ABSTRACT

MCVEY, JUSTIN MATTHEW. Assessing Food Habits of Red Wolves (*Canis rufus*) and Coyotes (*Canis latrans*) in Eastern North Carolina. (Under the direction of Dr. Christopher E. Moorman and Dr. David T. Cobb).

Red wolves (*Canis rufus*) and coyotes (*Canis latrans*) are recent co-inhabitants with the fauna of eastern North Carolina. The non-native coyote began appearing in the mid 1980's, and red wolves, which were once inhabitants of North Carolina but declared extinct in the wild in 1980, were reintroduced in 1987. The wolf reintroduction in North Carolina offers a unique opportunity to investigate the food habits of the sympatric congenerics. Information on the food habits of the two species also will aid in management of coyotes, red wolves, and their prey. Our objectives were to identify and compare food habits of red wolves and coyotes and to determine if food habits of these large canids change seasonally. We also used this opportunity to calculate upper and lower thresholds of scat diameters to distinguish between scats of red wolves and scats of coyotes and red wolf-coyote hybrids. Non-paved roads in agricultural, pocosin, and pine plantation habitats were surveyed once a month for 12 months. We used faecal DNA analysis to identify donor species and multinomial modeling designed of mark-recapture data to investigate diets of co-occurring red wolves, coyotes, and red wolf-coyote hybrids. Red wolf and coyote diets were similar and contained large proportions of white-tailed deer, rabbits, and small rodents. We found no difference in the diet over time when we divided the sampling period into biological seasons related to canid reproduction but did find a difference when we divided time by calendar season. Small rodents were more common in scat in the spring than in the summer, suggesting seasonal differences in prey availability in our study area. We believe that red wolves and coyotes coexist in eastern North Carolina due to temporal and spatial separation of the taxa, high abundance of prey, and high level of management of the coyote population.

Based on normal-distribution probability functions of scat diameters, scats ≥29 mm in diameter were at least 95% certain to be of red wolf origin. Conversely, scats ≤14 mm in diameter were 95% certain to be of coyote or hybrid origin. Scats >14 mm and <29 mm in diameter could not be identified by diameter alone. We suggest these upper and lower thresholds of scat diameters be used in concert with other methods (e.g., DNA genotyping) to monitor for red wolf, coyote, and hybrid activity to help conserve a lone, free-ranging population of wild red wolves.

Assessing Food Habits of Red Wolves (*Canis rufus*) and Coyotes (*Canis latrans*) in Eastern North Carolina

by
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A thesis submitted to the Graduate Faculty of
North Carolina State University
in partial fulfillment of the
requirements for the degree of
Master of Science

Fisheries, Wildlife, and Conservation Biology

Raleigh, North Carolina

2012

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BIOGRAPHY

Justin McVey grew up in a King, North Carolina, a small town in the foothills. His parents always encouraged him to pursue his interests with the caveat that once he started something, he must finish. Justin's childhood was that of a typical boy filled with explorations of adjacent woods, staying outside until Momma called him in for supper, going back out if there was still light, and somehow always managing to be the muddiest kid in the neighborhood. A bachelor's degree in Zoology from North Carolina State University in 2000 and a subsequent first job carried Justin from King to Raleigh, North Carolina to Dawsonville, Georgia. This first job at a kangaroo farm in the north Georgia mountains reaffirmed his compassion for animals and changed his outlook on life. With stories of hunting and fishing from coworkers and the exposure to Aldo Leopold's, *A Sand County Almanac*, Justin was able to put into words the feelings of his heart. A career in wildlife conservation would not only be his passion but his duty and occupation. With the support of a beautiful wife, stepping stones of several jobs finally allowed him to pursue his passion more formally by entering graduate school for wildlife and conservation biology. Graduate school has allowed Justin to meet some of his best friends who share his passion of wildlife and laughter. Justin is excited about the next chapter of life. Especially sharing hunting, fishing and passion for God's creation with his two boys, Braeden and Finn, and enjoying that creation with them.

ACKNOWLEDGEMENTS

I would like to thank the North Carolina Wildlife Resources Commission and the North Carolina State University Fisheries, Wildlife, and Conservation Biology Program for funding this project. I thank my committee, Chris Moorman, David Cobb, Roger Powell, and Michael Stoskopf for aiding in my education.

I especially want to thank the numerous graduate students and other folks that helped me through this process. Joey Hinton always provided insightful advice, interesting conservation, and good friendship. My collaboration with Justin Dellinger not only led to the second chapter of this thesis but also aided in the collection of samples. I could not have completed the mark-recapture analysis without the assistance of Aaron Facka and Patrick Lemons. Chelsea Daystar, Stephen Lasher, and Lauren Green were all subjected to countless hours in the lab with me and were very helpful.

The US Fish and Wildlife Service Red wolf recovery team was of great benefit. Not only did they help in scat collection but also offered advice. Chris Lucash gave Dellinger and me the idea for looking at scat diameters to distinguish species.

I am very thankful to the numerous landowners such as Weyerhaeuser, Matamuskeet Ventures, and Jamin Simmons that allowed me access to their properties. Justin Bohling and Lisette Waits identified scats via faecal DNA genotyping at a considerably reduced cost and Bohling was always up for explaining the DNA analysis numerous times.

Last but certainly not least, I would like to thank my sugar-momma and my boys.

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CHAPTER 1

Introduction

The taxonomic status of *Canis* populations in North America has been widely debated. It is generally accepted that gray wolves (*C. lupus*) evolved in Eurasia (Lehman et al. 1991; Nowak 1979; Wilson et al. 2000) but the ancestry and speciation of New World, derived canids (coyotes [*C. latrans*], red wolves [*C. rufus*], and eastern wolves [*C. lycaon*]) are more controversial.

Red wolves originally were described by Audubon and Bachman (1851) as a subspecies of *C.lupus,* a view later shared by Lawrence and Bossert (1967). Goldman (1937) suggested that red wolves were not a subspecies but a distinct species. This species distinction was based on morphology and paleontology and was generally accepted until 1990 (Goldman 1937, 1944; McCarley 1962; Nowak 1979, 1992, 1995, 2002, 2009).

Analyses of mitochondrial and nuclear DNA prompted some authors to suggest a hybrid origin for red wolves citing the appearance of *C. lupus* and *C. latrans* DNA genotypes in extant red wolf populations as evidence (Reich 1999; Wayne and Jenks 1991; Roy et al. 1994, 1996). Roy et al. (1996) also suggested that the intermediate size of *C. rufus* was the result of an evolutionary stage between *C. latrans* and *C. lupus*. Nowak (2009), however, pointed out that, while hybridization of *C. latrans* with *C. rufus* has led to the demise of the latter species, a hybrid origin has never been supported by morphometric analysis.

Recent hypotheses have suggested *C. rufus* is closely related to *C. lycaon* and may be the same species (Wilson et al. 2000, 2003; Kyle et al 2006). Wilson et al. (2000) suggested, based on morphological and genetic similarity between *C. lycaon* and *C. latrans*, that the two taxa may have diverged from *C. lupus* 1.2 million years ago followed by a separation of *C. lycaon* from *C. latrans*. vonHoldt et al. (2011) countered this view based on analysis of high density single nucleotide polymorphisms and concluded that there is no evidence of an association of *C. lycaon* and *C. rufus* and that the latter species appear to have 75%-80% of its genome attributed to *C. latrans* and the remainder attributed to *C. lupus*.

Another hypothesis regarding the hybrid origin of *C. rufus* is that it is the original small wolf of eastern North America descended from the Eurasian wolf, *C. mosbachensis*. *C. mosbachensis* was intermediate to the primitive wolves, *C. priscolatrans* and *C. etruscus*, as well as to the modern wolf, *C. lupus* (Nowak 2002). Support for designation of *C. rufus* as a distinct species comes from the lack of *C. lupus* and *C. latrans* specimens in southeastern United States during the time that would have given rise to hybrid populations (Nowak 2002).

Whatever the true evolutionary background of the red wolf, the United States Fish and Wildlife Service (USFWS) currently recognizes *C. rufus* as a distinct species based on mtDNA sequencing of a portion of the control region of nuclear DNA revealing a unique haplotype that has not been observed in coyotes, gray wolves, or dogs (Adams 2002; Adams et al. 2003; USFWS 2007). The USFWS designation of the red wolf as an endangered species in 1967, based solely on morphometric criteria, led to the development of a recovery plan for the species (USFWS 1990). Red wolf populations had been reduced or eliminated from much of their historical range by the early 1900s through direct persecution, forest clearing, road building, decreases in deer populations, and hybridization with coyotes (Nowak 1979; USFWS 1989).

To facilitate recovery, a captive breeding program was established in 1973 using red wolves captured from Louisiana and southeastern Texas (Phillips et al. 2003). Over 400 animals were captured for the breeding program (USFWS 1989). Forty-three animals were selected, based on morphological characteristics, to be included in the breeding program; but only 14 of the resulting offspring exhibited the morphological standards to serve as founders for the restoration program (McCarley and Carley 1979; USFWS 1990). In 1980, the species had been declared extinct in the wild (USFWS 1989).

In 1987, the first red wolves from the captive breeding program were reintroduced onto the Alligator River National Wildlife Refuge, North Carolina (hereafter The Refuge, often abbreviated as ARNWR in documents of the US Fish & Wildlife Service; Fig. 1, Phillips et al. 2003). The 640 km^2 refuge was chosen in part because of its location on the Albemarle Peninsula, which is isolated on 3 sides by water, and because of its abundance of prey, lack of human inhabitation, and, perhaps most importantly, apparent absence of coyotes (Phillips et al. 2003). A second reintroduction program was initiated in the Great Smoky Mountains National Park in western North Carolina in 1991 but was discontinued in 1999 due to poor pup survival and propensity of wolves establishing home ranges bordering and outside of the park (Henry 1998). Red wolves have slowly radiated from The Refuge throughout the Albemarle Peninsula to encompass the 5-county Red Wolf Recovery Experimental Population Area (hereafter called the Study Area, often referred to as the Peninsula in US

Fish & Wildlife documents; USFWS 2007). The current population is estimated to have ~130 red wolves all within the Study Area (USFWS 2007).

The biggest threat to the reintroduction of red wolves into North Carolina is hybridization with coyotes and the subsequent introgression of coyote genes (USFWS 1989). Except for a brief period at the end of the last glaciation 10,000 years ago, coyotes were not native residents of southeastern North America (Nowak 2002). Historically, coyotes occurred mostly in western North America and only recently entered the Southeastern United States. As early as 1938, coyotes were seen in Gaston County, North Carolina (Young 1978) through the escape of captive coyotes or the release of coyotes for chase with hounds (Hill et al. 1987). With the reduction of gray wolf populations and modification of habitats by humans, the range of the coyote also expanded eastward naturally and since 1972 has expanded dramatically in the Southeast (Hill et al. 1987; Nowak 2002). By the mid-1980s, coyotes were well distributed throughout the region. Coyotes currently inhabit all 100 North Carolina counties including the 5-county Albemarle Peninsula, where they co-occur with red wolves (Webber 2005).

The co-occurrence of red wolves and coyotes provided an opportunity for the 2 canids to hybridize, which has been documented in both captive and natural settings. In captivity, female red wolves have mated with male coyotes to produce fertile hybrid offspring (Marshall and Matthias 1971). More recently, red wolf-coyote hybrids have been documented in North Carolina (USFWS 2007). Hybridization and introgression can lead to the loss of parental genetics within a few generations of the initial hybridization, potentially threatening the red wolf reintroduction efforts (Kelly et al. 1999; Wolf et al. 2001).

To address hybridization between red wolves and coyotes, the USFWS developed an adaptive management work plan in April 2000 that uses several strategies to manage the canid populations and to conserve red wolf genetics (Kelly 2000; Fazio et al. 2005). The Albemarle Peninsula has been separated into 3 management zones (Figure 1, Kelly et al. 1999). The management strategy in zone 1 includes the trapping and extirpation of coyotes (Stoskopf et al. 2005). Stochastic simulations, using data and literature from the red wolf recovery program, showed that a decrease in coyote survival by 10% leads to doubling of red wolf numbers (Roth et al. 2008). In these simulations, total coyote extirpation is prevented by continual immigration of coyotes. The assumptions of the model are that wolves always displace coyotes and that habitat is homogeneous (Roth et al. 2008). Whether violation of these assumptions affects the applicability of the model seriously is unknown (Roth et al. 2008).

The strategy in zone 2 is to trap and sterilize coyotes (USFWS 2007). Sterilized coyotes are then released to act as placeholders and exclude other coyotes or hybrids from immigrating to the recovery area (USFWS 2007). These place-holding coyotes are eventually replaced naturally by red wolves via direct competition or removed by managers. Simulations of these sterilizations show that this approach to coyote management can improve the probability of successful red wolf recovery by 2.8- and 2.3 –fold in small and large initial wolf populations (Fredrickson and Hedrick 2006; Roth et al. 2008). Coyotes were not managed in zone 3 prior to the expansion of management boundaries in March 2002. Due to the expansion of red wolves from their initial release site, boundaries of the 3 management zones in the southern parts of the recovery area were moved west. Starting in

August 2003, canids captured in what had formerly been the eastern half of zone 3 were treated according to the guidelines for zone 2; coyotes were sterilized instead of euthanized (Stoskopf 2005).

In areas of low prey abundance or diversity, co-occurrence of similar taxa can be facilitated by resource partitioning as well as dietary shifts in prey size or life stage (Gittleman 1985; Johnson et al. 1996; Rozensweig 1966). For example, coyotes responded to the recolonization of gray wolves in northwestern Montana by separating themselves temporally and spatially from the wolves and exploiting different food resources (Arjo and Pletscher 1999). Following reintroduction of gray wolves into Yellowstone National Park, coyotes shifted their diets to include more wolf-killed carcasses (Switalski 2003). Conversely, in Manitoba where elk (*Cervus elephaus*) and white-tailed deer (*Odocoileus virginianus*) are common, coyotes and gray wolves have significant dietary overlap without conflict (Paquet 1992).

Although red wolves are typically animals of upland and bottomland forests, swamps, and coastal prairies, and coyotes are typically found in open grasslands, brush country, and broken forests (Nowak 1999), the two canids currently co-occur on a landscape of commercial pine plantations, pocosins, non-riverine swamp forests, and saltwater marshes. The occupation of both canids in the same area and their use of similar prey could lead to interspecific competition. Analysis of the diets of red wolves and coyotes may provide insight into the mechanisms of co-occurrence.

Coyotes are versatile scavengers and predators with a diverse diet (Hilton 1978). Throughout the southeastern United States, mammalian prey (rabbits, small rodents) typically occur most frequently in coyote diets, but vegetation, dump refuse, and domestic livestock are also present (Blanton and Hill 1989; Gipson 1974; Hall 1979; Lee 1986; Wooding et al. 1984). Contents of coyote scats in Florida and South Carolina, however, contain vegetation as the most frequent item (Schrecengost et al. 2008; Stratman and Pelton 1997)

The primary prey of red wolves before their extirpation in 1980 included nutria (*Myocastor coypus*), rabbits (*Sylvilagus* spp.), and cotton rats (*Sigmodon hispidus*, Riley and McBride 1972; Russell and Shaw 1971; Shaw 1975; Young and Goldman 1944). During an experimental release on Horn Island, Mississippi, raccoons (*Procyon lotor*) and nutria made up the largest portion of the diets of red wolves (Weller 1996). The only study of red wolf diet since the reintroduction in North Carolina found that the biomass of red wolf scats were 41% white-tailed deer, 36% raccoons, and 11 % marsh rabbits (*Sylvilagus palustris*, Kelly 1994). No one has evaluated the diets of red wolves and coyotes where they coexist.

Raccoons have consistently been documented as an important part of red wolves' diets. This is of particular interest as raccoons are mesopredators whose presence may affect prey diversity. The mesopredator release hypothesis states that, in the absence of large predators, populations of mid-sized predators (mesopredators) thrive (Estes 1996; Terborgh et al 1999). Thriving mesopredator populations then reduce populations of mammalian and avian prey, eventually leading to a reduction in prey abundance and diversity (Estes 1996; Henke et al. 1999; Terborgh et al 1999). Whether red wolves or coyotes in North Carolina prey on mesopredators is currently unknown.

