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(3) EVOLUTION AND DEVELOPMENT IN THE SPOTTED HYENA

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I will explore possible roles of external selection pressure and developmental constraint in shaping the evolution of novel patterns of behavior in mammals. Spotted hyenas (Crocuta crocuta) are long-lived, gregarious carnivores exhibiting a peculiar suite of traits that are sex-role reversed from mammalian norms; behaviorally, female Crocuta are more aggressive than, and socially dominant to, males. Here I will describe how my colleagues and students and I are testing two hypotheses suggesting explanations for the evolution of role-reversed behavior in female Crocuta. The first hypothesis suggests that female dominance and aggressiveness evolved to ensure adequate nutrition to lactating females and their dependent young during intense contest competition over food. The second hypothesis suggests that, rather than competition alone, a combination of two forces promoted the evolution of dominant, aggressive females in Crocuta; one involved external selection pressure imposed by intensive feeding competition as in the first hypothesis, and the other involved constraints imposed by slow or prolonged development of the complex feeding apparatus found in Crocuta and other bone-cracking hyenas. According to this second hypothesis, skull features that were superb adaptations in a solitary ancestor for scavenging effectively from large carcasses currently handicap young Crocuta during competitive feeding with conspecifics such that they need unusually high levels of maternal aid to feed on both soft and hard foods long after weaning. Thus aggressiveness and social dominance represent compensatory behavioral traits favored in mothers when development of the skull in offspring is refractory to selection pressure imposed by feeding competition. We are testing both these hypotheses with behavioral and morphological data. We anticipate that this research will ultimately teach us a great deal about the interaction of evolutionary forces promoting stasis with those promoting change.

(10) HOME RANGES AND ACTIVITY PATTERNS OF ENDANGERED DARWIN'S FOXES AND THEIR SYMPATRIC CONGENERS IN THE NAHUELBUTA MOUNTAINS, SOUTH-CENTRAL CHILE.

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Three canid species occur in the Nahuelbuta Mountains of south central Chile. One of them, the Darwin's fox, (or chilote; Pseudalopex fulvipes), is endemic to and endangered in Chile, and occurs in only one other location. The other two species, the grey fox (or chilla; P. griseus), and the culpeo fox (P. culpaeus) are found throughout Chile and neighboring countries. Because of the Darwin's fox's endangered status, we sought to identify differences in species behaviors that allow for coexistence. Thus, from September 1998 to May 2002 we gathered radio-telemetry data on the home ranges and activity patterns of 23 Darwin's foxes, 17 chilla foxes and 3 culpeo foxes within the 6,800-ha Parque Nacional Nahuelbuta (PNN). We plotted home ranges of both species on vegetation maps to estimate home range overlap within and among species, and to differentiate habitat selection among species. Seasonal activity patterns were estimated for comparison between species, sexes, and geographical area, as well. Preliminary analyses from 5079 independent activity readings for the Darwin's fox indicate that this species is nocturnal with low levels of activity between 7:00 and 18:00.

Daytime activity for male and female Darwin's fox increase during Fall/Winter. During Fall/Winter, foxes whose home ranges include areas outside the PNN have a higher daytime activity then those whose home ranges are restricted to PNN. Analyses of 3196 independent activity readings for chilla foxes indicate that this species is active throughout the day and night. Comparison of seasonal activity patterns indicates a drop in activity between 23:00 and 10:00 during Fall/Winter. Radio-collared culpeo foxes left the study area shortly after being collared and were only relocated after death, which occurred far outside the park. We were unable to determine home ranges and activity patterns for this species, but our findings indicate that their use of the park is limited.

(17) THE EVOLUTION OF POST-CRANIAL ECOMORPHS IN THE MUSTELIDAE

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A recent, comprehensive, molecular-based phylogeny of the Mustelidae allows for the mapping of ecological patterns within an evolutionary framework. The mustelids are a diverse group of mammalian carnivores, especially post-cranially, including semi-fossorial (badgers), arboreal (martens), terrestrial (wolverines) and aquatic taxa (otters), as well as elongate forms with bounding gaits (weasels). This study investigated possible morphological correlates of these locomotor styles by using a breadth of taxa across the mustelid family. The measures included simple vertebral counts as well as ratios of post-cranial measures that were thought to be functionally significant. Multivariate methods were used to explore these variables and find those that were best correlated with the primary locomotor mode of the taxa. These morphological indicators were then mapped to the phylogeny to determine the evolution of these traits, including polarity of transformations and the incidence of convergence across the family. Enhydra (the sea otter) is the most distinctive mustelid, with relatively long limbs, although it does group with other otters (Lutrinae). Both species of Martes used in this study (the fisher and the pine marten) do not group with other arboreal taxa, nor with their closest relatives, but with the similarly elongate Mustela (weasels). The evolution of locomotory styles is complex and driven both by phylogeny and ecology

(23) RANK-RELATED PARTNER CHOICE IN THE FISSION-FUSION SOCIETY IN SOCIETY OF SPOTTED HYENAS

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Biological market theory predicts that, when social partners vary in their relative value, choosy individuals should compete for partnerships with highly valued partners. In contrast to traditional optimality theory, it further predicts partner choice should be mutual because traders match assortatively within the biological marketplace. Here we tested these predictions in a wild population of spotted hyenas (Crocuta crocuta) in Kenya. Crocuta live in complex, fission-fusion societies structured by dominance hierarchies in which individuals vary greatly in their value as social companions. Because patterns of association among Crocuta reflect social preferences, we calculated Association Indices (AIs) to examine how social rank influences intrasexual partner choice among unrelated adult females. Highest-

ranking females were generally most gregarious. Females associated most often with dominant and adjacent-ranking females. Females joined subgroups based on the presence of particular conspecifics such that subordinates joined focal females at higher rates than did dominants. Dominants benefit from associations with subordinates by enjoying priority of access to resources obtained and defended by multiple group members, but the benefits to subordinates are unknown. To investigate this, we tested hypotheses suggesting how subordinate females might benefit from these associations by being harassed less away from food, better tolerated during feeding, and supported more often during coalitionary aggression by the higher-ranking females with whom they associate most often. We found support for the first two hypotheses, but not the third. Overall, our data resemble those documenting patterns of association among cercopithecine primates, and support the predictions of biological market theory.

(24) SEX, AGE AND SCENT IN THE SPOTTED HYENA

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An efficient communication system is a critical component of animal societies. In mammals, communication is often achieved via chemical signals that may convey information about the sender’s species, sex, age and individual identity, as well as social, reproductive and motivational condition. Previous research on the functions of mammalian scent-marking has often focused on marking by rodents, particularly adult males. Recent investigators have stressed that the functions of scent-marking vary not only between species, but also among age/sex classes within the same species. We investigated the functions of scent-marking (‘pasting’) in the spotted hyena, Crocuta crocuta. Specifically, we addressed the hypotheses that spotted hyena pasting functions in maintaining territories, advertising social status, male sexual advertisement, communicating female reproductive state, and facilitating recognition as a group member. We used naturalistic observational data to evaluate the social contexts in which pasting occurred, and conducted scent discrimination experiments with free-living hyenas in the Masai Mara National Reserve, Kenya. We confirm that pasting has a territorial function. Our results also suggest that pasting functions in communicating social status for adult males, although it does not appear to do so for adult females. We show that the frequency of adult male pasting behavior is not a predictor of reproductive success, and that adult females do not advertise sexual receptivity via pasting, although information about female reproductive state is clearly available in paste. Additionally, we found that, in contrast to captive female spotted hyenas, free-living adult females responded more strongly to scent from other adult females than from adult males. Lastly, we discuss preliminary evidence suggesting that frequent overmarking by spotted hyena cubs may facilitate their being recognized as group members before they are widely known as individuals.

