 *H. contortus* males to determine the proportion of Phe200Tyr SNP on codon 200 of β-tubulin isotype 1 within three different ruminant species. Among the worms, 110 were genotyped as homozygous susceptible (SS), 49 as heterozygous (RS) and 81 as homozygous resistant (RR), thus the total frequency of SS, RS and RR was 45.8% (CI95% = 39.58-52.22%), 20.4% (CI95% = 15.65-20.01%) and 33.8% (CI95% = 27.89-39.98%),
respectively. Considering the alleles, the proportion of susceptible (S) and resistant (R) allele was 56% (CI95% = 51.57-60.44%) and 44% (CI95% = 38.1-49.94%), respectively.

Distribution of the different genotype was showed a wide variety in hosts. The SS was the most representative in free-living red deer, where all of the worms belonged to this genotype group. The RR was highly prevalent in farmed red deer and sheep but was moderate in roe deer. Meanwhile, the RS was observed in a similar portion in these three host populations (Table 1). Except the comparison of the farmed red deer and sheep (P=0.708), the allele frequencies between the host populations were confirmed significantly different (P<0.05).
Body Temperature Patterns Vary with Pregnancy and Condition in Moose (Alces alces)

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Variation in body temperature of mammals is the result of endogenous regulation of heat from metabolism and the environment, which is affected by body size and life history. We studied moose (Alces alces) in Alaska to examine the effects of endogenous and exogenous factors on core body temperature at seasonal and daily time scales. We recorded continuous vaginal temperature (Tv) in adult female moose with a modified vaginal implant transmitter. Vaginal temperature in non-pregnant, wild moose showed a seasonal fluctuation, with a higher daily mean Tv during the summer (37.8°C) than in winter (37.4°C). Daily change in vaginal temperature (ΔTv) was greater in summer (0.98°C) than winter (0.67°C). In comparison with non-pregnant moose, body temperature of pregnant moose was warmer (0.2 °C higher Tv) and less variable (0.1 °C lower ΔTv). During winter, body temperature was lower (Tv) and more variable (ΔTv) as body fat decreased among female moose. Ambient and local temperature (collar temperature), precipitation, and solar radiation accounted for a large amount of the residual variation in Tv after accounting for season, reproductive status, population and individual. Temperature, wind, solar radiation and precipitation had the greatest effect on the residual variation of ΔTv. Our study shows that adult female moose exhibit hypothermia induced heterothermy, and that body temperature is influenced by pregnancy and body energy reserves within seasons and by environmental conditions within days. When studying northern Cervids, the influence of season and condition on heterothermic body temperature patterns should be considered when estimating critical thresholds for environmental stress (e.g. heat stress).
Camera Trap as a Tool for Monitoring the Sika Deer Density after Culling in the Forest, Japan

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Recently, the damage to forestry by sika deer (Cervus nippon) has drastically increased in Japan. Although the most effective action to reduce the forestry damage must be the reduction of sika deer population, it is difficult not only to evaluate the effect of reducing population size but also to monitor the results of culling. In this study, we used the value of sika deer appearance frequency trapped by the camera in the forest in order to monitor the fluctuation of population size.

From Jun. 2014 to Feb. 2016, we monitored the number of sika deer in the intensive culling area (2km×2km) compared to that in the surrounding area (4km×4km) located at the national forest of Izu Peninsula, central Japan. We set one or two sensor cameras every ca. 500m and harvested 31 sika deer in the intensive culling area from Jul. 2015 to Aug. 2015. After the culling, the mean number of sika deer trapped by cameras in the intensive culling area were drastically decreased and remained to be low compared to that of surrounding area. Camera trap have proven to be an effective tool to monitor the results of culling sika deer.
Camouflage Patterns Are Highly Heritable But Predictability Varies Among Three Populations Of White-Tailed Deer

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If ungulate neonate cryptic coloration provides a survival advantage, it should be heritable and adapted to their prevailing environment. However, recent changes in land-use and predation pressure may have created a mismatch between previously adapted camouflage and the current environment. In Mississippi, USA, row crop agriculture has altered some landscapes while recovery of native predators and establishment of novel predators may apply new directional pressures. We assessed if spotting characteristics of neonate white-tailed deer (*Odocoileus virginianus*) were heritable and if they accurately predicted region of origin, indicating adaptation to specific environmental characteristics. Spotting characteristics were moderately (total number of spotting clusters; $h^2=0.36$) to highly (number of single spots; $h^2=0.85$) heritable, suggesting specific characteristics may provide an adaptive advantage.

Camouflage patterns were moderately distinctive for neonates with lineages originating in the Lower Coastal Plain and Thin Loess (≥ 67% neonates accurately classified into their respective region) supporting previous selection for specific patterns at the regional level. However, camouflage patterns failed to predict region of origin for neonates originating from the Delta region (0%), suggesting disruption of previous adaptation. Of the three regions (Figure 1), the Delta is the most heavily converted from forested habitats, with over 70% in agriculture, while the Lower Coastal Plain and Thin Loess are less than 40% and 21% agriculture, respectively. Given that camouflage patterns are heritable and neonates displaying successful camouflage patterns should display increased survival, the lack of a predictable pattern within the dynamic Delta landscape suggests that major land use changes and new predatory pressures may have disrupted the neonate cryptic coloration best suited to this population’s current environment.
Can Passive Camera Grids Effectively Monitor Activity Patterns of White-tailed Deer?

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Temporal activity patterns of white-tailed deer (Odocoileus virginianus) have historically been evaluated using visual observations of deer or by monitoring a subsample of a population via VHF or GPS collars. However, inferring activity patterns through the use of VHF telemetry can be problematic due to infrequent sampling regimes and the inaccuracy of activity sensors. Higher location acquisition rates and greater location accuracy of GPS collars have improved identification patterns of collared animals. However, high costs often limit sample sizes and collared animals may not be representative of the population because variation in activity patterns has been reported among individual deer [1,2]. Additionally, due to behavioral differences among age groups, it is difficult to obtain a random sample of individuals that are representative of the population. High density trail camera grids may allow non-invasive monitoring of population-level activity patterns, and have been used to determine environmental effects on sika deer scientific name activity [3].

To evaluate temporal patterns of activity of white-tailed deer, and to investigate the influence of seasonal and environmental factors, we deployed cameras (1 camera/20 ha) on a 1,000-ha tract at the Joseph W. Jones Ecological Research Center at Ichauway in Georgia, USA. Between September 2014 and February 2017, we collected 13,036 observations of deer while simultaneously collecting weather data. During the study period, a record setting drought occurred in southwestern Georgia. Between 1 September 2016 and 1 December 2016, rainfall on our study site was 44% of normal. Therefore, we investigated how the drought affected deer activity. We used ANOVA to determine differences in activity rates between a year with normal rainfall (2015) and a drought year (2016). Activity rates of does (p<0.01) and adult bucks (p<0.01) were substantially higher during the drought period than the same months of the previous year (Fig. 1). We used linear mixed effects models to assess the effects of seasonal and diel factors on activity rates during the year with normal rainfall. Diel periods were considered dawn, day, dusk, and night, and biological seasons were considered rut, post-rut, gestation, fawning, rearing, and pre-rut. Diel period was the best year-round predictor of doe activity patterns, with dawn and dusk activity rates being greater than day or night. The best predictor of adult buck activity was biological season, with 61% of all detections occurring during the rut. We used linear mixed effects models to determine the effects of temperature, wind speed, and precipitation, along with changes in each factor from the last diel period and the previous 24 hours on activity rates within each biological season. Change in wind speed from the previous diel period had a negative effect on doe activity during the post-rut, and the average temperature value had a negative effect on doe activity during gestation. No weather variables accurately predicted activity for does or adult bucks during the other seasons. Because buck detection rates were low outside of the rut, small sample size prevented identification of environmental influences on activity. Although passive camera grids can be used to monitor white-tailed deer activity at a broad temporal scale (i.e. season, diel period), they are likely not appropriate to monitor fine scale influences on activity (i.e. weather factors) due to the low number of detections during certain biological seasons and diel periods.
Figure 1. Activity rates (photos/camera-day) of adult female and adult male white-tailed deer during 2015 (normal rainfall) and 2016 (drought) southwestern GA, USA. Period of drought indicated by grey shading.

References
Can Red Deer Male (*Cervus elaphus*) Intentionally Affect His Testosterone and/or Cortisol Concentrations via Selected Social Company?

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In a previous study on red deer, changing the social environment of adult red deer males resulted in a change of the relationship between dominance rank and testosterone (T) as well as cortisol (C) concentrations despite the fact that the rank position of the adults itself did not change [1]. In the present study we added an aspect of non-agonistic relationships among the red deer males. We predicted that some males will keep company with others for a long time, while others will not; those keeping together will be either “non-Fighters” (not attacking others) or “Fighters” (competing frequently); this will modify C and T.

Nineteen tame red deer males were kept in six enclosures, covering an area of approximately 4 ha. Each enclosure (of about 0.7 ha) contained a shelter, a water reservoir, and a mud pool for wallowing. During the observation period (from 1st May to 27th August 2014) all enclosures were interconnected by two permanently opened gates in each enclosure. The animals were identified with colored, numbered collars and equipped with GPS collars.

Based on GPS data, we applied cluster analysis and divided the pairwise average distances between males into two groups: “Associates” (number of pairs, mean ± SE; n=174, 25.53 ± 1.68 m) and “Non-associates” (n=58, 175.62 ± 4.13 m). Applying the same cluster procedure, pairwise average agonistic interactions were divided into “Fighters” (n=96, 13.65 ± 0.46 interactions) and “Non-Fighters” (n=133, 3.50 ± 0.17 interactions). Percentage of pair relationships with Non-Fighters was 69.47% in Associates and 59.26% in Non-associates. Proportion of Non-Fighters for an individual male ranged from 27.27% to 100%. Associates had higher mean C concentrations than Non-associates (LSMEANs ± SE, Associates 130.02 ± 1.35 ng/ml, Non-associates 124.07 ± 1.14 ng/ml). However, in both, Associates and Non-associates, C concentrations were decreasing with increasing proportion of Non-Fighters. (Other fixed effects were statistically eliminated in generalized linear mixed model.)

Associates did not differ in age, size, or aggressiveness from those who preferred less tight relationships with others (Non-associates). Both types did not differ in cortisol levels but Non-associates (LSMEANs SE, 0.42 ± 0.01 ± 0.91 ng/ml) had slightly higher T concentrations than Associates (0.39 ± 0.01 ng/ml). The males who tended to keep in proximity with others (Associates) benefitted from more peaceful relationships with a higher proportion of Non-Fighters which appeared a highly significant modifier of C and T. Increasing proportion on Non-Fighters decreased C in Associates as well as Non-Associates. On the other hand, proportion of Non-Fighters had different effect on T concentrations in Associates and Non-associates. Increasing proportion of Non-Fighters did not affect T concentration in Associates (P = 0.54), but decreased T in Non-associates (P < 0.01).

Influence of T on C: There was apparent dual effect according to low or high C concentrations (Table 2). In C High group, with increasing T concentrations, the concentrations of C were also increasing (P < 0.0001). On the contrary, in Cortisol Low group it was just opposite; C concentrations were decreasing with increasing T (P < 0.0001). With increasing body weight C decreased in Associates while increased in Non-Associates (at the end of observation).
Non-associates searched for the Fighters (the inverted value of Non-Fighters) more frequently than did Associates. Thus the Non-associates avoided stable social relationships and were more challenging than the Associates.

Associates and Non-Associates did not differ in the number of agonistic interactions per se. However, in accordance with the Challenge hypothesis [2] unlike in Associates, T was more pronounced to be related to aggression in the Non-associates who, living apart from others, were exposed to social instability and formation of dominance relationships when approaching other males. Any agonistic encounter thus could be more challenging first of all for Non-associates who initiated the encounter. The effects of the proportion of Non-Fighters and age therefore appeared influential in modifying T in Non-associates but not in Associates. With increasing proportion of Non-Fighters, T in Non-associates decreased. Thus the presence of close social partners had buffering effect not only for C as anticipated [3-5] but also for T in challenging situations.

Our results thus suggest that red deer males may intentionally modify their C and T concentrations, which are involved in antler growth [6] and they may theoretically increase their future reproductive success [7].

References
Catch Me if You Can: Behaviors Used by Male White-tailed Deer to Avoid Detection by Hunters

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In North America, white-tailed deer (Odocoileus virginianus) are the most abundant and widely distributed deer species, resulting in its popularity as a game species. Hunting accounts for most mortality; therefore, hunters influence population dynamics of the species. At the same time, hunters pose an indirect risk to deer whereby human predation risk [1] can alter the behavior and spatial distributions of animals. These risk effects can impact fitness-producing activities where animals must make trade-offs between avoiding risk and energy acquisition [2].

Response to human predation risk can be evaluated by examining movement behavior and those behaviors stemming from the movement process (e.g., space use patterns, distribution [resource selection]). Deer may adopt strategies such as decreased movement and space use, and increased use of security cover to minimize disturbance and the risk of being observed, which translates into reduced risk of harvest [3-5].

In this study, with spatial and temporal controls, we examined how hunters impacted adult (≥2.5 years), male white-tailed deer behavior (i.e., area of use size, refuge use, movement, resource selection, and observability) in southern Oklahoma at three risk treatment levels (i.e., control = no risk; low-risk = 1 hunter/250 ac; and high-risk = 1 hunter/75 ac) over the course of a 36-day study period, including both non-risk and risk periods. Deer were fitted with GPS collars programmed to record GPS relocations every 8 minutes over the 36-day study period. We captured 45 male deer, but analyzed data on 30 unique deer; 7 of which were collared during both years (2008: n = 19; 2009: n = 18).

Eleven deer succumbed to mortality as a result of illegal harvest (n = 8), legal harvest (n = 1), natural mortality (n = 1), and deer-vehicle collision (n = 1). Deer responded to the presence of hunters on the landscape by adapting movement and resource selection strategies both spatially and temporally to avoid potential contact with hunters. These altered behavioral patterns influenced the probability of being observed; collared male deer and all un-collared deer were observed more frequently early during the hunting season progressively declining to the end of the 16-day hunting season. During the study, deer reduced micro-ranges and movement distance, and increased site fidelity by using smaller areas more intensively; the greatest reduction in space use behavior occurred during the 16-day hunting season. Deer altered their resource selection by increasing use of forested areas to reduce the risk of detection, meaning that deer perceived open habitat types as the riskiest places and moved through these at greater speeds.

Understanding the effects of hunting pressure on deer behavior can be used to explain decreased observation rates later in the season, facilitate or reduce harvest based on population management objectives, and help manage hunter expectations regarding observations and harvest. Based on these findings, if the goal is to facilitate harvest, then encouraging early season harvest can help meet harvest management goals because deer have not yet responded to risk on the landscape where movement, resource selection and observability are altered. These data also highlight the adaptive ability of male white-tailed deer
to risk where deer show generalized changes in behavior, but also respond in situation-specific manners.

Figure 1. Spatially explicit depiction of the relative predicted probability of resource selection by male white-tailed deer in south-central Oklahoma from 2008 to 2009 during the (A) preseason, prior to any hunting or human risk on the landscape, and during the (B) hunting risk period for deer in the high-risk treatment. Predicted probability of selection changed as the result of hunter presence, which was more pronounced in some areas than others. Relative predicted probability of selection was placed into 5 equal-sized bins (lowest, low, moderate, high and highest) where 20% of raster cells fell within each bin.

References
As a large herbivore, the European roe deer (*Capreolus capreolus*) is faced on a daily basis with eating nutritional components that are partially difficult to digest. As a ruminant, it owes its ability to digest raw fibre to its rumen microbiome. Depending on the forage type, food situation and season, this is made up of many different groups and species of microorganisms [1]. The roe deer is classified as a so-called "concentrate selector" [2]. This means that roe deer are only able to digest raw fibre to a limited extent and are more likely to take in food with a high crude protein content [2,3,4].

In a preliminary study conducted from 2011 to 2014, we collected the rumina of 220 roe deer in two Bavarian habitat types, gathering the samples throughout the 12 months of each year. We wanted to investigate the adaption of the microbiome to conditions in a natural landscape and those in a cultivated landscape on the one hand, and to seasonal influences over the course of the year on the other. The raw fibre content of the rumen contents was determined and PCR was used to determine the proportions of individual genera known to be found in roe deer. The average proportion of fibre in the food intake of the deer was 25-29% (max. 48%). These high values are attributed to the intermediate feeder type or roughage feeder type of herbivores [2,5].

We found the highest proportions of fibre in forest roe deer, which also had a significantly higher (p < 0,001) total number of microorganisms in their rumen than animals living in the agricultural area. Particularly in the cases of the "general bacteria", the "archaea" and the "proteolytic alpha bacteria", the number was significantly higher. In the forest roe deer there were significantly more bacteria of the "Fibrobacter" and "anaerobic fungi" genera for the digestion of raw fibre.

In the course of the year, the number of microorganisms important for the digestion of raw fibre were also highest for the forest roe deer in winter and for the roe deer from the agricultural area in the summer. This demonstrates the adaption of the microbiome to both habitat and season.

As the roe deer can obviously digest far higher proportions of fibre and also adapt to the higher proportion, it would be better to describe it as a "browser" or "selector" rather than a "concentrate selector", as done in Germany and other parts in Europe.

In order to see whether the adaption is similar in other habitat types and to establish more detailed adaptation of the microbiome, this study is to be continued throughout Bavaria.

References
West Virginia began formal surveillance for Chronic Wasting Disease (CWD) in 2002. In 2005, after two and one-half years of surveillance, West Virginia became the 10th state to detect CWD within its borders. The first free-ranging white-tailed deer (*Odocoileus virginianus*) found to harbor the abnormal protein associated with CWD was a 2.5 years of age male that had been sampled as part of the statewide surveillance of road kill deer. Since that time, a total of 338 CWD positive deer have been detected through sample monitoring of predominately hunter harvested deer in the area of the first detection. Both, the known geographic distribution of the disease and disease agent prevalence, have increased in the area through the period from 2005 to present. The outbreak has expanded geographically approximately 33 sq.km. ($R^2 = 0.9344$) per year in Hampshire County and increased in periodic prevalence from 2.5% (±2.4%) to 36.5% (±13.1%) from 2005 to present in a designated monitoring area of 102 sq.km.

Generally accepted disease management actions to limit the spread of CWD focus on deer population manipulation, carcass disposal and transport, and curtailing supplemental feeding and baiting of deer. Disease management actions implemented to address CWD in West Virginia include, increase oversight of captive cervids, designation of an area to focus disease management actions, liberalize deer hunter opportunity for antlerless deer, impose a ban on supplemental feeding and baiting of deer, discourage the use of deer derived lures, impose restrictions on the disposal and transport of deer carcasses from within areas in West Virginia and surrounding states, and provide carcass disposal receptacles during deer hunting seasons to encourage proper deer carcass disposal. Evaluation and insight of the public involvement and compliance of these key elements to disease management will reduce risk to the remaining unaffected free-ranging deer populations. The “hunter friendliness” of management actions as evaluated with a hunter’s attitude survey will be shared [1].

The impact to the agency is significant. The agency’s challenges relating to operational changes for game harvest registration, expenditures, staffing, and agency stamina for sustained disease management actions will be discussed. Potential future challenges will be elucidated, such as the demand for food safety testing of harvested deer, outbreak geographical expansion impacts, landowner concerns regarding disease presence, and the agency’s ability to make adjustments to a declining deer population and/or declining hunter participation. Efforts to increase public awareness and compliance to maximize disease management actions that target deer hunters and landowners also need political support to be effective.

A well-documented method of spreading CWD across long distances is the movement of live species of deer for commercial purposes. Organizations such as the Quality Deer Management Association, Rocky Mountain Elk Foundation, and The Wildlife Society have recognized the threat that pen propagation and translocation of deer species represent to the wild deer and elk resources which are enjoyed by all citizens. This threat is not only CWD but also the introduction of other pathogens and genetic consequences, which have the potential to devastate our revered deer resources. A unified effort across state, federal, and public health
agencies is needed to make the risks for continued spread of CWD relevant not only to deer hunters, but to the agricultural community and the general public.

References
Missouri began Chronic Wasting Disease (CWD) surveillance in 2001 and first detected CWD in its free-ranging white-tailed deer (Odocoileus virginianus) population in 2012. Since that time, a total of 62 CWD positive deer have been detected, and although known geographic distribution of the disease has increased, disease prevalence in established locations has remained low (< 4%). Successes of the Missouri Department of Conservation (Department) CWD Management program include 1) a sustained high level of disease surveillance, enabling early detection of the disease; 2) continued intensive culling efforts in localized areas where positive deer have been detected, contributing to low prevalence of the disease. The primary mechanism driving these successes was the high priority placed on CWD management by the Department. The “all hands-on deck” approach to CWD management was integral to the success of the 2016 and 2017 Mandatory Sampling efforts during which more than 16,000-19,000 were collected in only 2 days each year. Although the intensive Department-wide approach to management of CWD has been successful, staff fatigue is and will continue to be an issue. Identifying avenues to increase efficiency for all CWD-related operations is paramount to succeeding in this effort.

Finding successes in on-the-ground management and highlighting hopeful findings in the scientific literature is important to improve staff and public morale for what can be a very bleak subject. Unfortunately, there are many obstacles and roadblocks to the continued success of CWD management. Principally, public communication, litigation, and the lack of appropriate federal funding stand in the way of Missouri’s success. Effective public communication regarding CWD management remains a struggle, as misinformation and confusion persists about CWD among the public and even some staff. This is not a problem unique to Missouri, but arguably in every state and Canadian province where CWD exists. A collaborative effort across state, federal, and provincial wildlife agencies would help boost public awareness and education. Specifically, it will become important to make this disease relevant not only to the hunting population, but to the general public. Litigation is an unfortunate obstacle that is simply part of the reality of public agencies, and Missouri is no exception. Lengthy lawsuits prevent needed management, erode staff morale, and serves as a detractor for other states considering similar regulations. Wildlife agencies should move forward CWD regulations with the expectation of litigation, and dedicate resources appropriately. Finally, the restoration of federal funding is important to increase surveillance efforts throughout the United States and increase scientific research into CWD management and treatment. Currently few states have resources to conduct surveillance for CWD at levels to detect the disease at low prevalence rates. Given CWD does not respect borders, a unified effort to increase surveillance across North America would benefit all. Despite these challenges, management of CWD remains one of the highest priorities for the agency.
Fear of predators can behaviorally-mediate prey population dynamics, particularly when predation risk influences reproductive investment [1,2]. However, nutritional costs of reproductive investment may negate predation risk aversion in species with relatively limited annual reproductive capacity. We hypothesized that intensity of reproductive investment should predict individual decision-making such that prey exhibit riskier behaviors when rearing young or breeding. We examined the activity patterns of sympatric white-tailed deer (*Odocoileus virginianus*), a sexually segregated polygynous ungulate, and Florida panthers (*Puma concolor coryi*) in the context of the ‘risky times – risky places hypothesis’ and the ‘reproductive strategy hypothesis’ [3]. We compared detection rates and diel activity overlap of both species using motion-triggered camera traps positioned on (*n* = 120) and off (*n* = 60) anthropogenic trails across 5 reproductive seasons of deer. Florida panthers were largely nocturnal and primarily observed on trails, providing an experimental framework with risky times and risky places (Fig. 1). Contrary to studies of other taxa inversely correlating prey reproductive investment to predation risk, deer were least risk averse during sex-specific seasons associated with intense reproductive investment (Fig. 2, 3) [2,4]. Our results suggest spatiotemporally variable predation risk influences sex-specific behavioral decision-making in deer such that reproductive success is maximized.

**Figure 1.** Panther detection rates per 1000 hours (01 Feb 2015 – 01 Nov 2015) at on- and off-trail camera locations in the Big Cypress Basin, Florida, USA. Error bars indicate 95% confidence intervals.
Figure 2. Male deer detection rates per 1000 hours (01 Feb 2015 – 01 Nov 2015) at on- and off-trail camera locations in the Big Cypress Basin, Florida, USA. Error bars indicate 95% confidence intervals.

Figure 3. Female deer detection rates per 1000 hours (01 Feb 2015 – 01 Nov 2015) at on- and off-trail camera locations in the Big Cypress Basin, Florida, USA. Error bars indicate 95% confidence intervals.

References

Comparing Two State-space Models for Estimating Dynamics of an Elk Population

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Mathematical models can predict how species respond to their environment, and they are a critical tool for global concerns including climate change, population management, pest control, and species conservation. The Gompertz and Ricker state-space models are both commonly used to estimate population parameters of large mammals using population counts, but few studies have compared the utility of these models while accounting for survey imprecision, or observer error. We used elk population abundance data collected by multiple sources in the U.S. Department of Energy’s Hanford site in southcentral Washington between 1983 and 1999 [1, 2, 3]. This dataset was useful since it includes observed counts over a wide range of abundances. We estimated the parameters of the Gompertz and Ricker hierarchical state-space models using Bayesian statistics in the RJAGS package in R. The Gompertz model estimated observer error following a log normal distribution, whereas the Ricker model estimated observer error following a Poisson distribution. When taking into account survey imprecision, the root mean square error of the Ricker hierarchical state-space model was almost half that of the Gompertz model. Furthermore, the projected 95% credible intervals of the Ricker model encompassed all observed counts, whereas 3 of 17 counts lied outside of the projected 95% credible intervals of the Gompertz model. Finally, the Ricker model, but not the Gompertz model, estimated carrying capacity. Therefore, the Ricker model appears to more precisely model population dynamics of this elk population than the Gompertz model when density dependent factors influence fluctuations in abundance.

References
Comparison of Aerial Survey Methods for Elk (Cervus canadensis) in Arizona

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Abstract: Elk (Cervus canadensis) populations in Arizona have historically been managed using estimates of relative abundance. Recent questions related to the influence of large wildfires, impacts to habitat, and predator-prey relations have increased the demand for absolute estimates of elk abundance. Between 2014 and 2016, we conducted experimental helicopter surveys of selected areas to compare several methods designed to model elk detection and estimate abundance. We conducted annual autumn helicopter surveys in 3 areas that contained radio-collared elk and recorded information on covariates affecting both detection (i.e., vegetative cover, vegetation type, burn category, group size, activity, and ambient light) and observer bias (i.e., observer position, pilot experience). We used information theory to rank a set of candidates a priori models to determine which covariates affected detection and select the most parsimonious models among sightability, double observer, and hybrid modeling methods. We then used the top model from each method to calculate annual site-specific elk abundance estimates for comparison to concurrent mark-recapture abundance estimates. The best supported models included all detection covariates, with the influence of covariates on elk detection generally adhering to expectations. Relative to mark-recapture estimates, the best performing hybrid model generally provided abundance estimates that were more accurate than double observer models and more precise than sightability models. The most economical methods to implement were the simultaneous double count and double observer methods, because these methods did not require model development or presence of marked animals. When applied to autumn helicopter survey data, our hybrid model should improve both precision and accuracy of elk abundance estimates.
Composition of Chinese Water Deer’s Digestive Tract Microbes

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The samples of digestive tract contents from just died Chinese water deer *Hydropotes inermis* and fresh feces were obtained in Shanghai, China. Microbial DNA was extracted and high-throughput sequencing was performed on the v3-v4 variable region of the 16S rRNA of microorganisms. The Digestive tract and feces can be measured more than 1% microbes about 16 phyla. Digestive tract accounted for 9 phyla, 104 genera. The feces accounted for 16 phyla, 148 genera. The feces contain all the phylum level microbes in the digestive tract. Digestive tract and fecal dominant bacteria are Firmicutes. The samples from Whole vegetation feeding was significant difference with which from half –vegetation feeding in the microbial diversity of the digestive tract. The digestive tract of microbial diversity was higher in the whole vegetation feeding, the Shannon index was 2.33 ± 0.24. The digestive tract of microbial diversity was lower in the half –vegetation feeding, the shannon index was 1.7 ± 0.19.
In Central America three species of cervids occur: the white-tailed deer *Odocoileus virginianus* (Zimmerman, 1780), the red brocket, *Mazama temama* (Kerr, 1792) and the Yucatan brown brocket, *Mazama pandora* (Merriam, 1901). A literature review and consultations with experts from Central American countries about its conservation of cervids, comes from studies using camera traps and records by sighting of technicians. Guatemala, Mexico, and Belize are the only central American cojntries with all 3 species. Distribution records come from the Calakmul Biosphere Reserve in Belize and the Ejido of Nuevo Becal in Mexico (Moreira et al, 2018). In Honduras, El Salvador, Nicaragua, Costa Rica and Panama, only the first two species are reported. The white-tailed deer (*O. virginianus*) shares the same common name throughout Central America and is distributed homogeneously throughout each country. *Mazama temama* has different common names, tilopo or güisisil, red goat, red deer or red brocket deer and its presence is restricted to primary forest. Its range of distribution includes diverse ecosystems and different altitudinal gradients. Information on population densities of the three species is limited although there have been estimations for white-tailed deer in Honduras and El Salvador. The species are included in the lists of the International Union for the Conservation of Nature (IUCN) and the Convention on International Trade in Species of Flora and Fauna (CITES) with some status of protection or monitoring. Cervids are of the most persecuted species by humans and natural predators, such as jaguar (*Panthera onca*), puma (*Puma concolor*), ocelot (*Leopardus pardalis*) and coyote (*Canis latrans*). As prey species, they are important in the structure of biotic communities (Marineros and Martínez, 1998, Portillo et al, 2015). Cervids are under strong pressure due to habitat loss and the increase in poaching (Secaira, 2013, Portillo et al, 2015). Poaching is a serious threat faced by these species in the region because their meat is valued for its good taste, protein value (in some cases it is the only available protein source). Its habitat loss is due to the advance of the agricultural frontier and infrastructure projects. Wild species have been captured and bred in zoos, exhibition centers and private collections and they have been raised with some ease, although in conditions not appropriate for the species. Even when cervids are resilient, precise studies of ecology and phylogeny are required to implement conservation projects at a regional level.