Methods used to study the food habits of animals include direct observation, examination of stomachs from carcasses, and examination of scats. Scat studies are one of the most common as they provide a low-cost, non-invasive way of analyzing food habits (Sperry 1941). Primary methods for estimating food habits from scats include estimating percent of occurrence, frequency of occurrence, and biomass of prey eaten. These approaches rely on identifying food items contained within scats by using reference collections and hair keys. The frequency of occurrence is simply the frequency that a food item (or category) occurs in all the scats in a sample, while percent occurrence is calculated as the percent of all scats containing a given food item. Prey biomass uses a conversion factor to convert the presence, or the dry mass, of a prey item in a scat to the fresh mass of that prey that was consumed (Rühe et al. 2008). This method provides useful information but the conversion factors must be predator and prey specific and the laboratory techniques used in estimating the biomass must be consistent with those used in deriving conversion factors (Rühe et al. 2008).

Food habits can be compared using contingency tables, analysis of variance, or other similar techniques (Dumond et al. 2001; Morey et al. 2007). These approaches can lead to pseudoreplication, as each sampling unit (scat) usually contains more than 1 food item, all of which are assumed to be independent of one another (Lemons et al. 2010). Lemons et al. (2010) suggested using multinomial models developed for analyzing capture-mark-recapture data to estimate diets.

Another challenge with using scats to estimate food habits is identifying the taxon of the animal that deposited the scat (hereafter called the donor animal). Identification of the donor animal using morphological characteristics of a scat and associated animal signs around the scat is common but becomes increasingly difficult when similar animals inhabit the same area (Davison et al. 2002). Recent advancements in technology include the use of nuclear DNA microsatellite markers on scats to identify species of origin and even individual identification of donor animals. This method, however, is costly and success rate of individual identification is low (Dellinger et al. 2011).

Hunting in the Study Area is an important social and economic aspect of coastal North Carolina culture. The large expanses of private and public lands support abundant game populations. Canid populations in the Study Area may reduce game populations (i.e. deer, rabbits, etc.) and may, thereby, affect hunter success, sportsmen’s activities, and the local economy (Seip 1995). Analyzing the food habits of red wolves and coyotes may have implications for animal and habitat management by state and federal fish and wildlife agencies.

The goal of this project was to document the food habits of red wolves and coyotes in the Study Area. I hypothesized that red wolves and coyotes would have similar diets and that white-tailed deer would make up a large portion of their diets. I also hypothesized that the diets of red wolves and coyotes would change over the course of my study. Foods change in abundance over time; for example, fruits and insects are most abundant during summer and early autumn. I divided my study year into calendar seasons and I also divided it into the reproductive periods of the canids (pair formation, denning, dispersal). Because I lack replication of seasons, I can not test for seasonal difference in diet. Yet, if analyzing diet by reproductive seasons detects differences not shown by calendar diets, then this result might be considered light support for diet change having biological causes.

Previews of chapters to follow

This thesis addresses the food habits of congeneric canids. In Chapter 2, I present a food habit study that used faecal DNA genotyping to identify donor animals and used mark-recapture techniques to quantify diets. This chapter has been written in manner to be submitted for publication with multiple authors. Both the analysis and methods pertaining to faecal DNA analysis were performed and written by my coauthors, Justin Bohling and Lisette Waits. Chapter 3 focuses on the morphological differences between scats of sympatric red wolves and coyotes, and presents practical guidelines for determining species-specific presence and movement. Using faecal DNA genotyping, scats were identified as red wolf, coyote, or ambiguous or hybrid and then the upper and lower scat diameter thresholds were estimated to aid in field identification of scats.

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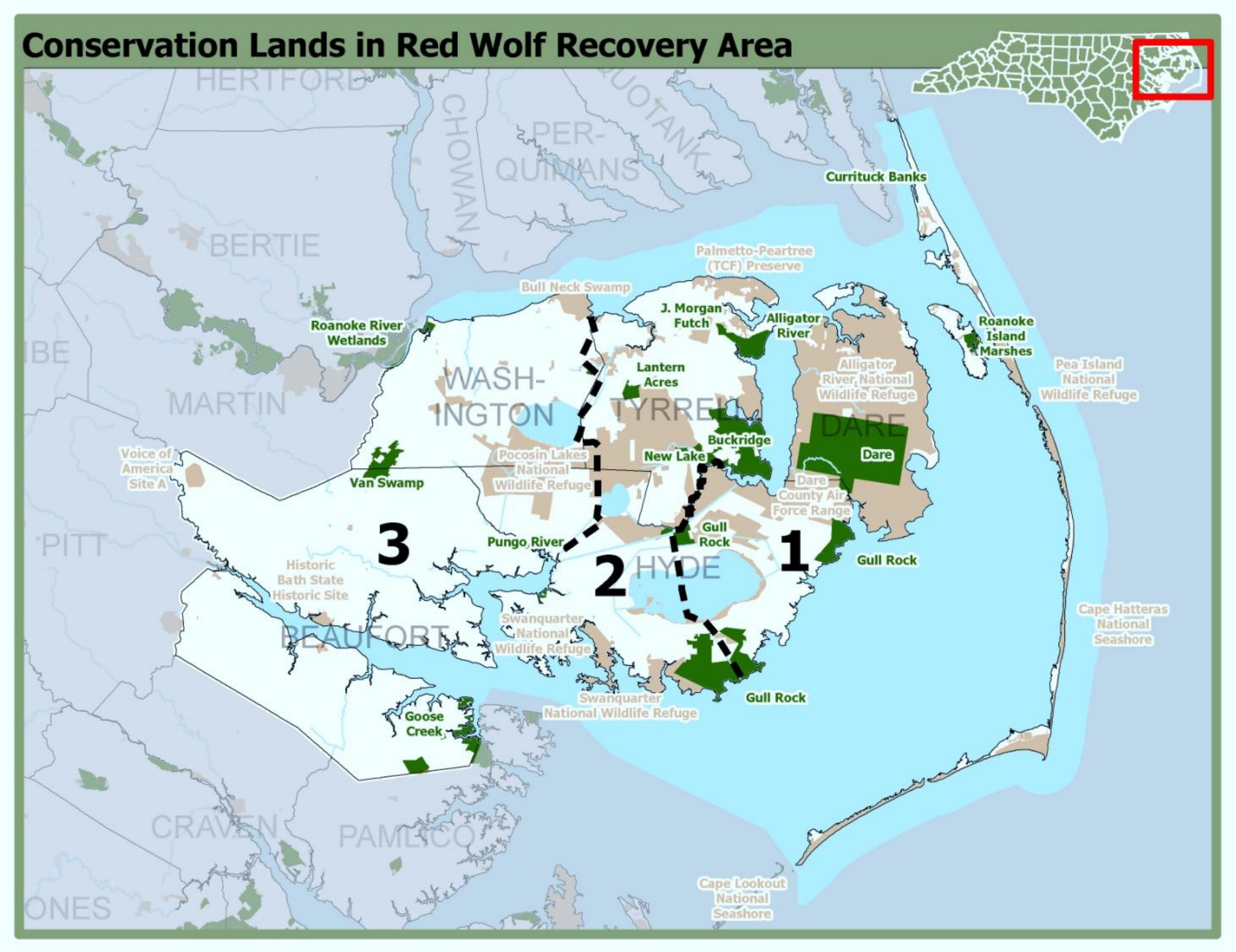

Figure 1. Conservation lands (green and tan) and United States Fish and Wildlife Service Adaptive Management Zones as of 2011.

CHAPTER 2

Evaluating food habits of co-occurring red wolves and coyotes using faecal DNA identification

The recent co-occurrence of red wolves (*Canis rufus*) and coyotes (*Canis latrans*) in eastern North Carolina provides a unique opportunity to study prey partitioning by sympatric canids. We collected scats from this region and examined them for prey contents. We used faecal DNA analysis to identify which taxa deposited each scat and multinomial modeling designed for mark-recapture data to investigate diets of co-occurring red wolves and coyotes. Diets of red wolves and coyotes did not differ, but the proportion of small rodents in the composite scats of both canids was greater in the spring than in the summer. White-tailed deer (*Odocoileus virginianus*), rabbits (*Sylvilagus* spp.), and small rodents were the most common diet items in canid scats. The similarity of diet between red wolves and coyotes suggests the 2 taxa may be affecting prey populations similarly.

Key words: dietary overlap, DNA genotyping, *Canis latrans*, *Canis rufus*, coyote, food habits, red wolf, scat.

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The eastern United States historically was occupied by a large canid, which may have been the red wolf (*Canis rufus,* Hall 1981; Nowak 1979, 1995). Red wolves may have evolved in North America and represent a transitional form between a coyote-like ancestor and gray wolves (*C. lupus*, Nowak 1979, 1995). Other hypotheses for the origin of red wolves are that these canids do not constitute a unique taxon but are hybrids of coyotes (*C. latrans*) and gray wolves (Roy et al. 1994, 1996; vonHoldt et al. 2011; Wayne and Jenks 1991). Whatever their taxonomic status, red wolves became extinct in the wild by 1980, were maintained in captivity only for several years, and were reintroduced to eastern North Carolina in 1986 (Phillips et al. 2003, US Fish & Wildlife Service 2007). Currently, the US Fish & Wildlife Service (USFWS) recognizes red wolves as a distinct taxon based upon morphological characteristics and upon mtDNA sequencing that reveals a unique haplotype (Adams 2002; Adams et al. 2003; USFWS 2007).

There has been little investigation of the dietary habits of red wolves and a better understanding of their food habits would provide insights into their potential ecological influences. Canids have the ability to reduce prey populations in some situations (Seip 1995). A population of black-tailed deer (*Odocoileus hemionus*) in Alaska was brought to near extinction by gray wolf predation (Klein 1995), and reintroduced gray wolves reduced ungulate abundance in Yellowstone National Park (Barber-Meyer et al. 2008). Canids also may have indirect effects on prey populations. For example, Crooks and Soulé (1999) suggested the disappearance of coyotes in California resulted in increased numbers of mesopredators and a subsequent increase in predation upon native prey by mesopredators.

Red wolves are opportunistic carnivores. In their historic range throughout the southeastern United States, red wolves preyed upon raccoons (*Procyon lotor*), rabbits (*Sylvilagus* spp.), and hispid cotton rats (*Sigmodon hispidus*, Riley and McBride 1972; Shaw

1975; Weller 1996). In the only diet study of the red wolves reintroduced to North Carolina, white-tailed deer (*Odocoileus virginianus*) also contributed significantly to the diet (Kelly 1994).

Following extirpation of large canids in the eastern United States, coyotes expanded their range eastward (Hill et al. 1987). Coyotes are smaller and are thought to eat fewer large prey items (e.g., white-tailed deer and raccoons) than red wolves. Coyotes have a diverse diet that includes small and medium-sized mammals, vegetation, dump refuse, white-tailed deer, and domestic livestock (Hilton 1978). Except in Florida and South Carolina, where vegetation was most abundant in scats, mammalian prey (e.g., rabbits and small rodents) have occurred most frequently in analyses of coyote diets in the southeastern United States (Blanton and Hill 1989; Gipson 1974; Hall 1979; Lee 1986; Schrecengost et al. 2008; Wooding et al. 1984). In addition, Schrecengost et al. (2008) reported white-tailed deer fawns to be the most common component of coyote diets during the period of deer parturition and fawn rearing in South Carolina, and coyotes have replaced gray wolves as an important predator of white-tailed deer in the northeastern United States (Gompper 2002, Kays et al. 2010). Thus, evidence suggests that the diets of coyotes and red wolves may overlap considerably and that coyotes may have filled a niche close to that historically occupied by red wolves across the eastern and southern United States.

The co-occurrence of red wolves and coyotes in eastern North Carolina provides a unique opportunity to directly compare food habits of these two taxa. Red wolves and coyotes only coexist in eastern North Carolina and the degree of dietary overlap and effect on prey populations is unknown. Diet can be influenced by intraspecific competition between the 2 canids and by changes in prey availability caused by seasonal or habitat differences (Andelt et al. 1987). Therefore, analysis of the diets of co-occurring red wolves and coyotes within the same time frame and across the same landscape would control for this spatial and temporal variability and provide initial data on the effects of these predators on prey populations.

We compared food habits of red wolves and coyotes using 2 recently developed methods: faecal DNA identification of canid taxa and multinomial analysis of food habits. Distinguishing the faeces of sympatric carnivores of similar size is difficult (Davison et al. 2002). A concurrent study revealed that scats of red wolves and coyotes with a diameter between 14 mm and 28 mm cannot be differentiated by size alone (Dellinger et al. 2011). Therefore, we used faecal DNA analysis to identify the taxon of the animal that deposited a scat and to reduce bias associated with inclusion of non-target taxa (Farrell et al. 2000). Food habits often are compared using contingency tables, analysis of variance, or similar techniques (Dumond et al. 2001; Morey et al. 2007). These approaches can lead to pseudoreplication as each sampling unit (scat) usually contains more than 1 food item, all of which are assumed to be independent of one another (Lemons et al. 2010). Lemons et al. (2010) suggested using multinomial models developed for analyzing capture-mark-recapture data to estimate diet selection accurately. We used a capture-mark-recapture model to test our hypothesis that the diets of red wolves and coyotes differ. Because diets of canids vary due to fluctuations of prey abundance (Morey et al. 2007), we included diet variation by biological and calendar periods in our tests.

MATERIALS AND METHODS

Study Area.—The study area was the 5-county Albemarle Peninsula (referred to as the Red Wolf Experimental Population Area in documents of the USFWS). The study area included >6,650 km^2 of federal, state, and private lands in Beaufort, Dare, Hyde, Tyrrell, and Washington counties, North Carolina. Public lands included Alligator River National Wildlife Refuge, Pocosin Lakes National Wildlife Refuge, a bombing range shared by the United States Navy and Air Force, and numerous state-owned game lands. Major land-cover types included agricultural fields (approximately 30%), pine (*Pinus* spp.) plantations (approximately 15%), pocosin (approximately 15%; including *P. serotina* and *Persea palustris*), non-riverine swamp forests (approximately 10%; including *Nyassa* spp., *Liquidambar styraciflua*, *Acer rubrum*, and *Chamaecyparis thyoides*), and saltwater marshes or open water (approximately 10%). Annual precipitation averaged 127 cm and temperatures ranged from an average of 5 °C in winter to 27 °C in summer (Beck et al. 2009). Elevation ranged from sea level to 50 m (Beck et al. 2009).

Potential prey species occurring in the study area included white-tailed deer, rabbits (*Sylvilagus floridanus, Sylvilagus palustris*), raccoons, feral hogs (*Sus scrofa*), nutria (*Myocastor coypu*), muskrats (*Ondatra zibethicus*), hispid cotton rats, house mice (*Mus musculus*), marsh rice rats (*Oryzomys palustris*), eastern golden mice (*Reithrodontomys humulis*), northern bobwhites (*Colinus virginianus),* and wild turkeys (*Meleagris gallopavo,* Phillips et al. 2003). Primary co-occurring carnivores were gray foxes (*Urocyon cineroargenteus*), red foxes (*Vulpes vulpes*), red wolves, coyotes, red wolf-coyote hybrids (*C.*

rufus x *C. latrans*), feral dogs (*C. familiaris*), bobcats (*Lynx rufus*), and black bears (*Ursus americanus*).

Sample collection.—We collected scats monthly from January 2009 through February 2010 by sweeping 190 km of non-paved roads comprehensively in areas known to be inhabited by red wolves or coyotes. Scats were placed in Ziploc® bags and labeled. We exposed tweezers to an open flame to sterilize and collected a 0.4-mL portion of each scat for DNA analysis and then immersed it in 1.2 ml of DET buffer contained in a 2-ml screw-top tube (Frantzen et al. 1998; Stenglein et al. 2010). We attempted to collect a scat subsample void of prey hair, bone, or vegetation, thus increasing the likelihood of obtaining the highest amount of usable canid DNA. The remainder of each scat sample was frozen.

