

TENNESSEE ELK RESTORATION PROJECT

26 August 2005

by

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USE OF POPULATION VIABILITY ANALYSIS TO IDENTIFY MANAGEMENT PRIORITIES FOR ELK REINTRODUCTION IN THE CUMBERLAND MOUNTAINS OF EASTERN TENNESSEE

Given high rate of annual mortality, it is prudent to examine stocking strategies to maximize the state's elk restoration program. We demonstrate how population viability analyses can be used to determine where best to invest manpower and money towards a successful restoration effort based on scientific data. As of January 2005, there have been 62 mortalities reported, with 55 transmitters censored (worn spacers, uncollared animals, transmitter malfunction). These data were analyzed with the Kaplan-Meier method of estimating survival. Results indicate an annual survival rate of 0.79 (annual mortality = 0.21). We found no significant separation of mean survival rates (Wilcoxon's rank sum test) between releases (3 groups, SE = 28.50, 2 df, $p = 0.478$), sexes (SE = 47.28, 1 df, $p = 0.297$) or age classes (3 age classes, SE = 66.68, 2 df, $p = 0.074$). Annual survival increases to 81% if deaths within the first 6 weeks post-release are ignored in the analysis.

We used Vortex 9.42 Population Viability Analysis Software to simulate population growth based on actual mortality data from the elk herd in eastern Tennessee and multiple stocking and reproductive scenarios based on elk herd demographics in scientific literature. In simulations based on current mortality rates and reproduction levels estimated by pregnancy rates at the time of release (79%), the data suggest a rapid decline in population levels resulting in herd extinction in 36–45 years. In simulations that included optimistic reproductive parameters (e.g. high percentage of twinning, high reproductive rates) results indicated stagnant population levels with no long-term growth. Results were similar in simulations with supplemental stockings of 200 and 400 individuals. However, in simulations where mortality is decreased by 25% simulations indicated positive population growth without supplemental stockings. This reduction in mortality is plausible through increased law enforcement efforts given that 8 of 62 known mortalities are known cases of poaching, with a high likelihood that several of the animals with unknown causes of death (26 of 62 deaths) were also killed illegally. Given the results of our analyses, we believe that further efforts at increasing herd size through labor-intensive translocation to be ineffective. Instead, we suggest that efforts be focused on reducing mortality by curtailing poaching and improving habitat in the restoration zone.

GENETIC RELATEDNESS AND SOCIAL STRUCTURE

The goal of this research is to determine the relationship between genetic diversity and post-release social structure of reintroduced elk in the Cumberland Mountains of Tennessee. In reintroduced populations of elk, post-release social structure will affect the

genetic variability of subsequent generations because spatial configuration of sub herds in relation to natural features will impact dispersal ability of males, and subsequently affect gene flow. Captive and reintroduced populations are especially susceptible to genetic bottlenecks resulting from low numbers of source animals and potential demographic influence on gene flow after release. Therefore, it is important to determine how social structure stabilizes in newly established populations. Combined with information on genetic diversity, social structure analysis will inform managers' decisions on selecting source populations for other future repatriation and restoration projects for cervids with regard to genetic diversity. I predict that there is greater genetic diversity among social groups than within due to female philopatry, and that genetic diversity will increase with distance between locations of sub herds.

Lack of allelic diversity may hinder elk restoration efforts; low levels of genetic diversity in early generations of can produce founder effects (e.g. decreased individual fitness, decreased adaptations to environmental or biological perturbations, higher probability of extinction. For example, in the recent reintroduction of elk to eastern Tennessee, meningeal worm (*Parelaphostrongylus tenuis*) has been implicated as a significant source of mortality for reintroduced animals. In this case, translocated elk came from a single population in Elk Island National Park (EINP), an area where meningeal worm is non-endemic. Furthermore, this source population originated from a small herd of about 20 animals that were enclosed in a 19,400 ha park and were allowed to reproduce beginning in 1906. It is possible that resistance to meningeal worm infection is hereditary, but low genetic variation in the new population may affect resistance to the parasite.

Prior to release, whole blood samples were collected from all elk to be released and were subjected to genetic analysis using 16 microsatellite markers by Wildlife Genetics International, Inc. (Nelson, British Columbia, Canada). Originally, these genetic data were intended for law enforcement use by the Tennessee Wildlife Resources Agency (TWRA) for determining whether samples of meat confiscated from suspected poachers came from reintroduced animals. However, these data present a unique opportunity to describe baseline genetics of released elk. I will calculate allelic heterozygosity to infer genetic diversity of the elk introduced to Tennessee and to serve as baseline information for future genetic analyses after a period of natural reproduction and possible supplemental releases in the future.

