GEOGRAPHIC DISTRIBUTION, MOLECULAR VARIABILITY, AND LANDSCAPE EPIDEMIOLOGY OF *EHRLICHIA CHAFFEENSIS* FROM WHITE-TAILED DEER IN THE SOUTHEASTERN UNITED STATES

by

MICHAEL JOHN YABSLEY

(Under the Direction of William R. Davidson)

ABSTRACT

The major objective of this research was to gain a better understanding of the epidemiology of *E. chaffeensis* and *E. ewingii*, both emerging zoonotic pathogens vectored by the lone star tick (LST; *Amblyomma americanum*). The natural history of *E. chaffeensis* includes the LST as a vector and white-tailed deer (WTD; *Odocoileus* virginianus) as both a natural reservoir for *E. chaffeensis* and a major host of LST. *Ehrlichia ewingii* is also vectored by the LST and natural infections have been reported from dogs and humans, but a reservoir has not been confirmed.

To delineate the geographic distribution of *E. chaffeensis*, a prototype surveillance system using WTD as natural sentinels was developed. To accomplish this goal, WTD from 563 counties from 18 states were tested for *E. chaffeensis* by serology, PCR, and culture. This sentinel system met critical criteria including diagnostic accuracy, adequacy of sample sizes and sampling intensity, key epidemiologic associations with the LST vector, and ability to detect spread of *E. chaffeensis*. To predict the distribution of *E. chaffeensis*, geostatistical (kriging) and logistic regression were conducted. Both analyses accurately predicted the distribution of *E. chaffeensis* and logistic regression detected climatic and land cover variables significantly associated with *E. chaffeensis* occurrence. The predicted *E. chaffeensis* distribution had good concordance with human case data. These comparisons are evidence that utilization of WTD as sentinels is an efficient alternative to human surveillance for predicting *E. chaffeensis* distribution and disease risk.

Molecular characterization of two antigen genes (VLPT and 120-kDa) of *E. chaffeensis* from 102 WTD showed that multiple genetic types were present. Genetic types were not geographically clustered and co-infection of single deer and populations of deer was common.

Because *E. chaffeensis* and *E. ewingii* are closely related and transmitted by the LST, deer were hypothesized to be susceptible to infection with *E. ew*ingii. To test for *E. ewingii* infection, polymerase chain reaction and inoculation of fawns with whole blood from wild deer were conducted. Natural infections of WTD were detected and captive fawns were successfully infected. These data suggest that white-tailed deer may be an important reservoir for *E. ewingii*.

INDEX WORDS: *Ehrlichia chaffeensis*, white-tailed deer, *Odocoileus virginianus*, surveillance system, sentinels, epidemiology, molecular characterization, geographic information system, *Ehrlichia ewingii*

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BS, Clemson University, 1997

MS, Clemson University, 2000

A Dissertation Submitted to the Graduate Faculty of The University of Georgia in Partial

Fulfillment of the Requirements for the Degree

DOCTOR OF VETERINARY PARASITOLOGY

ATHENS, GEORGIA

2004

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May 2004

ACKNOWLEDGEMENTS

I would like to thank my committee members for their guidance and help during my studies. Particularly, I would like to thank Randy who constantly serves as a source of inspiration. He juggles more than most professors I've ever met but still manages to find the time to offer help and is never to busy to step out of his office to see someone's new interesting finding (just be careful of the "thumbing"!). I would also like to thank Randy for allowing me the freedom to follow my interests and pursue outside research projects. I would like to thank Susan for the PCR training and guidance and Dave for his never ending enthusiasm about my project. I also thank Buffy and Ray for their support throughout my project. The work of Jackie Dawson and Mitch Lockhart added greatly to the completion of this project. I thank them for their excellent pioneering studies into the natural history of *E. chaffeensis*.

Most of all I thank my mom Elaine Yabsley for supporting me all of these years and trusting that I would one day be finished with school. And to Sam…while it is impossible to express on paper how much I appreciate all the help, love, and support that she have given me during these past three years, I do thank her from the bottom of my heart.

A countless number of individuals have provided help for this project by collecting for and adding to the SCWDS serum bank which provided many samples for this project. I would like to thank David Stallknecht, Britta Hanson, and others before them, for their hard work to provide such a valuable resource. Sarah Cross, Scott Danskin, and Mike Wimberly provided wonderful help with GIS and without their help, it may never have gotten done. Within the lab, I thank Danny for PCR guidance and Page Luttrell for help and support in the endless fight against the evil trypanosomes. I especially thank Andrea for bumbling through the past several years with me and providing a wonderful sounding board for any and all lab issues, which unfortunately involved a mysterious extra PCR band far too often. Andrew Allison, Dana Ambrose, Janaenne Brewton, Joe Corn, Caroline Duffy, Vivien Dugan, Robbie Edalgo, John Fisher, Joe Gaydos, Rick Gerhold, Nicole Gottdenker, Colin Hurd, Darryl Kavanaugh, Kali King, Cindy McElwee, Nate Mechlin, Gus Moore, Molly Murphy, Liz Nance, Rob Olsen, David Peterson, Cynthia Tate, Tracy Townsend, Marsha Ward, Lynn Lewis-Weis, Donna Wood, and Anna Yellin have all helped in various ways either with my research or as a friend, and I thank them. I especially thank Jennifer Smith for always having a smile and making the lab a happier place to work.

Numerous people helped in the collection of samples including people from Alabama (Chris Cook, David Smith, Kevin McKinstry), Florida (H.W. Harter, III, Neil Eicholz, John Morgan, Steve Glass, Don Coyner, Nancy Dwyer), Georgia (Mike Dzimianski, Bill Cooper, Greg Waters, Doug Hoffman, George Steele, Wes Abler, Don McGowan, Nic Nicholson, Terry Kyle, Vic Vansant, Kent Kammermeyer), Kansas (Lloyd Fox, Greg Harris, Randy Whiteaker, Marc Gray, Carolyn Sutton, Todd Pesch), Kentucky (Jon Gassett, Karen Alexi, Mike Henshaw, David Yancey, Tony Black, Wayne Tamminga, Hope Carlton, Keith Parker, Lee Cope, Charlie Logsdon, Scott Busen, Eric Williams, Jonathan Day), Maryland (Jonathan Shaw, Kent Adams), Missouri (Jeff Berringer, John Freihaut), New Jersey (Douglas Roscoe), North Carolina (Evin

Stanford, Ken Knight, Mike Tipton, George Strader, David Rowe, David Sawyer, Robbie Norville, Jr., Thomas Padgett), Oklahoma (A. Alan Kocan), South Carolina (Katie Bruce, Paul Johns, Sidney Haskey, Charles Ruth, Jr., Jeff Witt, Mark Bara, Bob Warren, Billy Freeman, Sam Stokes, Jr.), Tennessee (Ben Layton), Texas (John Morrill, Ken Waldrup, Mary Humphrey), Louisiana (Tom Bourland, David Moreland, R. Robert Rackley), Virginia (Phil West, Todd Engelmeyer, Ronald Hughes, Brad Howard, Mac Walls, Cale Godfrey, Jimmy Conner, Jennifer Cromwell, W. Matt Knox, Bob Duncan, Dan Lovelace, Jay Jeffreys, David Allaben), West Virginia (Jim Crum), and others at state wildlife agencies and USDA-APHIS.

Work was supported primarily by the National Institutes of Allergy and Infectious Diseases (5 R01 AI044235-02). Further support was provided by the Federal Aid to Wildlife Restoration Act (50 Stat. 917) and through sponsorship from fish and wildlife agencies in Alabama, Arkansas, Florida, Georgia, Kansas, Kentucky, Louisiana, Maryland, Mississippi, Missouri, North Carolina, Oklahoma, Puerto Rico, South Carolina, Tennessee, Virginia, and West Virginia.

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CHAPTER 1

INTRODUCTION

The major objective of this research was to gain a better understanding of the epidemiology of ehrlichial zoonoses, especially those vectored by the lone star tick (*Amblyomma americanum*). Both *Ehrlichia chaffeensis* and *E. ewingii* are small obligate intracellular bacteria and are emerging lone star tick-borne pathogens. *Ehrlichia chaffeensis* is the causative agent of human monocytotropic ehrlichiosis (HME) and *E. ewingii* is one causative agent of human granulocytotropic ehrlichiosis (also called E. ewingii ehrlichiosis (EWE) to differentiate it from *An. phagocytophilum* which also causes human granulocytotrophic ehrlichiosis/anaplasmosis). Both diseases are most often reported from the southeastern and south central United States (Walker and Dumler, 1996; McQuiston et al., 1999; Paddock and Childs, 2003). Severity of disease following infection with either of these *Ehrlichia* species varies from asymptomatic to fatal, with the most common clinical signs being fever, headache, nausea, and malaise; leucopenia and thrombocytopenia are often present (Dumler and Walker, 1991). Since the discovery of HME in 1986 over 2,000 cases have been reported to the CDC (McQuiston et al., 1999; Paddock et al., 2001; Childs and Paddock, 2003; Gardner et al., 2003). At least 20 cases of EWE have been reported since 1999 with the majority of cases being in immunocompromised patients (Buller et al., 1999; Paddock et al., 2001; Childs and Paddock, 2003).

Ehrlichia chaffeensis is maintained in a zoonotic cycle involving white-tailed deer (WTD; *Odocoileus virginianus)* as a vertebrate reservoir and *Am. americanum* as the principal biological vector. Several previous studies have shown that WTD are important factors in the epidemiology of *E. chaffeensis* as they serve as principal hosts to the vector and serve as persistent rickettsemic reservoirs (Dawson et al., 1994a; 1994b; Ewing et al., 1995; Lockhart et al., 1996; 1997a; 1997b; Davidson et al., 2001). *Ehrlichia chaffeensis* surveillance has relied on passive reporting of human cases to the CDC (McQuiston et al., 1999; Gardner et al., 2003) and limited active surveillance in a few locations (Standaert et al., 1995; Fritz et al., 1997; Carpenter et al., 1999; Marshall et al., 2002; Talbot et al., 2003). This system is fraught with problems including multiple states which do not consider ehrlichiosis reportable, inconsistent reporting of cases within states that consider ehrlichiosis reportable, and failure to diagnose cases. Multiple studies have indicated that WTD should be excellent sentinels for *E. chaffeensis* (Dawson et al., 1994a; Lockhart et al., 1995; 1996; Mueller-Anneling et al., 2000) but to be effectively utilized, additional work will be needed to implement a surveillance system. Seropositive populations have been detected in all south central and southeastern states with the exception of West Virginia; however it appears that the distribution within these regions is not continuous. Additional testing of WTD populations from unsampled areas will help better delineate the distribution of *E. chaffeensis* in WTD. Because of the lack of HME case data, no spatial analyses or logistic regression modeling has been conducted for *E. chaffeensis* to develop risk models and projected distribution maps. Intensive sampling of WTD provides surveillance data that currently is not possible using human case data; therefore, these data could be used to develop important distribution models and maps.

Molecular epidemiology is becoming a common way of investigating the transmission patterns, strain typing, immunobiology, immunity, and strain pathogenesis of disease causing organisms. To date, there are no known molecular markers that differentiate *E. chaffeensis* strains that cause severe disease from those detected in asymptomatic patients. Several *E. chaffeensis* nucleotide sequences have been characterized including the 16S rRNA gene, the variable length PCR target (VLPT) antigen, 120-kDa protein, the 106-kDa protein, the 37-kDa protein, the *groESL* heat shock operon (58-kDa), a quinolate synthetase A (nadA) gene, DsbA-like disulfide bond formation proteins, RNA polymerase beta-subunit, and a multigene family containing 22 homologous genes which encode for the p28 surface protein (Yu et al., 1997; Sumner et al., 1997; Yu et al., 1999; Sumner et al., 1999; Yu and Walker, 1997; Yu et al., 2000; McBride et al., 2002; Taillardat-Bisch et al., 2003). Two of these genes, the VLPT and 120-kDa antigen genes, encode for immunoreactive surface proteins which each contain repetitive elements with variable numbers of repeats. The number of repeats can be easily observed by gel electrophoresis, thus provide an easy and simple way to characterize *E. chaffeensis* from human, animal, and tick samples.

Little is known about the natural history of *E. ewingii*, although both dogs and humans can serve as vertebrate hosts. Natural infection of dogs was first recognized in the 1960's (Ewing, 1963) and since has been detected in dogs from several states (Goldman et al, 1998; Murphy et al., 1998; Anderson et al., 1992; Dawson et al., 1996; Kordick et al., 1999; Goodman et al., 2003; Liddell et al., 2003). Experimentally, *Am.*

americanum and *Dermacentor variabilis* are competent vectors and natural infection of these tick species has been reported from Missouri and North Carolina. Because both infected dogs and humans can develop clinical disease, we suggest that another host (e.g., WTD) may serve as a reservoir.

Because WTD (1) are important reservoirs of *E. chaffeensis*, (2) are heavily exposed to *Am. americanum* in endemic areas, (3) have limited home-ranges, and (4) have long life spans which increases their chance of becoming infected, we propose to use WTD to study the epidemiology of *Am. americanum*-vectored ehrlichiae.

Specific objectives of this study include the following:

1. To construct an extensive regional database on *E. chaffeensis*-reactive antibodies in WTD, confirm these serologic results using PCR assays and cell culture isolation, and evaluate a prototype surveillance system using WTD as natural sentinels for *E. chaffeensis*.
2. To characterize the variable length PCR target (VLPT) and 120-kDa antigen genes of *E. chaffeensis* from WTD and test the hypothesis that genetic types of *E. chaffeensis* are geographically clustered
3. Investigate the landscape epidemiology of *E. chaffeensis* in the southeastern United States using geographic information systems, spatial analyses, and computer modeling.
4. Investigate whether WTD are natural hosts for *E. ewingii*, a granulocytotropic ehrlichia closely related to *E. chaffeensis* and which is also vectored by *Am. americanum*.

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CHAPTER 2

LITERATURE REVIEW

Human Monocytotropic Ehrlichiosis (HME)

History

Ehrlichia chaffeensis, the causative agent of HME, was first recognized in 1986 in a Minnesota patient with a history of travel to Arkansas. This patient had symptoms compatible with Rocky Mountain spotted fever (RMSF), which is caused by *Rickettsia rickettsii* (Maeda et al., 1987). Serological testing of this patient for RMSF was negative; however, small rickettsia-like inclusions were observed in leukocytes. Further testing revealed that the patient's serum reacted with *E. canis* so the infection was attributed to *E. canis*. In 1991, the true causative agent was isolated from two ehrlichiosis patients who had acquired the infection at Ft. Chaffee, Arkansas and the agent was subsequently named *E. chaffeensis* (Anderson et al., 1991).

Interestingly, the first recognized cases of HME may have been detected in soldiers at Camp Bullis, Bexar and Comal Counties, Texas during the summers of 1942 and 1943 (Goddard, 1988). What was believed to be an undescribed rickettsial agent was detected in an outbreak of more than 1,000 soldiers who presented with fever, prostration, general weakness, anorexia, severe occipital headaches, and low white blood cell counts with rare cases of rashes and nausea (Woodland et al, 1943). Rocky

Mountain spotted fever, Q fever, typhus, and *Proteus vulgaris* tests were all negative. Furthermore, the cytoplasm of lymphoid cells was noted to contain minute coccobacillary bodies consistent with rickettisia. Because of the seasonal nature of the disease and the fact that hundreds of thousands of *Am. americanum* were detected on the base, the disease was suspected to be vectored by *Am. americanum* (Brennan, 1945). It was also noted that members of a preventive medicine unit at Camp Bullis removed 1,150 attached ticks from a soldier who had sat in a tick-infested thicket for only two hours (Webb, 1952). Although the name *Rickettsia texiana* was proposed for the causative agent of Bullis fever by Anigstein and Anigstein (1975), many researchers believe the true causative agent to be *E. chaffeensis*. Since the mid-1940s, no cases of Bullis fever have been reported from Camp Bullis; however, numerous cases of *E. chaffeensis* have been documented (Goddard, 2000).

Transmission

The primary route of transmission for *Ehrlichia chaffeensis* is via an infected tick bite. Two species of ticks (*Am. americanum* and *D. variabilis*) have been confirmed as competent vectors (Ewing et al., 1995; Wagner et al., 2002), although *E. chaffeensis* has been detected in several other tick species (see tick vectors of *E. chaffeensis* section below). The transmission period for *E. chaffeensis* is directly linked to *Am. americanum* activity and is greatest during the summer months (May-August), although cases can be diagnosed year-around in parts of the country where *Am. americanum* are active in winter (Gardner et al., 2003).

Following a tick bite, *E. chaffeensis* is phagocytosed by macrophages in the spleen, liver, lymph nodes, bone marrow, lung, and kidney where infection is established (Walker and Dumler, 2001; Yu et al., 1993; Dumler et al, 1991; Dumler et al., 1993a). Both L-selectin and E-selectin have been shown to mediate the attachment of *E. chaffeensis* to monocytes and macrophages (Zhang et al., 2003). Expression of the immunodominant 120-kDa antigen protein of *E. chaffeensis* in *Escherichia coli* allows attachment and internalization by Vero cells suggesting an important role for this protein for attachment and invasion of host cells (Popov et al., 2000).

Many cases of organ transplant transmission have been reported (Antony et al., 1995; Sadikot et al., 1999; Tan et al., 2001; Liddell et al., 2002; Safdar et al., 2002), and the survival of *E. chaffeensis* in ADSOL-treated red blood cells for 11 days suggests blood transfusion transmission could occur (McKechnie et al., 2000).

Symptoms

Infections with *E. chaffeensis* usually present with various non-specific symptoms and the clinical syndrome is commonly described as the "summer flu." Symptoms generally occur 7-10 days following a tick bite (Dumler and Walker, 2001) and consist of fever, malaise, headache, myalgia, rigor, arthralgia, nausea, diaphoresis, and anorexia (Rikihisa, 1999). Less commonly, patients may experience diarrhea, abdominal pain, lymphadenopathy, and confusion and may develop a rash. Because signs are non-specific, misdiagnosis is common and 40-62% of patients become progressively more ill and require hospitalization. Although generally easily treated with tetracyclines (doxycycline), infections can be life threatening as patients may develop hypertension, respiratory failure, meningeoncephalitis, acute renal failure, coagulopathies, hemorrhagic manifestations, and cardiac failure (see Dumler and Walker, 2001). In immunocompromised patients, *E. chaffeensis* causes extensive multi-system necrosis and frequently death (Paddock et al., 1993).

Diagnosis

Diagnosis of infection usually is based on the presentation of "summer flu" symptoms with a history of potential exposure to ticks and the absence of other causes for illness. If leucopenia or thrombocytopenia is present, treatment with doxycycline is recommended. Generally, morulae are not observed in a patient's white blood cells (with the exception of immunocompromised patients). At the onset of symptoms, few individuals (< 29%) have detectable antibody levels to *E. chaffeensis*. PCR has become a useful tool in the diagnosis of infection (Anderson et al, 1992b); however, PCR testing is not widely available and great care must be taken to avoid contamination of samples. Similarly, isolation of *E. chaffeensis* in DH82 cell cultures is an effective way to diagnose an early infection, but few hospitals have culture facilities available for human diagnostic work. Positive cultures are easily detected by the characteristic cytopathic effect created in the monolayer (Chen et al., 1995). In practice, diagnosis is often based on a compatible history and symptoms and is confirmed by a four-fold or greater increase in IFA titer to *E. chaffeensis*. Serologic confirmation requires that patients return after the sickness for collection of convalescent serum for comparison testing.

Human Monocytotropic Ehrlichiosis (HME) Surveillance

Currently the only estimate of HME risk in the United States is based on passive surveillance of human case data reported to the Centers for Disease Control and Prevention (CDC) through the National Electronic Telecommunications System for Surveillance (NETSS) and very limited active surveillance.

Passive Surveillance

In 1998, the Council of State and Territorial Epidemiologists and the Centers for Disease Control and Prevention recommended that ehrlichioses (HME and HGE) be added to the list of nationally notifiable diseases. Prior to this recommendation, several states (Arkansas, Arizona, California, Connecticut, Florida, Kentucky, Maine, Minnesota, Michigan, Missouri, New Hampshire, New Jersey, New York, North Carolina, Pennsylvania, Rhode Island, South Carolina, Tennessee, and Texas) reported ehrlichiosis case data to the CDC. In 1999, Delaware, Georgia, Iowa, Kansas, Massachusetts, Nebraska, Ohio, South Dakota, Utah, Virginia, West Virginia, and Wyoming began reporting cases. In 2000, Alabama, Indiana, Oklahoma, Washington, and Wisconsin began reporting and a new category (OE, other or unspecified ehrlichial agent) was added in part to recognize *E. ewingii* as a human pathogen. In 2001, Hawaii, Illinois, and Oregon began to report. Although the CDC and the Council of State and Territorial Epidemiologists (CSTE) recommended that human ehrlichioses be nationally reportable in 1998, currently 11 states (Alaska, Colorado, Idaho, Louisiana, Maryland, Mississippi, Montana, Nevada, New Mexico, North Dakota, and Vermont) do not report ehrlichiosis cases (Gardner et al., 2003). Three of these states (Louisiana, Maryland, and Mississippi) are in the region of the United States where the most HME cases are reported. Even in states that consider HME reportable, inconsistencies in diagnosis and reporting of HME limits the usefulness of this data for fine scale risk mapping.

From 1986-1997, 742 cases of HME were reported to the CDC by state health departments and another 754 were diagnosed by the CDC (McQuiston et al., 1999). For available data, the case fatality rate for HME was 2.7% (8 of 299 cases available for study). Most HME cases were reported from states in the southeastern quadrant of the United States. The highest annual incidence rates of HME were in Arkansas (5.53 per million), North Carolina (4.72 per million), Missouri (3.05 per million), and Oklahoma (2.90 per million), with Searcy County, Arkansas having the highest annual incidence per county (64.8 per million). Of note was that the incidence of *E. chaffeensis* infection was comparable with or exceeded that of Rocky Mountain spotted fever in some regions.

Gardner et al. (2003) report updated surveillance data for human ehrlichioses from 1997-2001. Data for HME cases were similar to those found in the previous review by McQuiston et al. (1996). Arkansas had the highest average annual incidence rate (6.2 per million) followed by Missouri (5.2 per million), Oklahoma (4.3 per million), Tennessee (2.5 per million), and North Carolina (1.4 per million). The majority of cases were among white males greater than 50 yrs of age and most cases were acquired between the months of May and August.

Active Surveillance

Accurate prevalence data for HME based on active surveillance are limited because certain populations were targeted (e.g., history of tick exposure, febrile) and studies have only been conducted in a few geographic regions. In general, active surveillance indicates that HME is more widespread and prevalence is higher than observed in passive surveillance. In southeastern Georgia, 8 of 75 (10.7%) febrile hospitalized patients (with no other etiology) seroconverted to *E. canis* (used as surrogate antigen for *E. chaffeensis*), resulting in a rate of 5.3 cases per 100,000 persons which is higher than that for RMSF in the same population during the study period (Fishbein et al., 1989). Similarly in North Carolina, of 35 patients with unexplained fever and history of tick bite, 16 (45.7%) had evidence of either *E. chaffeensis* or RMSF (Carpenter et al., 1999). Ten patients were infected with *E. chaffeensis* and 7 with RMSF (one patient was co-infected). A retrospective survey of 311 residents at a golf-oriented retirement community in Tennessee which experienced an outbreak of HME among residents indicated that 12.5% had prior exposure (Standaert et al., 1995). Interestingly, residents with average scores of > 100 for 18 holes were 2.4 times more likely to be seropositive and golfers who retrieved lost golf balls were 3.7 times more likely to be seropositive than those golfers who used a new ball. Residents at a nearby (10 miles) community with less wildlife and wooded areas only had a 3.3% seroprevalence rate. Few residents in either community reported a recent illness compatible with ehrlichiosis. The only study to investigate HME prevalence in children found that prevalence rates varied by geographic location (2%-

22%) but that older children were more likely to be seropositive than younger children (Marshall et al., 2002).

Military personnel are considered a high risk group because of the high exposure to ticks which occurs at certain bases. *Ehrlichia chaffeensis* was initially isolated from a patient at Ft. Chaffee in Arkansas (Dawson et al., 1991). Subsequent surveys of personnel at Ft. Chaffee indicate that 1.3-2.7% are exposed to *E. chaffeensis* while 2.5-6.4% are exposed to RMSF (Yevich et al., 1995; McCall et al., 2001). Even higher rates have been reported; during a single Army Reserve field training exercise in New Jersey, 12% of 74 personnel developed HME (Peterson et al., 1989).

HME surveillance outside of the United States

Reports of human infections with *E. chaffeensis* outside of the United States are primarily based on serologic evidence of exposure. Because of the cross-reactivity observed between *Ehrlichia* and *Anaplasma* species, confirmation of *E. chaffeensis* infection (either molecular or culture) is needed. One study reported that 4 of 35 (11.4%) blood samples from patients with fever and history of tick bite in northern China were PCR positive for *E. chaffeensis* (Wen et al., 2003). This finding was based on a small region of the 16S rRNA gene and was not confirmed with other more specific gene targets.

A recent study in Korea found that 39 of 271 (14.4%) serum samples reacted with *E. chaffeensis* in an IFA test with titers ranging from 80-320 (Park et al., 2003). Of these positive samples, 29 (74.4%) reacted with purified *E. chaffeensis* antigens by

Western blot analysis. All samples reacted with an antigen approximately 28 kDa, but only three weakly reacted with the 120-kDa antigen.

Serologic evidence of *E. chaffeensis* exposure has been reported in Israel, Poland, Slovenia, Netherlands, Croatia, Greece, Indonesia, Mali, Mozambique, Burkina Faso, Argentina, Mexico, Italy, Thailand, China, Korea, and Chile, but infection not been confirmed by other diagnostic assays (Morais et al., 1991; Uhaa et al. 1992; Brouqui et al., 1994; Heppner et al., 1997; Santino et al., 1998; Nuti et al., 1998; Gongora-Biachi et al., 1999; Keysary et al., 1999; Ripoll et al., 1999; Zikonov and Potasman, 1999; Brouqui and Dumler, 2000; Cizman et al., 2000; Groen et al., 2002; Kondrusik et al., 2002; Heo et al., 2002; Lopez et al., 2003; Richards et al., 2003; Topolovec et al., 2003; Wen et al., 2003).

Description and Phylogeny of *Ehrlichia chaffeensis* and Related Organisms

Ehrlichia chaffeensis and *E. ewingii*, members of the ∝-subdivision of the *Proteobacteria* in the family *Anaplasmataceae*, are small, gram negative, obligate intracellular bacteria (Dumler et al., 2001). Several genera in this family are of veterinary and medical importance, including *Ehrlichia*, *Anaplasma*, and *Neorickettsia*. *Ehrlichia* species characteristically grow in membrane-lined vacuoles which have a trilaminar cell wall found within the cytoplasm of infected cells (Smith and Ristic, 1977; Dawson et al., 1991). These intracellular bacteria, about 0.5 μm in size, may be found individually within the cytoplasm or as larger (up to 4.0 μm) groups called morula (McDade, 1990; Dawson et al., 1991). Members of the family *Anaplasmataceae* enter cells by induced phagocytosis (McDade, 1990), and *E. chaffeensis* entry and intracellular infection involves cholesterol-rich lipid rafts or caveolae and glycosylphosphatidylinositol (GPI)-anchored proteins (Lin and Rikahisa, 2003). Once inside the cell, *E. chaffeensis* replicate in early endosomes that are slightly acidic, are negative for lysosomal glycoproteins (Barnewall et al., 1997), and which accumulate tranferrin receptors (Barnewall et al., 1997, 1999). The ehrlichiae replicate within this membrane bound phagosome, form inclusion bodies, and are released when the host cell lyses (Dumler and Walker, 2001). In addition, individual *E. chaffeensis* bacteria were observed to replicate extracellularily in experimentally infected BALB/c mice (Li and Winslow, 2003).

This group of bacteria have historically been divided into three subgroups (genogroups) based on serological responses and host cell tropism; however, recently revisions have been published based on 16S rRNA and *groESL* gene analyses (Dumler et al., 2001). Former genogroup I included *E. canis, E. chaffeensis*, *E. ewingii*, *E. muris*, and *Cowdria ruminantium*. Revisions of this genogroup included the reassignment of *C. ruminantium* to the genus *Ehrlichia*. Former genogroup II included *E. platys*, *E. phagocytophila, E. equi, Anaplasma marginale*, and *An. ovis*. This genogroup also included the "HGE agent", the causative agent of human granulocytotropic ehrlichiosis. Reorganization of genogroup II reclassified all of these species into the genus *Anaplasma* and synonomized *E. equi* and the "HGE agent" with *An. phagocytophilum*. Former genogroup III included the trematode-borne ehrlichiae, *E. sennetsu*, *E. risticii*, *Neorickettsia helminthoeca, N. elokominica*, and the *Stellantchasmus falcatus* agent, and under the taxonomic revision, all were united in the genus *Neorickettsia*.

Vertebrate Hosts of *Ehrlichia chaffeensis*

<u>White-tailed deer (*Odocoileus virginianus*)</u>

White-tailed deer were examined as potential reservoirs because they are important hosts for all three mobile stages of *Am. americanum*, which at the time was suspected as the vector for *E. chaffeensis*. Dawson et al. (1994) examined serum samples from 1,269 WTD for anti-*Ehrlichia* antibodies. Using *E. chaffeensis*-infected DH82 cells as antigen, 544 (43%) tested positive. This was the first report that incriminated WTD as a potential reservoir for *E. chaffeensis*.

Soon after this finding, the susceptibility of WTD to infection with *E. chaffeensis* was investigated (Dawson et al., 1994). Two young seronegative WTD each were inoculated, via jugular vein, with either *E chaffeensis* or *E. canis*-infected DH82 cells. Both *E. chaffeensis*-inoculated deer seroconverted by 10 DPI and were culture positive from 13-24 DPI. Additionally, whole blood samples were PCR positive for *E. chaffeensis* from 10-27 DPI. Both *E. canis*-inoculated deer and one non-inoculated control deer were negative throughout the study.

To better understand the local epidemiology of *E. chaffeensis*, Lockhart et al. (1997b) investigated both the reservoirs (WTD and other potential mammalian reservoirs) and vectors in an area of high *E. chaffeensis* endemnicity at Whitehall Experimental Forest, Clarke County, Georgia. Ninety-four WTD were examined for ticks and serologically tested for *E. chaffeensis*. Additionally, WTD and questing *Am. americanum* were PCR tested for *E. chaffeensis*. Culture attempts were made from

WTD blood and tissues. White-tailed deer had a high prevalence of *E. chaffeensis* antibodies (92%) and PCR positivity (54%); however, none were culture positive. Three species of questing ticks were collected (*Am. americanum*, *D. variabilis*, and *Ixodes* sp.); however, over 99.9% of 52,924 ticks recovered were *Am. americanum*. PCR testing of individual adult *Am. americanum* for *E. chaffeensis* generated a higher minimal infection frequency (12%) compared to PCR testing of tick pools (3.5%).

Culture isolation of *E. chaffeensis* from 5 naturally infected WTD from Georgia (Whitehall Experimental Forest, Clarke County and Cedar Creek Wildlife Management Area in Jasper, Jones, and Putnam Counties) confirmed their role as a reservoir host (Lockhart et al., 1997a). A subsequent study obtained an additional WTD isolate from Ossabaw Island, Chatham County, Georgia (Little et al., 1998).

Although WTD had been confirmed as an important reservoir of *E. chaffeensis*, little was known about the pathogenicity or duration of infection in WTD. Previously, persistent *E. chaffeensis* infection had been described in both laboratory mice and humans (Dumler et al., 1993b; Telford and Dawson, 1996); however, no study of infection persistence had been conducted in WTD, the presumptive natural reservoir. A nine-month study was conducted to determine time of seroconversion, length of rickettsemia, and any tissue tropism in experimentally infected WTD (Davidson et al., 2001). Four WTD were inoculated intravenously with a WTD-isolate (GA-15B) of *E. chaffeensis* and the course of infection was monitored by IFA testing, PCR, and culture attempts. All exposed deer seroconverted (titer > 1:64) by 17 DPI and positive titers of antibodies persisted from 87 to 123 DPI. Approximately 44 days after becoming negative for *E. chaffeensis* antibodies, one deer developed a second period of antibody positivity which lasted for 64 days. Culture attempts on whole blood were successful on three infected deer, from 17 DPI through 108 DPI. The three deer also were intermittently PCR positive from 10-271 DPI. Following necropsy at 278 DPI, a bone marrow sample from one deer and a ruminal lymph node sample from another deer were positive for *E. chaffeensis* DNA.

While Dawson et al. (1994) and Davidson et al. (2001) successfully infected WTD with *E. chaffeensis*, infections were initiated by IV injection, a technique which does not mimic an infection via a tick-bite. To investigate the effect of various routes of infection, Varela et al., (2003) experimentally infected WTD by different routes of inoculation (intravenous, subcutaneous, and intradermal). All WTD, regardless of inoculation route, seroconverted (> or = 1: 64) and became PCR and/or cell culture positive by 15 DPI. There was no apparent difference in susceptibility to infection between deer inoculated by different routes.

A large scale serologic survey of *E. chaffeensis* in WTD was conducted statewide in Iowa (Mueller-Anneling et al., 2000). *Ehrlichia chaffeensis*-reactive antibodies were detected in 374 of 2,877 (13%) of WTD. Seropositive WTD were primarily in the southern and eastern parts of Iowa with the highest prevalence occurring in counties bordering northern Missouri. Other studies have detected antibodies reactive to *E. chaffeensis* in WTD which has provided distributional limits in the Midwestern and northeastern United States. Seropositive WTD have been detected as far north as southern Illinois, Indiana, and Ohio (Dawson et al., 1994a; Steiner et al., 1999; Irving et al., 2000). WTD in northern parts of these three states were seronegative (Dawson et al., 1994a; Steiner et al., 1999; Irving et al., 2000); however 9 of 337 (2.7%) WTD from Wisconsin were seropositive and all reacted to the 28- to 29-kDa antigens of *E. chaffeensis* in a western blot (Walls et al., 1998). All 9 WTD also were IFA positive for *An. phagocytophilum* and contained antibodies reactive with the 44-kDa antigen suggesting either dual infections with *An. phagocytophilum* and *E. chaffeensis* or another closely related organism.

Other Vertebrate Hosts

While WTD are the main reservoir responsible for maintenance of the enzootic cycle of *E. chaffeensis* in nature, several other species of animals have been shown to be experimentally susceptible, naturally infected, or to have evidence of exposure to *E. chaffeensis*.

Domestic dogs are susceptible to multiple *Ehrlichia* and *Anaplasma* spp. (*E. canis*, *E. ewingii, E. chaffeensis, An*. *platys*, and *An. phagocytophilum*) and are common hosts of *Am. americanum*. Soon after the discovery of *E. chaffeensis* as a human pathogen, domestic dogs were shown to be experimentally susceptible to IV inoculation with *E. chaffeensis* (Dawson and Ewing, 1992). Experimentally infected dogs showed no clinical signs but seroconverted. *Ehrlichia chaffeensis* was reisolated from blood samples of these experimentally infected dogs up to DPI 26. Natural infection of domestic dogs with *E. chaffeensis* was first detected in Virginia where 28 of 74 (38%) and 8 of 19 (42%) dogs were seropositive and PCR positive, respectively (Dawson et al., 1996). In central Oklahoma, 4 of 65 (6%) dogs tested positive for *E. chaffeensis* by PCR (Murphy et al., 1998). Despite the multiple reports of natural *E. chaffeensis* infections in dogs using molecular assays, *E. chaffeensis* has never been isolated in culture from a naturally infected dog.