(27) AN EVALUATION OF THE CURRENT DISTRIBUTION AND CONSERVATION STATUS OF THE EASTERN SPOTTED SKUNK (SPILOGALE PUTORIUS) IN KANSAS

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The eastern spotted skunk (Spilogale putorius) historically was reported as abundant or common throughout much of the central United States; however, three decades of population declines and limited records of recent occurrence present a need to confirm the current distribution and status of the species within the region. Our research focuses on the conservation issues that pertain to the biology, status, and distribution of the eastern spotted skunk in Kansas. At the onset of our research, our knowledge of the current distribution of the species was limited by a small number of recent voucher specimens and unsolicited sighting reports, which we used as a guideline for selecting our first field verification sites. In 2005, we confirmed the presence of the eastern spotted skunk in Cherokee County in southeastern Kansas, but failed to confirm the presence of the species at other locations within state. We selected the Cherokee County study site based on a voucher specimen from the past year; whereas, our other study sites were selected based on sighting reports from the past year. Because our efforts to confirm the presence of the eastern spotted skunk in all but one of our study areas were unsuccessful and study site selection was restricted to few widely separated locations, we solicited additional sighting information from several target groups. We will use the information from those reports for planning field verification sites and as a preliminary indication of the current distribution of the species within the state. Additional field studies are necessary to determine the distribution and population status of the eastern spotted skunk in Kansas.

(41) PRESERVING A PIECE OF THE PRAIRIE: PARTNERSHIPS ARE KEY FOR SWIFT FOX RESTORATION IN SOUTH DAKOTA

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For several decades, the swift fox (Vulpes velox), has experienced population declines throughout most of its range. Once numerous across western South Dakota, they are now listed as state threatened. A coalition of projects including a private landowner, the National Park Service (NPS), and two Native American Tribes are working independently, yet cooperatively, to restore the swift fox. In 2002, the Turner Endangered Species Fund (TESF) released the first cohort of 30 translocated swift fox. In 2003, the Badlands National Park (BNP) followed suit. The Lower Brule Sioux Tribe (LBST) has plans to conduct their first release in the fall of 2006. The Oglala Sioux Tribe (OST) is in the process of completing surveys to determine population status and the feasibility of releases within their borders. As individuals, each project has the potential to make a localized difference but together, managing over 2.2 million acres, they form a stronger whole that completes a broader, regional vision. As with many restoration projects, progress is often slow, yet important scientific and social milestones have been reached. Scientific milestones include documentation of second-generation foxes born in SD and confirmed dispersal between TESF and BNP and remnant SD populations. Our research has provided insights into the success of fox translocation techniques, patterns of fox dispersal, habitat selection, and has initiated four related graduate student projects. Meanwhile, ongoing education outreach and one-on-one landowner contacts have served to foster broad community awareness and support for swift fox, widely considered one of the deciding factors for the success of restoration efforts.

Conserving native species and their attending landscapes increasingly need to be conducted over large scales involving many partners. These efforts provide a valuable model on how groups with diverse backgrounds, but shared values can make a conservation impact.

(49) DIETARY RECONSTRUCTION OF CREODONTS AND NICHE OVERLAP WITH CARNIVORANS

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Living carnivores fill a range of dietary niches. However, “carnivory” is a broad term that masks a great deal of complex dietary variation. Identifying this kind of variation is important to understanding the ecology and interactions of extinct species. In this study, low-magnification dental stereomicroscopy was used to reconstruct the dietary ecology of creodonts, in order to learn about their biology and their place in fossil mammal communities. Creodonts are members of a taxon that is the extinct sister group to the Order Carnivora. To reconstruct diet, we compared the tooth wear of creodonts and fossil carnivorans to that of modern carnivorans. We made more than 100 molds of teeth with high-quality impression compound and used them to create epoxy resin casts which were examined under a stereomicroscope in order to observe the wear features. The averages of these counts directly reflect what an animal was chewing in its last days or weeks. Stereomicroscopy has proven to be a valuable tool to distinguish between different kinds of herbivory in extinct ungulates and primates, but had yet to be applied to creodonts. In this sample, we found a range of carnivorous niches in all species. Didymictis (Carnivora, Viverravidae) had heavy pitting and cross-scratching, which is associated with high amounts of grit or bone in the diet and with complex chewing; however, it also had puncture-pits, indicative of fruit in the diet. Hyaenodon (Creodonta, Hyaenodontidae) had intermediate levels of pitting and little to no cross-scratching, indicating mostly meat and bone with little variability in chewing stroke. Hesperocyon (Carnivora, Canidae) had the softest diet, with the lowest pitting and moderate cross-scratching.

(54) ACTIVITY PATTERNS OF TWO SYMPATRIC SKUNK SPECIES (MEPHITIS MEPHITIS AND SPILOGALE GRACILIS) IN TEXAS

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We used telemetry data to document and compare activity and movement patterns between Spilogale gracilis, the western spotted skunk, and Mephitis mephitis, the striped skunk, in west-central Texas. Mephitis mephitis had a higher rate of movement than S. gracilis. Both species had highest movement rates during fall, coinciding with dispersal of young. With the exception of summer, M. mephitis was significantly more active than S. gracilis and generally took shorter breaks during nightly activity. We documented statistical differences in activity patterns between the species for all seasons. The height in activity of one species occurred during the lowest activity of the other species, which may indicate avoidance of one species by the other. Spilogale gracilis may forage for shorter times due to increased foraging efficiency and smaller body size.

(59) A SHOT IN THE DARK: THE SEARCH FOR ACCURACY IN ESTIMATING SNOW LEOPARD ABUNDANCE

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Snow leopards (Uncia uncia) are an important cultural symbol and ecological component of the Central Asian Mountains, but habitat loss, poaching, and retribution killing continue to threaten their survival. Snow leopards' legendary camouflage and secretive nature historically have made their populations difficult to monitor, and conservation efforts are in need of dependable methods to estimate abundance. Here we assess the concordance of three methods for estimating snow leopard population size: camera capture-recapture estimates, standardized sign surveys, and predator-prey biomass ratios. Camera traps were used to capture 32, 12, and 1 snow leopard images, respectively, in three areas of varying environmental conditions in the Tien Shan Mountains of Kyrgyzstan and China. We identified individual snow leopards in photos by their unique pelage patterns and estimated population abundance using a capture-recapture statistical model. Densities in two study sites were 1.6 and 1.9 individuals/100 km2, and in the third study site one capture event limited our results to a minimum density of 0.2 individuals/100 km2. Average amounts of snow leopard sign (scats and/or scrapes) varied substantially (16-95/km searched), as did concurrent ibex (Capra ibex) counts used to estimate available ibex biomass (766-9,196 kg/100 km2) and thus potential snow leopard abundance (0.1-0.9/100 km2) ; however, neither estimator correlated with photo-trap estimates or with each other. Variance due to low capture rates, biased sign observations, limited sample size, or unknown environmental circumstances may have led to these inconsistent and unexpected results. Regardless of the reason, our results give no indication that any one of these three methods is accurate under short timeframes and standard operating conditions.