I will employ isolation by distance analyses and allele frequency analysis in the program STRUCTURE to establish baseline genetic diversity information for the translocated animals in Tennessee. It is likely that post-release social groups are a result of genetic relatedness, in that family groups were captured together at source herd locations and remained together after transport to the elk restoration zone and subsequent release. Therefore, genetic clustering should reveal distinct genetic structure at the local scale among sub-herd groupings of elk. I will also utilize genetic clustering algorithms in the program STRUCTURE to assign individuals to genetic populations. For this analysis, I will infer population structure by probabilistically assigning individuals to groups based on microsatellite genotype data. If genetic relatedness affects post-release

social structure of elk, spatial clusters (observed sub herds of elk) will be similar to genetic clusters determined via microsatellite analysis.

LANDSCAPE-SCALE HABITAT MODELING

I am currently investigating several potential predictive habitat modeling techniques from the literature, including classification and regression trees (CART), Mahalanobis distance statistic, ecological niche modeling, and genetic algorithm rule set prediction (GARP). An example of a favorable technique is Mahalanobis Distance Statistic (D^2). The technique has recently been used successfully to predict black bear and elk habitat in Arkansas, Northern saw-whet owl habitat, and the occurrence of rare plant species. A major advantage of the technique is that it requires no arbitrary 'absence' points, and only uses telemetry location to predict habitat. Mahalanobis distance is a measure of dissimilarity between a set of 'ideal' habitat characteristics as defined by, for example, telemetry locations and a set of sample habitat characteristics within pixels of GIS coverages (Clark et al. 1993). With decreasing values of D^2 a greater degree of similarity exists between that pixel and the 'ideal' habitat conditions as defined by telemetry locations. The habitat model will be developed from a suite of variables that have been suggested as important to elk ecology in recent literature and variables that may be unique to land use on the study area. A preliminary list of potential habitat variables follows.

Variable Type	Variable Name
Topographic	Elevation
	Slope
	Aspect
	Landform index
Land Cover	Forest connectivity
	Forest area density
	Landscape pattern types
	Land cover interspersions/juxtaposition
	Land cover diversity
Anthropogenic	Distance to edge
	"U-index"
	Road proximity
	Road density

Land Use

Mine proximity

SEX-BIASED BEHAVIOR IN FOOD HABITS

Currently, the University of Tennessee is investigating the diet and availability of food species for reintroduced elk (J. L. Lupardus, *unpublished data*). However, there exists the possibility that the sexes select forage differently. Recent advances in radioimmunoassay techniques may allow the determination of an individual's sex from unknown fecal samples that have been recently used to test dietary composition. If possible, sex-specific food plot and habitat management recommendations can be made.

To this end, we have begun field seasonal fecal collection from known sex and age classes of animals at USDA Forest Service Land Between the Lakes, Golden Pond, Kentucky. We will soon begin isolating sex steroids from the fecal samples, and use radioimmunoassay to assign sex based on hormone composition of the samples. If successful, the technique will be repeated with unknown-sex samples used to investigate diet. The resulting data will be used to test for differences in seasonal and overall diet composition and used to inform food plot and habitat management efforts in the elk restoration zone.

DIET USE AND FORAGE AVAILABILITY

Sampling Area

A sample area was delineated within the Royal Blue Wildlife Management Area (RBWMA) using location points ($n = 1450$) of radio-collared elk gathered through aerial telemetry from February 2001 to June 2003 to develop a herd home range. The core sampling area was chosen because of the size, abundant elk activity, and concentration of data points needed for effective habitat sampling. All location points for individual animals were censored from analyses if radio contact was lost, the collar was found dropped, or if the collar was found on a dead elk. We estimated 95% and 50% fixed kernel group home ranges using the Animal Movement Extension in Arc View 3.2[®] (ESRI, Redlands, California). The 95% and 50% fixed kernel home ranges covered 7,100 ha and 789 ha, respectively. The 50% fixed kernel home range was located in the southern part of RBWMA, encompassing the Montgomery Fork Creek area; it represented a statistical center of activity for the elk. The 50% kernel home range was used as the core sampling area, and it included 70% of the entire monitored elk herd ($n = 63$; 17 males and 46 females).