In northeastern Georgia, 21% of raccoons (*Procyon lotor*) and 8% of opossums (*Didelphis virginiana*) were seropositive for *E. chaffeensis* (Lockhart et al., 1997b). Both species of mammals were infested by larval, nymphal, and adult stages of *Am. americanum*. Similar results were observed by Comer et al. (2000) who reported that serum samples from 83 of 411 (20%) raccoons from Florida, Georgia, North and South Carolina, Texas, Virginia, West Virginia, and Washington had antibodies reactive to *E. chaffeensis*. A recent intensive survey of 60 raccoons from east-central Georgia for *Ehrlichia* and *Anaplasma* disclosed that 23 (38%) had antibodies reactive to *E. chaffeensis*, 13 (22%) had antibodies reactive to *E. canis*, and 1 (2%) had antibodies reactive to *A. phagocytophilum* (Dugan et al., unpublished). All 60 raccoons were PCR negative for *E. chaffeensis* and *E. ewingii*, but one was PCR positive for *E. canis*. Surprisingly 31 (53%) of raccoons were PCR positive for *A. phagocytophilum* but after sequencing, the products only had ~94% identity with *A. phagocytophilum*. Instead the sequences were ~99% identical to *Ehrlichia*-like sequences reported from *I. ricinus* ticks in the Netherlands (Schouls et al., 1999), *I. ovatus* ticks from Japan (Shibata et al., 2000), and rats (*Rattus* spp.) in China (Pan et al., 2003). The high seroprevalence of *E. chaffeensis* but the lack of molecular confirmation suggests that the *Ehrlichia*-like agent of raccoons cross-reacts serologically with *E. chaffeensis*; however, additional studies are needed to prove this theory.

No antibodies were detected in serum samples from 38 white-footed mice (*Peromyscus leucopus*), 20 cotton rats (*Sigmodon hispidus*), 10 Eastern gray squirrels

(*Sciurus carolinensis*), 8 house mice (*Mus musculus*), 4 Eastern cottontail rabbits (*Sylvilagus floridanus*), 4 Eastern harvest mice (*Reithrodontomys humulis*), and 3 Eastern chipmunks (*Tamias striatus*) from Whitehall Experimental Forest, Clarke County, Georgia (Lockhart et al., 1997b). Testing of 245 serum samples of 9 species of rodents (Cotton rats, gray squirrels, fox squirrels [*Sciurus niger*], Norway rats [*Rattus norvegicus*], house mice, white-footed mice, eastern harvest mice, rice rats [*Oryzomys palustris*], and cotton mice [*Peromyscus gossypinus*]) from South Carolina and Georgia also failed to reveal any IFA positives (Lockhart et al., 1998); however, anti-*E. chaffeensis* antibodies have been detected in white-footed mice from Connecticut (Magnarelli et al., 1997). Antibodies have also been detected in rabbits, red foxes (*Vulpus vulpes*), and gray foxes (*Urocyon cinereoargenteus*) (see Lockhart, 1996b), and experimentally red foxes are competent hosts (Davidson et al., 1999). *Ehrlichia chaffeensis* has not been isolated from any of these hosts in the wild and because serologic cross-reaction is known to occur among *Ehrlichia* spp. (Nyindo et al, 1991; Shankarappa et al., 1992), it is possible that some of this serologic reactivity was not due to *E. chaffeensis* infection. Studies are needed to confirm the susceptibility of these mammalian hosts via experimental infection or culture isolation of natural infections.

Molecular evidence of natural infection in coyotes in Oklahoma has been reported (Kocan et al., 2000). Of 21 coyotes tested by PCR, 15 (71%) were positive for *E. chaffeensis* and none were positive for *E. canis* or *E. ewingii*. Because coyotes have large home ranges and are common hosts of *Am. americanum*, they may be involved in the large-scale movement of infected ticks and possibly *E. chaffeensis* to naïve populations.

Natural infection of domestic goats has been documented (Dugan et al., 2000). Of 38 goats from a University of Georgia herd examined for *E. chaffeensis*, 28 (73.7%) were seropositive by IFA and six (15.8%) were PCR positive. A single goat was culture positive for *E. chaffeensis* on two separate sampling times 40 days apart (Dugan et al., 2000). However, two independent experimental trials have failed to infect domestic goats with *E. chaffeensis* (Dugan et al., 2004).

Molecular evidence of natural infections of lemurs was recently reported (Williams et al., 2002). Seven ring-tailed lemurs (*Lemur catta*) and 1 red ruffed lemur (*Varecia variegata rubra*) from the Duke University Primate Center developed clinical signs consistent with ehrlichiosis in May and June 2001. Anorexia, fever, lethargy, lymphadenopathy, thrombocytopenia, and hyperbilirubinemia were commonly observed in sick lemurs. All of the lemurs were infested by numerous ticks (*Am. americanum*, *Rhipicephalus sanguineus*, and *D. variabilis*). *Ehrlichia chaffeensis* infection was confirmed in six ring-tailed lemurs using PCR and by culture of a single infected red ruffed lemur. Additionally, morulae were observed in lymphocytes and monocytes in inguinal lymph node aspirates from three of the eight lemurs. None of the eight clinically ill lemurs or uninfected lemurs present at the Duke University Primate Center was serologically tested for *E. chaffeensis* exposure. To investigate the exposure rate of a group of free-ranging lemurs, Yabsley et al. (2004) tested 52 lemurs (3 species) from St. Catherine's Island, Liberty Co., GA for *E. chaffeensis* by IFA, culture, and PCR of whole blood. Twenty of the 52 (38.5%) lemurs had antibodies reactive for *E.*

chaffeensis (titer $\geq$ 1:128) and two ring-tailed lemurs were culture and PCR positive for *E. chaffeensis*. This study showed that at least 39% of the free-ranging lemurs on St. Catherine's Island are exposed to *E. chaffeensis*, and in contrast to the Williams et al. (2002) study, clinical disease was not observed in these two infected lemurs.

Other vertebrate hosts outside of the United States

Ehrlichia chaffeensis, or closely related ehrlichiae, has been detected in blood samples from 12 of 31 (38.7%) and spleens from 22 of 39 (56.4%) wild rats (*Rattus niviventer, R. losea, R. norvegics,* and *R. flavipects*) in southern China (Wen et al., 2003). However, this finding is suspect as the PCR target was the highly conserved 16S rRNA gene and products were not sequenced. Also, Pan et al. (2003) detected an *Ehrlichia*-like organism, related to but distinct from *E. chaffeensis*, in the blood and spleen of *R. norvegicus* from southern China. Analysis of 1,494-bp of this *Ehrlichia*-like species indicated that it was most closely related to a Dutch *Ehrlichia*-like species termed the "Schotti" variant. It is unknown if the *Ehrlichia* detected in the two studies are identical because sequencing was only conducted in the Pan et al. (2003) study.

Table 2.1. Summary data for 8 culture isolates of *Ehrlichia chaffeensis* from non-human vertebrates in the United States.

Species	County	State	Age	Reference
WTD	Clarke	GA	18 mo	Lockhart et al., (1997a)
WTD	Clarke	GA	9 mo	Lockhart et al., (1997a)
WTD	Clarke	GA	9 mo	Lockhart et al., (1997a)
WTD	Jasper/Jones/ Putnam	GA	11 mo	Lockhart et al., (1997a)
WTD	Jasper/Jones/ Putnam	GA	11 mo	Lockhart et al., (1997a)
WTD	Chatham	GA	2.5 yr	Little et al., (1998)
Domestic Goat	Clarke	GA	NA*	Dugan et al., (2000)
Red-Ruffed Lemur	Wake	NC	NA	Williams et al., (2002)
Ring-tailed Lemur	Liberty	GA	1yr 7mo	Yabsley et al., (2004)
Ring-tailed Lemur	Liberty	GA	5yr 7mo	Yabsley et al., (2004)

* Not available.

Table 2.2. Summary data for non-human vertebrate hosts of *Ehrlichia chaffeensis* (as determined by polymerase chain reaction) in the United States.

Species	Location	No. infected/ No. tested (%)	Reference
White-tailed deer	Clarke Co., GA	15/28 (54)	Lockhart et al. (1997a)
White-tailed deer	Clarke Co., GA	4/20 (20)	Lockhart et al., (1997b)
White-tailed deer	Jasper, Jones, and Putnam Cos., GA	3/10 (30)	Lockhart et al., (1997b)
White-tailed deer	Jasper and Jones Cos., GA	1/5 (20)	Little et al. (1997)
White-tailed deer	Beaufort Co., SC	2/5 (40)	Little et al., (1997)
White-tailed deer	Chatham Co., GA	1/5 (20)	Little et al., (1998)
White-tailed deer	Wilkes Co., GA	1/1 (100) *	Little and Howerth (1999)
White-tailed deer	Boone Co., MO	20/217 (23)	Arens et al., (2003)
Domestic Goats	Clarke Co., GA	6/38 (16)	Dugan et al., (2000)
Red-Ruffed lemur	Wake Co., NC	1/2 (50)*	Williams et al., (2002)
Ring-tailed lemur	Wake Co., NC	5/6 (83)*	Williams et al., (2002)
Lemur	Unknown Co., VA	1/NA†	See Williams et al., (2002)
Ring-tailed lemur	Liberty Co., GA	2/56 (4)	Yabsley et al., (2004)
Domestic dogs	Unknown Co., VA	8/19 (42)	Dawson et al., (1996)
Domestic dogs	Unknown Co., NC	9/27 (33)	Kordick et al., (1999)
Domestic dogs	Oklahoma and Tulsa Cos., OK	4/65 (6)	Murphy et al., (1998)
Domestic dogs	Unknown Co., NC	3/12 (25)	Breitschwerdt et al., (1998)
Coyotes	Unknown Co., OK	15/21 (71)	Kocan et al., (2000b)

* Clinically ill animals.
† Not available.

Tick Vectors of *Ehrlichia chaffeensis*

Amblyomma americanum (lone star tick)

Amblyomma americanum, a three host tick, is a major pest of humans and livestock, and recently has been recognized as a major vector of several pathogens of medical and veterinary importance. The distribution of *Am. americanum* is wide and encompasses the majority of the southeastern and midwestern United States (as far west as Texas, Oklahoma, Kansas, and Nebraska and as far north as Iowa, Illinois, Indiana, and Ohio). Recently, *Am. americanum* has been reported from the eastern coastline as far north as Maine (Keirans and Lacombe, 1998; Ijdo et al., 2000), but the distribution of *Am. americanum* in non-coastal regions of these northern states (e.g., Pennsylvania, New York) is not known. Historical isolated distribution reports include Canada (Labrador and Manitoba), Guatemala, Mexico, the Guianas, and Brazil (USDA, 1965; Parker et al., 1937; Bishopp and Trembley, 1945). These ticks were probably detected on people or livestock moved from *Am. americanum*-endemic areas. No current reports indicate that *Am. americanum* became established in these areas.

Prior to any knowledge of the natural history of *E. chaffeensis*, human infections were associated with tick exposure and *Am. americanum* was suspected as a possible vector based on the distribution of human cases, history of tick exposure or bites, and seasonality of disease occurrence (Fishbein et al., 1989; Harkess et al., 1989; Eng et al., 1990). Subsequent detection of *E. chaffeensis* DNA in *Am. americanum* utilizing PCR further incriminated this species (Anderson et al., 1993). A list of states where PCR positive *Am. americanum* have been detected is presented in Table 2.3.

A temporal relationship between the presence of *Am. americanum* and the prevalence of *E. chaffeensis*-reactive antibodies was demonstrated for a WTD population at Whitehall Experimental Forest in Georgia (Lockhart et al., 1995). *Amblyomma americanum* ticks were not present at Whitehall Experimental Forest prior to 1983, and did not become prevalent until after 1986. Testing of 50 WTD prior to 1986 failed to demonstrate any *E. chaffeensis* seropositive deer and a single deer in 1986 had a titer of 1:64. In 1987, 8 of 38 (21%) of WTD were seropositive for *E. chaffeensis*. Additional testing of WTD from 1988-1993 revealed a significant increase (up to 100%) in the number of *E. chaffeensis* seropositive deer. This study demonstrated an association between the introduction of *Am. americanum* to an area and the presence of *E. chaffeensis* in WTD at Whitehall Experimental Forest.

In addition to a temporal association, a spatial association was established for *Am. americanum* and *E. chaffeensis* antibodies in WTD populations (Lockhart et al., 1996a). Of 150 WTD tested from 30 *Am. americanum* endemic areas, 121 (80.7%) were seropositive. Additionally, each of the 30 populations sampled had at least 2 of 5 seropositive WTD. Of 150 WTD tested from 30 *Am. americanum* negative populations, 4 (2.7%) were seropositive with only 2 of 30 locations having seropositive WTD.

Experimental transmission of *E. chaffeensis* between WTD by *Am. americanum* has been demonstrated (Ewing et al., 1995). Laboratory-reared deer were needle-inoculated with *E. chaffeensis* infected DH82 cells. On PID 11, infected WTD were exposed to larval, nymphal, and adult *Am. americanum*. Resultant nymphs or adults were used to test transstadial transmission to naïve deer by allowing ticks to feed to repletion. Transmission WTD were tested for infection by culture attempts and PCR testing of whole blood. Ticks that were acquisition fed as larvae or nymphs and subsequently transmission fed as nymphs or adults, respectively, successfully transmitted *E. chaffeensis* to naïve deer based on serologic and molecular evidence.

Amblyomma maculatum (Gulf coast tick)

Amblyomma maculatum was suspected as a potential vector for *E. chaffeensis* since its distribution overlaps the range of *E. chaffeensis* endemnicity and this tick is a promiscuous feeder. However, neither field surveys nor experimental trials have provided evidence that *Am. maculatum* can serve as a vector of *E. chaffeensis* (Lockhart et al., 1996a; Kocan et al., 2000a; Yabsley et al., 2003 [Chapter 2]).

Dermacentor species

Although *Am. americanum* is considered to be the primary vector of *E. chaffeensis*, recent studies have suggested that *D. variabilis* may play a minor role in the transmission of *E. chaffeensis*. *Ehrlichia chaffeensis* DNA was initially detected in a *D. variabilis* collected from an opossum in Arkansas (Anderson et al., 1992b). Subsequent surveys of questing *D. variabilis* detected *E. chaffeensis* in 4 of 120 (3.3%) ticks from southwestern Missouri (Steiert and Gilfoy, 2002), 3 of 15 (20%) ticks from northern California (Kramer et al., 1999) and 4 of 58 (6.9%) ticks from southern California (Holden et al., 2003). Recently, Wagner et al. (2002) successfully transmitted *E. chaffeensis* between domestic dogs with *D. variabilis* confirming the vector potential of this tick species.

Ehrlichia chaffeensis has been detected in a single adult *D. occidentalis* (1 of 353, 0.028%) from southern California (Holden et al., 2003). This tick is probably not involved in the maintenance of *E. chaffeensis* in nature.

<u>*Ixodes pacificus* (Western black-legged tick)</u>

In California, *E. chaffeensis* has been detected in *Ixodes pacificus* (Kramer et al., 1999; Holden et al., 2003). In northern California, two pools of adult ticks (13.3% minimum infection rate) were positive for *E. chaffeensis,* and in southern California, 5 of 776 (0.64%) adult ticks were positive.

<u>Other potential tick vectors outside of the United States</u>

In southern China, *E. chaffeensis* has been reported from *Am. testudinarium* (16 of 29 adults) and *Haemaphysalis yeni* (28 of 240 adults and nine of 215 pools of nymphs) (Cao et al., 2000). In the Fujian region of China, *E. chaffeensis* was detected in 3 of 25 (12%) *I. ovatus* collected off of the cervid Reeves' muntjac (*Muntiacus reevesi*) (Gao et al., 2000a). In northern China, 7 of 70 (10%) adult *D. silvarum* and 25 of 64 (39.1%) adult *I. persulcatus* were positive (Gao et al., 2000b). Sequencing of nearly the entire 16S rRNA gene (1,463-bp) of *E. chaffeensis* from *H. yeni* in China revealed only 6 nucleotides (0.4%) difference between the *E. chaffeensis* from China and the USA, suggesting that the agent is either closely related to or a genetic variant of *E. chaffeensis* (Wen et al., 2003). In Korea, two single infections of *I. persulcatus* (one of two ticks and one of three ticks) have been reported (Chae et al., 2002; Kim et al., 2003)

Table 2.3. Tick species (host seeking) and states in which *Ehrlichia chaffeensis* has been detected by polymerase chain reaction in the United States.

Species	State	Reference
Amblyomma americanum	AL	Stromdahl et al., (2001)
	AR	Stromdahl et al., (2001)
	CT	Ijdo et al., (2000)
	FL	Stromdahl et al., (2001)
	GA	Lockhart et al., (1997b); Whitlock et al., (2000); Varela et al., (sub.)
	IN	Burket et al., (1998); Steiner et al., (1999); Irving et al., (2000)
	KS	Stromdahl et al., (2001)
	KY	Anderson et al., (1993); Yu et al., (1997b)
	MD	Stromdahl et al., (2001)
	MO	Anderson et al., (1993); Yu et al., (1997b); Roland et al. (1998)
	NC	Anderson et al., (1993); Stromdahl et al., (2001); Yu et al., (1997b)
	NJ	Stromdahl et al., (2001)
	RI	Ijdo et al., (2000)
	VA	Stromdahl et al., (2001)
Dermacentor variabilis	CA	Kramer et al., (1999) Holden et al., (2003)
	MO	Roland et al., (1998); Steiert and Gilfoy, (2002) Anderson et al., (1993)
Dermacentor occidentalis	CA	Holden et al., (2003)
Ixodes pacificus	CA	Kramer et al., (1999); Holden et al., (2003)

Molecular Characterization of *Ehrlichia chaffeensis*

Multiple genes of *E. chaffeensis* have been sequenced and/or characterized including those genes for the 16S rRNA, variable length PCR target (VLPT), 120-kDa antigen protein, 106-kDa antigen protein, 37-kDa protein, *groESL* heat shock proteins, quinolate synthetase A (nadA), DsbA-like disulfide bond formation proteins, RNA polymerase beta-subunit, and a multigene family containing 22 homologous genes which encode for the p28 surface protein (Yu et al., 1997a; Sumner et al., 1997; Yu et al., 1999; Sumner et al., 1999; Yu and Walker, 2000; Yu et al., 2000; McBride et al., 2002; Taillardat-Bisch et al., 2003). Two of these genes, the VLPT and 120-kDa genes, encode for immunoreactive surface proteins and each contain repetitive elements with variable numbers of repeats. The number of repeats can be easily observed by gel electrophoresis, thus provides a way to characterize *E. chaffeensis* from human, animal, and tick samples.

120-kDa antigen gene

The 120-kDa antigen gene encodes for an immunodominant surface protein. This protein is expressed on dense-core stages of *E. chaffeensis* and is also released into the intramorular fibrillary matrix (Popov et al., 2000). The 120-kDa gene contains a series of 240-bp tandem repeat units. Three genetic variants of the 120-kDa gene, containing two, three, or four repeats, have been reported from *E. chaffeensis* from human or tick samples. Despite having varying numbers of repeats, antisera recognized all p120 antigen types from different isolates suggesting that this protein fails to provide cross-immunity between strains. To date, only a single genetic variant of the 120-kDa gene has been detected in individual infected humans or in individual ticks.

Expression of the 120-kDa gene in *Escherichia coli* allows attachment and internalization by Vero cells suggesting an important role for this protein for attachment and invasion of host cells by *E. chaffeensis* (Popov et al., 2000). The first repeat unit of the 120-kDa gene contains four nucleotide substitutions compared to the subsequent repeats which are identical (Yu et al., 1997a).

Variable length PCR target (VLPT) antigen gene

The variable length PCR target (VLPT) antigen gene contains three to six tandem imperfect 90-bp repeat units. In addition, the VLPT gene has variations at the nucleotide level consisting of: 1) single-base substitutions at 4 specific locations, 2) presence or absence of an aspartic acid codon deletion upstream from the repeat region, and 3) a 9-bp deletion downstream from the stop codon. Sequencing of the tandem imperfect repeat units in the VLPT gene has revealed seven distinct amino acid repeat profiles (Sumner et al., 1999). Currently, the function of the VLPT protein is unknown, but the greater number of repeats compared with the 120-kDa antigen gene makes the VLPT gene useful for strain differentiation. Apparent geographic clustering of VLPT genetic types noted in previous surveys of ticks (Stromdahl et al., 2000) led to the suggestion that there might be a geographic clustering of *E. chaffeensis* genetic variants (Paddock and Childs, 2003).

Landscape Epidemiology of *Ehrlichia chaffeensis*

Geographic Information System analyses

Geographic information systems (GIS) development has provided researchers with a powerful tool to investigate the epidemiology of diseases. This system allows the capture, storage, retrieval, analysis, and display of spatial and nonspatial (attribute) data. The strength of this system is that in addition to mapping their data, researchers can perform statistical analyses to predict data in unsampled regions, predict future occurrence of an event, or determine predictive variables related to the data of interest. These analyses can investigate associations between disease presence and location, environment, or other variables. Examples include: identifying locations of high prevalence and monitoring of intervention and control programs for onchocerciasis in Guatemala (Richards, 1993); monitoring spread of trypanosomiasis in Africa (Roger and Williams, 1993); developing a risk map for various malaria mosquito vectors in Europe (Kuhn et al., 2002); determining landscape features associated with infection of lizards with *Plasmodium mexicanum* (Eisen and Wright, 2001); identifying risk factors for Lyme disease using a canine surveillance system (Guerra et al., 2001); and investigating remotely sensed characterizations of landscape composition and environmental factors affecting the distribution of *I. scapularis* and Lyme disease risk (Dister et al., 1997; Guerra et al., 2002).

One important tool in GIS analysis is the ability to identify potential predictors of disease presence or absence. These factors (e.g., reservoir host density, soil type, land use, temperature, precipitation, or other climate variables, etc.) can be tested using logistic regression analysis to see if they accurately predict the presence and absence of a disease. Once factors related to the disease are identified, analyses can be conducted to produce a predictive model. The model(s) and GIS are then used to construct a map of the predicted distribution of the disease or disease agent.

As a supplementary tool, geostatistical analyses (e.g., kriging) can be conducted to predict and map the distribution and risk of acquiring a disease. This technique analyzes data from sampled points and extrapolates data for unknown points based on a nearest neighbor analysis. This technique has been applied successfully to map malaria risk in Mali (Kleinschmidt et al., 2000) and to investigate the spatial distribution of human granulocytic ehrlichiosis (HGE, caused by *Anaplasma phagocytophilum*) in Connecticut (Chaput et al., 2002). In the latter study, HGE cases were mapped in census blocks and analyzed for clustering to see if the cases were randomly distributed. The results indicated several clusters of HGE risk in the region and provided the spatial distribution of HGE which can now be used to identify if any environmental or landscape characteristics are associated with increased risk of HGE infections.

Ehrlichia chaffeensis is maintained in nature in a cycle involving WTD and *Am. americanum* as the major reservoir and vector, respectively. Little is known about the climatic or environmental factors that limit the distribution or spread of *E. chaffeensis*. Based on *E. chaffeensis* antibodies in WTD, Dawson et al. (1994) found that elevation, latitude, longitude, mean air temperature, and mean soil temperature in summer were associated with presence or absence of *E. chaffeensis*. Neither probability modeling nor geospatial analyses were conducted in this study to predict the distribution of *E. chaffeensis* for unsampled counties.

The lack of additional geospatial or modeling analyses is primarily related to the inconsistent and nonuniform coverage of primary HME case data. As mentioned earlier, HME is a reportable disease, but not all states report cases to the CDC through the NETSS. Within the south central and southeastern United States where the risk of HME is considered to be the highest, three states (Louisiana, Maryland, and Mississippi) still do not report ehrlichiosis cases. Even within states where ehrlichiosis cases are reported, diagnosis and reporting are uneven (Gardner et al., 2003). Based on the limited data available from the NETSS, Gardner and others (2003) were able to discern areas with high incidence rates of HME but because of large regions of negative data were unable to analyze the spatial distribution of HME. Data acquired during this study (i.e., additional *Am. americanum* distribution records, *E. chaffeensis* distribution in WTD populations) provide the basis for both predictor and spatial analyses of the risk of HME because these data provide a more comprehensive assessment of *E. chaffeensis* distribution [Chapters 3 and 5].

Factors influencing distribution of *Am. americanum* and *E. chaffeensis*

Studies have linked the presence of *E. chaffeensis* with *Am. americanum* infestation of WTD populations (Lockhart et al., 1996a; 1997a; 1997b; Yabsley et al., 2003 [Chapter 3]), but again, little is known about what factors determine the range of the LST. Because of the high correlation between infestation of WTD with *Am. americanum* and infection of WTD with *E. chaffeensis*, the factors affecting these events are likely similar.

Amblyomma americanum reproductive success and survival depend on several environmental and climatic factors including temperature, humidity, amount of underbrush, soil cover, and the presence of large mammals (e.g., deer). The climatic factors that constrain the observed distribution of *Am. americanum* would be hypothesized to differ as the climate in southern Florida (where *Am. americanum* is absent) is vastly different than the climate in other regions of the United States where the tick is also absent (e.g., western Texas or in West Virginia). However, as discussed in the tick vector section of this introduction, if *Am. americanum* (and *E. chaffeensis*) are introduced into a susceptible previously non-endemic WTD or cervid population (e.g., in California), other tick vectors may serve as vectors of *E. chaffeensis* in that focal area, possibly without the establishment of *Am. americanum*.

Optimal temperature and relative humidity (RH) are important to the reproduction, development, and survival of *Am. americanum*. Laboratory studies indicate warm temperature and high RH is needed for reproduction and egg hatching. Females will not lay eggs at temperatures below 10 C and eggs fail to hatch at temperatures greater than 30 C (Koch and Dunn, 1980). At 30-31 C, eggs were laid five days following engorgement and at 27 C eggs hatched in 23 days whereas at 13 C eggs took up to 117 days for development (Hooker et al., 1912). One study found that when RH is less than 55%, eggs failed to hatch (Kock and Dunn, 1980), while at 65% RH almost 19% of eggs hatched. Another study found that eggs failed to hatch when

RH was less than 75% (Lancaster, 1957). These studies indicate that, in the laboratory, the optimum temperature for reproduction is between 20 and 30 C and optimum RH is greater than 75%.

Field studies have supported these findings, but few have been conducted because of the difficulty in accurately measuring these conditions in the microhabitat of the ticks. In Oklahoma, when temperatures rise and humidity decreases, tick activity decreases (Robertson et al., 1975). In support of the observations in the former study, Semter et al. (1975) also found that temperature was an important factor controlling the activity and development of ticks by tracking tick activity and development throughout the year using lab reared ticks released into cages placed in various habitats.

Amblyomma americanum are found predominantly in wooded habitats, particularly young second-growth forests containing thick underbrush with lower numbers occurring in grass-crop land or climax forest (Hair and Howell, 1970; Lancaster, 1957; Sonenshine et al., 1966). These wooded and brushy habitats provide a microhabitat for *Am. americanum* and also are utilized preferentially by WTD and other potential hosts. The habitats that provide low day temperatures, high humidity, and low variability among these variables during the day and night provide the best conditions for *Am. americanum*. When conditions change, *Am. americanum* can move considerable distances to find optimum temperature or humidity (Smittle et al., 1967).

The emergence of *Am. americanum*-vectored diseases has been partially related to the reestablishment and growth of WTD populations in the United States (Childs and Paddock, 2003). This population increase followed the cessation of uncontrolled harvests and substantial restocking of populations throughout the southeastern United

States. However, there are areas in the southeastern United States (e.g., West Virginia) where WTD have rebounded (SCWDS, unpublished data), but apparently, infections with *E. chaffeensis* have not. This would suggest that there is a non-WTD factor limiting the spread of *E. chaffeensis*. The presence, and possibly the density, of WTD are none the less important to the maintenance of high numbers of *Am. americanum* (Haile and Mount, 1987; Mount et al., 1993; Patrick and Hair, 1978) and likely *E. chaffeensis.* It has been shown that in the absence of large mammalian hosts, *Am. americanum* densities will decline and that the tick may go locally extinct (Mount et al., 1993). While WTD are important to the maintenance of high levels of *Am. americanum* and are important as reservoirs for *E. chaffeensis*, other factors such as land cover, environmental, or climatic factors may be directly or indirectly important in the maintenance of *E. chaffeensis*.

Literature Review for *Ehrlichia ewingii*

History and Description

Ehrlichia ewingii is a small, gram negative, obligate intracellular bacteria which is closely related to *E. chaffeensis* and *E. canis*. *Ehrlichia ewingii* was first reported based on observed leukocytic inclusion bodies in dogs in the early 1960's and was thought to be a new strain of *E. canis* (Ewing, 1963). Several more reports during subsequent years indicated that this *Ehrlichia* sp. was common in domestic dogs in Oklahoma (Ewing and Buckner, 1965; Ewing and Philip, 1966; Ewing, 1969) and was infectious to coyotes (Ewing et al., 1964). Nearly 30 years later, the 16S rRNA gene of this canine granulocytotropic ehrlichiosis agent was amplified and sequenced, after which the name *E. ewingii* was proposed for this new species (Anderson et al. 1992a). The most closely related species were *E. canis* (98.0% related) and *E. chaffeensis* (98.1% related). Experimentally, this organism has been studied by using serial passage in dogs because all attempts to date to culture the organism in multiple types of mammalian cell lines have failed.

Vertebrate Hosts of *Ehrlichia ewingii*

Ehrlichia ewingii infections of dogs have been diagnosed in several states including Oklahoma, North Carolina, Missouri, and Virginia (Goldman et al, 1998; Murphy et al., 1998; Anderson et al., 1992a; Dawson et al., 1996; Kordick et al., 1999; Goodman et al., 2003; Liddell et al., 2003). In a review of 15 *E. ewingii* clinical cases, fever and lameness (n = 8) were the most common findings followed by neurologic abnormalities (n = 5) including ataxia, paresis, proprioceptive deficits, anisocoria, intention tremor, and head tilt, and neutrophilic polyarthritis (n = 3). All 12 dogs for which platelet counts were available were thrombocytopenic (Goodman et al., 2003). Following treatment with doxycycline, most dogs improved rapidly. A survey of kennel dogs in North Carolina indicated that 8 of 27 (29.6%) were infected with *E. ewingii* (Kordick et al., 1999). All infected dogs had some clinical sign attributed to an ehrlichial infection; however, all dogs were infected with one or more additional tick-borne infections (e.g., *E. canis, E. chaffeensis, An. phagocytophilum, An. platys*, *Rickettsia* spp., *Bartonella vinsonii*, and *Babesia canis*) making interpretations of clinical disease associated with *E. ewingii* difficult. A cross-sectional study of *Ehrlichia* and *Anaplasma* infections in dogs in Missouri found that *E. ewingii* represented the predominant *Ehrlichia* found in dogs suspected of having ehrlichiosis (Liddell et al., 2003). In a study of 78 dogs suspected of having ehrlichiosis and 10 healthy dogs, 20 of the symptomatic and two of the asymptomatic dogs were found to be infected with an *Ehrlichia* or *Anaplasma* species by PCR. Of the 22 positive animals, 20 (91%) were infected with *E. ewingii* and one dog each was infected with *E. chaffeensis* and *An. phagocytophilum*. *Ehrlichia canis* was not detected in any of the dogs.

Prior to the current study, no known non-canine reservoir hosts for *E. ewingii* were known. Although many infected dogs develop disease, some remain asymptomatic suggesting that they may serve as reservoirs (Goodman et al., 2003; Liddell et al., 2003). In this study, we chose to examine WTD as potential reservoir hosts for *E. ewingii* [Chapter 6] because of the close molecular relatedness to *E. chaffeensis*, which also uses *Am. americanum* as a vector and WTD as important reservoirs. Subsequent to publication of that study (Yabsley et al., 2002), Arens et al. (2003) reported molecular evidence of *E. ewingii* infections in 44 of 217 (20%) WTD from central Missouri (Boone County).

Human *Ehrlichia ewingii* Ehrlichiosis (EWE)

Buller et al. (1999) reported the first cases of *E. ewingii* infection of humans. In that study, four patients positive for *Ehrlichia* or *Anaplasma* by broad-range PCR were negative for both *E. chaffeensis* and *An. phagocytophilum* using specific PCR assays. Sequencing revealed the causative agent to be *E. ewingii*. Morulae were observed in neutrophils in two patients and antibodies reactive with *E. chaffeensis* were detected in three patients. Disease was similar to that observed in other human ehrlichioses and was characterized by fever, headache, and thrombocytopenia with or without leukopenia. To date human infections with *E. ewingii* have been reported from Missouri, Oklahoma, and Tennessee (Buller et al., 1999; Paddock et al., 2001).

Tick Vectors of *Ehrlichia ewingii*

Experimentally, *Am. americanum* is a competent vector of *E. ewingii* (Anziani et al., 1990); however, natural infections of two other tick species, *R. sanguineus* and *D. variabilis*, have been reported from Oklahoma and Missouri (Murphy et al., 1998; Steiert and Gilfoy, 2002). Molecular evidence of naturally infected LST has been reported from multiple states including Missouri, North Carolina, Georgia, Florida, and Texas (Steiert and Gilfoy, 2002; Wolf et al., 2000; Varela et al., submitted; Sumner et al., unpublished; Labruna et al., unpublished).

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CHAPTER 3

EVALUATION OF A PROTOTYPE *EHRLICHIA CHAFFEENSIS* SURVEILLANCE SYSTEM USING WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) AS NATURAL SENTINELS[1]

[1] Yabsley, M.J., V.G. Dugan, D.E. Stallknecht, S.E. Little, J.M. Lockhart, J.E. Dawson, and W.R. Davidson. 2003. *Vector Borne and Zoonotic Diseases* 3:195-207. Reprinted here with permission of publisher.

ABSTRACT

The natural history of *Ehrlichia chaffeensis*, the causative agent of human monocytotropic ehrlichiosis, includes the lone star tick (LST, *Amblyomma americanum)* as a vector and white-tailed deer (WTD; *Odocoileus virginianus*) as both a natural reservoir of *E. chaffeensis* and a major host of LST. The goal of the current study was to implement and evaluate a prototype surveillance system to delineate the geographic distribution of *E. chaffeensis* using WTD as natural sentinels. To accomplish this goal, serologic testing using the indirect immunofluorescent antibody (IFA) test was performed on WTD serum samples, and to confirm serologic results, polymerase chain reaction (PCR) assays and culture isolation were conducted. Considerations relevant to the applicability of a surveillance system utilizing WTD were analyzed (e.g., age and gender relationships to serologic status, adequacy of sample sizes needed to distinguish between uninfected and infected populations, presence of LST, and ability to detect stability and spread of *E. chaffeensis* in WTD populations). Of 3,275 WTD serologically tested, 1,549 (47%) from 17 of 18 states had antibodies reactive to *E. chaffeensis* (IFA titer ≥1:128). No differences between age groups or gender were noted with serologic testing, thus these variables would not be a concern for a surveillance system using WTD. Significantly more deer in younger age groups (≤ 1.5 yr) were PCR and culture positive, and 46% of 122 seropositive WTD populations were confirmed positive by PCR or culture isolation. A significant association between LST infestation and *E. chaffeensis* seroreactivity was noted. Furthermore, the surveillance system was able to detect stability of *E. chaffeensis* within WTD populations and also spread to new populations, both of which were associated with LST status. These data

clearly demonstrate that WTD are useful as natural sentinels for this emerging human pathogen, and establish a prototypical framework for a WTD surveillance system. Key Words: *Ehrlichia chaffeensis*, *Amblyomma americanum*, tick-borne, serology, deer, surveillance system.

INTRODUCTION

Ehrlichia chaffeensis, the causative agent of human monocytotropic ehrlichiosis (HME), is maintained in a zoonotic cycle involving white-tailed deer (WTD; *Odocoileus virginianus)* as the primary vertebrate reservoir and lone star ticks (LST, *Amblyomma americanum*) as biological vectors (see Childs and Paddock, 2003). Many populations of white-tailed deer from the southeastern United States have been shown to have antibodies reactive to *E. chaffeensis* (Dawson et al., 1994a), and experimental and field studies have proven that WTD are competent and persistently infected reservoirs (Dawson et al., 1994b; Lockhart et al., 1997a; Davidson et al., 2001; Yabsley et al., 2002). The LST was initially suspected to be a vector based on the geographic distribution of HME cases and this was confirmed by polymerase chain reaction (PCR) detection of *E. chaffeensis* DNA in LST (Anderson et al., 1993; Roland et al., 1998; Steiert and Gilfoy, 2002) and by experimental transstadial transmission between WTD (Ewing et al., 1995). In addition to being important reservoirs for *E. chaffeensis*, WTD are an important host for all three mobile stages of LST (Bloemer et al., 1988).