**References**


Cryptic Genetic Population Subdivision and Conservation in Elk (*Cervus elaphus*)
Translocated from Elk Island National Park (Alberta, Canada) to Tennessee and North Carolina, USA

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Translocation of organisms from one site to another site is a commonly used tool to restore populations, species, or even ecosystem function. However, many of these reintroductions have not been successful in establishing viable populations (reviewed in [1]). Batson et al. [2] reviewed the available literature to develop 30 tactics to facilitate translocation success including maximizing genetic diversity and selection of organisms with similar genetic characteristics to the original stock (or adapted to the original range). Kelly and Phillips [3] even suggested using targeted gene flow and moving pre-adapted individuals to new locations to make sure favorable traits promote restoration success. These favorable adaptations may be for disease resistance or variations better suited to different climates. Also low genetic diversity may lead to inbreeding depression and a decrease in immunocompetence [1]. Therefore, genetic makeup may affect population growth and persistence of the reintroduced species. Given the significance of the source population for successful reintroduction, we should give high importance to genetic considerations.

Recent research has revealed the presence of so-called cryptic metapopulations (i.e., a spatially continuous distribution of organisms exhibiting metapopulation-like behaviors) in giraffes (*Giraffa camelopardalis*, [4]), and red deer (*Cervus elaphus*, [5, 6]). We have identified this phenomenon in 2 reintroduced populations of a large and highly mobile mammal, elk (*Cervus elaphus*) in Tennessee and North Carolina, which could have significant implications for conservation of elk but also all other reintroduced species [7].

Elk from Elk Island National Park (EINP), which is located 45 km northeast of Edmonton, Alberta, Canada have been used for restoration projects in Ontario, Canada, Kentucky at Land Between the Lakes (LBL), Cumberland Mountains, Tennessee, and Great Smoky Mountains National Park in North Carolina. What is unique about EINP elk is that there are 2 genetically distinct populations because animals from the north side have been isolated for over 100 years and the south side for over 50 years by a 2.2-m high fence. EINP (196 km$^2$) was established in 1906 to preserve a small herd of 75 elk and has many native herbivores and few large predators [8]. EINP is bisected by a major highway (Highway 16) and fence which was first established on the north side in 1907. Therefore, about 15 elk generation times have occurred which have brought about distinct genetic structuring between the north and south sides of the park. Elk are trapped on both sides of the road and brought to a central handling facility where they are mixed together, marked and processed for shipment to restoration sites. Given the separation of the 2 populations at EINP, we are interested in how genetic structuring affects reintroduction efforts when these animals are transported to new habitats.

**What We Know about Genetic Structure at EINP:** At the time of capture at EINP or LBL (originally from EINP), we were able to obtain blood or hair from 220 elk that were later translocated to GSMNP and TNCM [7]. Wildlife Genetics International (WGI; http://www.wildlifegenetics.ca/) analyzed 16 microsatellite markers commonly used in game-farmed elk. We used the program STRUCTURE [9], which provides a Bayesian clustering
algorithm to assign genetic structure without any prior assumption of group membership. We found 92.7% (n=220) strongly assigned to one of the 2 populations. Only 7.3% (n=16) of the population had indications of mixing between the 2 clusters. These distinct clusters are related to the road at the source site of EINP [7].

**Continued Elk Population Structure after Translocation from EINP:** We continue to observe population structure in LBL, TNCM and GSMNP, with few admixtures, despite overlapping ranges and potential breeding opportunities between the 2 genetic groupings 11+ years after reintroduction. This structure means the effective population sizes of these reintroduced populations are much smaller than originally thought, which could affect population persistence. The genetic consequences of smaller effective population sizes than presumed could lead to inbreeding and other deleterious genetic effects. More research needs to evaluate the effects of this genetic structure and identify possible mechanisms for continued reproductive isolation. We need to understand effects of cryptic population structuring on reintroductions or restoration of wildlife species.

**References**


Habitat-based prediction of equilibrium density (i.e., carrying capacity) typically requires a complete characterization of the relationship between landscape configuration and animal density; however, under the correct conditions models of habitat selection (e.g., Resource-Selection Probability Functions, RSPFs) may be solved and summed over space to produce a prediction of animal abundance. This suggests that simple models of habitat selection may enable prediction of carrying capacity using commonly collected and widely available datasets of animal presence. We demonstrate this possibility using a time series of moose (*Alces alces*) abundance based on aerial census and hunter harvest data from which we estimate the carrying capacities of 34 Wildlife Management Units (WMUs) across the province of Ontario, Canada. We then use regression and information theoretic procedures to relate carrying capacity to environmental covariates of biological and management relevance. The best model is then used to generate predictions of carrying capacity for all WMUs. Next, we fit a RSPF to site-specific aerial survey data collected from multiple sites in central Ontario. The RSPF is solved for every 30-m pixel across all WMUs, and the predicted equilibrium density from the RSPF within a WMU is simply the sum of the probabilities across pixels divided by the area of the WMU. We then compare the predictions from the carrying capacity model to those from the RSPF to evaluate the capability of models of habitat selection to accurately predict carrying capacity. We observe that the RSPF fails to accurately predict carrying capacities; however, the direction and magnitude of difference between carrying capacity and the equilibrium density calculated from the RSPF can be predicted based on the difference in landscape characteristics between the site where the RSPF was fitted and the site onto which a prediction is made. Our findings suggest that prediction of carrying capacity from simple models of habitat selection is possible provided characterization of the habitat functional response such that model coefficients may be adjusted based on resource availability. Such models also benefit from enabling estimation of both landscape-level and local densities, allowing examination of “neighborhood carrying capacities” relevant at sub-population scales.
Determining The Impact Of Free-ranging Livestock On Tufted deer (Elaphodus Cephalophus) In Wanglang National Nature Reserve, SW China

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During the past two decades, the dramatic increase in livestock that are freely dwelling in and around nature reserves has become to a major threat to protected areas across China [1-2]. Compared to wild ungulates, domestic animals were in general characterized by larger body size, higher density, less fear in behavior, higher foraging intensity, and more intensive disturbance [3-5]. Free-ranging livestock compete with wild ungulates for limited space and food resources, and greatly increase the risk of disease transmission. Overabundant livestock may also negatively impact seedling recruitment and alter the process of forest regeneration [6]. To examine the influence of free-ranging livestock on sympatric wild ungulates, we randomly selected 100 quadrats and conducted camera-trapping survey in the 25.2-ha Wanglang Alpine Conifer Forest Dynamics Plot, SW China, a natural habitat of the iconic giant panda (Ailuropoda melanoleuca), from 2013 to 2017. We recorded six wild ungulates and two livestock species with a sampling effort of 8220 camera-days. Three species with sufficient detections (N>200), including domestic horse (598 detections), cattle (454 detections) and tufted deer (Elaphodus cephalophus) (334 detections), were included in further analysis. Density estimation was used to evaluate the activity pattern of each species and calculate the temporal overlap between each species pair [7]. Time series analysis was used to describe the current and predict the future monthly active patterns of tufted deer [8]. The results showed that livestock were currently the dominant herbivores in this forest ecosystem. Tufted deer and horses utilized the plot throughout the year, whereas cattle occurred in the plot only during the growing season (May-September). The mean dwelling durations of domestic cattle (297s) and the horse (285s) at foraging site were both significantly longer than that of tufted deer (69s). Results of time serial regression indicated that livestock had a significant negative impact on the habitat use of tufted deer. When livestock, either horses or cattle, were present, tufted deer shifted their activity pattern accordingly to reduce temporal overlap. Our results indicated that tufted deer might use the strategy of temporal niche differentiations to reduce inter-specific competition with livestock, and therefore facilitate their co-existence. Our study provided preliminary data and valuable insights into the complicated interactions of free-ranging livestock and wild ungulates in the montane forest of SW China. The results will have further implications to protected area management and wildlife habitat conservation across the region and elsewhere.

References


Digestive plasticity of roe deer in response to changes in diet energy and diet quality

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The European roe deer (*Capreolus capreolus*) is a forest dweller [1] and classified as a typical “Browser” or “Concentrate Selector” [2]. This means that roe deer depend on a diet with a low fiber content and high proportion of crude protein [2,3,4]. This is why some hypothesize that roe deer are unable to digest agricultural plants, as these contain a relatively high proportion of fiber [5,6,7].

From 2011 to 2014, the rumena of 220 roe deer and data on the respective conditions were collected from legal hunts in both a forest habitat and in an agricultural habitat [8]. In order to observe seasonal influences, we gathered samples throughout all 12 months of each year. We thus acquired a permit from the local hunting authorities to collect roe deer outside the regular hunting seasons. Our aim was to measure the quality and energy content of the natural roe deer diet (in terms of metabolizable energy (ME)) found in the rumena. We used standard methods of dietary analysis; *in vitro* ruminal fermentation, crude nutrient analysis, and analysis of neutral/acid detergent fiber and acid detergent lignin [9, 10]. For an overview of the total energy budget of the roe deer, we used a wildlife systems approach to analyze the condition and physiological adaption of roe deer to local and seasonal changes in diet. In addition, the availability and quality of the local vegetation and stress of the deer were evaluated as a measure of human disturbance.

**Figure 1:** Mean energy concentration (ME MJ / kg DM) in roe deer diets in two different habitats

Roe deer diets in the agricultural habitat had a mean energy content of 6.3 ME MJ/ kg DM, which was significantly more metabolizable energy than was available to roe deer in the forest habitat, where the mean was 5.4 ME MJ/kg DM (Fig. 1). To compensate for the lower energy content, rumen contents of roe deer from the forest habitat was on average 300g heavier than that of deer from the agricultural habitat. Roe deer in the natural forest habitat thus compensate for the lower energy density of the vegetation with a higher intake and increased rumen capacity. According to literature, roe deer need an average energy intake of 3.5 to 5 (10) ME MJ/day [9,11, 12]. With our data we calculated a yearly average energy value between 8 ME MJ / day and 11 ME MJ / day for both populations, and on average both populations gathered the same average energy intake per year. However, in both habitats the proportion of fiber was not less than 21% of dry matter and in winter, roe deer were able to extract more energy from the fibrous diet than domestic sheep, a grazer.

During our study period we did not observe any energy gap between the two populations. In neither of the two areas was supplemental feeding necessary for the roe deer to survive the winter. In terms of dietary energy, the roe deer in agricultural habitat did not notice that it was winter. In general, the roe deer’s microbiome is adaptable to the local vegetation, permitting the animal to exploit energy from plants throughout the year, even with a high proportion of fiber.

**References**


In response to the risk of predation by wolves, elk in the northwest of the Yellowstone Ecosystem proactively increased vigilance, moved out of favored foraging habitat into protective cover and disaggregated, all of which are expected to reduce the likelihood of encounter or attack [1, 2]. These responses were associated with changes in diet, reduced food intake and increased mobilization of tissue nitrogen stores [3]. In eight populations, these responses have been accompanied by decreased levels of pregnancy-specific protein B, serum progesterone and fecal progesterone in the third trimester of pregnancy [4, 5]. In turn, these changes in reproductive physiology aligned spatially and temporally with decreased calf recruitment (Fig. 1). In an ecosystem-scale before-after-control-impact analysis of 12 Montana and Wyoming elk populations over 33 years, all populations exposed to wolves shifted from growth to decline at the time of wolf colonization, while adjacent populations that were not colonized by wolves continued to grow [6]. The decline in populations exposed to wolves was driven primarily by reduced recruitment (juveniles/adult female), rather than changes in adult survival [4, 7, 8]. Quantitatively, the decrease in recruitment could not be explained by the additive effects of predation [6, 9, 10] or by other limiting factors such as snow accumulation, rainfall and population density (Fig. 1). Debate over the causes of decreased elk recruitment is largely due to the uncertainty of inferences about causation when more than one limiting factor changed around the same time at a single study site. Multi-site, multi-variable analyses that apply a before-after-control-impact design help to resolve these uncertainties [6].

Figure 1. A before-after-control-impact analysis of data from 12 Wyoming and Montana elk populations over 33 years. Six populations colonized by wolves shifted from growth to decline at the time of colonization, while six adjacent populations that were not colonized by wolves continued to grow [6]. Each bar shows annual calf recruitment for the six elk management units within Yellowstone National Park that were colonized by wolves, for the period following colonization. In each year, the upper black line shows the calf recruitment expected from pre-wolf relationships for that year’s elk population density, snowfall and growing season precipitation. The upper dark gray bar shows losses explained by direct wolf predation, calculated from the number of wolves present and their seasonally adjusted rates of predation on adults and juveniles. The bottom grey line shows observed calf recruitment. After controlling for other limiting factors, the effect of direct wolf predation on calf survival explained, on average, only 52% of the difference between observed and expected recruitment; 48% of the difference (bottom light grey bar) was not explained by previously-established limiting factors other than risk effects. These calculations assume no change in predation by grizzly bears (because local increases in bear density did not spatiotemporally align with reductions in elk recruitment), but changes in prey selection by individual bears could explain some of the missing calves in some parts of the six units.
References


Does the Petal Fall Far from the Rose? Revealing the Ontogeny and Population Consequences of Ungulate Migration

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Seasonal migration often provides fitness benefits by allowing animals to secure access to high-quality forage, reduce predation risk, and ameliorate severe environmental conditions. For terrestrial migrants, the ontogeny of migration is poorly understood, but has implications for understanding why some species exhibit strong fidelity to their migration routes and seasonal ranges. One hypothesis is that migration routes and aspects of the mother’s seasonal ranges are transmitted from mother to offspring, resulting in surviving female offspring establishing summer ranges in close proximity to their natal range. The rose petal hypothesis describes these matrilineal clusters of related females, which may result in fine-scale genetic clustering and have implications for how biologists and managers understand behavioral constraints on the occupancy of seasonal ranges. Nevertheless, the mechanisms underpinning how this behavior develops, and whether landscape-scale population consequences follow, remain largely unknown. By building upon the framework of the behavioral transmission and rose petal hypotheses, we propose to test whether migratory patterns are transmitted from mother to daughter and assess the population-level consequences of this behavior. We will test the prediction that mothers pass their migratory routes and seasonal ranges to their daughters, resulting in matrilineal clusters that will form as a function of historical performance of the lineage and the seasonal ranges they occupy. We will characterize how mother-daughter pairs of mule deer (Odocoileus hemionus) in western Wyoming come to establish and occupy their seasonal ranges. To reveal how this behavior influences population dynamics and understand historical performance of matrilines, we will use genetic mark-recapture to quantify family-level density. The development and transmission of migration routes and seasonal ranges across generations may influence the occupancy and spatial distribution of migratory animals and, consequently, has implications for harvest management and conserving migration.
Driven to Mate: Male White-tailed Deer Alter Resource Selection during Breeding Season to Mirror Female Use of the Landscape

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In cervids, male mate search strategies are influenced by the spatial distribution and reproductive synchrony of females [1]. Roving is a common strategy employed by males in cases where receptive females are distributed in unpredictable patches across a landscape. However, roving is energetically costly compared to other search strategies, suggesting males should incorporate spatial knowledge during their searching to maximize encounter probabilities with females [2]. For example, males may increase their encounter probability with mates when selecting for patches used by females [3].

To improve our understanding of how males may increase their likelihood of encountering receptive females, we examined changes in resource selection of 21 male and 11 female white-tailed deer (*Odocoileus virginianus*) during pre-breeding (13 September – 25 October) and breeding seasons (26 October – 27 November) in Harris County, Georgia, USA. Because sexual segregation is common among white-tailed deer populations, we hypothesized that males and females would be sexually segregated during pre-breeding [4]. We also hypothesized that males would align their resource selection with females during breeding season to increase their encounter probabilities.

We observed differential resource selection between sexes and seasons. During pre-breeding, females selected for agriculture and shrub-scrub vegetation types, while avoiding deciduous and evergreen forests, riparian, and developed areas. Interestingly, during pre-breeding, males selected for vegetation types that females avoided (e.g., deciduous and evergreen forests, and riparian areas), suggesting some level of sexual segregation prior to breeding season. During breeding season, females altered their resource selection from pre-breeding by selecting for deciduous forests and water sources (e.g., ponds, impoundments), while avoiding evergreen forests, shrub-scrub, riparian, and developed areas. As expected, males maintained selection of deciduous forests and riparian areas, but avoided vegetation types that females were no longer using such as agriculture and shrub-scrub.

Spatial mapping revealed an overall pattern of shifted resource selection for females between the pre-breeding and breeding periods; this also was evident for males (Figure 1). Spatial depiction of landscape use revealed that the two sexes utilized resources much differently during pre-breeding, a sign of sexual segregation. As expected, the areas predicted to receive the greatest use by females during the breeding season appeared to influence resource selection and the spatial distribution of males. Our research provides insight into how males alter behavior and spatial use of the landscape to match that of females during the breeding season, which should increase encounter probabilities with mates. Future analyses will examine how encounter probabilities may influence male movement behaviors.
Ecological Drivers of Elk Survival in Idaho

Jon S. Horne, Mark Hurley, Scott Bergen, Kayte Groth – Idaho Department of Fish and Game

Effective management of elk (Cervus canadensis) populations is facilitated by an understanding of the factors that influence elk survival. From 2005 - 2016, we monitored elk across the state of Idaho for mortality and often times cause-specific mortality. We compiled known-fate survival data from 2,007 radio-collared elk (1,273 adult cows and 834 6-month-old calves). Statewide, lion and wolf predation were the main causes of mortality for cows (35% and 32%, respectively) and 6-month old calves (45% and 29%, respectively). Mortality rates were highly variable across elk populations and years. To examine factors potentially causing this variation, each elk was assigned to one of 29 populations based on its winter range. We then modeled risk of mortality as a function of winter severity, summer nutritional resources, and wolf abundance. For calves, we found a negative relationship between chest girth and risk of mortality and a positive relationship with wolf pack size and snow depth. For adult cows, we found a positive relationship between risk of mortality and wolf pack size and snow depth and a parabolic relationship with age. Overall, we found that elk survival is inherently complex but by utilizing a data set encompassing substantial spatial and temporal variation, we were able to identify the main drivers of elk survival in Idaho.
ECOLOGY AND CONSERVATION OF THE HUEMUL: REINTERPRETING HYPOTHESIS AND EVIDENCE

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The Patagonian huemul deer (Hippocamelus bisulcus) is the only South American cervid in danger of extinction. Only 1048-1500 individuals are remaining, fragmented into 101 subpopulations. 60% of those have only 10-20 deer, compatible with pseudoextinction levels. The past range contraction of huemul follows a north-south and an east-west gradient related to certain anthropogenic activities. The northern distribution has experienced the largest declines and fragmentation, with remaining huemul in high elevations of the Andes mountains.

Measures to reverse the effect of the supposed competition with livestock result in both success and failure generating discussions and little progress in understanding the cause-effect relationship. The present work characterizes observed patterns and proposes a hypothesis to explain them. One key observation is regarding the contradictions surrounding the biology of huemul. Studies on habitat selection based on remaining populations in northern Patagonia, even after the livestock removal, indicate a selection of high altitude areas which implicitly contradicts the knowledge about having lost traditional wintering areas as a cause of the contraction and population declines. Additionally, the causes of the population declines may be different to those resulting in failure of recovery. However, there is quantitative evidence that resident populations living at high elevations result in lower densities. There are some cases where management strategies had been successful: Reserva Nacional Lago Cochrane, Fiordo Témanos, Estancia Valle Chacabuco and the reintroduction in the National Park (NP) Torres del Paine. These cases have resulted in quite rapid recoveries (λ=1,14-1,21), they are located in the best preserved area of the habitat gradient - in valleys and at low elevation; with high deer densities; absence or low levels of livestock, dogs and hunting; with dispersing animals and/or having relatively high reproductive rates. Similar management applied in other cases though did not result in recoveries: NP Los Alerces or regarding habitat selection in Valle Esperanza could be merely consequences of failure in recovery. These cases differ from the previously mentioned examples in that resident huemul remain living at high elevations. We hypothesize that the loss of migratory behavior, at least altitudinal movements, is an ultimate factor which explains the failure to recover. Nutritional ecology is the first hypothesis to explain failure in recovery. Secondarily, we propose that low deer densities reduce the success of the 'rescue effect' and the recovery efforts. We understand that any hypothesis explaining such a dual response must generate hysteresis (loss of resilience). Huemul is strongly phylopatric and little or non-migratory, probably artificially. In Odocoileus virginianus, phylogenetically related to huemul, the use of summer ranges is an acquired behavior, passed from the mother to the young during the first year. They do not change their home range or migratory patterns, for instance, to colonize better habitat in neighboring areas, and show a high degree of site fidelity. If the migratory behavior is acquired in huemul similarly as in other cervids, then the permanency of small and isolated groups in high mountain areas for several generations could provoke their local and independent loss of migratory behavior in metapopulations. This could explain why the successful and non-successful cases of recovery, the reported patterns of habitat selection and non-migratory behavior, and why the causes of declines and those that prevent recovery are different in the northern distribution where the species has suffered the major impacts. Although most parsimonious hypothesis does not require migration to explain...
the observed, we believe that including them is suitable for the habitat and the phylogeny of huemul.

References
[10] Izquierdo, VM. 2017. Informe técnico sobre el proyecto “Aplicación de medidas para la mitigación de amenazas a la conservación del Huemul (*Hippocamelus bisulcus*)”. Informe APN.
Effect of Male Age Structure on Demography and Breeding Behavior in White-Tailed Deer


White-tailed deer (*Odocoileus virginianus*) populations throughout North America have endured harvest rates as high as 80% of antlered males resulting in a female-biased sex ratio throughout the 20th century with no adverse effects on overall abundance. In 2002, Pennsylvania implemented statewide harvest regulations that increased the survival rate of males by implementing antler point restriction (APR) regulations and reduced the survival rate of females by increasing the allocation of antlerless licenses.¹ These changes in harvest regulations created an older age structure in the male population (percentage of antlered males >2.5 years old increased from <4% to 11%), reduced overall population size by 27%, and created an adult (>1 year old) male:female ratio that was less skewed towards females (from 1:3.7 to 1:2.1).

During 1999–2006 we examined road-killed females to monitor pregnancy rates, conception dates, productivity (embryos/female), and embryo sex ratios to test if changes in sex-age structure of the population influenced timing and synchrony of breeding and productivity. We predicted the shift to an older age structure of males and a less skewed sex ratio would result in the average conception date occurring earlier, greater breeding synchrony (reduced variance in conception dates), increased productivity, and more male offspring produced.²,³ We examined 2,209 adult females (>2 years old), 1,397 yearling females (>1 year old), and 2,647 fawns for embryos and we calculated date of conception for 3,107 female deer (207–523 per year). We developed a hierarchical model with wildlife management unit (WMU) and year treated as random effects, in which both the date of conception and the variance around the date of conception changed after APRs were implemented. We failed to detect a change in conception date over years (mean date = 13 November) and any consistent change in the SD of conception dates. In contrast to our predictions, reproductive rates were greater before APRs were implemented (Yearlings: 1.51 embryos/female, SE = 0.053; Adults: 1.65 embryos/female, SE = 0.043) and declined to 1.39 embryos per yearling female (SE = 0.046) and 1.56 embryos per adult female (SE = 0.030). Also, we found no evidence that pregnancy rates for female fawns increased. Furthermore, we found no evidence that offspring sex ratios changed after APRs were implemented. The best linear mixed effects model, treating WMU as a random effect, included only an intercept term. During 1999-2006, yearling females produced 1.13 males per female (SE = 0.093) and adult females produced 1.09 males per female (SE = 0.031). We believe there are several reasons for the lack of change in breeding behavior and demography. First, breeding in white-tailed deer is not dominated by older age classes so increasing the proportion of older males in the population is unlikely to change who dominates breeding.⁴ Second, there may be limited flexibility regarding when breeding can occur. The timing of breeding should result in an optimal birth date for fawns such that it is not too early that they are exposed to environmental conditions that elevate the risk of mortality (e.g., cold temperatures) yet early enough to attain a body condition in autumn that maximizes winter survival. Synchrony of breeding in white-tailed deer increases with latitude but Pennsylvania is located within the portion of the range of white-tailed deer that exhibit little variation. Third, productivity has been adversely affected in ungulates when sex ratios were >25 females per male.³ In white-tailed deer, given typical reproductive rates, it is difficult to achieve a breeding age (≥1.5 year old) male:female sex ratio skewed beyond 1:4 unless adult male annual mortality rates exceed 0.90 and adult female annual mortality rates are <0.2. Harvest regulations, similar to what were implemented in Pennsylvania, that create an older male age structure and shift the sex ratio towards 1:1 are unlikely to affect the timing of breeding, synchrony of breeding, productivity, and sex ratio of offspring in white-tailed deer. As a result, efforts to identify a desired sex ratio or
manipulate sex ratios to achieve management goals relative to breeding behavior will be challenging.

References
Effects of Calf Predation and Nutrition on Elk Vital Rates in New Mexico

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Demographic data indicated a population of elk (Cervus elaphus) in northern New Mexico had reduced juvenile recruitment, resulting in a concern over quality hunting opportunities. Following several years of low calf:cow ratios of <25:100, we conducted a 4-year study from 2009–2012 to identify reasons for poor recruitment and evaluated the role of predation and nutrition in limiting productivity of an elk population. We captured and fixed ear-tag radio transmitters to 245 elk calves (126M, 119F) to determine cause-specific mortality and estimate calf survival. During the second half of our study, we implemented a new spring black bear (Ursus americanus) season resulting in higher spring black bear harvest and evaluated response in calf survival. We also quantified herd-wide nutritional condition and productivity. We estimated percent ingesta-free body fat (IFBF) and pregnancy rates by sampling 1,808 hunter-harvested female elk from autumn through winter. The primary cause of summer mortality for calves across all years was black bear predation. Estimates for annual calf survival were greater when spring black bear harvest was moderate to high (0.44–0.47) compared to periods with lower bear harvest (0.33–0.35; Table 1). For every additional bear harvested in spring, radio-tagged elk calves were 2.4% more likely to survive the summer. Across years and age classes 82% (SE = 1%) of females were pregnant (Table 2). Pregnancy rate was greatest for prime aged (2–14 years) females (88%, SE = 1%). Our herd-wide estimate of IFBF for prime-aged adult female elk IFBF was 11.9% (SE = 0.19) but varied by pregnancy and lactation status (Table 2). Our results that black bear predation was the primary cause of summer calf mortality and that adult females were in adequate nutritional condition suggested that black bear predation was limiting population productivity. Additionally, calf survival was higher in drought years, the same years when targeted spring black bear harvest was implemented. Our results demonstrated that productivity could be increased by implementing a spring black bear harvest strategy targeted around calving areas and could be applied in other areas experiencing low elk calf survival. Additionally, our methods could be applied in other areas experiencing low calf survival, with black bear predation being the primary cause of early calf mortality.
Table 1. Elk (*Cervus elaphus*) calves captured 2009–2012 in northern New Mexico to estimate survival. Data are presented by year: number of calves captured, number censored, median birth date, average birth mass, summer and annual calf survival, and number of bears harvested (current spring and previous fall).

<table>
<thead>
<tr>
<th></th>
<th>2009</th>
<th>2010</th>
<th>2011*</th>
<th>2012*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number calves captured</td>
<td>30 (19M, 11F)</td>
<td>51 (22M, 29F)</td>
<td>63 (34M, 29F)</td>
<td>101 (51M, 50F)</td>
</tr>
<tr>
<td>Number calves censored</td>
<td>4</td>
<td>2</td>
<td>3</td>
<td>10</td>
</tr>
<tr>
<td>Median birth date</td>
<td>June 1</td>
<td>June 6</td>
<td>May 29</td>
<td>June 7</td>
</tr>
<tr>
<td>Average birth mass (SE)</td>
<td>16.22 kg (0.32)</td>
<td>15.19 kg (0.26)</td>
<td>16.40 kg (0.29)</td>
<td>16.71 kg (0.25)</td>
</tr>
<tr>
<td>Summer calf survival (SE)</td>
<td>0.43 (0.09)</td>
<td>0.35 (0.07)</td>
<td>0.54 (0.06)</td>
<td>0.48 (0.05)</td>
</tr>
<tr>
<td>Annual calf survival (SE)</td>
<td>0.35 (0.09)</td>
<td>0.33 (0.07)</td>
<td>0.47 (0.06)</td>
<td>0.44 (0.05)</td>
</tr>
<tr>
<td>Current spring bear harvest</td>
<td>1</td>
<td>1</td>
<td>20</td>
<td>11</td>
</tr>
</tbody>
</table>

*a2011 and 2012 were when black bear population manipulation was occurring

*bCalves were censored because their fates could not be determined or because they were harvested by hunters (n = 3) and we were interested in evaluating non-anthropogenic causes of mortality.

Table 2. Ingesta-free body fat, lactation rates, and pregnancy rates for female elk (*Cervus elaphus*) harvested from autumn and winter 2009–2012 in northern New Mexico. Age class was categorical; young (1.5 years old), prime (2–14 years old), and old (>14 years old). Pregnancy was calculated for animals harvested on or after November 1 of each year. Ingesta-free body fat was calculated for elk harvested from November 1–December 20 and lactation rate was calculated for animals harvested in autumn (October 1 through December 20).