Molecular methods.—We extracted DNA from each scat using the Qiagen Stool Kit in a laboratory dedicated to extracting low-quality DNA. To differentiate scats deposited by canids from other carnivores, we performed a species identification test by amplifying a portion of the mitochondrial DNA (mtDNA) control region following methods used by Onorato et al. (2006). When scat samples tested positive for mtDNA from a *Canis* species, we attempted to identify individuals using 17 microsatellite loci following methods outlined by Bohling and Waits (2011). Loci were amplified in 2 separate multiplexes and alleles only were accepted if they were observed in ≥ 2 independent polymerase chain reaction (PCRs). We only accepted homozygous genotypes if they were observed in 3 independent PCRs. The probability of identity for siblings was previously calculated by Bohling and Waits (2011) at 6 loci and was sufficiently low (0.003-0.006) to differentiate individuals. We regrouped duplicate genotypes using GenAlEx to identify unique individuals (Peakall and Smouse

2006). Genotypes obtained from scats also were compared to genotypes of known red wolves and coyotes captured by the USFWS biologists.

Evaluating genetic ancestry.–Known individuals previously captured by the USFWS had been evaluated for genetic ancestry using the red wolf pedigree and a maximum likelihood-based assignment test (Adams 2006; Miller et al. 2003; Stoskopf et al. 2005). We assessed genetic ancestry (q-value) of unknown individuals using the Bayesian clustering programs STRUCTURE 2.2 (Pritchard et al. 2000) and BAPS 5.1 (Corander et al. 2003, 2006) using representatives of four species as training sets following the methods and parameters outlined by Bohling and Waits (2011). The 4 species used for this analysis were coyotes from North Carolina and Virginia (82), gray wolves from Idaho and Alaska (37), domestic dogs (27), and pure red wolves composing the current wild population (151). Pure red wolves were defined as individuals with 100% red wolf ancestry as determined by the pedigree.

A challenge with using the Bayesian programs is interpreting the output and determining criteria for assessing purity and the proportion of gene flow from an outside population (admixture). Typically, studies evaluating hybridization using Bayesian clustering programs, primarily STRUCTURE, rely solely on setting arbitrary thresholds for q-values when determining admixture (Vaha & Primmer 2006). We analyzed individuals of known ancestry using these programs to develop standardized thresholds for assessing admixture (Bohling 2011). First, an individual was automatically considered a hybrid if there was statistical evidence for admixture using BAPS or STRUCTURE. For STRUCTURE, ancestry was considered statistically significant if the credibility interval surrounding a q-value did not overlap 0. Thus, any individual with q-values for 2 or more species for which the credibility intervals did not overlap 0 was considered a hybrid. BAPS uses simulations to assess the statistical significance of ancestry coefficients and considers an individual admixed if the values are significant at $p < 0.1$ (Corander et al. 2006; Corander & Marttinen 2006), which we also used as a threshold of admixture for our samples. If either the STRUCTURE credibility intervals or BAPS classified an individual as admixed, we considered it a hybrid. If the STRUCTURE credibility intervals and BAPS classified an individual as a pure member of different groups, we also classified the individual as hybrid.

We developed an additional criterion based on STRUCTURE q-values: any individuals with q-values < 0.75 for all 4 putative taxonomic groups were classified as hybrids. Our experience suggests that a maximum q-value for any one group between 0.75 and 0.8 typically indicates hybrid ancestry. To be conservative, we also classified those individuals as hybrids. We considered any individual with a q-value >0.8 to be a member of that taxonomic group. Although, the 0.9 q-value threshold has been frequently used in the literature, our experience and other studies strongly suggest that the 0.8 q-value is adequate (Barilani et al. 2007; Beaumont et al. 2001; Oliveira et al. 2008; Sanz et al. 2009; Trigo et al. 2008; Vaha & Primmer 2006; Yokoyama et al. 2009).

Diet Analysis.—We placed any scat identified as red wolf or coyote in nylon hosiery and laundered it in a washing machine using the gentle cycle, hot water, and detergent; contents that remained in the hosiery after washing were dried in a 65 ^{o}C oven for 4 hours. We identified prey species by microscopically and macroscopically comparing hair, bone, tooth, claw, and hoof fragments found in a scat to reference collections and identification manuals (Debelica and Theis 2009; Moore et al. 1997). Food items visually estimated to comprise

<1% by volume of the scat were excluded to minimize bias associated with overestimation (Kelly 1991; Knowlton 1964).

Data Analysis.—Recording each food item as present or absent in a single scat yields a structure similar to capture histories for closed-capture, capture-mark-recapture data and thus allows the use of Program MARK to analyze diets (Lemons et al. 2010). We placed food items into 6 categories: white-tailed deer, rabbits, small rodents (house mice, marsh rice rats, white-footed mice, eastern harvest mice, hispid cotton rats), other mammals (muskrats, raccoons, domestic and feral hogs), vegetation [corn (*Zea mays*), blackberry (*Rubus* spp.), persimmon (*Diospyros virginianas)*, Poaceae)], and other (e.g. insects, trash). Each category was recorded as present or absent with a 0 or 1 in a multinomial sequence for each scat. We analyzed diet data using Huggins' (1989) models for closed populations in Program MARK and calculated the overdispersion parameter $\hat{c}$ using a goodness of fit statistic (Anderson et al. 1994; Burnham and Anderson 2002; Lemons et al. 2010; Williams et al. 2002). Because $\hat{c}$ was determined to be 1.23, we used quasi–AIC_c ($QAIC_c$) values for our analysis.

We built 6 models to examine the best predictor of canid diets; the variables in these models included canid taxon, time divided into biological periods, and time divided into calendar periods (Table 1). Biological periods were defined as pair bonding (December-February), pup rearing (March-May), and dispersal (June-November, Morey 2007). Calendar periods were spring (March-May), summer (June-August), fall (September-November), and winter (December-February). The first three models used calendar period, biological period, or canid taxon individually as the predictor. Models 4 and 5 included interaction between canid taxon and biological period and interaction between canid taxon and calendar period. The last model was a fully parameterized model and included all 3 variables.

To develop results comparable to previous studies, we also calculated percent occurrence for diet categories. We defined percent occurrence for each canid as the number of times a food item occurred divided by the total number of occurrences of all food items (Schrecengost et al.2008).

RESULTS

From 1,163 scats, we identified an individual genotype for 228 scats (Appendix B). The remaining scats were either those of hybrids or non-target taxa or were unable to be identified using faecal DNA genotyping due to low quality DNA of the scats. Of those 228 scats, 179 were identified as red wolf (49 individuals) and 64 as coyote (34 individuals). No identifiable coyote scats were collected in February or October - December 2009.

Rabbits, white-tailed deer, and rodents were the prey most frequently eaten by red wolves and coyotes (Figure 1; Table 2). The scats of red wolves contained white-tailed deer in every month. Rodents appeared in 15% of red wolf scats and 33% of coyote scats (Table 2). Raccoons appeared only in 4 red wolf scats and 2 of these occurrences were from scats from the same individual that were collected close together. Other mesopredators were not detected in any scats. A single item made up greater than 95% of the scat volume in 55% of the coyote and 71% of the red wolf scats.

The only competitive mark-recapture model ($\Delta QAIC_c \leq 2$) included only calendar period as a predictor for canid diet (Table 1) and models including taxon comparisons all had

$\Delta QAIC_c > 12$ and had extremely low weights. Parameter estimates from this model indicated more rodents were consumed during the spring than during the summer (Figure 2). Diets did not differ over time when the sampling period was divided into biological periods, nor did diet differ between red wolves and coyotes (Figure 1; Table 1).

DISCUSSION

Diets of red wolves and coyotes were similar, indicating significant year round overlap in the diets of members of the 2 taxa. Although there are no previous comparisons of diets of red wolves and coyotes, comparisons between gray wolf and coyote diets have shown varying degrees of overlap and resource partitioning (Meleshko 1986; Thurber 1992). Similar diets of co-occurring taxa may imply spatial or temporal separation between the 2 or a super abundance of prey (Johnson et al. 1996). Given the low human populations, large expanses of open space, and extensive cover of agricultural fields in our study area, high prey abundance was likely.

The change in the diet of red wolves and coyotes between the spring and summer calendar periods likely was related to changing prey availability. Seasonal variation in food items has been reported in canid food habit studies (Gese et al. 1988; Smith and Kennedy 1983). Litvaitis and Shaw (1980) noted the highest trapping success of rodents and greatest frequency of rodents in coyote scats occurred during winter, and Harrison and Harrison (1984) documented a correlation between availability and amount of berries found in coyote scats. However, further study of prey abundance and diet items across replicated seasons is needed to determine if changes in canid diets in our study area can be attributed to seasonal prey availability.

The diet of coyotes in eastern North Carolina appears generally similar to coyote diets in other areas in the southeastern United States. Our results suggest insects and vegetation are relatively unimportant for these coyotes, which is in contrast to results of some other studies in the southeastern United States (Blanton 1988; Schrecengost et al. 2008; Smith and Kennedy 1983, Stratman and Pelton 1997). We suspect, however, that our results may underestimate insects and vegetation. We commonly detected orthopterans, primarily grasshoppers, in scats but these items rarely contributed >1% of the scat volume, and were thus excluded from our analysis. Additionally, we collected several scats composed entirely of orthopterans or persimmon and blackberry seeds, but lack of faecal material prevented collection of useable DNA samples and species identification was unsuccessful in these cases.

Several recent studies have suggested that coyotes may be suppressing white-tailed deer populations in the eastern United States through fawn, and possibly adult, mortality (Kilgo et al. 2010; Schrecengost et al. 2008). Our diet analyses showed white-tailed deer was an important component of red wolf and coyote diets year round. Although we did not differentiate adult deer from fawns, several scats contained small hooves, bones, and teeth indicative of fawns. Coyote diet studies in other states suggested cervid carrion may make up a large proportion of the diet (Arjo and Pletscher 1999; Switalski 2003), but we were unable to determine the amount of deer consumed as carrion.

Species identification using faecal DNA ensured scats used in our analyses were of target taxa (Bohling and Waits 2011, Farrell et al. 2000). Previous food habit studies of wolves and coyotes used scat size as a determinate of animal origin, excluding extremely large or small scats to avoid inclusion of feral dogs, foxes, and bobcats (Arjo et al. 2002; Carrera et al. 2008; Schrecengost et al. 2008). Despite the poor success rate of species identification (26.5% for our study), excluding non-canid scats from our analysis and positively identifying scats from red wolves and coyotes increased the accuracy of our study.

Our results show that the diets of red wolves and coyotes do not to differ significantly in eastern North Carolina where their ranges overlap. Although food may have been abundant during our study, thereby masking potential resource partitioning, we believe that red wolves and coyotes coexist in eastern North Carolina due to mechanisms other than prey partitioning. Additionally, the diet similarity between the 2 taxa suggests that red wolves and coyotes affect prey populations similarly and may be partially fulfilling the historic, ecological, large carnivore niche in the southeastern United States.

ACKNOWLEDGMENTS

This project was funded by the North Carolina Wildlife Resource Commission and the North Carolina State University Fisheries, Wildlife, and Conservation Biology Program. A. Facka and P. Lemons provided help with data analysis. J. Hinton and J. Dellinger provided assistance with scat collection and diet analysis. C. Daystar, S. Lasher, and L. Green helped with diet analysis. Lab assistance was provided by E. Herrera, A. Knapp and M. Sterling. We also thank the USFWS Red Wolf Recovery team for help in scat collection and facilitating access to USFWS properties. Weyerhaeuser Company, Matamuskeet Ventures, and other local landowners also allowed access to their properties.

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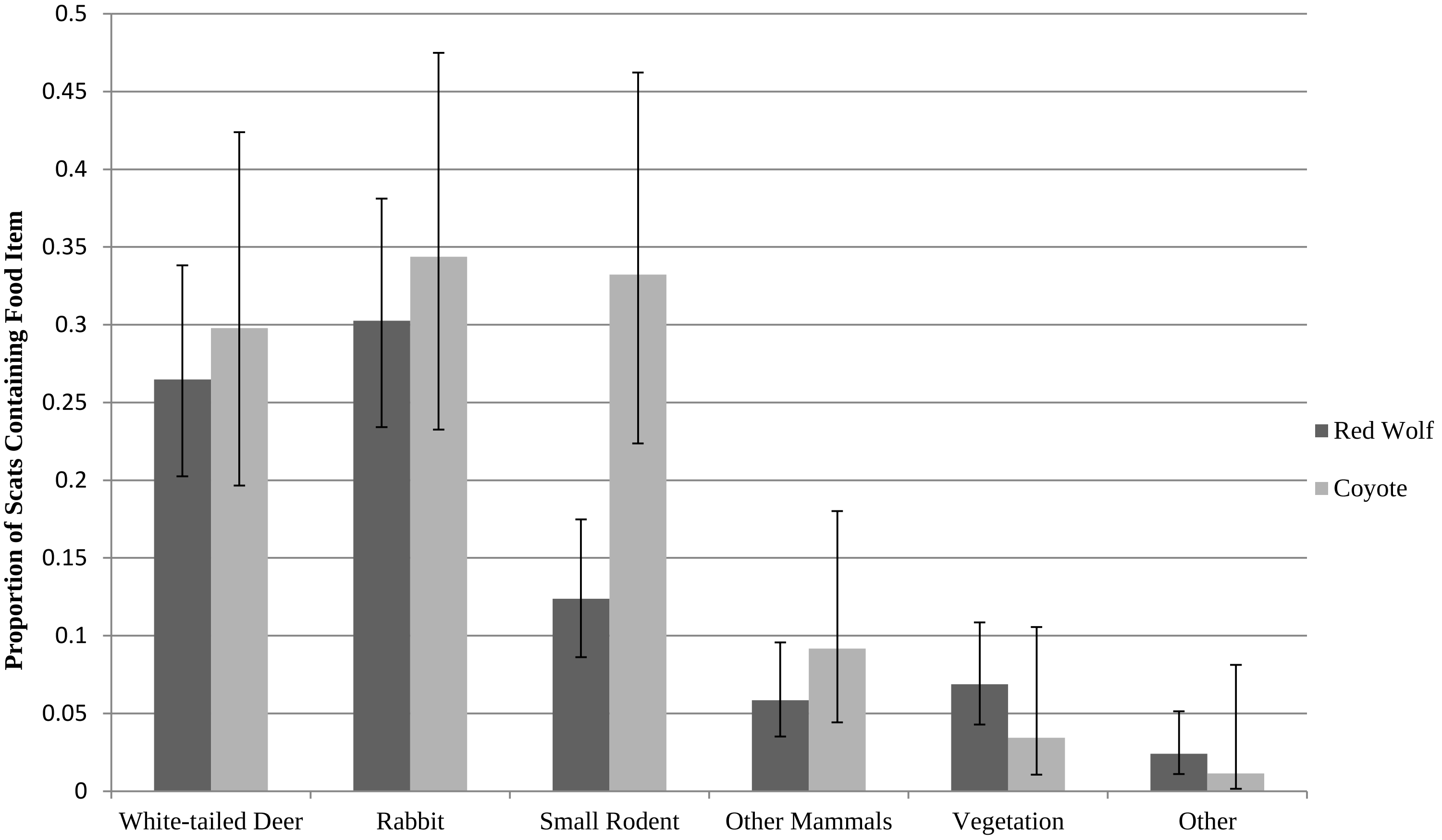

Figure1.—Diet estimates for red wolves and coyotes from Program MARK from January 2009 to February 2010 in eastern North Carolina. Error bars represent 95% confidence intervals.