The potential utility of WTD as a sentinel for determining the distribution of *E. chaffeensis* was first suggested when antibodies reactive to *E. chaffeensis* were detected in WTD (Dawson et al., 1994a), and a prototype WTD serologic surveillance system for *E. chaffeensis* recently was applied statewide in Iowa (Mueller-Anneling et al., 2000). White-tailed deer have been utilized as sentinel animals to monitor numerous human and livestock pathogens including Jamestown Canyon virus (Boromisa and Grimstad, 1987), Venezuelan equine encephalitis (Smart and Trainer, 1975), Lyme disease (Gill et al., 1993), vesicular stomatitis virus (Fletcher et al., 1991), and bluetongue and epizootic hemorrhagic disease viruses (Stallknecht et al., 1991). The advantages associated with surveillance systems utilizing deer include: 1) a distribution that includes 45 states allowing development of national, regional, or state-wide surveillance systems; 2) relatively high abundances allowing use as sentinels in most locations; 3) regulated harvests in all states enhancing the ease and reducing the cost of collecting samples from hunter-killed animals; 4) limited size of deer home ranges (mean approximately 400 ha) allowing identification of exposure location compared to potential domestic animal sentinels which may be transported to and infected in distant locations; 5) a much higher rate of exposure to tick vectors compared to humans or potential domestic animal sentinels; 6) relatively long life spans and increased opportunity for exposure compared to short-lived medium sized mammals or rodents; 7) opportunities to simultaneously monitor for presence of tick vectors and avoid separate entomologic surveys for vectors; 8) association of deer with both natural habitats and areas proximal to human habitation; and 9) freedom from prior treatment with antibiotics or acaracides as could occur with domestic animal sentinels.

Field studies have demonstrated that serologic monitoring of deer would allow for fine-scale mapping of the distribution of *E. chaffeensis* (Lockhart et al., 1996; Mueller-Anneling et al., 2000). Using a sample size of only five animals per population, Lockhart et al. (1996) successfully discriminated between LST infested populations which had a 100% antibody prevalence and populations believed to be LST-free which had a seroprevalence of 6.7%. Although *E. chaffeensis*-reactive antibodies are reported for many WTD populations, confirmation of infection using PCR and/or culture has only been reported for 10 seropositive populations in Arkansas, Georgia, Kentucky, North Carolina, and South Carolina (Lockhart et al., 1997a, 1997b; Little et al., 1997, 1998; Yabsley et al., 2002).

In addition to *E. chaffeensis*, WTD are hosts to at least 3 other members of the Family *Anaplasmataceae*: *Ehrlichia ewingii*, *Anaplasma phagocytophilum*, and as yet undescribed *Anaplasma* sp. (WTD-agent) (Dawson et al., 1996; Little et al., 1998; Magnarelli et al., 1999; Yabsley et al., 2002). Serologic cross-reactivity, which potentially could confound serologic studies, is common among members of the family *Anaplasmataceae*; however, the extent of cross-reaction is not fully understood among the four species that occur in WTD.

The overall goal of this study was to implement and evaluate an extensive fine-scale (county) serologic surveillance system for *E. chaffeensis* utilizing WTD as natural sentinels. Specific objectives to achieve this goal were to: 1) combine current and prior WTD serologic data to construct an extensive regional database on *E. chaffeensis*-reactive antibodies in WTD; 2) use PCR assays and cell culture isolation testing to confirm *E. chaffeensis* infection in seropositive WTD populations; 3) document any age class or gender relationships to antibody prevalence and PCR detection; 4) evaluate sample sizes that would be functionally effective at distinguishing between infected and uninfected populations; 5) affirm that infection status of WTD populations corresponds with the presence of LST; and 6) investigate the ability of a WTD surveillance system to consistently discern the distribution or spread of *E. chaffeensis* among WTD populations over time.

MATERIALS AND METHODS

Sample collections

White-tailed deer samples specifically for this project were collected from sites selected to complement and further expand four previous studies where WTD in the south central and southeastern United States were tested for *E. chaffeensis*-reactive antibodies (Dawson et al., 1994a; Lockhart et al., 1996; Little et al., 1997; Yabsley et al., 2002). Blood samples were collected from 2,101 WTD from 471 populations in 18 states (AL, AR, GA, FL, KS, KY, LA, MD, MO, MS, NC, NJ, OK, SC, TN, TX, VA, and WV) during Southeastern Cooperative Wildlife Disease Study herd health evaluation activities, other research projects, or in cooperation with state wildlife agency personnel from hunter-harvested animals. Blood samples were collected either aseptically from the heart, from the jugular vein, or from the body cavity. One exception was that blood samples from 40 of 79 deer from Missouri were collected on Nobuto strips and eluted in phosphate-buffered saline (PBS), pH 7.4 as described (Mueller-Anneling et al., 2000). Serum, plasma, or eluted blood samples were frozen at –20°C until serologic testing. From a subset of WTD (368 deer from 112 seropositive populations and 61 deer from 20 seronegative populations), whole blood samples were collected and frozen at –20°C for PCR testing. A second subset of 715 WTD (117 populations) was examined visually for ticks and if present, a representative sample was collected and submitted to the National Veterinary Services Laboratories (U.S. Department of Agriculture, Ames, IA) for identification. Animals were handled and samples collected by procedures approved by the Animal Care and Use Committee at the University of Georgia (A3437-01).

Serologic assays

Serum, plasma, or eluted blood samples were tested for antibodies reactive to *E. chaffeensis* by the indirect immunofluorescent antibody (IFA) test as previously described (Dawson et al., 1994; Lockhart et al., 1996) with the following two modifications. Samples were screened at a dilution of 1:128 using *E. chaffeensis* antigen slides (Focus Technologies, Cypress, CA). A 1:50 dilution of fluorescein isothiocyanate-labeled rabbit anti-deer immunoglobulin G (Kirkegaard & Perry Laboratories, Gaithersburg, MD) was used as conjugate. Geometric mean titer (GMT) was computed for 152 seropositive deer.

Molecular assays

DNA from 300 μl of 429 whole blood samples was extracted using the GFX Genomic Blood DNA Purification Kit (Amersham Pharmacia Biotech, Piscataway, NJ) following the manufacturer's protocol. Two gene targets, the 16S rRNA gene and the variable length PCR target (VLPT) antigen gene, were utilized for screening of whole blood for *E. chaffeensis* DNA using a nested PCR format. Primary outside amplification for the 16S rRNA gene consisted of 5 μl of DNA (from whole blood) in a 25 μl reaction containing 10 mM Tris-Cl (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 0.2 mM each dNTP

(Promega, Madison, WI), 2.5 units Taq DNA Polymerase (Promega), and 0.8 μM of primers ECC and ECB (Dawson et al., 1994b; 1996a). For the nested PCR, 1 μl of primary product was used as template in a 25 μl reaction containing the same PCR components except *E. chaffeensis* specific primers, HE1 and HE3 (Dawson et al., 1994b), were used.

Nested PCR for the VLPT antigen gene was conducted on 429 blood samples collected during this study as previously described (Sumner et al., 1999). In addition, 101 blood samples from an additional ten populations previously tested using 16S rRNA primers (Yabsley et al., 2002) were tested for *E. chaffeensis* using the VLPT gene target. Amplified products were separated in 2% agarose gels, stained with ethidium bromide, and visualized with UV light. To confirm identity, representative secondary VLPT gene amplicons were purified with a Microcon spin filter (Amicon Inc., Beverley, MA), sequenced at MWG-BIOTECH (High Point, NC), and compared to published *E. chaffeensis* VLPT sequences in the GenBank database.

Stringent protocols and controls were utilized in all PCR assays to prevent and detect contamination. DNA extraction, primary amplification, secondary amplification, and product analysis were performed in separate dedicated laboratory areas. Two negative water controls were included in each set of DNA extractions and one water control was included in each set of primary and secondary PCR reactions.

Culture isolation

During 2001-2003, aseptically collected blood samples from 72 WTD from 15 LST positive populations were cultured in DH82 cells for isolation of *E. chaffeensis* as previously described (Lockhart et al., 1997a). Cultures were fed biweekly with MEM medium (Sigma, St. Louis, MO) supplemented with 10% fetal bovine serum (Sigma) and monitored for evidence of cytopathic effect or for a maximum of 45 days. Cultures showing cytopathic effect and cultures completing the 45 day incubation period were harvested with a cell scraper and tested by direct fluorescent antibody assay as previously described (Lockhart et al., 1997a).

Data analysis

Serologic data from this study (n = 2,101) were combined with data from previous studies conducted independently by SCWDS researchers (n = 425; Lockhart et al., 1996, Little et al., 1997, Yabsley et al., 2002) or collaboratively with others (n = 749, Dawson et al., 1994a) to construct a comprehensive map delineating the distribution of *E. chaffeensis* seroreactive WTD in the southeastern and south central United States. Some of the previous studies used different cutoff values for IFA testing (e.g., 1:64 or 1:128), but in order to standardize results from this study and previous studies, IFA assays were classified as positive only if a sample had a titer of ≥ 1:128. To facilitate graphic presentation, data for each population were categorized by county or parish; if one or more deer with antibodies reactive to *E. chaffeensis* was detected, that county or parish was classified as seropositive.

To confirm serologic data, PCR and/or culture isolation were conducted on a total of 541 deer from 122 seropositive populations and on 61 deer from 20 seronegative populations. Chi-square analysis was used to test for differences of PCR prevalence between seropositive and seronegative populations.

Prevalence of antibodies reactive to *E. chaffeensis* among different age classes and gender categories were only determined for WTD in seropositive populations. Serologic data from Dawson et al. (1994), Lockhart et al. (1996), Little et al. (1997), Yabsley et al. (2002), and this study were combined for determining prevalence among age classes because analysis of WTD age data had not been previously conducted. PCR testing was not conducted by Dawson et al. (1994) and Lockhart et al. (1996); therefore, analysis of age and PCR positivity was conducted only on deer from Little et al. (1997), Yabsley et al. (2002), and this study. Chi square analysis was used to test for differences in both seroprevalence and PCR positivity among age classes.

To accurately classify the serostatus of a population, an appropriate sample size needs to be tested. In previous studies, testing of five deer from a population consistently detected *E. chaffeensis*-reactive antibodies in deer populations infested with LST (Lockhart et al., 1997; Little et al., 1997, 1998), and based on Dawson et al (1994) testing a mean of 21 deer failed to detect seroreactive deer in seronegative populations. However, additional evaluation of the sample sizes required to reliably classify the serologic status of populations was conducted in this study. To determine minimal number of samples needed to detect the presence of a seropositive deer in a population, the formula $n = (1 – (1\text{-}a)^{1/D}) (N – (D –1)/2)$ was used as described (Thrusfield, 1995). Because seronegative populations are more difficult to accurately classify, two methods were used to examine adequacy of sample size. Larger numbers of deer (n = 8 - 16) were tested from nine seronegative populations to enhance detection of potentially low prevalences in those populations. Also, four populations with no history of LST infestation were repeatedly tested for several years (see below).

To assess the predicted epidemiologic association between LST infestation and serologic status of WTD populations, the tick status and seroprevalence for populations were calculated. Chi-square analysis was used to test for an association between LST presence and seroreactors at the population level. Furthermore, 11 populations for which both tick and serologic data were available were evaluated during multiple years; three populations had LST infestation each sample year, four never had any evidence of LST infestation, and four were negative for LST during earlier sampling period(s) but became LST positive during subsequent test years. Chi-square analysis was used to test for differences between groups.

RESULTS

Regional serologic database for WTD

Among the 2,101 WTD collected specifically for this study, 984 (46.8%; CI95% = 44.7%, 48.9%) had antibodies reactive ($\geq$ 1:128 titer) to *E. chaffeensis* by IFA testing (Table 1). The mean prevalence of antibodies reactive to *E. chaffeensis* in seropositive populations was 73.8% (SD = 25.8%, range 20-100%). White-tailed deer with antibodies reactive to *E. chaffeensis* were detected in all states tested except West Virginia. The modal antibody titer for seropositive deer was 1:128 with a maximum titer of 1:4,096. The GMT of a subset of 152 seropositive WTD was 355.

The combined dataset of WTD serologically tested during this and four prior studies (Dawson et al., 1994a; Lockhart et al., 1996; Little et al., 1997; Yabsley et. al., 2002) contained a total of 3,275 WTD from 18 southeastern and south central states.

In the combined data set, 1,549 (47.3%) WTD examined had antibodies reactive to *E. chaffeensis* with seropositive populations detected in 17 of 18 states (Figure 3.1).

The highest overall seroprevalences were in Arkansas and Missouri. Although high prevalences were detected in local WTD populations in most states, considerable variation in prevalence occurred between different regions of many states (e.g., Florida, Kansas, North Carolina, Oklahoma, and Virginia). A western boundary for the distribution of *E. chaffeensis* was evident in the states of Kansas, Oklahoma, and Texas. Similarly, a southern boundary was noted in peninsular Florida. Multiple populations of seronegative deer were detected in southern Mississippi and Louisiana, along the lower Mississippi River floodplain and in the Appalachian Mountains from western Maryland to northern Alabama.

PCR and culture validation of *E. chaffeensis* serologic data

Eighty-six of 368 (23.4%) WTD from 50 seropositive populations were PCR positive for *E. chaffeensis* by either 16S or VLPT PCR. Of 101 WTD previously tested by 16S PCR (Yabsley et al., 2002), nine deer from seven populations were positive by VLPT PCR. Collectively for this study and Yabsley et al. (2002), 95 of 469 (20.3%) WTD from 56 of 122 (46%) seropositive populations have been confirmed using PCR (Table 1); 70 of 95 deer with both gene targets, 2 of 95 for only the 16S rRNA gene, and 23 of 95 only for the VLPT gene. In contrast, 16S rRNA and VLPT PCR assays on 61 deer from 20 seronegative populations were all negative. Presence of PCR positive deer was strongly associated with seropositive populations ($\chi^2 = 11.6$, $p < 0.001$).

Of 72 culture attempts, 34 (44.2%) were lost to contamination with bacteria and/or *Trypanosoma cervi*. Seven of the remaining 38 cultures (18.4%) were positive for *E. chaffeensis*. Positive cultures were obtained from two WTD from Greene Co., AR; two from Woodruff Co., AR; and one each from Clarke Co., GA; Anson Co., NC; and Georgetown Co., SC. All isolates were confirmed as *E. chaffeensis* by PCR of the 16S rRNA and VLPT gene targets.

Relationship of age class and gender to antibody prevalence and PCR detection

Age was available on 1,882 deer tested serologically; 1,086 deer from this study, 517 from Dawson et al. (1994), 165 from Lockhart et al. (1996), five from Little et al., (1997), and 109 from Yabsley et al (2002). For this combined data set, differences were not noted (χ^2 = 5.65, p = 0.46) in seroprevalance among age classes (Figure 3.2). Similarly, seroprevalence did not differ between males and females (Figure 3.4; 69.3% vs. 69.6%; χ^2 = 0.016, $p > 0.05$).

Age was available for 393 deer from seropositive populations that were tested by PCR. Higher proportions of deer were PCR positive in the younger age classes (χ^2 = 71.7, $p < 0.001$). Among deer $<$ 0.75 years old, 53.1% were PCR positive, within the next age group (0.76 – 1.5 yr) the prevalence decreased significantly to 27% (χ^2 = 14.7, $p < 0.001$), and less than 8% of deer $>$ 1.5 yr old were PCR positive (Figure 3.3). The mean age of PCR positive WTD was 1.1 yr (range 0.25-4 yr). Insufficient culture isolates were made to examine age-related associations; however, the mean age for culture positive deer was 3.2 yr (range 0.3-9.5 yr). Similar to antibody prevalence, PCR positivity did not differ between males and females (Figure 3.4; 19% vs. 22.8%; χ^2 = 0.89, $p > 0.05$).

Evaluation of sample size adequacy

Regarding sample size for seropositive populations, post hoc statistical analysis utilizing a mean 73% seroprevalence (results above) indicated that testing of only three or four deer gives a high probability (95% and 99%, respectively) of detecting a positive population (Thrusfield, 1995). Although validation of seronegative populations is more problematic, testing of larger numbers of deer per population and repeated testing of selected populations both produced consistent negative results. In a combined dataset from Dawson et al., 1994a and this study, 250 deer from 17 seronegative populations (9-30 deer per population) were negative for antibodies to *E. chaffeensis* with means of 20.8 and 10.4 deer tested per seronegative population, respectively. Similarly, none of the 131 deer from four populations consistently negative for LST infestation had antibodies reactive to *E. chaffeensis* (see data below). The mean number of WTD tested per population in this study was 6.2 (SD = 6.1, range 1-58) and data for populations with sample sizes less than four deer were used only if a seropositive animal was detected.

Association between LST and serologic status at population level

Of 117 WTD populations examined for ticks, 82 were infested with LST, 29 with *Am. maculatum*, 4 with *Ixodes affinis*, and 13 with *I. scapularis*. Eighty of the 82 (97.6%) populations infested with LST contained at least one seropositive WTD while only 4 of 35 (11.4%) populations not infested with LST contained seropositive deer. One LST negative population (Harris Co., GA) was both seronegative and tick negative in 1986; however, in 2002 the deer population was seropositive but the LST status was not evaluated. The prevalence of antibodies reactive to *E. chaffeensis* was significantly higher among LST infested populations of WTD than populations not infested by LST (χ^2 = 89.9, p <0.001). None of the six populations infested only with *Am. maculatum* contained seropositive deer; there were insufficient populations with *I. affinis* or *I. scapularis* alone to permit evaluation.

Stability and spread of *E. chaffeensis* and LST among WTD populations

Fifty-seven populations which were tested during previous studies (Dawson et al., 1994a; Lockhart et al., 1996) were retested during this study. The serologic status for 50 of these populations (88%) was the same as the previously published serologic status; 35 seropositive populations remained seropositive and 15 seronegative populations remained seronegative. Six populations which previously tested seronegative were seropositive during this study. Three of these representing Anson Co., NC, Haywood Co., TN, and Stewart Co., GA had documented invasion of LST between the first reported testing and this study. One Texas population (Travis Co.) was seropositive (n = 7, 71.4%) when tested in 1992 (Dawson et al., 1994a) but was seronegative when sampled (n=10) in 2002 for this study. The LST status for this county was not known for either sampling period.

Among the 11 populations where LST infestation and serologic status were monitored repeatedly over time, there was complete concordance between LST presence and seropositive deer (Table 2). All three LST positive populations were consistently seropositive each year tested. The mean seroprevalence for these three populations was 83%, and two of these populations (Jones Co., GA and Ashley Co., AR) were confirmed PCR positive for *E. chaffeensis*. None of the four populations where LST was consistently absent contained seropositive deer at any sampling time. Among the four populations where LST status changed from absent to present, seropositive deer were only detected following the appearance of LST. The mean prevalence of antibodies reactive to *E. chaffeensis* in the most recently tested year was significantly higher for populations infested with LST for multiple years (mean = 100%) compared to populations only recently infested (mean = 53.8%, $\chi^2 = 15.5$, $p < 0.001$). One recently infested population (Anson Co., NC) was confirmed by isolation of *E. chaffeensis* from a single WTD in 2001.

DISCUSSION

The overarching goal of this study was to implement and evaluate a prototype surveillance system using WTD as natural sentinels to determine the geographic distribution of *E. chaffensis* across most of the suspected HME endemic region of the United States. To this end, the data obtained demonstrate the following critical attributes: 1) serologic findings reflect *E. chaffeensis* infection, 2) effective surveillance can be achieved with small sample sizes, 3) any deer >6 mo old is suitable for surveillance purposes, 4) enzootic and consistently negative locales were identified repeatedly across time, 5) surveillance of deer has the ability to detect spread to new locales, and 6) serologic, molecular, and culture diagnostic findings among deer could be related to presence of the principal tick vector, *Am. americanum*. These findings compliment and expand on a recent WTD serologic surveillance effort within Iowa (Mueller-Anneling et al., 2000); however, that study exclusively used serologic assays and did not include either confirmatory microbiological diagnostics or contemporaneous tick vector monitoring. Collectively, these two studies confirm the effectiveness of this prototypical surveillance system for monitoring the distribution of this emerging human pathogen.

Although several studies have examined the prevalence and distribution of *E. chaffeensis* antibodies among many southeastern and south central WTD populations (Dawson et al., 1994a; Lockhart et al., 1996; Little et al., 1997; Yabsley et al., 2002), the extensive additional testing filled many geographic gaps and provided a finer scale distribution of *E. chaffeensis* among WTD throughout the regions of the United States with the highest HME risk (Paddock and Childs, 2003). The combined data evaluated herein disclosed a wide distribution of seropositive WTD populations across all of the 18 states represented except for West Virginia; however, some distributional limits also were discerned including a western boundary extending across Kansas, Oklahoma, and Texas, a southern boundary across peninsular Florida, and a cluster of many seronegative populations centered along the Appalachian Mountains (Figure 3.1). Other prior studies of WTD have documented an apparent northern range limit for *E. chaffeensis* in southern portions of Iowa, Illinois, Indiana, and Ohio (Dawson et al., 1994a; Irving et al., 2000; Mueller-Anneling et al., 2000). Along the East coast, surveys have indicated that *Am. americanum* and *E. chaffeensis* are present as far north as Connecticut, Maine, and Rhode Island (Keirans and Lacombe, 1998; Ijdo et al., 2000).

The accuracy of diagnostic assays utilized is critical to any pathogen surveillance system. Infection with *E. chaffeensis* was confirmed in nearly half (46%) of 122 seropositive WTD populations tested by PCR and was supplemented by isolation from others. In contrast, PCR evidence of infection was not detected in any of 20 seronegative WTD populations. Thus, PCR and culture testing applied at the population level were effective at confirming infection in many seropositive populations and demonstrating a strong association between the serologic status of populations and infection with *E. chaffeensis*.

Because WTD in these regions are known to be infected with three other related rickettsiae (*E. ewingii, An. phagocytophilum*, and an *Anaplasma* sp. [WTD-agent]) in addition to *E. chaffeensis* (Dawson et al., 1996b; Little et al., 1998; Brandsma et al., 1999; Magnarelli et al., 1999; Yabsley et al., 2002), the potential for serologic cross-reaction is an important consideration. Although antibodies reactive with *E. chaffeensis* in WTD from Maryland have been confirmed by immunoblotting using the 28- to 29-kDa antigens of *E. chaffeensis* (Walls et al., 1998), the extent of serologic cross-reactions among these four species is not fully understood (Dumler and Walker, 2001). However, data from other studies suggests that infection with these other rickettsiae may not commonly result in production of antibodies that cross-react with *E. chaffeensis.* Cross-reactions between *E. chaffeensis* and *E. ewingii* have been noted in infected humans and dogs; however, not all *E. ewingii* infected dogs or humans develop antibodies to *E. chaffeensis* antigens (Murphy et al., 1998; Paddock et al., 2001). Similarly, a WTD fawn experimentally infected with *E. ewingii* did not develop antibodies reactive with *E. chaffeensis* (Yabsley et al., 2002). Cross-reactions between *E. chaffeensis* and *An.*

phagocytophilum have been reported in humans and may complicate diagnosis (Comer et al., 1999). Far fewer WTD in the southeastern states have antibodies reactive to *An. phagocytophilum* (<25%) than to *E. chaffeensis* antigens; however, although some deer reacted to both *E. chaffeensis* and *An. phagocytophilum* at or above the 1:128 cut-off, many also reacted to only one of these antigens at titers ≥1:128 (Little et al., 1998; Walls et al., 1998; V. G. Dugan and M. J. Yabsley, unpublished data). The high percentage of populations where seropositive or seronegative status was confirmed by PCR or culture, together with data from these other studies, provide considerable evidence that the seroreactivity reported herein largely represents specific seroconversion to *E. chaffeensis*.

The distribution of antibodies within WTD age and gender categories was investigated because these variables are an important consideration for a WTD natural sentinel system. Only a limited investigation of geometric mean titers among age categories has been reported for WTD (Lockhart et al., 1995), and any significant influence of age or gender on the occurrence of antibodies would require sampling stratified according to these host attributes. Importantly, differences in antibody prevalence were not noted among age or gender categories indicating that all WTD, particularly animals ≥ 6 mo of age, are suitable for use in a WTD surveillance system. In contrast to the high, stable prevalence of antibodies among age classes (Figure 3.2), PCR evidence of rickettsemia declined with age (Figure 3.3). This pattern conforms to proposed infection dynamics in naturally infected WTD whereby animals from ~6 mo to ~1.5 yr of age are more likely to be rickettsemic than older adults (see Paddock and Childs, 2003; Dawson et al., 1994; Lockhart et al., 1997a; Davidson et al., 2001). In the present study, the prevalence of PCR positivity dropped dramatically from over half (53%) of WTD younger than 0.75 yr to less than 8% of WTD older than 1.5 yr. The majority of deer tested from some seropositive populations were >1.5 yr and only deer >1.5 yr from other populations were available for PCR testing which may explain why not all seropositive populations were confirmed by PCR. Because the probability of a WTD being rickettsemic declines with age, serology represents a better surveillance tool than PCR, and under natural conditions of re-exposure to ticks, titers do not decline over time as often occurred in single exposure experimental infections of WTD (Dawson et al., 1994b; Ewing et al., 1995; Davidson et al., 2001).

Previous serologic surveys of *E. chaffeensis* in WTD (Dawson et al., 1994a; Lockhart et al., 1996; Little et al., 1997; Yabsley et al., 2002) have utilized relatively small sample sizes per population but, except for one (Mueller-Anneling et al., 2000), have not addressed the adequacy of these sample sizes to correctly classify infected and uninfected populations. Data from the current and prior studies (Dawson et al., 1994a; Lockhart et al., 1996; Little et al., 1997) have shown that infected WTD populations in the southeastern and southcentral United States typically have high (>70%) seroprevalences. Calculations (Thrusfield, 1995) based on a mean 73% seroprevalence indicated that use of a sample size of five WTD per population should reliably detect nearly all positive populations. Although it was beyond the scope of this study to test enough deer to detect very low population prevalences, larger sample sizes and repeated sampling of seronegative populations did not reveal seropositive populations that would have been misclassified as seronegative based on smaller sample sizes. A chance of misclassifying newly infected populations of WTD exists because seroprevalence may be low initially; however, field evidence shows that antibody prevalence can increase rapidly once a population becomes infected with *E. chaffeensis* (Lockhart et al., 1995). Utilizing per county sample sizes equivalent to this study, statewide serotesting of WTD from Iowa demonstrated a clear north-south gradient of seroprevalence that corresponded to key epidemiologic factors (e.g. distributions of ticks, deer, and habitats) (Mueller-Anneling et al., 2000).

Because the distributions of pathogens often are reflected by some combination of both static and changing geographic distributions, an important attribute of an effective surveillance system is the ability to identify both persistently enzootic locales and spread to new locations. Testing of WTD from LST infested populations over the span of 20 yr showed that once this biologically important vector is present and WTD populations are infected with *E. chaffeensis*, there is a high probability that the populations will remain infected and that WTD sentinels reflect these enzootic conditions. Conversely, populations with no history of LST infestation remained consistently seronegative when tested multiple times. These results are compatible with a strong site-specific association between *E. chaffeensis* antibodies and the presence of LST (Lockhart et al., 1996). Of interest, each of two populations (Choctaw Co., AL and Bolivar Co., MS) that were earlier reported as seropositive but LST negative (Lockhart et al., 1996) were shown in this study to be both LST positive and seropositive for *E. chaffeensis*. The rare failure to find LST in seropositive WTD populations may have occurred because many collections were made during the fall hunting season when LST infestations are undergoing rapid seasonal declines (see Allan, 2001).

Four instances of *E. chaffeensis* spread to new locations were detected by monitoring WTD for multiple years (Table 2). At each of these locations, the change in population serologic status from negative to positive coincided with documented appearance of LST. These findings are very similar to those from a 12 yr long monitoring of a WTD population that demonstrated the introduction of *E. chaffeensis* was attributable to the establishment of LST (Lockhart et al., 1995). Multiple instances of spread by *E. chaffeensis* to previously uninfected populations were identified, and since these changes in population serostatus were linked to the principal vector, they provide further evidence that this surveillance system reflects important epidemiologic factors and that it should discern changing local HME risks.

In summary, the biological reasons a sentinel WTD surveillance system functions effectively are that the force of transmission of *E. chaffeensis* is focused on WTD and that aspects of WTD biology allow attribution of infection to a specific geographic location. From an operational perspective, the system has the desirable attributes of applicability on a wide geographic scale and logistic feasibility by using "free" (hunter-harvested) samples. The present work was done in a research context; however, it is possible to implement sentinel WTD serologic surveillance for *E. chaffeensis* in an operational public health context as clearly demonstrated previously in Iowa (Mueller-Anneling et al., 2000).

ACKNOWLEDGMENTS

We are indebted to over 100 individuals representing state wildlife agency personnel, SCWDS staff, and white-tailed deer researchers for help in field collection of samples, but especially the following individuals for coordinating specific collections: Chris Cook (AL), John Morgan (FL), Lloyd Fox (KS), Jon Gassett and David Yancy (KY), Jeff Beringer (MO), Douglas Roscoe (NJ), A. Alan Kocan (OK), Charles Ruth, Jr. (SC), Ben Layton (TN), Matt Knox (VA), and Jim Crum (WV). Sarah Cross, Page Luttrell, and Darrell Kavanaugh from SCWDS provided excellent field and laboratory help. Work was supported primarily by the National Institutes of Allergy and Infectious Diseases (5 R01 AI044235-02). Further support was provided by the Federal Aid to Wildlife Restoration Act (50 Stat. 917) and through sponsorship from fish and wildlife agencies in Alabama, Arkansas, Florida, Georgia, Kansas, Kentucky, Louisiana, Maryland, Mississippi, Missouri, North Carolina, Oklahoma, Puerto Rico, South Carolina, Tennessee, Virginia, and West Virginia.

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TABLE 3.1. RESULTS OF SEROLOGIC AND POLYMERASE CHAIN REACTION TESTING FOR *EHRLICHIA CHAFFEENSIS* IN WHITE-TAILED DEER FROM 18 STATES[a]

State	*Years*	*Counties tested by IFA test*	*Number IFA positive/ no. tested (%)*	*Number PCR positive/ no. tested (%)*
Alabama	1981-2001	33	59/141 (42)	NT[b]
Arkansas	1982-2002	29	111/154 (72)	7/46 (15)
Florida	1983-2002	15	43/104 (40)	9/36 (25)
Georgia	1973-2002	50	119/243 (49)	26/98 (27)
Kansas	1998-2002	38	39/76 (51)	3/26 (12)
Kentucky	1983-2001	27	26/99 (26)	2/23 (9)
Louisiana	1981-2001	34	54/166 (33)	1/18 (6)
Maryland	1999-2002	5	12/25 (48)	1/7 (14)
Mississippi	1995-2001	38	80/152 (53)	1/19 (5)
Missouri	1994-2002	19	57/79 (72)	3/23 (13)
North Carolina	1982-2002	33	75/131 (57)	15/72 (21)
New Jersey	2001	2	6/10 (60)	0/5
Oklahoma	1985-2002	13	30/50 (60)	0/3
South Carolina	1991-2001	26	52/124 (42)	4/60 (7)
Tennessee	1981-2001	20	54/100 (54)	0/10
Texas	1992-2002	33	73/123 (59)	0/13
Virginia	1983-2002	37	94/168 (56)	23/57 (40)
West Virginia	1977-2001	18	0/156	0/14
Total		471	984/2101 (47)	95/530 (18)

[a]Includes PCR results for the VLPT antigen gene for 101 WTD previously tested by PCR for the 16S rRNA gene (Yabsley et al., 2002).

[b]NT, not tested.

TABLE 3.2. SEROLOGIC AND TICK SURVEY RESULTS FROM SEVEN POPULATIONS OF WTD COLLECTED DURING MULTIPLE TIME PERIODS AND TESTED FOR ANTIBODIES REACTIVE FOR *E. CHAFFEENSIS*.

Site	Years	# of years sampled	Tick status (years)	# deer tested	Mean IFA prevalence (%) (range)
Sites positive for ticks					
Jones Co., GA	1979-2001	6	+ (6)	41	92 (80-100)
Ashley Co., AR	1982-2001	7	+ (7)	37	84 (71-100)
Franklin Co., FL	1984-1996	5	+ (5)	25	68 (40-100)
Sites negative for ticks					
Floyd Co., GA	1973-2001	6	- (6)	58	0
Tyler Co., WV	1985-2000	4	- (4)	21	0
Hardy Co., WV	1977-1999	7	- (7)	37	0
Monroe Co., FL	1992-2001	4	- (4)	15	0
Sites where tick status changed					
Anson Co., NC	1987, 2001	2	-, +[a]	10	0, 40[b]
Concordia Pa., LA	1986, 1991, 1999	3	-, +, +	22	0, 38, 60
Haywood Co., TN	1989, 1994, 1998	3	-, -, +	16	0, 0, 20
Stewart Co., GA	1986, 1998	2	-, +	10	0, 20

[a]Tick status at sequential sampling periods.

[b]Prevalence of IFA seropositive deer at sequential sampling periods.

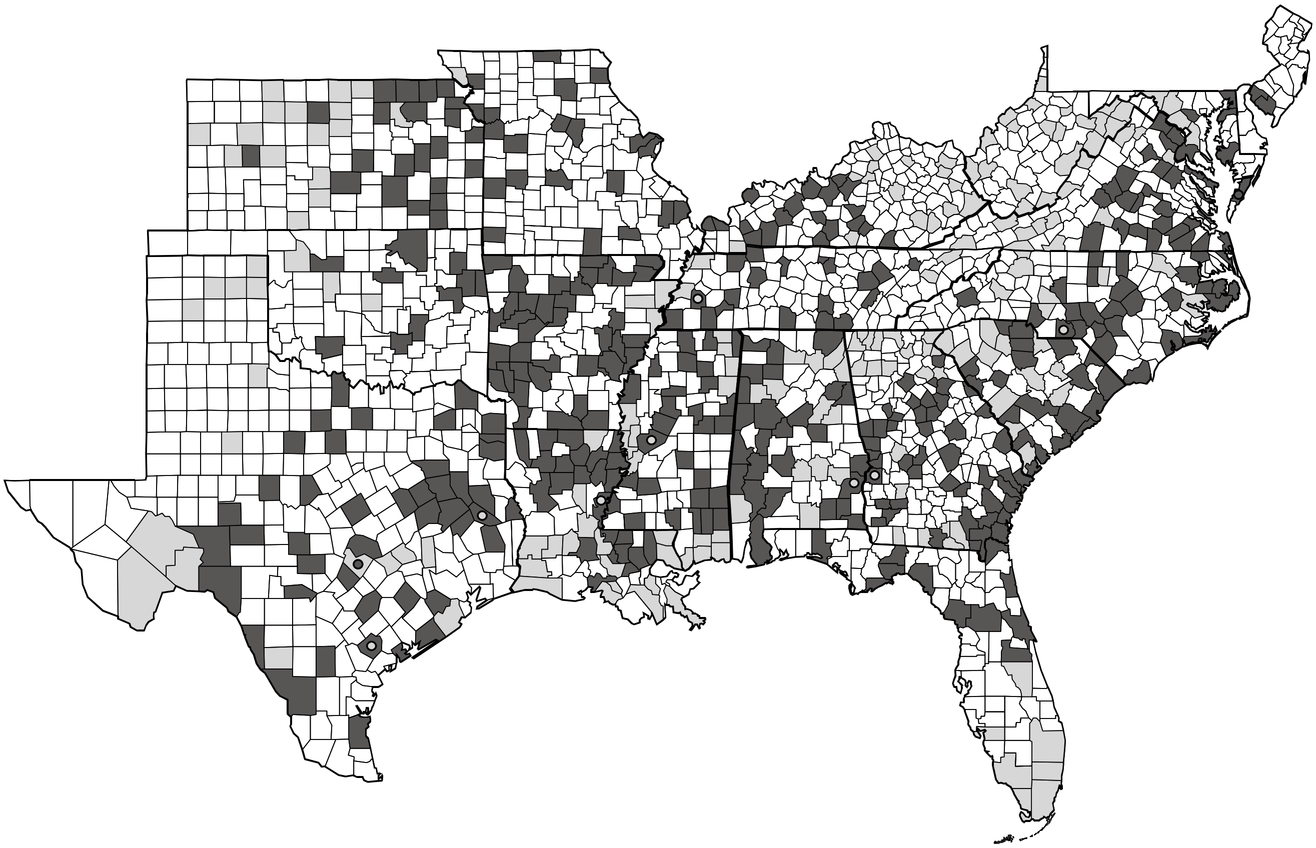

FIG. 3.1. Indirect immunfluorescent antibody results for *Ehrlichia chaffeensis* in white-tailed deer. Results are from the current study and from previously published work obtained in collaboration with SCWDS. Darkly shaded counties positive and lightly shaded counties negative for antibodies (≥1:128) reactive for *E. chaffeensis*. Previous serologic results that differed from the results of the current study are shown as small circles within the county. ● = previously positive for antibodies (≥1:128) reactive for *E. chaffeensis*; ○ = previously negative for antibodies reactive for *E. chaffeensis*.