<table>
<thead>
<tr>
<th>Age class (n)</th>
<th>Lactating (SE)</th>
<th>Pregnant (SE)</th>
<th>Lactating</th>
<th>Non-lactating</th>
<th>Lactating and non</th>
</tr>
</thead>
<tbody>
<tr>
<td>Young</td>
<td>0</td>
<td>0.14 (0.04)</td>
<td>0</td>
<td>8.46% (0.50)</td>
<td>8.46% (0.50)</td>
</tr>
<tr>
<td>Prime aged</td>
<td>0.35 (0.02)</td>
<td>0.88 (0.01)</td>
<td>10.23% (0.34)</td>
<td>12.83% (0.20)</td>
<td>11.94% (0.19)</td>
</tr>
<tr>
<td>Senescent</td>
<td>0.22 (0.06)</td>
<td>0.47 (0.05)</td>
<td>5.63% (1.17)</td>
<td>8.53% (0.83)</td>
<td>7.90% (0.71)</td>
</tr>
<tr>
<td>Herd wide</td>
<td>0.27 (0.02)</td>
<td>0.82 (0.01)</td>
<td>9.98% (0.34)</td>
<td>12.07% (0.21)</td>
<td>11.41% (0.19)</td>
</tr>
</tbody>
</table>
Effects of Habitat Selection and Predation on Cause-specific Mortality of White-tailed Deer Fawns in the Appalachian Mountains of Georgia, USA

Adam C. Edge, Cheyenne J. Yates, Gino J. D’angelo, Andrew R. Little – Daniel B. Warnell School of Forestry and Natural Resources, University of Georgia; Charlie H. Killmaster, Kristina L. Johannsen – Game Management Section, Wildlife Resources Division, Georgia Department of Natural Resources; David A. Osborn, Karl V. Miller – Daniel B. Warnell School of Forestry and Natural Resources, University of Georgia

White-tailed deer (Odocoileus virginianus) population densities have declined over the past few decades throughout the Chattahoochee National Forest in northern Georgia, USA. From 1979-2015, deer harvests on wildlife management areas (WMAs) within this Southern Appalachian Mountains region have declined by 85% and 97% for males and females, respectively [1]. However, nutritional condition indicators (body mass, yearling antler size, etc.) of harvested deer have steadily improved during this same time period, suggesting that habitat-related declines in fecundity are an unlikely cause of population declines. The area is characterized by a closed-canopy, forested habitat with a suppressed understory, possibly lacking adequate escape cover for fawns. Populations of black bears (Ursus americanus), coyotes (Canis latrans), and bobcats (Lynx rufus) have expanded in this region [2,3,4]. These species are known to impact fawn survival [5] and may be reducing fawn recruitment rates. High fawn predation rates can cause negative effects on long-term stability of deer populations [6].

To investigate survival and cause-specific mortality rates of white-tailed deer neonates in the southern Appalachians, we will capture 90 does ≥1.5 years of age, affix GPS collars, and insert vaginal implant transmitters (VITs) over 3 years (2018-2020) on the Blue Ridge and Cooper’s Creek WMAs in North Georgia. The resultant offspring will be captured within 24 hours of parturition and VHF collars will be affixed to 120 neonate fawns. We will monitor survival to 16 weeks of age and investigate fawn mortalities using saliva DNA analysis for predator identification and necropsies for other cause-specific indicators. We will triangulate locations to form minimum convex polygons for each collared fawn using ArcMap 10.4.1. and complete habitat surveys of each fawn’s home range recording both micro-habitat and landscape variables. Mortality rates with associated causes will be described and the effects of both biological characteristics and habitat variables on survival probabilities of fawns will also be assessed. We hypothesize fawn survival rates to fall within the range of similar studies in the southeastern United States where predation is prevalent at 14-33% [7,8,9,10]. We also expect habitat variables associated with closed-canopy forests to have a negative effect on neonate survival.

References
Effects of Lysine and Methionine Supplementation on Fattening and Blood Protein Metabolites in Fallow Deer (*Dama dama*)

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Amino acid supplementation is an almost unexplored research area in cervids. Only three studies have been previously conducted, all with a low sample size (four animals per experimental group) leading to inconclusive results[1,2,3]. These previous studies were conducted on *Cervus elaphus* and *Cervus nippon*. For that reason, in this study we focused on the effects of supplementation with ruminally protected amino acids in a large herd of fallow deer (*Dama dama*), which is the most commonly farmed deer species in Europe.

This study was designed to investigate the effects of lysine and methionine supplementation on growth performance, body condition, carcass traits, and blood plasma metabolites related to protein and fat metabolism, of fallow deer during the fattening period. A second goal was to determine the influence of two culling seasons on these parameters. Forty-five farmed male fallow deer were randomly allocated to three groups of 15 animals each, balanced by body weight. The supplementation experiment started at 11 months of age (calves from the previous year). All three groups were pasture-fed and supplemented with barley (500 g/animal/day) and mineral premix *ad libitum*. The groups received varying levels of ruminally-protected lysine and methionine: 1) no amino acids (Control), 2) 9 g/day of lysine (Lys), and 3) 9 g/day of lysine plus 3 g/day of methionine (Lys+Met). Animals were culled in two separate seasons: late autumn (LA; 6 animals/group), and late winter (LW; 9 animals/group). To compensate for the lack of pasture during winter, the animals received grass silage during this period. Generalized Linear Mixed Models tested the effects of treatment and culling period on selected carcass traits (culling weight, average daily weight gain ADG, carcass weight, dressing percentage, blood weight, percentage of meat, body condition score [BCS], kidney fat index [KFI], total kidney fat weight, percentage of internal fat) and blood biochemistry (creatinine, blood urea nitrogen, total proteins, albumin, globulins and tryglicerides).

Supplementation had no significant effects on final weight, while ADG significantly decreased in the LW (p=0.002). Lys+Met supplementation positively influenced BCS (p=0.024), while animals culled in LW showed decreased BCS (p<0.001). Lys+Met (p=0.005) and LW culling (p=0.004) had a positive effect on KFI. That was expected because of the cessation of growth in cervids during winter due to changes in photoperiod[4]. Carcass weight, bone percentage, and blood weight were lower in LW (p<0.05) but were not influenced by treatment. Dressing percentage was higher in Lys+Met treatment (p=0.002) and LW group (p<0.001). Body condition score (p=0.024), kidney fat index (p=0.005), total kidney fat (p=0.001), and percentage of internal fat (p<0.001) increased significantly with Lys+Met supplementation. During LW, kidney fat index (p=0.004) and kidney fat (p=0.001) were also significantly higher than in LA. Deer that received Lys or Lys+Met supplementation showed elevated values of creatinine, blood urea nitrogen, and triglycerides (all p<0.001). The increased concentration of creatinine was correlated with BCS (r=0.450; p=0.019).

In summary, even if the treatment does not seem to improve weight gain, it affected dressing percentage, especially at autumn culling. The increase in this very important parameter in animal production is supported by the increase of protein-related metabolites (creatinine and blood urea nitrogen). Lys and Lys+Met treatments also affected fat deposition, especially during the winter period, reflected also in the increased values of triglycerides. Thus, apparently, both treatments affected muscle formation during the growth period (summer and autumn) and fat...
storing during winter. These results suggest a good potential of amino acids to increase muscle development and production during the following spring, since supplemented animals will finish the summer in better condition and with greater fat stores.

Culling, or selective harvest, is a widely practiced strategy aimed at increasing antler size in managed populations of cervids. Recognizable microevolution of phenotypic traits through selection has long been practiced in laboratory or domestic populations, but the effect of culling on wild populations is poorly documented because of the difficulty in the field experimental settings [1]. Ideally, antler sizes of selected individuals between intergeneration at each age class are consistent or larger, and antler traits generationally improve via culling [2]. However, selective-harvesting young males can be genetically random due to unclear expression of their phenotypic potential in variable environments [3], and the environmental variations may also baffle the genetic potential for the mature antler growth [4]. We evaluated the effects of culling on demographic, genotypic, and phenotypic traits as part of a long-term experimental study of male white-tailed deer in southern Texas, USA. We established 3 treatments including, males at all age classes subjected to the intensive culling criteria (14.2 km$^2$), males at the middle and mature age classes subjected to the moderate culling criteria (72.8 km$^2$), and males without culling applications as control (20.2 km$^2$). Each autumn during 2006–2016, we captured male deer, estimated age, and measured antler characteristics. Deer that did not meet culling criteria for their age class were sacrificed during 2006–2012. We recorded 5,447 captures of 2,937 individual bucks, and culled 1,333 of them. Most bucks were sired by males that exceeded the culling criteria. Nonetheless, the annual culling intensity for 1.5-year-old males at the intensive treatment ranged from 85 to 100% of bucks captured. Sixty-seven percent of 1.5-year-old males classified as culls would transition from cull to acceptable at 2.5 years old, while 56% would transition from acceptable to culls. The proportion of males changing, originally from acceptable to keep next year ranged 30 to 33% across all age classes. Heritability of antler points at 1.5-year-old males is only 24% (Table 1). In other words, contributions of environmental effects to young antler growth are large. In the south Texas environment, phenotypes of physically immature males may not correlate to their genetic potential. Even though heritabilities of antler traits increased as deer aged, the empirical response for the genetic component of antler traits to culling were not recognizable due to the long interval between generations (Mean = 5-6 years), small numbers of male-offspring per sire (Mean = 1.0-1.3 male offspring), and the presence of phenotypically superior males with relatively lower breeding values. The results of this study will have important management implications for harvest management in male white-tailed deer.
Table 1. Age distribution of estimated heritabilities of antler traits, antler points for 1.5-, 2.5-, 3.5-4.5-year-old males and GBC for ≥3.5 and ≥5.5-year-old males, were quantified using the male pedigree records collected from 2006 to 2016 from the Comanche Ranch, Texas, USA.

<table>
<thead>
<tr>
<th>Age class</th>
<th>Traits</th>
<th>h² (SE)⁺⁺</th>
<th>PE (SE)ᵇ</th>
<th>e (SE)ᶜ</th>
<th>Repeatability</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.5</td>
<td>Antler points</td>
<td>0.24 (0.11)*</td>
<td>—</td>
<td>0.76 (0.11)**</td>
<td>—</td>
</tr>
<tr>
<td>2.5</td>
<td>Antler points</td>
<td>0.25 (0.14)</td>
<td>—</td>
<td>0.75 (0.14)**</td>
<td>—</td>
</tr>
<tr>
<td>3.5-4.5</td>
<td>Antler points</td>
<td>0.36 (0.12)*</td>
<td>0.16 (0.13)</td>
<td>0.49 (0.04)**</td>
<td>0.58</td>
</tr>
<tr>
<td>≥3.5</td>
<td>GBS</td>
<td>0.45 (0.09)**</td>
<td>0.13 (0.09)</td>
<td>0.42 (0.02)**</td>
<td>0.58</td>
</tr>
<tr>
<td>≥5.5</td>
<td>GBS</td>
<td>0.67 (0.18)**</td>
<td>0.00 (0.18)</td>
<td>0.33 (0.03)**</td>
<td>0.67</td>
</tr>
</tbody>
</table>

⁺⁺ P < 0.05, ** P < 0.01

⁺ Heritability of the Boone and Crockett Score at ≥5.5-year old male was based on the year effects, the year of measurements.

ᵇ PE indicated the permanent environment effects.

ᶜ e indicated the residual effects of the unknown factors as a proportion of the male antler phenotypic variance (σ²P).

References
Environmental Influences on Ages Estimated from Tooth Replacement and Wear

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White-tailed deer are often aged by tooth replacement and wear (TRW). It is unknown whether environmental factors or visual bias influence estimated TRW age. For instance, sandy soils may accelerate tooth wear, whereas supplemental feeding may have the opposite effect. Further, visual cues, such as body size and antler size, may influence estimated TRW age. Cementum annuli (CA) is another ageing technique that is unbiased; thus, the differentials between TRW and CA may provide information about external influences on TRW ages. We obtained CA and TRW ages from 7,389 male deer harvested on King Ranch during 2000-2014 and performed a mixed-effects analysis, with the difference between CA and TRW ages as the dependent variable, antler size, feeder site density, body mass, soil characteristics, and harvest date as exploratory variables, and TRW as a random effect. Results indicated that fixed effects explained little of the variation in age differences ($R^2 = 0.01$). The largest influence came from body mass; the greater the body mass, the higher the TRW age than the CA age. This indicates that visual bias may influence TRW age; however, the effect size was small. A 9 kg (20 pound) increase in dressed body mass decreases the difference between TRW and CA by 0.1 years. Sand and supplemental feed had small influences on age differentials. Our results agree with previous studies that differences between true ages and estimated ages are likely a function of variability in teeth among individual deer. Despite the variability, CA and TRW were ± 1 year ~70% of the time, indicating that TRW has value for management purposes.
Estimating Carrying Capacity of Roosevelt Elk Herds using State-Space Models and variation in strength of density dependence

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Estimates of $K$ carrying capacity are useful for conserving and managing large herbivores as this parameter is integral to understanding population dynamics and trophic interactions. Population growth models estimate parameters such as $K$ carrying capacity from time series of abundances. Furthermore, when implemented using a state-space formulation these models can accommodate bias in population survey methods (observer error) so that estimated parameters are more accurate [1,2]. We estimated population parameters of five, non-migratory Roosevelt elk ($Cervus elaphus roosevelti$) herds in Redwood National and State Parks, California, USA, to assess variation in $K$ and how variation in $K$ can be used to understand population dynamics across herds [3]. Our objectives were: (1) evaluate three commonly used population growth models to understand Roosevelt elk herd dynamics in the parks, (2) estimate the maximum intrinsic rate of population increase ($R_{max}$) and $K$ of each of the five herds in the parks, and (3) assess how variation in $K$ might affect strength of density dependence for each herd. We fitted the Gompertz, Ricker, and theta-logistic models to these data. Although these models indicated differing population dynamics and estimates of $K$ for the same herd (Fig. 1), we based our inferences on the results from the Ricker model after considering elk life history, a comparison of the model estimates to the fit of the observed time series of abundances, and the precision of parameter estimates. Across herds estimates of $K$ ranged over an order of magnitude from 22 to 246, yet $R_{max}$ was constant (0.21). As such, the strength of density dependence should be inversely related to $K$ [4], a pattern that has been detected at larger regional scales, but not at a landscape scale. The strong density dependence of smaller herds might also explain why one of the herds that originated 27 years ago and has experienced changes in available forage resources has yet to establish density-dependent population growth, resulting in imprecise estimates of $K$. 


**Figure 1.** Plot of estimated intrinsic rate of population growth ($R = \ln(N_{t+1}/N_t)$) from low abundance to $K$ carrying capacity of one herd based on three population growth models. The Gompertz model is the black line, the Ricker model is the green line, and the theta-logistic model is the red line. The interior tick marks on the X axis are the 21 abundance estimates of the herd gathered across 41 years.

**References**


Changes in forest management over the last century, such as fuels reductions through thinning and prescribed burning, has the potential to influence populations and distributions of both mule deer (*Odocoileus hemionus*) and white-tailed deer (*Odocoileus virginianus*) in forested landscapes. However, because deer are difficult to survey in forested landscapes using traditional methods (e.g., capture and telemetry, transect surveys), biologists currently lack a method to reliably estimate densities within these landscapes. Furthermore, we have a poor understanding of the spatial and temporal segregation of mule deer and white-tailed, or of differences between the species in how they select habitat. Our project aims to address these problems by testing and validating a novel method that uses camera traps to estimate species-specific densities within the Colville National Forest in northeastern Washington, especially in relation to forest management initiatives aimed at reducing the risk of forest fires [1].

During October 2017, we deployed cameras for 26 days in the Colville National Forest to test the feasibility of a larger study to be carried out during the summer of 2018. The camera grid had an array of 30 cameras spaced 500 m apart (Fig. 1). At each camera location, we measured visual obstruction using a cover pole at 7 m and 15 m from the camera to provide an estimate of detectability by the camera in different habitats. During installation of the cameras, we measure distances from the camera and recorded videos of researchers holding distance markers at 1-m intervals out to 20 m to provide a reference for estimating distances to filmed deer. To separately estimate densities of mule deer, white-tailed deer, and moose we estimated distances to recorded animals by comparing their distances to those of researchers in the reference videos. We fit point transect models, adapted to camera trap data, in program Distance [1]. We included visual obstruction at 7 and 15 m as covariates in the detection function to account for differences in detectability of animals because of vegetation. We sampled a total area of 12.25 km². Eleven of the 30 cameras had at least one image of a moose, 12 had mule deer, and 21 had white-tailed deer. The density estimates, without including visual obstruction in the model, were 11.98 / km² for mule deer, 15.77 / km² for white-tailed deer, and 0.68 / km² for moose (Table 1). The inclusion of visual obstruction in the model slightly improved the fit of the model (i.e., reduced AIC) and increased the density estimates (Table 2). Our next step is to sample deer and moose across a larger area and variety of habitat types within the Colville National Forest and compare our new camera-based method of density estimate with density estimated by traditional techniques (i.e., pellet group counts and line transect sampling).
Figure 1. Configuration of cameras that were deployed for 26 days during October 2017 in the Nancy Creek region on the Colville National Forest, Washington.

Table 1. Density estimates for mule deer, white-tailed deer, and moose during October 2017 in the Nancy Creek region of the Colville National Forest. Estimates were obtained using the hazard rate model with no adjustments and no covariates in program Distance.

<table>
<thead>
<tr>
<th>Species</th>
<th># Observations</th>
<th>Density</th>
<th>SE</th>
<th>Estimated # animals</th>
<th>SE</th>
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</table>

Table 2. Density estimates for mule deer, white-tailed deer, and moose during October 2017 in the Nancy Creek region of the Colville National Forest. Estimates were obtained using the hazard rate model with no adjustments and visual obstruction at 7 m and 15 m in program Distance.

<table>
<thead>
<tr>
<th>Species</th>
<th># Observations</th>
<th>Density</th>
<th>SE</th>
<th>Estimated # Animals</th>
<th>SE</th>
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</thead>
<tbody>
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References
Decades of fire suppression, logging, and overgrazing have altered the conditions of southwestern forests resulting in increased densities of small diameter trees and an overall increase in fuel loads. These increasing tree densities have been associated with decreases in biodiversity, reduced habitat quality, degraded foraging conditions for ungulates, and more frequent and severe wildfires. In response, land managers are increasingly implementing landscape-scale forest restoration treatments through the use of prescribed fire and forest thinning in an attempt to mitigate the risk of catastrophic wildfires and improve habitat conditions for a variety of wildlife species. Similar vegetation treatments are commonly implemented by wildlife managers specifically to improve habitat conditions for mule deer (*Odocoileus hemionus*). We monitored responses of female mule deer to forest restoration treatments and wildfires in northern New Mexico. Our specific objectives were to: 1) assess changes in abundance of key forage species; 2) estimate differences in forage quality; and 3) determine habitat selection patterns of mule deer in relation to recent wildfires, forest restoration treatments (including the time since treatments), and other habitat characteristics. Herbaceous forage biomass was greater in wildfire burned areas than prescribed burns, forest thinning, and untreated areas. Oak forage biomass was greater in wildfire burned areas compared to prescribed burns, forest thinning, and untreated areas. Thinned areas tended to have higher oak forage biomass than untreated areas. Mule deer selected for areas burned by prescribed fire and avoided wildfire burned and thinned areas less than 5 years old. Mule deer strongly selected for thinned areas >5 years old. At both the landscape and within home range scale, grasslands were avoided during all seasons, pinyon-juniper woodlands were selected for in winter, and oak vegetation and mixed conifer forests were selected during summer. Data collected during our study suggests mule deer benefit from recent prescribed burns and older forest thinning. The lack of selection for wildfire burned areas was unexpected given the differences in forage biomass observed. Knowledge of the short- and long-term effects of restoration treatments will provide managers with guidance for making informed decisions regarding implementation of vegetation treatments to benefit mule deer.
Exotic ungulates play a major role in the current biodiversity crisis [1]. Axis deer (*Axis axis*) are expanding its range and causing increasing concern in multiple regions, though its negative impacts have only been described in a few places [e.g. 2]. A long-term management program of wild boar (*Sus scrofa*) and axis deer in a protected area in north-eastern Argentina (El Palmar National Park, covering 8,500 ha) documented an unexpected increasing trend in deer numbers despite lethal removal through controlled still shooting performed by recreational hunters over a 12-year period [3,4]. In order to assess the effects of the overabundant axis deer population and contribute to the park’s management goals, our ongoing work there seeks to describe deer habitat use and the prevalence of tree damage by fraying and bark-stripping across a gradient of distance to water courses and associated refuge availability. We used a systematic sampling design consisting of 28 equidistant strip transects measuring 1000 x 1 m, each one subdivided in three blocks (200 x 1 m), deployed across the park’s northern zone (approximately half the park’s area) open for public use. On each block we counted deer fecal pellet groups, trees and woody shrubs, and recorded for each individual its diameter at breast height (DBH), presence and type of damage, and wound area [5]. At each block we recorded a set of environmental variables every 50 m: degree of invasion by exotic trees, overstory and understory cover, average height of grasses, and type of habitat. Deer fecal pellet groups were found in all transects and habitats, and at most blocks (73 of 81, 90.1%), but its spatial distribution was not uniform. The density of deer pellets steadily increased starting at 4 km from the Uruguay River (eastern limit of the park) up to the coast (Figure 1). Deer pellet groups reached maximal density in the riverine forest, which is densely invaded by seven exotic species of trees and shrubs, and is probably key for deer activities [6]. We registered 444 trees or woody shrubs of which 113 (25.5%) presented some type of debarking attributable to axis deer (Figure 2).

Among native trees with more than 10 individuals examined, the most frequently affected species were *Myrcianthes cisplatensis* (55.0%), *Allophylus edulis* (34.3%), *Acacia caven* (8.7%), and other 2 low-density species (*Cordia boissieri* and *Daphnopsis racemosa*); the relative frequency of affected specimens differed highly significantly among these species (p < 0.001). We detected five types of debarking affecting 9 species in a widely variable manner. The exotic shrub *Pyracantha atalantoides* was frequently (39.3%) affected with signs attributable to axis deer, presenting bark stripping by feeding in 83% of the specimens showing some damage. Regarding the severity of damage, nearly half (48.6%) of all individuals with fraying damage occurred in specimens with DBH values below 9 cm, potentially causing lethal effects. Girdling (the most severe type of damage) occurred very frequently in *M. cisplatensis* (22% of specimens displaying any sign of damage), a relatively common native tree species. Deer presence through the park reflected in a spectrum of levels of damage to several native trees and exotics woody species. Our preliminary results suggest a positive association between axis deer habitat use and the increasing expansion of exotic trees and woody shrubs. Additional studies are needed to assess deer habitat use over different seasons in the context of culling actions, and their impacts on forest regeneration and trees growth rates.
Figure 1. Relative frequency of axis deer pellet groups per strip transect (n = 28) and block oriented from west to east of the Uruguay River at the eastern park limit.

Figure 2. Relative frequency of woody individuals with signs of debarking attributable to axis deer (113 individuals) according to species among all specimens examined for damage (n = 444).

References
Sea Pines (SP) is a 5,300-acre residential/resort community on Hilton Head Island, SC. Traditional white-tailed deer (*Odocoileus virginianus*) hunting is not feasible due to municipal ordinance. As development in SP neared completion, the property owners association (Community Services Associates [CSA]) began receiving complaints regarding deer-human conflicts. In 1995 the University of Georgia (UGA) developed a research project to provide CSA and the South Carolina Department of Natural Resources (SCDNR) with biologically sound data needed to manage deer on SP. The project received a great deal of local, state, national and even international media attention. Local newspapers questioned the project and editorials included professional ridicule. In 1998 the original project was completed and UGA proposed a follow-up project that included lethal removal. Five local, state and national animal activist groups organized a coalition and in 1998 filed a lawsuit, ultimately heard by the South Carolina Supreme Court (SCSC) in 2000. In 2001 the SCSC ruled in favor of CSA and SCDNR; however, CSA decided to forgo the follow-up project and opted instead to implement a culling program made possible by recently approved SCDNR Urban Deer Management Guidelines. Since 2001 CSA has utilized sharpshooting to discretely remove 985 deer without incident. Deer-vehicle collisions and complaints of landscape depredation have decreased substantially. Local media, once a source of ridicule, now recognize the merit of these programs. Successfully managing deer in an emotionally, legally, and politically charged environment can be challenging for wildlife professionals. A description of lessons learned while operating amid such controversy will be presented.
Antler size of white-tailed deer (*Odocoileus virginianus*) is a trait that is controlled by a variety of factors including nutrition, age, and host genetics [1]. As white-tailed deer are an intensively managed and hunted species, understanding the underlying genetic factors associated with variation in phenotypes can provide information for managers to target in the optimization of traits such as antler size. We used genomic techniques that utilized pooled whole genome re-sequencing of individuals representing extreme antler phenotypes to identify quantitative trait loci of large effect across the entire genome. Samples were selected from a database containing phenotypic data for 3974 male white-tailed deer from Anticosti Island, Quebec, with DNA from the top individuals for large and small antlers being combined in equal quantities in two representative pools. Sequencing for each pool was performed on the Illumina HiSeq-X platform for overall coverage of 50x per pool. As expected the genome-wide analysis revealed a largely homogenous genome, but also detected significant and highly diverged regions between large and small antler pools [2]; these regions represent putative antler genes. We have identified and will discuss the underlying genes of interest that are related to extreme antler phenotypes.

References
Cervus elaphus subspecies red deer and wapiti have been farmed in New Zealand for over 40 years, with the first deer farming license issued in 1970. As the industry moved beyond an establishment phase, selective breeding has occurred for traits that improve product quality and farming system profitability. Antler traits, velvet and hard antler weight and style were initially the production traits focussed on [1]. Being a highly heritable trait [2] which is measured during harvest, velvet antler allowed breeders to make good genetic progress without the aid of quantitative genetic tools. Liveweight traits were mostly selected from the mature sire and dam liveweights in the early years, as regular progeny data collection was not generally common practice. Liveweight traits only became a major focus in the last 20-years when quantitative tools for the estimation of breeding values became readily available to breeders [3]. Deer Select, the New Zealand deer industry performance recording system, has been providing estimated breeding values since 2005 [3, 4]. The majority of venison-focussed red deer and wapiti stud breeders’ record on Deer Select, whereas less than half of the antler-focussed stud breeders do. Deer Select measures a range of velvet, liveweight and carcass traits, conception success and date. It reports estimated breeding values (EBV) and multiple trait economic indexes [5] produced across-herds, but within breeds [4]. Over half, 15 red and 7 wapiti breeders, of the estimated 40 stud breeders in New Zealand record on Deer Select. This represents 2% of the national herd being recorded and satisfies >30% of replacement breeding sire requirements annually [4]. These recorded herds provide the opportunity to quantify the genetic progress, or genetic trends for the New Zealand farmed herd for any traits recorded since 1995 (Figs. 1 & 2). The industry has made genetic progress in red deer velvet antler weight both at 2-years of age and older over the past two decades, while it has really only been in the past 10-15 years that there has been genetic progress made on other traits. Growth traits in the past decade are making around 250% more genetic progress than during the previous decade (Figs. 1 & 2). These trends are averages across all herds recording on Deer Select, so some individual breeders are making much more dramatic genetic gains in antler, liveweight, reproductive and carcass traits, e.g. the EBV of the trait leading red sire for 12-month liveweight in 2005 was +14.9kg, whereas the current trait leader is +35.6kg. Gains have primarily been made by focussing on single-trait selection which can present risks long term, so now many breeders are adopting a more multiple-trait approach and/or using the economic indexes. This appears to be reflected in a slight reduction in liveweight EBV rates of gain (Figs 1 & 2). The genetic progress made since 1995 has added $8.60 per hind mated, to a red deer replacement early-kill venison system or $17.58 to a red deer terminal venison system [5]. Commercial producers who actively source the best improved genetics from stud breeders should be able to match the rates of genetic progress of their breeders to realise the gains for themselves. In many cases commercial producers are seeing much greater phenotypic gains above the estimated genetic gain, by improving their farm management, especially the nutrition of the animals.
Figure 1. Genetic trends for all red deer recorded on Deer Select from 1995-2016 for 12-month liveweight, 12-month carcass weight; 2-year-old, and mature (>2-year-old), velvet weight; estimated breeding values (EBV), all in kg.

Figure 2. Genetic trends for all wapiti and wapiti-red deer crossbreds recorded on Deer Select from 1995-2016 for 12-month liveweight, 12-month carcass weight; 2-year-old, and mature (>2-year-old), velvet weight; estimated breeding values (EBV), all in kg.

References
Genetic Variability of the Red Deer (*Cervus elaphus*) in the Carpathian Basin

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Fragmentation of landscapes and deer habitats results in disintegration of natural populations into several subpopulations having a more or less pronounced genetic exchange. The presence of a genetic pattern is an important wildlife management issue, because the reduced gene flow between different populations may lead to genetic depletion [1]. Gene flow, maintained by the dispersal of animals, enhances genetic diversity, thus knowledge of the genetic diversity and the genetic exchange between neighboring populations is a precondition to discovering and evaluating potential problems and to determining the appropriate countermeasures [2]. Our objectives were to quantify genetic diversity and assess genetic structure of red deer (*Cervus elaphus*) populations in the Carpathian Basin. Samples were obtained from 267 free-ranging red deer legally harvested in six regions of the Carpathian Basin, 81 from Gemenc, 56 from Baranya, 58 from Somogy, 27 from Bakony, 9 from Csorna and 36 from Zemplén Mountains (Fig. 1). Samples were genotyped using 10 autosomal microsatellites [3]. Allele frequencies as well as allelic richness and diversity indices were calculated based on individual genotypes with the help of the Cervus and GenAIEx softwares; individual genotypes were also processed with the Structure software.