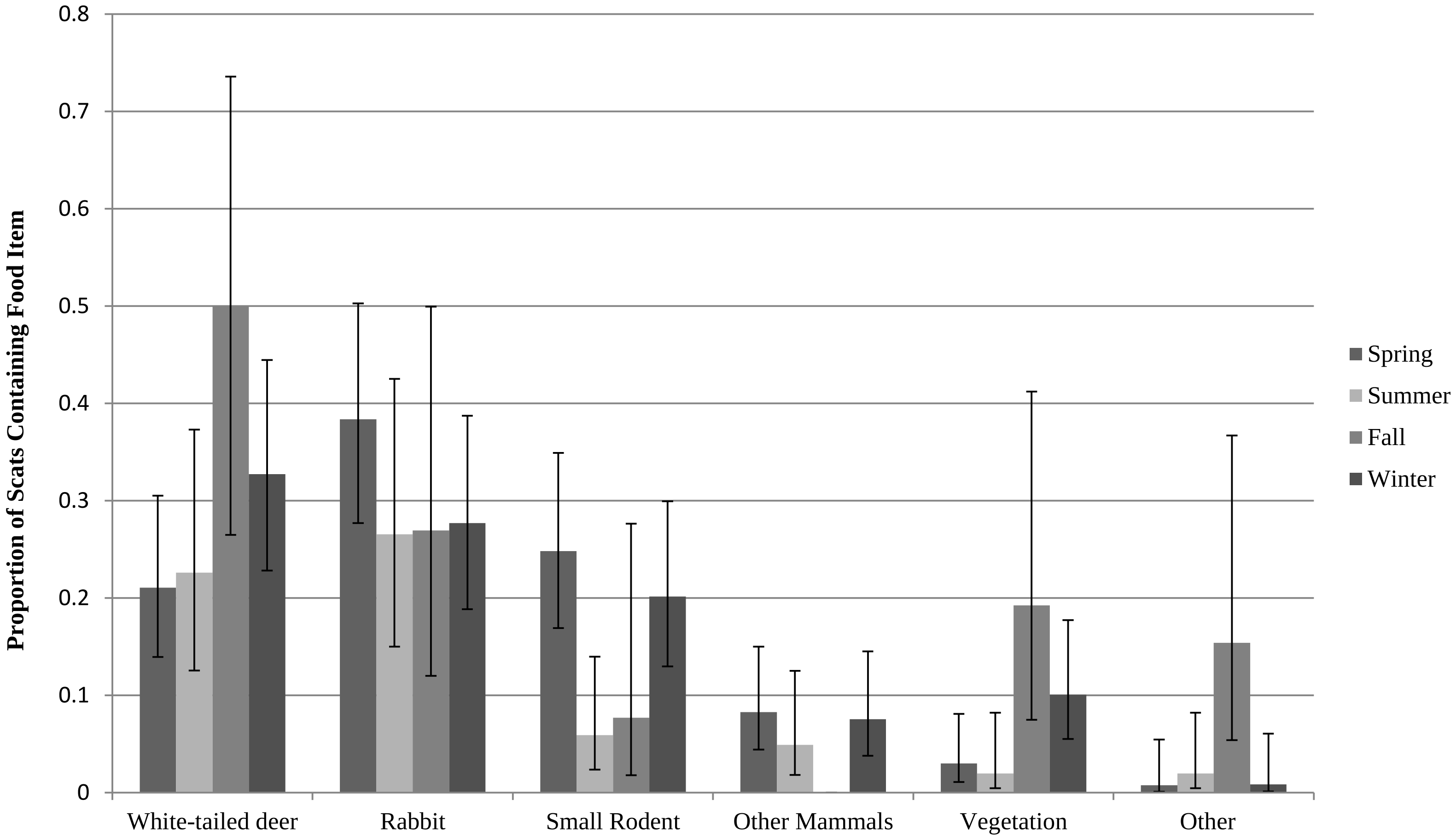

Figure 2.—Diet estimates of large canids by calendar period from Program MARK from January 2009 to February 2010 in eastern North Carolina. Error bars represent 95% confidence intervals.

Table 1. —Model sets and model results used to estimate diets of red wolves and coyotes from January 2009 to February 2010 in eastern North Carolina.

Model[a]	$QAIC_c$	ΔQAICc	Model Weight	K[b]
cl	1135.8714	0	0.94108	24
bp	1141.5873	5.7159	0.05401	18
tx	1148.0088	12.1374	0.00218	12
tx*bp	1148.9833	13.1119	0.00134	36
tx*cl	1150.2845	14.4131	0.0007	48
tx*bp*cl	1150.2845	14.4131	0.0007	48

[a] Model notation: cl = calendar period, bp = biological period , tx= taxon
[b] K = number of parameters in model

Table 2.—Number of occurrences and percent occurrence of food items in *Canis rufus* (n=179) and *Canis latrans* (n=64) scats from January 2009 to February 2010 in eastern North Carolina.

Taxa	*Canis rufus* No. (%)	*Canis latrans* No. (%)
White-tailed deer	77 (31.2)	25 (24.8)
Rabbits (*Sylviligus* spp.)	88 (35.6)	30 (29.7)
Small Rodents	38(15.4)	33(32.7)
Other Mammals	15(6.1)	8(7.9)
Vegetation	22(8.9)	3(3.0)
Other	7(2.8)	2(2.0)

CHAPTER 3

Diameter Thresholds for Distinguishing Between Red Wolf and Other Canid Scat

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Abstract: Differentiation between scats of sympatric canid species is important for determining species-specific presence and movements, but distinction in the field is difficult. We calculated upper and lower thresholds of scat diameters to distinguish between scats of red wolves and scats of coyotes and coyote-wolf hybrids in the field. We used DNA genotyping to identify scats collected in the field and took diameter measurements of those scats. Based on normal-distribution probability functions of scat diameters, scats ≥29 mm in diameter were at least 95% certain to be of red wolf origin. Conversely, scats ≤14 mm in diameter were 95% certain to be of coyote or hybrid origin. Scats >14 mm and <29 mm in diameter could not be identified by diameter alone. We suggest these upper and lower thresholds of scat diameters be used in concert with other methods (e.g., DNA genotyping) to monitor for red wolf, coyote, and hybrid activity to help conserve a lone, free-ranging population of wild red wolves.

WILDLIFE SOCIETY BULLETIN 35(4):416-420

Key words: **Red wolf, *Canis rufus*, scat, coyote, *Canis latrans*, hybrid, DNA genotyping.**

Since 1987, the United States Fish and Wildlife Service (USFWS) has managed the only free-ranging population of red wolves (*Canis rufus*) in the 6,650- km^2 Red Wolf Recovery Experimental Population Area (RWREPA) on the Albemarle Peninsula in North Carolina, USA. A major threat to this endangered species in the wild is hybridization with coyotes (*Canis latrans*; Phillips et al. 2003). Biologists routinely monitor location and movement of packs of red wolves within the recovery area as well as co-occurring coyotes to attempt to reduce hybridization between the two canids.

Current monitoring techniques include tracking animals fitted with GPS and VHF collars and identification of scats using faecal DNA genotyping methods (Adams and Waits 2007, Chadwick et al. 2010). While faecal DNA genotyping is a generally reliable method, it has some drawbacks: high cost (~$60/sample); taking several months to conduct genetic testing to determine species of origin of scats; and requiring high-quality DNA, typically from fresh scats (Adams et al. 2003). Direct identification of scats in the field would aid in monitoring presence and movement of red wolves across the RWREPA, but criteria to distinguish scats of red wolves from scats of coyotes and coyote-wolf hybrids are not available. Herein, we describe guidelines for distinguishing scats of coyotes and hybrids from red wolves based on scat morphology.

STUDY AREA

The RWREPA is comprised of >6,650 km^2 of federal, state, and private lands in five counties (Beaufort, Dare, Hyde, Tyrrell, and Washington) on the Albemarle Peninsula in North Carolina. Federal lands included Alligator River National Wildlife Refuge, Pocosin Lakes National Wildlife Refuge, and a bombing range shared by the United States Navy and Air Force. State lands included numerous game lands, while private lands were primarily pine plantations and agricultural fields. Types of land cover and approximate percentage of area were agricultural fields (30%); commercial pine (*Pinus* spp.) plantations (15%); pocosin (15%; *Pinus serotina* and *Persea palustris*); non-riverine swamp forests (10%; *Nyassa* spp., *Liquidambar styraciflua*, *Acer rubrum,* and *Chamaecyparis thyoides*); saltwater marsh or open water (10%); and other types of land cover (10%). Climate was characterized by four full seasons of nearly equal length with annual precipitation averaging 127 cm. Temperatures averaged 5°C in and to 27°C in summer. Elevation was from sea level to 50m (Beck et al. 2009). Potential prey included white-tailed deer (*Odocoileus virginianus*), rabbits (*Sylvilagus floridanus and Sylvilagus palustris*), raccoons (*Procyon lotor*), feral hogs (*Sus scrofa*), nutria (*Myocastor coypus*), muskrats (*Ondatra zibethicus*), small rodents (*Sigmodon hispidus, Mus musculus, Oryzomys palustris,* and *Reithrodontomys humulis*), and ground-dwelling birds (*Colinus virginianus* and *Meleagris gallopavo*; Phillips et al. 2003).

Co-occurring carnivores included gray foxes (*Urocyon cinereoargenteus*), red foxes (*Vulpes vulpes*), red wolves (*Canis rufus*), coyotes (*Canis latrans*), coyote-red wolf hybrids (*Canis rufus x latrans*), feral dogs (*Canis lupus familiaris*), bobcats (*Lynx rufus*), and American black bears (*Ursus americanus*).

METHODS

During February 2009-March 2010, scats of canids were collected by systematically traveling game trails and unpaved roads within the RWREPA at least once per month (Fig. 1). Maximum diameter of scats at the widest point was measured once to the nearest 1 mm using calipers. Following measurements, faecal matter was removed from each scat and stored in a buffer solution for DNA genotyping (Adams et al. 2003). We attempted to identify all scats using faecal DNA genotyping. Fecal matter was extracted from vials using the 13 Qiagen DNA Stool Kit (Qiagen Inc., Valencia, CA) and a mitochondrial-DNA fragment test was conducted to determine if the animal that produced the scat was a canid (Onorato et al. 2006). Scats that tested positive for mtDNA of *Canis* were screened at nine microsatellite loci (CXX172, CXX173, CXX20, CXX200, CXX109, CXX250, Ostrander et al. 1993; AHT103, AHT121, Holmes et al. 1995; CXX377, Mellersh et al. 1997). Two PCRs were performed using the nine microsatellite loci above, and scats that failed to amplify at ≥5 loci were removed from further analysis. Genotypes of scats that amplified at ≥5 loci for the two PCRs combined were compared to genotypes of known red wolves and coyotes within the RWREPA (Adams et al. 2007). Scats with genotypes not matching those of known individuals were analyzed in program Structure 2.3.3 (Pritchard et al. 2000). Scats with genotypes not matching those of known individuals but having ≥85% probability of being red wolf or coyote based on program Structure 2.3.3 were labeled accordingly; otherwise scats were labeled as hybrid (Pritchard et al. 2000). Once faecal DNA genotyping was complete, all comparative analyses involved two groupings: 1) scats of red wolves and 2) scats of coyotes and hybrids combined.

Because items in scats could potentially influence scat diameters, composition of scats was determined. Scats were washed individually and dried for 48 hours and food items were identified using reference keys. We used percent frequency of occurrence to determine contribution of prey items to scats (Ciucci et al. 1996). Scats containing more than one prey item were listed as containing only the prey item representing the majority of the scat. In all cases, prey items representing the majority of the scat accounted for the majority of the mass. An Anderson-Darling test for normality demonstrated that diameters of scats grouped by prey item were not normally distributed ($P < 0.05$), furthermore sample sizes were unequal. Thus, we used a Kruskal-Wallis test to assess the influence of prey items in scats on diameters of scats of red wolves and scats of coyotes and hybrids.

An Anderson-Darling test for normality demonstrated that diameters of scats grouped by species of origin were not normally distributed ($P < 0.05$), furthermore sample sizes were unequal. Thus, we used a Mann-Whitney U-test to determine if diameters of scats of red wolves and scats of coyotes and hybrids differed. We constructed normal-distribution probability functions to estimate an upper threshold in diameter of scats of coyotes and hybrids, above which one could be 95% certain scats greater than or equal to this diameter were not of coyote or hybrid origin. Similarly, we used normal-distribution probability functions to estimate a lower threshold in diameter of scats of red wolves, below which one could be 95% certain scats less than or equal to this diameter were not of red wolf origin. All normal-distribution probability functions were based on mean and standard deviation of scats of interest (i.e., diameters of scats of coyotes and hybrids for upper threshold and diameters of scats of red wolves for lower threshold).

RESULTS

Of 1377 scats collected, we identified 254 as red wolf, 57 as coyote, and 54 as hybrid using faecal DNA genotyping. We were unable to identify the remaining scats using faecal DNA genotyping due to low quality of DNA of scats. We were able to amplify only 26.5% of scats which is similar to Adams et al. (2007). Diameters of scats of the two groups overlapped considerably (Fig. 2). Mean (± 1 SD) maximum diameter of scats of coyotes and hybrids was 19 ± 6 mm (range: 10-35 mm). Mean (± 1 SD) maximum diameter of scats of red wolves was 24 ± 6 mm (range: 10-43 mm). Median diameters of scats of red wolves (24 mm) and scats of coyotes and hybrids (19 mm) were different ($P < 0.01$).

Analysis of scats of red wolves revealed seven prey groups (Table 1). The dominant prey item in scats had no effect on median diameters of red wolf scats ($P = 0.28$) or median diameters of scats coyote and hybrid scats ($P = 0.32$).

Normal-distribution probability functions resulted in upper and lower 95% certainty thresholds of 29 and 14 mm, respectively. Scats within the RWREPA ≥29 mm in diameter were 95% certain not to be of coyote or hybrid origin. Conversely, scats within the

RWREPA ≤14 mm in diameter are 95% certain not to be of red wolf origin. Scats with diameters > 14 mm and < 29 mm could not be assigned based on diameter alone.

Four percent of scats of coyotes and hybrids were equal to or exceeded the separation point of 29 mm established using normal-distribution probability functions. The largest diameter for scat of a coyote or hybrid was 35 mm. Conversely, 24% of scats of red wolves in our study were equal to or exceeded this same separation point. Five percent of scats of red wolves were equal to or less than the separation point of 14 mm established using normal-distribution probability functions. The smallest diameter for scat of a red wolf, at 10mm, was equal to the smallest diameter for scat of a coyote or hybrid. Conversely, 24% of scats of coyotes and hybrids were equal to or less than 14 mm.

DISCUSSION

Scat diameters and ranges from our study were similar to those of Weaver and Fritts (1979) who reported mean diameters of 21 and 27 mm (range = 7-34 and 13-47 mm) for coyotes and gray wolves (*Canis lupus*), respectively. Also, diameters of scats and ranges were similar to those of Reed (2004) who reported mean diameters of 23 and 26 mm (range = 17-28 and 16-36 mm) for coyotes and Mexican gray wolves (*Canis lupus baileyi*), respectively. Our results agree with Weaver and Fritts (1979) that the dominant prey item has no effect on median diameters of scats of large canids. Diameters and ranges from these studies have been accepted and used to study and compare diets and movements of both Mexican and gray wolves with those of coyotes where they co-occur (Arjo et al. 2002, Carrera et al. 2008). Thus we suggest diameters and ranges from our study are acceptable standards for distinction between coyote and red wolf scats where they co-occur.

Domestic dogs (*Canis lupus familiaris*) are present in the RWREPA but in low numbers and experience low survival (C. Lucash, USFWS, personal communication). Thus canid scats ≥29 mm in diameter are likely red wolf. We suggest 29 mm as an upper threshold for distinguishing scats of red wolves from scats of coyotes, hybrids and smaller canids (e.g., red foxes and gray foxes) within the RWREPA. We suggest DNA genotyping need not be used to identify scats of red wolves when the diameter is ≤ 14mm or ≥ 29mm.

Use of these thresholds alone is likely to lead to considerable loss of information due to exclusion of scats of red wolves <29 mm in diameter. In this study, 76% of red wolf scats collected could not be distinguished from coyote and hybrid scats based on diameter. Similarly, 76% of coyote and hybrid scats collected could not be distinguished from red wolf scats based on diameter. Scats of canids with diameters of 15-28 mm will not be identifiable based on diameter alone so other techniques such as DNA genotyping will be required (Adams et al. 2003, Adams and Waits 2007). Co-occurrence of scats ≥29 mm in diameter and scats <29 mm in diameter could represent the pairing of a red wolf with a coyote or hybrid, different sized scats from the same red wolf or pack of red wolves, or a transient coyote or hybrid.