(70) REMOVAL OF MAMMALIAN PREDATORS REDUCES PREDATION RATE ON ARTIFICIAL BEACH-NESTS ON THE VIRGINIA BARRIER ISLANDS

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Do islands on which mammalian predators have been reduced provide more secure beach-nesting habitat than untreated islands? Does predation management reduce overall “predation intensity” on the eggs of beach-nesting birds? We ran a study to estimate “predation intensity” on eggs in artificial beach nests (scrapes) on two of the Virginia (U.S.A.) barrier islands. We compared predation intensity on scrapes on (1) predator-removal (Metompkin) and control (Parramore) islands in August 2003 and (2) on Parramore Island before (2003) and after

(June-July 2004) an intensive predator removal campaign. On each island, we established 100 artificial scrapes at randomly-selected points along a 4-km transect oriented parallel to the beach face and located above the high tide line. Each scrape was stocked with a “clutch” of 2 eggs, including 1 Japanese quail egg and 1 clay (Plasticene) egg. Each nest was monitored and restocked daily for 4 days. Metompkin was thought to be free of raccoons (Procyon lotor) and red foxes (Vulpes vulpes) in 2003, while Parramore harbored large numbers of both species. Mammalian predation rates on these unattended nests were vastly higher on Parramore (~99% per day) than on Metompkin (~0%). Nevertheless, gulls and ghost crabs depredated ~19% of the nests per day on Metompkin in the absence of mammalian predators. We repeated this trial in June and July 2004, using the same artificial nest stations. Metompkin harbored 1-2 raccoons at this time, while Parramore still harbored both species even after a large number of raccoons and red foxes had been removed in autumn 2003. Mammalian predation rates on Parramore (18% per day) were still higher than on Metompkin (~0% per day), but were down dramatically from 2003. Once again, gulls and ghost crabs depredated ~6% of the nest per day on Metompkin. These results suggest that predation management has significant potential for reducing nest predation on islands.

(79) DO TWO SPECIES OF AMERICAN MARTENS EXIST? – A LOOK AT FECUNDITY

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Current research has raised questions concerning the taxonomy of the two subspecies groups (lineages) of American marten (Martes americana). These lineages, “americana” and “caurina”, were once recognized as distinct species, M. americana and M. caurina, but were lumped into one species in the 1950’s; however, these lineages have distinctive morphological and genetic differences. Through donations by trappers, we have collected samples from an area of sympatry in western Montana to further explore similarities and differences between these two lineages. Previous researchers studying in this same region identified a difference between fecundity rates of martens from northwestern and southwestern Montana and attributed this difference to ecological factors. However, previous genetic research has shown that the two lineages exist in Montana, “americana” in the northwestern region and a mix of “americana” and “caurina” in the southwestern section. Therefore, we are testing an alternative hypothesis that the difference in fecundity rates is due to genetic differences that exist between the lineages. DNA was extracted and a portion of the cytochrome b gene was amplified. A restriction enzyme digestion generated a diagnostic RFLP pattern for each individual, which was used to identify lineage type. Fecundity was indirectly measured using corpora lutea counts. Approximately 400 samples of both male and female have been collected over the past 6 years. Of these samples, 102 samples have been genotyped with 64 represent the “americana” lineage and 38 represent the “caurina” lineage. Mean corpora lutea counts were 2.85 (N=20) and 2.61 (N=18) for the “americana” and “caurina” lineages, respectively. This information adds to existing morphological and genetic data and should assist in the determination of the proper classification of these lineages.

(82) USE OF NON-INVASIVE SAMPLING TO STUDY RELATIVE PATTERNS OF DISTRIBUTION AND ABUNDANCE OF CANIDS AT MARINE CORPS BASE QUANTICO, VIRGINIA.

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Determining presence, distribution and abundance of wild canids is the first step in designing wildlife management plans for these species, particularly in areas where there is potential conflict with human use of the landscape. Non-invasive fecal DNA sampling has the potential to provide a wealth of information necessary for monitoring and managing canid species while eliminating the need to capture, handle or observe individuals. In this project we used non-invasively collected samples from scat to determine the presence and the relative distribution and abundance of wild canids that occur at Marine Corps Base Quantico located in Northern Virginia. We extracted DNA from 300 scat samples and amplified a short fragment of the mtDNA control region using primers specifically designed from North American canids. We demonstrate that these primers consistently amplified PCR products that varied in length for different canid species and confirm that this method is a reliable and quick way to differentiate between sympatric canids using non-invasive methods. Our analysis of 223 scat samples showed that gray foxes (Urocyon cinereoargenteus), red foxes (Vulpes vulpes) and coyotes (Canis latrans) occur sympatrically. Preliminary results suggest that gray foxes have a wider distribution and are more abundant than red foxes and coyotes in this area.

(90) PHYLOGEOGRAPHY AND DEMOGRAPHIC HISTORY OF GRAY FOXES (UROCYON CINEREOARGENTEUS) FROM EASTERN NORTH AMERICA

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Gray foxes, Urocyon cinereoargenteus, are widely distributed in North America, Central America and northern South America. In spite of their extensive range there is suprisingly little known concerning their basic ecology, demography and phylogeography. In this study we used a phylogeographic approach to analyze gray fox populations along the east coast of North America. We examined mitochondrial DNA variation in 109 foxes from areas distributed throughout the Eastern USA including samples from South Carolina (n=48), Virginia (22), New England (n=19), and New York (n=22). These samples cover the range of two subspecies: U. c. borealis in the northeast, and U. c. cinereoargenteus occurring east of the Mississippi and north of Georgia. Analyses of the mtDNA control region revealed 13 haplotypes, each closely linked in a star-shaped phylogenetic network; several of the most frequent haplotypes were internal, while the majority were unique to single populations and presented distal positions in the network. Overall there was a lack of genetic structure amongst populations with most of the variance explained by within population genetic diversity. Results of a “mismatch distribution analysis” and the deviation from neutrality suggest that the northern populations have experienced a recent rapid demographic/ range expansion. Preliminary analyses of 6 microsatellite loci suggest similar patterns of genetic diversity. Our expansion hypothesis is supported by paleontological evidence that during the last glaciation gray foxes did not extend into the current range of U. c. borealis. Additionally, historical evidence suggests a second southward range shift in the 17th century when they disappeared from Canada at the same time red foxes were introduced. They have since recolonized and extended the previous northernmost limit of their range. We will discuss our results and compare them to studies of other furbearers in eastern North America.

(91) DENSITY AND SPATIAL DISTRIBUTION OF BLACK BEARS IN SOUTHEASTERN OKLAHOMA USING HAIR-SNARE SAMPLES

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Historically, black bears (Ursus americanus) were present in Oklahoma but extripated in the early 1900s due to habitat loss and unregulated hunting. Reintroduction of black bears in the Ozark and Ouachita national forests of Arkansas between 1958–1968 by the Arkansas Game and Fish Commission successfully reestablished populations in these regions. Recent expansion of this black bear population into eastern Oklahoma has led to management questions regarding abundance and distribution. To learn more about the population in Oklahoma, 128 hair snares were set in 4.8 x 4.8-km grid cells over approximately 3,400 km2 of the Ouachita Mountains. The hair snare enclosures consisted of barbed wire stretched around 3–6 trees at a height of 30.5–61.0 cm and baited with sardines and raspberry extract. Hair snares were checked for hair samples and rebaited approximately every 7 days. After 7 weeks of sampling in June–August, 2004 and 2005, 650 hair samples were collected. Hair was collected from 57.8% (n=74) hair snare enclosures, averaging 2.87 hair samples/snare in 2004 and 2.70 hair samples/snare in 2005. Genetic analysis of 299 samples identified 272 (88.9%) unique individuals and 14 (4.6%) recaptures. Initial density estimates indicate a higher density of bears in eastern parts of the study area compared with western parts.

(96) PHYLOGENY OF THE AELUROID CARNIVORA

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Evolutionary relationships within the aeluroid Carnivora ((Felidae, Hyaenidae, Viverridae, Herpestidae) have long been problematic. I present a combined evidence phylogeny of the aeluroid Carnivora, including both molecular and morphological information and both recent and fossil taxa. This combined evidence phylogeny, which includes over 40 recent taxa and over 40 fossil forms, adds significantly to our understanding of patterns of diversification between families and major clades, and adds support to recent hypotheses of relationships.