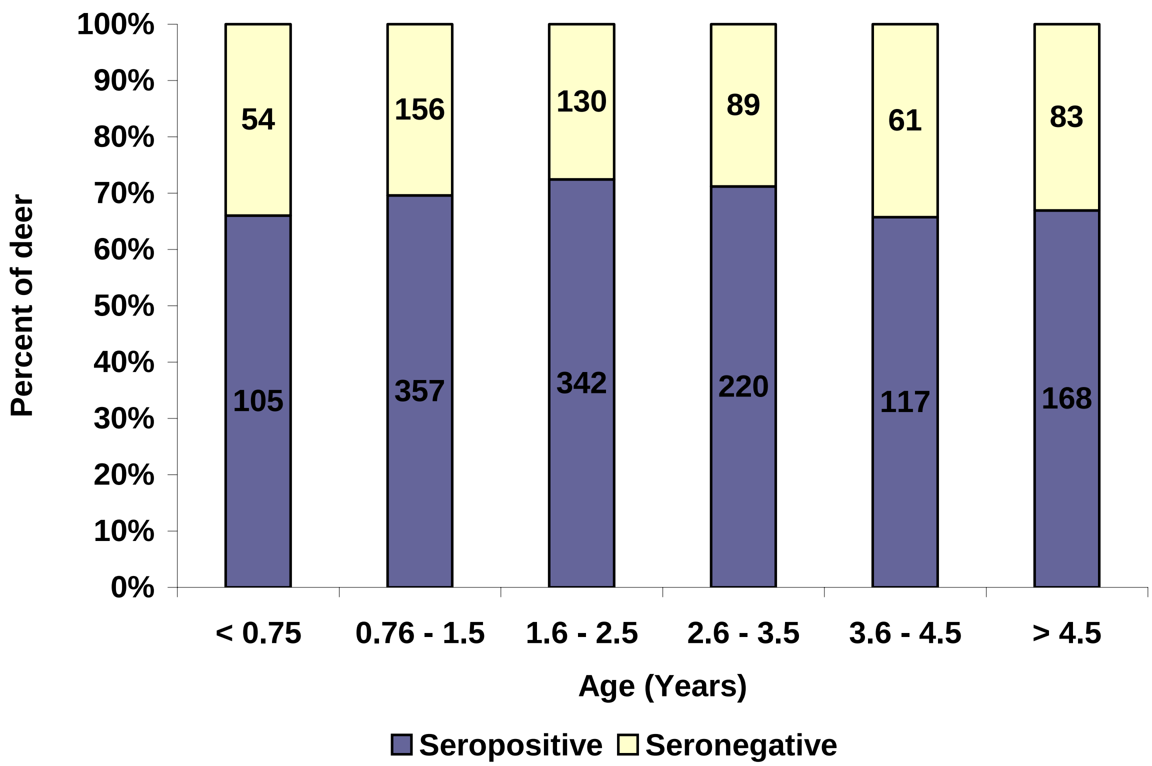

FIG. 3.2. Prevalence of antibodies reactive to *E. chaffeensis* in WTD among age classes. Numbers in bars represent number of deer tested.

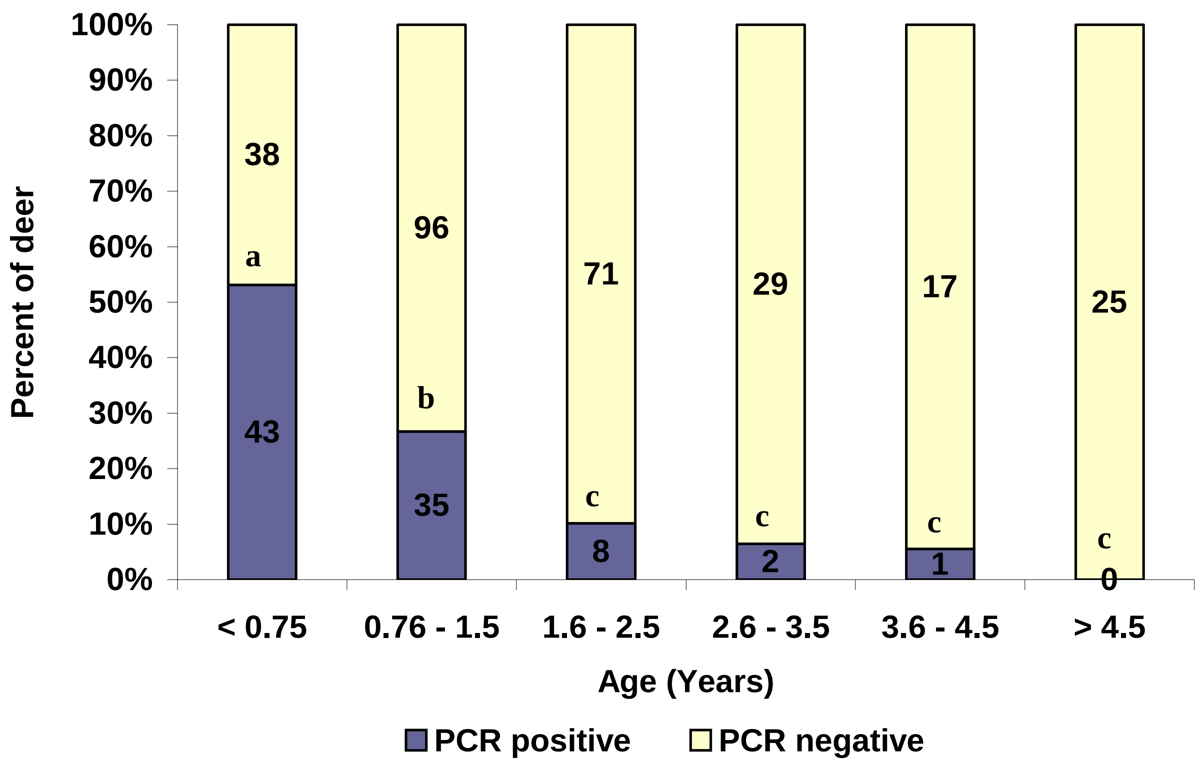

FIG 3.3. Prevalence of PCR positive WTD among age classes. Numbers in bars represent number of deer tested and different letters represent significant differences at $p < 0.05$.

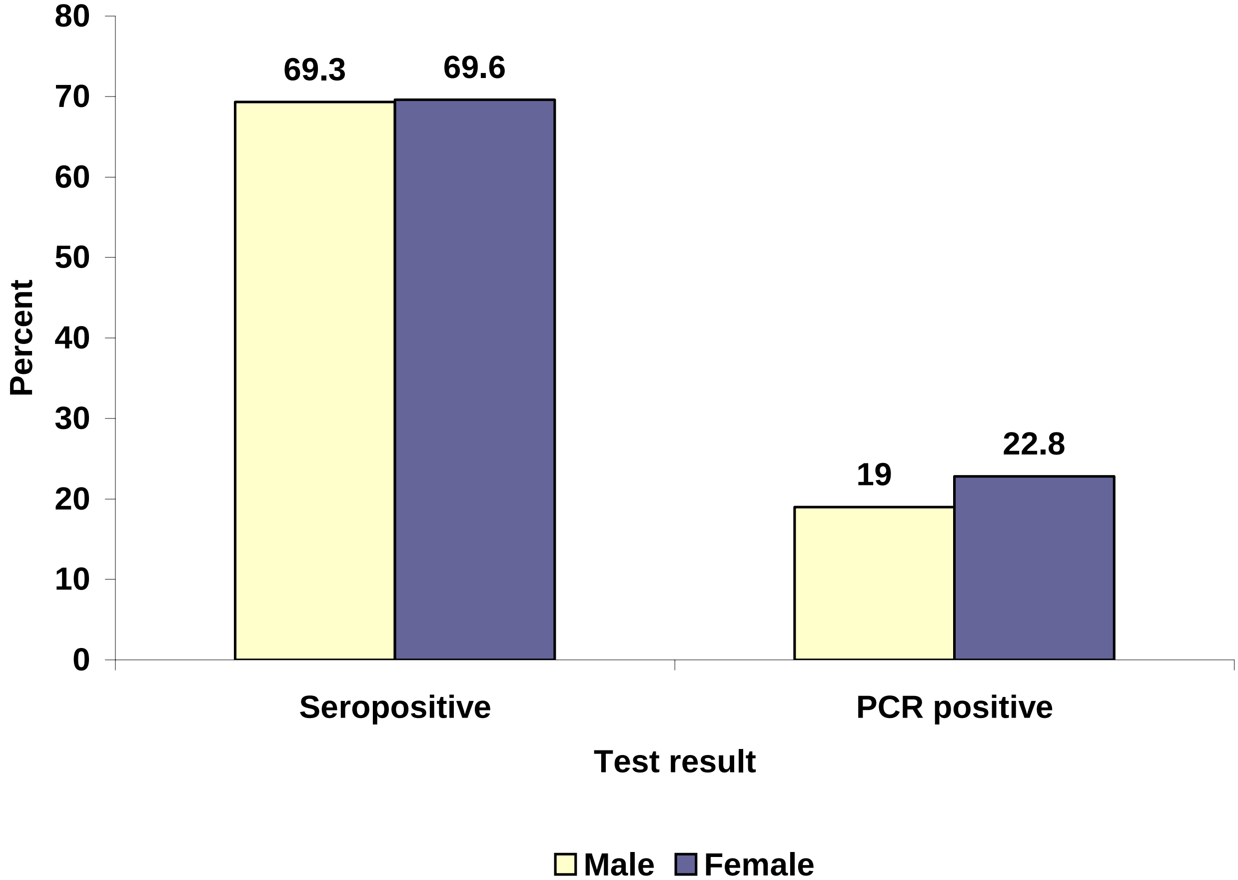

FIG 3.4. Prevalence of seropositive and PCR positive WTD among sex classes.

CHAPTER 4

MOLECULAR VARIATION IN THE VARIABLE LENGTH PCR TARGET (VLPT) AND 120-KILODALTON ANTIGEN GENES OF *EHRLICHIA CHAFFEENSIS* FROM WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*)[1]

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[1] Yabsley, M.J., S.E. Little, E.J. Sims, V.G. Dugan, D.E. Stallknecht, and W.R. Davidson. 2003. *Journal of Clinical Microbiology* 41: 5202-5206. Reprinted here with permission of publisher.

ABSTRACT

White-tailed deer are the principal reservoir for *Ehrlichia chaffeensis*, an obligate intracellular bacterium which causes human monocytotrophic ehrlichiosis, the most important emerging tick-bone disease in the southeastern United States. Genes encoding two surface expressed antigens of *E. chaffeensis*, the variable length PCR target (VLPT) and 120-kDa, have been shown to contain variable numbers of tandem repeats. In this study these genes were characterized for *E. chaffeensis* from deer. The VLPT and 120-kDa genes from infected deer contained numbers of repeats similar to those reported from humans and ticks, although a new variant of the 120-kDa gene containing 5 repeat units was found in deer. Sequence analysis of the VLPT and 120-kDa genes of *E. chaffeensis* from deer revealed more nucleotide variation than previously reported for *E. chaffeensis* from infected humans or ticks; a novel VLPT amino acid repeat type unit was also found. Geographic clustering of various repeat variants was not apparent among deer from 12 southeastern and south central states. In addition, two or more genetic variants of *E. chaffeensis* were present within single populations and in the same individual deer. This is the most extensive study of the genetic variation of the VLPT and 120-kDa genes of *E. chaffeensis* to date, and is the first to examine genetic variation in *E. chaffeensis* from a nonhuman vertebrate host. Inclusion of reservoir-source organisms in the comparison of *E. chaffeensis* isolates provides a more comprehensive understanding of the intraspecific genetic variation of this important human pathogen.

INTRODUCTION

Ehrlichia chaffeensis, the causative agent of human monocytotrophic ehrlichiosis (HME), is the most important emerging tick-borne pathogen in the southeastern and south-central United States. *E. chaffeensis* is maintained in a zoonotic cycle involving white-tailed deer (WTD; *Odocoileus virginianus)* as the principal vertebrate reservoir and lone-star ticks (LST; *Amblyomma americanum*) as a biological vector. Severity of disease following infection varies from asymptomatic to fatal, with the most common clinical signs being fever, headache, nausea, and malaise; leucopenia and thrombocytopenia are often present (6). Since the discovery of HME in 1986, over 1,100 cases have been reported to the CDC (1).

The variable length PCR target (VLPT) and 120-kDa antigen genes of *E. chaffeensis* contain variable numbers of tandem repeats. The VLPT gene contains three to six 90-bp repeat units and the 120-kDa gene contains two to four 240-bp repeat units. In addition, the VLPT gene has variations at the nucleotide level consisting of 1) single-base substitutions at 4 specific locations, 2) presence or absence of an aspartic acid codon deletion upstream from the repeat region, and 3) a 9-bp deletion downstream from the stop codon. Sequencing of the tandem imperfect repeat units in the VLPT gene has revealed seven distinct amino acid repeat profiles (19). Currently, the function of the VLPT protein is unknown, but the greater number of repeats compared with the 120-kDa antigen gene makes the VLPT gene useful for strain differentiation. Apparent geographic clustering of genetic types noted in previous surveys of ticks (18), led to the suggestion that there may be a geographic correlation with repeat number (13).

The 120-kDa antigen gene encodes an immunodominant surface protein that is mainly expressed on dense-core stages of *E. chaffeensis* and is released into the intramorular fibrillary matrix (16). Expression of this gene in *Escherichia coli* causes attachment and internalization by Vero cells suggesting an important role for this protein for attachment and invasion of host cells by *E. chaffeensis* (16). The first repeat unit of the 120-kDa gene contains four nucleotide substitutions that make it different from the other repeats, which are all identical in sequence (22).

Both the VLPT and 120-kDa genes have been amplified from infected human and tick samples, but have not been reported from infected WTD. The objectives of this study were to 1) characterize the VLPT and 120-kDa antigen genes of *E. chaffeensis* from WTD and 2) test the hypothesis that genetic types of *E. chaffeensis* are geographically clustered.

MATERIALS AND METHODS

Sample collections. A total of 11 culture isolates and 91 infected whole blood samples from WTD were utilized in this study. Culture isolates from WTD were obtained during previous studies conducted at the Southeastern Cooperative Wildlife Disease Study (10, 11, 21; M. J. Yabsley, V. G. Dugan, D. E. Stallknecht, S. E. Little, J. M. Lockhart, J. E. Dawson, and W. R. Davidson, submitted for publication). Whole blood samples from infected deer were obtained during a prior study of WTD as reservoirs of *E. chaffeensis* (M. J. Yabsley, V. G. Dugan, D. E. Stallknecht, S. E. Little, J. M. Lockhart, J. E. Dawson, and W. R. Davidson, submitted for publication).

Molecular analysis. DNA from 300 μl of whole blood was extracted using the GFX Genomic Blood DNA Purification Kit (Amersham Pharmacia Biotech, Piscataway, New Jersey) following the manufacturer's protocol. For culture samples, a single-step PCR for the VLPT and 120-kDa genes was conducted as described (19, 23). For whole blood samples, a nested PCR was conducted using 1 μl of primary product as template in a 25 μl reaction containing the same PCR components except for substitution with internal primers FB5/FB3 and PXCF3B/PXAR5 for the VLPT and 120-kDa genes, respectively (19, 23). Amplified products were separated in 2% agarose gels, stained with ethidium bromide, and visualized with UV light. Stringent protocols and controls were utilized to prevent and assay for contamination. DNA extraction, primary amplification, secondary amplification, and product analysis were performed in separate dedicated laboratory areas. Water controls were included in each set of DNA extractions and one water control was included in each set of primary and secondary PCR reactions.

Nucleotide sequencing. Eleven amplicons from the primary VLPT PCR were sequenced for ten culture isolates of *E. chaffeensis* and amplicons from the secondary PCR for 22 infected WTD whole blood samples. Because enough template was not present in infected whole blood samples to sequence the primary product, a hemi-nested PCR was developed in order to obtain a larger sequence fragment of the VLPT gene. Four whole blood samples (E937, E990, E915, and E521) were subjected to the hemi-nested PCR using primers FB5A and FB3A in a primary reaction and FB5 and FB3A in a secondary reaction. Thermocycler conditions for the hemi-nested PCR were 94°C for 1 min, 52°C for 90 s, and 70°C for 90 s for 36 cycles followed by 68°C for 5 min. The secondary product for the 120-kDa gene of the OSLN2 isolate of *E. chaffeensis* was sequenced to verify identity of the novel five repeat variant. Products were purified with a Microcon spin filter (Amicon Inc., Beverley, Mass.), sequenced at MWG-BIOTECH (High Point, North Carolina), and the resultant sequences compared to published *E. chaffeensis* sequences in the GenBank database. Samples with multiple amplicons were purified as described above, separated in 1.5% agarose, and each amplicon separately purified using the Qiaquick Gel Extraction Kit (Qiagen, Valencia, Calif.).

Nucleotide sequence accession numbers. The VLPT sequences obtained in this study have been submitted to the GenBank Database under accession numbers: 15B, AY307329; 40S, AY307330; 22B, AY307341; OSLN2, AY307328; 604-2, AY307322; 604-5, AY307324; 628-5, AY307321; 543-6, AY307336; E937, AY307333; E990, AY307327; H02-66, AY307338; H02-68 4 repeat, AY307345; H02-68 3 repeat, AY307353; H02-72, AY307339; 125B, AY307331; E914, AY307337; E915, AY307334; 601-5 3 repeat, AY307335; 601-5 5 repeat, AY307323; E905, AY307348; E897, AY307349; E521, AY307332; 529-3, AY307343; E890, AY307346; 606-1, AY307344; 623-4, AY307326; 590-4, AY307347; CC377-02, AY307350; E886, AY307325; CC228-02, AY307340; E1058, AY307352; E1059, AY307342; and CC343-02, AY307351. The accession number for the OSLN2 isolate 120-kDa sequence is AY307354.

RESULTS

VLPT antigen gene analysis. *E. chaffeensis* from WTD exhibited heterogeneity in the number of repeats (n = 3, 4, 5, or 6) present in the VLPT antigen gene (Table 1). Each culture isolate of *E. chaffeensis* contained either a single 4 or 5 repeat amplicon except for one culture isolate (601-5; Jones Co., GA) which had amplicons corresponding to 3, 4, and 5 repeats. All 91 infected WTD whole blood samples were positive by VLPT PCR. Eighty of these 91 (87.9%) WTD had single amplicons corresponding with 3 repeats (n = 1 WTD), 4 repeats (n = 54), and 5 repeats (n = 25). The remaining 11 WTD had two amplicons corresponding to 3 and 5 repeats (n = 1 WTD), 4 and 5 repeats (n = 9), or 4 and 6 repeats (n = 1).

Several populations of WTD were coinfected with multiple genetic variants of the VLPT gene (e.g., two variants were detected in four infected deer from Gwinnett Co., GA, two variants in seven deer from Chatham Co., GA, and 2 variants in eight infected deer from Culpepper Co., VA). As mentioned earlier, 11 individual deer were coinfected with two variants. In contrast, several other locations with multiple infected deer contained the same variant (e.g., four deer with four repeats in Albemarle Co., VA, six deer with 4 repeats in Dare and Hyde Co., NC, and 4 deer with 4 repeats in Wakulla Co., FL).

The profiles of sequence repeat units were similar to those reported for human and tick samples (Table 2). All 4 repeat unit samples were 1, 2, 3, 4, the single 3 repeat unit sample had a deletion of the third unit type (1, 2, 4), and the five repeat unit samples had an addition of a fifth unit type or a repeat of unit type 3 (i.e., 1, 2, 3, 4, 5 or 1, 2, 3, 3, 4). A nucleotide substitution (C for a T) at position 247 in three WTD samples (from Georgetown Co., SC; Yazoo Co., MS; and Culpepper Co., VA) resulted in a substitution of a proline for a serine. This substitution created an eighth unique repeat type unit which is most similar to the second repeat type unit. Substitutions (A or G) were noted at positions -69, 6, 27, and 487, but only 3 of 31 (9.7%) WTD contained the nucleotide guanosine at position 6. A deletion within the 9-base gap region (5'-

GTTTTATAT) of a single WTD sample compared with infected human or tick samples (19) was noted; the first two thymidines (643 and 644) within the gap region were deleted from a culture isolate of *E. chaffeensis* from a deer from Greene Co., AR.

120-kDa antigen gene analysis. Similar to the VLPT antigen gene, varying numbers of repeats (2, 3, 4, or 5) in the 120-kDa antigen gene were observed for *E. chaffeensis* in WTD (Table 1). Each culture isolate contained a single amplicon corresponding to 3, 4, or 5 repeats, with one exception, an isolate from Georgetown Co., SC (E886) which had amplicons corresponding to both 3 and 4 repeats. Only 62 of 91 (68.1%) infected blood samples were positive for the 120-kDa antigen gene. Single 120-kDa amplicons corresponding to 2, 3, 4, and 5 repeats were detected in 1, 24, 33, and 2 WTD, respectively. Two WTD had two amplicons corresponding to 3 and 4 repeats. One deer from Putnam Co., GA with two 120-kDa amplicons also contained two amplicons with the VLPT PCR (4 and 5 repeats).

Sequence analysis of a 1,311-bp fragment of the 120-kDa gene (OSLN2 isolate) revealed a series of 5 tandem 240-bp repeat units. The five units differed by five nucleotides at positions 46, 138, 146, 202, and 232 from the beginning of the repeat region resulting in two amino acid substitutions (Table 3). Each repeat unit of the OSLN2 isolate differed between two and four nucleotides from each repeat unit of the 120-kDa genes of *E. chaffeensis* in the GenBank database (accession numbers U49426, U74670, AF474890-AF47499).

DISCUSSION

This study reports the first molecular characterization of *E. chaffeensis* from WTD, the natural vertebrate reservoir host. Similar to previous studies of human and tick samples of *E. chaffeensis*, we detected variable numbers of repeat units in both the VLPT and 120-kDa antigen genes and also additional sequence variations in the VLPT antigen gene. *E. chaffeensis* has only been isolated from two other hosts, a domestic goat (*Capra capra*) from Clarke Co., GA (7) and a red ruffed lemur (*Varecia variegata rubra*) from Durham Co., NC (20), although molecular evidence of infection has been detected in domestic dogs and coyotes (*Canis latrans*) (3, 8). The genetic types of *E. chaffeensis* infecting the coyotes, domestic dogs, and lemur are unknown but a fragment of the VLPT gene for a goat isolate from Clarke Co., GA was identical in sequence to those from WTD isolates from Clarke Co. tested during this study (E. J. Sims and M. J. Yabsley, unpublished data). In contrast, the 120-kDa gene of the goat isolate differed from WTD *E. chaffeensis* samples collected from Clarke Co.; the goat isolated contained 4 repeats (M. J. Yabsley, unpublished data), while the WTD samples contained 3 repeats (n = 1) or 4 repeats (n = 2).

For both the VLPT and 120-kDa antigen genes, only a single genetic type has been detected in individual infected humans or in individual ticks. A single tick pool containing 10 ticks tested by Sumner et al. (19) had two amplicons, a strong one corresponding to 3 repeat units and faint one for 4 repeat units; however, because of pooling co-infection of a single tick could not be confirmed. In this study, 11.8% and 2.7% of individual WTD were infected with at least two genetic variants of the VLPT and 120-kDa antigen genes.

The 4 and 5 repeat types of the VLPT gene were the most commonly detected genetic variant in WTD which is similar to other studies of humans and ticks (19, 13, 17). The 3 and 6 repeat types of the VLPT gene were the least common variants observed in this study and have only been reported from infected humans on five and one occasion, respectively. The 3 VLPT repeat type has only been reported from humans in Georgia, Tennessee, and Nebraska (2, 14); however, in the current study this genetic variant was found in WTD from Kansas, thereby extending the geographic distribution of this genetic type. Similarly, the 6 VLPT repeat profile has only been reported once from a human from Wakulla Co., FL (19). In this study, four infected WTD from Wakulla Co., FL were infected with *E. chaffeensis* of the 4 repeat variant and none were infected with the 6 repeat variant; however, we did detect a WTD infected with the 6 repeat variant in Florence County, SC. Because the 4 and 5 repeat variants were detected in all states examined in this study and multiple genetic variants were detected in single populations and single deer, it appears unlikely that there is a specific geographic distribution of the VLPT genetic variants. Additional studies are needed to fully understand the importance of the VLPT protein and any corresponding distribution of genetic variants.

At the nucleotide level, the VLPT antigen gene of *E. chaffeensis* from WTD was similar to isolates from humans or ticks, but some differences were noted. A single nucleotide substitution resulted in a unique VLPT repeat type unit; thus there are now eight described repeat type units, with two types [types 6 and 7] having only been reported once each from an infected human and tick, respectively (19). Single adenosine and guanosine substitutions were detected at four previously reported A or G variable positions; however, only 3 of 31 (9.7%) WTD samples had a G at position 6 while 41% of human isolates (9, 19) and 25% of tick samples contained a G at this position (19). Previously in human isolates, the presence of the aspartic acid deletion was associated with the presence of the 9-base gap; however, no association was noted for infected tick pools (19). Similar to ticks, *E. chaffeensis* from WTD had no association between the aspartic acid deletion and the presence of the 9-base gap in *E. chaffeensis* from WTD was observed. The 9-base gap region of the *E. chaffeensis* VLPT gene, located 45 nucleotides downstream from the putative stop codon, from a single infected WTD contained a two nucleotide deletion not previously reported. The significance of these variations is unknown, but more variation is present in this gene than previously reported.

As with the VLPT antigen gene, variable numbers of repeats were detected in the 120-kDa gene of *E. chaffeensis* from WTD. A new variant of the 120-kDa antigen gene with 5 repeats was detected indicating that there also is a broader range of variation in this gene than previously reported. Numerous nucleotide substitutions were noted in the repeat region of a single novel 5 repeat variant resulting in several amino acid substitutions, the importance of which is unknown. This novel 120-kDa 5 repeat variant was only detected in a single population of WTD located on Ossabaw Island in Chatham Co., GA. Two genetic variants of the 120-kDa gene were detected on Ossabaw Island where two deer were infected with the novel 5 repeat variant and two other deer were infected with the 3 repeat variant. This new 120-kDa 5 repeat variant was not detected in 36 other populations, including other coastal populations.

Additional testing of WTD from barrier islands may reveal additional populations infected with this genetic variant or possibly additional new variants.

The finding of multiple genetic variants of the VLPT and 120-kDa genes in individual deer is interesting because it suggests that *E. chaffeensis* fails to exclude infection in individuals with multiple genetic variants unlike a related rickettsial organism, *Anaplasma marginale*. *An. marginale* can establish multiple msp1∝ genotypes in a herd of chronically infected cattle but only one genotype has been found in each infected animal (15). Similarly, when tick cell cultures or cattle are inoculated with two different genotypes of *An. marginale*, only one strain successfully establishes (5). This exclusion also occurs in tick cell cultures co-infected with *An. marginale* and the sheep rickettsia, *An. ovis*. Furthermore, when *Dermacentor variablis* were fed sequentially on cattle inoculated with two different genotypes of *An. marginale*, only one genotype was detected in infected ticks, suggesting that genotype exclusion also occurred in ticks (4).

The finding of only one genetic variant of *E. chaffeensis* in humans but not in WTD may be related simply to the number of potentially infectious ticks parasitizing an individual. Deer commonly are infested with hundreds to thousands of ticks while a human generally is only infested with one or a few ticks which decreases the chance of exposure to multiple genetic types of *E. chaffeensis*. Sequential infections in humans is possible based on a report of reinfection. Two years after a liver transplant patient recovered from an infection with *E. chaffeensis*, a second infection with a genetically distinct variant of *E. chaffeensis* was detected (9). The above data suggest that either the immune response to one genetic type of *E. chaffeensis* is insufficient to prevent infection with another genetic variant or that neither the VLPT or 120-kDa antigens are involved in clearance or prevention of reinfection with *E. chaffeensis*.

The significance of the 120-kDa and VLPT proteins to the relative virulence of different strains of *E. chaffeensis* infecting humans is not understood. However, inclusion of reservoir-source organisms in the comparison of *E. chaffeensis* isolates provides a more comprehensive view of the intraspecific variation present in this pathogen. Further studies of the genetic variations of the VLPT, 120-kDa, and other genes, in human, tick, and reservoir populations will help in understanding the epizootiology and pathogenicity of *Ehrlichia chaffeensis*.

ACKNOWLEDGEMENTS

We would like to thank numerous staff at federal, state, and private wildlife agencies and Southeastern Cooperative Wildlife Disease Study for collecting samples used in this study. This work was supported primarily by the National Institutes of Allergy and Infectious Diseases (5 R01 AI044235-02). Further support was provided by the Federal Aid to Wildlife Restoration Act (50 Stat. 917) and through sponsorship from fish and wildlife agencies in Alabama, Arkansas, Florida, Georgia, Kansas, Kentucky, Louisiana, Maryland, Mississippi, Missouri, North Carolina, Oklahoma, Puerto Rico, South Carolina, Tennessee, Virginia, and West Virginia.

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TABLE 4.1. Summary of VLPT[a] and 120-kDa genetic types of *Ehrlichia chaffeensis* detected in white-tailed deer from 12 southeastern and south central states

State	VLPT		120-kDa	
	# of WTD[b]	Repeat variants detected in population (# of each repeat type)	# of WTD[c]	Repeat variants detected in population (# of each repeat type)
Arkansas	9	4 (2), 5 (7)	7	3 (2), 4 (5)
Florida	9	4 (8), 5 (1)	5	3 (2), 4 (3)
Georgia	30	4 (17), 5 (8), 3+5 (1), 4+5 (3), 3+4+5 (1)	23	3 (12), 4 (7), 5 (3), 3+4 (1)
Kansas	3	3 (1), 4 (1), 5 (1)	2	4 (2)
Kentucky	2	4 (1), 5 (1)	1	4 (1)
Louisiana	1	5 (1)	0	
Maryland	1	4 (1)	0	
Mississippi	1	5 (1)	1	4 (1)
Missouri	3	4 (2), 5 (1)	2	3 (1), 4 (1)
North Carolina	15	4 (12), 5 (2), 4+5 (1)	9	2 (1), 3 (3), 4 (5)
South Carolina	5	4 (1), 5 (3), 4+6 (1)	4	3 (1), 4 (2), 3+4 (1)
Virginia	23	4 (13), 5 (5), 4+5 (5)	19	3 (6), 4 (12), 3+4 (1)

[a] Variable length PCR target antigen gene of *Ehrlichia chaffeensis*.

[b] Number of white-tailed deer positive for the VLPT antigen gene.

[c] Number of white-tailed deer positive for the 120 kDa antigen gene.

TABLE 4.2. Summary of VLPT sequence variation for *Ehrlichia chaffeensis* from white-tailed deer

Sample	Location	No. of repeats	Repeat profile	A or G at position –69	A or G at position 6	A or G at position 27	A or G at position 487	Asp deletion	Nine-bp gap
15B[a]	Clarke, GA	4	1,2,3,4	A	A	G	G	No	No
40S[a]	Clarke, GA	4	1,2,3,4	A	A	G	G	No	No
22B[a]	Jasper, GA	5	1,2,3,4,5	ND	A	A	ND	Yes	ND
OSLN2[b]	Chatham, GA	4	1,2,3,4	A	A	G	G	No	No
604-2[c]	Greene, AR	5	1,2,3,3,4	A	A	G	G	No	No
604-5	Greene, AR	5	1,2,3,4,5	G	G	A	A	Yes	No[d]
628-5	Phillips, AR	5	1,2,3,3,4	G	A	G	G	No	No
543-6	Phillips, AR	5	1,2,3,3,4	ND	A	G	ND	No	ND
E937	Levy, FL	4	1,2,3,4	ND	A	G	G	No	No
E990	Taylor, FL	5	1,2,3,4,5	ND	A	A	A	Yes	No
H02-66	Chatham, GA	5	1,2,3,4,5	ND	A	A	ND	Yes	ND
H02-68	Chatham, GA	4	1,2,3,4	ND	A	G	ND	No	ND
H02-68	Chatham, GA	3	1,2,4	ND	A	G	ND	No	ND
H02-72	Chatham, GA	5	1,2,3,4,5	ND	A	A	ND	Yes	ND
125B	Clarke, GA	4	1,2,3,4	A	A	G	A	No	No
E914	Gwinnett, GA	5	1,2,3,3,4	ND	A	G	ND	No	ND
E915	Gwinnett, GA	4	1,2,3,4	ND	A	G	A	No	No
601-5	Jones, GA	3	1,2,4	A	A	G	G	No	No
601-5	Jones, GA	5	1,2,3,3,4	A	A	G	G	No	No
E905	Lowndes, GA	4	1,2,3,4	ND	A	G	ND	No	ND
E897	Washington, GA	4	1,2,3,4	ND	A	G	ND	No	ND
E521	Jefferson, KS	5	1,2,3,4,5	ND	A	A	A	Yes	Yes
529-3	Madison, LA	5	1,2,3,3,4	ND	ND	G	ND	No	ND
E890	Kent, MD	4	1,2,3,4	ND	A	G	ND	No	ND
606-1	Yazoo, MS	5	1,8,3,4,5	ND	ND	A	ND	Yes	ND

cont…

cont…

TABLE 4.2. Summary of VLPT sequence variation for *Ehrlichia chaffeensis* from white-tailed deer

Sample	Location	No. of repeats	Repeat profile	A or G at position –69	A or G at position 6	A or G at position 27	A or G at position 487	Asp deletion	Nine-bp gap
623-4	Anson, NC	5	1,2,3,4,5	ND	G	A	A	Yes	Yes
590-4	Dare, NC	4	1,2,3,4	ND	A	G	ND	No	ND
CC377	Johnston, NC	4	1,2,3,4	ND	A	G	ND	No	ND
E886	Georgetown, SC	5	1,8,3,4,5	G	G	A	A	No	Yes
CC228	Buckingham, VA	5	1,2,3,4,5	ND	A	A	ND	Yes	ND
E1058	Culpepper, VA	4	1,2,3,4	ND	A	G	ND	No	ND
E1059	Culpepper, VA	5	1,8,3,4,5	ND	A	A	ND	Yes	ND
CC343	Cumberland, VA	4	1,2,3,4	ND	A	G	ND	No	ND

[a] Culture isolates from reference 9.
[b] Culture isolate from reference 8.
[c] Remaining samples from reference 18.
[d] The first two thymidines (T_{643} and T_{644}) of the 9 base region were deleted.

TABLE 4.3. Nucleotide and amino acid differences for the units of the novel 5 repeat genetic variant of *Ehrlichia chaffeensis*

	Nucleotide[a]					Amino Acid[b]				
	46	138	146	202	232	15	46	49	67	77
Unit 1	G	A	A	C	T	K	K	M	L	N
Unit 2	A	.	.	.	.	.	.	.	.	.
Unit 3	.	.	.	.	.	.	.	.	.	.
Unit 4	.	G	G	A	C	.	R	V	.	.
Unit 5	.	G	G	.	C	.	R	V	.	.