Vegetation Sampling

We determined major habitat types in the core area using 1995 land cover maps developed by TWRA. The major cover types located within the core group home range were deciduous forest and grassland. An additional cover type called “edge” was added. The importance of elk use of edge areas has been documented; therefore we incorporated this component into our analysis to ensure effective habitat analysis. A buffer distance of 10-m around fields, unimproved roads, improved roads, and grasslands was used as the edge-cover type.

We conducted preliminary sampling ($n = 23$, $\sigma^2 = 34.51$) in summer 2003 to determine the necessary sample size to distinguish significant differences at $p \leq .05$. Preliminary data, constraints from logistics, and sampling costs determined the quantity of vegetation plots ($n=150$). We randomly placed these points throughout the three major cover types. The proportional area of the cover types was used to derive the number of sampling points distributed within each. Vegetation sampling was conducted from November 2003 to October 2004. Square 1-m² samples were taken 5 m from plot center in the 4 cardinal directions, and all forbs, grasses, and seedlings within each 1-m² sample were recorded. Saplings and shrubs (1 to 2m height) were recorded in a 10-m² square plot surrounding plot center, and basal area was recorded at each plot.

Microhistological Analysis

We collected fresh elk scat during vegetation sampling from November 2003 to October 2004. We collected 30 groups of scat during each season (120 samples per year). All pellet samples were sent to the Habitat Lab at Washington State University (Pullman, Washington, USA) for microhistological analysis of plant cells to derive a composite seasonal elk diet. Plants in the diet were described to species if possible.

Analysis and Results

We used analysis of variance for a repeated measures design to test plant availability means (independent variable) against the repeated fecal sample means (n=30) to determine significant differences ($p \leq .05$). Tests between forage availability and diet composition were based on linearly independent pairwise comparisons among the estimated means each season. Positive mean differences represent plants used in less proportion to availability, and negative mean differences represent plants used in greater proportion to availability (preferences).

Winter

The lowest diversity of plants found within the diet for all seasons was winter (n=45). Grasses (65.9%) were the dominant forage class (Table 1). We believe that elk were using any available green forage in the area. The most frequently consumed grass overall was tall fescue (*Festuca arundinacea*; 35.1 %). Fescue was highly preferred during winter because it was the only species available in large quantities, however nutrition may be limited for tall fescue. Christmas fern (*Polystichum acrostichoides*; 12%) dominated the fern diet composition (13.1%), however it was not found to be significantly used when compared to its widespread availability. The largest, significant negative mean difference (-7.82) found in the diet was big bluestem (*Andropogon gerardii*).

Spring

The diet shifted in the spring to a mixture of woody plants (28.1%) and forbs (19.4%), however grasses (38.4%) were the dominant forage class. Autumn olive (*Elaeagnus spp.*) was found significant with the largest negative mean difference (-10.06). Sedges/rushes (*Carex/Juncus spp.*) were the most frequently used (12.7 %) grasses, and sedges/rushes were found significant. Jewelweed (*Impatiens spp.*) was the only forb found significantly in the diet with a mean negative difference.

Summer

Forb use increased to 45% in the summer, and legumes (23%) were a large forage component of the diet. Our results suggest that jewelweed (27%) was a highly valuable plant utilized by elk during summer. Elk use succulent and nutritious vegetation (e.g., forbs, legumes) during calving and the subsequent neonatal period. Briars (*Rubus spp.*) and maples (*Acer spp.*) were significantly found to not be selected by elk.

Fall

The dominant forage class was woody plants (37.4%) with oaks (14.3%) being the most used woody plant. Elk viability in the deciduous forest may be somewhat dependent upon the hard mast crop. Acorns composed only 9.7 % of the fall diet, but the nutritional value from this food source probably was substantial. Interspecific competition for acorns may influence populations of other species. Food consumption for 1 adult elk is equivalent to that of 3 white-tailed deer.

Conclusions

Much emphasis is placed upon intensively managing small food plots to provide additional sources of nutrition for animals in the winter, but our findings suggests on a nutritional basis that spring, summer, and fall forages are more important than winter forages in limiting elk populations. Attention should be focused to manage forages for all seasons over a broader scale using landscape level techniques (e.g., silviculture, prescribed burning). The conversion of monocultures of tall fescue and lespedeza to more diverse, palatable, and nutrient rich forages is desirable. Elk herbivory and interspecific competition for key resources (e.g., acorns) should be monitored. Future research is necessary to determine the effects of elk upon the flora and fauna in deciduous forests.