Though the above thresholds only appear to allow for identification of ~25% of red wolf scats and coyote and hybrid scats in the RWREPA, this cost-effective monitoring alternative translates into a savings of $1500 for every 100 canids scats sampled at present analysis cost ($60/sample). While diameters of scats can be influenced by environmental factors, we feel that the simplicity of this method coupled with financial savings facilitate its use. Faecal DNA genotyping is precise, but requires fresh scats to ensure high quality DNA, costly equipment, training to use the equipment, and an advance understanding of genetics (Adams et al. 2007). Use of scat diameters to identify scats would be most beneficial to studies with low budgets and interested in monitoring the distribution of a species at the population level, while faecal DNA genotyping would be most beneficial to studies wanting to monitor and distinguish individuals within a population.

Though the above thresholds are only immediately applicable to biologists in and around the RWREPA, it is important to realize that the methodology is applicable to other species. For example, distinguishing scats of endangered Canada lynx (*Lynx canadensis*) from those of bobcats, or scats of endangered grizzly bears (*Ursus arctos*) from those of American black bears. This method could allow biologists to rapidly and cost-effectively monitor the distribution and location of a number of rare and endangered species. However, datasets used to develop diameter thresholds of scats for distinguishing among co-occurring species should be as large as is feasibly possible to develop robust thresholds. Failing to do so could result in thresholds that are poor at discriminating scats of co-occurring species and could lead to misinterpreting the location or distribution of the species of interest. For example, misidentification of a coyote scat in the RWREPA as a red wolf scat could result in the occupation of a coyote in red wolf territory. This individual than has the potential to mate with a red wolf, resulting in a hybrid offspring, which is the number one threat to the existence of the red wolf (Adams et al. 2006).

MANAGEMENT IMPLICATIONS

Biologists routinely monitor location and movement of packs of red wolves within the recovery area as well as co-occurring coyotes to attempt to reduce hybridization between the two canids. Effective restoration and management of the only free-ranging population of red wolves requires biologists to have access to and knowledge of fast and efficient field identification techniques. Rapid identification of scats of red wolves from scats of coyotes, coyote-wolf hybrids, and smaller canids based on diameters of scats provides a cost effective alternative to DNA genotyping for monitoring movements of red wolves and co-occurring canids. However, DNA genotyping is an important method for distinguishing between red wolf scats and coyote and hybrid scats and will likely be required to identify ~75% of canid scats collected in the RWREPA. Use of such field identification techniques, whether based on diameters of scats or other metrics of identification (e.g. mass of scats or size of tracks), is easily adapted to other situations of management concern and would be useful elsewhere to rapidly and cost-effectively monitor the distribution and location of a number of rare and endangered species.

Acknowledgments. We thank C. Lucash for help in collection of scats and gaining access to public and private lands. The North Carolina Wildlife Resources Commission; The Fisheries, Wildlife, and Conservation Biology Program at North Carolina State University; and Auburn University provided funding and resources. Weyerhaeuser Company provided access to its lands. J. Bohling and L. Waits identified scats via faecal DNA genotyping at a considerably reduced cost.

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Table 1. Diameters of scats of red wolves and scats of coyotes and hybrids grouped by primary prey found in scats collected within the Red Wolf Recovery Experimental Population Area from 2009-2010. Species: RW (red wolf), C/H (coyote and hybrid). N = number of scats with corresponding prey as primary prey item. M = median diameter of scats with corresponding primary prey item.

Prey Item	Red wolf		Coyote and Hybrid	
	N	M (mm)	N	M (mm)
White-tailed deer (*Odocoileus virginianus*)	97	25	36	20
Large rodent[a]	13	25	2	24
Small rodent[b]	32	23	22	20
Rabbit[c]	84	23	49	16
Feral and domestic hog (*Sus scrofa*)	11	23	2	26
Raccoon (*Procyon lotor*)	12	28	n/a	
Insect[d]	5	22	n/a	

[a] Nutria (*Myocastor coypu*) and muskrat (*Ondatra zibethicus*)

[b] Primarily hispid cotton rat (*Sigmodon hispidus*) and house mouse (*Mus musculus*)

[c] Marsh rabbit (*Sylvilagus palustris*) and eastern cottontail (*Sylvilagus floridanus*)

[d] Primarily grasshoppers family *Acrididae*

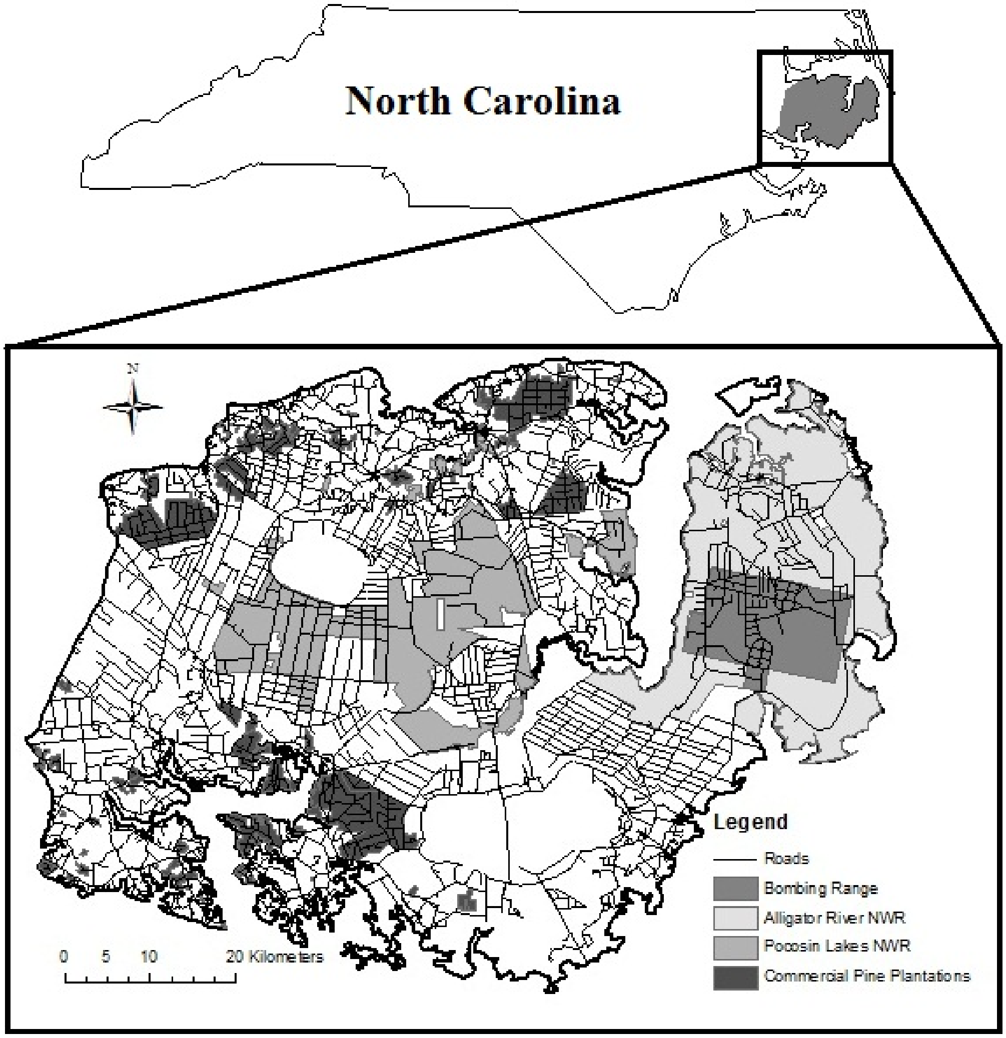


Figure 1. Landownership in the Red Wolf Recovery Experimental Population Area in northeastern North Carolina, USA (2009-2010).

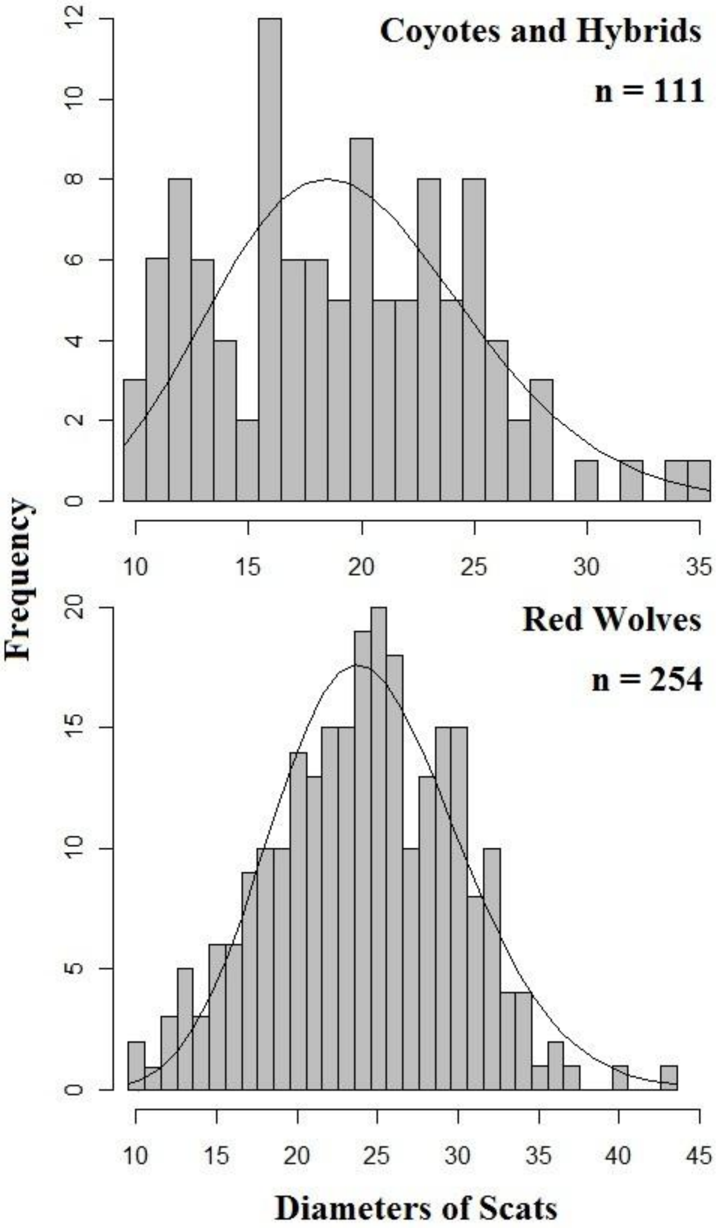


Figure 2. Diameters of coyote and hybrid scats (top; n = 111) and red wolf scats (bottom; n = 254) in the Red Wolf Recovery Experimental Population Area in northeastern North Carolina, USA (2009-2010).

Appendices

Appendix A

Results from Structure 2.2

	Structure P-values				Confidence intervals				
Individual	Coyote	Gray wolf	Dog	Red wolf	Coyote 95% CI	Gray wolf 95% CI	Dog 95% CI	Red wolf 95%CI	Assessment
Canid1	0.8	0.102	0.08	0.018	(0.535,0.988)	(0.000,0.354)	(0.000,0.268)	(0.000,0.089)	Coyote
Canid2	0.819	0.018	0.072	0.091	(0.596,0.985)	(0.000,0.091)	(0.000,0.271)	(0.000,0.275)	Coyote
Canid3	0.088	0.018	0.013	0.881	(0.003,0.236)	(0.000,0.090)	(0.000,0.067)	(0.722,0.983)	Red Wolf
Canid4	0.029	0.017	0.019	0.934	(0.000,0.140)	(0.000,0.087)	(0.000,0.094)	(0.792,0.999)	Red Wolf
Canid5	0.81	0.033	0.066	0.09	(0.519,0.994)	(0.000,0.161)	(0.000,0.272)	(0.000,0.333)	Coyote
Canid6	0.843	0.043	0.079	0.035	(0.574,0.997)	(0.000,0.201)	(0.000,0.316)	(0.000,0.165)	Coyote
Canid7	0.872	0.022	0.048	0.059	(0.632,0.998)	(0.000,0.107)	(0.000,0.213)	(0.000,0.248)	Coyote
Canid8	0.783	0.057	0.051	0.109	(0.529,0.976)	(0.000,0.229)	(0.000,0.212)	(0.000,0.309)	Likely Hybrid
Canid9	0.319	0.028	0.051	0.602	(0.117,0.537)	(0.000,0.136)	(0.000,0.208)	(0.401,0.782)	Hybrid
Canid10	0.703	0.088	0.051	0.158	(0.426,0.949)	(0.000,0.313)	(0.000,0.219)	(0.000,0.394)	Hybrid
Canid11	0.822	0.092	0.06	0.026	(0.505,0.996)	(0.000,0.366)	(0.000,0.269)	(0.000,0.131)	Coyote
Canid12	0.619	0.179	0.067	0.136	(0.258,0.948)	(0.000,0.542)	(0.000,0.310)	(0.000,0.405)	Hybrid
Canid13	0.776	0.171	0.034	0.018	(0.447,0.994)	(0.000,0.489)	(0.000,0.168)	(0.000,0.090)	Likely Hybrid
Canid14	0.858	0.048	0.07	0.023	(0.584,0.997)	(0.000,0.217)	(0.000,0.306)	(0.000,0.115)	Coyote
Canid15	0.725	0.174	0.06	0.041	(0.447,0.960)	(0.000,0.453)	(0.000,0.259)	(0.000,0.184)	Hybrid
Canid16	0.037	0.043	0.872	0.047	(0.000,0.186)	(0.000,0.215)	(0.600,0.998)	(0.000,0.220)	Dog
Canid17	0.913	0.018	0.046	0.024	(0.712,0.999)	(0.000,0.089)	(0.000,0.216)	(0.000,0.118)	Coyote
Canid18	0.119	0.019	0.025	0.837	(0.005,0.323)	(0.000,0.095)	(0.000,0.125)	(0.614,0.977)	Red Wolf
Canid19	0.032	0.063	0.056	0.849	(0.000,0.155)	(0.000,0.252)	(0.000,0.231)	(0.629,0.994)	Red Wolf
Canid20	0.077	0.366	0.434	0.123	(0.000,0.299)	(0.077,0.662)	(0.082,0.765)	(0.000,0.364)	Hybrid
Canid21	0.213	0.087	0.613	0.086	(0.018,0.471)	(0.000,0.337)	(0.272,0.891)	(0.000,0.300)	Hybrid
Canid22	0.021	0.025	0.015	0.939	(0.000,0.103)	(0.000,0.119)	(0.000,0.077)	(0.808,0.999)	Red Wolf
Canid24	0.884	0.051	0.039	0.026	(0.644,0.999)	(0.000,0.233)	(0.000,0.192)	(0.000,0.129)	Coyote
Canid25	0.831	0.073	0.048	0.047	(0.583,0.992)	(0.000,0.286)	(0.000,0.201)	(0.000,0.185)	Coyote
Canid26	0.033	0.129	0.779	0.06	(0.000,0.159)	(0.000,0.385)	(0.489,0.980)	(0.000,0.245)	Likely Hybrid
Canid27	0.141	0.114	0.693	0.052	(0.000,0.597)	(0.000,0.492)	(0.064,0.994)	(0.000,0.240)	Hybrid
Canid28	0.034	0.129	0.783	0.055	(0.000,0.163)	(0.000,0.365)	(0.520,0.975)	(0.000,0.234)	Likely Hybrid
Canid29	0.163	0.194	0.544	0.099	(0.000,0.471)	(0.000,0.523)	(0.196,0.863)	(0.000,0.340)	Hybrid
Canid30	0.935	0.018	0.025	0.022	(0.787,1.000)	(0.000,0.092)	(0.000,0.124)	(0.000,0.109)	Coyote
Canid31	0.028	0.08	0.045	0.848	(0.000,0.130)	(0.000,0.250)	(0.000,0.181)	(0.686,0.962)	Red Wolf
Canid32	0.805	0.037	0.131	0.026	(0.488,0.996)	(0.000,0.180)	(0.000,0.444)	(0.000,0.131)	Coyote
Canid33	0.819	0.067	0.098	0.016	(0.535,0.995)	(0.000,0.251)	(0.000,0.344)	(0.000,0.082)	Coyote
Canid34	0.911	0.044	0.03	0.015	(0.731,0.999)	(0.000,0.195)	(0.000,0.137)	(0.000,0.076)	Coyote