[a]Nucleotide numbering begins at first nucleotide of repeat unit 1 of OSLN2.

[b]Deduced amino acid sequence numbers based on open reading frame of U49426 and deduced sequence begins at the second nucleotide of repeat unit 1.

CHAPTER 5

SPATIAL ANALYSIS OF THE DISTRIBUTION OF *EHRLICHIA CHAFFEENSIS*, CAUSATIVE AGENT OF HUMAN MONOCYTOTROPIC EHRLICHIOSIS, ACROSS A MULTI-STATE REGION[1]

[1] Yabsley, M.J., M.C. Wimberly, V.G. Dugan, S.E. Little, D.E. Stallknecht, and W.R. Davidson. To be submitted to *Emerging Infectious Diseases*.

ABSTRACT

Using data from a prototypic white-tailed deer *Ehrlichia chaffeensis* surveillance system, we mapped the probability of *E. chaffeensis* occurrence using geostatistical analysis (kriging) and logistic regression. The analyses included the *E. chaffeens*is serostatus for 563 counties from 18 south-central and southeastern states. Cross-validation showed that kriging accurately predicted counties positive for *E. chaffeensis* (84%). Logistic regression modeling of the entire region and three subregions detected climatic and land cover variables significantly associated with *E. chaffeensis* occurrence. The accuracy of each subregional model (78-85%) was higher than the regional model (75%). The predicted *E. chaffeensis* distribution had good concordance with human case data. The integration of a deer surveillance system with geostatistical and logistic regression analyses was useful in developing HME risk maps.

INTRODUCTION

Ehrlichia chaffeensis, which causes human monocytotrophic ehrlichiosis (HME), is an important emerging tick-borne pathogen in the southeastern and south-central United States. *Ehrlichia chaffeensis* is maintained in a zoonotic cycle involving white-tailed deer (WTD; *Odocoileus virginianus*) as a principal vertebrate reservoir and the lone star tick (LST; *Amblyomma americanum*) as the biological vector (Dawson et al., 1994a; Dawson et al., 1994b; Ewing et al., 1995; Lockhart et al., 1997a; Lockhart et al., 1997b). The LST ranges from mid Texas north to Iowa and east to the Atlantic coast and recently has been detected as far north as Maine (Childs and Paddock, 2002). Evidence of *E. chaffeensis* has been detected in WTD and/or ticks throughout the range of the LST; however, the distribution of *E. chaffeensis* in these states is not continuous (Paddock and Childs, 2003). Some known distributional limits of *E. chaffeensis* in WTD include a western boundary extending across Kansas, Oklahoma, and Texas, a southern boundary across peninsular Florida, and a cluster of many seronegative populations centered along the Appalachian Mountains (Dawson et al., 1994b; Yabsley et al., 2002, Yabsley et al., 2003). Other studies of WTD have documented an apparent northern range limit for *E. chaffeensis* in southern portions of Iowa, Illinois, Indiana, and Ohio (Dawson et al., 1994a; Irving et al., 2000; Mueller-Anneling et al., 2000).

Currently the only estimate of HME risk is based on human case data reported to the Centers for Disease Control and Prevention (CDC) through the National Electronic Telecommunications System for Surveillance (NETSS) (McQuiston et al., 1995; Gardner et al., 1999). Although the CDC and the Council of State and Territorial Epidemiologists (CSTE) recommended that human ehrlichioses be nationally reportable in 1998, currently 11 states do not report ehrlichiosis cases (Gardner et al., 2003). The incidence of HME in three of these states (Louisiana, Maryland, and Mississippi) is suspected to be high based on numbers of cases in neighboring states. Even for states that consider HME reportable, inconsistencies in diagnosis and reporting of HME limits the usefulness of these data for risk mapping (Gardner et al., 2003).

Recently, an extensive relatively fine-scale (county) serologic surveillance system using WTD as natural sentinels was evaluated as a means of discerning the distribution of *E. chaffeensis* (Yabsley et al., 2003). This alternative surveillance system included 563 populations of WTD throughout 18 states in the south central and southeastern United States. The overall goal of the present study was to evaluate whether data from this WTD surveillance system reflected HME risk by examining its spatial correlation with the distribution of reported HME cases. To accomplish this goal, we conducted two analyses 1) geostatistical analyses (kriging) to estimate the spatial pattern of *E. chaffeensis* and 2) logistic regression modeling to identify ecological predictor variables that could be useful in estimating distributional limits of locales suitable for *E. chaffeensis* transmission. The distributions of *E. chaffeensis* projected by kriging and logistic regression were then compared with NETSS HME case data extracted from McQuiston et al. (1999) and Gardner et al. (2003).

Materials and Methods

Ehrlichia chaffeensis *database*

The WTD *E. chaffeensis* serologic database used (Yabsley et al., 2003) was derived from samples collected by Southeastern Cooperative Wildlife Disease Study researchers (Dawson et al., 1994a; Lockhart et al., 1996; Little et al., 1997; Yabsley et al., 2002). The database comprised a total of 563 WTD populations tested for antibodies reactive to *E. chaffeensis* by the indirect immunofluorescent antibody (IFA) test as previously described (Dawson et al., 1994a; Lockhart et al., 1996; Yabsley et al., 2003). Serologic data for each population were categorized by county or parish and linked to a map of county boundaries in a geographic information system (GIS). If one or more deer with antibodies reactive to *E. chaffeensis* was detected, that county or parish was classified as positive.

Geostatistical modeling (kriging)

Because county serostatus was coded as an indicator variable (present = 1 and absent = 0), the spatial distribution of *E. chaffeensis* was interpolated using indicator kriging (Isaaks and Srivastava, 1989). The predictions obtained by this technique are based on the assumptions that 1) spatial variability in *E. chaffeensis* serostatus is related to the distance between counties and 2) the presence of *E. chaffeensis* in an unsampled county can be predicted based on the status of nearby sample locations. An empirical semivariogram was calculated over twelve 50-km lag intervals using data for the sampled counties (n = 563), with the spatial location of each county represented by its centroid. A spherical model was fitted to this semivariogram and used to generate a kriged map of the probability of *E. chaffeensis* presence or absence.

Kriging accuracy was assessed using cross-validation, in which the observed value for each sampled county was compared with its predicted value when the observed value was excluded from model. Counties were classified as positive for *E. chaffeensis* if the predicted probability was > 0.5, and negative otherwise. Accuracy (percent of counties correctly classified), sensitivity (percent of positive counties correctly classified), and specificity (percent of negative counties correctly classified) were computed based on the cross-validation. Semivariogram analysis, kriging, and cross-validation were conducted using ArcGIS 8.3 (ESRI, Redlands, CA 92373).

Logistic regression modeling

<u>Explanatory variables</u>

Spatial predictor variables for the logistic regression model were obtained as GIS datasets from a variety of sources and a full description of variables is given in Table 5.1. Climate variables included average monthly and annual minimum temperature, maximum temperature, number of frost days, precipitation, and water vapor pressure summarized for 1980-1997. These data were obtained as 1-km grids generated using the DayMet model (Thornton et al., 1997). Seasonal data were summed from average monthly data (winter, Dec-Feb; spring, Mar-May; summer, June-Aug; fall, Sept-Nov). Relative humidity was calculated using water vapor pressure and minimum and maximum temperatures using the method described by Thornton et al. (2000). Land cover data were obtained from the Global Land Cover Characteristics Database and were derived from 1-km Advanced Very High Resolution Radiometer data collected from April 1992 to March 1993 (Loveland et al., 2000). Elevation data was obtained as a 1-km digital elevation model. A soil drainage index was computed for each county using the State Soil Geographic (STATSGO) database (1:250,000). Low values characterized frequently saturated soils, whereas high values characterized well-drained soils. For each mapped soil polygon, a composite index for each polygon was computed based on the area-weighted average of drainage indices of the associated soil series. Deer density data from 1999 were obtained as a paper map from the Quality Deer Management Association. These data were mapped as polygons with five density levels: deer rare, absent, or urban with unknown population; <15 deer/km^2; 15-30 deer/km^2; 30-45 deer/km^2; and >45 deer/km^2. The states included in this study were digitized, georeferenced, and converted to a 1-km grid.

The above data sets were overlaid on the county boundaries to compute summary values for each county. Climate variables and soil drainage were summarized as mean values for each county. Land cover was summarized as the percentage of each county occupied by various land cover classes. Elevation was summarized as mean value for each county, and a ruggedness index was computed by subtracting the lowest elevation from the highest elevation within each county. Deer density was summarized by assigning the density class that covered the majority of each county to represent the entire county.

Ecological predictive models

Logistic regression analysis was carried out in SAS 8.2 (SAS Institute Inc., Cary, NC 27513) using the serostatus of WTD populations as the dependent variable. We used stepwise regression with a $p < 0.05$ cutoff to reduce the large set of potential predictor variables to a more parsimonious subset. Because we had *a priori* reasons (e.g., differing climates in western vs. eastern states) to believe that different predictive variables were important in different portions of the 19-state study region, we analyzed the region as a whole and then analyzed three separate subregions containing 18 of the 19 original states. The western subregion included Kansas, Oklahoma, and Texas (n = 110/563 counties), the central subregion included Alabama, Arkansas, Louisiana, Mississippi, and Missouri (n = 179), and the eastern subregion included Georgia, Delaware, Kentucky, New Jersey, North Carolina, South Carolina, Tennessee, Virginia, and West Virginia (n = 256). Florida was excluded from other subregions because of its semi-isolated geography and unique climate. Because of small sample size (n = 18), data for Florida could not be analyzed separately.

The logistic regression models were applied in ArcView 3.2 (ESRI, Redlands, CA 92373), using spatial predictor variables from all of the counties in the 19-state region to create a map of the probability of *E. chaffeensis* occurrence (hereafter termed “endemnicity probability”). The overall fit of the models was measured by comparing observed and predicted values for the sampled counties, with *E. chaffeensis* classified as present when the predicted probability of occurrence was greater than 0.5, and absent otherwise. Accuracy, sensitivity, and specificity were computed as described previously. We also calculated the area under the receiver operating characteristic curve (AUC ROC) (Fielding and Bell, 1997) and the pseudo-R^2 (Nagelkerke, 1991) as overall indices of model fit.

Comparison of predicted Ehrlichia chaffeensis *distribution with HME case data*

Incidence rates of HME reported under NETSS were obtained by combining data from McQuiston et al., (1999) and Gardner et al. (2003). In both studies, annual incidence rates (per million human population) had been calculated using the corresponding yearly census estimate. Incidence groups were low (<2.5), low-medium (2.5-<5), medium-high (5-<15), and high ($\geq$15) by McQuiston et al. (1999) and low (<3.5), low-medium (3.5-<8.3), medium-high (8.3-<17), and high ($\geq$17) by Gardner et al., (1999). Although category limits differed slightly in the two studies, the four levels of incidence (low to high) were combined to obtain unified sequential incidence estimates. If a county was positive in both studies but classified in different incidence categories, the higher of the two was used in this study. These incidence estimates per county were entered into ArcView 3.2 and compared with the endemnicity probability maps generated using our geostatistical and logistic regression modeling.

Results

Geospatial modeling (kriging)

The fitted semivariogram had a range of 463.3 km, a nugget value of 0.13014, and a sill of 0.21846 (Figure 5.1). The high nugget value, relative to the structural variance, suggested that additional fine-scale (< 50km) spatial variability in *E. chaffeensis* distribution was present but not accounted for in the kriging model. With a cutoff value of 0.5, the accuracy of the model was 87.2%, the sensitivity was 96.9%, and the specificity was 67% (Table 5.2).

Large irregularly shaped clusters of both positive and negative counties were detected in the study region (Figure 5.2). Positive counties were clustered in Atlantic coastal states from Florida to New Jersey and in a broad area extending north from Texas to Missouri east to Kentucky and south to Mississippi. Two large negative clusters were apparent. One along the western edge of the region through western portions of Kansas, Oklahoma, and Texas and a second centered along the Appalachians in Virginia, Kentucky, West Virginia, Tennessee, and Georgia. Two smaller negative clusters were observed; one in southern Louisiana and Mississippi and one in southern Florida. Sixty counties, both scattered and clustered within the study region, were misclassified as positive when they were observed to be negative (Figure

5.2). These misclassified counties occurred in close proximity to several positive counties.

Ecological predictive models

For the entire 19-state region-wide model, five variables were significantly related to *E. chaffeensis* serostatus in WTD (Table 5.3, Figure 5.3). The endemnicity probability of *E. chaffeensis* decreased with elevation, increased with percent savannah, increased with percent mixed deciduous forest (combination of deciduous and mixed), decreased with percent wooded wetlands, and increased with summer maximum temperature. With a cutoff value of 0.5, this model accurately predicted the *E. chaffeensis* serostatus of 421 of 563 (74.8%) counties (Table 5.2). Only 30 counties were misclassified as negative (sensitivity = 92.1%). The predicted distribution of seropositive WTD populations in some areas (southern Louisiana, Mississippi, and along the Mississippi River alluvial basin) was overestimated using this region-wide model and the predicted distribution in eastern Kansas and northern Missouri was underestimated (Figure 5.3).

In the eastern subregion model, five variables were significantly related to *E. chaffeensis* serostatus (Table 5.3, Figure 5.4). Predicted distribution decreased with elevation, and increased with percent total forest, soil moisture content, annual minimum temperature, and summer relative humidity. Three explanatory variables were associated with serostatus of WTD populations in the central subregion model (Table 5.3). The predicted distribution decreased with percentage cropland and annual precipitation, and increased with the density of WTD (Table 5.3, Figure 5.4). In the western subregion model, predicted positive counties were associated with increasing annual precipitation and increasing summer minimum temperature (Table 5.3, Figure 5.4).

The overall fit of the three subregion models was better than the region-wide model. The accuracy of the eastern subregion model compared with the region-wide model only increased by 3.3% but the specificity increased by 15.1% (Table 5.2). The accuracy of the central subregion model was greater than the region-wide model (79.3% vs. 74.8%, Table 5.2). The sensitivity was slightly lower than the region-wide model, but the specificity was higher (47.7% vs. 38.5%). The western subregion model correctly classified the serostatus of 84.5% counties resulting in a 9.7% increase in predictive power over the region-wide model (Table 5.2). The sensitivity of the region-wide and western subregion models was the same, but the specificity of the western model was 29.1% higher than that of the region model. All three subregion models had higher max-rescaled r^2 values and AUC ROC (Table 5.2) indicating that they better fit the data.

Comparison with HME case data

Within our 19 state study region, 270 counties in 15 states (Figure 5.5) had reported cases of HME during the years 1997-2002 (McQuiston et al., 1999; Gardner et al., 2003). The highest correlation with human case data was observed for the kriging analysis, with a total of 251 counties (93%) with human cases being classified as positive by our analysis (Figure 5.6). Overall, a high correlation was noted for the three subregion logistic models; 244 counties (90.4%) with reported HME cases were predicted to be positive. As HME incidence increased, there was higher correlation with correctly classified positive counties and nearly 100% of high incidence counties were classified as positive by our analyses (Figure 5.6).

Discussion

We used two different modeling methods to predict the endemnicity probability of *E. chaffeensis* within the southeastern and south-central United States and, by implication, identify locations with risk for HME. This is first large scale study to use geospatial analyses to estimate the geographic distribution of *E. chaffeensis* and was conducted using data from a prototypic surveillance system that employed WTD as natural sentinels (Yabsley et al., 2003). Data for this deer sentinel system was derived by serologically testing deer from 563 populations (counties) in 18 southcentral and southeastern states (Yabsley et al., 2003). Because geographic gaps existed since deer were not tested from every county, the present study used kriging and logistic regression modeling to predict the distribution of *E. chaffeensis* across all counties in these states. Logistic regression analyses also identified several climatic and landcover variables useful as predictors of *E. chaffeensis* occurrence. To relate these geospatial analyses to the occurrence of HME, comparisons were made with the geographic distribution of laboratory confirmed cases of HME for 1997-2002 compiled by public health agencies as published previously (McQuiston et al., 1999; Gardner et al., 2003). These comparisons disclosed spatial concordance between HME cases and *E. chaffeensis* endemnicity projected by both geospatial models.

The usefulness of modeling is dependent upon the reliability of input data, how well model predictions fit the actual status of variables being modeled, and, in regard to geospatial modeling especially, the issues of scale and scope of sampling (Matthews, 1990). Input data from the WTD surveillance sentinel system used in this study has previously been demonstrated to meet critical reliability criteria including diagnostic accuracy, adequacy of sample sizes and sampling intensity, key epidemiological associations with the LST vector, and ability to detect spread of *E. chaffeensis* (Yabsley et al., 2003). Data for the present study included over a third (33.8%) of counties in the 19 state study region, and measures of reliability for both kriging and logistic regression models disclosed high accuracy, sensitivity, and somewhat lower specificity (Table 5.2). Furthermore, analyses confirm that the logistic regression models fit the data well and that variables in the models included had biological relevance based on previous studies (Haile and Mount, 1987; Mount et al., 1993).

Kriging accurately estimated the distribution of *E. chaffeensis* across the entire study region. Kriging investigates and projects the spatial pattern of *E. chaffeensis* based on populations sampled independent of any landcover or climatic variables. This purely spatial analysis is dependent on a sufficient number of populations being sampled because an increase in distances between sampled populations leads to increased uncertainty. Large clusters of counties with similar serologic status were accurately detected; however, when variability in *E. chaffeensis* serostatus occurred among counties in close proximity, this model tended to over predict the presence of *E. chaffeensis*. Two prominent clusters of seronegative populations in the Mississippi River alluvial basin were misclassified as seropositive, in this case, small numbers of seronegative counties were encircled by seropositive counties. Three smaller negative clusters in central Alabama, south-central Georgia, and southeastern Texas also were projected to have moderate risk (0.5 < probability < 0.7). Similarly, two positive counties in western Kansas, one in southern Louisiana, and one in western North Carolina fell well within areas projected to have a low probability of *E. chaffeensis* occurrence. The failure to correctly classify individual or small clusters of counties reflects the high nugget value of our semivariogram which indicated that some fine scale variability (<50 km) was present but not being detected.

Logistic regression analyses also accurately classified the *E. chaffeensis* status within the study region and identified several ecological variables associated with the distribution of *E. chaffeensis*. In contrast to kriging, logistic regression modeling relies on correlations with ecological variables which are then used to estimate the distribution of *E. chaffeensis*. The region-wide model had good accuracy (75%) and high specificity (92%) but low sensitivity (39%). *Ehrlichia chaffeensis* distributions were accurately predicted in many states, but the region-wide logistic regression model produced results which conflicted with observed distributions in northern portions of Kansas and Missouri, central South Carolina, New Jersey, and portions of the Mississippi River alluvial basin. and Gulf Coast Partitioning into three subregions improved the accuracy, sensitivity, and specificity of the logistic regression modeling method. The most significant changes were the increased ability of subregion models to accurately predict positive status in northern Kansas/Missouri and New Jersey and to predict negative status for areas in eastern Kentucky, within the Mississippi River alluvial basin, and along the central Gulf coast. Both region-wide and subregional logistic regression models projected limited positive areas in north-central Kentucky, northeastern Alabama, northwestern Georgia, and central South Carolina that were outside the current distribution based on observed serostatus and kriging analysis.

Both kriging and subregion logistic regression models provided very reliable portrayals of *E. chaffeensis* occurrence, and the similarity of maps produced by these two modeling processes tends to substantiate the projected distributions. Because kriging was more accurate than logistic regression, models the observed distribution of serostatus, and does not require collection of additional ecological variables for use in a GIS, the kriging analysis probably provides the most accurate estimate of current *E. chaffeensis* distribution and would be more useful in monitoring spread to new locations. On the other hand, because logistic regression analysis is based on association with ecological variables, the projected extensions of *E. chaffeensis* into currently negative areas suggests these areas probably are suitable for maintenance of *E. chaffeensis* and that they are likely locations of future expansion.

The distribution of *E. chaffeensis* is highly dependent on the presence of WTD to serve as reservoirs (Lockhart et al., 1997a; Lockhart et al.,1997b) and the presence of LST to serve as a vector (Ewing et al., 1995), and indirectly on any factors that limit the distribution of WTD or LST. Based on extensive biological data relevant to LST, five critical variables, and interactions thereof, have been identified as being important to LST population dynamics (Haile and Mount, 1987; Mount et al., 1993). These variables consist of measures of moisture, temperature, habitat type, day length, and host density (WTD and/or cattle). During warm months, temperature and moisture are positively correlated with LST survival and activity while day length is negatively correlated with LST activity. LST abundance and survival are positively associated with wooded habitats, particularly young second-growth forests containing thick underbrush which provides proper microhabitat, but are negatively associated with grass or crop land habitats (Hair and Howell, 1970; Lancaster, 1957; Sonenshine et al., 1966). The landcover variables in our models (Table 5.3) conformed in general terms with these previously identified critical variables important to LST population dynamics. *Ehrlichia chaffeensis* presence was correlated with higher soil moistures and higher proportions of forest/savannah, which are habitats that provide better microhabitat for LST, while wooded wetlands, cropland (Figure 5.7), and high elevations (probably to some extent reflecting temperature) (Figure 5.7) were negatively correlated with *E. chaffeensis*.

Regarding climatic variables, our logistic regression models were in agreement with previous laboratory and field studies on LST. High annual precipitation and high relative humidity are thought to prevent desiccation and higher average temperatures (Figure 5.7) help prolong questing, all of which conspire to increase LST survival and densities (Hooker et al., 1912; Lancaster, 1957; Robertson et al., 1975; Koch and Dunn, 1980; Mount et al., 1993). Of interest was that *E. chaffeensis* presence was negatively correlated with increasing annual precipitation in the central subregion model, possibly because high precipitation in this low-lying region may lead to flooding or excessive wetness. The abundance of another ixodid tick, *Ixodes scapularis*, is negatively impacted by excessively wet soils (Bunnell et al., 2003), and our negative correlation with wooded wetlands suggests that *A. americanum* also may not be well suited for habitats subject to standing ground water.

The presence of WTD is clearly important to maintenance of high LST densities (Mount et al., 1993); however, interestingly, we found that WTD density was not a significant predictor variable in the region model or two of the three subregion models. While deer were important to modeling LST population dynamics (Mount et al., 1993), there are critical differences between LST modeling and modeling the probability of *E. chaffeensis* infection in WTD. Because the force of transmission is so heavily focused on WTD, low numbers of LST can quickly introduce and maintain *E. chaffeensis* within WTD populations (Lockhart et al., 1995; Yabsley et al., 2003). Furthermore, based on almost 100% concordance between LST presence and *E. chaffeensis* presence in WTD (Lockhart et al., 1996; Yabsley et al., 2002; Yabsley et al., 2003) and PCR detection of *E. chaffeensis* in nearly all surveys of LST (Childs and Paddock, 2003; Paddock and Childs, 2003; Anderson et al., 1993; Burket et al., 1998; Ijdo et al., 2000; Irving et al., 2000; Steiert and Gilfoy, 2002; Steiner et al., 1999; Stromdahl et al., 2001; Whitlock et al., 2000), it is reasonable to conclude that a very high proportion of LST populations are infected. WTD were present throughout our study area (Figure 5.7), frequently at high densities. Only the central subregion logistic regression model included deer density as a variable, and this appeared attributable to sizable highly agriculturalized areas within the Mississippi River alluvial basin where deer are rare, absent, or exist at low densities or in semi-isolated populations.

Comparison of the predicted distribution for *E. chaffeensis* with HME case data showed that >90% of counties with HME cases were predicted positive for *E. chaffeensis* by both kriging and logistic regression. In fact, counties in the high HME incidence category were nearly always (>98%) identified as *E. chaffeensis* positive based on our analyses. Several counties with a low incidence of HME were predicted to be negative. This could be because our analyses misclassified the county status or that the HME cases were acquired in another locale but reported in the county of residence. This comparison provides evidence that utilization of WTD as sentinels is an efficient alternative to human surveillance for predicting *E. chaffeensis* distribution and HME risk.

The distribution for E. chaffeensis projected in the current study should be validated by testing additional WTD populations from unsampled counties, especially in areas where the prediction data were inconsistent between the two models. Although highly correlated with HME case data, a better means for validation of the sentinel deer surveillance system validation is needed because HME case data are known to contain a variety of biases and under-represent the distribution and magnitude of HME (McQuiston et al., 1999; Gardner et al., 2003). An extensive cross-sectional serosurvey of humans for *E. chaffeensis* antibodies, which would provide a less biased and more accurate estimate of exposure to *E. chaffeensis* than does HME case data, should be conducted to validate the ability of the sentinel WTD surveillance system to accurately predict HME risk.

Acknowledgements

The authors would like to thank Scott Danskin and Sarah Cross for excellent help with building the GIS databases used in this study. We also would like to thank numerous staff at federal, state, and private wildlife agencies and SCWDS for collecting samples used in this study.

Work was supported primarily by the National Institutes of Allergy and Infectious Diseases (5 R01 AI044235). Further support was provided by the Federal Aid to Wildlife

Restoration Act (50 Stat. 917) and through sponsorship from fish and wildlife agencies in Alabama, Arkansas, Florida, Georgia, Kansas, Kentucky, Louisiana, Maryland, Mississippi, Missouri, North Carolina, Oklahoma, Puerto Rico, South Carolina, Tennessee, Virginia, and West Virginia.

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Table 5.1. Description of variables used in logistic regression modeling.

Variable		Variable description	Units	Range
Elevation		Average elevation per county	Meters	1 - 1501
Ruggedness		Difference in maximum and minimum elevation values	Meters	1 - 1843
Soil drainage value		Represents the natural drainage condition of the soil and refers to the frequency and duration of periods when the soil is free of saturation	None	1.9 - 80.7
Temperature		Average monthly and annual minimum and maximum temperature from 1980-1997	Celsius	Monthly -9.9 - 29.6 Annual 2.3 - 29.6
Precipitation		Average monthly and annual precipitation from 1980-1997	Centimeters	Monthly 0.6 - 24.6 Annual 23.5 - 189.6
Frost days		Average number of frost days per year from 1980-1997	Days	0.4 - 164.5
Relative humidity		Average relative humidity calculated from the monthly and annual water vapor pressure and the monthly and annual minimum and maximum temperatures	%	Monthly 20.5 - 82.5 Annual 35.7 - 85.8
Deer density		Categories of deer density for each county based on 1999 population estimates	No. deer/km^2	5 categories for densities of 0 - 45+ deer/km^2
Land cover	Urban	Percentage of urban and built-up land	% cover	0 - 100
Land cover	Crops	Percentage of dryland and irrigated cropland, grassland and woodland mosaic, and pasture	% cover	0 - 100
Land cover	Savanna	Percentage of savannah	% cover	0 - 95
Land cover	Dbroadmix	Percentage of deciduous broadleaf forest and mixed forest (no type of tree exceeds 50% of tree types)	% cover	0 - 100
Land cover	Evneedlemix	Percentage of evergreen needleleaf forest and mixed forest (no type of tree exceeds 50% of tree types)	% cover	0 - 98
Land cover	Total forest	Percentage of all forest types	% cover	0 - 100
Land cover	Wdwet	Percentage of wooded wetlands	% cover	0-63

Table 5.2. Logistic regression models for predicting distribution of *Ehrlichia chaffeensis*.

Region	Variable	Coefficient	X^2	*p* value
All states	Intercept	-11.51	14.73	0.0001
	Elevation	-0.09	35.45	<0.0001
	Savannah	3.78	4.67	0.0308
	Deciduous forest mix	1.18	10.79	0.0010
	Wooded wetlands	-214.9	5.06	0.0244
	Summer maximum temp	0.41	20.62	<0.0001
Eastern	Intercept	-36.72	11.06	0.0009
	Elevation	-0.31	28.61	<0.0001
	Forest	1.88	8.36	0.0038
	Soils	0.08	14.30	0.0002
	Annual minimum temp	0.20	5.62	0.0178
	Summer relative humidity	0.52	11.63	0.0006
Central	Intercept	18.99	23.80	<0.0001
	Annual precipitation	-1.55	21.69	<0.0001
	Crops	-2.69	11.47	0.0007
	Deer density	0.59	7.65	0.0057
Western	Intercept	-13.95	19.45	<0.0001
	Annual precipitation	0.85	16.66	<0.0001
	Summer minimum temp	0.37	7.16	0.0074

Table 5.3. Comparison of four models for predicting distribution of *Ehrlichia chaffeensis* based on a white-tailed deer surveillance system.

Analysis [a]	**Kriging**	**19-State**	**Eastern**	**Central**	**Western**
Accuracy (%)	87.2	74.8	78.1	79.3	84.5
Sensitivity (%)	96.9	92.1	93.1	89.6	92.1
Specificity (%)	67.0	38.5	53.6	47.7	67.6
Max-rescaled R^2	NA[b]	0.24	0.45	0.31	0.43
AUC ROC [c]	NA	0.724	0.834	0.804	0.845

[a] A county was classified as positive for *E. chaffeensis* if probability (*p*) was > 0.5 and compared to the actual serologic status of that county.

[b] NA, not applicable.

[c] AUC ROC, Area under the receiver operating characteristic curve.

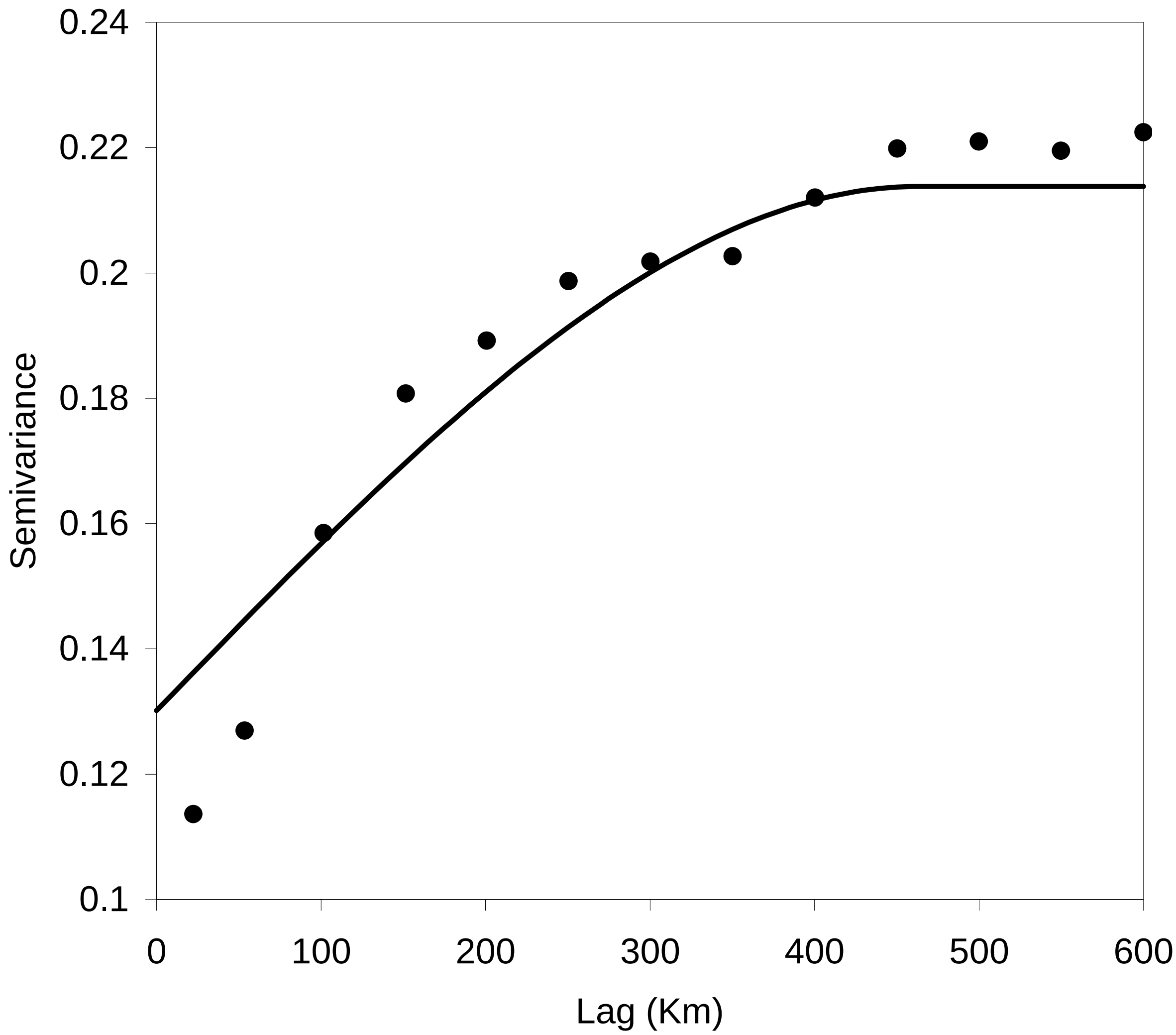


Figure 5.1. Semivariogram of *E. chaffeensis* occurrence. Lag = 50 km, nugget variance c_0 = 0.13014, sill c = 0.08832, and range a = 463.3 km.

Figure 5.2. Map of endemnicity probabilities for *E. chaffeensis* and risk of HME based on kriging. Solid circles represent positive *E. chaffeensis* serologic data and open circle represent negative serologic data obtained from a previous WTD surveillance studies (Chapter 3; Yabsley et al., 2003).

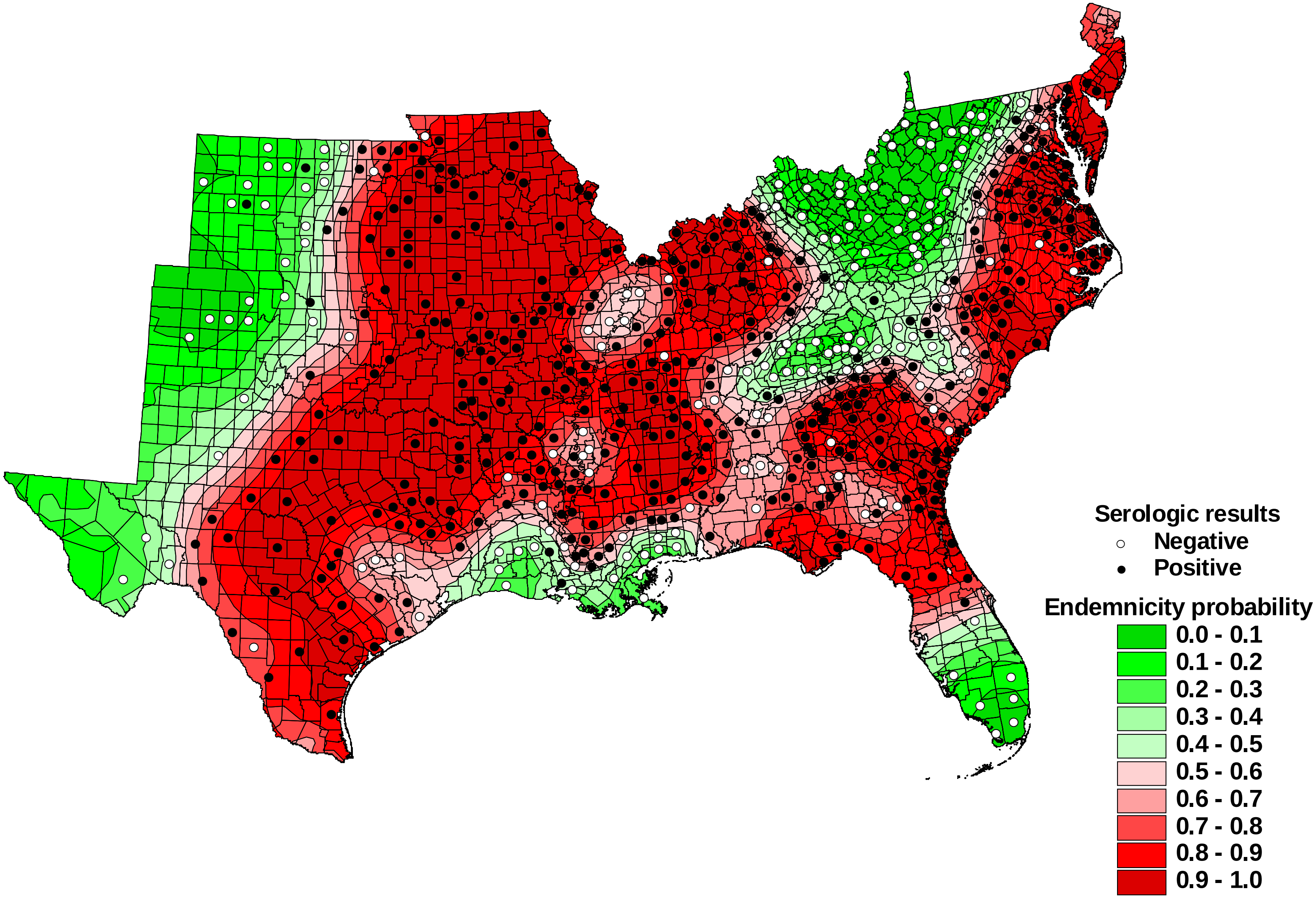

Serologic results
Negative
Positive
Endemnicity probability
0.0 - 0.1
0.1 - 0.2
0.2 - 0.3
0.3 - 0.4
0.4 - 0.5
0.5 - 0.6
0.6 - 0.7
0.7 - 0.8
0.8 - 0.9
0.9 - 1.0

Figure 5.3. Map of endemnicity probabilities for *E. chaffeensis* based on a region-wide logistic regression model derived for the entire 19-state region. Solid circles represent positive *E. chaffeensis* serologic data and open circle represent negative serologic data obtained from a previous WTD surveillance studies (Chapter 3; Yabsley et al., 2003).