Table1. Mean differences between available forage and composition of elk diet (\bar{x} % \pm SE). Diet composition determined from microhistological analysis of plant material in feces, November 2003 to October 2004, Royal Blue Wildlife Management Area, Tennessee, USA.

Plant Taxa	Winter (n=30)			Spring (n=30)			Summer (n=30)			Fall (n=30)		
	\bar{x} (%)	SE	\bar{x} difference ^a	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference
Woody Plants												
Acer spp.	0.2	0.14	3.25 *	0.4	0.10	5.47 *	0.2	0.04	6.18 *	0.7	0.54	5.28 *
Aralia spinosa	0.1	NA	-7.82 *	0.2	0.16	-0.18	0	NA	NA	0.0	NA	NA
Betula lenta	0.0	NA	NA	1.0	0.41	-1.02	1	0.70	-0.67	0.0	NA	NA
Carya spp.	0.5	0.31	-1.86 *	0.3	0.12	0.31	0.2	0.12	0.38	0.1	0.05	1.34
Ceanothus spp.	0.3	0.05	-0.29	0.6	0.33	-0.18	0	NA	NA	0.2	0.13	0.36
Celtis spp.	0.1	0.04	-0.29	0.0	NA	NA	0	NA	NA	0.0	NA	NA
Cercis canadensis	0.2	0.23	-0.61	0.4	0.13	0.48	0.3	0.25	0.34	0.7	0.30	-0.47
Cornus florida	0.1	0.03	-0.05	0.0	NA	NA	0.8	0.46	-0.79	0.6	0.29	-0.50
Elaeagnus spp.	1.7	0.74	-1.81 *	9.7	1.82	-10.06 *	2.3	0.52	-2.35 *	8.7	2.50	-7.73 *
Fagus grandifolia	0.0	NA	NA	0.1	0.05	0.03	0	NA	NA	0.1	0.05	0.06
Fraxinus americana	0.0	NA	NA	0.0	NA	NA	0	NA	NA	0.3	0.33	-0.15
Ilex opaca	0.0	NA	NA	0.0	NA	NA	0	NA	NA	0.1	0.05	-0.04
Juniperus virginiana	0.0	NA	NA	3.2	1.12	-3.50 *	0	NA	NA	0.3	0.20	-0.30
Lindera benzoin	1.3	0.67	-1.47	0.3	0.21	-0.36	1.5	0.45	-1.59 *	3.9	0.95	-4.34
Liriodendron tulipifera	0.0	NA	NA	0.0	NA	NA	0.1	0.07	2.55 *	0.0	NA	NA
Magnolia spp.	0.0	NA	NA	0.1	0.07	0.07	0.1	0.07	0.13	0.5	0.20	-0.21
Oxydendrum arboreum	0.0	NA	NA	0.0	NA	NA	0.5	0.29	0.78	0.0	NA	NA
Pinus spp.	0.9	0.40	-0.99	2.0	0.71	-2.13 *	0.1	0.11	-0.14	0.3	0.24	-0.35

Table 1. Continued.

Plant Taxa	Winter (n=30)			Spring (n=30)			Summer (n=30)			Fall (n=30)		
	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference
Woody Plants												
Prunus spp.	0.4	0.13	-0.18	0.2	0.15	0.11	0.1	0.13	0.11	0.1	0.09	-0.80
Quercus Acorns	0.0	NA	NA	0.0	NA	NA	0	NA	NA	9.7	2.64	-6.72*
Quercus spp.	2.1	0.42	-0.79	3.4	0.94	-2.49 *	3.1	0.53	-1.57*	4.6	0.91	-3.34*
Rhododendron spp.	0.1	0.05	-0.41	0.9	0.43	-0.58	0	NA	NA	0.7	0.35	0.45
Rhus spp.	2.6	0.76	-1.29	0.1	0.09	2.99 *	0	NA	NA	3.5	1.04	-4.00*
Rosa spp.	1.5	0.25	-1.18	1.8	0.67	-1.67	0	NA	NA	0.1	0.04	0.05
Sambucus canadensis	0.1	0.06	0.12	0.0	NA	NA	0	NA	NA	0.5	0.17	-0.48
Sassafras albumin	0.1	0.07	0.50	0.0	NA	NA	0.5	0.27	1.17	0.0	NA	NA
Tilia americana	0.0	NA	NA	0.7	0.34	-0.69	0	NA	NA	0.0	NA	NA
Tsuga canadensis	0.0	NA	NA	0.1	0.05	-0.04	0	NA	NA	0.0	NA	NA
Vaccinium spp.	0.5	0.12	1.23	2.5	0.52	-1.16	0.5	0.21	0.55	0.7	0.17	0.75
Viburnum acerifolium	1.0	0.21	-0.57	0.1	0.07	0.29	0	NA	NA	1.0	0.42	-1.02
Unknown woody spp.	1.3	0.18	NA	2.2	0.25	NA	2	0.25	NA	3.1	NA	NA
<i>Total Woody Spp.</i>	<i>15.1</i>			<i>28</i>			<i>13</i>			<i>37.4</i>		
Forbs												
Allium	0.0	NA	NA	0.1	0.05	0.04	0.3	0.21	-0.29	0.0	NA	NA
Ambrosia spp.	0.0	NA	NA	0.1	0.06	-0.09	0.3	0.08	1.32	0.1	0.02	0.13
Antennaria spp.	0.0	NA	NA	0.2	0.14	-0.09	0.6	0.23	-0.59	0.1	0.14	-0.01
Arisaema triphyllum	0.0	NA	NA	0.0	NA	NA	0.7	0.24	0.08	0.0	NA	NA