Appendix A

Results from Sructure 2.2

	Structure P-values				Confidence intervals				
Individual	Coyote	Gray wolf	Dog	Red wolf	Coyote 95% CI	Gray wolf 95% CI	Dog 95% CI	Red wolf 95%CI	Assessment
Canid35	0.057	0.029	0.865	0.05	(0.000,0.276)	(0.000,0.144)	(0.585,0.998)	(0.000,0.220)	Dog
Canid36	0.896	0.045	0.027	0.032	(0.680,0.999)	(0.000,0.211)	(0.000,0.130)	(0.000,0.157)	Coyote
Canid38	0.711	0.075	0.105	0.109	(0.335,0.987)	(0.000,0.329)	(0.000,0.440)	(0.000,0.396)	Hybrid
Canid39	0.121	0.087	0.778	0.015	(0.000,0.414)	(0.000,0.283)	(0.506,0.966)	(0.000,0.074)	Likely Hybrid
Canid40	0.708	0.094	0.149	0.049	(0.364,0.984)	(0.000,0.396)	(0.000,0.504)	(0.000,0.224)	Hybrid
Canid41	0.848	0.062	0.045	0.045	(0.548,0.998)	(0.000,0.292)	(0.000,0.216)	(0.000,0.201)	Coyote
Canid42	0.727	0.036	0.156	0.081	(0.394,0.981)	(0.000,0.173)	(0.000,0.468)	(0.000,0.283)	Hybrid
Canid43	0.882	0.022	0.062	0.034	(0.624,0.999)	(0.000,0.110)	(0.000,0.284)	(0.000,0.167)	Coyote
Canid44	0.057	0.246	0.672	0.025	(0.000,0.274)	(0.000,0.816)	(0.058,0.995)	(0.000,0.128)	Hybrid
Canid45	0.56	0.058	0.308	0.074	(0.197,0.919)	(0.000,0.260)	(0.000,0.672)	(0.000,0.256)	Hybrid
Canid46	0.83	0.033	0.121	0.017	(0.493,0.998)	(0.000,0.162)	(0.000,0.447)	(0.000,0.085)	Coyote
Canid47	0.914	0.024	0.032	0.03	(0.720,0.999)	(0.000,0.122)	(0.000,0.159)	(0.000,0.149)	Coyote
Canid48	0.465	0.286	0.191	0.058	(0.113,0.838)	(0.000,0.682)	(0.000,0.577)	(0.000,0.265)	Hybrid
Canid49	0.488	0.087	0.404	0.021	(0.169,0.833)	(0.000,0.365)	(0.044,0.748)	(0.000,0.104)	Hybrid
Canid50	0.853	0.03	0.065	0.053	(0.609,0.996)	(0.000,0.144)	(0.000,0.271)	(0.000,0.211)	Coyote
Canid51	0.011	0.015	0.012	0.962	(0.000,0.054)	(0.000,0.075)	(0.000,0.063)	(0.870,1.000)	Red Wolf
Canid52	0.777	0.054	0.14	0.029	(0.475,0.989)	(0.000,0.239)	(0.000,0.414)	(0.000,0.139)	Likely Hybrid
Canid53	0.034	0.059	0.041	0.865	(0.000,0.161)	(0.000,0.234)	(0.000,0.182)	(0.667,0.993)	Red Wolf
Canid54	0.802	0.058	0.071	0.069	(0.541,0.987)	(0.000,0.239)	(0.000,0.269)	(0.000,0.244)	Coyote
Canid56	0.138	0.054	0.031	0.776	(0.000,0.344)	(0.000,0.211)	(0.000,0.151)	(0.585,0.931)	Likely Hybrid
Canid57	0.929	0.022	0.026	0.023	(0.768,0.999)	(0.000,0.109)	(0.000,0.129)	(0.000,0.114)	Coyote
Canid58	0.173	0.048	0.052	0.727	(0.002,0.420)	(0.000,0.220)	(0.000,0.228)	(0.458,0.929)	Hybrid
Canid59	0.193	0.065	0.171	0.571	(0.003,0.512)	(0.000,0.287)	(0.000,0.532)	(0.211,0.874)	Hybrid
Canid60	0.128	0.105	0.096	0.671	(0.000,0.508)	(0.000,0.399)	(0.000,0.398)	(0.268,0.945)	Hybrid
Canid61	0.157	0.161	0.088	0.594	(0.000,0.448)	(0.000,0.520)	(0.000,0.357)	(0.264,0.879)	Hybrid
Canid62	0.841	0.035	0.103	0.022	(0.566,0.996)	(0.000,0.166)	(0.000,0.369)	(0.000,0.110)	Coyote
Canid63	0.068	0.072	0.07	0.79	(0.000,0.337)	(0.000,0.338)	(0.000,0.336)	(0.372,0.997)	Likely Hybrid
Canid64	0.023	0.027	0.024	0.926	(0.000,0.117)	(0.000,0.135)	(0.000,0.122)	(0.749,1.000)	Red Wolf
Canid65	0.399	0.075	0.223	0.303	(0.101,0.744)	(0.000,0.297)	(0.000,0.536)	(0.061,0.562)	Hybrid
Canid66	0.739	0.085	0.124	0.052	(0.376,0.988)	(0.000,0.347)	(0.000,0.433)	(0.000,0.234)	Hybrid
Canid67	0.395	0.39	0.187	0.028	(0.104,0.731)	(0.001,0.774)	(0.000,0.557)	(0.000,0.140)	Hybrid
Canid68	0.604	0.037	0.229	0.13	(0.246,0.937)	(0.000,0.175)	(0.000,0.573)	(0.000,0.373)	Hybrid
Canid69	0.732	0.034	0.119	0.115	(0.436,0.963)	(0.000,0.160)	(0.000,0.403)	(0.000,0.343)	Hybrid

Appendix A
Results from Sructure 2.2

	Structure P-values				Confidence intervals				
Individual	Coyote	Gray wolf	Dog	Red wolf	Coyote 95% CI	Gray wolf 95% CI	Dog 95% CI	Red wolf 95%CI	Assessment
Canid70	0.856	0.062	0.04	0.041	(0.608,0.997)	(0.000,0.260)	(0.000,0.185)	(0.000,0.183)	Coyote
Canid71	0.276	0.046	0.645	0.033	(0.046,0.558)	(0.000,0.207)	(0.359,0.892)	(0.000,0.153)	Hybrid
Canid72	0.568	0.139	0.168	0.125	(0.269,0.861)	(0.000,0.427)	(0.000,0.459)	(0.000,0.308)	Hybrid
Canid73	0.633	0.112	0.158	0.097	(0.323,0.917)	(0.000,0.379)	(0.000,0.419)	(0.000,0.284)	Hybrid
Canid74	0.6	0.139	0.113	0.148	(0.264,0.910)	(0.000,0.443)	(0.000,0.405)	(0.000,0.374)	Hybrid
Canid77	0.05	0.051	0.142	0.757	(0.000,0.222)	(0.000,0.225)	(0.000,0.423)	(0.496,0.963)	Likely Hybrid
Canid75	0.76	0.044	0.158	0.038	(0.442,0.988)	(0.000,0.210)	(0.000,0.470)	(0.000,0.166)	Likely Hybrid
Canid76	0.135	0.029	0.027	0.809	(0.001,0.355)	(0.000,0.142)	(0.000,0.137)	(0.579,0.967)	Red Wolf
Canid78	0.022	0.023	0.026	0.93	(0.000,0.109)	(0.000,0.113)	(0.000,0.130)	(0.768,0.999)	Red Wolf
Canid79	0.552	0.088	0.2	0.16	(0.136,0.903)	(0.000,0.352)	(0.000,0.590)	(0.000,0.423)	Hybrid
Canid80	0.856	0.038	0.073	0.033	(0.557,0.998)	(0.000,0.187)	(0.000,0.333)	(0.000,0.162)	Coyote
Canid81	0.131	0.097	0.6	0.172	(0.000,0.485)	(0.000,0.418)	(0.071,0.968)	(0.000,0.488)	Hybrid
Canid82	0.402	0.085	0.097	0.416	(0.054,0.769)	(0.000,0.358)	(0.000,0.430)	(0.078,0.721)	Hybrid
Canid83	0.56	0.025	0.062	0.352	(0.281,0.817)	(0.000,0.124)	(0.000,0.278)	(0.130,0.581)	Hybrid
Canid84	0.494	0.297	0.127	0.083	(0.134,0.891)	(0.000,0.710)	(0.000,0.468)	(0.000,0.339)	Hybrid
Canid85	0.502	0.069	0.285	0.144	(0.224,0.794)	(0.000,0.273)	(0.011,0.590)	(0.000,0.361)	Hybrid
Canid86	0.454	0.154	0.35	0.042	(0.161,0.780)	(0.000,0.470)	(0.033,0.674)	(0.000,0.191)	Hybrid
Canid87	0.027	0.027	0.925	0.021	(0.000,0.134)	(0.000,0.135)	(0.755,0.999)	(0.000,0.106)	Dog
Canid88	0.791	0.148	0.035	0.025	(0.493,0.993)	(0.000,0.428)	(0.000,0.171)	(0.000,0.125)	Likely Hybrid
Canid89	0.572	0.222	0.149	0.058	(0.234,0.902)	(0.000,0.567)	(0.000,0.464)	(0.000,0.247)	Hybrid
Canid90	0.419	0.224	0.276	0.081	(0.099,0.794)	(0.000,0.569)	(0.005,0.610)	(0.000,0.323)	Hybrid
Canid91	0.71	0.109	0.156	0.025	(0.345,0.983)	(0.000,0.444)	(0.000,0.465)	(0.000,0.125)	Hybrid
Canid92	0.909	0.037	0.026	0.029	(0.714,0.999)	(0.000,0.178)	(0.000,0.128)	(0.000,0.138)	Coyote
Canid93	0.769	0.053	0.084	0.094	(0.418,0.993)	(0.000,0.247)	(0.000,0.351)	(0.000,0.387)	Likely Hybrid
Canid94	0.574	0.253	0.089	0.084	(0.262,0.891)	(0.000,0.592)	(0.000,0.339)	(0.000,0.265)	Hybrid
Canid95	0.064	0.271	0.577	0.088	(0.000,0.289)	(0.033,0.529)	(0.275,0.847)	(0.000,0.306)	Hybrid
Canid96	0.82	0.053	0.052	0.075	(0.553,0.991)	(0.000,0.226)	(0.000,0.223)	(0.000,0.287)	Coyote
Canid97	0.694	0.148	0.059	0.1	(0.372,0.958)	(0.000,0.451)	(0.000,0.257)	(0.000,0.357)	Hybrid
Canid98	0.075	0.021	0.043	0.861	(0.000,0.256)	(0.000,0.106)	(0.000,0.172)	(0.668,0.981)	Red Wolf
Canid99	0.799	0.118	0.066	0.017	(0.532,0.990)	(0.000,0.365)	(0.000,0.289)	(0.000,0.086)	Likely Hybrid
Canid100	0.823	0.035	0.095	0.047	(0.532,0.996)	(0.000,0.171)	(0.000,0.345)	(0.000,0.199)	Coyote
Canid101	0.442	0.287	0.182	0.089	(0.033,0.872)	(0.000,0.660)	(0.000,0.612)	(0.000,0.346)	Hybrid
Canid102	0.03	0.044	0.055	0.871	(0.000,0.150)	(0.000,0.217)	(0.000,0.266)	(0.598,0.998)	Red Wolf

Appendix A

Results from Sructure 2.2

	Structure P-values				Confidence intervals				
Individual	Coyote	Gray wolf	Dog	Red wolf	Coyote 95% CI	Gray wolf 95% CI	Dog 95% CI	Red wolf 95%CI	Assessment
Canid103	0.234	0.051	0.101	0.615	(0.011,0.527)	(0.000,0.246)	(0.000,0.407)	(0.314,0.860)	Hybrid
Canid104	0.211	0.1	0.672	0.018	(0.000,0.629)	(0.000,0.341)	(0.290,0.940)	(0.000,0.088)	Hybrid
Canid105	0.515	0.383	0.043	0.059	(0.139,0.941)	(0.000,0.791)	(0.000,0.205)	(0.000,0.279)	Hybrid
Canid106	0.039	0.088	0.818	0.056	(0.000,0.193)	(0.000,0.386)	(0.456,0.997)	(0.000,0.252)	Dog
Canid107	0.818	0.091	0.059	0.033	(0.532,0.994)	(0.000,0.346)	(0.000,0.244)	(0.000,0.153)	Coyote

Appendix B

Results from BAPS

	Coyote	Gray wolf	Dog	Red wolf	p-value
Canid1	1	0	0	0	1
Canid2	1	0	0	0	1
Canid3	0	0	0	1	1
Canid4	0	0	0	1	1
Canid5	1	0	0	0	1
Canid6	1	0	0	0	1
Canid7	1	0	0	0	1
Canid8	1	0	0	0	1
Canid9	0.3	0.03	0.04	0.63	0
Canid10	1	0	0	0	1
Canid11	1	0	0	0	1
Canid12	1	0	0	0	1
Canid13	1	0	0	0	1
Canid14	1	0	0	0	1
Canid15	1	0	0	0	1
Canid16	0	0	1	0	1
Canid17	1	0	0	0	1
Canid18	0	0	0	1	1
Canid19	0	0	0	1	1
Canid20	0	0	1	0	1
Canid21	0	0	1	0	1
Canid22	0	0	0	1	1
Canid24	1	0	0	0	1
Canid25	1	0	0	0	1
Canid26	0	0	1	0	1
Canid27	0	0	1	0	1
Canid28	0	0	1	0	1
Canid29	0	0	1	0	1
Canid30	1	0	0	0	1
Canid31	0	0.13	0	0.87	0.01
Canid32	1	0	0	0	1
Canid33	1	0	0	0	1
Canid34	1	0	0	0	1
Canid35	0	0	1	0	1
Canid36	1	0	0	0	1
Canid37	1	0	0	0	1