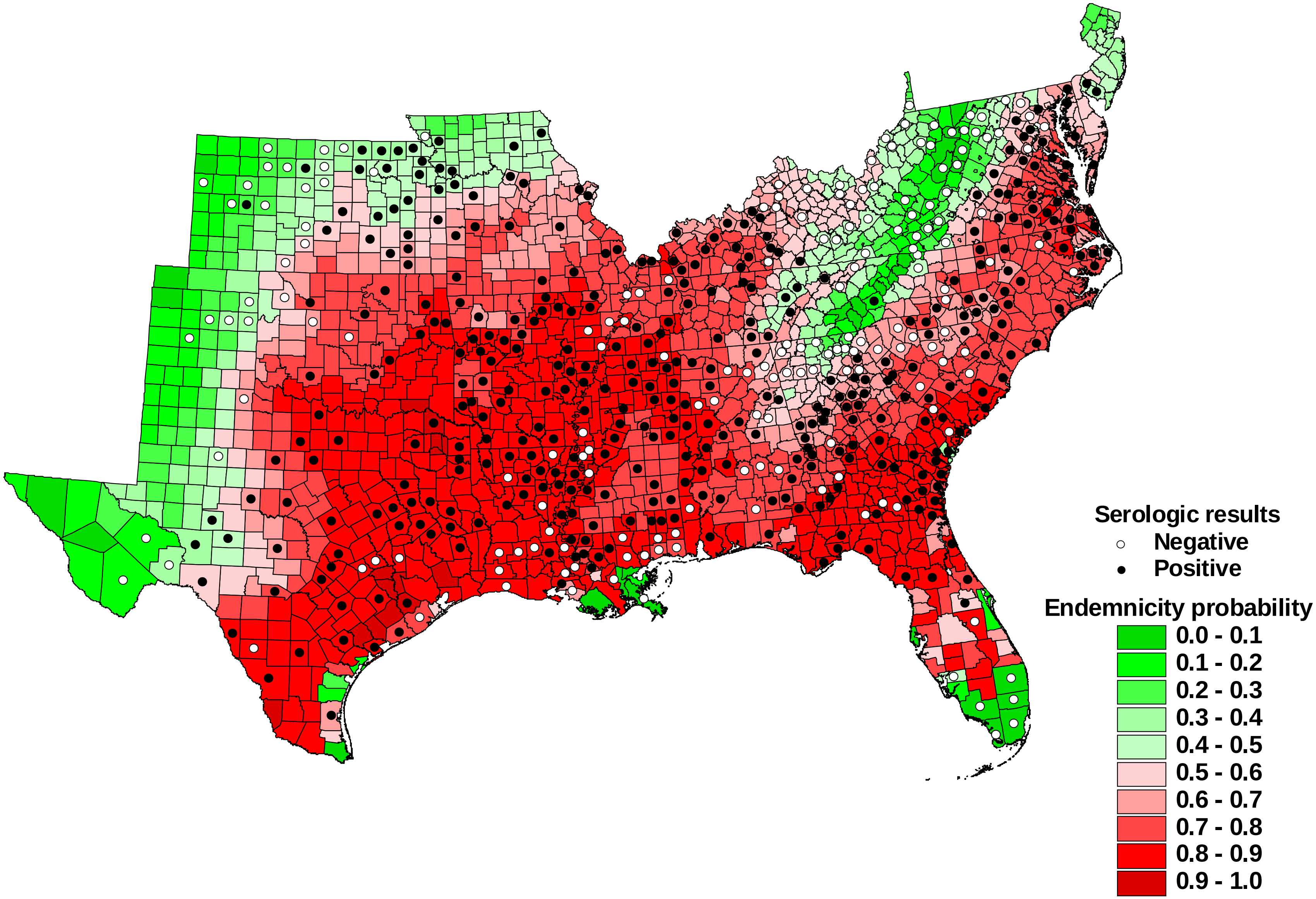
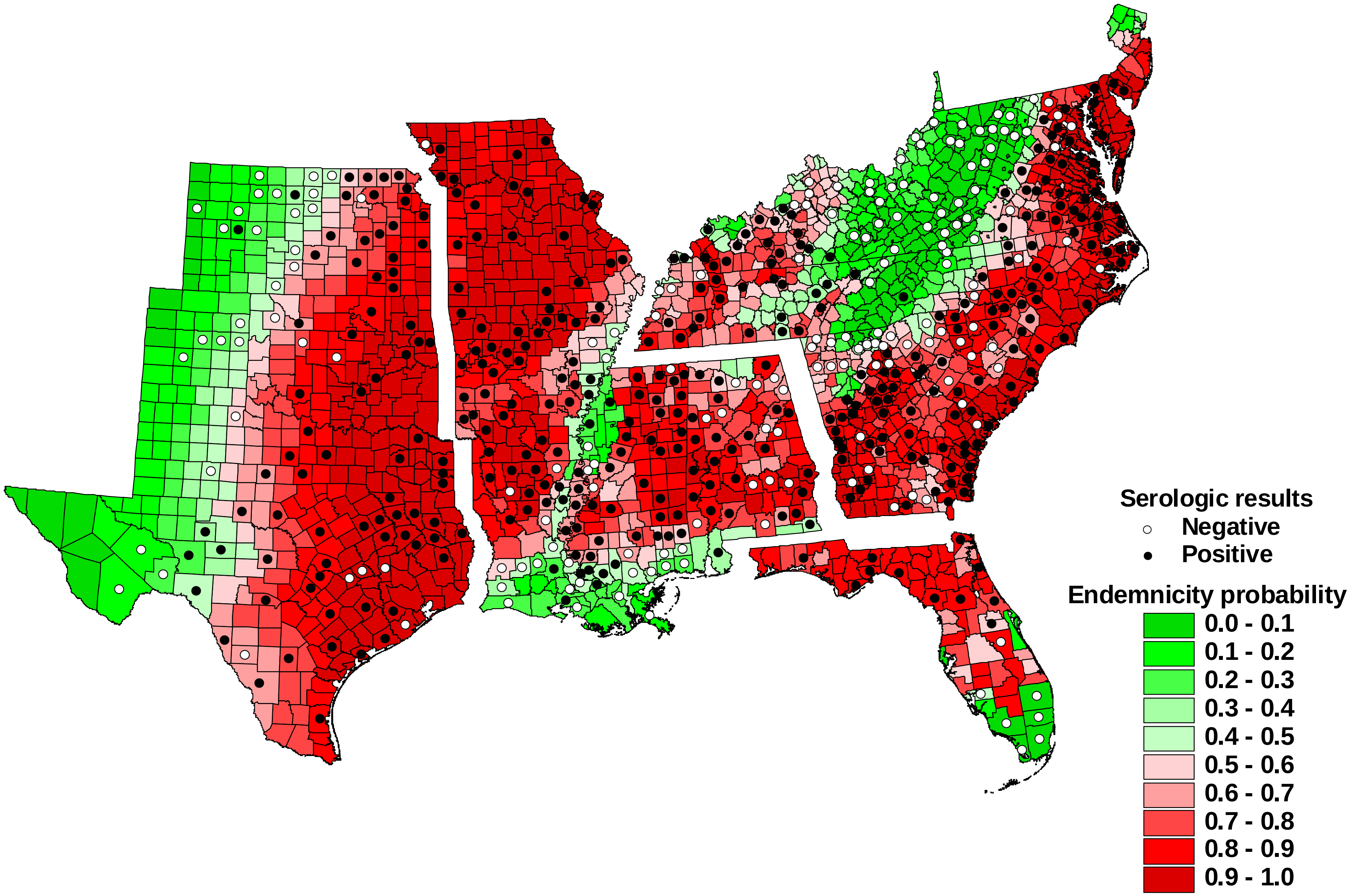
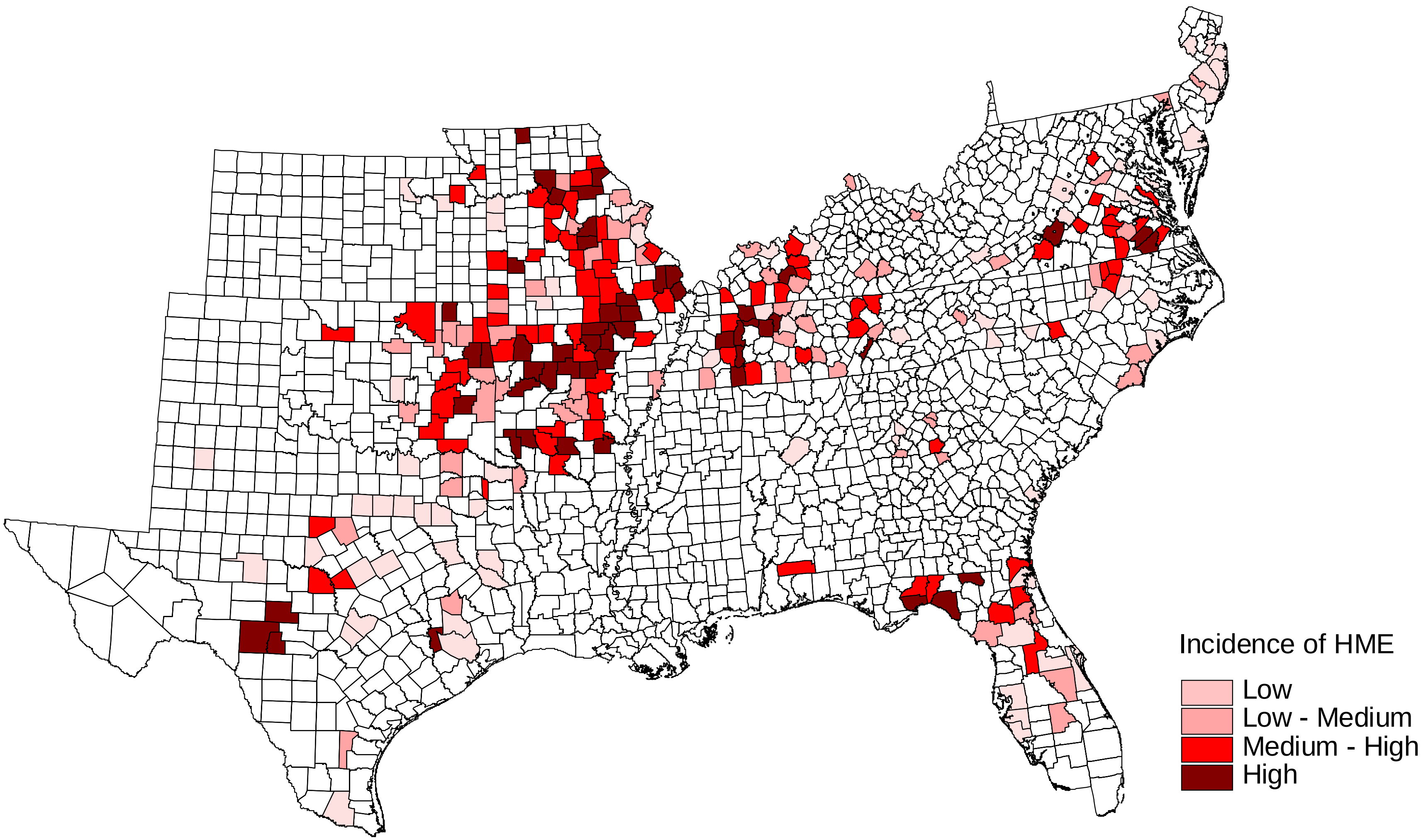

Serologic results
Negative
Positive
Endemnicity probability
0.0 - 0.1
0.1 - 0.2
0.2 - 0.3
0.3 - 0.4
0.4 - 0.5
0.5 - 0.6
0.6 - 0.7
0.7 - 0.8
0.8 - 0.9
0.9 - 1.0

Figure 5.4. Maps of endemnicity probabilities for *E. chaffeensis* based on separate logistic regression models for the eastern, central, and western subregion models and Florida extracted from the original entire 19-state region-wide model. Solid circles represent positive *E. chaffeensis* serologic data and open circle represent negative serologic data obtained from a previous WTD surveillance studies (Chapter 3; Yabsley et al., 2003).



Serologic results
Negative
Positive
Endemnicity probability
0.0 - 0.1
0.1 - 0.2
0.2 - 0.3
0.3 - 0.4
0.4 - 0.5
0.5 - 0.6
0.6 - 0.7
0.7 - 0.8
0.8 - 0.9
0.9 - 1.0

Figure 5.5 County-level average annual incidence rates for HME reported under NETSS. Data obtained from McQuiston et al. (1999) and Gardner et al. (2003).


Incidence of HME
Low
Low - Medium
Medium - High
High

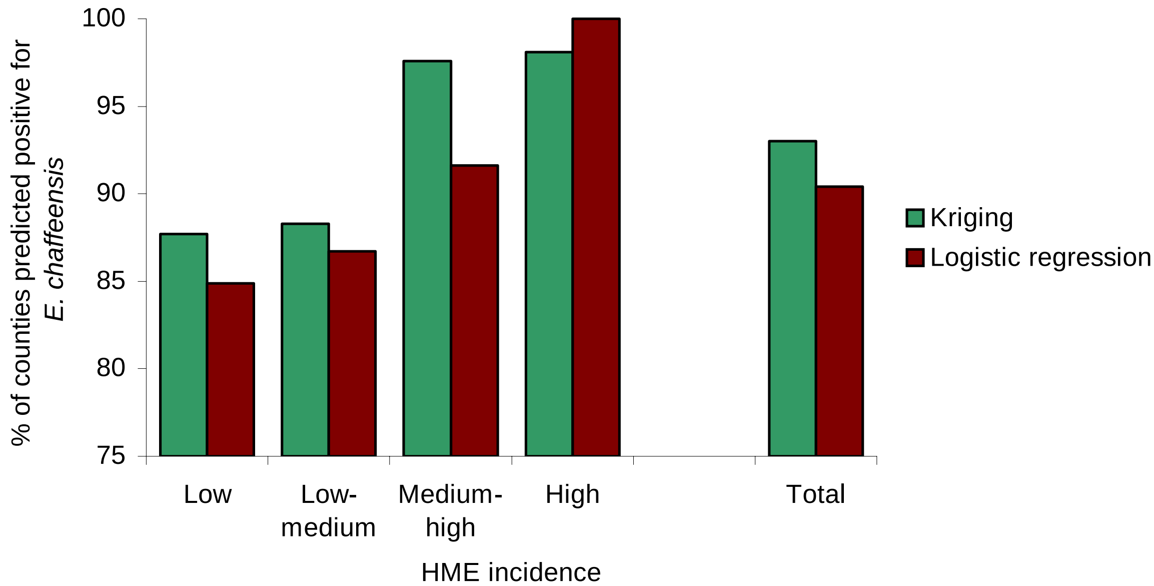
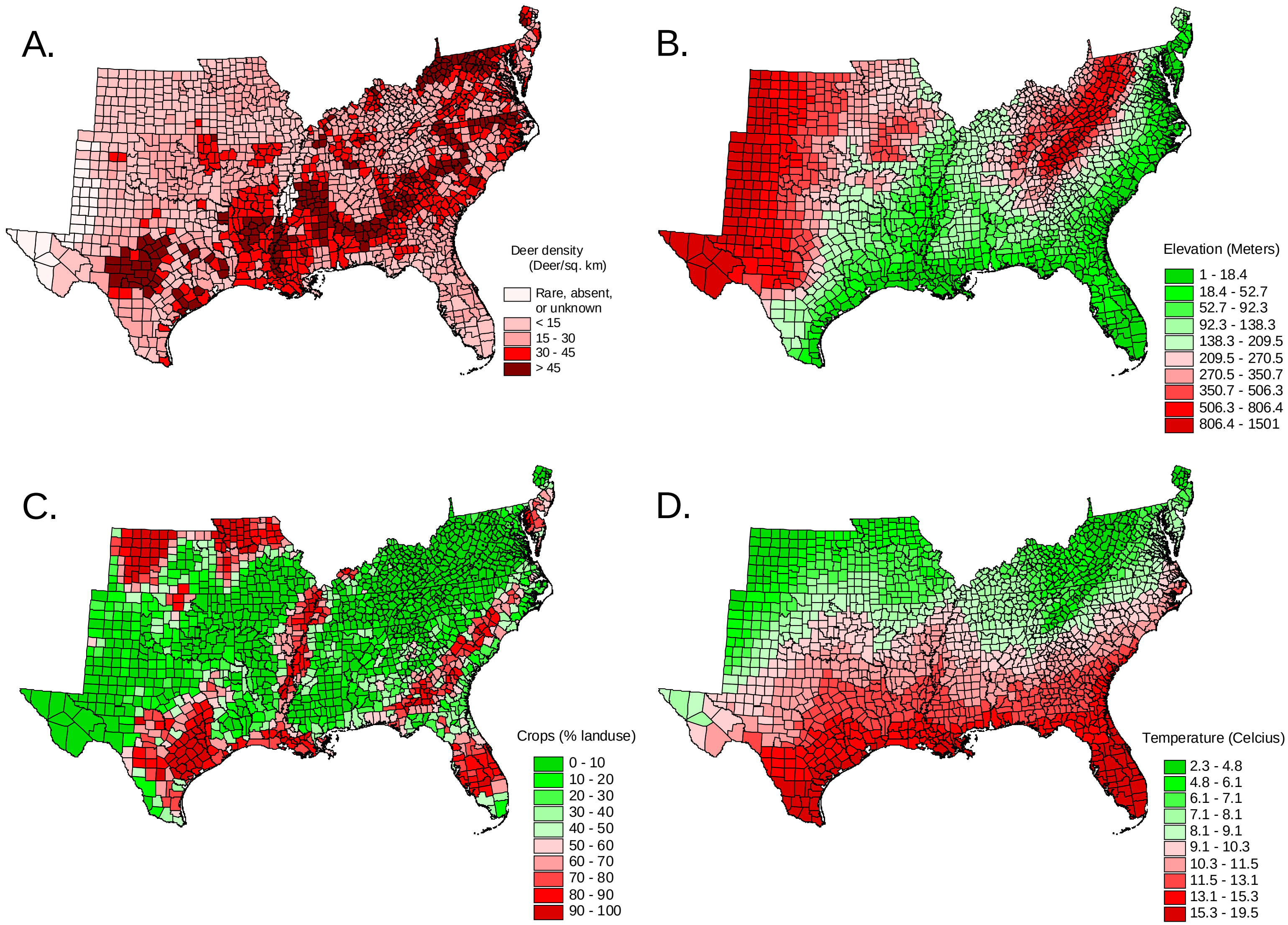


Figure 5.6. Comparison of HME case data with the predicted presence of *E. chaffeensis* based on kriging and logistic regression analyses.

Figure 5.7. GIS overlay maps for selected key explanatory variables used in development of logistic regression models.

A. WTD density; B. Elevation; C. Percentage of all crops; and D. Annual minimum temperature.


A.
Deer density
(Deer/sq. km)
Rare, absent, or unknown
< 15
15 - 30
30 - 45
> 45
B.
Elevation (Meters)
1 - 18.4
18.4 - 52.7
52.7 - 92.3
92.3 - 138.3
138.3 - 209.5
209.5 - 270.5
270.5 - 350.7
350.7 - 506.3
506.3 - 806.4
806.4 - 1501
C.
Crops (% landuse)
0 - 10
10 - 20
20 - 30
30 - 40
40 - 50
50 - 60
60 - 70
70 - 80
80 - 90
90 - 100
D.
Temperature (Celcius)
2.3 - 4.8
4.8 - 6.1
6.1 - 7.1
7.1 - 8.1
8.1 - 9.1
9.1 - 10.3
10.3 - 11.5
11.5 - 13.1
13.1 - 15.3
15.3 - 19.5

CHAPTER 6

EHRLICHIA EWINGII INFECTION IN WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*)[1]

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[1] Yabsley, M.J., A.S. Varela, C.M. Tate, V.G. Dugan, D.E. Stallknecht, S.E. Little, and W.R. Davidson. 2002. *Emerging Infectious Diseases*. 7: 668-671. Reprinted here with permission of publisher.

Abstract

Two closely related zoonotic ehrlichiae, *Ehrlichia chaffeensis* and *E. ewingii*, are transmitted by *Amblyomma americanum*, the lone star tick. Because white-tailed deer (WTD) are critical hosts for all mobile stages of *Am. americanum* and are important vertebrate reservoirs of *E. chaffeensis*, we investigated whether WTD are infected with *E. ewingii*, a cause of granulocytotropic ehrlichiosis in humans and dogs. Polymerase chain reaction and inoculation of fawns with whole blood from wild WTD were used to test for *E. ewingii* infection. Of 110 deer tested from 20 locations in 8 states, 6 (5.5%) WTD were positive for *E. ewingii*. In addition, natural *E. ewingii* infection was confirmed through infection of captive fawns. These findings expand the geographic distribution of *E. ewingii*, and risk of human infection, to include areas of Kentucky, Georgia, and South Carolina. Further, these data suggest that WTD could be an important reservoir for *E. ewingii*.

Key words: ehrlichiosis, zoonoses, southeastern United States, disease reservoirs, tick-borne diseases, deer, indirect immunofluorescence antibody test, PCR

Ehrlichia ewingii, one of the causative agents of canine granulocytic ehrlichiosis, has been reported from dogs in several states, including Oklahoma, North Carolina, and Virginia (1-4). Human infections with *E. ewingii* have been reported from Missouri, Oklahoma, and Tennessee (5,6); clinical disease is similar to that caused by other *Ehrlichia* spp. and is characterized by fever, headache, and thrombocytopenia, with or without leukopenia. (5-7). Experimentally, the lone star tick (*Amblyomma americanum*) has been shown to be a competent vector (8); however, natural infection of two other tick species, *Rhipicephalus sanguineus* and *Dermacentor variabilis*, has been reported in Oklahoma (2).

White-tailed deer (*Odocoileus virginianus*) are an important host for all three mobile stages of *Am. americanum* and white-tailed deer and lone star ticks serve as a major reservoir and vector, respectively, for *E. chaffeensis* (9-11). Because *E. ewingii* is closely related to *E. chaffeensis* and both share the same vector, we aimed to determine if white-tailed deer are naturally infected with *E. ewingii*. In some human and canine infections with *E. ewi*ngii, cross-reactions with *E. chaffeensis* antigens have been reported (5,6); however, not all infections with *E. ewingii* result in positive serologic tests to *E. chaffeensis* antigen (2,6). Because *E. ewingii* has not been isolated in culture and because serological test reagents are not readily available, we utilized several techniques to detect infections. These included: 1) serum samples were tested for antibodies reactive with *E. chaffeensis* antigen, 2) white blood cells or whole blood were tested by polymerase chain reaction (PCR) using primers specific for *E. ewingii* and *E. chaffeensis*, and 3) captive white-tailed fawns were inoculated with whole blood from deer collected in an *Am. americanum* endemic area.

Methods

Sample collections

From September 1996 to July 2001, whole blood samples and serum from 110 deer from 20 sites (Table 1) in the southeastern United States were collected in Vacutainer® EDTA tubes (whole blood) and serum tubes (Becton Dickinson, Franklin Lakes, NJ). For PCR, two blood preparation protocols were utilized. During the 1996-1997 collection period, white blood cells were separated from whole blood as previously described (9) whereas during the 2000-2001 period whole blood was extracted for PCR assays. Both white blood cells and whole blood samples were frozen at –20°C until PCR testing. Serum was aliquoted into serum vials and held at –20°C until serologic testing. Because *Am. americanum* is the only experimentally proven vector for *E. ewingii*, only locations with deer infested with *Am. americanum* were selected for this study.

Serologic analysis

Serum collected from each deer was tested for antibodies reactive to *E. chaffeensis* by the indirect immunofluorescent antibody (IFA) test as previously described (10) with the following modifications. Briefly, sera were screened at a dilution of 1:128 using *E. chaffeensis* antigen slides obtained from Focus Technologies (formally MRL Diagnostics, Cypress, CA). A 1:50 dilution of fluorescein isothiocyanate-labelled rabbit anti-deer immunoglobulin G (Kirkegaard & Perry Laboratories, Gaithersburg, MD) was used as conjugate.

Molecular analysis

DNA from 200 μl of whole blood or 20 μl of white blood cells was extracted using the GFX Genomic Blood DNA Purification Kit (Amersham Pharmacia Biotech, Piscataway, NJ) and InstaGene™ Purification Matrix (Bio-Rad Laboratories, Hercules, CA), respectively, following the manufacturer's protocol. Primary outside amplification consisted of 5 μl of DNA (from whole blood) or 10 μl (from white blood cells) in a 25 μl reaction containing 10 mM Tris-Cl (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 0.2 mM each dNTP, 2.5 units Taq DNA Polymerase (Promega, Madison, WI), and 0.8 μM of primers ECC and ECB (11). For the nested PCR, 1 μl of primary product was used as template in a 25 μl reaction containing the same PCR components except *E. ewingii* specific primers, EE72-ewingii (5'-CAATTCCTAAATAGTCTCTGACTATT-3') and HE3 (4), or *E. chaffeensis* specific primers, HE1 and HE3 (11), were added. Amplified products were separated in 2% agarose gels, stained with ethidium bromide, and visualized with UV light. Representative secondary PCR products for *E. ewingii* were purified with a Microcon spin filter (Amicon Inc., Beverley, MA), sequenced at the Molecular Genetics Facility at The University of Georgia using an ABI 3100 automated sequencer (Applied Biosystems, Perkin Elmer Corp, Foster City, CA), and then compared to published *E. ewingii* sequences (GenBank accession no. M73227 (3) and U96436 (1)).

Inoculation of fawns

Two 4-mo-old, laboratory-reared white-tailed fawns (76 and 81) were housed in a tick-free facility at the College of Veterinary Medicine, University of Georgia prior to inoculation. Both fawns were negative for antibodies reactive to *E. chaffeensis* and PCR negative for both *E. chaffeensis* and *E. ewingii* prior to inoculation. Whole blood for inoculation was obtained from five wild source deer (WTD1-5) collected at Piedmont National Wildlife Refuge (NWR) in Jones County, GA on July 24, 2001. A whole blood sample from each of the wild deer also was cultured in DH82 canine macrophage cells as previously described (12). For inoculation, fawns were anesthetized by intramuscular injection of tiletamine HCL and zolazepam HCL (4.4 mg/kg body weight; Ft. Dodge Animal Health, Fort Dodge, IA) and xylaxine (2.2 mg/kg; Butler, Columbus, OH) and were reversed with intravenous injection of yohimbine (0.125 mg/kg; Lloyd Laboratories, Shenandoah, IA). Equal volumes of whole blood in EDTA from WTD1 and WTD2 were pooled and a total of 8 ml was inoculated into fawn 76 in 2 ml aliquots by each of 4 routes (intravenous, intradermal, subcutaneous, and intraperitoneal). Fawn 81 was inoculated in the same way with a total of 8 ml of pooled blood from WTD3-5. Blood samples were collected from both fawns on 5, 9, 15, 20, 47, 68, and 110 days post inoculation (DPI) for PCR, serology, and blood smears. Blood was tested by PCR for *E. ewingii* and *E. chaffeensis*, as described above, and also for the human granulocytic ehrlichiosis (HGE) agent (*Anaplasma phagocytophila*) as previously described using primers GE9f and GA1UR (13).

Results

Ninety-seven of the 110 (88.1%) wild deer had antibodies reactive (≥1:128 titer) to *E. chaffeensis* by IFA testing and all locations examined contained seropositive deer (range of 57-100%). A 407 base pair product, characteristic of *E. ewingii*, was generated in 6 (5.5%) deer by nested PCR and 6 (5.5%) deer were also positive for *E. chaffeensis* (Table 1). Positive PCR results for *E. chaffeensis* and *E. ewingii* were obtained with both blood preparation processes. Only 1 deer (0.9%) was positive for both *E. ewingii* and *E. chaffeensis* by PCR.

All 5 source deer (WTD1-5) were positive for antibodies to *E. chaffeensis* but all were negative for *E. ewingii* and *E. chaffeensis* by PCR (Table 2). However, blood from deer WTD5 was culture positive for *E. chaffeensis*. Fawn 81 was first positive for antibodies reactive with *E. chaffeensis* at 15 DPI and also was positive on 47, 68, and 110 DPI. Fawn 76 was seronegative on all days tested. Both inoculated fawns were PCR positive for *E. ewingii* on 47 DPI and fawn 81 remained PCR positive on 68 DPI (Table 2). Whole blood samples from fawn 81 were PCR positive for *E. chaffeensis* on 15, 20, 47, 68, and 110 DPI. On thin blood smears from 47 DPI, morulae characteristic of *E. ewingii* were observed in ~2-3% and <1% of neutrophils of fawns 81 and 76, respectively (Figure 1). Both deer remained PCR negative for the HGE agent.

Sequences of three *E. ewingii* products (Dare County, North Carolina, Fawn 76, and Fawn 81) were identical to published gene sequences M73227 and U96436. The *E. ewingii* product from Benton County, Arkansas differed from others at base 225 (corresponds to accession number AY093439). The *E. ewingii* sequences have been deposited in the GenBank Database under the accession numbers AY093439-AY093441 and AY497628.

Discussion

This is the first evidence that white-tailed deer are naturally infected with *E. ewingii* and these data also extend the geographic distribution of *E. ewingii* to include areas of Kentucky, Georgia, and South Carolina. Prior to this report, the only reported vertebrate hosts for *E. ewingii* were humans and dogs. By combining PCR and inoculation data, a minimum of 8 of 110 deer (7.3%) were infected with *E. ewingii* which is similar to prevalence rates previously reported for dogs. A range of 6.2-15.8% of dogs from southeastern Virginia, Oklahoma, and southeastern North Carolina has been reported infected with *E. ewingii* (2,4,14). As discussed below, this percentage may represent a substantial underestimation of the actual prevalence of *E. ewingii* infection in WTD due to the limited sensitivity of PCR for detection of this organism. Our data suggests that the distribution of *E. ewingii* and hence the risk of human and canine infection may be more widespread than previously reported and may correspond with the distribution of *Am. americanum*.

Although whole blood samples from all 5 deer (WTD1-5) collected at Piedmont NWR in Georgia were negative by PCR, both inoculated fawns developed *Ehrlichia* spp. infections. At least 2 of the Piedmont NWR deer were infected with *E. ewingii* since both inoculated fawns developed *E. ewingii* infections. Also, at least 1 Piedmont NWR deer was positive for *E. chaffeensis* since fawn 81 became infected and WTD5 was culture positive. Because a much smaller volume of blood was used for PCR (20-200 μl) than for culture (5 ml) or inoculation of fawns (8 ml), low numbers of organisms may have been more readily detected by the latter 2 methods. Consistent with previous studies (12,15), our data indicate that use of PCR alone as a screening tool may fail to detect acute infections of white-tailed deer with *Ehrlichia* spp.

Although fawn 76 was clearly infected with *E. ewingii* based on PCR and detection of morulae, it was never positive by serology. Serologic cross-reactions between *E. ewingii* and *E. chaffeensis* have been reported by some authors (5,6);

however, not all *E. ewingii* infected dogs or humans develop antibodies to *E. chaffeensis* antigens (2,6). Compared to previous experimental infections of white-tailed deer with *E. chaffeensis* (11,15), an extended period of time was required before *E. ewingii* was detected. Low numbers of *E. ewingii* in the original inoculum may explain the longer time required for PCR detection of *E. ewingii* in fawns 76 and 81. Because this experimental infection was a small pilot study it provides limited insight concerning the course of *E. ewingii* infection in white-tailed deer. However, since *E. ewingii* was detected in fawn 81 over a three-week period, this indicates that *E. ewingii* was capable of replicating in white-tailed deer.

White-tailed deer have been demonstrated as important reservoirs for *E. chaffeensis* (11,12,15). In this study, using PCR, culture, and inoculation of fawns, at least 7 of 110 deer (6.4%) were positive for *E. chaffeensis*. In previous studies in *Am. americanum* endemic areas, as many as 40-100% of white-tailed deer have been shown to have antibodies reactive with *E. chaffeensis* and up to 20% of deer are PCR positive (10,12). Five of the 7 populations of WTD positive for *E. chaffeensis* also were positive for *E. ewingii*. This finding is not surprising as both pathogens share the same vector. Although evidence of the HGE agent has been detected in white-tailed deer by both serology and PCR (13,16), the relative importance of deer as reservoirs for the HGE agent has not been fully evaluated. While this study demonstrates that white-tailed deer harbor a third human ehrlichial pathogen, the importance of deer as reservoirs is not known.

Data from this study raise several important issues: (1) because of epidemiological similarities between *E. chaffeensis* and *E. ewingii*, deer could be an important reservoir for *E. ewingii*; (2) because of potential serologic cross-reactivity, it is clear that *E. chaffeensis* seroreactors in the current and prior surveys of white-tailed deer (10,17) could actually represent *E. chaffeensis*, *E. ewingii* or mixed infections; and (3) because at least 4 *Ehrlichia* spp. infect white-tailed deer (*E. chaffeensis*, *E. ewingii*, *An. phagocytophila*, and an undescribed *Ehrlichia* sp.) (9,12,13,16) it is important to utilize an array of diagnostic assays for detecting *Ehrlichia* spp. infections. Consequently, further studies to examine the reservoir potential of white-tailed deer for *E. ewingii* infection need to be conducted.

Acknowledgments

Work was supported primarily by the National Institutes of Allergy and Infectious Diseases (5 R01 AI044235-02). Further support was provided by the Federal Aid to Wildlife Restoration Act (50 Stat. 917) and through sponsorship from fish and wildlife agencies in Alabama, Arkansas, Florida, Georgia, Kansas, Kentucky, Louisiana, Maryland, Mississippi, Missouri, North Carolina, Oklahoma, Puerto Rico, South Carolina, Tennessee, Virginia, and West Virginia.

The authors would like to thank John Sumner for an *E. ewingii* positive DNA sample, M. Page Luttrell and Victor Moore for laboratory assistance, and numerous staff at Southeastern Cooperative Wildlife Disease Study for field and technical assistance.