Autosomal microsatellites showed a high genetic diversity in red deer: the number of alleles per locus varied between 6 and 25, with an average number of 16.4 alleles per locus. Heterozygosity values were also high; mean expected and observed heterozygosities were 0.832 and 0.773, respectively. Heterozygosity and allelic richness values per population were in the same range as for the whole sample set. Other diversity indices also showed high values for all populations; PIC was between 0.722 and 0.837 with an average value of 0.832, Shannon-Weaver Index values were between 1.668 and 2.046 with an average value of 1.940. Genetic structure was detected by the software Structure, the second order rate of change in log Pr indicate the presence of three clusters (K=3). Although the weak differentiation found in our samples (Fig. 2) could indicate some structuring, the numerous mixed genotypes suggest an extensive admixture between populations of different sites. Various demographic and historical factors may contribute to the lack of a clear genetic structure. A more extensive sampling would be desired in the Carpathian Basin, associated with genotyping and evaluation of results.
Figure 1. Sampling sites for genetic study of red deer in the Carpathian Basin. Dots – Gemenc, Diamonds – Baranya, Squares – Somogy, Stars – Bakony, Circle – Csorna, Triangles – Zemplén.

Figure 2. The cluster assignment of the red deer in different sites of the Carpathian Basin based on autosomal microsatellites in the case of three clusters (K=3). 1 – Gemenc, 2 – Baranya, 3 – Somogy, 4 – Bakony, 5 – Csorna, 6 – Zemplén.

References
Habitat Selection by Columbian White-tailed Deer Along the Lower Columbia River

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Columbian white-tailed deer (*Odocoileus virginianus leucurus*) were one of the original 78 species to be granted federal protection under the Endangered Species Preservation Act of 1966, pre-dating the Endangered Species Act of 1973. Columbian white-tailed deer originally inhabited river valleys and surrounding foothills dominated by shrubs [1]. By the early 1900s, due to habitat loss and unregulated harvest Columbian white-tailed deer were extirpated throughout most of their historic range, with two remnant distinct population segments (DPS) remaining [2]. These DPSs are geographically isolated, separated by about 320 km of mostly unsuitable habitat (Figure 1). The lower Columbia River population occupies diked bottomlands and islands in the lower Columbia River in southwest Washington and northwest Oregon, and the Douglas County population occupies oak woodlands in the Umpqua River Basin in Douglas County, Oregon [3]. In 2003, after 25 years of active management, the Douglas County DPS was removed from the Endangered Species Act. However, the lower Columbia River population only recently improved from endangered to threatened, a designation achieved in 2016. Improvements in their conservation status were driven by harvest restrictions, acquisition of critical lands and habitat restoration. Yet, because habitat along the Columbia River is fragmented, translocations may be the most effective means of re-establishing Columbian white-tailed deer throughout their historic range.

We examined habitat selection and the effect of current vegetation management (i.e., cattle grazing and mowing) by adult female deer at 3 sites in the lower Columbia River population. From 2013-2018 GPS location data was collected for deer translocated to Ridgefield National Wildlife Refuge (n = 16) and non-translocated resident deer at the Julia Butler Hansen Refuge (n = 14). We fit generalized linear mixed models to estimate habitat characteristics influencing selection. Selection declined as distance to concealment cover increased (P<0.00). Likewise, selection decreased as distance to open increased (P<0.01). All habitat types were significantly different from grazed pastures, with only ‘other’ (urban areas, roads, water, sand, mud, etc.) and ‘coniferous forest’ having a lower selection index (Table 1). Adult females at all 3 sites preferred pastures and open areas managed without cattle grazing. Deer selected strongly against cattle pastures even when cattle were not present, supporting previous research observations [3, 4]. Our results may inform habitat suitability at future translocation sites. Habitat selection appears to be primarily influenced by availability of concealment cover and access to the cover-open interface. Planting of native tree and shrub species to fragment cattle pastures and other open areas may increase habitat suitability and connectivity by creating preferable edge habitat. Continuing to advance our understanding of this threatened population is essential to the conservation, recovery, and future viability of this species.
Figure 1. Study sites, current distribution, and historic range of Columbian white-tailed deer.

Table 1. Standardized parameter estimates ($\beta$) for the best model predicting habitat selection by Columbian white-tailed deer ($n=30$) along the lower Columbia River in Washington and Oregon.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Standardized $\beta$ Estimate</th>
<th>Standardized $\beta$ SE</th>
<th>Lower CI</th>
<th>Upper CI</th>
<th>Relative Habitat Rank$^a$</th>
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$^a$ Ranking based on standardized coefficients of habitat types relative to ‘grazed pasture.’

* Denotes significance; $p<0.05$, when compared to reference habitat type ‘grazed pasture.’

References

Habitat Selection by Mule Deer Within Migration Corridors in Nevada

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Migration is an important ecological phenomenon that allows ungulates to increase their exposure to high quality nutrients throughout the year. Although much is known about ungulate migration strategies, causes of migration, and habitat selection on seasonal ranges; few studies have identified those variables that are selected within migratory corridors. Additionally, there is limited information regarding how wildlife managers should account for shifts in corridors caused by seasonal and annual changes in resource availability and climatic conditions. To address this, we examined movement patterns and resource selection along migration routes to understand the effects of environmental stochasticity on corridor selection and the habitat preferences within the migration corridors of female mule deer, *Odocoileus hemionus*. We captured and applied radio collars to female mule deer (n=98) on their migratory pathway in the Pequop Mountains of eastern Nevada from 2012-2017. We used Brownian Bridge Movement Models to delineate stopover sites for each individual during seasonal migrations. We then used a machine learning analysis, random forest, to determine which climatic and environmental variables individuals selected across seasons in stopover locations and along movement paths within the migration corridors through a step-selection framework. We also compared corridors annually to determine the differences that existed due to environmental stochasticity and if corridors shifted in response to these environmental changes. Our research will benefit scientists by describing mule deer habitat selection within different parts of migration corridors which will allow them to identify high priority zones along migration routes where no collar information is available. It will also give managers a better understanding of environmental impacts on migration corridor selection as well as how corridors change in a stochastic environment. This research will assist managers with the conservation of vital corridors for migratory ungulates and address the importance of managing for larger and multiple corridors across the landscape.
Historical Perspective and Current State of Deer Conservation and Sport Hunting in Mexico

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ANGADI It is the Mexican Association of owners of private properties, ejidos and communal lands, dedicated to the conservation, management and sustainable use of the resources of the flora and fauna that is developed and produced on their lands as well as people interested in knowing and participate in what refers to diversified Livestock. The mission of ANGADI is to disseminate, promote and support knowledge, conservation and sustainable use of wildlife (flora and fauna) as a fundamental pillar of the ecological and socio-economic cultural heritage of Mexico, and holders of properties where this it is developed through the rural production model based on the Diversified Livestock. Our commitment is to conserve Mexico’s biodiversity and take advantage of opportunities for economic diversification for the rural sector, help the federal government through the Diversified Livestock model to the production of sustainable use of wildlife, as well as in the application of the General Law of Wildlife, instrument that was requested by the ANGADI and promulgated by the congress of the union in the year 2000. Currently, ANGADI is the most important organization in Mexico of producers of wildlife, and congregates over one thousand five hundred owners and holders of "Units of Management for the Conservation of Wildlife (UMAS)“, which cover about 10 million hectares of natural habitats where more than 70 species of wildlife of hunting interest and more than a thousand species of non-hunting wildlife are present, White-tailed deer is the most important game species in the country. For its efficient operation, ANGADI has State Delegations in Aguascalientes, Baja California, Coahuila, Chihuahua, Guanajuato, Jalisco, Nuevo Leon, Sonora and Tamaulipas.
White-tailed Deer Management Continuum in the USA: A History of Slippery Slopes and Potential Diminishing Returns

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White-tailed deer (deer) have long been recognized as the most popular and economically important game species in the USA. In recent decades, as the appetite for deer hunting increased, the intensity of the tools used to manage deer herds in many states grew, as well. The continuum of deer management practices is broad, ranging from what could be described as traditional practices on one end of the continuum, to extreme practices on the other end of the continuum. Emphasis on growing bigger antlers to supply hunting markets has been the impetus behind the integration of some of the more extreme practices into commercial deer hunting programs. Some of these practices include captive propagation of deer in small pens, line breeding strategies, artificial insemination, sexing of semen, use of various performance enhancing medicaments, embryo transfer, and bottle-feeding fawns. Though these practices have pushed antler sizes that now exceed 600” on the Boone & Crockett measuring system, there has also been a degree of chaos that has been created among the hunting community due to many of these extreme practices being perceived as controversial and antagonistic to the greater good of hunting and wildlife conservation. Further, there are also concerns that some of these controversial practices lead to erosion of support for hunting by the non-hunting community. All of this does beg the question of whether there are points along the deer management continuum that yield diminishing returns, resulting in decreased participation in deer hunting, decreased support for hunting, decreased financial economies associated with deer and deer hunting, and compromised sustainability of conservation funding that benefits all terrestrial wildlife in this country.
The introduction of sika deer in the United States has occurred several times at different locales and with several different subspecies. The first introduction was onto James Island, Maryland in 1916. Results of genetic analysis found that five sika deer arrived in Maryland from Yakushima Island, Japan via a multigenerational stopover in the United Kingdom [1]. In the 1920’s, a small number of sika deer from the James Island population were transported east to Assateague Island along the Atlantic coast. These deer dispersed onto neighboring Chincoteague Island, and by 1963 the eastern population was estimated to be 1,300 individuals. A population of 10,000 – 12,000 sika deer is presently established on the eastern shores of Maryland (Fig. 1) and is increasing in abundance and expanding in range. Densities can reach as high as 42 deer/km² in managed areas [2].

Sika deer outcompete native white-tailed deer, resulting in a decrease in the nutritional value of white-tailed deer diet when ranges overlap with sika deer [3]. The presence of white-tailed deer, however, does not affect the diet quality of sika deer. This dietary competition could lead to competitive exclusive of white-tailed deer in areas with high sika densities. While habitat in their native range of Yakushima Island was primarily mountainous, sika deer habitat in Maryland consists of tidal marsh, agricultural fields and thick, forested wetlands. Sika deer in Maryland also maintain larger home ranges (464 – 4121 ha) than both white-tailed deer and native sika populations and occasionally exhibit seasonal migrations and nomadic behaviors [4,5].

Harvest of sika deer began on James Island and mainland Maryland as early as 1938 but was sporadic through the early 1960’s with only a few harvested annually [6]. Sika deer were distinguished from white-tailed deer as a large game animal in 1973 and regulations allowed for greater rates of harvest on sika deer than white-tailed deer [7]. Regulations regarding sika deer harvest have changed several times as hunting has become increasingly popular in the region. Professional guide services are available that cater exclusively to sika deer hunters, and recent survey figures indicate that 3,000 – 5,000 hunters annually pursue sika deer for over 30,000 hunter days per year [8]. Sika deer harvest dates run concurrently with white-tailed deer harvest, typically the first week of September to the end of January with a mix of archery, muzzleloader, and firearms seasons. Current regulations permit the harvest of 3 sika deer, no more than 1 antlered male, per each weapon type. The Maryland Department of Natural Resources manages sika deer as a local economic and social benefit to the region, and recently increased harvest bag limits for the 2014 – 2015 hunting season. Harvest management is the most effective means of controlling population growth, and the spread of sika deer across Maryland and neighboring states has led to efforts to curtail the range expansion.
Figure 1. Counties with established sika deer populations (gray) on the eastern shore of the Chesapeake Bay, Maryland, USA.

References
In 2016, chronic wasting disease (CWD) was detected in both elk (*Cervus canadensis*) and white-tailed deer (*Odocoileus virginianus*) in 10 counties in northwestern Arkansas (Fig. 1). To evaluate the relationships between proximity to CWD and perceived risk, from 7 March to 8 May 2017, we conducted a statewide telephone survey of Arkansas resident licensed hunters. Up to 12 contact attempts were made to increase the likelihood of hunter participation. A total of 1302 interviews were conducted. The response rate was 82%. Nonresponse bias was not determined. We interviewed 459 hunters residing within a 10-county region where CWD had been detected (red zone), 414 hunters residing within a 13-county region immediately adjacent to the red zone (yellow zone), and 429 hunters located in other counties in Arkansas (green zone; Fig. 1). More than 80% of hunters in each zone indicated they hunted deer during the 2016 season. Of those who did not hunt deer in 2016, most indicated that they did not hunt for reasons unrelated to CWD. Only 8% of hunters indicated they had read, heard, or seen nothing at all about CWD. More hunters in the red zone had read, heard, or seen “a lot” about CWD compared to respondents in the other 2 zones. One of 4 hunters (25%) who hunted most often in a county located in the red zone were not aware that CWD had been detected in the county they hunted. Regardless of the zone they most often hunt, hunters shared the same levels of concern about CWD. Most (79%) hunters were very or somewhat concerned about CWD. Hunters in the red zone were not as concerned about consuming untested deer meat harvested in the red zone than hunters in the green zone (39% vs 24%, respectively). Most hunters (56%) strongly supported mandatory CWD testing for deer harvested within the red zone. A higher proportion of hunters supported mandatory testing if it was limited to opening weekend of the modern firearm deer hunting season. Fewer red zone hunters strongly supported mandatory CWD testing than green zone hunters (46% vs. 58%, respectively). Most hunters who initially opposed mandatory CWD testing indicated less of an opposition if it was limited to the opening weekend of the modern firearm deer hunting season. Most (63%) hunters indicated that they were very likely to hunt deer during the 2017 deer hunting season. Hunters indicated that detection of CWD will not affect their choice of hunting locations. Most (66%) hunters in the yellow and green zones indicated they will very likely continue hunting in the same county, even if CWD is eventually detected in that county. We plan to repeat our survey at 3-year intervals to track changes in hunter perceptions of CWD and the relationships between proximity to CWD and perceived risk.
Figure 1. Spatial distribution of Chronic Wasting Disease (CWD) in Arkansas, USA, in 2016. For purposes of examining the relationships between proximity to CWD and perceived risk, 3 zones were created. The 10 counties where CWD was detected were considered the red zone. The 13 counties that bordered the red zone were considered the yellow zone. All other counties in Arkansas were considered the green zone.
Hunting Moose (*Alces alces*), Building Community in Norway

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In Norway at the end of the 1990s forest owners and farmers struggled with low timber prices and reduced income from farming. These major landowners explored alternative sources of income, one of which was to commercialize moose (*Alces alces*) hunting. Supported by rural- and regional development program and motivated by a growing consumer interest for moose meat, these landowners and a few butchers and meat processors developed an infrastructure for buying moose carcasses from hunters and landowners, processing and packing it for distribution to consumers or the supermarkets. Concurrently, there was a growing interest from the urban population to gain access to moose hunting and an increased willingness to pay for the hunting experience, an interest which stimulated additional landowners to start renting out the hunt.

This presentation reports on an ethnographic study of the conflicts and controversies related to the ongoing process of commercializing moose hunting in Norway. My objective was to describe how local hunters define themselves in comparison to visiting hunters from “out-of-town” and gain insights about potential changes. The researcher joined a hunting team for eight days, and used both observation and interviews to collect data on the possible effects of the commercialization process to local hunting cultures.

There is a strong collective narrative among local hunters, which distinguishes between local and the non-local hunters “hunting ethos”. In the local hunter’s stories about themselves, they perceived themselves as “working” harder, more skilled, and in general more serious about hunting than non-locals. I discovered that the materiality of wild-harvested moose meat – the sense of being the physical object carrying the complex set of symbolic values among people – is important in the construction of the local in the local moose hunt.

The local practice for how moose meat is distributed between landowners and non-landowners, hunters and non-hunters generally involves more than just the hunters. The distribution of meat connects and ties together people and the community to the hunt, the hunter to the household, the man to the women and children and it even brings families and friends that once moved out from the community back for a short visit. Wild-harvested moose meat secures the continuity of the moose hunt as a common cultural event in the community, and makes the hunt relevant for the community and the community relevant for the hunt.
Impact of Sea-Level Rise on Florida Key Deer Population Abundance

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Sea-level rise (SLR) due to global climate change is expected to occur and impact the low-elevation Lower Florida Keys (LFK). The Florida Key deer (*Odocoileus virginianus clavium*; hereafter Key deer) is an endangered white-tailed deer subspecies endemic to the LFK and one of several local endemics likely to be negatively impacted by SLR due to loss of habitat. Adding complexity to the issue, the Key deer has experienced recent population declines due to an outbreak of New World screwworm (*Cochliomyia hominivorax*) and the destruction caused by Hurricane Irma. We created a compartment model using available data of extant Key deer demographic, habitat and environmental data. This allowed us to broadly determine potential impacts on the Key deer population in the face of hypothesized SLR scenarios (amount of habitat lost to inundation at different levels of SLR) at different time scales (2040, 2070, 2100). In order to comprehensively model potential scenarios and account for recent population fluctuations, we used high (pre-population decline) and low (30% population decline) starting population abundances, various intrinsic growth rates (stable, declining, or increasing), and different rates of environmental catastrophes (e.g., hurricanes and diseases). Best case starting variables that included high starting population, high intrinsic growth rate, and low probability of catastrophe resulted in population declines over all hypothesized levels of SLR (2040:17–24% decline, 2070: 25–64% decline, 2100: 39–91% decline). Various combinations of reduced starting population abundances reduced intrinsic growth rate and increased probability of catastrophes had relatively little impact on population abundance declines (often within 5–15% of best case) under all SLR scenarios. However, an increase in hurricane abundance did result in decreases in population abundance in the near- and long-term under low SLR scenarios (20–40% lower than best case scenario). Impacts increased dramatically when SLR was removed from model simulations; indicating inundation of habitat was the primary driver of population change. Our model indicates that widespread loss of habitat will cause decreases in population abundance in the near-term and these decreases will continue in the long-term due to SLR. This is likely to be exacerbated by an increase in hurricane intensity or frequency over the same time period.
The dominant paradigms of large herbivores predict a first irruption, followed by a recovery to a reduced carrying capacity, however, supporting evidence has tended to be anecdotal [1]. The sika deer (*Cervus nippon*) population on Nakanoshima Island (5.2 km²), Hokkaido showed repeated irruption which imposed irreversible changes on the vegetation. The sika deer reached the first peak (52.5 deer/km²) in 1984 and the second peak (83.5 deer/km²) in 2001 that was 1.6 times higher than the first peak. The population relatively remained stable at 45-59 deer/km² during 2008-2012. Thus annual rate of increase (λ) changed from 16% in the initial irruption (Phase 1) to 7% in the second irruption (Phase 2) and stabilize thereafter (Phase 3) [2]. Under heavy browsing, deer eliminated dwarf bamboo during the first irruption and plum yew during the second irruption, thereafter fallen leaves were staple food in all season. Fallen leaves occupied 92% of the potential food supply and contributed 76% of the total consumption of the deer in Phase 2 [3]. Crude protein of fallen leaves was over requirement level for body growth in summer and declined in autumn and fall, however, which exceeded the requirement for maintenance level. The deer herd exhibited density dependent changes in life history trait, such as delayed sexual maturity, lower calf recruitment, lower body mass and smaller body size (jaw length) in the post-initial irruption (Phase 2-3). The body mass of adult female (≥3 yrs old) was related to pregnancy rate, which decreased as body mass decrease. Corresponding to the change in food habits, the molar wear rate accelerated in Phase 2-3 [4]. Nevertheless, female adult survival was maintained at a high level with a mean of 0.84 (95% CI: 0.80–0.88), which might contribute to the maintenance of a high-density sika deer population even under severe resource limitation [5].

In the absence of predation, hunting or culling may be the only management tool available to control ungulate populations and negative impacts on vegetation.

References

In Search of Does: Male White-Tailed Deer Exhibit Unique Movement Patterns During the Breeding Season

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Mate searching strategies in male white-tailed deer (*Odocoileus virginianus*) have been attributed to random walks informed by olfactory cues, with little variation assumed across individuals. Recent research in the arid southwestern U.S. demonstrated repeated visitation of focal areas by 56% of bucks during the breeding season, presumably as a strategy for locating receptive does. We evaluated focal area use during the breeding season of 30 adult male deer in south eastern U.S. deciduous forests. Sixty-seven percent of mature male deer exhibited focal area use, providing evidence that the focal area search strategy persists across other portions of the white-tailed deer’s range. Understanding that different patterns in mate searching behavior exist among groups of males and that spatial memory contributes to an animal’s mating strategy could aid management and hunting efforts.
Incorporating Behavior and Social Associations into Modeling Transmission and Disease Spread

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Behavior obviously plays a fundamental role in determining contact rates and transmission dynamics of disease. However, assessing the connections between host density, contact rates and disease transmission remains very challenging. I will review a series of empirical and modeling studies at multiple spatial scales that address this issue. Contact rates in social species are likely to depend upon both the group size distribution as well as how group size changes with regional population size. For some ungulates the group size distribution appears to be constant despite changing population size, which can lead to disease transmission that is not a function of population size. The largest groups of elk, however, get even larger as populations increase, creating a connection between population size and contact rate. However, directly correlating density to disease may still be difficult if movement rates among groups, or among areas of different densities, is high. In addition, the presence of an environmental disease reservoir may further obscure the correlations between density and disease, due to potentially long time lags between deposition of pathogen and subsequent infections. Modeling results suggest that this can, in turn, create ecological traps—attractive habitats that begin as high quality due to their resources, but become heavily contaminated with pathogens and later become population sink. I conclude with some potential future research on how movement data may be used to model future disease spread and identify seasonal patterns of disease transmission.
Influences of Fuel Reduction Logging on The Nutritional Ecology of Deer in Northeastern Washington

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Inland northwestern forests of the United States were historically structured to support light fuel loads and frequent low-severity fires. For over 100 years, fire suppression has shifted these forests to have thick, continuous overstories, dense tree stocking, and heavy fuel loads, which increase the chances of catastrophic wildfires that threaten human safety and further alter natural forest communities [1]. To restore historic conditions, promote healthy forests, and reduce wildfire risk, a group of state, federal, and private forest managers in northeastern Washington State have used commercial thinning to remove a portion of the overstory canopy and reduce fuel loads in the Colville National Forest. In addition to unnatural wildfire risks, closed canopy, densely-stocked forests limit light penetration to the forest floor, which can limit production of herbaceous and woody understory vegetation. Therefore, these thinning projects have the potential to improve productivity of understory forage resources for native herbivores that reside in these forests, including mule deer (*Odocoileus hemionus*), white-tailed deer (*Odocoileus virginianus*), Rocky Mountain elk (*Cervus elaphus*), and moose (*Alces alces*). To examine the effects of these thinning projects on the quality and quantity of forage resources for mule deer and white-tailed deer, we measured biomass, plant species composition, and nutritional quality of understory vegetation over four seasons in 78 stands that ranged from 0 – 100% canopy closure, 1 – 20 years post-thinning, along with unharvested stands. Within these stands, we also measured diet quality and composition, nutrient intake, and nutritional carrying capacity using bite-count methods with tractable, hand-raised deer.

Our preliminary results indicate that, non-conifer forage biomass increased as canopy cover declined (Fig. 1) and with time since thinning (Fig. 2). Additionally, we found that digestible energy and protein in deer diets decreased with high canopy cover. The amount of time spent active, based on accelerometer data calibrated with behavioral observations, showed that deer spent more time active as canopy cover increased and less time active as available biomass increased. Deer also spent a lower proportion of each day traveling with time since thinning. Deer bite and harvest rates increased with years following thinning and greater available biomass. Likewise, dry matter intakes increased with higher available biomass. Results from this project suggest that deer benefit from fuel reduction thinning projects. Higher available forage led to higher nutrient consumption and daily digestible energy and protein intakes. Daily intake of digestible protein and energy are directly related to deer fitness because they affect pregnancy, twinning rates, and fawn survival, which are good metrics for population sustainability [2]. Our data also indicate that the benefits of thinning increased until 15 – 20 years post-thinning, when canopies begin re-closing and light penetration again becomes reduced. Results from this project can help identify how deer adapt to changing, human-influenced habitats, aid in management decisions, and promote interdisciplinary natural resource management that supports biodiversity and sustainability.
**Figure 1.** The relationship of non-conifer understory biomass and canopy cover in dry conifer forests of northeastern Washington.

![Figure 1](image1.png)

**Figure 2.** The relationship of non-conifer understory biomass and years following thinning in dry conifer forests of northeastern Washington.

![Figure 2](image2.png)

**References**
Intraspecific Temporal Resource Partitioning at White-tailed Deer Feeding Sites: Implications for Differential Predation Risk

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Individuals may reduce competition by temporally or spatially partitioning their use of a shared resource [1,2]. Temporal resource partitioning, in particular, can be vital to the coexistence of species, or reduce competition among conspecifics, that share a common resource [2]. Sex-specific behavioral differences in ungulate resource use increases segregation as individuals attempt to avoid antagonistic interactions [3]. However, interference competition from dominant cohorts may reduce subordinates’ access to food resources, regardless of sex [4,5,6]. We hypothesized that white-tailed deer (Odocoileus virginianus) temporally segregated at supplemental feeding sites based on social rank and that segregation was affected by phase of the breeding season (pre-breed, breed, and post-breed) and diel cycle (diurnal or nocturnal hours). If cohorts do segregate temporally, we predicted that the resulting activity patterns would manifest in one cohort being relatively more susceptible to hunter-induced mortality. We used camera traps to record the presence of each cohort at feeding sites. To quantify temporal segregation, we used multi-state modeling to determine the probabilities for feeding sites (n = 16) to transition from 1 of 4 states (1-no deer present, 2-subordinate cohort present, 3-dominant cohort present, 4- both subordinate and dominant cohort present) to a different state. Additionally, we calculated the probability that a feeding site was in a particular state during diurnal and nocturnal hours during the 3 phases of the breeding season. We determined that transition probabilities differed by season and diel cycle and dominant and subordinate cohorts clearly avoided each other at the feeding sites. During the pre-breeding season, the probability of a subordinate being present during diurnal hours was 3.0x more likely than a dominant being present, but did not differ during nocturnal hours (Fig. 1). There was no difference for dominants and subordinates during diurnal or nocturnal hours during the breeding season (Fig. 1). In the post-breeding season, subordinates were 1.7x more likely to be at the feeding site than a dominant during diurnal hours but cohorts did not differ during nocturnal hours (Fig. 1). Our study illustrates how patterns in temporal resource partitioning at feeding sites may influence relative risk to different sources of mortality. Subordinates used the shared resource at similar rates, but the pattern of temporal partitioning evidently would make subordinates more susceptible to human predation.
**Figure 1.** Probability for a feeding site to transition from state 1 – state 2 (solid circle), state 1 – state 3 (hollow circle), and state 1– state 4 (triangle) during diurnal and nocturnal hours. State 1 = no deer present, state 2 = subordinate (adult females and yearling males) present, state 3 = dominant (adult males) present, and state 4 = subordinate and a dominant present.

### References


Knowledge of Foraging Behavior Influences Estimates of Forage Resources for Columbian Black-tailed Deer.

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Evaluating the ability of a landscape to support wild herbivores is critical for understanding and predicting the effects of habitat characteristics and land management activities on these populations. Because plants vary in nutritional quality, the abundance of nutritious forage directly influences survival and reproduction of herbivores and the number of herbivores that a unit of habitat can support [1]. Therefore, accurately assessing forage resources requires assessing both the quality and quantity of forage and is necessary for evaluating habitat quality and the effects of habitat changes. One method that combines quality and quantity of forage to determine how much vegetation biomass ungulates can actually use is the Forage Resource Evaluation System for Habitats (FRESH) model. The FRESH-model uses linear programming to find the maximum biomass that, taken together, meets a minimum specified nutritional requirement (i.e., useable biomass, kg/ha) [2]. Because measuring quantity and quality of forage across landscapes is time- and resource-intensive, we examined the effect of using prior knowledge of diet selection and reducing resolution of plant sampling on estimating useable biomass for Columbian black-tailed deer (Odocoileus hemionus columbianus) in the Pacific Northwestern United States. We calculated useable biomass for 98 sites that varied greatly in composition and amount of understory vegetation using two different scenarios and compared the resulting useable biomass estimates. In one scenario, we accounted for knowledge about what foraging deer will eat and separated stems and leaves of important plant groups and limited use of plants with plant secondary compounds known to limit intake. In the second scenario, we did not account for a priori knowledge of what deer would select and combined plant parts.

On average, useable biomass calculated accounting for deer knowledge was higher than useable biomass calculated with no knowledge of deer diets (paired t-test, \( t_{97} = 4.57, p <0.0001 \), \( n = 98 \)). Additionally, as total understory biomass in the plot increased so did the magnitude of difference between the useable biomass values calculated the different methods. For every 100 kg/ha increase in biomass, the useable biomass calculated when separating leaves and stems was 7 kg/ha greater than useable biomass estimates calculated combining stems and leaves (linear regression, \( F_{97}=13.83, p =0.0003 \)). That means that at 100 kg/ha of understory biomass the estimate of useable biomass difference between both methods was only about 7 kg/ha, but for 3,500 kg/ha of understory biomass the estimate of useable biomass difference was 240 kg/ha. When leaves and stems were entered separately, the higher quality leaves were included in the useable biomass, but the stems were not. When stems and leaves were combined as one model entry, the stems might reduce the nutritional quality of the plant enough to move some plant species into the “unuseable” biomass category. Assessing the value of habitats and the effects of habitat manipulation is limited by the ability to measure variables at the correct scale. Our study shows when estimating useable biomass using the FRESH-Deer model, separating plant biomass into as fine–scale units of similar nutritional quality as practical and as likely to be detected and selected by deer will improve the resolution of the model and its ability to measure habitat quality for large herbivores.