Appendix B
Results from BAPS

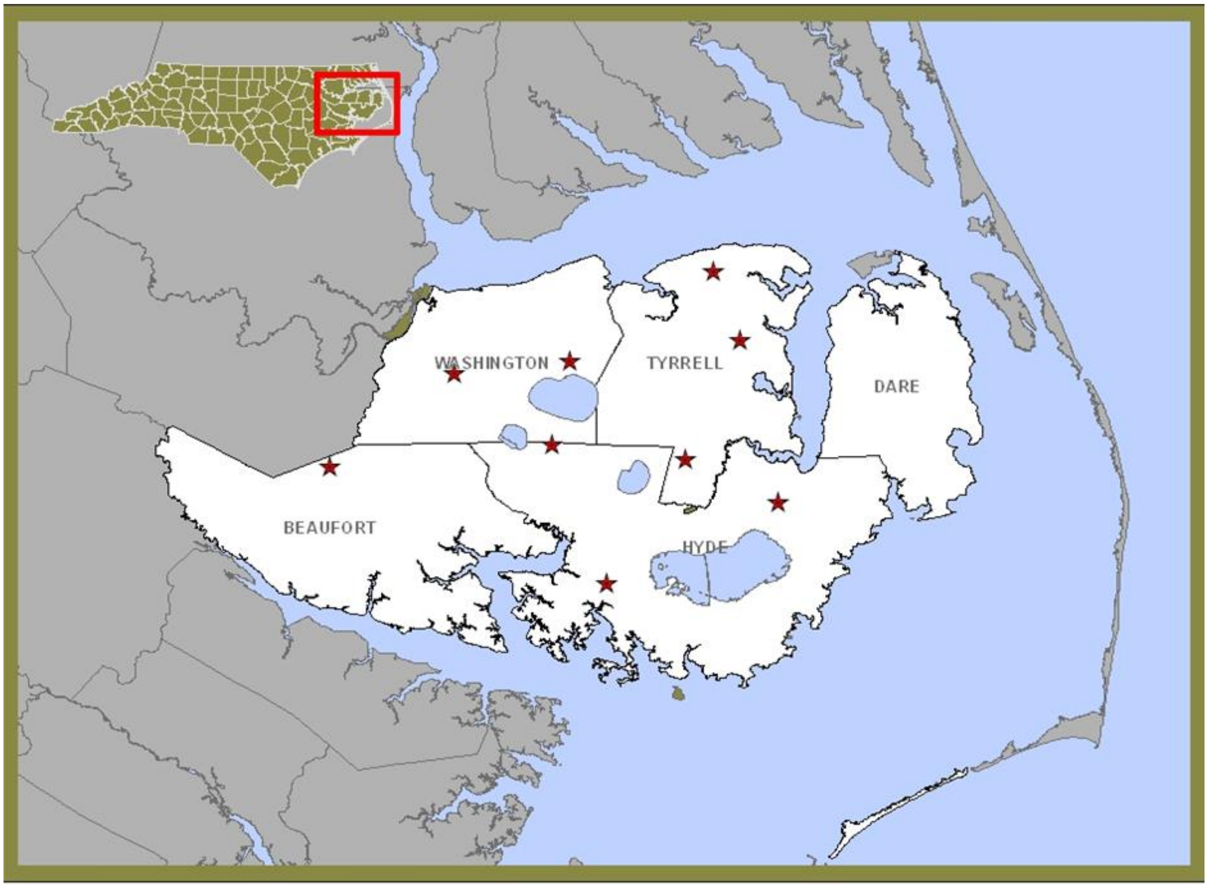
	Coyote	Gray wolf	Dog	Red wolf	p-value
Canid38	1	0	0	0	1
Canid39	0	0	1	0	1
Canid40	1	0	0	0	1
Canid41	1	0	0	0	1
Canid42	1	0	0	0	1
Canid43	1	0	0	0	1
Canid44	0	0.31	0.69	0	0
Canid45	1	0	0	0	1
Canid46	1	0	0	0	1
Canid47	1	0	0	0	1
Canid48	0	1	0	0	1
Canid49	0	1	0	0	1
Canid50	1	0	0	0	1
Canid51	0	0	0	1	1
Canid52	1	0	0	0	1
Canid53	0	0	0	1	1
Canid54	1	0	0	0	1
Canid56	0	0	0	1	1
Canid57	1	0	0	0	1
Canid58	0	0	0	1	1
Canid59	0	0	0	1	1
Canid60	0	0	0	1	1
Canid61	0	0	0	1	1
Canid62	1	0	0	0	1
Canid63	0	0	0	1	1
Canid64	0	0	0	1	1
Canid65	0	1	0	0	1
Canid66	1	0	0	0	1
Canid67	0	1	0	0	1
Canid68	1	0	0	0	1
Canid69	1	0	0	0	1
Canid70	1	0	0	0	1
Canid71	0	0	1	0	1
Canid72	0	1	0	0	1
Canid73	0	1	0	0	1
Canid74	0	1	0	0	1

Appendix B
Results from BAPS

	Coyote	Gray wolf	Dog	Red wolf	p-value
Canid75	1	0	0	0	1
Canid76	0	0	0	1	1
Canid77	0	0	0	1	1
Canid78	0	0	0	1	1
Canid79	1	0	0	0	1
Canid80	1	0	0	0	1
Canid81	0	0	1	0	1
Canid82	0.52	0.01	0.01	0.46	0.025
Canid83	0.65	0	0	0.35	0.085
Canid84	0	1	0	0	1
Canid85	0	1	0	0	1
Canid86	0	1	0	0	1
Canid87	0	0	1	0	1
Canid88	1	0	0	0	1
Canid89	0	1	0	0	1
Canid90	0	1	0	0	1
Canid91	1	0	0	0	1
Canid92	1	0	0	0	1
Canid93	1	0	0	0	1
Canid94	0	1	0	0	1
Canid95	0	0	1	0	1
Canid96	1	0	0	0	1
Canid97	1	0	0	0	1
Canid98	0	0	0	1	1
Canid99	1	0	0	0	1
Canid100	1	0	0	0	1
Canid101	1	0	0	0	1
Canid102	0	0	0	1	1
Canid103	0.27	0	0.05	0.68	0.005
Canid104	0	0	1	0	1
Canid105	0	1	0	0	1
Canid106	0	0	1	0	1
Canid107	1	0	0	0	1

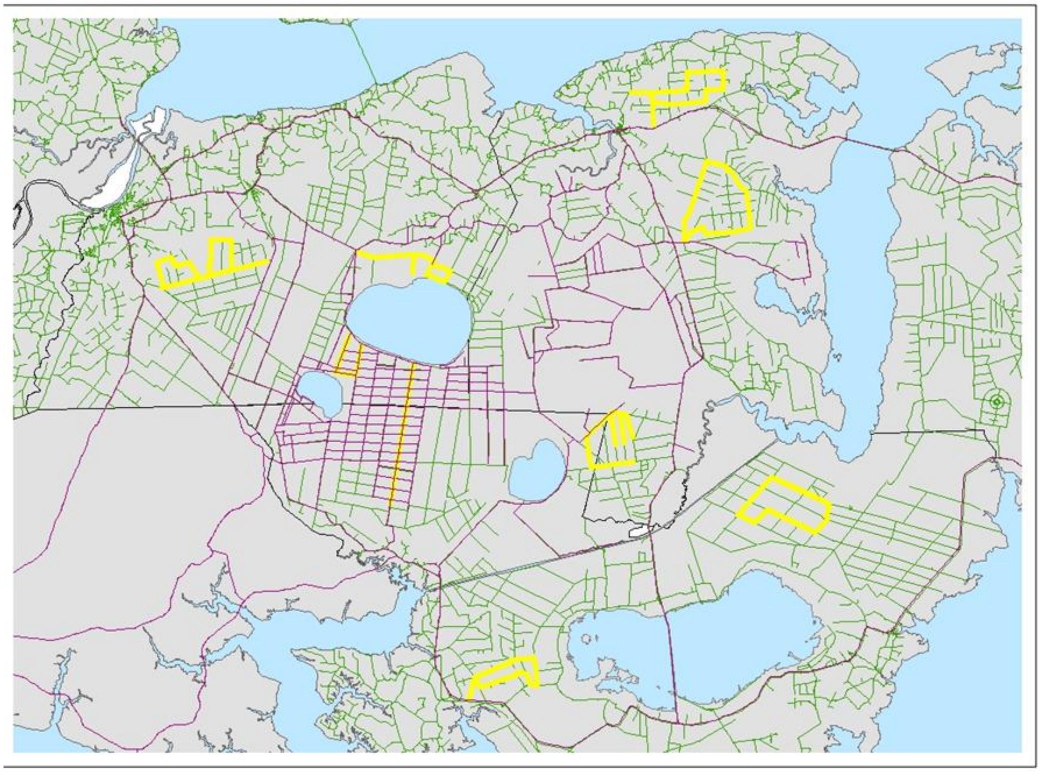
Appendix C

Sampling locations and route driven



Appendix B

Results from BAPS



Appendix D
GPS location and species identification of scats

Date	Sample ID		Easting	Northing	Species ID
6/15/09	JD	284	394894	3978788	20463
6/15/09	JD	288	396098	3978765	20463
6/15/09	JD	297	415242	3970362	20463
3/10/09	JH	25	368300	3963954	20463
3/10/09	JH	26	368263	3963954	20471
3/10/09	JH	27	367590	3965143	20478
3/10/09	JH	28	369695	3963735	20478
3/10/09	JH	29	375026	3963152	40330
3/11/09	JH	32	378714	3966919	40458
3/13/09	JH	35	373924	3965754	BLANK
3/17/09	JH	36	363852	3975744	Canid1
3/17/09	JH	38	363507	3973915	Canid1
3/17/09	JH	40	369951	3975619	Canid1
4/19/09	JH	64	371322	3974216	Canid1
4/19/09	JH	66	363443	3974633	Canid100
4/19/09	JH	68	361941	3974597	Canid107
6/15/09	JH	81	365823	3951375	Canid11
1/14/09	JM	3	396516	3978754	Canid11
1/14/09	JM	19	398299	3967872	Canid11
1/30/09	JM	20	398293	3968055	Canid11
1/30/09	JM	23	398247	3968670	Canid11
3/20/09	JM	9	399033	3941256	Canid14
3/21/09	JM	17	398375	3966871	Canid14
3/22/09	JM	35	372035	3926670	Canid17
3/22/09	JM	45	347029	3965407	Canid2
4/17/09	JM	1	354502	3964959	Canid2
4/17/09	JM	2	354502	3964959	Canid24
4/17/09	JM	3	354502	3964959	Canid30
4/17/09	JM	5	354239	3964930	Canid30
4/17/09	JM	10	346899	3965864	Canid32
4/17/09	JM	12	346899	3965864	Canid33
4/17/09	JM	17	346899	3965864	Canid33
4/17/09	JM	22	346291	3963112	Canid34
4/17/09	jm	28	352724	3964578	Canid36
4/18/09	JM	45	393141	3966221	Canid37
4/19/09	JM	106	414767	3941743	Canid41

Appendix D

GPS location and species identification of scats

Date	Sample ID		Easting	Northing	Species ID
5/14/09	JM	303	332133	3950489	Canid43
5/14/09	JM	315	354248	3964918	Canid43
5/14/09	JM	323	349245	3963865	Canid46
5/14/09	JM	324	347811	3966309	Canid47
5/14/09	JM	332	347440	3963586	Canid5
5/16/09	JM	378	396520	3979593	Canid5
5/16/09	JM	383	396797	3966352	Canid5
5/17/09	JM	395	362317	3958095	Canid5
5/17/09	JM	411	358517	3955578	Canid6
6/30/09	JM	458	329627	3950885	Canid6
6/30/09	JM	459	330076	3950597	Canid6
6/30/09	JM	463	327510	3947256	Canid6
7/1/09	JM	483	368336	3964739	Canid6
7/1/09	JM	484	368324	3964549	Canid66
7/1/09	JM	485	346556	3965748	Canid66
8/17/09	JM	574	383216	3947028	Canid7
9/16/09	JM	623	366995	3950911	Canid7
9/17/09	JM	653	394907	3978771	Canid7
1/23/10	JM	972	354702	3965017	Canid7
1/28/10	JM	983	329877	3952403	Canid7
2/9/10	JM	1003	352242	3966890	Canid70
2/9/10	JM	1004	352242	3966890	Canid70
2/10/10	JM	1014	367961	3955627	Canid80
2/12/10	JM	1047	361739	3956746	Canid88
2/18/10	JM	1154	363724	3964207	Canid96
2/18/10	JM	1160	363724	3964207	11358
2/18/10	JM	1162	362731	3964324	11684
2/19/10	JM	1164	339053	3937612	11440
4/19/09	JH	67	363012	3974318	Canid40
1/30/09	JM	8	392884	3978779	Canid26
1/30/09	JM	13	394282	3967559	Canid27
1/30/09	JM	15	394399	3967578	Canid29
2/27/09	JM	30	362446	3958408	Canid9
2/27/09	JM	32	361840	3956985	Canid9
2/27/09	JM	33	361589	3956643	Canid13
2/27/09	JM	35	362981	3955327	Canid9

Appendix D

GPS location and species identification of scats

Date	Sample ID		Easting	Northing	Species ID
3/25/09	JM	47	333188	3953025	Canid10
3/25/09	JM	48	331649	3953029	Canid48
4/17/09	JM	9	346968	3965663	Canid49
4/17/09	JM	25	352204	3965918	Canid8
4/17/09	JM	27	351926	3964414	Canid8
4/18/09	JM	54	373208	3927804	Canid12
4/18/09	JM	58	375564	3928953	Canid12
4/18/09	JM	60	375897	3929041	Canid12
4/18/09	JM	61	376418	3929021	Canid42
5/14/09	JM	305	332213	3953587	Canid10
5/14/09	JM	307	332005	3954868	Canid15
5/14/09	JM	308	333172	3954333	Canid10
5/14/09	JM	316	354124	3964890	Canid38
5/14/09	JM	328	347305	3964228	Canid39
5/14/09	JM	333	348013	3963591	Canid20
5/14/09	JM	334	348140	3963620	Canid21
5/16/09	JM	386	372252	3927453	Canid12
5/16/09	JM	387	372252	3927453	Canid12
5/17/09	JM	398	361834	3956969	Canid9
5/17/09	JM	399	361834	3956969	Canid9
5/17/09	JM	400	361834	3956969	Canid9
5/17/09	JM	407	361174	3955442	Canid13
5/17/09	JM	413	362238	3954806	Canid13
6/5/09	JM	511	360210	3957231	Canid9
6/14/09	JM	505	379270	3955645	Canid45
6/30/09	JM	464	330157	3951187	Canid15
7/1/09	JM	480	363245	3965720	Canid44
7/29/09	JM	553	366618	3949083	Canid13
8/18/09	JM	596	330334	3951694	Canid15
8/18/09	JM	609	327983	3952013	Canid99
9/2/09	JM	738	355413	3950231	Canid103
9/18/09	JM	657	362256	3964411	Canid9
10/16/09	JM	664	330023	3948997	Canid101
11/19/09	JM	1150	391680	3978831	Canid95
12/28/09	JM	805	392854	3965785	Canid69
1/19/10	JM	850	372364	3927203	Canid12

Appendix D

GPS location and species identification of scats

Date	Sample ID		Easting	Northing	Species ID
1/19/10	JM	852	386683	3924490	Canid74
1/19/10	JM	857	386507	3924589	Canid68
1/20/10	JM	888	391755	3978785	Canid75
1/20/10	JM	946	385305	3950407	Canid77
1/20/10	JM	947	385305	3950407	Canid77
1/20/10	JM	949	385305	3950407	Canid77
1/20/10	JM	950	384736	3949939	Canid105
1/25/10	JM	978	349246	3963849	Canid71
1/27/10	JM	981	330335	3951688	Canid72
1/29/10	JM	984	329519	3952982	Canid72
2/10/10	JM	1015	390097	3977183	Canid81
2/10/10	JM	1016	390077	3978756	Canid82
2/11/10	JM	1019	394920	3980426	Canid75
2/12/10	JM	1021	391677	3977630	Canid75
2/12/10	JM	1026	362418	3958318	Canid73
2/12/10	JM	1028	362418	3958318	Canid73
2/12/10	JM	1030	362418	3958318	Canid73
2/12/10	JM	1031	362418	3958318	Canid73
2/12/10	JM	1034	362240	3957912	Canid73
2/12/10	JM	1036	362221	3957860	Canid85
2/12/10	JM	1039	362196	3957802	Canid86
2/12/10	JM	1049	361608	3956439	Canid89
2/12/10	JM	1072	376463	3929030	Canid90
2/12/10	JM	1079	377770	3927521	Canid67
2/12/10	JM	1080	377777	3927417	Canid67
2/12/10	JM	1082	372505	3926860	Canid91
2/12/10	JM	1083	386672	3924513	Canid68
2/12/10	JM	1085	386657	3924477	Canid74
2/12/10	JM	1086	386657	3924477	Canid74
2/12/10	JM	1090	395165	3965973	Canid93
2/12/10	JM	1098	396774	3966741	Canid69
2/23/10	JM	1171	364592	3955215	Canid97
2/28/10	JM	1107	400986	3943423	Canid94
2/28/10	JM	1130	387102	3949217	Canid77
2/28/10	JM	1131	386990	3950377	Canid77
2/28/10	JM	1135	385541	3948048	Canid77