Table 1. Continued.

Plant Taxa	Winter (n=30)			Spring (n=30)			Summer (n=30)			Fall (n=30)		
	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference
Forbs												
Aster spp.	0.0	NA	NA	1.2	0.35	-0.57	0.9	0.21	-0.43	0.3	0.11	0.60
Centrosema virginianum	1.1	0.30	-1.01	1.1	0.45	-0.19	2.6	0.70	-0.59	1.4	0.37	-0.06
Chamaecrista fasciculata	0.0	NA	NA	0.8	0.28	0.06	0	NA	NA	0.0	NA	NA
Chenopodium album	0.0	NA	NA	0.1	0.09	-0.14	0	NA	NA	0.2	0.24	0.11
Erigeron annuus	0.0	NA	NA	0.2	0.14	-0.07	0.6	0.21	-0.37	0.0	NA	NA
Euonymus americana	0.2	0.06	0.72	0.7	0.35	0.02	0.7	0.22	-0.03	0.5	0.26	0.21
Galium spp.	0.0	NA	NA	1.0	0.40	1.28	0.9	0.27	-0.25	0.1	0.05	0.24
Geranium maculatum	0.0	NA	NA	0.9	0.28	0.15	1.5	0.26	-1.47	0.1	0.08	-0.12
Helianthus spp.	0.0	NA	NA	0.0	NA	NA	0.8	0.23	4.32*	0.0	NA	NA
Heuchera spp.	0.0	NA	NA	0.0	NA	NA	0.1	0.09	1.15	0.0	NA	NA
Impatiens spp.	0.0	NA	NA	7.9	2.61	-4.56 *	27	3.65	-24.15*	0.0	NA	NA
Ipomoea spp.	0.2	0.15	-0.36	0.1	0.07	-0.11	0	NA	NA	0.1	0.12	-0.09
Lathyruss pp.	0.6	0.23	-0.48	0.0	NA	NA	0.5	0.21	0.06	0.1	0.10	0.26
Mitchella repens	0.9	0.34	-1.02	0.0	NA	NA	0.2	0.09	-0.14	0.9	0.40	-3.25*
Monarda spp.	0.0	NA	NA	0.0	NA	NA	0.2	0.19	-0.03	0.0	NA	NA
Phytolacca americana	0.2	0.17	0	0.0	NA	NA	0.5	0.26	0.69	0.0	NA	NA
Potentilla spp.	0.0	NA	NA	0.5	0.22	0.818	1	0.45	0.05	0.2	0.09	0.64
Rubus spp.	0.5	0.28	21.17 *	1.0	0.23	2.99 *	1.3	0.40	10.88*	1.4	0.20	10.16*
Smilacina racemosa	0.0	NA	NA	0.6	0.26	1.32	0.1	0.08	0.93	0.0	NA	NA

Table 1. Continued.