Landscape Genetic Analysis of Mule Deer to Guide Management for Chronic Wasting Disease

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Chronic Wasting Disease (CWD) was discovered in North American cervids in 1980 and has become a major management concern in the following decades. This disease has spread throughout the country and entered Texas through the Hueco Mountain range in 2012. The disease has reduced survival rates within herds of wild and captive cervids up to 30%, which has influenced the economic and ecological well-being of many areas. Management has focused on containment of CWD as the most viable and economically efficient option. Landscape genetics is an emerging field that could play a large role in understanding the potential spread of diseases. The influence of landscape features on movements and dispersal of mule deer (Odocoileus hemionus) can inform managers how this disease may spread across the landscape in coming years. Tissue samples have been collected from 2100 deer at Texas Parks and Wildlife Department CWD check stations across the Trans-Pecos and Panhandle regions of Texas to analyze genetic relationships. Results so far show statistically significant but low levels of population structuring, suggesting high dispersal rates. The combination of genetic and landscape data provides a powerful tool in predict the movement of CWD within Texas. Understanding dispersal routes and the possibility of environmental barriers will inform future management decisions throughout the state.
Learning from Others: Modeling the Growth and Spread of Chronic Wasting Disease in an Emergent Area.

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Chronic wasting disease (CWD) is a transmissible spongiform encephalopathy that affects at least seven North American cervid species, including white-tailed deer [1, 2]. Since its discovery in Colorado in 1967, CWD has become a serious threat to the sustainable future of susceptible host species because of long-term population declines in deer herds where the disease is well established. To prevent disease establishment, wildlife managers need information regarding the current state of disease to make rapid assessments and implement aggressive management actions. However, their decisions are almost always made with limited information regarding the local extent of CWD in an area. In this study, our objective was to leverage research findings from Wisconsin [3], a state where CWD is established, to make predictions on the spatial extent of CWD in Michigan, a state where CWD has recently emerged. The model utilizes partial differential equations to generate forecasts regarding where CWD may spread and grow in prevalence. Factors affecting spread and prevalence include sex and age of susceptible animals and landscape features in close proximity to disease detections. To assess the model fit for Michigan, we performed repeated simulations across a range of times and points of disease origin and evaluated results based on their ability to predict spread to known locations of disease. Our results provide a potential origin site in western Michigan that occurred prior to the first-free ranging detection in the state. The results also indicate that CWD will spread and grow most quickly in locations of high forest density, such as the Huron-Manistee National Forest, a nearly one-million acre forest immediately north of areas known to hold CWD-affected deer. Based on these findings, we generate a spatially-explicit map that provides the estimated probability of infection for each 1-square mile unit across the entire study area.

Utilizing model extrapolation and validation is critical to the prevention of CWD establishment because these approaches can leverage information from a few disease detections to provide managers with insight into where and when CWD may occur next.

References
Linking White-tailed Deer Density, Nutrition, and Vegetation in a Stochastic Environment: Deer Foraging and Nutrition


Density dependent responses in cervids are often mediated through changes in diet quality resulting from deer foraging impacts on vegetation. In regions where vegetation communities have high biomass of poor- and moderate-quality forage and in which production of high-quality forage is dependent on unpredictable precipitation and therefore highly variable, classical density dependent responses may be muted. Furthermore, biologists managing deer in regions of highly variable or poor-quality forage may enhance deer nutrition by providing supplemental feed. The effects of enhanced nutrition on deer foraging behavior could cause increased foraging pressure on preferred forages or could help protect preferred forages. We used tractable female white-tailed deer and the bite count technique to explore the effects of deer density and enhanced nutrition on diet composition, diet quality, and intake rate of deer in semi-arid rangelands of southern Texas, USA.

Our study of deer density was conducted in 4 81-ha enclosures, 2 of which had a target deer density of 12 deer/km² and 2 of which had a target density of 48 deer/km². These population densities had been maintained for 5 years before the study began. The proportion of shrubs, forbs, mast, cacti, and subshrubs in deer diets did not differ (P > 0.31) between deer-density treatments. Percent grass in deer diets was higher (P < 0.06) at high deer density but composed only 1.3±0.4% of the diet. Digestible protein and metabolizable energy of diets were similar (P > 0.45) between deer-density treatments. Likewise, bite rate, bite size, and dry matter intake did not vary (P > 0.23) with deer density. Unlike deer density, drought had dramatic (P < 0.05) effects on foraging of tractable deer. During drought, the proportion of shrubs and flowers increased in deer diets while forbs declined. Digestible protein was 31%, 53%, and 54% greater (P = 0.06) during non-drought than drought during autumn, winter, and spring, respectively. We studied the effects of enhanced nutrition on the composition and quality of deer diets in 4 enclosures each of which had a target deer density of 12 deer/km². We estimated proportion of pelleted feed in diets of tractable deer and non-tractable deer using ratios of stable isotopes of carbon. Averaged across seasons and nutrition treatments, shrubs composed a majority of the vegetation portion of deer diets (44%), followed by mast (26%), and forbs (15%). Enhanced nutrition influenced the proportion of mast, cacti, and flowers in the diet, but the nature and magnitude of the effect varied by season and year. The trend was for deer in natural nutrition enclosures to eat more mast. We did not detect a statistical difference (P = 0.15) in the proportion of shrubs in diets between natural and enhanced nutrition, but deer with enhanced nutrition consumed 7–24% more shrubs in 5 of 8 seasonal study periods. In the enhanced nutrition treatment, supplemental feed averaged 47–80% of the diet of tractable deer. Of non-tractable deer in all density treatments with enhanced nutrition, 97% (n = 128 deer) ate supplemental feed. For non-tractable deer averaged across density treatments, study sites, and years, percent supplemental feed in deer diets exceeded 70% for all sex and age groups.

We found that a 4-fold difference in white-tailed deer density did not have a large effect on deer diets or foraging behavior, a finding consistent with results from other aspects of this project. Deer density had little influence on vegetation communities and, although deer density had some effects on deer morphology and population dynamics, the effects were subtle. Conversely, variable precipitation had large effects on deer diets, vegetation communities, and
deer populations. Our results support the contention that in the western portion of southern Texas, abundant browse and sporadic, precipitation-dependent forbs disrupt the linkage between deer density and vegetation documented in other systems. Furthermore, provision of supplemental food by managers improves the quality of deer diets and does not cause deer to concentrate their foraging on high-quality but rare forages such as forbs.
Density-dependent behavior underpins white-tailed deer (*Odocoileus virginianus*) theory and management application in North America. Researchers have not focused on linking vegetation dynamics, nutrition, and deer dynamics, which has left a gap in our knowledge of the mechanisms underlying density dependence. We conducted a series of designed experiments during 2004-2012 to determine how strongly white-tailed deer density, vegetation composition, and deer nutrition (natural and supplemented) are linked in a semiarid environment where the coefficient of variation (CV) of annual precipitation exceeds 30%. Our study was replicated on 2 sites with thornshrub vegetation in Dimmit County, Texas, USA. During late 2003, 6 81-ha enclosures surrounded by 2.4-m tall woven wire fence were constructed on each study site. The experimental design included 2 nutrition treatments and 3 deer densities in a factorial array, with study sites as blocks. Abundance targets for low, medium, and high deer densities in enclosures were 10 deer (equivalent to 13 deer/km²), 25 deer (31 deer/km²), and 40 deer (50 deer/km²). Each study site had 2 enclosures with each deer density. Deer in 1 enclosure at each density were provided with a high-quality pelleted supplement *ad libitum*, which we termed enhanced nutrition; and the other enclosure at each density provided natural nutrition from the vegetation. We conducted camera surveys of deer in each enclosure twice per year and added or removed deer as needed to approximate the target densities. We maintained >50% of deer ear-tagged for individual recognition. We used reconstruction, validated by comparison to known numbers of bucks, to make monthly estimates of density in each enclosure for use in analysis of treatment effects. We analyzed fawn:doe ratios, growth rates of fawns and yearlings, survival from 6–14 months of age and for adults >14 months of age, adult body mass, and population growth rates (lambda apparent, λ_APP) to determine density and nutrition effects on deer populations in the research enclosures during 2004-2012. Fawn:doe ratios declined (*P* = 0.04) from low-medium density to high density in natural nutrition enclosures but were not affected (*P* = 0.48) by density in enhanced nutrition enclosures. Enhanced nutrition resulted in increased fawn:doe ratios of 0.15 ± 0.12 fawns:doe at low-medium density and 0.44 ± 0.17 fawns:doe at high density. Growth rate of fawns was not affected by deer density under natural or enhanced nutrition (*P* > 0.14) but increased 0.07 ± 0.01 kg/day in enhanced nutrition enclosures compared to natural nutrition (*P* = 0.02). Growth rate of yearlings was unaffected (*P* > 0.24) by deer density but growth rate increased for both sexes in enhanced nutrition enclosures. Adult body mass declined in response to increasing deer density in natural nutrition enclosures for both adult males (*P* < 0.01) and females (*P* = 0.10). Enhanced nutrition increased male body mass but female mass did not increase compared to natural nutrition. Survival of adult males was unaffected by deer density in natural (*P* = 0.59) or enhanced (*P* = 0.94) nutrition enclosures. Survival of adult females was greatest (*P* = 0.04) in medium density enclosures with natural nutrition but similar at low and high density. Enhanced nutrition increased survival of females (*P* < 0.01) and marginally for males (*P* = 0.11). Survival of fawns 6-14 months old was unaffected (*P* ≥ 0.35) by density in either natural or enhanced nutrition treatments but was greater (*P* = 0.04) under enhanced nutrition. Population growth rate declined (*P* = 0.06) with increasing density in natural nutrition enclosures but not (*P* = 0.55) in enhanced nutrition. Enhanced nutrition resulted in an increase of 0.32 in λ_APP. Some researchers have reported that density dependence is weak in environments where the coefficient of variation (CV) of annual precipitation exceeds 30%. Despite the high variation in precipitation in our study area, we found evidence of density dependence with natural nutrition.
because fawn:doe ratios, adult body mass, and population growth rate declined with increasing deer density. However, sequential wet years are usually necessary to attain deer densities approximating our medium and high density treatments under natural nutrition. Density dependent effects may be weak or non-existent at other times. Additionally, plant communities and deer diets did not reflect the density dependent response. We hypothesized that variation in quality of small home ranges in enclosures may have disadvantaged some deer, resulting in density effects at higher densities.
Density-dependent behavior underpins white-tailed deer (*Odocoileus virginianus*) theory and management application in North America. Researchers have not focused on linking vegetation dynamics, nutrition, and deer dynamics, which has left a gap in our knowledge of the mechanisms underlying density dependence. We conducted a series of designed experiments during 2004-2012 to determine how strongly white-tailed deer density, vegetation composition, and deer nutrition (natural and supplemented) are linked in a semiarid environment where the coefficient of variation (CV) of annual precipitation exceeds 30%. Our study was replicated on 2 sites with thornshrub vegetation in Dimmit County, Texas, USA. During late 2003, 6 81-ha enclosures surrounded by 2.4-m tall woven wire fence were constructed on each study site. The experimental design included 2 nutrition treatments and 3 deer densities in a factorial array, with study sites as blocks. Abundance targets for low, medium, and high deer densities in enclosures were 10 deer (equivalent to 13 deer/km²), 25 deer (31 deer/km²), and 40 deer (50 deer/km²). Each study site had 2 enclosures with each deer density. Deer in 1 enclosure at each density were provided with a high-quality pelleted supplement *ad libitum*, which we termed enhanced nutrition; and the other enclosure at each density provided natural nutrition from the vegetation. We determined if increasing deer density and enhanced nutrition resulted in a decline in preferred forbs and shrubs and an increase in plants less preferred by deer as predicted by traditional theories on succession and retrogression. We sampled all 12 enclosures via 20, 50-m permanent transects in each enclosure. Percent canopy cover of preferred forbs was similar \((P = 0.13)\) among deer densities averaged across nutrition treatments and sampling dates \((8 \pm 2 \text{ [mean \pm SE]}, 5 \pm 1, \text{ and } 4 \pm 1 \text{ in low, medium, and high deer density enclosures, respectively}). Averaged across deer densities, preferred forb canopy cover was similar between nutrition treatments in 2004; but by 2012 averaged 20 \pm 3\% in enhanced nutrition enclosures compared to 8–13\% in natural nutrition enclosures. Percent canopy cover of other forbs, preferred shrubs, other shrubs, and grasses, as well as Shannon’s index, evenness, and species richness were similar \((P > 0.01)\) among deer densities, averaged across nutrition treatments and sampling dates. The density dependent response by the deer population was not directly reflected by vegetation responses. Vegetation in our study area was more strongly linked to variation in precipitation than to deer density. In addition, the ephemeral nature of annual forbs, asynchrony in phenology of the vegetation, and plant attributes that act as herbivore defenses may have constrained vegetation responses. Foraging by deer with enhanced nutrition did not result in a reduction in preferred plants in the vegetation community and enhanced nutrition may have had a protective effect on preferred forbs because \(\leq50\%\) of deer diets consisted of vegetation. Comparison of vegetation responses to different combinations of deer density and enhanced nutrition revealed an indirect response to deer density. Preferred forbs increased over time in enclosures with enhanced nutrition compared to enclosures with natural nutrition. This can be interpreted as a density effect because deer consumed less vegetation with enhanced nutrition. Preferred forbs increased more in enhanced nutrition enclosures with low densities than in enhanced nutrition enclosures with high deer densities, provided further evidence of an effect of deer density. Linkages between vegetation and herbivores may be partial in highly stochastic environments, making detection of density-dependent effects more difficult.
Localized Management For Reducing Agricultural Damage Caused By White-tailed Deer (Odocoileus virginianus) In Minnesota

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Minimizing damage caused by white-tailed deer (Odocoileus virginianus) is an important consideration for managing deer populations throughout the range of the species. Damage caused by white-tailed deer can be severe in the United States with >$100 million lost annually by agricultural producers [1]. Previous research demonstrated that intensified population reduction of deer in a small geographic area, also known as localized management, effectively reduced the abundance of deer to maintain lowered deer densities over time [2]. In theory, damage to resources targeted for protection should be reduced because fewer deer are available to cause damage. However, studies of the effectiveness of localized management for reducing damage on specific properties in agricultural settings are lacking. Results from previous studies have demonstrated only through anecdotal evidence that population reduction of deer can reduce damage to agriculture [3,4,5]. We conducted this study to assess the effectiveness of localized management of deer to reduce damage to agricultural crops in southeast Minnesota, USA. Our objectives were to evaluate the effectiveness of localized management for reducing fine-scale deer abundance and to examine whether damage caused by deer to agricultural crops was reduced on properties where deer densities were lowered. During 2014-2016, we used baited infrared camera surveys to estimate deer abundance on focal properties. We evaluated yields of corn in fenced and unfenced plots to estimate the impacts of browsing by deer. Corn yield loss was seemingly low on most properties, and there was no difference in corn damage between properties where localized management was utilized versus normal sport-hunting. Corn damage could not be explained solely by deer abundance at the property level. However, extra deer harvest opportunities were utilized when requested by landowners. Deer management was >2 times as intensive on properties where localized management was used versus normal sport-hunting. Deer on adjacent properties likely filled any voids created by localized management. Increased deer harvest pressure on properties with localized management may have prevented corn damage from being worse had additional deer not been harvested. The results of this study will provide a basis for improving the framework for future application of localized management in agricultural regions.

References:
Population expansion models are often used in conservation planning practices. However, the long-term reliability of such models has rarely been tested. In 1996 the Nature and Parks Authority, Israel, initiated the reintroduction Persian fallow deer (Dama mesopotamica) in the Kziv reserve. Over the next 9 years 188 individuals (equal sex ratio) were released [1]. Based on the first 2.5 years of data we developed an individual-based spatially realistic population expansion model and tested its prediction against empirical data 2.5 years later [2]. We then simulated the population’s numerical growth and spatial expansion 100 years into the future based on the current landscape and based on regional development plans [3]. Now, 22 years after the reintroduction began, we re-assess the model by comparing the models projections on range expansion, direction and activity centers the 20th year projection with empirical data based on camera traps surveys conducted in the area for the past 4 years. Cameras were placed within and beyond the predicted range of expansion and in a variety of habitats including those considered in the model as preferred to those considered less desirable. We analyzed the empirical data using N-mixture models and extracted an accurate measure of the population expansion trends and compared them with the model predictions. Our results suggest that the model based on the original landscape when the model was constructed was able to accurately predict the range of expansion relative to the release site but was less successful in predicting the direction of the expansion and the location of population cores (habitat use). The model based on development plans was more successful in predicting the direction of the expansion. Using N-mixture models we could assess what other factors, other than those originally considered, such as predation risk, affected the spatial expansion patterns of the population. Spatial population expansion models for reintroduced species provide a comparative backdrop against which empirical data can be assessed, focusing on the progress of the project evaluated and identifying new factors (that either did not exist in the past or have been overlooked) that affect the current expansion of the population. In addition, our findings emphasize the importance of including future developmental plans in spatial models.

Managing White-tailed Deer at the Intersection of Ecosystem Restoration, Game Management and Endangered Species Conservation

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Management of white-tailed deer (*Odocoileus virginianus*) in southern Florida involves a complex association of biological, social, political, and economic forces. Deer are the most popular game species and the primary prey of the endangered Florida panther (*Puma concolor coryi*), a predator that generates strong and diverse opinions. Managers must therefore assess deer management from both game and prey management perspectives, while balancing the societal complexities of restoration of an apex predator in the system. In recent decades, harvest and aerial monitoring data suggest that deer populations are declining in portions of southern Florida; however, the causes are unknown as population declines have coincided with changing hydrological regimes, habitat conditions, and predator community. The Comprehensive Everglades Restoration Plan, a $7.8 billion, 30-year project, has changed the hydrological flow through the Greater Everglades ecosystem since 2000, influencing the suitability of habitat for deer. Habitat conditions also have changed as a result of altered fire ecology and the invasion of nonnative plant species. Furthermore, recent additions of coyotes (*Canis latrans*) and Burmese pythons (*Python bivittatus*) and increases in Florida panther abundance have substantially altered the predator community. We explore the biological and cultural history of deer management in southern Florida to illustrate the challenges of deer management in a system where a multitude of competing conservation and management goals and numerous interacting factors influencing deer population dynamics. Understanding these complex factors is critical to long term conservation and management of this popular game species while ensuring a sustainable prey base for Florida’s native carnivores.
Migration is an important adaptation for species inhabiting variable ecosystems. Many ungulate populations make seasonal migrations between summer and winter ranges; however, peer-reviewed literature indicates migration routes and distances traveled can be highly variable. Few studies have quantified these migration strategies in the context of true measures of fitness such as body condition or population-level effects on survival. We used data from over 750 radio-collared mule deer (Odocoileus hemionus) to test hypotheses relating survival to body condition, sex, environmental conditions, and migratory strategy. Adult survival was most parsimoniously explained by models containing co-variates for sex, season, body condition and migration distance. Over-winter survival of juvenile mule deer was best explained by models containing co-variates for sex, body mass, and a winter severity index. Adult and juvenile survival was lower for males than for females, even after accounting for mortality caused by human harvest. These results suggest population models may overestimate male survival outside of harvest reporting. We also provide preliminary results that suggest adult survival varies with respect to migratory behavior and body condition, which may have direct management implications for decisions affecting harvest quotas, habitat improvements, and energy development policies.
Chronic wasting disease (CWD) is a transmissible disease that affects members of the Cervid family. Recently, multiple cases of CWD have been discovered in captive white-tailed deer facilities in Texas. There is concern about how CWD would impact free-ranging deer populations especially in South Texas where the variable rainfall results in variable and, on average, low fawn recruitment rates. We developed a model based on data from 55,505 ha of rangelands where deer harvests were light (~2%), no supplemental feed was provided, and deer counts were conducted annually for 20 years. Our models with survival rates, fawn:doe ratios, and rates of hunter harvest produced projections that were comparable with observed trends. CWD parameters were inputted into the model based on data from CWD-affected states. Initial prevalence was set at 1% of the population with a 0.26% increase in prevalence per year and mortalities occurred 1-3 years after being infected. With no CWD and no harvest, populations increased 1.43% annually and the population was able to sustain a 2% annual rate of harvest. Incorporation of CWD did not result in a decline in population size if there was no harvest; however, populations declined when 1% harvest of both sexes occurred. Limiting harvest to males did not cause populations to decline but proportion of mature males declined because males are more susceptible to CWD. Our results indicated that if CWD emerged in free-ranging deer populations in South Texas, the economics and culture of deer management and recreational hunting would be altered.
Modeling Individual Deer Variation in Resource Selection to Improve Management and Demographic Outcomes

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Resource selection modeling has strong applications in conservation because resource selection is a fundamental ecological process shaping movement and distribution [1], and offers spatially explicit guidance for targeted management. As animals move across the landscape, they must make trade-offs associated with resource selection to meet needs of survival and reproduction, and for minimizing risk [2]. Fitness is influenced by resource-related decisions by individuals where each resource choice has costs and benefits associated with it. Therefore, individual variation (also referred to as heterogeneity) warrants further investigation in resource selection modeling and how it structures demographic performance such as survival.

Studies of Rocky Mountain elk (Cervus elaphus) and white-tailed deer (Odocoileus virginianus) will be presented to highlight the conceptual framework to study individual variation in resource selection and its applications for modeling demographic outcomes and functional responses, and improving conservation and management. The general approach included estimating resource selection functions (RSFs) and estimating Cox proportional hazards models to quantify risk of mortality as a function of covariates depicting landscape-level features. Spatial models of occurrence and risk are combined to provide a spatially-explicit assessment of the relationship between habitat and demographic performance, wherein low-performance habitat (e.g., sink habitat) was defined as high probability of occurrence coupled with high risk of mortality, and high-performance habitat (e.g., source habitat) was high probability of occurrence coupled with low risk of mortality. For white-tailed deer, fully random effects models are used to estimate conditional (i.e., representing an individual) and marginal (i.e., representing the population-level response) coefficient estimates from RSFs to study behavioral strategies that may influence survival or encounter probability of mates during rut.

Variability in the occurrence of elk was driven by selection for specific resource features as well as responses to human activity. Risk of mortality in elk was a function of human modification of the landscape with little variation explained by resource features. Proximity to industrial (i.e., oil and gas) development was associated with increased risk of mortality whereas proximity to residences and agricultural structures was associated with decreased risk. Individual-level results revealed added complexity – risk of mortality was associated with a consistent pattern of occurrence relative to industrial development, yet the association between risk and occurrence relative to structures (e.g., houses, barns, buildings) was highly variable and likely a function of disparate land-use practices [3]. Using individual elk RSF coefficients (i.e., conditional responses) revealed functional responses for human disturbance and security cover. Elk selected randomly for disturbed areas when level of disturbance was low, but elk showed stronger avoidance as disturbance increased. Elk also used greater security cover relative to its availability especially when exposed to human disturbance [4]. Results from white-tailed deer are forthcoming based on data from [5] and [6].

Prioritizing management based on occurrence without a connection to a demographic outcome risks poor performance because occurrence alone can be a misleading indicator of fitness. Therefore, management may be most effective when individual variation is considered and linked to demographic outcomes.
References


Females of many ungulate species, including red deer hinds, often nurse non-filial offspring. Causes of such at first sight strange and non-economical investment are not yet fully understood and seem to differ among species. Across studies, large individual variability in the incidence of allosuckling has been reported. Allosuckling has been discussed as an artefact caused by unnatural breeding conditions or reproductive errors on farms (e.g., lack of maternal experience, misdirected maternal care, may be combined with “milk thievin” by the infant). On the other hand, allosuckling may be explained from evolutionary perspective in terms of altruism that evolved either through kin selection, or through reciprocity (or another mechanism) in small stable social groups. Allosuckling females could thus help balance growth deficiencies of their (related) herd mates’ progeny.

We tested hypothesis of compensatory function of allosuckling in farmed red deer. The predictions were (i) through allosuckling calves compensate their growth and/or maternal nutrient insufficiencies; (ii) nursing of non-filial calves does not negatively affect maternal care provided to filial calves, as well as their growth; (iii) allosucking calf should not find an energy demanding tactic get non-maternal milk; and (iv) red deer hinds discriminate young they nurse (allonursing is not accidental or random).

From 3952 suckling bouts recorded in a group of red deer, 13.5% were non-filial. Nursing non-filial calves did not mean failure of maternal care provided to filial calves. Neither growth rate nor weaning weight of calves was affected by alonursing behavior of the mother. Calves suckling beside mothers also non-maternal females grew less and were lighter at weaning, and were also less successful in sucking the mother. Despite large individual variance in dams’ allonursing incidence, allosucking calves had well chance (more to 70%) to be nursed when solicited, without use any special tactic. Variability in calves’ allosuckling behavior reflected their actual needs, and alonursing behavior of the dams seemed to reflect their possibilities above maternal investment. As presumed, nursings were not equally distributed among the calves, occurring most frequently within filial pairs. The hinds nursed filial calves almost 3times more frequently than non-filial calves when being solicited. Two types of non-filial allosuckers were detected, “preferred” (suckling mostly accepted by the particular hind) and “non-preferred” (suckling mostly rejected). Preferred non-filial calves had even higher success to be nursed than filial calves (P<0.001).

Our results support the hypothesis that calves through allosuckling compensate growth and/or nutritional deficiency rather than it was some kind of reproductive error. Allonursing was not a matter of random solicitation by the calves. The hinds were not only discriminative in nursing filial vs. non-filial calves, but also in nursing individual non-filial calves. Supported by project MZE-RO0718.
New World Screwworm Impacts on the Endangered Florida Key Deer

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In July 2016, Florida Key deer (*Odocoileus virginianus clavium*), were confirmed to have New World screwworm (*Cochliomyia hominivorax*). Screwworm is a threat to U.S. agricultural interests and wildlife populations, prompting an immediate response from federal, state, and local agencies to stop further expansion in North America and eradicate the current infestation in the Lower Florida Keys.1 Study objectives were to (1) characterize screwworm-related mortalities and (2) assess infestation impacts on population density, sex-age structure, and viability. Approximately 15% of the Key deer population were euthanized and/or died due to screwworm infections (n=135 deer mortalities) between July 2016–August 2017 (Fig. 1). The majority of these mortalities occurred during October 2016. However, screwworm-related mortality decreased by 95% in November 2016 (n=7 since 1 November 2016) as a result of doramectin treatments and sterile fly release efforts by USDA and USFWS. No additional screwworm-related mortalities were recorded after January 2017. Adult males were disproportionately impacted by screwworm infestations (92%) which is attributed to rut-related injuries. Sex ratios shifted with adult male mortalities and were slightly higher (4.12:1 females:males, current) compared to the historic average (3.76:1). An estimated 925 (CI=698-1353) Key deer occupy Big Pine and No Name keys (core population) post-screwworm incident as of April 2017. Population metrics (i.e., mean encounter rate, monthly deer density, and screwworm mortalities) presented as potential indicators of Key deer population status suggests the Key deer population is stable and above the population viability analysis “trigger points” requiring more active management by USFWS personnel. Successful resolution of the screwworm incident reduced the need for intensive Key deer data collection efforts (i.e., less radiotelemetry and fewer driving surveys) after April 2017. At this time, it is recommended that USFWS continue baseline monitoring efforts for the Key deer population.
Nutrition and Ontogeny Influence Weapon Development in a Long-lived Mammal


Selection in male cervids should optimize allocation of nutritional resources to the competing demands of body growth versus weapon development. We investigated allocation decisions of growing and mature male white-tailed deer (*Odocoileus virginianus*) from three regions of low, moderate, and high diet quality. We tested (i) if deer under greater nutritional limitations would allocate proportionally less to antler growth; (ii) if antler and body mass became less variable with age; and (iii) if antler size consistently exhibited positive allometry with body mass across age classes and nutritional planes. Greater nutrition increased antler allocation in 2.5- to 4.5-year olds, but not in yearlings or prime-aged males. Variability of antler mass decreased with age and was generally less in more fertile regions, but body mass was equally variable across all ages and regions. Antler mass was positively allometric with body mass for all combinations of age class and region, but exhibited age- and region related differences. Our results suggest that accruing body mass is more important to lifetime reproductive success than increasing weapon size. Reduced allometric coefficients in older males likely stems from increasing use of skeletal mineral reserves, selective pressures favoring greater body mass, and possible selection for optimal weapon strength and structure.
Historically, Texas mule deer (*Odocoileus hemionus*) were most common in the Trans-Pecos, but population numbers have dramatically increased in the Panhandle. Little is known about mule deer population structure in the Panhandle and how the agriculture-rangeland habitat structure affects population performance. Here, we evaluate body condition and mass, antler size, and lactation status of mule deer in 3 regions throughout the Texas Panhandle. We captured 74 adult male, 81 adult female, and 123 juvenile mule deer during autumn of 2015–2017. Though age structure was consistent across sites, morphometric measurements varied greatly. On average, adult (over 3 year old) males in the southwest Panhandle had greater body mass (114 kg SD=11 vs. 90 kg SD=29), had more rump fat (28 mm SD=10 vs. 22 mm SD=7), and larger antlers (142 in. SD=20 vs. 103 in. SD=26; B&C score) than deer in the southeast Rolling Plains and northern Canadian River breaks. Adult females were larger in the southwest Panhandle (70 kg SD=11 vs. 62 kg SD=13) and lactated at a higher rate (0.50 vs 0.25), however, there was no difference in rump fat measurements. Juvenile size and body mass did not vary between years and sites and overall observed antler growth was 30 B&C inches per year averaged across all age classes. Our data show high heterogeneity in population health indices across the Texas Panhandle. Creating baseline population measures will aid in establishing an adaptive management plan as mule deer population levels in the Panhandle continue to increase.
Persistent Transmission Of Bovine Tuberculosis From White-tailed Deer To Cattle In Michigan, USA: Mitigation Strategies And Needs

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Free-ranging white-tailed deer (Odocoileus virginianus) are a self-sustaining reservoir for bovine tuberculosis (bTB) in northeastern lower Michigan, U.S.A., with a prevalence rate of about 1-2% persisting over recent decades. Though a comprehensive program is in place and on-farm mitigation strategies to manage against bTB transmission from deer to cattle have been implemented for over a decade, cattle continue to become infected with the disease. Continual detections of bTB in cattle on farms in the region is of mounting concern for state and federal agricultural agencies, producers, wildlife managers and the public. Current on-farm efforts to curtail transmission include a variety of fencing options, using livestock protection dogs, and clean cattle feeding and watering practices. Liberal harvest of antlerless deer through hunter harvest and permits issued to cattle producers and agency sharp shooters has also been ongoing. Though all of these strategies have merit and the level of effort to reduce prevalence in deer and protect cattle is high, additional management actions are needed to overcome this incessant problem. These actions could include the implementation of a program to vaccinate deer against bTB, landscape-scale habitat alteration, and fine-scale removal of deer in proximity to vulnerable farms. Vaccine development and foundational research to address delivery to free-ranging deer is complete. Deer population responses to the manipulation of forest vegetation types are generally understood and sustainable habitat management could reduce deer numbers and their distribution in the region while enhancing regional wildlife, forestry and agricultural goals. The responses of local deer populations to targeted removal of individuals are also generally understood, and the potential exists to greatly decrease deer densities and presence around agricultural operations while they persist on natural foods in nearby forested habitat. Here we summarize the progress to date, discuss the merit of these newly suggested strategies, and provide options for a way forward to rid deer and cattle in Michigan of bTB.
Overabundant sika deer (*Cervus nippon*) cause serious agricultural damages and huge impacts to natural vegetation in the whole Japan. The number of recreational hunter has decreased from over 500 thousands in 1970’s to around100 thousands in 2010’s. The Japanese Government pays rewards to local hunters to kill around 400 thousand deer as pests per year, except around 200 thousand harvest in recreational hunting. Consumption of game meat was not popular in Japan. Most of carcasses are abandoned not consumed as food. I discuss perspectives of community-based deer management referring to two areas. A local NPO has set a special hunting area in Nishiokoppe village, 308 km$^2$, Hokkaido, and managed deer as natural resources based on the hunting and wildlife law since 2004[1]. Guest hunters must follow local guides to shoot deer in order not to make deer smart. The proportion of encounters possible to fire in guided hunting did not decrease between 30 and 40%, while the proportion of encounters resulting in escape slightly increased from 10% to 30%. Around two hundred deer are culled through 160 hunter-days annually. It contributed to employment of a few local hunters and lodging in the local hotel. Three deer were introduced by a local private company in Nakanoshima Island (5.2 km$^2$) in Lake Toya, Shikotsu-Toya National Park, Hokkaido, between 1956 and 1966. The deer population rapidly increased and became overabundant without annual culling, causing irreversible impacts to natural vegetation [2]. The local deer management council consisting of stakeholders started to reduce and maintain the deer number in low density in 2013 supported by the Ministry of Environment. Eradication is an option in areas where deer were introduced artificially. Platforms to make a decision by local stakeholders are necessary in community-based deer management in cases of sustainable use or eradication.