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Table 6.1. Polymerase chain reaction (PCR) results for *Ehrlichia chaffeensis* and *Ehrlichia ewingii* in 110 white-tailed deer collected from 20 locations in the southeastern United States

Location[*]	County/State	*E. chaffeensis* PCR No. positive / No. tested (%)	*E. ewingii* PCR No. positive / No. tested (%)
White River NWR	Arkansas, AR	0/5	0/5
Felsenthal NWR	Ashley, AR	0/5	0/5
Pea Ridge NMP	Benton, AR	1/6 (17)	1/6 (17)
Shirey Bay WMA	Lawrence, AR	0/5	0/5
Cache River NWR	Monroe, AR	1/5 (20)	0/5
St. Vincent NWR	Franklin, FL	0/4	0/4
White Oak CC	Nassau, FL	0/5	0/5
Piedmont NWR	Jones, GA	0/5[†]	0/5[‡]
St. Catherines Is.	Liberty, GA	0/5	0/5
Blackbeard Is.	McIntosh, GA	1/7 (14)	2/7 (29)
Harris Neck NWR	McIntosh, GA	0/5	0/5
Ballard WMA	Ballard, KY	0/5	0/5
Fort Knox	Hardin, KY	0/5	0/5
West Kentucky WMA	McCracken, KY	1/5 (20)	1/5 (20)
Tensas River NWR	Madison, LA	0/3	0/3
Dahomey NWR	Bolivar, MS	0/3	0/3
Cape Hatteras NS	Dare, NC	1/4 (25)	1/4 (25)
Mattamukseet NWR	Hyde, NC	1/5 (20)	0/5
Sea Pines	Beaufort, SC	0/18	1/18 (6)
Kiawah Island	Charleston, SC	0/5	0/5
Total		**6/110 (5.5)**	**6/110 (5.5)**

[*]NWR = National Wildlife Refuge; NMP = National Military Park; WMA = Wildlife Management Area; CC = Conservation Center; NS = National Seashore.

[†]At least 1 of 5 (20%) was positive based on transmission to fawn 81.

[‡]At least 2 of 5 (40%) were positive based on transmission to both fawns 76 and 81.

Table 6.2. Summary serologic and polymerase chain reaction (PCR) data for source deer and inoculated fawns

Source deer	IFA results*	PCR *E. ewingii*	PCR *E. chaffeensis*	PCR HGE	Inoculation deer	IFA results	PCR *E. ewingii* (DPI)†	PCR *E. chaffeensis* (DPI)	PCR HGE
WTD1	+	-	-	-	76	-	+ (47)	-	-
WTD2	+	-	-	-					
WTD3	+	-	-	-					
WTD4	+	-	-	-	81	+	+ (47, 68)	+ (15, 20, 47, 68, 110)	-
WTD5	+	-	-	-					

*Indirect immunofluorescent antibody test, positive IFA test is titer ≥ 128.

† DPI = days post inoculation.

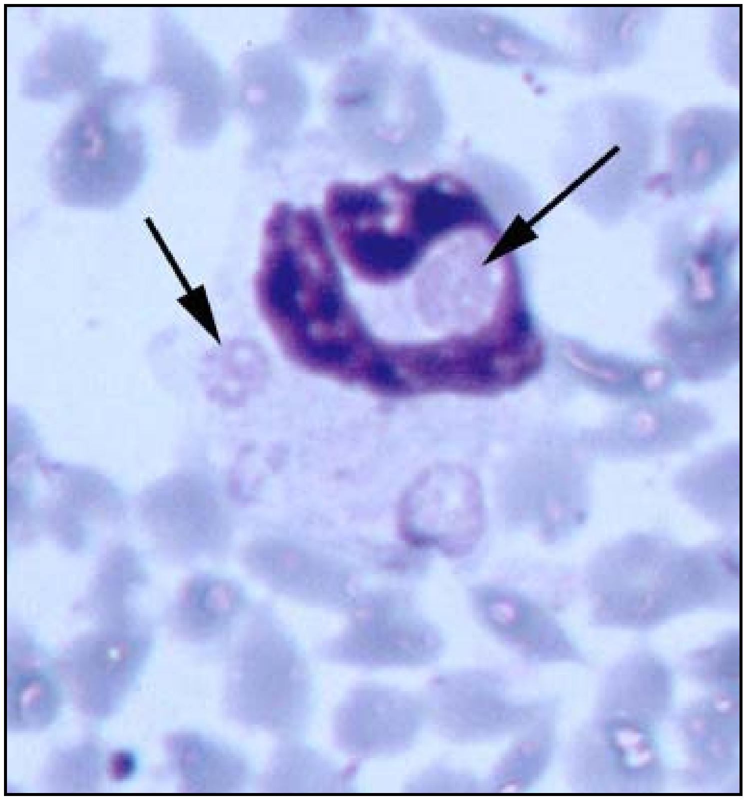

Figure 6.1. Multiple morulae consistent with *Ehrlichia ewingii* in a neutrophil from fawn 81 experimentally inoculated with pooled whole blood from 2 wild white-tailed deer (Giemsa stain, 100X).

CHAPTER 7

CONCLUSIONS

The major objective of this research was to gain a better understanding of the epidemiology of ehrlichial zoonoses, especially those vectored by the LST. Both *E. chaffeensis* and *E. ewingii* are emerging LST-borne zoonotic pathogens. *Ehrlichia chaffeensis* is the causative agent of human monocytotropic ehrlichiosis (HME) and *E. ewingii* is one causative agent of human granulocytotropic ehrlichiosis.

Study 1 (Chapter 2)

The overarching goal of this study was to implement and evaluate a prototype surveillance system using WTD as natural sentinels to determine the geographic distribution of *E. chaffeensis* across most of the suspected HME endemic region of the United States. To this end, the data obtained demonstrate the following critical attributes: 1) serologic findings reflect *E. chaffeensis* infection, 2) effective surveillance can be achieved with small sample sizes, 3) any deer >6 mo old is suitable for surveillance purposes, 4) enzootic and consistently negative locales were identified repeatedly across time, 5) surveillance of deer has the ability to detect spread to new locales, and 6) serologic, molecular, and culture diagnostic findings among deer could be related to presence of the principal tick vector, *Am. americanum*. These findings compliment and expand on a recent WTD serologic surveillance effort within Iowa

(Mueller-Anneling et al., 2000); however, that study exclusively used serologic assays and did not include either confirmatory microbiological diagnostics or contemporaneous tick vector monitoring. Collectively, these two studies confirm the effectiveness of this prototypical surveillance system for monitoring the distribution of this emerging human pathogen.

Study 2 (Chapter 3)

This study reports the first molecular characterization of *E. chaffeensis* from WTD, the natural vertebrate reservoir host. Similar to previous studies of human and tick samples of *E. chaffeensis*, we detected variable numbers of repeat units in both the VLPT and 120-kDa antigen genes and also additional sequence variations in the VLPT antigen gene. Multiple genetic variants were detected in single populations and single deer, so it appears unlikely that there is a specific geographic distribution of the VLPT genetic variants. A novel VLPT repeat type (type 8) was detected and a novel variant of the 120-kDa antigen gene with 5 repeats was detected indicating that there also is a broader range of variation in these genes than previously reported. The finding of multiple genetic variants of the VLPT and 120-kDa genes in individual deer is interesting because it suggests that *E. chaffeensis* fails to exclude infection in individuals with multiple genetic variants.

The significance of the 120-kDa and VLPT proteins to the relative virulence of different strains of *E. chaffeensis* infecting humans is not understood. However, inclusion of reservoir-source organisms in the comparison of *E. chaffeensis* isolates provides a more comprehensive view of the intraspecific variation present in this pathogen. Further studies of the genetic variations of the VLPT, 120-kDa, and other genes, in human, tick, and reservoir populations will help in understanding the epizootiology and pathogenicity of *Ehrlichia chaffeensis*.

Study 3 (Chapter 4)

Two different modeling methods were used to predict the geographic distribution of *E. chaffeensis* within the southeastern and south-central United States and, by implication, identify locations with risk for HME. This is first large scale study to use geospatial analyses to estimate the geographic distribution of *E. chaffeensis* and was conducted using data from a prototypic surveillance system that employed WTD as natural sentinels (Yabsley et al., 2003). Data for this deer sentinel system was derived by serologically testing deer from 563 populations (counties) in 18 south-central and southeastern states (Yabsley et al., 2003). Because geographic gaps existed since deer were not tested from every county, the present study used kriging and logistic regression modeling to predict the distribution of *E. chaffeensis* across all counties in these states. Logistic regression analyses also identified several climatic and landcover variables useful as predictors of *E. chaffeensis* occurrence. To relate these geospatial analyses to the occurrence of HME, comparisons were made with the geographic distribution of laboratory confirmed cases of HME for 1997-2002 compiled by public health agencies as published previously (McQuiston et al., 1999; Gardner et al., 2003). These comparisons disclosed spatial concordance between HME cases and *E. chaffeensis* endemnicity projected by both geospatial models.

Study 4 (Chapter 5)

This is the first evidence that white-tailed deer are naturally infected with *E. ewingii* and these data also extend the geographic distribution of *E. ewingii* to include areas of Kentucky, Georgia, and South Carolina. Prior to this report, the only reported vertebrate hosts for *E. ewingii* were humans and dogs. By combining PCR and inoculation data, a minimum of 8 of 110 deer (7.3%) were infected with *E. ewingii* which is similar to prevalence rates previously reported for dogs. And, this percentage may represent a substantial underestimation of the actual prevalence of *E. ewingii* infection in WTD due to the limited sensitivity of PCR for detection. Our data suggests that the distribution of *E. ewingii* and hence the risk of human and canine infection may be more widespread than previously reported and may correspond with the distribution of *Am. americanum*. Also, WTD could be an important reservoir of *E. ewingii*, but additional studies are needed to examine the reservoir potential of WTD for *E. ewingii*.

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APPENDIX A

DEMOGRAPHIC, *EHRLICHIA CHAFFEENSIS* DATA (SEROLOGIC AND MOLECULAR), AND LONE STAR TICK STATUS FOR EACH WHITE-TAILED DEER UTILIZED IN THIS STUDY.

Legend:

Demographic information: Unique identifier number, locality, county and state of collection, collection date, gender, and age for each deer tested.

E. chaffeensis serologic results: IFA results given as- (negative) or + (positive).

PCR results: For 16S rRNA gene are give as - (negative) or + (positive). Blanks indicate that the sample was not tested. PCR results for the variable length PCR target (VLPT) and 120-kDa antigen genes are given as - (negative) or if positive, given as a number which represents the number of repeats. Blanks indicate that the sample was not tested.

Amblyomma americanum (LST) status: A subjective estimate of the tick infestation intensity according to the following criteria: 0, no ticks observed; 1, <20 ticks observed; 2, between ~20-100 ticks observed; and 3, >100 ticks observed. Blanks indicate that that deer was not examined for ticks.

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
248-3	River Styx Lodge	Baldwin	AL	8/10/1981	F	3	+				1
248-1	River Styx Lodge	Baldwin	AL	8/10/1981	F	1	-				0
248-2	River Styx Lodge	Baldwin	AL	8/10/1981	M	1	-				1
248-4	River Styx Lodge	Baldwin	AL	8/10/1981	F	1	-				0
248-5	River Styx Lodge	Baldwin	AL	8/10/1981	F	2	-				0
SE91-297	Barbour Co. WMA	Barbour	AL	2/7/1991	M	1.5	+				
SE91-299	Barbour Co. WMA	Barbour	AL	2/7/1991	F	4.5	+				
SE91-303	Barbour Co. WMA	Barbour	AL	2/7/1991	M	2.5	+				
SE91-304	Barbour Co. WMA	Barbour	AL	2/7/1991	M	1.5	+				
SE91-307	Barbour Co. WMA	Barbour	AL	2/7/1991	M	1.5	+				
SE91-309	Barbour Co. WMA	Barbour	AL	12/28/1991	M	1.5	+				
SE91-310	Barbour Co. WMA	Barbour	AL	12/28/1991	F	4.5	+				
SE91-311	Barbour Co. WMA	Barbour	AL	12/28/1991	M	1.5	+				
SE91-312	Barbour Co. WMA	Barbour	AL	12/28/1991	F	0.5	+				
SE91-316	Barbour Co. WMA	Barbour	AL	1/17/1991	F	4.5	+				
SE91-317	Barbour Co. WMA	Barbour	AL	1/17/1991	F	0.5	+				
SE91-318	Barbour Co. WMA	Barbour	AL	1/17/1991	M	1.5	+				
SE91-319	Barbour Co. WMA	Barbour	AL	1/17/1991	M	2.5	+				
SE91-320	Barbour Co. WMA	Barbour	AL	1/17/1991	F	1.5	+				
558-2	Eufaula NWR	Barbour	AL	8/10/1998	F	2	+				0
SE91-298	Barbour Co. WMA	Barbour	AL	2/7/1991	M	0.5	-				
SE91-300	Barbour Co. WMA	Barbour	AL	2/7/1991	M	1.5	-				
SE91-301	Barbour Co. WMA	Barbour	AL	2/7/1991	M	1.5	-				
SE91-302	Barbour Co. WMA	Barbour	AL	2/7/1991	M	1.5	-				
SE91-305	Barbour Co. WMA	Barbour	AL	2/7/1991	M	2.5	-				
SE91-306	Barbour Co. WMA	Barbour	AL	2/7/1991	M	1.5	-				
SE91-313	Barbour Co. WMA	Barbour	AL	12/28/1991	M	1.5	-				
SE91-315	Barbour Co. WMA	Barbour	AL	12/28/1991	F	2.5	-				
326-01	Eufaula NWR	Barbour	AL	7/16/1986	F	5	-				0
326-02	Eufaula NWR	Barbour	AL	7/16/1986	M	4	-				0
326-03	Eufaula NWR	Barbour	AL	7/16/1986	F	2	-				0
326-04	Eufaula NWR	Barbour	AL	7/16/1986	F	3	-				0
326-05	Eufaula NWR	Barbour	AL	7/16/1986	M	1	-				0
558-1	Eufaula NWR	Barbour	AL	8/10/1998	F	3	-				0

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
558-3	Eufaula NWR	Barbour	AL	8/10/1998	F	5	-				0
558-4	Eufaula NWR	Barbour	AL	8/10/1998	F	1	-				0
558-5	Eufaula NWR	Barbour	AL	8/10/1998	F	3	-				0
SE95-0757	Barbour Co. WMA	Barbour/ Bullock	AL	6/17/1905		1.5	-				
SE95-0760	Barbour Co. WMA	Barbour/ Bullock	AL	6/17/1905		0.5	-				
SE95-0761	Barbour Co. WMA	Barbour/ Bullock	AL	6/17/1905		2.5	-				
SE95-0766	Barbour Co. WMA	Barbour/ Bullock	AL	6/17/1905		2.5	-				
SE95-0768	Barbour Co. WMA	Barbour/ Bullock	AL	6/17/1905		3.5	-				
EHRL-0101	Oakmulgee WMA	Bibb/Hale	AL	11/11/2000	F	5.5	+				
EHRL-0102	Oakmulgee WMA	Bibb/Hale	AL	11/11/2000	F	3.5	+				
EHRL-0103	Oakmulgee WMA	Bibb/Hale	AL	11/11/2000	F	4.5	+				
EHRL-0104	Oakmulgee WMA	Bibb/Hale	AL	11/11/2000	F	3.5	-				
EHRL-0105	Oakmulgee WMA	Bibb/Hale	AL	11/22/2000	M	2.5	-				
479-1	Fort McClellan/ Main Post	Calhoun	AL	8/19/1993	F	2.5	+				2
479-3	Fort McClellan/ Main Post	Calhoun	AL	8/19/1993	M	1.5	+				2
479-4	Fort McClellan/ Main Post	Calhoun	AL	8/19/1993	F	3.5	+				2
479-5	Fort McClellan/ Main Post	Calhoun	AL	8/19/1993	F	1.5	+				2
479-2	Fort McClellan/ Main Post	Calhoun	AL	8/19/1993	F	1.5	-				1
EHRL-0141	David Smith Prop. near Ft. Payne	Cherokee	AL	4/25/2001			-				
EHRL-0142	David Smith Prop. near Ft. Payne	Cherokee	AL	4/25/2001			-				
EHRL-0143	David Smith Prop. near Ft. Payne	Cherokee	AL	4/25/2001			-				
EHRL-0144	David Smith Prop. near Ft. Payne	Cherokee	AL	4/25/2001			-				
EHRL-0145	David Smith Prop. near Ft. Payne	Cherokee	AL	4/25/2001			-				
308-05	Choctaw NWR	Choctaw	AL	7/9/1985	F	6	+				0
557-2	Choctaw NWR	Choctaw	AL	8/3/1998	F	0.75	+				1
557-3	Choctaw NWR	Choctaw	AL	8/3/1998	F	4	+				1
557-4	Choctaw NWR	Choctaw	AL	8/3/1998	F	3	+				1
557-5	Choctaw NWR	Choctaw	AL	8/3/1998	M	1	+				1
308-01	Choctaw NWR	Choctaw	AL	7/9/1985	F	1	-				0

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
308-02	Choctaw NWR	Choctaw	AL	7/9/1985	F	1	-				0
308-03	Choctaw NWR	Choctaw	AL	7/9/1985	M	1	-				0
308-04	Choctaw NWR	Choctaw	AL	7/9/1985	F	2	-				0
557-1	Choctaw NWR	Choctaw	AL	8/3/1998	F	0.75	-				1
SE95-0454	Scotch WMA	Clarke	AL	6/17/1905		1.5	+				
SE95-0456	Scotch WMA	Clarke	AL	6/17/1905		3.5	+				
SE95-0457	Scotch WMA	Clarke	AL	6/17/1905		3.5	+				
SE95-0458	Scotch WMA	Clarke	AL	6/17/1905		5.5	+				
SE95-0459	Scotch WMA	Clarke	AL	6/17/1905		5.5	+				
EHRL-0092	Hollins WMA	Clay/ Talladega	AL	12/29/2000	F	7.5	-				
SE91-329	Choccolocco WMA	Cleburne	AL	12/13/1991	M	1.5	+				
SE91-330	Choccolocco WMA	Cleburne	AL	12/13/1991	M	2.5	+				
SE91-331	Choccolocco WMA	Cleburne	AL	12/13/1991	F	4.5	+				
SE91-332	Choccolocco WMA	Cleburne	AL	12/14/1991	M	4.5	+				
SE91-334	Choccolocco WMA	Cleburne	AL	12/14/1991	M	3.5	+				
SE95-0621	Freedom Hills WMA	Colbert	AL	6/17/1905		1.5	+				
SE95-0624	Freedom Hills WMA	Colbert	AL	6/17/1905		1.5	+				
SE95-0625	Freedom Hills WMA	Colbert	AL	6/17/1905		5.5	+				
SE95-0622	Freedom Hills WMA	Colbert	AL	6/17/1905		0.5	-				
SE95-0623	Freedom Hills WMA	Colbert	AL	6/17/1905		0.5	-				
EHRL-0093	Coosa WMA	Coosa	AL	1/3/2001	F	0.5	+				
EHRL-0094	Coosa WMA	Coosa	AL	1/4/2001	M	1.5	+				
EHRL-0095	Coosa WMA	Coosa	AL	1/30/2001	M	2.5	+				
489-1	Solon Dixon Forest Ed Center	Covington	AL	8/9/1994	F	2	-				0
489-2	Solon Dixon Forest Ed Center	Covington	AL	8/9/1994	M	3	-				0
489-3	Solon Dixon Forest Ed Center	Covington	AL	8/9/1994	F	2	-				0
489-4	Solon Dixon Forest Ed Center	Covington	AL	8/9/1994	M	1	-				0
489-5	Solon Dixon Forest Ed Center	Covington	AL	8/9/1994	M	3	-				0
262-1	Fort Rucker	Dale/Coffee	AL	7/13/1982	M	1	+				1
262-3	Fort Rucker	Dale/Coffee	AL	7/13/1982	F	3	+				1
262-4	Fort Rucker	Dale/Coffee	AL	7/13/1982	F	1	+				1
262-2	Fort Rucker	Dale/Coffee	AL	7/13/1982	F	5	-				1
262-5	Fort Rucker	Dale/Coffee	AL	7/13/1982	F	2	-				1

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE00-858	White Bluff HC	Dallas	AL	5/2/2001	F	2.5	+				
SE00-860	White Bluff HC	Dallas	AL	5/9/2001	F	2.5	+				
SE00-862	White Bluff HC	Dallas	AL	5/23/2001	F	2.5	+				
SE00-859	White Bluff HC	Dallas	AL	5/9/2001	F	2.5	-				
SE00-861	White Bluff HC	Dallas	AL	5/9/2001	F	3.5	-				
EHRL-0121	Little River WMA	DeKalb/ Cherokee	AL	11/28/2000	M	1.5	-				
EHRL-0122	Little River WMA	DeKalb/ Cherokee	AL	11/28/2000	M	1.5	-				
EHRL-0123	Little River WMA	DeKalb/ Cherokee	AL	11/29/2000	M	1.5	-				
EHRL-0124	Little River WMA	DeKalb/ Cherokee	AL	11/29/2000	M	1.5	-				
EHRL-0096	Wolf Creek WMA	Fayette/ Walker	AL	12/16/2000	M	1.5	-				
EHRL-0097	Wolf Creek WMA	Fayette/ Walker	AL	12/16/2000	M	4.5	-				
EHRL-0098	Wolf Creek WMA	Fayette/ Walker	AL	1/12/2001	M	1.5	-				
EHRL-0099	Wolf Creek WMA	Fayette/ Walker	AL	1/13/2001	M	1.5	-				
EHRL-0100	Wolf Creek WMA	Fayette/ Walker	AL	1/27/2001	M	1.5	-				
404-1	Solomon Farm	Houston	AL	8/28/1990	F	2.5	+				1
404-3	Solomon Farm	Houston	AL	8/28/1990	F	1.5	+				1
404-5	Solomon Farm	Houston	AL	8/28/1990	F	4.5	+				1
404-2	Solomon Farm	Houston	AL	8/28/1990	F	2.5	-				1
404-4	Solomon Farm	Houston	AL	8/28/1990	F	2.5	-				1
EHRL-0132	James D Martin-Skyline WMA	Jackson	AL	11/18/2000	M	2.5	+				
EHRL-0133	James D Martin-Skyline WMA	Jackson	AL	12/8/2000	F	2.5	+				
EHRL-0134	James D Martin-Skyline WMA	Jackson	AL	11/24/2000	F	3.5	+				
EHRL-0131	James D Martin-Skyline WMA	Jackson	AL	11/18/2000	M	3.5	-				
EHRL-0135	James D Martin-Skyline WMA	Jackson	AL	1/12/2001	M	5.5	-				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
EHRL-0119	Sam R Murphy WMA	Lamar/Marion	AL	1/13/2001	M	3.5	+				
EHRL-0120	Sam R Murphy WMA	Lamar/Marion	AL	1/13/2001	M	2.5	+				
EHRL-0118	Sam R Murphy WMA	Lamar/Marion	AL	12/16/2000	F	2.5	-				
EHRL-0125	Black Warrior WMA	Lawrence/ Winston	AL	11/25/2000	M	2.5	+				
EHRL-0127	Black Warrior WMA	Lawrence/ Winston	AL	12/1/2000	M	2.5	+				
EHRL-0128	Black Warrior WMA	Lawrence/ Winston	AL	12/2/2000	M	1.5	+				
EHRL-0126	Black Warrior WMA	Lawrence/ Winston	AL	12/1/2000	M	1.5	-				
EHRL-0129	Black Warrior WMA	Lawrence/ Winston	AL	12/8/2000	M	2.5	-				
406-1	G. E. Property	Lowndes	AL	8/31/1990	F	2.5	-				0
406-2	G. E. Property	Lowndes	AL	8/31/1990	M	1.5	-				0
406-3	G. E. Property	Lowndes	AL	8/31/1990	F	2.5	-				0
406-4	G. E. Property	Lowndes	AL	8/31/1990	M	1.5	-				0
406-5	G. E. Property	Lowndes	AL	8/31/1990	M	1.5	-				0
SE00-871	Cadwallader Place	Marengo	AL	3/21/2001	F	2.5	+				
SE00-872	Cadwallader Place	Marengo	AL	3/26/2001	F	5.5	+				
SE00-873	Cadwallader Place	Marengo	AL	3/26/2001	F	3.5	+				
SE00-874	Cadwallader Place	Marengo	AL	3/26/2001	F	2.5	+				
SE00-876	Cadwallader Place	Marengo	AL	3/26/2001	F	2.5	+				
364-01	Chambers Place	Marengo	AL	7/20/1988	M	1	-				0
364-02	Chambers Place	Marengo	AL	7/20/1988	F	2	-				0
364-03	Chambers Place	Marengo	AL	7/20/1988	F	1	-				0
364-04	Chambers Place	Marengo	AL	7/20/1988	F	1	-				0
364-05	Chambers Place	Marengo	AL	7/20/1988	M	1	-				0
567-1	Lake Guntersville SP	Marshall	AL	9/8/1999	F	2	-				0
567-2	Lake Guntersville SP	Marshall	AL	9/8/1999	F	3	-				0
567-3	Lake Guntersville SP	Marshall	AL	9/8/1999	F	2	-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
567-4	Lake Guntersville SP	Marshall	AL	9/8/1999	F	3	-				0
567-5	Lake Guntersville SP	Marshall	AL	9/8/1999	F	3	-				0
AL AF3	Purdue Hill	Monroe	AL	1/1/1987			+				
AL AF	Purdue Hill	Monroe	AL	1/1/1987			+				
AL AF4	Purdue Hill	Monroe	AL	1/1/1987			+				
AL AF5	Purdue Hill	Monroe	AL	1/1/1987			+				
AL AF7	Purdue Hill	Monroe	AL	1/1/1987			-				
387-1	Chapel Gray Estate	Montgomery	AL	8/22/1989	F	1	-				0
387-2	Chapel Gray Estate	Montgomery	AL	8/22/1989	F	4	-				0
387-3	Chapel Gray Estate	Montgomery	AL	8/22/1989	F	4	-				0
387-4	Chapel Gray Estate	Montgomery	AL	8/22/1989	F	1	-				0
387-5	Chapel Gray Estate	Montgomery	AL	8/22/1989	F	1	-				0
589-5	Wheeler NWR	Morgan	AL	9/14/2000	F	2.5	-				0
589-2	Wheeler NWR	Morgan	AL	9/14/2000	F	3.5	-				0
589-3	Wheeler NWR	Morgan	AL	9/14/2000	F	5.5	-				0
589-1	Wheeler NWR	Morgan	AL	9/14/2000	F	2.5	-				0
589-4	Wheeler NWR	Morgan	AL	9/14/2000	F	2.5	-				0
SE99-001	Westervelt Lodge	Pickens	AL	3/17/1999	M	1.5	+				
SE99-002	Westervelt Lodge	Pickens	AL	3/17/1999	F	2.5	+				
SE99-003	Westervelt Lodge	Pickens	AL	3/17/1999	F	0.5	+				
SE99-004	Westervelt Lodge	Pickens	AL	3/17/1999	F	1.5	+				
SE99-005	Westervelt Lodge	Pickens	AL	3/17/1999	M	1.5	+				
478-1	Fort Benning	Russell	AL	8/18/1993	F	1.5	+				0
478-3	Fort Benning	Russell	AL	8/18/1993	F	1.5	+				1
478-2	Fort Benning	Russell	AL	8/18/1993	M	1.5	-				1
478-4	Fort Benning	Russell	AL	8/18/1993	M	1.5	-				1
478-5	Fort Benning	Russell	AL	8/18/1993	F	2.5	-				0
566-1	Oak Mountain State Park	Shelby	AL	9/8/1999	F	2	+				2
566-2	Oak Mountain State Park	Shelby	AL	9/8/1999	F	3	+				3
566-4	Oak Mountain State Park	Shelby	AL	9/8/1999	F	2	+				1
566-3	Oak Mountain State Park	Shelby	AL	9/8/1999	M	2	-				2
566-5	Oak Mountain State Park	Shelby	AL	9/8/1999	M	2	-				2
364-06	Lee Haven Area	Sumter	AL	7/19/1988	F	3	+				1
364-07	Lee Haven Area	Sumter	AL	7/19/1988	F	3	+				1

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
364-08	Lee Haven Area	Sumter	AL	7/19/1988	M	1	+				1
364-09	Lee Haven Area	Sumter	AL	7/19/1988	M	1	+				1
364-10	Lee Haven Area	Sumter	AL	7/19/1988	M	1	+				1
SE00-878	McGiffert Farms	Tuscaloosa	AL	2/27/2001	F	4.5	+				
SE00-879	McGiffert Farms	Tuscaloosa	AL	2/27/2001	F	2.5	+				
SE00-881	McGiffert Farms	Tuscaloosa	AL	2/27/2001	F	2.5	+				
SE00-882	McGiffert Farms	Tuscaloosa	AL	2/27/2001	F	3.5	+				
SE00-883	McGiffert Farms	Tuscaloosa	AL	2/27/2001	F	2.5	+				
EHRL-0111	Mulberry Fork WMA	Tuscaloosa/ Walker	AL	11/24/2000	F	.5	-				
EHRL-0112	Mulberry Fork WMA	Tuscaloosa/ Walker	AL	11/25/2000	M	4.5	-				
EHRL-0113	Mulberry Fork WMA	Tuscaloosa/ Walker	AL	12/8/2000	M	6.5	-				
EHRL-0114	Mulberry Fork WMA	Tuscaloosa/ Walker	AL	1/20/2001	M	1.5	-				
EHRL-0115	Mulberry Fork WMA	Tuscaloosa/ Walker	AL	1/20/2001	M	5.25	-				
SE93-408	Bull Pen Hunting Club	Washington	AL	12/26/1993		1.5	-				
SE93-409	Bull Pen Hunting Club	Washington	AL	12/26/1993		1.5	-				
SE93-410	Bull Pen Hunting Club	Washington	AL	12/26/1993		0.5	-				
SE93-411	Bull Pen Hunting Club	Washington	AL	12/27/1993		4.5	-				
SE93-412	Bull Pen Hunting Club	Washington	AL	12/27/1993		1.5	-				
542-1	White River NWR	Arkansas	AR	9/8/1997	F	5	+	-	-		1
542-4	White River NWR	Arkansas	AR	9/8/1997	F	4.5	+	-			1
542-5	White River NWR	Arkansas	AR	9/8/1997	F	6	+	-			2
542-2	White River NWR	Arkansas	AR	9/8/1997	F	2	-	-			1
542-3	White River NWR	Arkansas	AR	9/8/1997	F		-	-			1
494-2	Overflow NWR	Ashley	AR	8/22/1994	F	3.5	+				1
494-4	Overflow NWR	Ashley	AR	8/22/1994	M	1.5	+				2
494-5	Overflow NWR	Ashley	AR	8/22/1994	F	3.5	+				1
494-1	Overflow NWR	Ashley	AR	8/22/1994	M	1.5	-				0
494-3	Overflow NWR	Ashley	AR	8/22/1994	M	3.5	-				1

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
371-2	Felsenthal NWR	Ashley/ Union	AR	9/16/1988	M	1.5	+				1
371-3	Felsenthal NWR	Ashley/ Union	AR	9/16/1988	F	1.5	+				1
371-4	Felsenthal NWR	Ashley/ Union	AR	9/16/1988	F	1.5	+				1
371-5	Felsenthal NWR	Ashley/ Union	AR	9/16/1988	M	1.5	+				1
493-1	Felsenthal NWR	Ashley/ Union	AR	8/22/1994	M	1.5	+				1
493-2	Felsenthal NWR	Ashley/ Union	AR	8/22/1994	F	2.5	+				1
493-3	Felsenthal NWR	Ashley/ Union	AR	8/22/1994	F	4.5	+				1
493-4	Felsenthal NWR	Ashley/ Union	AR	8/22/1994	F	3.5	+				1
493-5	Felsenthal NWR	Ashley/ Union	AR	8/22/1994	F	2.5	+				1
541-1	Felsenthal NWR	Ashley/ Union	AR	9/6/1997	F	1.5	+	-			1
541-2	Felsenthal NWR	Ashley/ Union	AR	9/6/1997	M	2.5	+	-			1
541-3	Felsenthal NWR	Ashley/ Union	AR	9/6/1997	M	1.5	+	-			1
541-4	Felsenthal NWR	Ashley/ Union	AR	9/6/1997	F	5	+	-	-		1
541-5	Felsenthal NWR	Ashley/ Union	AR	9/6/1997	F	3.5	+	-	-		1
371-1	Felsenthal NWR	Ashley/ Union	AR	9/16/1988	M	1.5	-				1
541-6	Felsenthal NWR	Ashley/ Union	AR	9/6/1997	M	0.25	-	-	-		1
541-7	Felsenthal NWR	Ashley/ Union	AR	9/6/1997	M	0.25	-	-	-		1

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
588-1	Pea Ridge Nat'l Military Park	Benton	AR	9/12/2000	M	1.5	+	-	-		3
588-2	Pea Ridge Nat'l Military Park	Benton	AR	9/12/2000	F	1	+	-	-		3
588-3	Pea Ridge Nat'l Military Park	Benton	AR	9/12/2000	F	5.5	+	-	-		3
588-4	Pea Ridge Nat'l Military Park	Benton	AR	9/12/2000	F	2.5	+	-	-		3
588-5	Pea Ridge Nat'l Military Park	Benton	AR	9/12/2000	F	3.5	+	-	-		3
588-6	Pea Ridge Nat'l Military Park	Benton	AR	9/12/2000	F	0.5	+	+	5 (b)	4 (b)	2
SE01-032	Felsenthal NWR	Bradley	AR	11/2/2001	M	1.5	+	-	-		
SE01-033	Felsenthal NWR	Bradley	AR	11/2/2001	M	4.5	+				
SE01-036	Felsenthal NWR	Bradley	AR	11/2/2001	M	2.5	+				
284-1	The Ross Foundation Property	Clarke	AR	9/14/1983	M	1	+				1
284-2	The Ross Foundation Property	Clarke	AR	9/14/1983	F	1	+				1
284-3	The Ross Foundation Property	Clarke	AR	9/14/1983	M	1	+				1
284-4	The Ross Foundation Property	Clarke	AR	9/14/1983	F	0.5	+				1
284-5	The Ross Foundation Property	Clarke	AR	9/14/1983	M	0.5	-				1
528-2	Dave Donaldson/Black River WMA	Clay	AR	8/21/1996	F	2.5	+	-			0
528-3	Dave Donaldson/Black River WMA	Clay	AR	8/21/1996	F	1.5	+	-			1
528-4	Dave Donaldson/Black River WMA	Clay	AR	8/21/1996	F	2.5	+	-			1
528-1	Dave Donaldson/Black River WMA	Clay	AR	8/21/1996	F	2.5	-	-			0
528-5	Dave Donaldson/Black River WMA	Clay	AR	8/21/1996	F	3.5	-	-			1
520-1	Ed Gordon/Point Remove WMA	Conway	AR	9/15/1995	F	5.5	+	-			1
520-2	Ed Gordon/Point Remove WMA	Conway	AR	9/15/1995	F	2.5	+	-			1
520-3	Ed Gordon/Point Remove WMA	Conway	AR	9/15/1995	M	2.5	+	-			1
520-4	Ed Gordon/Point Remove WMA	Conway	AR	9/15/1995	M	1.5	+	-			2
520-5	Ed Gordon/Point Remove WMA	Conway	AR	9/15/1995	F	3.5	+	-			1
627-1	Wapanocca NWR	Crittendon	AR	9/9/2002		7	-	-	-		0
627-2	Wapanocca NWR	Crittendon	AR	9/9/2002		1	-	-	-		0
627-3	Wapanocca NWR	Crittendon	AR	9/9/2002		1.5	-	-	-		0
627-4	Wapanocca NWR	Crittendon	AR	9/9/2002		1.5	-	-	-		0
627-5	Wapanocca NWR	Crittendon	AR	9/9/2002		2.5	-	-	-		0
492-3	Management Unit 9	Franklin	AR	8/24/1994	F	1.5	+				1
492-4	Management Unit 9	Franklin	AR	8/24/1994	F	3.5	+				1
492-1	Management Unit 9	Franklin	AR	8/24/1994	F	1.5	-				1
492-2	Management Unit 9	Franklin	AR	8/24/1994	F	2.5	-				1
492-5	Management Unit 9	Franklin	AR	8/24/1994	M	1.5	-				1