(104) GRIZZLY BEAR ABUNDANCE ESTIMATION WITH DNA MARK-RECAPTURE IN TAKU RIVER WATERSHED, BRITISH COLUMBIA

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The Taku River is a large, unroaded watershed that supports grizzly bears and wild runs of the 5 species of Pacific Salmon. During summer and fall, grizzly bears congregate along the Taku River and its tributaries to feed on salmon, but concern about the population is prompting efforts to estimate current abundance and begin long-term monitoring. Because bears congregate along the river during summer and fall runs of salmon, sampling DNA from bears along the linear river corridor should be an effective and efficient way to estimate abundance within portions of the watershed. Two mainstem river reaches (each ~55 km long) were separately, and repeatedly, sampled during salmon runs in 2000, 2001, and 2003. DNA from hair follicles was genotyped to individual with 6 polymorphic microsatellite loci; sex was determined from the amelogenin gene. In most years, a simple Huggins closed population model with no temporal variation or individual covariates was the most parsimonious for abundance estimation. We determined “bears per river km” by adding a buffer strip based on distances between relocations. The upper reach held ~1.2 grizzlies per km. The lower reach held ~0.3 grizzlies per km. This area was predicted to support high quality bear habitat and indigenous and local knowledge indicates that high numbers of bears have historically used the area, but that population has declined over the last several years. It is possible that high mortality due to increasing human access and/or the collapse of the fall chum populations have reduced grizzly populations. In each reach, the “bears per river km” was relatively consistent across all 3 years. We infer that the population was approximately closed during each summer of sampling based on the short recorded movement distances, and on low movement rate estimates from Pradel models. We conclude that mark-recapture sampling for grizzly DNA along rivers, during salmon runs, appears to be reliable for abundance estimation.

(118) INFLUENCE OF INTERNAL PARASITES (BAYLISASCARIS COLUMNARIS) AND FOOD MANIPULATION ON INTERNAL BODY FAT STORES OF CAPTIVE STRIPED SKUNKS (MEPHITIS MEPHITIS).

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Striped skunks accumulate large amounts of body fat in order to survive the period of winter inactivity and food scarcity. Individuals that accumulate larger body fat reserves have increased survival over the winter season. Energy stores can potentially be influenced by energy intake and energy expenditures. Energy intake in the captive skunks is simplified by feeding the skunks a homogenous commercially prepared diet (that has a consistent energy value. Energy expenditures of the captive skunks are also similar with one possible difference being attributed to costs associated with parasitic infection. Baylisascaris columnaris is a common nematode found in the intestinal tract of skunks. Ivermectin, a drug belonging to the avermectin family that interferes with the nervous system of invertebrates, was tested for efficacy and subsequently used to determine impact of helminthes on storage of body fat in

captive striped skunks. A follow up experiment was performed to determine if there were interactions between food intake and anthelmintic treatment.

(125) MECHANISTIC HOME RANGE MODELS CAPTURE SPATIAL PATTERNS AND DYNAMICS OF COYOTE TERRITORIES IN YELLOWSTONE NATIONAL PARK

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Patterns of space-use by individuals are fundamental to the ecology of animal populations influencing their social organization, mating systems, demography, and the spatial distribution of prey and competitors. To date, the principal method used to analyze the underlying determinants of animal home range patterns has been Resource Selection Analysis (RSA), a spatially implicit approach that examines the relative frequencies of animal relocations in relation to landscape attributes. In this analysis, we adopt an alternative approach, using a series of mechanistic home range models to analyze observed patterns of territorial space-use by coyote packs in the heterogeneous landscape of Yellowstone National Park. Unlike RSAs, mechanistic home range models are derived from underlying correlated random walk models of individual movement behavior, and yield spatially-explicit predictions for patterns of space-use by individuals. As we show here, mechanistic home range models can be used to determine the underlying determinants of animal home range patterns, incorporating both movement responses to underlying landscape heterogeneities and the effects of behavioral interactions between individuals. Our analysis indicates that the spatial arrangement of coyote territories in Yellowstone is determined by the spatial distribution of prey resources and an avoidance response to the presence of neighboring packs. We then show how the fitted mechanistic home range model can be used to correctly predict observed shifts in the patterns of coyote space-use in response to perturbation.

(156) PHYLOGEOGRAPHY OF THE LONG-TAILED WEASEL, MUSTELA FRENATA

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The long-tailed weasel, Mustela frenata, ranges widely throughout North and Central America and extends primarily along the western slopes of the Andes to Bolivia in South America. Although it has the largest distribution of any mustelid in the western hemisphere, it has been poorly studied. This study represents the first attempt to genetically characterize Mustela frenata. Using primarily samples from frozen tissues, I sequenced the complete cytochrome-b gene for 25 of Hall's 42 designated subspecies. In an expanded data set representing 34 subspecies, I used DNA extracted from skins of museum specimens to sequence a large portion of the control region (d-loop) for animals collected across the range. Analyses suggest structured clades in each of the Americas. This study also includes the first genetic sequences of a tropical weasel, Mustela africana, for outgroup comparison with M. frenata's sister taxon, Mustela vison.

(158) A GENETIC ANALYSIS OF BOBCATS LYNX RUFUS IN THE MIDWEST

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The bobcat Lynx rufus is a highly adaptable and mobile species, as demonstrated by its expansive distribution ranging from southern Canada to northern Mexico. Prior to European settlement, the Midwest was comprised of a diverse array of land cover types including prairies, forests, and wetlands, much of which was suitable habitat for bobcats. However, during the last century, the Midwest underwent increased urbanization and conversion of suitable bobcat habitat to intensive agricultural land cover. It is unknown whether these landscape changes or other potential dispersal barriers (i.e., the Missouri and Ohio Rivers) have affected gene flow among Midwestern bobcat populations. Therefore, we examined the effects of habitat discontinuities and extent of genetic differentiation among bobcat populations throughout Illinois, Indiana, Kentucky, and Missouri using ten microsatellite markers. Preliminary analysis from 190 bobcats using five microsatellite loci have revealed significant fine scale genetic structure between these areas (global FST = 0.0139, p value = 0.004), thus habitat discontinuities or large rivers may be affecting gene flow in Midwestern bobcats. These results will allow wildlife biologists to better assess the management needs of bobcats and indicate how habitat may facilitate or impede gene flow among bobcat populations over large scales.

(152) COMPETITION LIMITS THE SOUTHERN DISTRIBUTION OF BOBCATS

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Bobcats Lynx rufus are opportunistic felids occurring in a diverse range of habitats and with a widespread distribution from southern Canada to southern Mexico. We modeled the ecological niches of the felid community in southern Mexico to explore why the bobcat distribution stops abruptly at the Isthmus of Tehuantepec (IT). The IT, a lowland region with subtropical swamp habitat, is unlikely to serve as a geographic and ecological barrier to bobcats. Mammal inventories conducted for over a century rejects the hypothesis that bobcats are present but have not yet been recorded south of the IT. No evidence of fossil records south of the IT provides little support for a past presence of bobcats in that region. We show that the ecological niche of bobcats extends south of the IT, suggesting that ecological conditions exist for the establishment of populations in that region. The overlap of the bobcat geographic niche was lowest with margay and ocelot, both felids with similar size and feeding habits. We propose that interspecific competition with other felids limits the southern distribution of bobcats, preventing dispersal to a suitable but geographically reduced niche south of the IT.