References
Mule deer (*Odocoileus hemionus*) have experienced periodic declines across most of their range in recent decades. While most populations are considered to have stabilized in recent years, mule deer continue to be at the forefront of management concern among state and federal wildlife agencies. Mule deer in temperate regions face varying seasonal challenges with respect to nutrition and environmental conditions, as well as, variation occurring from year to year. Despite these challenges, adult survival is generally high and stable across most populations. We focused our efforts on assessing juvenile survival and recruitment as an indicator of population performance. Effective management of mule deer requires an understanding of the factors that influence survival. We used the nest survival module in program MARK to investigate juvenile survival in an environment experiencing years of variable winter severity. We investigated the relative effects of body size, body weight, mother’s nutritional status, timing of parturition, snow depth, and location or characteristics of birth site on survival of young. We modeled juvenile survival out to weaning (120 days). Juvenile survival to weaning was 0.34 (SE= 0.06) across three years of the study. Juvenile age was positively correlated with survival. We observed the highest rate of juvenile mortality during the first month of life. Supplemental feeding of the mother during winter and being born with a sibling increased the probability of survival. Females on a higher plane of nutrition have a higher probability of successfully rearing young to weaning.
White-tailed deer (*Odocoileus virginianus*) populations on 8 Wildlife Management Areas (WMAs) on Chattahoochee National Forest in northern Georgia, USA have declined substantially during the past 36 years. Harvest has declined by 85% and 97% for antlered and antlerless deer, respectively [1]. Georgia Department of Natural Resources-Wildlife Resources Division restricted harvest of antlerless deer, but populations have failed to recover. However, deer condition indicators (i.e., body mass and antler measurements) have improved during this same period [1], suggesting improved nutritional conditions. Acorn (*Quercus* spp.) mast production is an important seasonal resource for deer, black bears (*Ursus americanus*), and feral pigs (*Sus scrofa*) in this region [2][3]. Populations of black bears, coyotes (*Canis latrans*), bobcats (*Lynx rufus*), and feral pigs have increased which could influence fawn survival and habitat use by deer and thus fawn survival may be a limiting factor in long-term population sustainability. We will capture and GPS collar 90 adult female deer to investigate space use and survival (2018-2020) on Blue Ridge and Cooper’s Creek WMAs in the north Georgia mountains. Additionally, in a concurrent study we will capture and collar (VHF) 120 neonates to monitor their survival to 16 weeks of age during 2019-2020. We will estimate survival rates for both fawns and adult does using the Kaplan-Meier estimator for the generalized staggered entry case. Subsequently we will simulate population growth under various harvest management regimes using parameters collected in our study area and for similar deer populations in the southeastern United States. In addition, we will monitor space-use of adult female deer throughout the year. We will evaluate annual and seasonal home range size and habitat selection using dynamic Brownian bridge movement models and resources selection functions. Finally, we will establish one 3,000-ha passive camera grid on each WMA (camera density of 1/50 ha) to examine the occupancy of fawns, adult deer, feral pigs, bears, bobcats, and coyotes. We will investigate occupancy during white-tailed deer parturition, lactation, mast production, the rut, and hunting seasons. The results of this study will help determine population vital rates for deer in the region and allow informed decisions to potentially reverse population declines of deer in the region.

References


Predominance of Venison in a System of Sharing and Consuming Wild-Harvested Meat

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Wild-harvested meats, such as venison, are used and distributed for their nutritional, economic, ecological, and sociocultural importance in societies throughout the world [1,2]. Sharing and consumption of wild-harvested meat has a positive effect on attitudes toward hunting in rural and urban settings in Sweden, even when socialization to hunters and hunting are controlled for in the analysis [3,4]. This evidence suggests that the culturally significant acts of sharing and consuming wild-harvested meat may function to connect hunters and non-hunters. Our objective was to gain a greater understanding of how wild-harvested meat, and wild-harvested venison in particular, is used and distributed by hunters and the people with whom they share. We will report results from three separate studies to discuss the predominance of venison in a system of sharing and consuming wild-harvested meat.

Study 1: We assessed maximum yield of edible, wild-harvested venison and hunter sharing behaviors by including questions on the annual 2013 statewide Michigan Deer Harvest Study [5]. We estimated 11,402 – 14,473 metric tons of wild-harvested venison were procured during the 2013 Michigan hunting season. Of hunters who harvested a deer, 85% shared wild-harvested venison. Hunters shared with an average of 5.6 people (SD = 4.5). Sharing of venison occurred most frequently within tight social networks: members of hunters’ households (68%), relatives (52%), and friends, neighbors, or coworkers (50%).

Study 2: We sought to determine factors predicting venison consumption by including questions in the Michigan State University (MSU) Institute for Public Policy and Social Research’s (IPPSR) Office for Survey Research (OSR) 68 th State of the State Survey (SOSS); a longstanding quarterly telephone survey with standardized protocol aimed at providing a statistically robust representation of the Michigan population. A total of 997 telephone interviews were completed. Seventy-two percent of all respondents and fifty-seven percent of all non-hunters reported consuming wild-harvested venison. Of respondents who reported consuming wild-harvested meat, venison was the most popular. The most common reason for never having consumed wild-harvested meat cited by both groups was never having the opportunity, followed by taste and smell, diet/lifestyle, don’t know any hunters, don’t hunt and don’t like venison. Attitudes toward hunting or moral ethical concerns were rarely cited as a reason for not consuming wild-harvested meat. Hunting experience and strength of relationships with hunters were positive predictors of venison consumption. Being of a race other than white and living in an urban community were negative predictors of venison consumption.

Study 3: We used a mail-back questionnaire, sent to a stratified random sample of Michigan residents in spring-summer 2016, to assess wild meat consumption patterns, attitudes toward hunting, hunters and wild-harvested meat, and hunting associated experiences and relations. A telephone questionnaire was used to assess sources and extent of non-response bias. Ninety percent of respondents reported consuming wild-harvested meat with 56% reporting consuming wild-harvested meat within 12 months prior to receiving the questionnaire. Forty-three different types of wild-harvested meat were identified, of which venison was exceedingly the most popular (89% of respondents reported consuming venison). A majority of respondents strongly agreed that wild-harvested meat was a local, lean nutritious food and sharing and consuming wild-harvested meat were reported as culturally important activities. Increased frequency of wild
meat consumption was a positive predictor of attitudes toward hunting, however, the effect size was relatively small.

Our findings demonstrate a system of sharing and consumption operated by informal institutions appears to have evolved in place of formal markets for wild-harvested meat. Despite a lack of legal U.S. markets, venison and other meat from wildlife is widely shared and distributed beyond the population of hunters, however hunter social networks bias distribution. From a public health management perspective, the network of sharing we describe also identifies pathways for exposure to zoonotic disease and chemical contaminants from wild-harvested meats, and in particular venison. Wild meat sharing and consumption are culturally important activities to some people and consumption of wild-harvested meat positively effects attitudes towards hunting. Increasing access to wild-harvested meat may be one way to maintain the relevancy of traditional uses and users of natural resources in a changing society.

References:
Preliminary Development of an Un-baited Camera Survey for Estimating White-tailed Deer Densities

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The most widely employed method of estimating population parameters of white-tailed deer (*Odocoileus virginianus*) is likely the baited camera survey technique developed by Jacobson et al. (1997) [1]. While the protocol is relatively easy to follow, the process of identifying individual bucks can be difficult and time consuming, no error terms are estimated, and the use of bait is illegal in some places and may be used only outside of hunting seasons in others. In addition, there have been relatively few improvements to using cameras as a survey tool over the past 20 years, therefore the need to investigate and implement recent advances in ecological modelling approaches [2][3] are warranted. We propose a novel technique for generating parameter estimates using a spatially explicit modelling approach with only the use of trap level count data. We conducted passive (un-baited, 1/~20 ha) and baited (1/~40 ha) camera surveys on four 1000-ha camera grids in southwestern Georgia, USA in 2014 and 2015. September baited camera survey density (deer / km$^2$) estimates for the four properties were 34, 25, 20, and 17, and preliminary passive survey estimates (95% CI) during October were: 26 (23-31), 24 (17-33), 20 (12-25), 12 (7-17), respectively (Figure 1). The passive survey produced similar estimates to the baited survey, however, actual densities for each site are still unknown. The passive model is currently under refinement and beta testing of the model will be necessary before full deployment. However, the use of un-baited cameras shows promise for generating population estimates at a relatively low cost without the need to identify individual deer.

Figure 1. Comparison of density (deer / km$^2$) estimates between the passive un-baited surveys and baited camera surveys.
References


Quantifying the Drivers of Individual Variation in Mule Deer Migration

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Migration, defined as seasonal movement between home ranges [1], is fundamental to the life history of many ungulate species. Although the importance of migration is widely recognized, many ungulate species have experienced declines in migration behaviour, due primarily to climate change and habitat loss [2]. Migration behaviour is not uniform between species, populations, or even individuals, and while it is largely driven by the environment, additional causes of individual variation in migration behaviour, particularly genetic or physiological factors, have not been tested. Our objectives were to 1) quantify individual variation in timing and directionality in mule deer (Odocoileus hemionus) during seasonal migrations; 2) assess the repeatability and consistency of behaviours within and among individuals across years; and 3) identify target genes that explain population level differences in timing and directionality of migration. We used high-resolution GPS data and genetic data collected from 240 mule deer in Colorado from 2008-2015. The mule deer population exhibits near-complete migration to two different summer ranges with high variance in migration timing [3]. We quantified migration behaviours (i.e., timing and direction) using GPS data and assessed genetic differences in these behaviours using a high throughput Restriction site Associated DNA Sequencing (RAD-Seq) approach.

References
Red Deer in Belarus: Insight from Genetic Structure for Management Policy

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After almost total extirpation of the red deer in the territory of Belarus at the end of the 18-th century there were several lines of approach for repopulation since 1865 [1]. Moreover, during the recent decade a number of new local populations were founded in several regions of the country for hunting purposes, with different deer farms across Europe being the main source of new animals. As an important game species, red deer has been translocated in Europe for centuries [2]. Furthermore, translocation of non-European subspecies, i.e. American wapiti and other Asian subspecies, with the purpose of improving trophy quality was common [3]. Therefore, the current practice of reintroduction without any genetic control poses a threat of hybridization and, as a consequence, blurring of the genetic structure of red deer population in Belarus on intraspecific scale. The aim of the present study is to describe the genetic variation and recent population structure of the Belarusian red deer in the light of intensive uncontrolled translocation of animals in the recent decade. Altogether 532 red deer individuals from different parts of Belarus were analyzed for 13 autosomal microsatellite loci. Additionally, part of mitochondrial DNA D-loop and a part of ZFY region of Y-chromosome were sequenced for 464 and 383 individuals respectively. First, we analyzed a sample of 140 individuals representing subpopulations formed in the territory of Belarus during the XX century. Analyzing autosomal microsatellite data using STRUCTURE [4] has showed that the genepool of these subpopulations can be best modeled as consisting of three genetic components, with one of them being typical for subpopulations inhabiting the eastern part of the country, while the two other components are found almost exclusively in the western subpopulations with no clear geographic subdivision between the two. Analysis of mtDNA showed that “western” and “eastern” mtDNA lineages are present in Belarus, but their distribution is uneven over its territory. The “western” haplogroup comprises 99% in the western subpopulations and only 5% in the eastern ones. The “western” haplogroup is represented by 5 haplotypes, one of which comprises 95%, while the “eastern” haplogroup is represented by only one haplotype. Based on the analysis of the Y-chromosome 3 haplotypes were revealed with non-uniform distribution between the West and the East of Belarus. One of them comprises 70% in the western subpopulations, two others comprise 60% in the eastern subpopulations. Thus, the results for all three data types are consistent between each other and show a subdivision of the red deer population into two geographic subpopulations with clear genetic differences between them. The observed structure reflects the recent history of reintroduction of the red deer in Belarus in the XX century.

Additionally, 392 individuals from newly founded local populations were analyzed. This analysis revealed 41 new haplotypes of western and eastern mtDNA lineages and 3 haplotypes of southern lineage with the latter being new for Belarus. In the case of Y-chromosome 1 new haplotype was detected. Furthermore 4.3% and 5.3% of tested animals belong to the Wapiti lineage based on the mtDNA and Y-chromosome analysis respectively. Analysis of autosomal microsatellites for all samples using STRUCTURE [4] has showed that recently founded local populations contain genetic components different from those found in previously established population in Belarus. Thus, despite tremendously increasing the local genetic diversity, animal’s translocation can potentially be a source of alleles, alien for the European genepool and jeopardize Belorussian native biodiversity. Therefore, it is recommended to undertake genetic control actions during quarantine procedures before animal translocating.
Abstract: Large wildfires in the western USA have increased in both frequency and intensity and may have significant impacts on wildlife use of habitats. The impacts of increased fire severity can be problematic and may not follow well known recovery trajectories. Responses of mule deer (*Odocoileus hemionus*) to habitat treatments designed to enhance shrub forage availability after two large, recent fires on the Kaibab Plateau in northern Arizona are not well documented. We examined location data from mule deer on the Kaibab plateau to determine the relative influence of wildfire severity, habitat treatments, and other environmental variables on winter habitat selection patterns. We used locations from 30 adult female mule deer fitted with global positioning system (GPS) collars to model probability of use as a function of habitat covariates using negative binomial regression. The best model describing habitat use by mule deer on the Kaibab plateau winter range included covariates describing the amount of treated area, fire severity, distance to developed water, snow depth, terrain ruggedness, vegetation height and solar radiation. Deer use increased in areas with lower average fire severity, reduced snow depths and closer to developed water sources. Similarly, lower terrain ruggedness and higher solar radiation were associated with increased deer use. This information may be important in designing landscape treatments to improve winter range habitat conditions for mule deer.
Cervids have variable degrees of sociality, within and among species and oftentimes between sexes. The premise that social behavior confers a net fitness benefit is not novel nor is its corollary that pathogens carefully hitchhike on the evolutionary balance of costs and benefits of social behavior to ensure they persist. At the fine scale, however, there is still much to learn by understanding the role ecological contexts has on manipulating the ties that bind social animals, their shared affiliation or association, and the implication for fine-scale behaviors upon which pathogens persistence and spread depend. To better understand the potential dynamics of pathogen transmission and density we studied fine-scale social associations of elk in captivity and in the field across a range of conspecific densities. Here we will illustrate how density affects different scales of social behavior: from fine-scale pairwise social associations, to how pairwise social associations affect individual position in a social networks, and to how social network architecture affects pathogen prevalence for male and female elk. These results are then scaled up and discussed in the context of a spatially structured population elk where disease has historically been confined into one subpopulation. Though some surprises emerge during this synthesis, what is likely most remarkable is how similar are the patterns and outcomes across scales.
Kashmir musk deer is confined to a small geographic range and nothing is known about its ecology. We studied seasonal food habits and habitat use of musk deer in a temperate system. The study was carried out in Kainag NP during two contrasting periods – resource limited, snow bound and least disturbed winter and also resource abundant but highly disturbed summer. We expected diet shift and altitudinal migration by the musk deer to adapt to the extreme weather. We recorded elevation, slope, aspect, vegetation variables (vegetation type, vegetation cover) and the snow cover, at each sighting to examine altitudinal migration of musk deer. We assessed the diet of musk deer through pellet analysis and direct observations. Musk deer primarily occurred at higher elevations (with average elevation above 3100 m) during summer and primarily used alpine meadows, subalpine scrub and subalpine forest (about 70% of sightings). It partially migrated to middle elevations (with average elevation below 3100 m) during winters. Musk deer used areas with high snow cover (average 50%) and low emergent ground plant cover (with average plant cover 30%) during winter but occurred along mixed forest and woodland (more than 60%) to seek shelter and forage in snow. The seasonal shift in diet by musk deer to conifers and monocots was surprising. In summer, it fed on forbs and shrubs (95%), but in winter it also fed on conifers and monocots, which made up about 40% of its diet. These adaptations have probably helped musk deer persist through the harsh winters and enabled it to widely use subalpine and alpine habitats of the Himalaya.

Figure 1. Seasonal diet (%) of musk deer as estimated through pellet analysis.

Reference
Seeing Spots: An SCR Model to Estimate Spatial and Temporal Variation in Fawn Survival and Recruitment

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In South Florida, white-tailed deer (*Odocoileus virginianus*) are an economically and culturally important game species. Deer populations in South Florida are unique due to their low density, low productivity, and wide window of reproductive activity [1]. The white-tailed deer is also the primary prey of the endangered Florida panther (*Puma concolor coryi*), which currently persists in a single population in South Florida [2]. Due to recently reported declines in South Florida deer populations, more information is needed about the factors influencing fawn survival and recruitment in this seasonally-inundated and predator-rich environment. We deployed 3 passive trail camera grids in the Florida Panther National Wildlife Refuge and Big Cypress National Preserve. Each 30 km² grid consisted of 60 cameras. We visually identified 123 unique fawns in 5200 fawn photos from December 1, 2015-June 30, 2016 and created a spatially-referenced capture history detailing each detection. We developed a novel spatial capture-recapture (SCR) model that uses capture histories to estimate population parameters such as birth rate, survival, and recruitment (180 days). Our model allows individual detection and survival probabilities to vary with fawn age and provides the ability to model spatiotemporal variation in birth rate and daily survival probability. We estimated the peak fawning date to be January 25th across this study site, with most fawning events occurring from January to March. Model estimates indicated that 208 fawns (95% CI 179-245) fawns were born within our camera grids during the 2016 fawning season, of which 37 individuals (95% CI 29-48) survived to 180 days (18%). We modeled fawn density, fawn detection probability, and daily survival rate as functions of environmental covariates including vegetation type, frequency of fire, seasonal water level changes, human activity and vehicle use, and the activity of potential fawn predators. Our goals were (A) to provide direct estimates of South Florida fawn survival and recruitment and (B) to elucidate which environmental variables had significant effects on fawn success in this landscape. We found that predicted fawn density significantly increased with frequent fire in an area, but decreased in open canopy vegetation types, such as marsh and prairie. Our model demonstrates a flexible, cost-effective, and non-invasive method for agencies and researchers to estimate fawn recruitment at broad spatial and temporal scales while addressing questions about the underlying birth and juvenile survival processes. We intend to make this innovative method accessible to other researchers for non-invasively studying population dynamics in a variety of target species.

References:
Anthropogenic activities have influence on wild animal populations. Sika deer (Cervus nippon) in Japan currently face no predators because Japanese wolves (Canis lupus), the only predator for deer, became extinct, in 1890 in Hokkaido Island and in 1905 in Honshu Island, through the intensive predator control against livestock loss [1]. A combination of severe winter conditions and overexploitation of deer due to the consumptions of furs, meats, and antlers contributed to the deer population decline in the late 19th century [2]. However, the harvest regulations, including restricting female harvests, between 1950s and 1980s ameliorated the population decline. The deer populations also positively responded to the additional food availabilities from the expansion of farmlands, pastures, and plantations which were developed near their habitats during the same period. As a result, the distribution of deer habitats and their abundance have greatly recovered since the 1980s [3]. Even though the restoration of deer populations was successful, deer were subjected to nuisance animals causing severe damage to agriculture, forestry, and regional ecosystems. Therefore, evaluating deer populations is important information to the sika deer management. I constructed records including hunter populations and captured deer populations in Japan from 1975 to 2014. The hunter population in Japan from 1975 to 2014 has decreased from 518,000 to 194,000 (Fig.1). On the other hand, the number of captured deer individuals between 1975 and 2014 has increased from 15,000 to 586,000. We developed the harvest-based Bayesian model to estimate the deer population [4]. Estimated population size in 2015 was 3,040,000 [5]. Sika deer populations have increased in last three decades. The unmanaged deer populations can generate negative effects on the agriculture, forestry, and ecosystem. Hunting and/or culling is a tool for resource management and ecosystem conservation. Encouraging the recruitment of hunters and establishing the culling regimes are important for wildlife implications in Japan.
Figure 1. Changes in sika deer harvest and number of hunters in Japan. The gray bars indicate the number of sika deer (*Cervus nippon*) harvested by hunting, the white bars indicate that by culling, and the black line indicates the number of sport hunters (Data from Ministry of the Environment, unpublished).

References
Social Dominance Increases Pelleted Feed Consumption by White-tailed Deer in South Texas

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Providing pelleted feed for white-tailed deer (Odocoileus virginianus) is a common management practice in Texas. Previous research has shown that not all deer consume the same amount of supplemental feed, suggesting that social interactions at the feed sites may restrict access to the feeder for subordinate deer, such as young and female deer. Social dominance at feed sites may benefit dominant deer by reducing competition. Changing deer density and supplemental feeder density may change the accessibility of supplemental feeders. To test these hypotheses, pelleted feed was provided year round, ad libitum within three, 81-ha enclosures on two ranches in South Texas with the following numbers of deer and feeders, respectively: 20/1, 60/1, and 60/3. We used stable carbon isotope ratios (δ¹³C) in deer serum to estimate supplemental feed in deer diets during March 2015. Social interactions at the feed sites were analyzed using trail cameras that recorded 30-s videos with no delay in March 2015. Elo Rating in Program R was used to recreate the social hierarchy within each enclosure. We used a mixed model to determine the effect of a deer’s Elo rating (dominance) on supplement consumption within the different treatments. As a deer’s dominance increased, feed consumption increased (P<0.01), but the importance of dominance was greatest in the 20/1 treatment (P<<0.01; Fig. 1). These results suggest that during spring, dominance at feed sites allow those deer to consume more supplemental feed but that the effect of dominance on feed access diminishes at high deer densities.

Figure 1.
Spatial Mortality Risk for Elk (Cervus elaphus) in a Multi-Predator Community in the Rocky Mountains, Alberta, Canada

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There is evidence that prey perceive the risk of predation, as they navigate a “landscape of fear” and alter their behaviour in response. Previous approaches to mapping spatial risk use predator and prey distributions to estimate potential encounters, yet this approach does not account for attack success resulting in mortality. Locations of prey kill sites represent mortality in space, but obtaining kill site data can be cost intensive and require time to accumulate adequate sample sizes. We address an alternative to these approaches for mapping predation risk based on mortality by relating features within a buffer to not only the spatial location but contents of predator scats in Ya Ha Tinda, a multi-predator community adjacent to Banff National Park in west-central Alberta, Canada. Scats collected from four large carnivores (wolves, cougars, coyotes and bears) across a 1200-km² study area from summer 2013-2016 have been analyzed for presence of elk (Cervus elaphus). We compared summer diets of large carnivores through microhistological and DNA scat analysis methods to determine landscape factors influencing spatial predation and validated the risk predictions with known elk kill sites. Elk comprised a larger part of wolf scats compared to cougar and coyote scats, while vegetation dominated bear diets. Juvenile elk (young of year) occur more frequently than adult elk in all predator scats except cougars. In addition to measuring spatial mortality risk through non-invasive sampling, this study also provides baseline data on predation in Banff National Park before the bison reintroduction as part of a 16-year study investigating the role of predation in the changing migratory behaviour of the YHT elk.

References
Stopover Use By A Migratory Ungulate 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 both Rocky Mountain Mule deer (*Odocoileus hemionus hemionus*) and Columbian Black-tailed deer (*Odocoileus hemionus columbianus*) located on the western slope of the Sierra Nevada Mountains, California. We hypothesize that stopover use will influence adult survival in a migratory ungulate population. Iridium satellite collars were applied to female deer within this population (n=34). Collar data was analyzed using the Brownian Bridge Movement Model (BBMM). BBMM uses consecutive GPS points to estimate stopover sites and migration routes. The collar data shows a mean migration distance of 31 km, and BBMM estimated that 58% of the individuals within the Pacific Deer Herd exhibit stopover behavior. Stopover use varied from 1 to 88 days during migration. Patterns of mortality were also assessed. Survival comparisons were made based on whether an individual was migrating or occupying seasonal range. Differences in survival probability were also examined based on whether an individual was migrating or occupying seasonal range; 5 of the 12 observed mortalities occurred during migration. However, 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. We have also found that environmental conditions may influence individuals to use stopover sites as winter range. 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 conservation importance.
Strategic Use Of Deer Management Cooperatives In Landscape Conservation Planning

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Habitat fragmentation and loss are the leading causes of decreasing global biodiversity and create barriers for conservation delivery [1]. Engaging private landowners to achieve landscape-level conservation is widely practiced [2]; however, established mechanisms to encourage voluntary conservation practices are lacking. White-tailed deer (Odocoileus virginanus) management by landowners and hunters is an increasingly popular conservation tool available to conservation planners. Annually, 12 million hunters own or lease approximately 356 million acres for hunting purposes [3]. However, targeting deer hunters for landscape-level conservation planning has not been explored. Deer management cooperatives (DMCs) are a novel approach by private landowners and hunters working collaboratively to improve deer herds and hunting quality. DMCs are defined as ‘a group of landowners and hunters voluntarily working together to improve the quality of wildlife (white-tailed deer), habitat, and hunting experiences on their collective acreages’ [4]. By aggregating multiple properties to cooperatively manage collective acreage, hunters and landowners may facilitate a larger, more connected managed land area within the landscape matrix. The potential increase in cooperative habitat management conducted within DMCs may increase conservation value within the surrounding landscape and to conservation planners. Thus, DMCs may provide a method to counter decreasing connectivity between habitat patches, while simultaneously increasing active habitat management within DMC boundaries. We compared land cover percentages between DMCs and adjacent landscapes to illustrate the utility of DMCs as a conservation-planning tool to increase active habitat management that may benefit species other than white-tailed deer within a fragmented landscape. We quantified the habitat composition and configuration of DMCs compared to the adjacent landscape using FRAGSTATS® software. We also sampled 32 DMCs across four representative U.S. states: Georgia (Southeast, USA), Michigan (Northern, USA), Missouri (Midwest, USA), and New York (Northeast, USA). DMCs totaled over 190,000 acres. Land cover was randomly sampled inside DMCs, and within the adjacent landscape, using a fishnet grid. We describe higher amounts of various ‘wildlife centric’ land cover within DMCs in all four states (Fig. 1), along with lower amounts of ‘agriculture centric’ land cover within DMCs in three of four states (Fig. 2). We additionally surveyed DMC participants in the previously mentioned states, with the addition of Texas (Mid South, USA), totaling over 560 responses. Their motives, importance-performance analysis, and willingness to engage in habitat management will be described. Thus, described landscape-level differences, triggered by DMC landowner motivations, may provide conservation benefits to other game and non-game cohabitating species.
**Figure 1.** Percentage land cover of ‘wildlife centric’ cover types on Deer Management Cooperatives versus the adjacent landscape in Georgia, USA (GA), Missouri, USA (MO), Michigan, USA (MI), and New York, USA (NY). Cover types include: early successional, herbaceous wetland, wildlife opening, woody wetland, and open evergreen (pine savanna).

**Figure 2.** Percentage land cover of ‘agriculture centric’ cover types on Deer Management Cooperatives versus the adjacent landscape in Georgia, USA (GA), Missouri, USA (MO), Michigan, USA (MI), and New York, USA (NY). Cover types include: row crop and managed exotic grass (hay/pasture).