Appendix D

GPS location and species identification of scats

Date	Sample ID		Easting	Northing	Species ID
2/28/10	JM	1137	385531	3948175	Canid77
2/28/10	JM	1144	385531	3948175	Canid77
6/15/09	JD	275	379074	3965924	11163
6/15/09	JD	277	380364	3965659	11132
6/15/09	JD	286	394904	3977742	11170
6/15/09	JD	301	394773	3972422	11170
6/15/09	JD	303	394361	3971340	11170
6/15/09	JD	304	393574	3971077	11170
6/15/09	JD	307	392379	3969816	11170
6/15/09	JD	308	392303	3967267	11170
6/15/09	JD	313	380395	3965272	11170
6/15/09	JD	315	380438	3965669	11170
6/15/09	JD	317	380222	3966003	11170
6/15/09	JD	320	380918	3963105	11170
6/15/09	JD	321	392973	3967843	11170
6/15/09	JD	322	392466	3968062	11170
6/15/09	JD	323	392466	3968920	11170
6/15/09	JD	324	393299	3969461	11170
3/11/09	JH	31	379067	3965949	11170
3/18/09	JH	43	426429	3964238	11170
3/18/09	JH	45	390181	3965363	11170
4/16/09	JH	54	388701	3978813	11170
4/16/09	JH	55	388979	3978808	11173
4/16/09	JH	56	389975	3977629	11173
4/16/09	JH	57	389096	3977638	11173
4/17/09	JH	58	388608	3977644	11185
4/19/09	JH	61	378990	3966157	11185
4/19/09	JH	83	368840	3951546	11185
4/19/09	JH	90	367973	3947537	11185
1/30/09	JM	11	386892	3975319	11185
2/27/09	JM	34	362093	3954840	11185
2/28/09	JM	44	398577	3942380	11185
3/20/09	JM	2	400363	3940568	11185
3/20/09	JM	7	399226	3941157	11185
3/20/09	JM	8	399226	3941157	11185
3/20/09	JM	10	400815	3941222	11185

Appendix D

GPS location and species identification of scats

Date	Sample ID		Easting	Northing	Species ID
3/20/09	JM	11	401733	394074	11185
3/22/09	JM	23	386118	3950404	11185
3/22/09	JM	24	386118	3950404	11185
3/22/09	JM	25	386118	3950404	11185
3/22/09	JM	27	386088	3950405	11199
3/22/09	JM	28	385430	3950498	11207
3/22/09	JM	29	385340	3950448	11207
3/22/09	JM	36	372240	3927409	11207
3/22/09	JM	42	376115	3927877	11207
4/18/09	JM	43	396517	3979072	11207
4/18/09	JM	57	375643	3928756	11207
4/18/09	JM	59	375897	3929041	11207
4/19/09	JM	64	383849	3948847	11207
4/19/09	JM	65	383849	3948847	11207
4/19/09	JM	81	385717	3946224	11207
4/19/09	JM	84	398215	3940765	11207
4/19/09	JM	85	398253	3940798	11207
4/19/09	JM	87	398861	3941342	11207
4/19/09	JM	88	399035	3941256	11207
4/19/09	JM	89	399035	3941256	11207
4/19/09	JM	92	401734	3939850	11207
4/19/09	JM	94	402322	3939539	11207
4/19/09	JM	95	402322	3939539	11207
4/19/09	JM	97	402322	3939539	11207
4/19/09	JM	98	402549	3939427	11207
4/19/09	JM	99	402549	3939427	11207
4/19/09	JM	100	402549	3939427	11207
4/19/09	JM	101	403169	3939227	11207
4/19/09	JM	103	403673	3939739	11207
4/19/09	JM	104	403673	3939739	11207
4/19/09	JM	108	414590	3938984	11207
4/23/09	JM	1184	375317	3941279	11207
5/15/09	JM	341	397075	3941800	11207
5/15/09	JM	343	398229	3940780	11207
5/15/09	JM	345	398971	3940423	11207
5/15/09	JM	349	402104	3938795	11207

Appendix D

GPS location and species identification of scats

Date	Sample ID		Easting	Northing	Species ID
5/15/09	JM	357	390869	3978854	11207
5/17/09	JM	410	358575	3955567	11207
6/17/09	JM	419	388415	3978812	11207
6/17/09	JM	431	398606	3940613	11207
6/17/09	JM	432	401648	3939035	11207
6/18/09	JM	437	398249	3968696	11207
6/18/09	JM	438	398249	3968696	11207
6/19/09	JM	452	361833	3956966	11238
6/30/09	JM	472	403050	3939106	11300
6/30/09	JM	473	403793	3939869	11300
6/30/09	JM	474	404207	3940870	11300
6/30/09	JM	475	404207	3940870	11300
6/30/09	JM	508	364356	3946333	11301
6/30/09	JM	509	398076	3975776	11301
7/15/09	JM	522	399397	3944209	11316
7/15/09	JM	527	399786	3939998	11316
7/15/09	JM	528	399786	3939998	11316
7/15/09	JM	530	402034	3938836	11316
7/15/09	JM	531	403050	3939105	11316
7/15/09	JM	532	403050	3939105	11316
7/15/09	JM	537	383079	3948436	11316
7/15/09	JM	540	384271	3945758	11316
7/29/09	JM	560	397975	3940933	11316
7/29/09	JM	561	397975	3940933	11316
7/29/09	JM	575	396416	3941136	11316
8/17/09	JM	585	401648	3939037	11316
8/18/09	JM	595	330334	3951694	11316
9/17/09	JM	643	387100	3949180	11357
9/17/09	JM	645	386732	3950259	11358
9/17/09	JM	646	398517	3943303	11358
10/18/09	JM	703	386018	3950427	11358
10/18/09	JM	707	385160	3950318	11419
10/18/09	JM	721	383190	3947272	11429
10/18/09	JM	722	383190	3947272	11439
10/18/09	JM	725	403624	3939694	11439
10/18/09	JM	726	354152	3939117	11439

Appendix D

GPS location and species identification of scats

Date	Sample ID		Easting	Northing	Species ID
10/18/09	JM	727	354357	3939100	11439
10/18/09	JM	728	354318	3939105	11440
10/18/09	JM	729	354206	3939113	11440
10/18/09	JM	730	354140	3939117	11440
10/18/09	JM	731	354659	3939101	11440
10/18/09	JM	739	383477	3948810	11440
11/19/09	JM	764	397159	3941889	11440
11/19/09	JM	766	386386	3947742	11452
11/19/09	JM	768	383240	3948604	11458
12/28/09	JM	804	392854	3965785	11458
12/29/09	JM	827	386991	3950376	11469
12/29/09	JM	834	385590	3947564	11469
12/29/09	JM	835	385590	3947564	11469
12/29/09	JM	837	383112	3948062	11469
12/29/09	JM	841	397704	3941074	11469
12/29/09	JM	842	397704	3941074	11469
12/29/09	JM	843	398540	3940647	11533
1/19/10	JM	861	397679	3941096	11539
1/19/10	JM	862	397971	3940938	11541
1/19/10	JM	864	399673	3940050	11628
1/19/10	JM	865	401864	3938919	11628
1/19/10	JM	866	402525	3938570	11634
1/20/10	JM	939	386108	3950407	11635
1/20/10	JM	940	386004	3950430	11643
1/20/10	JM	942	385554	3947919	11677
1/20/10	JM	953	383969	3949248	11684
1/20/10	JM	960	383210	3947099	11686
1/20/10	JM	968	365577	3943996	11687
2/12/10	JM	1058	361021	3955078	11693
2/12/10	JM	1060	365601	3944136	11693
2/12/10	JM	1061	365389	3943032	11693
2/12/10	JM	1062	371810	3925876	11693
2/12/10	JM	1063	372645	3927603	11697
2/12/10	JM	1064	372701	3927627	11703
2/12/10	JM	1065	373978	3928085	11703
2/12/10	JM	1067	375480	3928649	11703

Appendix D

GPS location and species identification of scats

Date	Sample ID		Easting	Northing	Species ID
2/12/10	JM	1074	377290	3929025	11703
2/12/10	JM	1075	377719	3928548	11703
2/12/10	JM	1076	377726	3928354	11705
2/12/10	JM	1081	372739	3926605	11705
2/12/10	JM	1088	379919	3923293	11185
2/12/10	JM	1089	394438	3966024	11706
2/12/10	JM	1091	395560	3965994	11706
2/12/10	JM	1096	396789	3966503	11706
2/12/10	JM	1178	361971	3950583	11706
2/18/10	JM	1157	345290	3954887	11706
2/18/10	JM	1158	346208	3954710	11706
2/18/10	JM	1159	346205	3954708	11706
2/28/10	JM	1109	397084	3941811	11706
2/28/10	JM	1110	396809	3941532	11706
2/28/10	JM	1111	396809	3941532	11706
2/28/10	JM	1112	397628	3941112	11706
2/28/10	JM	1113	397628	3941112	11706
2/28/10	JM	1114	397628	3941112	11706
2/28/10	JM	1115	397628	3941112	11725
2/28/10	JM	1116	397628	3941112	11727
2/28/10	JM	1117	397708	3941672	Canid102
2/28/10	JM	1119	398251	3940794	Canid18
2/28/10	JM	1120	398970	3940422	Canid19
2/28/10	JM	1121	398970	3940422	Canid22
2/28/10	JM	1122	398970	3940422	Canid3
2/28/10	JM	1123	399014	3940399	Canid31
2/28/10	JM	1125	400166	3939803	Canid4
2/28/10	JM	1126	403234	3939289	Canid4
2/28/10	JM	1127	403234	3939289	Canid4
2/28/10	JM	1128	404196	3940905	Canid4
2/28/10	JM	1129	387224	3947991	Canid4
2/28/10	JM	1134	385538	3948080	Canid4
2/28/10	JM	1136	385541	3948048	Canid4
2/28/10	JM	1139	385531	3948175	Canid76
2/28/10	JM	1143	385531	3948175	Canid78
2/28/10	JM	1153	345304	3954908	Canid78

Appendix D

GPS location and species identification of scats

Date	Sample ID		Easting	Northing	Species ID
2/28/10	JM	1156	345709	3954130	Canid98

Appendix E
Frequency of occurrence

Red Wolf Diet (frequency of occurrence)

	2009												2010	
Taxa	January	February	March	April	May	June	July	August	September	October	November	December	January	February
Mammalia														
Artiodactyla														
Cervidae														
Odocoileus virginianus	1	1	4	9	2	12	4	1	1	8	3	6	6	19
Carnivora														
Procyonidae														
Procyon lotor	0	0	1	0	0	0	0	0	0	0	0	0	1	0
Lagomorph														
Leporidae														
Sylvilagus spp.	0	1	10	19	2	12	9	1	2	3	0	2	6	21
Rodentia														
Cricetidae														
Ondatra zibethicus	0	1	3	0	2	0	0	0	0	0	0	0	0	0
Oryzomys palustris	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Peromyscus leucopus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Reithrodontomys humulis	0	2	0	0	0	0	0	0	0	0	0	0	0	0
Sigmodon hispidus	0	1	4	5	2	2	0	0	0	1	1	0	0	11
Muridae														
Mus musculus	0	0	3	2	0	3	0	0	0	0	0	0	0	1
Suidae														
Sus scrofa (domestic)	0	0	0	0	0	2	0	0	0	0	0	1	0	1
Sus scrofa (feral)	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Aves	0	0	0	0	0	1	0	0	0	0	0	0	0	1

Appendix E
Frequency of occurrence

Red Wolf Diet (frequency of occurrence) continued

	2009												2010	
Taxa	January	February	March	April	May	June	July	August	September	October	November	December	January	February
Insecta	0	0	0	0	0	1	0	0	0	3	1	0	0	0
Planta	0	2	0	2	0	1	1	0	1	3	0	2	5	5
Other	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total number of scats	1	2	16	31	6	28	11	2	3	12	3	8	11	45

Coyote Diet (frequency of occurrence)

	2009												2010	
Taxa	January	February	March	April	May	June	July	August	September	October	November	December	January	February
Mammalia														
Artiodactyla														
Cervidae														
Odocoileus virginianus	2	0	3	2	7	5	0	1	1	0	0	0	1	3
Carnivora														
Procyonidae														
Procyon lotor	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Lagomorph														
Leporidae														
Sylvilagus spp.	1	0	10	4	6	2	3	0	2	0	0	0	1	1
Rodentia														
Cricetidae														

Appendix E

Frequency of occurrence

Coyote Diet (frequency of occurrence) continued

	2009												2010	
Taxa	January	February	March	April	May	June	July	August	September	October	November	December	January	February
Ondatra zibethicus	0	0	1	1	0	1	0	0	0	0	0	0	0	0
Oryzomys palustris	0	0	0	2	0	0	0	0	0	0	0	0	0	0
Peromyscus leucopus	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Reithrodontomys humulis	0	0	0	1	1	0	0	0	0	0	0	0	0	0
Sigmodon hispidus	0	0	2	4	1	0	1	0	0	0	0	0	0	4
Muridae														
Mus musculus	4	0	6	1	1	0	0	0	0	0	0	0	1	3
Suidae														
Sus scrofa (domestic)	0	0	0	3	0	0	0	0	0	0	0	0	0	0
Sus scrofa (feral)	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Aves	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Insecta	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Planta	0	0	1	0	1	0	0	0	1	0	0	0	0	0
Other	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Total number of scats	7	0	24	19	19	8	4	1	4	0	0	0	3	12

Appendix E
Frequency of occurrence

Red Wolf-Coyote Hybrid Diet (frequency of occurrence)

	2009												2010	
Taxa	January	February	March	April	May	June	July	August	September	October	November	December	January	February
Mammalia														
Artiodactyla														
Cervidae														
Odocoileus virginianus	3	2	1	4	7	3	1	2	0	0	0	1	3	11
Carnivora														
Procyonidae														
Procyon lotor	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lagomorph														
Leporidae														
Sylvilagus spp.	1	1	0	4	7	0	1	2	1	1	1	0	3	17
Rodentia														
Cricetidae														
Ondatra zibethicus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oryzomys palustris	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Peromyscus leucopus	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Reithrodontomys humulis	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Sigmodon hispidus	0	2	0	2	3	0	0	0	1	0	0	0	4	1
Muridae														
Mus musculus	0	0	1	1	2	0	0	0	0	0	0	0	1	1
Suidae														
Sus scrofa (domestic)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sus scrofa (feral)	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aves	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Appendix E

Frequency of occurrence

Red Wolf-Coyote Hybrid Diet (frequency of occurrence) continuted

	2009												2010	
Taxa	January	February	March	April	May	June	July	August	September	October	November	December	January	February
Insecta	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Planta	0	0	1	1	0	0	0	0	0	0	0	0	1	2
Other	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Total number of scats	4	5	3	14	20	3	2	4	2	1	1	1	12	33

Appendix F
Frequency of occurrence (Stomach contents)

Sample Id	Date of Death	Sex	Stomach empty	Horse meat	Odocoileus virginianus	Sylviligus spp.	Sigmodon hispidus	Mus musculis	Oryzomys palustris	Peromyscus leucopus	Sus scrofa (Feral)	Grass	Veg	Seeds	Feathers	Acrididae	Trash	Comments
11702													1					Vegetation seems incidental
10768M	6/10/2004	M			1	1							1					Muscadine, Euthanized, mange, heartworms
10871M		M			1					1								
10980M		M			1													Iridescent beetles, roadkill-gator pack
11030F	2/15/2006	F																Mange
11117M		M	1															
11187M	4/15/2003	M	1															
11240F		F			1												1	Plastic in stomach
11303F		F				1												
11311M	none	M	1															
11322F	11/9/2005	F	1															Gunshot
11438F	1/23/2006	F	1															Euthanized at Ventures
11461M	3/4/2008	M				1												
11523F		F			1											1	1	
11709F	12/9/2008	F			1													
11770F		F			1						1	1				1		Small hoof found (fawn)
20457F		F			1			1			1		1			1		Muscadine, small leg bones (fawn)

Appendix F
Frequency of occurrence (Stomach contents)

Sample Id	Date of Death	Sex	Stomach empty	Horse meat	Odocoileus virginianus	Sylviligus spp.	Sigmodon hispidus	Mus musculis	Oryzomys palustris	Peromyscus leucopus	Sus scrofa (Feral)	Grass	Veg	Seeds	Feathers	Acrididae	Trash	Comments
20494M		M					1	1	1	1								Worms in stomach
20497F		F			1													
20488F	2/27/2009	F			1													Missing Foot
20519M		M						1				1		1		1		
30456M		M			1													
30490M		M										1	1		1			Persimmon in stomach
30498M		M			1													Snapping turtle foot
ST4151	none	M	1															Species unknown, DNA identification unsuccessful
ST4152	none	M		1														Species unknown, DNA identification unsuccessful