(171) EFFECTS OF URBANIZATION AND HABITAT FRAGMENTATION ON RODENT AND CARNIVORE COMMUNITIES IN COASTAL SAGE SCRUB COMMUNITIES

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Rapid, sprawling urbanization in southern California coastal sage scrub has created fragments of varying sizes within an urban matrix. As urban development and fragmentation continue, it is important for land managers to understand the impacts in order to devise and implement effective conservation plans. Fragmentation resulting in habitat loss and lack of connectivity is credited with altering basic ecological processes as well as population and community dynamics. This study focused on how fragmentation impacts carnivore activity and rodent communities. We sampled over four site types: edges and interiors of large reserves and small and large fragments within urban San Diego. We sampled carnivore activity with remote trigger cameras and rodent populations using mark-recapture. The results show a positive overall edge effect impacting coyote (Canis latrans) activity, an apex mammalian predator in this system. Other carnivore species, excluding bobcat (Felis rufus), were most commonly detected in fragments in relatively low numbers. In addition, rodent richness was higher at edges and lower at small fragments. Rodent abundance was higher at interiors compared to the other three site types and did not vary with carnivore activity. These results suggest habitat fragmentation has an important impact on both carnivores and rodents. Densities or activity levels of coyotes may be artificially high along edges due to allochthynous urban resource subsidies. High rates of coyote activity may negatively impact smaller carnivore species. Rodent species displayed differential responses to the site types indicating resource availability and competition play an important role in species composition. Habitat quality and human influences on edges may strongly affect essential resources and intraguild processes for both groups of mammals. Thus, factors other than overall area must also be considered in management decisions in San Diego’s fragmented landscape.

(189) ASSESSING THE HEALTH OF FLORIDA PANTHERS FROM STABLE ISOTOPE GEOCHEMISTRY AND OTHER MEANS

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The Florida Panther (Puma concolor) is the only surviving population of puma in the Eastern U.S. Habitat loss and human persecution once reduced Florida Panther populations to as few as 30 individuals and its distribution to the southernmost (and not necessarily the most productive) regions of Florida. As a result, the Florida Panther has the lowest heterozygosity recorded among panther populations. Monitoring of the Florida Panther has revealed serious health problems associated with malnutrition and inbreeding, including congenital heart defects, cryptorchidism; poor semen quality, and elevated pathogen/parasite loads. Intense recovery efforts, such as genetic enrichment, through the introduction of Texas pumas, as well as land acquisition and new management practices, appear to be reversing these trends. The genetic restoration program has reduced the number of deleterious manifestations of inbreeding unique to Florida Panthers such as cowlicks, kinked tails, cryptorchidism, congenital heart defects, and population numbers have increased to an estimated 80

individuals. However, human population growth, restricted range size, and the landscape features of peninsular Florida continue to limit these efforts. This begs the question, "are the individuals in the population healthier than in the past?" We have examined two distinctly different types of data to assess Florida Panther health. Harris lines are transverse lines through long bones that are associated with arrested bone development, and have been used to document periods of dietary stress in other animals. Stable isotopes can be used to evaluate differences in diet, and can at times be used to indicate periods of dietary stress. Our data consistently show dramatic differences in male and female panther diet as well as small changes associated with habit and age.

(206) JAGUAR (PANTHERA ONCA) CURRENT DISTRIBUTION IN TABASCO, WESTERN CAMPECHE AND NORTHERN CHIAPAS, MEXICO

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During the Jaguar Conservation Symposium carried out by Wildlife Conservation Society in 1999, extensive regions of southern Mexico, such as the state of Tabasco, northern Chiapas and western Campeche were identified as areas where the long term survival of jaguar populations is high. However, only 20% of the original terrestrial ecosystems in the western portion of this area is preserved. In this same region, other areas where human population is almost inexistent were recognized as areas where jaguar population status was unknown, such as the largest wetland system composed mostly by the Laguna de Terminos Wildlife Protection Area (LTWPA) and the Pantanos de Centla Biosphere Reserve (PCBR). To clarify the current jaguar distribution in the area, we looked for reports (skins, skulls, photographs or trustable references) of jaguar presence in the last 10 years. We found 55 jaguar records, most of them distributed around the LTWPA, the PCBR, and the Mexico-Guatemala border. To determine the possible habitat and human population characteristics that allow jaguars to persist in the area, we divided the study area in a 10x10km grid using a GIS, in which terrain, habitat and human population characteristics where obtained for each cell where recent jaguar records were found. Jaguar records were obtained in cells with a mean altitude of 42.5 m a s l (SD=70.8), a mean terrain complexity of 20.5m (SD=58.9), a mean percentage of preserved area of 70.2% (SD=26.5), a mean percentage of protected area of 37.7% (SD=43.8), a mean number of human inhabitants of 724 inhabitants per 100 square km (SD= 1000.4) and a mean road length of 13.5 km per 100 square km (SD 11.6). These results imply that recent jaguar records tend to be present in areas with low elevation, low human population and road density and highly preserved areas but not necessarily associated to protected areas.

(209) RUN FASTER; JUMP HIGHER; ANATOMIC VARIATIONS IN THE PAWS OF CLOUDED LEOPARDS (NEOFELIS NEBULOSA)

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The clouded leopard (Neofelis nebulosa) is a medium-sized, highly arboreal cat. In this study the structure of the fore and hind limb paw pads was examined. The metacarpal and

metatarsal pads are covered by a cornified epidermis, beneath which is a supple subcutaneous fat pad that is extensively anchored to the tendon sheaths of the metacarpal and metarsal phalangeal joints, respectively. In the hind paw, three tendinous branches extend from the flexor digitorum superficialis muscle (flexor digitorum superficialis runs deep to the flexor retinaculum) that project through the fat pad and attach to the middle, medial and lateral sides of the paw pad epidermis. Previous reports have described tendinous extensions of the flexor digitorum superficialis muscle (previously known as the palmaris longus muscle) into the forepaw of the domestic cat, but not the hind paw. The combined effect of these tendinous extension insertions and the flexibility of the paw pad may allow contraction of the pad, thus enhancing the animal's ability to grip tree branches more effectively while hunting.

(228) ONTOGENETIC CHANGE IN SKULL MORPHOLOGY AND FEEDING PERFORMANCE IN THE SPOTTED HYENA (CROCUTA CROCUTA)

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Ontogeny in the spotted hyena (Crocuta crocuta) is characterized by dramatic behavioral and morphological change. These large, gregarious carnivores feed in intensely competitive environments in which the ability to consume large quantities of food in a short period of time is highly advantageous. Furthermore, spotted hyenas have a highly durophageous diet in which they must crack open and consume bones of large diameter. Consequently, their skulls are highly specialized for durophagy, with enormous sagittal crests and wide zygomatic arches providing increased attachment area for muscles critical in bite force generation. In this study we used geometric morphometric techniques to quantify ontogenetic changes in skull size and shape in Crocuta crocuta. We analyzed the ventral and lateral views of 65 Crocuta skulls ranging in age from 1 day to 17 years. Although selection should favor rapid improvement in feeding performance in such competitive feeding environments, we found that Crocuta skulls continued to change in size and shape until 30 months of age. This delayed maturation is long after the average weaning age of 14 months and therefore presents limitations on aspects of feeding performance such as feeding speed and bite force generation. Feeding speed continues to increase significantly past 35 months of age, when post-cranial growth reaches its asymptote in both captive and wild hyenas. This delayed development in the feeding apparatus ultimately may provide insight into the adaptive significance of the unusual trait of female dominance in this species.