**References**


Different species of animals, even those closely related, are normally kept from reproducing through reproductive isolating mechanisms such as: geographic isolation, breeding season timing, occupying different types of habitat, or by having different courtship and breeding behavior. In the case of white-tailed and mule deer, all these factors help keep the two species from hybridizing. These mechanisms have worked remarkably well throughout their evolutionary coexistence. However, in rare cases these isolating factors break down resulting in interspecific hybridization. Hybrids of these two species have been reported from captive facilities as early as 1898 when a whitetail x mule deer cross was produced at the Cincinnati Zoo. Male hybrids are sterile, however, female hybrids are fertile and can breed back to either of the parental species. This hybridization in *Odocoileus* is rare in most areas, but does occur where their ranges overlap. Hybrid deer show characteristics that are intermediate between mule deer and whitetails but most are not universally diagnostic of a hybrid individual. The most informative physical feature to diagnose a hybrid in the wild is the size and location of the metatarsal gland on the outside of the lower portion of the rear legs. Two loci visualized by protein electrophoresis have been used in the past as a genetic test of hybridization. New advances in genetic techniques have been developed and are now being employed to learn more about hybridization in *Odocoileus*. In addition to the identification of F1 hybrids, a suite of microsatellites appear to offer some clarity regarding the results of backcrossed individuals.

Figure 1. Dorsal surface of the tail in white-tailed deer x mule deer hybrids are variable, but usually dark and intermediate in coloration. Photo by Gerald Day.
Figure 2. White-tailed deer x mule deer hybrid showing the classic intermediate tail coloration and metatarsal glands. Photo by George Andrejko.
Temporal Resolution of the White-tailed Deer

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Temporal resolution is the rate at which the visual system of an organism can acquire and process visual information. High temporal resolution allows animals to process movement at an efficient rate, enhancing their ability to quickly negotiate complex environments as well as avoid fast moving predators [1, 2, 3]. Although the central nervous system can process large quantities of visual information, animals’ finite amount of cognitive ability within the brain means cognitive function for another sensory system must be reduced. Thus, the resolution at which temporal information is perceived varies greatly across animal taxa [4, 5]. Aspects of white-tailed deer (Odocoileus virginianus) visual perception have been previously studied. However, temporal resolution has not been measured in any wild cervid to date. Understanding the temporal resolution of deer provides insight into how visual processing and deer’s ability to react to their visual environment influences their behavior and ecology.

Critical flicker fusion frequency (CFF), the frequency at which a flashing light source is perceived as constant, is one measure of the rate at which temporal information is processed by an animal’s visual system. High CFF means the perception of a moving object is less likely to be blurred, and determination of its nature, direction, and velocity is facilitated [3, 6]. We used ERG methods to assess CFF for dark- and light-adapted vision in deer. Average CFF for 7 deer ranged from 41.0 - 77.5 Hz for rod function. Mixed rod-cone function CFF values ranged from 56.0 - 77.5 Hz for dark-adapted vision and 98.9 - 106.7 Hz for light-adapted vision. Cone function CFF ranged from 98.1 - 106.8 Hz. Our results provide a comparative context between human and deer vision, and suggest that white-tailed deer have high temporal resolution and are adapted to low-light conditions for enhanced movement detection, particularly at dawn and dusk.

References
The brief story of the IBDC

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As a child I spent every summer in a village at my grandparents enjoying the great variety of domestic animals and wildlife including roe deer. I first decided to become a vet at about the age of ten. At university I pursued studies concerning wildlife. Then in 1972 I got a job at the new Game Biology Station nearby to Budapest. As a vet my main interest was primarily on parasites. Nevertheless my favorite animals were deer from the beginning: the native red deer and roe deer as well as fallow deer, what was introduced to Hungary around the 15th century. I started to collect as much information as possible, especially reproduction and general health status to understand the impact of parasites in deer species. In 1982 I gained employment at the Agricultural College, Kaposvár, when I began to monitor and study red deer of Somogy county. In connection with the research activity I tried to take every opportunity to learn and share ideas and experiences especially at conferences like the Congress of the International Union of Game Biologists (IUGB). I interacted with many scientists including just a few names: Anton and George Bubenik (Canada), Norma Chapman (GB), Hermann Ellenberg and Rudolf. R. Hofmann (Germany). I think it is time to put my experiences on paper about my favorite world: the familiar atmosphere of the IDBC.

1. Capturing Somogy red deer for NZ
On a midsummer day 1983 one well known New Zealand (NZ) deer farmer Bernard Pinney visited Kaposvár, the center of the Somogy Forestry Company. The aim was to discuss the possibilities of capturing feral red deer (Cervus elaphus) for export to New Zealand. Somogy county red deer were chosen after evaluating the antler characteristics observed on international trophy shows: Somogy stags' antlers beside the good measurements (length and diameter of the beam) also showed just 3-4 (not too many) but long and thick branches in the coronet compared to those of other good quality populations in Hungary/Europe. (Note that that the optimal time for cutting velvet antler for the traditional Chinese market is just before the branching of the coronet, which is ~60 days after shedding the old antler.) After discussions the decision was made: to capture live deer of both sexes undergo local quarantine and then transport to NZ via England. After two winters of successful captures about 120 were transported to the new home. To illustrate the reputation of these deer in NZ, two stags born in Hungary were sold at auctions for record prices in the early 90's: Kapos - $100,000 NZ, later Magyar (Hungarian) - $120,000 NZ.

2. Proceedings of the Deer Biology Conference NZ
In 1995 one of the New Zealand visitors gave me a brand new copy of the "Biology of Deer Production": The Proceedings of an International Conference held at Dunedin NZ 13-18 February 1983. This book served as a bible for our deer research group for many years.

3. IUGB Congress in Krakow, Poland 1987
In 1986 while perusing the 18th Congress of the International Union of Game Biologists (IUGB), I came upon the "Deer Farming" session held by Peter Fennessy (Invermay, NZ). This gave me an idea. Why not invite him to visit Kaposvár to discuss on our plan to hold a second congress on the "Biology of Deer" in the future. I have shared the idea with our university leader, Prof. Peter Horn, who agreed. Soon we sent a letter to Peter Fennessy. In the response he apologized for not being able to attend but Colin Mackintosh form Invermay, New Zealand would be attending. We met at the IUGB Congress in Krakow in 1987 and spent several days together at the post-congress tour to Popielno to see Prof. Z. Jacewski's famous deer research unit (antler physiology). During the 3 day tour I also spent a lot of time with Whitley Otway (NZ), a physician educated in traditional Korean medicine, as one of the founders of the NZ Deer Farmers
Association. I spent an unforgettable time visiting him in 1988: seeing the wonderful Mesopotamian fallow deer and watching the intrauterine fertilization of red deer hinds with Père David’s deer semen for the successful hybridization. Some days later Colin arrived in Hungary. Visiting our campus and deer farm he accepted that our university would be a good host of the deer congress somewhat later.

4. Letter from Prof. Robert Brown
But our envisaged program would not be fulfilled immediately. Soon a letter arrived from Mississippi. Prof. Robert Brown wrote that had received a sponsorship offer: if they organize an international congress on the biology of deer they could get 30 thousand USD. He was interested in holding the second congress in Starkville (Mississippi, USA) instead of Kaposvár, if it suited everyone. Our deer research team accepted the proposal, stressing our intention to organize the following conference in Kaposvár.

5. The newer congresses
2nd International Conference on the Biology of Deer, 28 May – 1 June, 1990, Starkville, MS, USA Chairman of the Local Organizing Committee: Robert D. Brown; 3rd International Conference on the Biology of Deer, 28 August – 2 September, 1994, Edinburgh, Scotland Chairman of the Local Organizing Committee: John Milne; (Then in Edinburgh we were given the task to organize the next one in Hungary)

The new name of the congress
For the preparation of the congress, I was fortunate that e-mail had become the mean tool of communication by then making our task much easier and effective. We exchanged e-mails frequently, sometimes daily with Ken Drew (the chairman of the Scientific Steering Committee), discussing on the session topics, plenary speakers, and the most suitable schedule. It was not easy sometimes because the second World Deer Congress was also organized in the same summer (Limerick, Ireland; June 1998). After a lot brain-storming I have put forward the idea to change the name of the congress to 4th International Deer Biology Congress. And Ken accepted it.

5th International Deer Biology Congress, 25-30 August, 2002, Quebec City, Canada Chairman of the Local Organizing Committee: Michele Créte
6th International Deer Biology Congress, 7-11 August, 2006, Prague, Czech Republic Chairman of the Local Organizing Committee: Ludek Bartos
7th International Deer Biology Congress, 1-6 August, 2010. Huilo-Huilo, Chile Local Organizing Committee: Werner Flueck, Alexandra Petermann and Jo Anne Smith
And now Harbin is coming: 8th International Deer Biology Congress, July 27-31, 2014, Harbin, China Chairman of the Local Organizing Committee: Zhi Xiaoliang

And why was China chosen as the next site? The cradle of the deer is somewhere here too without doubt. Think of the existing unique antlerless forms: musk deer, Chinese water deer or others like muntjac and Père David's deer (milu). After the early differentiation, ancient deer started to disperse to west and east, north and south. Moving eastward they walked through the Bering land bridge to Alaska, other parts of North America, and slowly down-down to the Tierra del Fuego - Argentina, and Chile...On the way they were followed by predators and parasites resulting in further differentiation due to co-adaptation, and co-evolution. And now we see the result: the colorful diversity. Amazing...!
The Efficacy of Zolvix Plus® (monepantel + abamectin) and a Combination of Abamectin and Oxfendazole in Young Farmed New Zealand Deer

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Anthelmintic resistance has become an issue in farmed red deer (Cervus elaphus) in New Zealand. The main focus of control when the industry started in the 1970s was for lungworm Dictyocaulus eckerti [1]. At that time, it was considered that gastrointestinal nematodes were of secondary concern, and were controlled by the treatments given for lungworm. Since their release onto the market in the 1980s, control has largely relied on use of macrocyclic lactones (MLs) [2]. Early research indicated that levamisole was not highly effective against lungworm [3], and whilst benzimidazoles were used this declined after the release of the MLs. In recent years, there has been growing evidence that gastrointestinal nematodes are important [4] and that commonly used anthelmintics were no longer as effective as previously observed [1, 5]. On this farm, there is a history of resistance to the MLs by Ostertagia leptospicularis and Spiculopteragia asymmetrica [5]. The anthelmintic that had been used in young deer during the year in question was a combination of abamectin and oxfendazole but there was some doubt as to its efficacy, which prompted this particular study. The aim of this study was to assess the efficacy of Zolvix Plus® (monepantel + abamectin) and a combination of abamectin with oxfendazole using a faecal egg count reduction test combined with larval cultures.

Animals were rising one-year-old red deer with a mean weight of 65kg (range 50kg to 78kg) and of both sexes. These deer were pasture grazed. They were arbitrarily allocated into two groups. Faecal samples were collected, then one group (n=24) was treated with Zolvix Plus® (2.5mg/kg monepantel, 0.2mg/kg abamectin) and the other group (n=19) with two separate treatments given at the same time being abamectin (0.2mg/kg; Mectin Drench for Sheep®) and then oxfendazole (9mg/kg; Bomatak C®). All samples were subject to a modified McMaster egg count where each counted represents 50 eggs/g. Faeces were also cultured by mixing with vermiculite and incubating for at least 14 days. In addition, a modified Baermann procedure was conducted to count the number of lungworm larvae. Post treatment samples were obtained 14 days later and subject to the same tests.

Faecal egg counts were allocated to genera based on larval morphology. However, as it was not possible to separately identify between those larvae of Ostertagia leptospicularis, Spiculopteragia spiculoptera and Spiculopteragia asymmetrica they were included together as Ostertagia-type and their efficacy calculated the same way. The efficacy against Ostertagia-type parasites was 87% for Zolvix Plus® and 65% for the abamectin and oxfendazole combination. Both were highly efficacious against Dictyocaulus with no larvae found in the post-treatment samples. The commonly defined definition of anthelmintic resistance is 95% reduction in faecal egg counts. Neither treatment was found to achieve this level of efficacy. These findings indicated that further
work is required to determine if an appropriate dose of Zolvix Plus® can be determined for use in deer.

References

Nutritional relationships animals have with their winter environments often underpin survival and reproduction, consequently, influencing population dynamics [1]. Severe winter conditions can compound the nutritional bottleneck common to winter environments because increased snowfall can further reduce access to forage and increase energy expenditure associated with thermoregulation and locomotion [2]. As a result, severe winter conditions may result in reduced nutritional condition (i.e., fat reserves) of individual animals that is needed to promote overwinter survival and future reproductive efforts. Although the deleterious effects of severe winters on adult and juvenile survival are well documented [1], the duration and influence of carryover effects on reproduction following severe winter conditions are rarely identified. We aim to understand the enduring effects of a severe winter on population dynamics of mule deer. We expected that the suppression in nutritional condition following a severe winter would have cascading effects on reproductive allocation and success, regardless of improved foraging conditions on summer range. Following extreme winter conditions in 2016-2017, we evaluated the relationship between nutritional condition and trends in reproduction of 75 adult and 67 neonate mule deer of the Wyoming Range in western Wyoming. Nutritional condition of female mule deer following severe winter conditions was lower than the preceding 4 years (2.3%IFBFat in 2017 compared with 4.0–5.3%IFBFat in 2013–2016, Figure 1), which resulted in suppressed fetal development (1 mm smaller eye diameter), delayed timing of parturition (4-7 days later), reduced birth mass of neonates (0.5kg lower), and a rise in neonate mortalities resulting from stillbirths (>100% increase). Our preliminary findings unveil the lasting effects of severe winter conditions on population dynamics resulting from the carryover effects of nutritional condition and its subsequent effect on reproductive success the following summer.
**Figure 1.** Percent ingesta-free body fat (IFBFat ±SE) in March and December for adult (>1yr) female mule deer in the Wyoming Range, 2013–2017.

![Seasonal Changes in Body Fat](image)

**References**


The Next Frontier for Recovering Endangered Huemul (*Hippocamelus bisulcus*): How to Avoid Recurrent Misdiagnoses of Health Status

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There remain only 350 - 500 huemul in Argentina, fragmented into some 50 subpopulations along 1,850 km of Andean mountains. No groups are documented to be recovering, rather the process of local extinctions is continuing. The difficult accessibility to remote locations of extant huemul has hindered research; thus, only in 2016 was a first female captured and marked, with six more being marked in 2017. Evaluations of intact cases, besides the 7 marked deer, were based on a few animals that died soon after confinement or were found freshly dead. Although few, these examined animals could serve as highly valuable case studies to reveal important sanitary issues. Instead, a high incidence of misdiagnosing the health status raises the question about what strategies to consider in order to minimize these diagnostic errors and consequential inappropriate treatments, and thereby reduce any unfavorable consequences. Here we present several cases involving misdiagnoses, then add our corresponding alternative interpretations.

Case 1: a female found in a delicate state and taken to a pen for veterinary supervision died soon after. Based on a subsequent necropsy, it was reported that she likely died from intoxication from plant consumption (*Astragalus* sp.). However, our subsequent analyses showed clear signs of osteopathological processes in the mandibular and maxillary bones, and moreover, columnar and appendicular lesions. Additionally, bone fluoride levels reached 2209 ppm, explaining the lesions resembling fluorosis, most likely explained by the high fluoride concentrations in volcanic ashes deposited from the 2008 eruption of Mt. Chaitén. Case 2: a male in the same region was found in a delicate state and taken to a pen for supervision. He died soon after. The veterinarians who performed the necropsy did not report any health problems. However, our subsequent analyses also showed this second case to have clear signs of osteopathological processes in the column, and *in vivo* photos clearly show an affected mandibula (park bureaucracy has not yet allowed an evaluation of the skull). This deer also had very high bone fluoride levels, even reaching 2979 ppm. Case 3: a male from another region was cornered by dogs in the evening, then roped and attached to a post by the farmer. Authorities, who were contacted, arrived in the afternoon of the next day. After sedation, the male was evaluated by veterinarians. Considered healthy, he was thus translocated to another site nearby for release, where he died shortly after, not recovering from the drug. Although the carcass was initially left at the site of death, it was later removed and buried elsewhere. In contrast to the veterinarian report, the subsequent recovery and necropsy of the carcass revealed skeletal health issues, particularly severe in the mandible and maxilla. Case 4: a female in another region, immobilized to be marked, was evaluated by a team of veterinarians. The animal was considered healthy and apt for release. However, photos of the animal before capture, during immobilization, and later after her release indicate that she had a swelling on the left mandibular site. These types of swellings frequently indicate underlaying osteopathological processes. Case 5: a population in Chile was recently evaluated for the status of the trace mineral selenium (Se). Given the samples with values below the detection limit were removed from analysis, the population was considered to have adequate Se levels. However, when all values were included, a re-analysis determined that at least 75% of the values were indeed in the deficiency range. Moreover, that population was shown to have numerous cases of advanced osteopathy compatible with Se deficiency. The prevalence of this osteological
disease pattern has been shown to be at least 57% in remains of dead adult huemul, and 86% among recently examined live adults. Additionally, the impact from volcanic ashes containing high amounts of fluoride also has been described for livestock and other wild ungulates. Reducing diagnostic errors is an important goal because of its associated morbidity and potential preventability. These repeated cases of diagnostic errors reported here are nontrivial given the few opportunities to evaluate live specimens of this highly endangered species. Aftermaths of failed diagnosis include a reduced life expectancy, when the alternative could be to take a debilitated individual to a rehabilitation center. Furthermore, at the current precarious state of this species, individuals under controlled conditions can provide useful opportunities to answer numerous research questions. Given the repeated evidence of osteopathology occurring in huemul over a broad geographical range and the high prevalence found in both dead and live huemul, it is essential that live huemul be examined utmost professionally. Special attention must be given to the hitherto described pathophysiology among huemul, which requires a thorough inspection of the oral cavity.

The Red Deer *Cervus elaphus* Reference Genome CerEla1.0

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The first reference genome assembly CerEla1.0 (NCBI, MKHE00000000) for red deer (*Cervus elaphus*) has been presented [1]. The CerEla1.0 could prove useful in many cervid Genome Wide Association Studies (GWAS). Red deer are an emblematic member of the natural megafauna of the Northern Hemisphere and have been present in human culture since the Neolithic. Humans introduced and spread the species to many places, including the Southern Hemisphere. Red deer, the mythological Wonder Deer, also the Royal Game of the Middle Ages in Europe, is respected and revered in many cultures. Today red deer are not only one of the most desired game, but also farmed for venison, velvet antler products and tonic. Red deer are becoming increasingly recognized as an animal model for bone, osteoporosis and regeneration research, as well as for population and evolutionary studies.

Red deer stag DNA was sequenced by Illumina technology at 74x coverage. The ALLPATHS-LG assembly of the reads resulted in 34.7x10^3 scaffolds. For building the red deer pseudochromosomes a pre-established genetic (recombination) map was used as the main anchor point [2]. A nearly complete co-linearity appeared between the array of the deer map points/map marker scaffold sequences and the order and orientation of the orthologous sequences in the syntenic bovine regions. Syntenies were also conserved at the in-scaffold level. The final CerEla1.0 assembly contains 26108 scaffolds and contigs and spans 3.4 Gbp including the NNN-s inserted between contigs during the scaffolding and between scaffolds. In nearly all genomic segments the cM distances corresponded uniformly to 1.34 Mbp, due to the many “NNN-s” inserted by the ALLPATHS-LG, 1.25-fold uniformly more than in the bovine homologous regions. In the resulting red deer pseudochromosome sequences, 2.8 million heterozygous sites/SNPs, 365 thousand indels and 19368 protein coding genes were identified along with positions for centromerons. This de novo assembly demonstrates the use of an approach of dual references, i.e. when a target genome (red deer) has already a pre-established genetic map, and is combined with the well-established whole genome sequence of a closely related species (cattle).

The reference genome CerEla1.0 of *Cervus elaphus hippelaphus* and its annotation, in accordance with new data from other programmes, is under continuous monitoring and updating. If the sequence data of a SNP-based map markers will be available the updating of
CerEla1.0 will be possible using the approach described in this work. A large number of SNP/heterozygotic sites were identified (2.8x10^6 SNVs, 3.6x10^5 indels) and aligned to the deer pseudochromosomes. The sequence and the pseudochromosome complement of CerEla1.0 may provide a basis and a rich source for broader interests, including, among others, conservation genetics, refined evolution and population studies within the family Cervidae as well as in a wider neighborhood of ruminants and Pecora. CerEla1.0 also provides a source for chromosome-specific microsatellite sets, which may shed light on inbreeding/outbreeding, help in the identification of gene introgressions, of descents for autosomal, maternal and paternal lineages, forensic identification, or defining allelic compositions behind of phenotypes important, for example, in game management. The exploration of the genetic component of record antlers becomes possible by Genome Wide Association Studies. The applications and use in several fields of medical research (e.g. bone and osteoporosis research, organ development and regeneration, robust tissue proliferation/tumor biology) are also feasible.Data availability: the raw reads have been deposited into the SRA database (SRR4013902). The reference genome sequence has been submitted to the NCBI database and can be accessed at the accession number MKHE00000000. The gene annotation and the variation tracks are available for browsing and downloading from the JBrowse web page http://emboss.abc.hu/wonderdeer/JBrowse.

References
The Red Desert to Hoback Mule Deer (*Odocoileus hemionus*) Migration: A Case Study in Common Interest as a Basis for Coexistence

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Human-human interactions that underlie human-wildlife coexistence are often overlooked in the conservation biology research, management, and practice [1]. However, human-wildlife coexistence depends on the ability of diverse human-interest groups, often with competing values, to accommodate wildlife [2]. Interdisciplinary approaches to integrating human-wildlife and human-human coexistence challenges offer a promising path forward [3]. In our work on mule deer (*Odocoileus hemionus*) migrations in southwestern Wyoming, USA, we applied an interdisciplinary framework—the policy sciences—to map the social and cultural context that exists alongside ecological concerns of migration. We conducted 45 semi-structured qualitative interviews with members of eight stakeholder communities whose interests were impacted by the Red Desert to Hoback mule deer migration. We solicited perspectives on challenges surrounding the migration, and the values that drive stakeholders to engage with it. We also conducted informal key-informant interviews, participant observation, and document analysis of popular press articles, organizational websites, and professional publications. We coded interview transcripts, field notes, and supporting materials for value claims and problem definitions. Our results revealed that many of the key values driving humans to interact with wildlife in this case were shared across stakeholder groups that exist in conflict with each other over an appropriate policy response to the migration. We also found four competing problem definitions at play in the discourse, each supported by a distinct set of value claims, that undergirded policy preferences. These findings clarify the basis of human-human conflicts that threaten to stymie efforts to ensure a coexistence outcome with mule deer along the Red Desert to Hoback migration corridor. However, results also suggest that strong shared values exist surrounding the migration, which could be developed to promote common-interest policy and long-term human-wildlife coexistence.

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The Selenium Distribution In Velvet Antler Of Sika Deer

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Velvet antler of sika deer is a traditional Chinese Medicine (TCM), which has been used for thousand years. Selenium is an essential trace mineral in human and animals that is important for many biology processes [1]. Both velvet antler and selenium have been reported to protect against cancer, virus, oxidative damage, immunodeficiency and several other diseases. Therefore, selenium might be one of active factors in velvet antler of sika deer. Herein, we developed a selenium measurement method by ICP-MS (inductively coupled plasma mass spectrometry) with a detection limit of ppm. Selenium amounts in different regions of velvet antler were measured. The selenium amounts in wax slices, powders slices and bone slices of velvet antler of sika deer were 0.750 ppm, 0.300 ppm and 0.244 ppm, respectively. The selenium amount in wax slices in reindeer was also measured and it was 0.594 ppm, which is less than that of sika deer (0.750 ppm). It should be noted that wax slices are from the growth region at the tip of the antler, where neuron and blood vessel grow extremely fast. Wax slices had the highest concentration of selenium in velvet antler, which indicates that selenium may play a key functional role in antler growth. Based on our unpublished genome of sika deer, we screened the selenium enrich gene and predicted the selenium proteins in antler. These results will help to clarify the role of selenium in velvet antler of sika deer and its TCM use.

References
The Waiting Game: Assessing Behavioral Differences Among Migratory Elk in Response to Risk From Multiple Predators

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The success of different migratory strategies among the Ya Ha Tinda (YHT) elk herd has changed following two decades of population decline, with fewer animals summering in Banff National Park and more becoming year-round residents or migrating east onto industrial forest lands every year.\(^1\,^2\) Resident elk wintering at YHT are habituated to human disturbance affording them more foraging opportunities (via multi-tasking) in winter than western migrants not habituated to humans. If eastern migrants also are habituated to humans in summer because of high recreational use on forest lands, this may partially explain their recent increase. To investigate how elk respond to predation risk—and how these responses may influence each migratory strategy’s vulnerability to predation—we compare the fine-scale spatiotemporal responses of migratory herd segments to humans and predators using time-to-event (TTE) modeling\(^4\) with data from 44 remote cameras placed throughout the winter range of the YHT. Cameras were distributed evenly among open, closed, and edge habitats at various distances from human activity. Photographs document when elk, wolves, cougars, grizzly bears, and humans use each site and provide estimates of how many individuals were present. We used a mixed effects Cox proportional hazards model to determine how the time between elk visitations (TTE) is influenced by time of day, elk group size and composition, recent predator presence, and site characteristics (e.g. distance to roads, vegetative cover, and topography). Preliminary results indicate the time between elk visitations is longer after wolves have been detected and shorter with the presence of bulls, larger group sizes, and in predominantly open habitats. With camera traps becoming an increasingly common tool for wildlife research, this purpose-driven sampling design offers a novel and non-invasive approach for determining how landscape features and human disturbance can alter the relative importance of space and time in shaping predator-prey interactions.

References
Tooth-loss Syndrome (TLS) in Deer and Implications on Diet of Endangered Patagonian Huemul (Hippocamelus bisulcus)

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Even though only 350-500 Patagonian huemul (Hippocamelus bisulcus) remain in Argentina, information on their population ecology and dynamics is severely lacking. For the first time, radio-telemetry collars were placed on a group of huemul in Argentina to better understand the factors behind the population’s failure to recover. Six adult huemul (3 of each gender) were captured during the winter of 2017 at Shoonem Protected Park, Chubut province. Physical examinations of these six during the capture, plus a necropsy of a fresh female carcass found under a fallen tree, revealed all to be under 5 years of age, yet 86% with clinical pathophysiognomies [1] (Flueck & Smith-Flueck 2017), which included lameness, an affected hoof, and exfoliation of from 2-7 incisor teeth. Skeletal remains collected between 1993 and 2007 from this same population had already revealed a high prevalence of osteopathy[2](Flueck & Smith 2008), with at least 57% of the adults affected, with lesions of the mandibula (63%), maxillary (100%), and appendices (78%). Many of those mandibles were found lacking incisors and we attributed this to the natural decomposition process of skeletal remains, since single conical roots have little hold in the alveoli. Only now, through these live marked huemul, do we realize that the absence of incisors on those carcasses might have actually occurred before the animals’ died. Additionally, there is some preliminary evidence that this tooth-loss syndrome (TLS) might be a common phenomenon throughout other parts of the huemul’s distributional range. For example, aware of the discovery of TLS in Shoonem Protected Park, Chilean veterinarians, while treating abscesses on a male huemul in the wild in February of 2018, checked the oral cavity to discover that some of his incisors were also lacking. Moreover, he was thin and in poor physical condition [3]. In our study at Shoonem Protected Park, 5 of the 7 animals were missing teeth [1]. The worst case (Huemul #1), a young male of an estimated 4-5 years of age, had only one full incisor tooth remaining (Figure 1) at the winter capture, at which time palpation of the spine revealed a progressive stage of muscular atrophy. These would be animals for a rehabilitation center, would such a center be available [4]. But instead, as they are left to fend for themselves in the wild, we are concerned about their foraging efficiency. Limited by their disability, some type of modification to their feeding behavior must have occurred, which ultimately could affect the quality and quantity of aliments consumed. To determine if the diet of these tooth-lacking huemul is affected, we collected fresh fecal droppings from Huemul #1 in January, 2018 (summer). These feces were unusual in shape, texture, moisture and content, and not at all similar to average huemul pellets. Instead, the fecal matter appeared more like that of a horse or wild boar, and contained a bit of undigested fibers. Additionally, we collected fresh pellets from two other adult huemul in the same habitat type during the same week of fieldwork; these appeared more like normal deer feces, and from the size, also from males. After air-drying the specimens, plant content was determined using microhistological analysis [5,6] at the Instituto Nacional Tecnología Agropecuaria. The plant content of these samples is being compared with that of fecal pellets (n= 12) collected in the summer of 1999 in the same habitat at the same study area [7]. The 1999 samples showed huemul to be predominantly browse feeders, with woody species and forbs comprising 71.8% and 27.2% of the diet, respectively. The main two woody species in the diet were Maitenus disticha and Gaultheria spp., which comprised 54.4% and 8.4% of the diet, respectively. Given the rigid-textured, tiny leaves (5-15 mm in length) of these woody species, we do not expect this
male huemul with TLS to be able to consume these types of plants, neither with help from the tongue. Normally deer press their bottom incisive teeth upon the upper dental pad to grab, pull and remove leaves from shrubs and forbs. Instead, we assume individuals with severe TLS, such as this male, might be forced to eat more tender plant material, such as forbs (those that predominated in the 1999 samples: *Osmorhiza chilensis*, *Adenocaulen chilensis*, and *Rosaceae* spp.), or instead focus on a completely different diet, perhaps foraging on aquatic species growing at the lake’s edge. During the winter capture, huemul were seen feeding on some submerged vegetation. We predict that this male with only 1 remaining incisive tooth has modified his diet to that of forbs over woody plants. Data from the three deer samples collected in January of 2018 will soon be ready for analysis and the results will be described and discussed in this presentation.