Plant Taxa	Winter (n=30)			Spring (n=30)			Summer (n=30)			Fall (n=30)		
	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference
Forbs												
Smilax spp.	0.1	0.06	6.55	0.3	0.15	3.12 *	1	0.40	1.45	0.3	0.24	3.08 *
Solidago spp.	0.1	0.03	0.06	0.2	0.09	2.25 *	0.6	0.20	4.00 *	0.8	0.32	3.63 *
Vicia spp.	0.1	0.05	-0.06	0.3	0.14	-0.24	0.4	0.16	-0.37	0.0	NA	NA
Unknown forbs	0.6	0.18	NA	2.1	0.41	NA	2.5	0.29	NA	3.4	0.39	NA
<i>Total Forbs</i>	4.6			19.4			45			10.0		
Ferns												
Athyrium filix	0.5	0.21	-1.14	0.4	0.20	2.90 *	0.3	0.23	1.96 *	0.0	NA	NA
Polystichum acrostichoides	12.0	2.07	7.86 *	2.5	0.98	4.39 *	0.2	0.16	5.13 *	0.6	0.37	7.59 *
Unknown ferns	0.6	0.17	NA	4.3	2.01	NA	0.6	0.05	NA	0.4	0.19	NA
<i>Total Ferns</i>	13.1			7.2			1.1			1.0		
Grasses												
Andropogon gerardii	8.5	1.21	-7.82 *	4.6	1.05	-4.94 *	2.3	0.60	-2.35 *	2.4	0.69	-2.48 *
Carex/Juncus	1.4	0.24	2.76 *	12.7	3.09	-8.36 *	1.3	0.37	1.26	2.0	0.41	1.28
Dactylis glomerata	3.3	0.56	-2.98 *	2.5	0.61	-2.62 *	1.1	0.42	-1.19	1.2	0.49	-1.26
Echinochloa crusgalli	0.2	0.15	-3.75 *	0.0	NA	NA	0.4	0.36	-0.10	0.0	NA	NA
Festuca arundinacea	35.1	2.81	-5.59 *	10.7	1.85	2.75 *	5	1.16	4.71 *	10.8	2.34	8.82 *
Microstegium japonicum	0.0	NA	-0.44	0.0	NA	NA	0	NA	NA	0.1	0.12	3.25 *
Panicum virgatum	3.9	0.53	-1.52	1.0	0.28	1.59	0.5	0.23	2.72 *	1.0	0.31	2.41 *
Phleum pratense	2.3	0.61	-0.39	1.8	0.94	-1.79	0.5	0.27	1.07	0.9	0.33	0.39

Table 1. Continued.

Plant Taxa	Winter (n=30)			Spring (n=30)			Summer (n=30)			Fall (n=30)		
	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference	\bar{x} (%)	SE	\bar{x} difference
Grasses												
Schizachyrium scoparium	4.9	0.84	-4.88 *	1.4	0.42	-1.34	0.2	0.13	-0.10	1.1	0.37	-1.04
Setaria spp.	0.5	0.19	-0.65	0.2	0.11	-0.16	0	NA	NA	0.3	0.20	-0.29
Sorghum spp.	0.7	0.26	-0.87	0.9	0.24	-0.74	0.1	0.07	0.07	0.8	0.42	-0.87
Triticum spp.	3.5	0.73	-3.03 *	1.0	0.35	-0.55	0.9	0.37	-0.70	1.5	0.60	-1.34
Unknown grasses	1.6	0.18	NA	1.6	0.24	NA	1.7	0.33	NA	1.9	NA	NA
<i>Total Grasses</i>	65.9			38.4			14			24.0		
Crops												
Zea mays	0.0	NA	NA	0.2	0.14	-0.2	0.6	0.26	-0.68	0.6	0.26	-0.69
<i>Total Crops</i>	0.0			0.2			0.6			0.6		
Legumes												
Lespedeza spp.	0.2	0.13	-0.15	1.6	0.67	2.63 *	7.5	1.36	-0.90	12.8	3.47	-5.67 *
Trifolium & Melilotus spp.	0.3	0.10	3.97 *	2.4	0.84	0.66	15	2.73	-12.16 *	6.5	1.34	-4.98 *
<i>Total Legumes</i>	0.5			4			23			19.3		
Other												
Lichen/Moss	0.1	NA	NA	0.2	NA	NA	0.2	NA	NA	0.4	NA	NA
Insect	0.1	NA	NA	0.1	NA	NA	0.7	NA	NA	0.2	NA	NA
Unknown	0.6	NA	NA	0.2	NA	NA	2.5	NA	NA	4.0	NA	NA
Number of plants	45			57			55			54		

NA Not applicable because items (plants and insects) were not in the diet or unknown.

a Positive numbers represent plants used in less proportion to availability. Negative numbers represent plants used in greater proportion to availability.

* Significance ($p \leq .05$)