(229) DEVELOPMENTS IN MAMMALIAN DIETARY RECONSTRUCTION OF CARNIVORES USING LOW-MAGNIFICATION STEREOMICROSCOPY OF DENTAL MICROWEAR

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Living carnivorans have dietary preferences that range from strictly carnivorous to omnivorous and even herbivorous diets. Some of these diets are not predictable from dental form alone. I employed a stereoscopic dental microwear method to examine the use wear of living carnivorans with a range of observed diets. This microwear method has been shown to be a reliable indicator of diet in large, primarily herbivorous mammals, but is applied here to

living carnivores for the first time. I examined dental casts of 242 individuals from 23 species of living carnivorans with known diets in order to relate those diets to microwear patterns. I found that particular carnivoran diets shared common microwear fabrics, and that these fabrics were distinct from those that have been recognized for herbivorous mammals. In contrast to the microwear patterns of ungulates and primates, I found the primary discriminator of diet in carnivorans to be the number of small pits. Bivariate and multivariate statistical analyses of microwear on the first molar reliably separate the larger species (> 8 kg) into meat specialist, meat and bone, omnivore, and tough fibrous groupings. I concluded that the microwear fabrics of larger species had somewhat different functional implications than for medium-sized species (0.5-8 kg), because of the difficulty of distinguishing between pitting caused by chewing skeletal parts of prey and pitting caused by incidentally-ingested environmental grit. Microwear of the slicing carnassial teeth has a similar predominance of a pitting signal, but dietary interpretations are complicated by masticatory differences among species. Finally, an assessment of omnivory uses microwear features most associated with particular food types. The database developed here is being extended to facilitate dietary reconstructions of Paleogene mammals.

(230) SEXUAL SHAPE DIMORPHISM AND RENSCH'S RULE IN UROCYON

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Bernhard Rensch (1960) demonstrated that an allometric relationship exists between sexual size dimorphism (SSD) and body size such that SSD increases with body size in taxa where males are larger than females and decreases with body size in taxa where females are larger. With some exceptions, various studies show support for this phenomenon now known as Rensch’s rule. However, Rensch’s rule has not been tested with regard to sexual shape dimorphism, nor has its effect been contrasted between different body regions. Two species within the genus Urocyon (Urocyon cinereoargenteus and Urocyon littoralis) provide an excellent vehicle for such an examination given their close phylogenetic relationship and difference in body size due to dwarfism in U. littoralis. Landmark-based morphometric techniques were used to quantify cranial and pelvic shape differences between males and females of each species. 14 cranial and 14 pelvic landmarks, along with centroid size were examined in order to determine: 1) the presence of sexual shape dimorphism in the cranium and pelvis of each species, 2) the effect of body size as a covariate on sexual shape dimorphism, 3) variation in levels of shape dimorphism between the cranium and the pelvis, 4) variation in levels of shape dimorphism between U. cinereoargenteus and U. littoralis, and 5) to test the application of Rensch’s rule to shape dimorphism.

(232) BRAIN SIZE EVOLUTION IN THE CANIFORMIA (CARNIVORA): INCORPORATING DATA FROM FOSSIL TAXA

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Brain-body size allometries in the order Carnivora have been studied with respect to the pattern and timing of brain size evolution, as well as to correlated aspects of life history, adaptation, and ecology. However, incorporating fossil data into investigations of brain size evolution has been hindered by a lack of data. Endocasts require special preservation of the interior of the braincase, while CT scanning can be time-consuming and expensive. A method for rapidly, inexpensively, and accurately estimating endocranial volumes from external skull measures, which has not yet been developed for Carnivora, has the potential to greatly increase the understanding of brain size evolution in fossil taxa. Endocranial volumes were estimated for 126 extant terrestrial carnivoran speciesfrom 825 museum specimens, spanning all major monophyletic carnivoran clades. Multiple linear regression combined with an AIC-based model averaging was employed to predict endocranial volume from three external skull measures. The AIC-averaged model accurately predicts endocranial volumes for modern carnivoran taxa (R-squared = 0.983), and is robust to potential sampling problems with respect to taxa represented by only a few specimens. Moreover, the results do not reflect phylogenetic autocorrelation nor does it represent correlation induced by general body size scaling. Application of the model equation to fossil taxa, for which endocranial volumes have been directly measured from endocasts, demonstrates that the scaling relationship for modern taxa also pertains to extinct Carnivora. The robustness of this estimator across all Carnivora allows reconstructions of brain volumes for a diverse array of fossil taxa, and explicit testing of hypotheses of brain size evolution across the caniform clade. Preliminary data from an extensive sample of the Canidae reveals a pattern of phylogenetic control over encephalization that is decoupled from simultaneous trends in body size evolution.

(240) SPATIAL ASSOCIATION OF RACCOONS AND OPOSSUMS IN ILLINOIS: NO EVIDENCE FOR COMPETITION

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We examined data from 24 years (1981-2004) of annual spotlight surveys in Illinois to determine if sightings of raccoons (Procyon lotor) and opossums (Didelphis virginiana) showed patterns suggesting avoidance or competition. The 48 spotlight survey routes were stratified across Illinois, sampled following standard protocols each spring before leaf-out, and each 25 mi (40.3 km) long. Raccoons and opossums showed latitudinal gradients, with raccoons more abundant in the north and opossums more abundant in the south. Statewide, sightings of raccoons in surveys doubled since the 1980s, but sightings of opossums changed little. Considering 29 individual survey routes where raccoon sightings increased in number, opossum sightings decreased along only one, increased along five, and did not change along 23. Considering 28,276 individual 1-mi segments along survey routes over the 24-yr period, a coefficient of association indicated a slightly positive, but near zero, association between raccoons and opossums. Coyotes (Canis latrans) and red foxes (Vulpes vulpes), which have been shown to interact negatively in several studies, showed inverse population trends since the mid 1980s and a negative association at the scale of 1-mi segments of survey routes in spite of much sparser data, but no clear trend at the scale of the entire survey route. Thus, we found no clear evidence for competition between raccoons and opossums although the patterns revealed for coyotes and red foxes show such evidence can be found when expected.

(249) TESTING REMOTE CAMERAS FOR DETECTING CANADA LYNX IN MAINE

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The Canada lynx Lynx canadensis is a federally-threatened species whose status is of considerable concern throughout their range in North America. Although snow-tracking and hair snares have been used to survey lynx populations, there is considerable interest in devising an alternative, effective technique for surveying lynx that does not face the challenges of previously-used methods. Our goal was to evaluate the use of remote cameras as a potential survey technique for lynx at the township scale. We placed 36 remote cameras (Moultrie Digital GameSpy; 1 camera/section) on an intensive lynx study area near Clayton Lake, Maine, and collected digital images during August-October 2005. Images were evaluated to determine lynx presence and make recommendations regarding the effectiveness of using this technique more widely. A total of 4,651 images were collected in 2,512 camera-nights. Of these images, 1,686 contained animals (36%); we suggest many of the blank photographs occurred due to animals just outside of the camera sensor range. Forty-five lynx events were recorded, for a lynx encounter rate of 1%; 1.8 lynx were recorded per 100 camera-nights. Lynx were detected in 17 of the 36 sections in the township (47%). We also modeled camera density and camera-days needed to detect lynx presence according to different combinations of cameras placed throughout the township. Finally, we provide recommendations for the proper use of remote cameras for surveying lynx in terms of proper camera placement, set-up, and equipment performance.