**References**


**Figure 1.** Live male huemul 4 to 5 years of age at Shoonem Protected Park: only one front tooth remains; the right canine is broken and only part of the root of the left canine remains at gum level.
Ungulates commonly select habitat with higher edible forage biomass and nutritional quality to maximize individual fitness [1]. However, predators can indirectly alter ungulate habitat selection and foraging behavior, and consequently their nutritional condition [2]. Ungulates will often choose areas with decreased predation risk, sometimes sacrificing higher quality forage [3]. This tradeoff between ideal forage and predation risk can be an important life strategy with major effects on body condition of individuals, and subsequently population vital rates. We determined if this tradeoff existed in a mule deer (Odocoileus hemionus) population in central New Mexico, and then examined mule deer habitat selection to see how they approached it. We utilized GPS collar data to model mule deer habitat selection based on covariates that included multiple metrics for forage as well as measurements of stalking cover and predation risk. We also examined microsite characteristics of mountain lion kill sites and mule deer foraging points to assess tradeoffs at a finer scale. Our data showed a moderate correlation ($r = 0.43$) between forage biomass and stalking cover, which indicates that deer are faced with a tradeoff between forage and risk. We also found that deer selection of foraging sites was best explained by increased quantities of edible biomass, further supporting the potential for a tradeoff scenario. As a whole, deer selected for areas of higher edible biomass when mountain lion predation risk and stalking cover were lower. Likewise, they utilized areas with lower stalking cover when predation risk was higher, also indicating that risk affects their behavior. Additionally, we found that actual kill sites were best explained by increasing stalking cover and grams of digestible protein, suggesting deer may be selecting for forage quality at the cost of predation risk. The mean visibility (i.e. stalking cover) at kill sites was $10.47m (± 0.94 [95%CI])$ compared to $14.43m (± 1.63)$ at random points, and a site was 1.5 times more likely to be a kill site with each 1-meter decrease in visibility. The often inconspicuous indirect effects of predation usually manifest themselves as nutrition deficiencies have a high potential to be mistaken for bottom-up forcing, which could lead to a misinterpretation of results and subsequently to flawed management strategies.

References
Understanding the Relative Roles of Nutrition and Predation in Regulating Sympatric Mule Deer and Elk in a High-Desert Ecosystem

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Demography of large ungulates is typified by relatively high and invariable survival of adults. Consequently, survival of young is the demographic that often underpins population trajectories. In systems where ungulates co-occur with predators, predation is commonly the leading cause of mortality among neonates. Moreover, predator avoidance by females during parturition is common among ungulates to minimize risk of predation to newborns; this behavior involves increased use of habitat that provides adequate cover for neonates. If habitats that minimize predation risk are not consistent with those that offer energetic gain, however, such behavior may conflict with the need for females to acquire adequate forage to meet the energetic demands of lactation. Behaviors in response to forage acquisition and predation risk can have important consequences for fitness, and therefore, we aim to link behavior, nutrition, and predation to survival and reproduction in mule deer (*Odocoileus hemionus*) and elk (*Cervus elaphus*), two species that differ both in body size and behavioral strategies during parturition. We expect the sensitivity of habitat selection to predation risk by coyotes (*Canis latrans*) to vary as a function of body size and time post-parturition. Further, we expect that nutritional condition at the end of winter will influence whether parturient females adopt a risk-prone or risk-averse strategy, and such behavior should be related to neonate survival. Behavior is one of the primary mechanisms by which females cope with constraints on survival and reproduction. Thus, understanding the interacting roles of predation, habitat, and nutrition on behavior is key to identifying the mechanisms underpinning ungulate dynamics. High-desert systems in particular are ubiquitous across the West, therefore, identifying the factors contributing to thriving elk herds alongside of stagnant populations of mule deer in such a system is key to maintaining robust herds of elk and enhancing population growth of mule deer.
The Swedish model of forest and wildlife management has been a conservation success by restoring cover, food and hunted species of wildlife over the last 150 years, including 4 species of deer: moose (Alces alces), roe deer (Capreolus capreolus), red deer (Cervus elaphus), and fallow deer (Dama dama). Key components of the model are strong focus of commonality and efficiency, utilitarian use and sustainability [1]. Commonality and efficiency resulted in hunters organizing in teams based on long lasting land tenures, which in turn enabled a sustainable flow of wild-harvested into to the society either via social networks or legally sold on the consumer market. The flow of wild-harvested meat has increased commensurate with increases in deer abundance and an increase of hunters since World War II. Various market mechanisms exist in Sweden to allow hunters and landowners to sell deer meat into formal markets as opposed to the North American practices of banning commercial uses of wildlife. Previous studies found that social networks are the main source of wildlife-harvested meat, yet market channels are important for those consumers without connections to hunting or hunters [2, 3]. Using national, regional and local survey data in combination with data on harvested deer species we explore the relative contribution of meat from various species of deer, relationships between household use of wild-harvested meat, sources of meat, and subsequent attitudes towards hunters, hunting, and wildlife management in general. We disentangle the effect of distribution channel – hunter provided or consumer market – and which source (species) of meat are most influential on people’s attitudes. and if households with a member being an active hunter differs from those with connection to hunting.

Using Low-Depth Genotyping-by-Sequencing for Genomic Analyses in Farmed New Zealand Deer

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Summary: In New Zealand, there are currently ~1 million commercially farmed deer, farmed mainly for venison and for velvet. The New Zealand deer industry uses genomic testing to obtain parentage and pedigrees for the purposes of breeding and selection. Recently, a new direct sequencing method (Elshire et al., 2011) has been applied to New Zealand deer. It involves direct sequencing of DNA from ear punch tissue. The method, genotyping-by-sequencing (GBS) has been used to obtain ~80,000 marker genotypes per animal without the need to develop commercial assays or to have a sequenced genome. The New Zealand deer industry is using GBS for parentage (Dodds et al., 2018) as deer behaviour prohibits intensive management of hinds, but these genotypes also offer new opportunities to harness genomic information. The purpose of this study was to explore further utility for the genotypes generated for parentage. Here we use over 1,000 recorded deer to show use of the method for parentage verification, breed/species assignment, finding major genes using genome-wide association studies (GWAS), and genomic prediction in New Zealand deer. Challenges of using this method involve handling sequence data of varying depth within a commercial platform to estimate genomic relationships (Dodds et al., 2015). Advantages include tens of thousands of markers at a price point equivalent to parentage. Accuracies for genomic prediction of commercial farm traits were assessed. Quantitative trait loci were identified for yearling weight and a candidate gene was proposed. An added challenge for genomic prediction in deer is the presence of two distinct species and the use of cross-breds. To address this, we adjusted genomic relationships based on the underlying marker allele frequencies in each species (Hess et al., 2018). This tool was developed for commercial parentage and breeding but has potential for many uses including population and conservation genetics.

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References
Disease models are a useful tool to understand disease transmission and spread, predict future disease trends, estimate epidemiological parameters, test mechanistic explanations for observed patterns, and integrate data from different scales. Network models are a type of model that is exceptionally suited for situations where some individuals, or groups of individuals, have more contacts than others. Wildlife often have heterogeneous contacts due to their spatial structure, social structure, and/or seasonal mixing patterns. For modeling CWD transmission in deer, network models could assume that deer congregate on high quality landscape patches (called 'nodes') that are identified based on resource selection metrics. Within patches, CWD could be transmitted by direct contact between individuals as well as indirect transmission with environmentally-persisting prions. Relative risk of being infected from the environment is related to the density of animals, residence times within patches, and return patch rates. CWD could be transmitted between patches by movements of animals between patches, and the strength of the 'edges' between patches could be related landscape connectivity, and could vary seasonally. In this talk we address advances in movement models of individual animals to show how movement ecology can improve predictions with respect to where hosts may be exposed, either through the environment or from other individuals. Integrating more movement-based aspects into network models may allow a further understanding of disease transmission dynamics and open the door to new questions.
The Western Association of Fish and Wildlife Agencies (WAFWA) established the Mule Deer Working Group (MDWG) in 1997 to address common management issues facing black-tailed and mule deer (collectively called mule deer) and to optimize cooperative research and management. The MDWG consists of a representative from all 23 western mule deer states and provinces and it was designed to (1) develop strategies to assist in management of declining mule deer populations, (2) improve communication among mule deer biologists, and (3) provide a forum to respond to information needs from agency administrations. Additionally, the group attempts to bridge the communication gap between agencies, universities, nongovernmental organizations, and citizens interested in mule deer. The group’s range-wide approach to conservation better equips mule deer biologists to face new challenges with a wider body of knowledge, helps natural resource administrators make science-based decisions, and provides up-to-date and accurate information to stakeholders.

Since inception, the MDWG has been successfully addressing concerns about mule deer that are shared among wildlife agencies in western North America. The many accomplishments of the MDWG include: a book summarizing the current knowledge, challenges, and opportunities for the important issues identified by leading mule deer experts (Mule Deer Conservation: Issues and Management Strategies 2003), a popularized version of this book for easy reading by non-biologists (Mule Deer: Changing Landscapes, Changing Perspectives), the North American Mule Deer Conservation Plan, Mule Deer Habitat Guidelines for 7 North American ecoregions, Energy Development Guidelines for Mule Deer, Methods for Monitoring Mule Deer Populations, Range-wide Status of Black-tailed and Mule Deer, Mule Deer Movement and Barriers, and a growing collection of 22 Fact Sheets addressing the most important issues facing mule deer today. The MDWG also collaborated with the WAFWA Wildlife Health Committee to publish 2 documents that address mule deer management in the face of major health concerns (Consideration of Disease Risks in Translocation of Deer by Wildlife Management Agencies and Recommendations for Adaptive Management of Chronic Wasting Disease in the West). In addition to the many published documents, the group is currently coordinating workshops to teach western state biologists how to use advanced statistical methodology to analyze GPS movement and migration data for rangewide planning and conservation decisions.

This is an opportunity to learn what the MDWG has been up to and become familiar with the tools available to help you conserve the most important member of Cervidae. All of these products are available at: www.muledeerworkinggroup.com.
What Can Genetic Relatedness Tell Us About Social Behavior, CWD Transmission, and Management Alternatives?

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The ultimate goal of integrating host behavior and disease transmission is to define what an infectious contact is and how to measure such contacts. The frequency, distribution, and relation to host density of those contacts (exposure) make up one of the fundamental mechanisms of disease transmission (the other key mechanism is susceptibility). Social behaviors that promote stable group structure and philopatry can have large impact on disease transmission by structuring infectious contacts on the same axis of variation as social contacts. When such behaviors are based on kinship, genetic relationships can be used to infer the social and infectious structures. Alternatively, social behaviors that promote less structured mixing of individuals, such as seasonal migrations and transient grouping, can decouple social behaviors from infectious contacts and genetic patterns. In addition, making the link among behaviors that structure infectious contacts also requires properly defining an infectious contact based on the transmission route of a pathogen. Since chronic wasting disease (CWD) can be transmitted directly and through the environment, the relative importance of each route in an infected population has an impact on how strongly social behaviors structure infectious contacts and how to interpret the empirical patterns of genetic relatedness and infection.

The social structuring of white-tailed deer in eastern North America remains the clearest example of where the overlap in social structuring, host genetics, and disease has revealed insights into CWD transmission heterogeneities. The matrilineal structure of white-tailed deer behavior is well-described and the emergence of CWD, as well as other diseases such as bovine tuberculosis, in high-density populations in the last 20 years have provided empirical evidence of how strong structuring of social groups along familial lines can influence disease patterns. Here, I present a synthesis of how the range of social behaviors in North American CWD host species may generate heterogeneities in transmission, when social behaviors are likely to be less important to transmission relative to competing factors, and what characteristics of social behaviors can be examined using genetic techniques.
Heterogeneity in availability and quality of forage on the landscape constitute the foodscape within which animals make behavioral decisions in acquisition of food resources. Novel changes to the foodscape, such as human disturbance, can alter behavioral decisions by prompting behaviors that favor risk-aversion over food acquisition. Although behavioral alterations and population declines often coincide with the introduction of human disturbance, the mechanistic link between behavior and population trajectory are largely undocumented. We aimed to elucidate the pathway by which human disturbance effects ungulate populations by testing the Behaviorally Mediated Forage-Loss Hypothesis, wherein risk-averse behavior is expected to compromise use of the foodscape. We used GPS collar data and behavioral observations of migratory mule deer (*Odocoileus hemionus*) in three populations exposed to a gradient in energy development (Fig. 1) to evaluate habitat selection, movement patterns, and foraging in response to varying levels of forage availability and human disturbance. Subsequently, we linked animal behavior with measured use of forage relative to human disturbance, and forage availability and quality. Mule deer exhibited behaviors of risk-aversion in response to human disturbance across multiple behavioral scales. Deer avoided habitat near, selected for movements away from, and increased vigilance near human disturbance—all behaviors consistent with risk-aversion. Although use of winter food (i.e., sagebrush) increased as production of new annual growth of sagebrush increased, use of available food decreased with proximity to disturbance. Consequently, behavioral avoidance prompted loss of otherwise available forage that was 4.6-times greater than forage lost to direct habitat loss from infrastructure development (Fig. 2); thus, further reducing the capacity of the foodscape to support mule deer populations. Our findings unveil the mechanisms by which human disturbance can affect populations of large herbivores and provide a missing link between altered behavior and population declines coincident with the introduction of human disturbance.
Figure 1. Study area including three discrete winter ranges for mule deer in western Wyoming, USA (Sublette, North Wyoming Range, and South Wyoming Range), 2013–2015.

Figure 2. Predicted use of forage across winter ranges (A: Sublette, B: North Wyoming Range, and C: South Wyoming Range) in western Wyoming, USA, 2013–2015, resulting from the negative binomial GLM with value of weighted distance to disturbance set to the maximum value (“Use of Forage without Disturbance”) and with the actual values of the weighted distance to disturbance (“Use of Forage with Disturbance”).
While Males Fight, Females Choose: Male Phenotypic Quality Informs Female Mate Choice In Mammals

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Theoretical support exists for male secondary sexual characteristics to signal quality and promote female choice [1]. However, there is little, if any, evidence to support this theory in male-male competition breeding systems. Using white-tailed deer (*Odocoileus virginianus*) as a model species, we manipulated antler size (Fig. 1), body size and age of bucks while controlling for other allometrically related traits and allowed estrus does the opportunity to choose between pairs of segregated bucks with large or small antlers, large or small body size, and old or young age. Segregating bucks removed intrasexual male competition and isolated the effects of female choice. Using various behavioral indications of female choice [2], we demonstrate that does prefer bucks with large antlers to those with small antlers (P = 0.002). Surprisingly, does display no preference for body size (P = 0.645) or age (P = 0.356). Because antler size is heritable in deer [3], this female preference for larger antlers may be adaptive by increasing the reproductive success of her male offspring. Our unique antler manipulation study supports antlers functioning as ornaments to females in male-male competition breeding systems.

**Figure 1.** Schematic representing antler manipulation.

![Antler manipulation schematic](image)

**References**

In 2007, U.S. trade rates due to economic growth of developing countries, combined with tight global grain supplies, resulted in record high prices for corn and other food/feed grains [1]. The higher corn prices have motivated farmers to increase corn acreage at the expense of other crops and native habitat [1]. With corn prices nearing record highs, farmers are more likely to use more land for corn crop production, causing habitat loss for wildlife. Overtime, land has been converted into highly cultivated landscapes, a land area with >80% agricultural land, which can negatively affect the wildlife that once inhabited the area. Alterations to the environment cause patches to develop, making it difficult for wildlife to find the appropriate cover needed. Cover is not the only thing lost during landscape transition, but the development of irrigation systems can cause water availability to become scarce. Water table levels in Nebraska over the past few years have dropped 10-15 feet, in some areas and as much as 15-25 feet. South of Kearney NE, where this study is taking place, the water table has dropped about 10-15 feet [3]. As the seasons transition from growing corn and heavy irrigation to a drastic change in habitat when corn is harvested, and irrigation has stopped, it makes it harder for animals to find certain resources. These changes may be causing a push for these animals to move to other locations where resources, such as water, is more readily available. In landscapes dominated by agricultural production, deer movements and migrations are influenced by extrinsic forces, such as changes in weather, food availability, and vegetation structures [2]. During this study, we plan to investigate the movement patterns and habitat use of white-tail deer over the changing seasons. This information will help population management by providing valuable information on deer movements and habitat use in an intensively cultivated landscape, which is currently lacking.

References
White-tailed Deer Conservation and Management in the United States of America

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The white-tailed deer is the most widely distributed and recreationally hunted large mammal in the United States. It is present in 46 of 50 states and provides many billions of dollars in recreational value and financial support to management agencies via sale of hunting licenses. Management focuses on optimizing recreational harvest while considering conflicting land uses and human safety. Management goals and intensity of effort vary greatly by state and landowner, but include: 1) male-biased harvest, which leads to a young male age structure and unbalanced adult sex ratio, 2) quality deer management, which includes protecting younger males, and 3) trophy management, which includes protecting males until maturity. Antler-based harvest restrictions are a widely used regulatory approach to protect younger males from harvest. Interest in habitat management and/or providing supplemental nutrition increases with management intensity. Harvest rate of females is a function of management goals, regional soil quality, land use, and predator communities. Human safety concerns in urban areas related to vehicle-deer collisions and prevalence of Lyme Disease increase interest in density reduction. The expansion of Chronic Wasting Disease across much of the United States complicates management efforts.
White-tailed Deer Management Challenges in Mexico

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White-tailed deer represents a huge income in terms of hunting and recreation enterprises, especially in northern Mexico. However, the cultural, ecological and technological issues in different regions in Mexico have a different effect on conservation and management of the species.

Most of the 14 white-tailed deer subspecies are located in central and south regions of Mexico where poverty is more accentuated. Additionally, the northern Mexico region has acquired more experience in terms of population and habitat management techniques for white-tailed deer because of the proximity of the United States and the fact that some of the white-tailed deer subspecies are sharing distribution ranges between USA-Mexico borders.

This is the case of Texas white-tailed deer which is present on most of the southern part of Texas and northeastern Mexico represented by the states of Coahuila, Nuevo Leon and Tamaulipas. Even when white-tailed deer conservation and management in northeastern region is more advanced as compared to western states in northern Mexico, gaps of knowledge exist in conservation and management of the species.

At the national level, Mexico possesses wildlife management units called UMA´s, which is wildlife utilization scheme that promotes conservation, management and proper level of harvest of game species. However, this scheme has been criticized because it does not consider the proper space scale of management to avoid the “tragedy of the commons”, especially in very small UMA´s.

The lack of use of ecological sound management techniques such as prescribed fire has been underestimated to improve the habitat for white tailed deer. In this regard, in the United States, the use of fire as ecological tool has been used for many years as habitat management technique for multiples species of wildlife. However, in Mexico, the prescribed fire has not been used extensively and it is being used just as prevention of wildfires without specific goal for game species management and, the time of utilization is restricted to fall and winter seasons. The validation of this technique in different ecoregions such as Chihuahuan desert, Sonora desert and Tamaulipan thornscrub must be evaluated to know the effect of this tool to improve white tailed deer habitat.

Another important issue that is threatening the conservation of native genetics of white tailed deer subspecies, especially in northeastern Mexico is the fact of the introduction of “northern blood lines” as a strategy to improve the B&C scores, and thus, losing the native genetic of WTD subspecies. Mexico have tremendous opportunities to use management techniques to improve white-deer conservation and management and to promote the sport hunting heritage in North America.
References


White-tailed Deer Neonate Survival in the Functional Absence of Predators

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Survival and cause-specific mortality of neonate white-tailed deer has been the focus of recent research, particularly in regards to predation mortality. An understanding of the true impact of predation on survival rates requires a predator-free population to serve as a control. We captured 109 neonates using opportunistic capture (n = 55) and vaginal implant transmitters (VIT; n = 54) in Sussex County, Delaware, USA during 2016 and 2017 (Fig. 1). Predators (i.e., black bear, bobcat, and coyotes) were functionally absent from the study area. We calculated 30-day survival using a Kaplan-Meier estimator and determined the importance of covariates on survival using Cox proportional hazard models. The overall 30-day survival estimate was 0.61 (95% CI = 0.51 – 0.72). The survival estimates for neonates captured using random searches (0.76) was greater (P < 0.01) than those for VIT neonates (0.53; Table 1). Natural causes (n = 34) accounted for all of our observed mortality, including one potential predation by red fox. The top supported models included covariates for birth weight, doe maturity, and precipitation (Table 2). Survival estimates for the functionally predator-free study area were comparable to those found in other studies where predators were present and predation was identified as the primary source of mortality. Predation could be less of a limiting factor for survival than many studies have suggested. Data derived from opportunistically captured neonates may inflate estimates of survival and misrepresent cause-specific mortality due to inobservance of early-life mortalities [1,2]. Although the influence of birth weight on survival has been reported previously [3,4], the impact of doe maturity and precipitation has not been readily documented in this environment. The current emphasis on predator management and the impact on deer abundance in this ecosystem may be misplaced.

Table 1. Survival estimates by capture method for 30, 60 and 90-day survival of neonates in Sussex county, Delaware, USA.

<table>
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<th>Survival Window</th>
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<tr>
<td>90 Days</td>
<td>Random</td>
<td>0.69</td>
<td>0.08</td>
<td>0.55 - 0.87</td>
</tr>
</tbody>
</table>
Table 2. Cox proportional hazard model ranking for neonates in Sussex county, Delaware, USA.

<table>
<thead>
<tr>
<th>Model</th>
<th>AIC</th>
<th>ΔAIC</th>
<th>AICw</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth Weight + Doe Maturity</td>
<td>184.03</td>
<td>0.00</td>
<td>0.36</td>
</tr>
<tr>
<td>Birth Weight + Precipitation</td>
<td>185.54</td>
<td>1.51</td>
<td>0.17</td>
</tr>
<tr>
<td>Birth Weight</td>
<td>185.55</td>
<td>1.53</td>
<td>0.17</td>
</tr>
<tr>
<td>Birth Weight * Minimum Temp</td>
<td>186.67</td>
<td>2.65</td>
<td>0.10</td>
</tr>
<tr>
<td>Birth Weight + Minimum Temp</td>
<td>187.42</td>
<td>3.39</td>
<td>0.07</td>
</tr>
<tr>
<td>Birth Weight * Precipitation</td>
<td>187.55</td>
<td>3.52</td>
<td>0.06</td>
</tr>
<tr>
<td>Global</td>
<td>188.69</td>
<td>4.67</td>
<td>0.04</td>
</tr>
<tr>
<td>Precipitation</td>
<td>190.91</td>
<td>6.88</td>
<td>0.01</td>
</tr>
<tr>
<td>Doe Maturity</td>
<td>191.28</td>
<td>7.25</td>
<td>0.01</td>
</tr>
<tr>
<td>Precipitation + Minimum Temp</td>
<td>192.54</td>
<td>8.51</td>
<td>0.01</td>
</tr>
<tr>
<td>Precipitation * Minimum Temp</td>
<td>192.58</td>
<td>8.55</td>
<td>0.01</td>
</tr>
<tr>
<td>Null</td>
<td>192.86</td>
<td>8.83</td>
<td>0.00</td>
</tr>
<tr>
<td>Minimum Temp</td>
<td>194.59</td>
<td>10.56</td>
<td>0.00</td>
</tr>
<tr>
<td>Birth Weight* Precipitation *Minimum Temp</td>
<td>195.08</td>
<td>11.05</td>
<td>0.00</td>
</tr>
</tbody>
</table>

References
White-tailed Deer Population Recovery in Private Lands in Mexico

J. Alfonso ORTEGA-S. and Jorge G. VILLARREAL G.

1Caesar Kleberg Wildlife Research Institute, Texas A&M University-Kingsville
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White-tailed deer was almost extinct in Mexico in the 1970’s because of excessive harvesting and other problems like the screwworms. One of the major challenges for wildlife sustainability in general is the impact of the growth of the population on the environment; most of the landscapes in Mexico have been modified to be used by humans. Habitat deterioration and fragmentation is one of the most important problems for wildlife sustainability. Approximately, 70% of the country shows some level of desertification and 50% of the original plant communities have been lost. Introduction of exotic grasses such as buffelgrass (*Pennisetum ciliare*) to improve forage productivity for feeding domestic animals is an activity that negatively affects habitat for wildlife species. However, introduction of exotic grasses will continue for as long as livestock production remains an important economic activity. Information to determine the middle point to optimize cattle production and wildlife is necessary to implement management programs to achieve this objective. Some examples of successful habitat and wildlife restoration in cattle operations include the case of the “Cuenca Palo Blanco” in the state of Nuevo Leon, Mexico, where owners of 130,000 ha comprised of 51 management units were organized to manage habitat, cattle, and wildlife with specific objectives and have shown excellent results. The awareness of the importance of wildlife conservation in Mexico has increased, however, education efforts focusing on land owners, managers, wildlife professionals, as well as politicians and government employees that participate in policy development and wildlife conservation decisions is crucial. Natural resources education from elementary to high school need to be considered in education programs to develop conservation principles in the new generations. The need for wildlife professionals is unquestionable, one of the main reasons for this is the lack of institutions offering degrees in wildlife management, some universities in the country in an attempt to solve this problem offer some specific courses in wildlife management, which is good but not enough. In terms of generation of knowledge, many of the basic questions pointed out by Leopold in the 50’s still valid especially in tropical regions even when in the last 25 years the understanding and interest for conservation and sustainable wildlife management has increased dramatically. Groups of researchers in different areas of the country continue working on specific regional problems on wildlife management and the efforts to build strong relationships among institutions to solve common problems are commendable, however, a stronger and stable support is needed to consolidate these relationships.
Wildlife Governance and Venison Sharing: Coupling Humans and Nature

John F. Organ, U.S. Geological Survey, Cooperative Fish and Wildlife Research Unit Program, Reston, VA; Shawn J Riley, Department of Fisheries and Wild, Michigan State University; Göran Ericsson, Department of Wild, Fish, and Environmental Studies, Swedish University of Agricultural Sciences, Sweden; Amber D. Goguen, Department of Fisheries and Wildlife, Michigan State University; Shane Mahoney, Conservation Visions, Canada

Wildlife governance, the totality of processes used in governing, whether undertaken by a government, market or social network used to guide human activities involving wildlife resources, takes various forms across the planet. One aspect of wildlife governance – the laws, policies and regulation affecting the exchange of wild-harvested deer meat (venison) – reflects broad differences in governance models across the planet. Hunting for deer throughout the world, and the yield of wild-harvested venison, has provided ecosystem goods and services for millennia. Yet, these goods and services are in many cases unrecognized, unquantified, or largely ignored. To set the context for the special session on wild-harvested venison, we will review recent evidence from Europe and North America that suggests venison is a coupler of humans to nature across cultures and lifestyles, urban and rural. We will review and compare the extent of venison sharing and consumption, and the effects of this immense biomass of legal, wild-harvested venison on societal connections to hunters, hunting, and nature. We provide an overview of formal commercial markets and informal non-commercial vehicles for sharing venison derived from legally-hunted deer, and explore differences in governance systems and their effect on how venison moves through society, hunters’ sharing of wild-harvested venison, and potential implications to conservation. Finally, we provide a framework for considering wild-harvested venison as a coupler of humans and nature.
Wildlife Park Oleniy: Reproduction and Management of Cervidae in Central European Russia

Eugene Yu. Likhatskiy, Yuri P. Likhatskiy, and Andrey E. Subbotin*, Wildlife Park «Oleniy», Krasnoye

Wildlife Park Oleniy (WPO) is a privately owned 1,500 ha area established in 2012, that lies 400 km south of Moscow. The goal of WPO is to sustain and manage the entire zonal ecosystem of feather-grass steppe and associated agricultural land.

There are five species of wild ungulates in WPO: red deer (*Cervus elaphus*), roe deer (*Capreolus capreolus*), sika deer (*Cervus nippon*), fallow deer (*Dama dama*), and European mouflon sheep (*Ovis musimon*). Only red and roe deer are native.

Since 2012, the abundance of all 5 species has increased three to five-fold. There are three main objectives of ungulate management in WPO:

1. Creation of a genetic reserve of red deer with high trophy quality to preserve their unique gene pool. At present, this part of Russia contains a genetically isolated and rather highly polymorphic group of the red stag that originated from the Voronezh region. Our studies showed that deer from the Voronezh region have rare genetic variants that have been lost in Western Europe, where mixed lineages have prevailed for the purpose of meat production. It is these deer possessing unique genetic characteristics that should serve as source stock for the further restoration of this species. Conservation of this genetic reserve provides for replenishment of the group with the translocation of animals of only “Voronezh” origin, breeding work with the herd and the formation of the optimal sex-age ratio.

2. Development of high-quality reindeer stock for translocation in hunting areas. This source stock will serve as a resource for hunting and for the restoration of self-sustaining populations of this species into suitable habitat. Over the past three years, more than 500 individual ungulates from WPO have been translocated in the hunting grounds of Central Russia. The work on the restoration includes the development of methods for catching, overexposing, transporting and releasing animals into a new habitat.

3. Translocation of a group of sika deer to WPO and development of a velvet production center at WPO. This sika facility will require the development of a scientific program that provides facilities for the full cycle of activities related to the collection of velvet raw materials (antlers and blood), methods for handling animals, the ability to store selected raw materials, and the processing methods to allow the entire complex of biologically active substances to be preserved until the production of products can be accomplished with further certification.

Further increasing the number of individuals of each species at WPO along with the objectives mentioned above should open the prospect for the beginning of wild meat production. However, a stable market is needed, which today remains quite unpredictable in Russia.