(255) MORPHOLOGICAL EVIDENCE SUPPORTS THE STATUS OF THE EXTINCT SEA MINK (MAMMALIA:CARNIVORA:MUSTELIDAE) AS A SEPARATE SPECIES

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The sea mink (Neovison macrodon) was probably the most aquatic member of the Mustelinae, and the only musteline restricted to coastal habitats. Its status as a separate species has not been resolved. A larger relative of the American mink (N. vison), it inhabited the shores of New England and possibly southern Canada until the 19th century. Skeletal specimens were not collected by zoologists, but are known from Native American archaeological sites. The hypothesis that the sea mink showed dental divergence from N. vison, an indication of phylogenetic and ecological distinctness, was tested on 111 archaeological mink specimens collected from Penobscot Bay, Maine and housed at the Maine State Museum. These were compared with 158 specimens measured for this study and 78 others from the published literature, representing 4 subspecies of N. vison and 22 additional musteloid genera. A total of 13 dental measurements were taken on all species, and studied using linear regression, principal components analysis and bivariate plots of residuals. In general, the distribution of these measurements was bimodal in the archaeological specimens, with most of the smaller individuals separable into two distinct categories. One category correlated very strongly ($r \geq 0.98$) with the mean values for N. vison. The other showed a somewhat weaker correlation with N. vison ($r \leq 0.96$), but a high correlation with the larger archaeological specimens. It appears likely that the archaeological specimens included primarily N. macrodon but also N. vison. The dental proportions of the several N. vison subspecies were nearly identical, while pairs of species within the Lutridae and genus Mustela showed divergence comparable to that of N. vison and N. macrodon. This suggests N.

macrodon was sufficiently distinct from N. vison to support its classification as a separate species.

(259) RECOVERY OF FISHERS, MARTES PENNANTI, IN EASTERN CANADA

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I present an overview of research initiated to understand the recovery of fisher populations in Ontario, Canada. Fishers have recolonized much of this province following widespread extirpation during the 1930s. The research program had several components, including a genetic analysis of 800 fishers from across Ontario; a telemetry study of a putative source population in an untrapped refugium (Algonquin Park); a telemetry study of a population in a settled, agricultural landscape; and an analysis of 10 years of fisher abundance data obtained from 450,000 trap nights. The genetic analysis identified several subpopulations within the small geographic area studied; evidence that historical fragmentation of fishers through overharvest has structured the population. Trapping refugia (Algonquin and Adirondack parks, in particular) have played an important role in providing emigrants to recolonize habitats. Densities were much higher in the agricultural landscape than in Algonquin Park, suggesting that fishers benefitted from the large, diverse food supply of the settled area, and a net flow of migrant fishers from south to north implicated snow depth and food supply as limiting factors.

(274) DEN SITE SELECTION BY FEMALE FLORIDA PANTHERS

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The Florida panther (Puma concolor coryi) is listed as an endangered subspecies under the United States endangered species act due to its restricted geographic range and low population numbers. Currently, panthers are restricted to 1 population in south Florida which likely consists of <100 individuals. Habitat loss and fragmentation appear to be among the main threats to persistence, but to date there has not been an adequate assessment of panther habitat preferences. Understanding which habitats are important to panther reproduction is especially critical for the conservation of this subspecies. During 1990-2006, >80 dens of 38 female panthers across the occupied range of the subspecies have been visited to monitor reproduction and mark offspring. I will use a Euclidean distance based approach to assess den habitat selection, by comparing the distances between den locations and random sites to habitat types available to panthers within individual home ranges. Additionally, distances from den locations and random sites to landscape features (e.g., roads and habitat edges) will be compared to investigate potential selection or avoidance of these features. These results should identify habitats and landscape features associated with reproduction and kitten rearing and allow for improved habitat management and conservation efforts for this endangered species.

(276) LIVESTOCK GRAZING INFLUENCES DAILY PATTERNS OF ACTIVITY IN THE SPOTTED HYENA

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Despite the relative rarity of large carnivores in human-altered habitat, behavioral plasticity with respect to use of both time and space has allowed some carnivores to coexist with humans in shared landscapes. Consequently, changes in carnivore activity patterns or movements can potentially be used as early behavioral indicators of the extent and severity of human disturbance. In the Maasai Mara National Reserve, Kenya, human disturbance in the form of livestock grazing and tour vehicle presence occurs at varying intensities throughout the Reserve. From 2002-2004 we monitored the density of both tour vehicles and livestock herds utilizing the territories of three separate social groups of spotted hyenas (Crocuta crocuta) to compare their relative exposure to human disturbance. Over the same period, we used long-term (2-15 hr) follows and behavioral observations of female adult hyenas from these groups to investigate the degree to which these disturbances influenced activity patterns, movement rates and timing of den use. Female hyenas in territories with daily livestock grazing and high tourist visitation rates showed reduced activity and den use relative to hyenas in an undisturbed territory during the times of day when human activity coincided with potential hyena activity. Specific times of day when activity was reduced indicated that livestock grazing, not tourist activity, was probably responsible for observed shifts in activity. We discuss possible indirect costs associated with observed alterations in timing of den use and activity in this species, as well as broader implications for carnivore conservation and management.

(279) SOCIAL AND MATERNAL FACTORS INFLUENCE SURVIVAL IN THE SPOTTED HYENA (CROCUTA CROCUTA)

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Understanding survivorship patterns is critical for elucidating selective pressures shaping life histories. Here, we examined two key aspects of survival: ontogenetic variation, and the influence of social and maternal factors, in the spotted hyena (Crocuta crocuta). Spotted hyenas are large, gregarious carnivores that live in complex social groups structured by linear dominance hierarchies. In many mammals, mortality risks are unevenly distributed among life-history stages. We tested hypotheses suggesting that three life-history events (departure from the den, weaning, and first parturition) are particularly dangerous events in the lives of female hyenas. While mortality increased after departure from the den and weaning, there was no evidence of increased mortality associated with first parturition. We next examined whether sex, social rank, litter size, and maternal parity influence survivorship. Sex did not affect survivorship in the first two years of life, but social rank and maternal parity influenced lifelong survival in females. Though litter size influenced early survival, this effect vanished by 6 years of age. Finally, we examined whether social rank affects survival during dangerous ontogenetic transitions. High social rank increased the probability of surviving after weaning, but not after den independence. Our results indicate that social rank has an even greater impact on fitness in this species than previously recognized, and point to at least one mechanism by which rank influences survival.

(293) USING SITE OCCUPANCY MODELS TO DETERMINE THE EFFECTS OF HABITAT FRAGMENTATION AND LANDSCAPE CONTEXT ON MEDIUM-SIZED MAMMALIAN PREDATORS IN NORTHEASTERN NATIONAL PARKS

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Human disturbance is a significant source of land use change around the world, particularly in the northeastern United States, where expanding human populations are causing increased landscape development, habitat fragmentation, and pressure on wildlife populations. The effects of fragmentation on a number of wildlife species have been well-documented, but for species like medium-sized mammalian predators that are often cryptic and elusive, these effects are difficult to evaluate and not well understood. To gain a better understanding of these relationships, we used remote cameras, track plates, and hair traps to collect presence/absence data on 10 mammalian predators within 8 National Park Service (NPS) sites across the northeast. We collected data on environmental variables at multiple spatial scales and modeled the responses of these species using site occupancy models that incorporate the probability of detection. Detection probabilities for the target species varied among time, space, and species, and all were <1 and most frequently <0.4. Using site occupancy models to account for this variation in detection, we determined that landscape scale variables were effective at describing differences in the occurrence of predators. Variables that focused on the amount of human disturbance, such as the amount of landscape development, fragmentation, and distance to the nearest occupied building, were the most important in describing the probability of site occupancy. Our research suggests that landscapes surrounding NPS sites should be considered as important sources of variation in species occurrence and patterns of distribution. Detection is an important parameter to incorporate when sampling wildlife populations because detectability varies over time and space and non-detection of a species does not imply absence.

(280) INDIVIDUAL PATTERNS OF LATRINE USE BY RACCOONS

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Raccoons (Procyon lotor) defecate at preferred locations, or latrines, which typically occur on fallen logs or stumps. Although latrine use can be of both social and ecological importance due to disease and parasite transmission, little is known regarding raccoon behavior at latrines. In June 2004, we fitted 42 raccoons (20 males, 22 females) within a 20-ha portion of a natural area in northeastern Illinois with proximity detectors. We monitored raccoon behavior at 15 latrines and 21 control logs within our trapping area during a 2-wk period in October 2004 and 2005. Monitoring was accomplished by placing proximity detectors beneath logs such that detection of other collars occurred only if they were above or immediately next to the log. Ten males and 10 females visited latrine logs, whereas 6 males and 9 females visited controls. The number of visits/log was greater for latrine than control logs ($P = 0.004$), as was time spent at latrine logs ($P = 0.045$). Individual latrines were visited 3 to 20 times (mean = 9.13, SD = 5.26) for a total duration of 17 to 556 sec (mean = 220.93,

SD = 178.82). Up to 6 individuals visited a latrine during a single night. One to 5 unique individuals visited a single latrine over the 2-wk period for both males (mean = 2.13, SD = 1.38) and females (mean = 1.93, SD = 1.30). Individual males visited 1 to 8 different latrines (mean = 3.20, SD = 2.31), whereas individual females visited 1 to 6 latrines (mean = 2.90, SD = 1.64) during the 2-wk period. The number of visits to latrines by males and females did not differ (P = 0.935), although time spent at latrines was greater for males (P = 0.026). Typically only 1 or 2 new scats were deposited over the 2-wk period at each latrine (mean = 1.5, SD = 0.707). Patterns of latrine visitation during this study suggested that latrines may serve social functions for the local raccoon population.

(281) SOCIAL ORGANIZATION AND GROUP FORMATION OF RACCOONS AT THE NORTHERN EDGE OF THEIR DISTRIBUTION

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We examined the spatial and temporal relationships of 104 radio-collared raccoons at the northern edge of their distribution to test hypotheses regarding social regulation and group formation of adult males. Female social tolerance varied among years, but adult females generally maintained relatively exclusive home ranges (percent overlap ranged from 2.2-12.5%) that were dispersed in a uniform pattern throughout the duration of the study (R values ranging from 1.32-1.87). Even though female home ranges were dispersed regularly in the landscape, there were instances where females shared common resources and tolerated overlap. This behavior likely precludes the ability of raccoons to self regulate their densities by spacing behavior. Male social interactions were more complex than previously described for low density populations of raccoons, with most adult males (ca. 80%) forming coalition groups. We identified 15 coalitions that had extensively overlapping home ranges and positively associated nightly movements within group members (overlap indices ranging from 85.3-97.3%); while maintaining relatively exclusive territories between groups (annual overlap indices ranging from 0-3.2%). Male coalition groups in carnivores are hypothesized to form in response to aggregations of females, but our data suggests this is not a prerequisite for the formation of male spatial groups. We propose a dominance hierarchy where subordinate males benefit through increased likelihood of territory inheritance while dominate males benefit through increase efficiency of territory defense.

(283) SUB-STAND SELECTION OF CANADA LYNX (LYNX CANADENSIS) NATAL DENS IN NORTHWEST MAINE, USA

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Canada lynx were listed as threatened in the contiguous United States under the Endangered Species Act in March 2000. Little information on lynx ecology at the southern extent of their

range was available at the time of listing, and no ecological studies had been conducted in eastern USA. A long term ecological study of lynx was initiated in 1999 in Maine in northeast USA. As part of this study, natal den habitat selection was investigated to address questions posed during the listing process as to importance of certain forest conditions to denning requirements. Lynx used both regenerating stands (n=16) and mature stands (n=9) for den sites. Sub stand characteristics of 26 den sites were compared to characteristics of stands containing the dens. We used logistic regression to identify sub stand components that distinguished natal dens from the residual stand and used the information-theoretic approach to select the models that best explained the data. Two models of the fifteen tested were good predictors of den sites. The top ranked model had three variables: tip-up mounds of blown down trees, visual obscurity as measured with a cover pole at 5 meters, and volume of above-ground solid coarse woody debris (Wi = 0.39). The second ranked model had visual obscurity and tip-up mounds as the only two variables (Wi = 0.36). Lynx select for structure and cover within stands independent of stand age for natal den sites.

(290) POPULATION STRUCTURE OF FISHERS (MARTES PENNANTI) ACROSS NEW YORK AND NEW ENGLAND

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Population structure was examined in fishers (Martes pennanti) across the northeastern United States using genotypic data (n=433) from 11 microsatellite loci. Both spatial and non-spatial methods of Bayesian clustering of genotypes resulted in the highest posterior probability of K at four populations across the study area. The uppermost level of structuring in the data set was determined to be K = 3 from the method of Evanno et al. (2005) and corresponded geographically to populations in New York, New Hampshire, and Maine & Vermont combined. Bayesian assignment of individuals to each of the three pre-defined populations (NY, NH, and ME & VT) ranged from 73.8-97.9% depending on the method used. Significant deviations from Hardy-Weinberg were detected at a few loci in all populations except Maine. Admixture analysis identified 34 samples with significant admixture, 18 of which were located in the vicinity of population boundaries or in areas of overlap between populations. Significant heterozygote deficiencies and positive FIS values in each population suggests further substructuring exists that was not detected using the Bayesian clustering methods. Both admixture and the Wahlund effect may be contributing to the deviation from Hardy-Weinberg equilibrium at loci in each population. Significant differentiation was detected between all pairs of populations using FST and allelic and genotypic differentiation. Current population structure of fishers in the northeastern United States appears to be derived from recolonization from the three refugial populations (ME, NY, and NH) described by Brander and Books (1973) and appears to have been influenced by the reintroductions of fishers that occurred between 1959 and 1991 at a few locations within the study area.

(291) GENETIC STATUS AND ABUNDANCE OF A RECOLONIZING BLACK BEAR (URSUS AMERICANUS) POPULATION IN OKLAHOMA

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Extirpation of black bears (Ursus americanus) in Oklahoma and near extirpation in Arkansas occurred in the early 1900s. The translocation of 254 individuals from Minnesota and Canada during 1958-1968 led to the restoration of black bears to Arkansas by the mid-1990s. Black bears are dispersing west across mountain ridges of the Ouachita Mountains from Arkansas into areas in southeastern Oklahoma devoid of bears since 1915. The situation in which quality habitat is within dispersal range of a large demographically healthy bear population is rare due to increasing spatial limitations on available habitat. Genetic monitoring of this dispersal event provides a unique opportunity to examine characteristics of recolonizing populations. Natural recolonization is valuable as a potential tool for maintenance and enhancement of wildlife populations in the absence of adequate funding and public support, and populations involved can provide sources of novel genetic variation to species. We used noninvasive hair sampling to examine characteristics of the black bear population currently recolonizing its former range in Oklahoma. We collected hair samples from 128 hair snares set at a frequency of 1 trap per 23 km2 across the 3,420 km2 study area to ensure ≥1 trap per female homerange. Hair collection occurred during two 7-week periods from June–August 2004 and 2005. We collected 650 hair samples, of which 640 (98.5%) were extracted; 299 (46.7%) of these have been successfully sexed and genotyped at ≥7 of 10 microsatellite loci. Of these, 272 (91%) are unique individuals represented by a male-biased sex ratio of 1.4:1, and 14 (4.7%) are recaptures. The remaining 13 are duplicate samples. Genetic diversity in this population (0.77) is similar to its source population in Arkansas (~0.75) as well as other large black bear populations in North America (~0.79). No negative effects from inbreeding or reduced population size are evident.