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
352-02		Fulton	AR	9/15/1987	F	2.5	+				2
352-03		Fulton	AR	9/15/1987	M	1.5	+				1
352-04		Fulton	AR	9/15/1987	F	3.5	+				2
352-05		Fulton	AR	9/15/1987	F	2.5	+				1
352-01		Fulton	AR	9/15/1987	M	1.5	-				2
460-1	Scatter Creek WMA/W.E. Brewer	Greene	AR	9/9/1992			+				1
460-6	Scatter Creek WMA/W.E. Brewer	Greene	AR	9/9/1992			+				1
582-1	Grandview Prarie WMA	Hempstead	AR	9/22/1999	F	1.5	+				1
582-3	Grandview Prarie WMA	Hempstead	AR	9/22/1999	F	2	+				2
582-4	Grandview Prarie WMA	Hempstead	AR	9/22/1999	F	2	+				2
582-2	Grandview Prarie WMA	Hempstead	AR	9/22/1999	F	2	-				1
582-5	Grandview Prarie WMA	Hempstead	AR	9/22/1999	F	2	-				1
555-1	Lake Catherine SP, Diamondhead Area	Hot Springs	AR	7/28/1998	F	3	+				3
555-2	Lake Catherine SP, Diamondhead Area	Hot Springs	AR	7/28/1998	F	3	+				3
555-3	Lake Catherine SP, Diamondhead Area	Hot Springs	AR	7/28/1998	M	1	-				3
555-4	Lake Catherine SP, Diamondhead Area	Hot Springs	AR	7/28/1998	M	1	-				3
555-5	Lake Catherine SP, Diamondhead Area	Hot Springs	AR	7/28/1998	F	6	-				3
518-4	Wickes Area	Howard	AR	9/14/1995	F	2.5	+	-			1
518-5	Wickes Area	Howard	AR	9/14/1995	F	2.5	+	-			1
518-6	Wickes Area	Howard	AR	9/14/1995	F	4.5	+	-			1
518-8	Wickes Area	Howard	AR	9/14/1995	F	1.5	+	-			2
352-06		Izard	AR	9/15/1987	M	2.5	+				1
352-07		Izard	AR	9/15/1987	F	1.5	+				2
352-08		Izard	AR	9/15/1987	M	1.5	+				1
352-09		Izard	AR	9/15/1987	F	5.5	+				1
352-10		Izard	AR	9/15/1987	F	2.5	+				2
350-1	Pine Bluff Arsenal	Jefferson	AR	9/17/1987	F	4.5	+				3
350-2	Pine Bluff Arsenal	Jefferson	AR	9/17/1987	M	5.5	+				3
350-3	Pine Bluff Arsenal	Jefferson	AR	9/17/1987	F	7	+				2

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
350-4	Pine Bluff Arsenal	Jefferson	AR	9/17/1987	M	2.5	+				3
350-5	Pine Bluff Arsenal	Jefferson	AR	9/17/1987	F	2.5	-				3
490-4	Brown's Apple Orchard	Johnson	AR	8/24/1994	F	2.5	+				2
490-5	Brown's Apple Orchard	Johnson	AR	8/24/1994	M	1	+				1
490-1	Brown's Apple Orchard	Johnson	AR	8/24/1994	F	1	-				2
490-2	Brown's Apple Orchard	Johnson	AR	8/24/1994	M	1.5	-				1
490-3	Brown's Apple Orchard	Johnson	AR	8/24/1994	F	1	-				1
311-01	Lafayette WMA	Lafayette	AR	8/20/1985	F	3	+				1
311-02	Lafayette WMA	Lafayette	AR	8/20/1985	M	2	+				1
311-03	Lafayette WMA	Lafayette	AR	8/20/1985	F	7	+				1
311-04	Lafayette WMA	Lafayette	AR	8/20/1985	F	2	+				1
311-05	Lafayette WMA	Lafayette	AR	8/20/1985	F	4	+				1
527-2	Shirey Bay/Rainey Brake WMA	Lawrence	AR	8/21/1996	F	3	+	-	-		1
527-4	Shirey Bay/Rainey Brake WMA	Lawrence	AR	8/21/1996	F	5.5	+	-	-		2
527-5	Shirey Bay/Rainey Brake WMA	Lawrence	AR	8/21/1996	F	2.5	+	-	-		0
527-1	Shirey Bay/Rainey Brake WMA	Lawrence	AR	8/21/1996	F	4.5	-	-			1
527-3	Shirey Bay/Rainey Brake WMA	Lawrence	AR	8/21/1996	F	4	-	-	-		1
527-6	Shirey Bay/Rainey Brake WMA	Lawrence	AR	8/21/1996	F	2.5	-	-	-		3
556-1	St. Francis Forest WMA	Lee/Phillips	AR	7/30/1998	F	7	+				1
556-2	St. Francis Forest WMA	Lee/Phillips	AR	7/30/1998	F	7	+				1
556-3	St. Francis Forest WMA	Lee/Phillips	AR	7/30/1998	F	5	+				1
556-4	St. Francis Forest WMA	Lee/Phillips	AR	7/30/1998	F	3	-				1
556-5	St. Francis Forest WMA	Lee/Phillips	AR	7/30/1998	F	8	-				1
264-06	Mountain Magazine	Logan/Yell	AR	7/31/1982	F	1	+				1
264-07	Mountain Magazine	Logan/Yell	AR	7/31/1982	F	3	+				1
264-08	Mountain Magazine	Logan/Yell	AR	7/31/1982	F	4	+				1
264-09	Mountain Magazine	Logan/Yell	AR	7/31/1982	M	2	+				1
264-10	Mountain Magazine	Logan/Yell	AR	7/31/1982	F	1	+				1
491-1	Don Huet Farm (Unit 1)	Madison	AR	8/24/1994	F	4.5	+				1
491-2	Don Huet Farm (Unit 1)	Madison	AR	8/24/1994	F	4.5	+				1
491-3	Don Huet Farm (Unit 1)	Madison	AR	8/24/1994	F	2.5	+				1
491-5	Don Huet Farm (Unit 1)	Madison	AR	8/24/1994	F	5.5	+				2
491-4	Don Huet Farm (Unit 1)	Madison	AR	8/24/1994	F	2.5	-				1
463-1	Big Lake NWR	Mississippi	AR	9/22/1992	M	1.5	-				0

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
463-2	Big Lake NWR	Mississippi	AR	9/22/1992	F	3.5	-				0
463-3	Big Lake NWR	Mississippi	AR	9/22/1992	F	4.5	-				0
463-4	Big Lake NWR	Mississippi	AR	9/22/1992	F	3.5	-				0
463-5	Big Lake NWR	Mississippi	AR	9/22/1992	M	1.5	-				0
543-1	Cache River NWR	Monroe/ Phillips	AR	9/9/1997	F	2.5	+	-	-		1
543-2	Cache River NWR	Monroe/ Phillips	AR	9/9/1997	F	3.5	+	-	-		1
543-3	Cache River NWR	Monroe/ Phillips	AR	9/9/1997	F	4.5	+	-	-		0
543-6	Cache River NWR	Monroe/ Phillips	AR	9/9/1997	F	0.25	+	+	5 (b)	-	0
543-4	Cache River NWR	Monroe/ Phillips	AR	9/9/1997	F	1.5	-	-	-		0
543-5	Cache River NWR	Monroe/ Phillips	AR	9/9/1997	F	2.5	-	-			0
372-1	Muddy Creek WMA	Montgomery	AR	9/15/1988	F	3	+				1
372-4	Muddy Creek WMA	Montgomery	AR	9/15/1988	F	3	+				1
372-2	Muddy Creek WMA	Montgomery	AR	9/15/1988	M	1	-				1
372-3	Muddy Creek WMA	Montgomery	AR	9/15/1988	F	2	-				1
372-5	Muddy Creek WMA	Montgomery	AR	9/15/1988	F	2	-				1
294-01	Bayou DeView WMA	Poinsett	AR	9/11/1984	M	1.5	-				0
294-02	Bayou DeView WMA	Poinsett	AR	9/11/1984	M	1.5	-				0
294-03	Bayou DeView WMA	Poinsett	AR	9/11/1984	F	2.5	-				0
294-04	Bayou DeView WMA	Poinsett	AR	9/11/1984	F	2.5	-				0
294-05	Bayou DeView WMA	Poinsett	AR	9/11/1984	F	7.5	-				0
423-2	Caney Creek WMA	Polk	AR	7/23/1991	F	4	+				2
423-3	Caney Creek WMA	Polk	AR	7/23/1991	F	4	+				2
423-4	Caney Creek WMA	Polk	AR	7/23/1991	F	2	+				2
423-5	Caney Creek WMA	Polk	AR	7/23/1991	M	1	+				2
423-1	Caney Creek WMA	Polk	AR	7/23/1991	F	1	-				1
AR Pope 06	Holla Bend NWR	Pope	AR	10/1/1985			+				
AR Pope 17	Holla Bend NWR	Pope	AR	10/1/1985			+				
AR Pope 47	Holla Bend NWR	Pope	AR	10/1/1985			+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
AR Pope 19	Holla Bend NWR	Pope	AR	10/1/1985			-				
AR Pope 30	Holla Bend NWR	Pope	AR	10/1/1985			-				
283-1	Wattensaw WMA	Prairie	AR	9/14/1983	F	2	+				1
283-3	Wattensaw WMA	Prairie	AR	9/14/1983	F	1	+				1
283-4	Wattensaw WMA	Prairie	AR	9/14/1983	F	3	+				1
283-5	Wattensaw WMA	Prairie	AR	9/14/1983	F	3	+				1
283-2	Wattensaw WMA	Prairie	AR	9/14/1983	M	1	-				1
409-06	private lands in south Searcy	Searcy	AR	9/19/1990	M	1.5	+				1
409-07	private lands in south Searcy	Searcy	AR	9/19/1990	F	3.5	+				2
409-08	private lands in south Searcy	Searcy	AR	9/19/1990	M	1.5	+				1
409-09	private lands in south Searcy	Searcy	AR	9/19/1990	F	1.5	+				1
409-10	private lands in south Searcy	Searcy	AR	9/19/1990	F	2.5	+				1
SE91-411	Fort Chaffee	Sebastian	AR	12/30/1991	M	3.5	+				
SE91-412	Fort Chaffee	Sebastian	AR	12/30/1991		0	+				
SE91-416	Fort Chaffee	Sebastian	AR	12/30/1991	F	6.5	+				
SE91-423	Fort Chaffee	Sebastian	AR	12/30/1991	F	2.5	+				
SE91-427	Fort Chaffee	Sebastian	AR	12/30/1991	F	0.5	+				
SE91-431	Fort Chaffee	Sebastian	AR	12/30/1991	M	1.5	+				
SE91-442	Fort Chaffee	Sebastian	AR	12/30/1991	F	1.5	+				
SE91-444	Fort Chaffee	Sebastian	AR	12/30/1991	F	2.5	+				
SE91-445	Fort Chaffee	Sebastian	AR	12/30/1991	F	4.5	+				
SE91-446	Fort Chaffee	Sebastian	AR	12/30/1991	F	0.5	+				
SE91-447	Fort Chaffee	Sebastian	AR	12/30/1991	F	3.5	+				
SE91-448	Fort Chaffee	Sebastian	AR	12/30/1991	F	5.5	+				
SE91-449	Fort Chaffee	Sebastian	AR	12/30/1991	F	3.5	+				
280-01	Fort Chaffee WMA	Sebastian	AR	8/1/1983	F	4	+				1
280-02	Fort Chaffee WMA	Sebastian	AR	8/1/1983	F	1	+				1
280-03	Fort Chaffee WMA	Sebastian	AR	8/1/1983	M	1	+				1
280-04	Fort Chaffee WMA	Sebastian	AR	8/1/1983	F	2	+				2
280-05	Fort Chaffee WMA	Sebastian	AR	8/1/1983	M	1	+				1
SE91-413	Fort Chaffee	Sebastian	AR	12/30/1991	F	3.5	-				
SE91-414	Fort Chaffee	Sebastian	AR	12/30/1991	M	1.5	-				
SE91-415	Fort Chaffee	Sebastian	AR	12/30/1991	F	4.5	-				
SE91-417	Fort Chaffee	Sebastian	AR	12/30/1991	F	0.5	-				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	VLPT	120-kDa	LST
SE91-418	Fort Chaffee	Sebastian	AR	12/30/1991	M	1.5	-				
SE91-419	Fort Chaffee	Sebastian	AR	12/30/1991	M	1.5	-				
SE91-420	Fort Chaffee	Sebastian	AR	12/30/1991	F	2.5	-				
SE91-421	Fort Chaffee	Sebastian	AR	12/30/1991	F	3.5	-				
SE91-422	Fort Chaffee	Sebastian	AR	12/30/1991	M	0.5	-				
SE91-424	Fort Chaffee	Sebastian	AR	12/30/1991	F	4.5	-				
SE91-425	Fort Chaffee	Sebastian	AR	12/30/1991	F	5.5	-				
SE91-426	Fort Chaffee	Sebastian	AR	12/30/1991	F	1.5	-				
SE91-428	Fort Chaffee	Sebastian	AR	12/30/1991	F	2.5	-				
SE91-429	Fort Chaffee	Sebastian	AR	12/30/1991	F	3.5	-				
SE91-430	Fort Chaffee	Sebastian	AR	12/30/1991	F	4.5	-				
SE91-432	Fort Chaffee	Sebastian	AR	12/30/1991	F	3.5	-				
SE91-433	Fort Chaffee	Sebastian	AR	12/30/1991	F	0.5	-				
SE91-434	Fort Chaffee	Sebastian	AR	12/30/1991	F	4.5	-				
SE91-435	Fort Chaffee	Sebastian	AR	12/30/1991	F	2.5	-				
SE91-436	Fort Chaffee	Sebastian	AR	12/30/1991	F	0.5	-				
SE91-437	Fort Chaffee	Sebastian	AR	12/30/1991	F	0.5	-				
SE91-438	Fort Chaffee	Sebastian	AR	12/30/1991	F	1.5	-				
SE91-439	Fort Chaffee	Sebastian	AR	12/30/1991	M	0.5	-				
SE91-440	Fort Chaffee	Sebastian	AR	12/30/1991	M	0.5	-				
SE91-441	Fort Chaffee	Sebastian	AR	12/30/1991	M	1.5	-				
SE91-443	Fort Chaffee	Sebastian	AR	12/30/1991	F	1.5	-				
SE91-450	Fort Chaffee	Sebastian	AR	12/30/1991	F	1.5	-				
612-6	Pond Creek NWR	Sevier	AR	9/19/2001	F	0.33	+	+	5 (b)	3 (b)	1
612-1	Pond Creek NWR	Sevier	AR	9/19/2001	M	1.1	+	-	-		2
612-2	Pond Creek NWR	Sevier	AR	9/19/2001	M	4.5	+				1
612-3	Pond Creek NWR	Sevier	AR	9/19/2001	M	2.5	+				1
352-11		Sharp	AR	9/15/1987	M	1.5	+				1
352-12		Sharp	AR	9/15/1987	M	1.5	+				1
352-13		Sharp	AR	9/15/1987	M	1.5	+				2
352-14		Sharp	AR	9/15/1987	M	2.5	+				2
352-15		Sharp	AR	9/15/1987	F	1.5	+				1
280-11	Sylamore WMA	Stone	AR	8/3/1983	F	2	+				1
280-12	Sylamore WMA	Stone	AR	8/3/1983	F	4	+				1

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
280-13	Sylamore WMA	Stone	AR	8/3/1983	F	4	+				1
280-14	Sylamore WMA	Stone	AR	8/3/1983	F	2	+				1
280-15	Sylamore WMA	Stone	AR	8/3/1983	M	1	+				2
SE91-290	Shallow Lake	Union	AR	11/8/1991	F	4.5	+				
SE91-291	Shallow Lake	Union	AR	11/22/1991	F	3.5	+				
SE91-292	Shallow Lake	Union	AR	11/22/1991	F	0.5	+				
SE91-293	Shallow Lake	Union	AR	11/22/1991	F	1.5	+				
SE91-294	Shallow Lake	Union	AR	11/22/1991	M	0.5	+				
SE91-295	Shallow Lake	Union	AR	11/22/1991	F	2.5	+				
SE91-296	Shallow Lake	Union	AR	11/23/1991	F	2.5	+				
421-1	Felsenthal NWR	Union	AR	7/24/1991	M	1	+				0
421-2	Felsenthal NWR	Union	AR	7/24/1991	F	5	+				1
421-3	Felsenthal NWR	Union	AR	7/24/1991	F	2	+				1
421-4	Felsenthal NWR	Union	AR	7/24/1991	F	8	+				0
421-5	Felsenthal NWR	Union	AR	7/24/1991	F	1	+				1
258-2	Felsenthal NWR	Union	AR	8/5/1982	F	4	+				1
258-3	Felsenthal NWR	Union	AR	8/5/1982	F	3	+				1
258-4	Felsenthal NWR	Union	AR	8/5/1982	M	1	+				1
258-5	Felsenthal NWR	Union	AR	8/5/1982	M	2	+				1
SE01-034	Felsenthal NWR	Union	AR	11/2/2001	M	2.5	+				
258-1	Felsenthal NWR	Union	AR	8/5/1982	F	1	-				1
SE01-030	Felsenthal NWR	Union	AR	11/2/2001	F	4.5	-				
314-01	Felsenthal NWR	Union/ Bradley	AR	8/24/1985	F	1	+				1
314-03	Felsenthal NWR	Union/ Bradley	AR	8/24/1985	F	3	+				1
314-04	Felsenthal NWR	Union/ Bradley	AR	8/24/1985	F	3	+				1
314-05	Felsenthal NWR	Union/ Bradley	AR	8/24/1985	F	4	+				1
314-02	Felsenthal NWR	Union/ Bradley	AR	8/24/1985	F	3	-				1
SE91-034	Gulf Mountain WMA	Van Buren	AR	10/19/1991	M	0.5	+				
SE91-035	Gulf Mountain WMA	Van Buren	AR	10/19/1991	M	1.5	+				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
SE91-037	Gulf Mountain WMA	Van Buren	AR	10/19/1991	M	1.5	+				
SE91-038	Gulf Mountain WMA	Van Buren	AR	10/19/1991	F	2.5	+				
SE91-040	Gulf Mountain WMA	Van Buren	AR	10/19/1991	M	1.5	+				
SE91-041	Gulf Mountain WMA	Van Buren	AR	10/20/1991	F	2.5	+				
SE91-042	Gulf Mountain WMA	Van Buren	AR	10/20/1991	M	1.5	+				
SE91-043	Gulf Mountain WMA	Van Buren	AR	10/23/1991	M	2.5	+				
SE91-044	Gulf Mountain WMA	Van Buren	AR	11/9/1991	F	5.5	+				
SE91-045	Gulf Mountain WMA	Van Buren	AR	11/9/1991	M	1.5	+				
SE91-046	Gulf Mountain WMA	Van Buren	AR	11/9/1991	M	2.5	+				
SE91-048	Gulf Mountain WMA	Van Buren	AR	11/10/1991	M	0.5	+				
SE91-049	Gulf Mountain WMA	Van Buren	AR	11/10/1991	M	1.5	+				
SE91-050	Gulf Mountain WMA	Van Buren	AR	11/13/1991	M	1.5	+				
SE91-051	Gulf Mountain WMA	Van Buren	AR	11/13/1991	M	1.5	+				
SE91-039	Gulf Mountain WMA	Van Buren	AR	10/19/1991	F	3.5	-				
628-1	Cache River NWR	Woodruff	AR	9/12/2002	M	1.5	+	-	-		1
628-4	Cache River NWR	Woodruff	AR	9/12/2002	F	4.5	+	-	-		2
628-5	Cache River NWR	Woodruff	AR	9/12/2002	M	3.5	+	-	5 (b,c)	4 (c)	2
628-2	Cache River NWR	Woodruff	AR	9/12/2002	F	9.5+	-	- (b)	- (b), 5 (c)		0
628-3	Cache River NWR	Woodruff	AR	9/12/2002	F	4.5	-	-	-		1
553-3	Mount Nebo State Park	Yell	AR	2/23/1998	F	0.5	+				1
553-5	Mount Nebo State Park	Yell	AR	2/23/1998	M	0.5	+				1
554-1	Mount Nebo State Park	Yell	AR	7/28/1998	F	6	+				1
554-2	Mount Nebo State Park	Yell	AR	7/28/1998	F	5	+				2
554-3	Mount Nebo State Park	Yell	AR	7/28/1998	F	3	+				1
554-4	Mount Nebo State Park	Yell	AR	7/28/1998	M	1	+				1
554-5	Mount Nebo State Park	Yell	AR	7/28/1998	F	2	+				1
553-1	Mount Nebo State Park	Yell	AR	2/23/1998	F	4.5	-				1
553-2	Mount Nebo State Park	Yell	AR	2/23/1998	F	3.5	-				1
553-4	Mount Nebo State Park	Yell	AR	2/23/1998	F	5.5	-				1
273-01	The Everglades Conservation Area 3-A, Levee #5-North and #28-South	Broward	FL	7/16/1982	F	0.75	-				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
273-02	The Everglades Conservation Area 3-A, Levee #5-North and #28-South	Broward	FL	7/16/1982	M	0.33	-				
273-03	The Everglades Conservation Area 3-A, Levee #5-North and #28-South	Broward	FL	7/16/1982	F	2	-				
273-04	The Everglades Conservation Area 3-A, Levee #5-North and #28-South	Broward	FL	7/16/1982	M	0.33	-				
273-05	The Everglades Conservation Area 3-A, Levee #5-North and #28-South	Broward	FL	7/16/1982	M	0.33	-				
EHRL-1076		Charlotte	FL		M	2.5	-				
EHRL-1077		Charlotte	FL		M	1.5	-	-	-		
EHRL-1078		Charlotte	FL		M	1.5	-	-	-		
EHRL-1079		Charlotte	FL		M	2.5	-				
468-01	Florida Panther NWR	Collier	FL	11/4/1992			-				
468-02	Florida Panther NWR	Collier	FL	11/4/1992			-				
468-03	Florida Panther NWR	Collier	FL	11/4/1992			-				
468-04	Florida Panther NWR	Collier	FL	11/4/1992			-				
468-05	Florida Panther NWR	Collier	FL	11/4/1992			-				
FL Dade 1		Dade/ Broward	FL				-				
FL Dade 2		Dade/ Broward	FL				-				
FL Dade 3		Dade/ Broward	FL				-				
FL Dade 4		Dade/ Broward	FL				-				
FL Dade 5		Dade/ Broward	FL				-				
337-01	St. Vincent NWR	Franklin	FL	8/18/1986	F	4	+				1
337-04	St. Vincent NWR	Franklin	FL	8/18/1986	F	3	+				1
337-05	St. Vincent NWR	Franklin	FL	8/18/1986	M	2	+				0
376-1	St. Vincent NWR	Franklin	FL	9/21/1988	F	2.5	+				1
376-2	St. Vincent NWR	Franklin	FL	9/21/1988	F	3.5	+				1
376-3	St. Vincent NWR	Franklin	FL	9/21/1988	M	2.5	+				1
376-4	St. Vincent NWR	Franklin	FL	9/21/1988	M	1.5	+				1

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
376-5	St. Vincent NWR	Franklin	FL	9/21/1988	F	1.5	+				1
453-1	St. Vincent NWR	Franklin	FL	9/17/1992	M	1	+				2
453-2	St. Vincent NWR	Franklin	FL	9/17/1992	F	1	+				1
531-1	St. Vincent NWR	Franklin	FL	10/2/1996	F	2.5	+	-	-		1
531-2	St. Vincent NWR	Franklin	FL	10/2/1996	F	2.5	+	-	-		1
531-3	St. Vincent NWR	Franklin	FL	10/2/1996	F	1.5	+	-	-		1
531-4	St. Vincent NWR	Franklin	FL	10/2/1996	F	1.5	+	-	-		0
531-5	St. Vincent NWR	Franklin	FL	10/2/1996	M	0.75	+	-	-		1
298-01	St. Vincent NWR	Franklin	FL	10/23/1984	F	4.5	+				1
298-03	St. Vincent NWR	Franklin	FL	10/23/1984	M	1	+				1
337-02	St. Vincent NWR	Franklin	FL	8/18/1986	F	2	-				1
337-03	St. Vincent NWR	Franklin	FL	8/18/1986	M	0.5	-				1
453-3	St. Vincent NWR	Franklin	FL	9/17/1992	M	2.5	-				1
453-4	St. Vincent NWR	Franklin	FL	9/17/1992	M	3.5	-				1
453-5	St. Vincent NWR	Franklin	FL	9/17/1992	F	3.5	-				1
298-02	St. Vincent NWR	Franklin	FL	10/23/1984	F	2.5	-				1
298-04	St. Vincent NWR	Franklin	FL	10/23/1984	M	1	-				1
298-05	St. Vincent NWR	Franklin	FL	10/23/1984	M	1	-				1
288-1	St. Marks NWR	Leon	FL	9/1/1983	M	1.5	+				
288-2	St. Marks NWR	Leon	FL	9/1/1983	F	3.5	+				
288-3	St. Marks NWR	Leon	FL	9/1/1983	F	3.5	+				
288-4	St. Marks NWR	Leon	FL	9/1/1983	M	1.5	+				
288-5	St. Marks NWR	Leon	FL	9/1/1983	M	1.5	+				
530-1	Lower Suwannee NWR	Levy	FL	9/30/1996	F	3.5	+				1
530-2	Lower Suwannee NWR	Levy	FL	9/30/1996	F	5.5	+				1
530-3	Lower Suwannee NWR	Levy	FL	9/30/1996	M	2.5	+				1
530-4	Lower Suwannee NWR	Levy	FL	9/30/1996	F	3.5	+				1
530-5	Lower Suwannee NWR	Levy	FL	9/30/1996	F	0.5	+				1
EHRL-0935		Levy	FL	10/26/2002	M	1.5	+	-	-		
EHRL-0937	Goethe WMA	Levy	FL	10/26/2002	M	1.5	+	+	4 (b)	3 (b)	
EHRL-0941		Levy	FL	10/25/2002			+				
EHRL-0943		Levy	FL	10/25/2002	M	2.5	+				
EHRL-0938		Levy	FL	10/26/2002	M	2.5	-				
FL Marion 1		Marion	FL				+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
FL Marion 4		Marion	FL				+				
FL Marion 2		Marion	FL				-				
FL Marion 3		Marion	FL				-				
FL Marion 5		Marion	FL				-				
KD 98-1	National Key Deer Refuge	Monroe	FL				-				
KD 98-2	National Key Deer Refuge	Monroe	FL				-				
KD 98-3	National Key Deer Refuge	Monroe	FL				-				
KD 98-4	National Key Deer Refuge	Monroe	FL				-				
KD 98-5	National Key Deer Refuge	Monroe	FL				-				
KD 01-1	National Key Deer Refuge	Monroe	FL				-				
KD 01-2	National Key Deer Refuge	Monroe	FL				-				
KD 01-3	National Key Deer Refuge	Monroe	FL				-				
KD 01-4	National Key Deer Refuge	Monroe	FL				-				
KD 01-5	National Key Deer Refuge	Monroe	FL				-				
470-02	National Key Deer Refuge	Monroe	FL	5/1/1993			-				
470-03	National Key Deer Refuge	Monroe	FL	3/19/1992	F	3.5	-				0
470-05	National Key Deer Refuge	Monroe	FL	7/4/1992	F	.5	-				0
470-07	National Key Deer Refuge	Monroe	FL	7/20/1992	F	2.5	-				0
470-10	National Key Deer Refuge	Monroe	FL	10/27/1992	F	.25	-				0
EHRL-0203	White Oak Conservation Center	Nassau	FL	7/10/2001	F	1.0	+	-	-		1
EHRL-0204	White Oak Conservation Center	Nassau	FL	7/10/2001	M	1.0	+	-	-		1
EHRL-0205	White Oak Conservation Center	Nassau	FL	7/10/2001	F	2.5	+	-	-		2
EHRL-0206	White Oak Conservation Center	Nassau	FL	7/10/2001	F	2.5	+	-	-		1
EHRL-0207	White Oak Conservation Center	Nassau	FL	7/10/2001	F	2.5	+	-	-		1
SE91-111	Tosohatchee WMA	Orange	FL	10/12/1991	F	4.5	+				
SE91-112	Tosohatchee WMA	Orange	FL	10/12/1991	M	3.5	+				
SE91-113	Tosohatchee WMA	Orange	FL	10/12/1991	M	0.5	+				
SE91-114	Tosohatchee WMA	Orange	FL	10/16/1991	F	0	+				
SE91-115	Tosohatchee WMA	Orange	FL	10/16/1991	F	2.5	+				
SE91-116	Tosohatchee WMA	Orange	FL	10/17/1991	F	0.5	+				
SE91-117	Tosohatchee WMA	Orange	FL	10/17/1991	M	1.5	+				
SE91-119	Tosohatchee WMA	Orange	FL	10/20/1991	F	1.5	+				
SE91-120	Tosohatchee WMA	Orange	FL	10/24/1991	F	0.5	+				
SE91-121	Tosohatchee WMA	Orange	FL	11/13/1991	M	1.5	+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE91-122	Tosohatchee WMA	Orange	FL	11/13/1991	F	0.5	+				
SE91-123	Tosohatchee WMA	Orange	FL	11/13/1991	M	3.5	+				
SE91-124	Tosohatchee WMA	Orange	FL	11/13/1991	F	3.5	+				
SE91-125	Tosohatchee WMA	Orange	FL	11/14/1991	F	1.5	+				
SE91-127	Tosohatchee WMA	Orange	FL	11/16/1991	M	2.5	+				
SE91-128	Tosohatchee WMA	Orange	FL	11/17/1991	M	3.5	+				
SE91-130	Tosohatchee WMA	Orange	FL	11/29/1991	M	1.5	+				
SE91-131	Tosohatchee WMA	Orange	FL	11/29/1991	M	2.5	+				
SE91-132	Tosohatchee WMA	Orange	FL	11/30/1991	F	0	+				
SE91-108	Tosohatchee WMA	Orange	FL	10/5/1991	F	4.5	-				
SE91-109	Tosohatchee WMA	Orange	FL	10/6/1991	F	0.5	-				
SE91-110	Tosohatchee WMA	Orange	FL	10/9/1991	M	5.5+	-				
SE91-129	Tosohatchee WMA	Orange	FL	11/29/1991	M	3.5	-				
SE95-0219	Three Lakes WMA	Osceola	FL	6/17/1905		1.5	-				
SE95-0220	Three Lakes WMA	Osceola	FL	6/17/1905		1	-				
SE95-0221	Three Lakes WMA	Osceola	FL	6/17/1905		2.5	-				
SE95-0222	Three Lakes WMA	Osceola	FL	6/17/1905		2.5	-				
SE95-0223	Three Lakes WMA	Osceola	FL	6/17/1905		3.5	-				
EHRL-0966	Three Lakes WMA	Osceola	FL	11/9/2002			-				
EHRL-0971	Three Lakes WMA	Osceola	FL	11/9/2002			-				
EHRL-0972	Three Lakes WMA	Osceola	FL	11/9/2002	M		-				
EHRL-0973	Three Lakes WMA	Osceola	FL	11/9/2002	M		-				
EHRL-0976	Three Lakes WMA	Osceola	FL	11/11/2002	M		-				
FL Palm 1		Palm Beach	FL				-				
FL Palm 3		Palm Beach	FL				-				
FL Palm 4		Palm Beach	FL				-				
FL Palm 5		Palm Beach	FL				-				
FL Palm 6		Palm Beach	FL				-				
524-1	Gordon Spratt/Twelve Mile Swamp	St. Johns	FL	2/28/1996	F	0.75	+				0
524-3	Gordon Spratt/Twelve Mile Swamp	St. Johns	FL	2/28/1996	F	1.75	+				0
524-4	Gordon Spratt/Twelve Mile Swamp	St. Johns	FL	2/28/1996	F	2.75	+				0
524-5	Gordon Spratt/Twelve Mile Swamp	St. Johns	FL	2/28/1996	F	3.75	+				1
524-2	Gordon Spratt/Twelve Mile Swamp	St. Johns	FL	2/28/1996	F	2.75	-				1

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
EHRL-0992	Big Bend/Spring Warrior Spring Creek Unit	Taylor	FL	11/16/2002	M	2.5	+	-	-		
EHRL-0993	Dallus Creek Check Station	Taylor	FL	11/9/2002	M		+	-	-		
EHRL-0936	Tide City	Taylor	FL	10/25/2002			+				
EHRL-0940		Taylor	FL	10/25/2002	M	1.5	+	-	4 (b)	-	
EHRL-0939		Taylor	FL	10/26/2002	M	4+	-				
EHRL-0958	Rima Ridge WMA	Volusia	FL	11/7/2002	M	4.5	+				
EHRL-0959	Rima Ridge WMA	Volusia	FL	11/7/2002	M	2.5	+				
EHRL-0961	Rima Ridge WMA	Volusia	FL	11/7/2002	M	0.5	+	+	-	-	
EHRL-0960	Rima Ridge WMA	Volusia	FL	11/7/2002	M	2.5	-				
358-1	St. Marks NWR (Wakulla Unit)	Wakulla	FL	9/30/1987	M	1.5	+				3
358-3	St. Marks NWR (Wakulla Unit)	Wakulla	FL	9/30/1987	M	4.5	+				3
358-4	St. Marks NWR (Wakulla Unit)	Wakulla	FL	9/30/1987	F	6.5	+				3
358-5	St. Marks NWR (Wakulla Unit)	Wakulla	FL	9/30/1987	F	3.5	+				3
358-2	St. Marks NWR (Wakulla Unit)	Wakulla	FL	9/30/1987	M	1.5	-				3
FL Walton B		Walton	FL				+				
FL Walton C		Walton	FL				+				
FL Walton E		Walton	FL				+				
FL Walton H		Walton	FL				-				
FL Walton J		Walton	FL				-				
H99-068	Chickasawhatchee WMA	Baker/ Calhoun	GA	10/16/1999	F	2.5	+				
H99-067	Chickasawhatchee WMA	Baker/ Calhoun	GA	10/16/1999	F	3.5	-				
H99-220	Chickasawhatchee WMA	Baker/ Calhoun	GA	11/5/1999	M	3.5	-				
H99-221	Chickasawhatchee WMA	Baker/ Calhoun	GA	11/6/1999	M	1.5	-				
H99-222	Chickasawhatchee WMA	Baker/ Calhoun	GA	12/27/1999	M	3.5	-				
519-1	Red Top Mountain State Park	Bartow/ Cherokee	GA	10/4/1995	F	3.5	-	-			0
519-2	Red Top Mountain State Park	Bartow/ Cherokee	GA	10/4/1995	F	5.5	-	-			0

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
519-3	Red Top Mountain State Park	Bartow/ Cherokee	GA	10/4/1995	F	2.5	-	-			0
519-4	Red Top Mountain State Park	Bartow/ Cherokee	GA	10/4/1995	M	1.5	-	-			0
519-5	Red Top Mountain State Park	Bartow/ Cherokee	GA	10/4/1995	M	5.5	-	-			0
EHRL-0904		Brooks	GA	10/19/2002	F	1.5	-	-	-		
GA Bryan 01	Sterling Bluff	Bryan	GA	7/31/1990			+				
GA Bryan 02	Sterling Bluff	Bryan	GA	7/31/1990			+				
GA Bryan 03	Sterling Bluff	Bryan	GA	7/31/1990			+				
GA Bryan 04	Sterling Bluff	Bryan	GA	7/31/1990			+				
GA Bryan 05	Sterling Bluff	Bryan	GA	7/31/1990			+				
378-1	Kings Bay Submarine Base	Camden	GA	8/29/1988	F	7	+				2
378-2	Kings Bay Submarine Base	Camden	GA	8/29/1988	F	1	+				2
378-3	Kings Bay Submarine Base	Camden	GA	8/29/1988	F	1	+				2
378-4	Kings Bay Submarine Base	Camden	GA	8/29/1988	F	1	+				1
378-5	Kings Bay Submarine Base	Camden	GA	8/29/1988	M	1	+				1
383-1	Okefenokee NWR, West Side	Charlton	GA	9/29/1988	M	4.5	+				
383-2	Okefenokee NWR, West Side	Charlton	GA	9/29/1988	M	3.5	+				
383-3	Okefenokee NWR, West Side	Charlton	GA	9/29/1988	F	2.5	+				
383-5	Okefenokee NWR, West Side	Charlton	GA	9/29/1988	M	1.5	+				
383-4	Okefenokee NWR, West Side	Charlton	GA	9/29/1988	M	2.5	-				
H91-148	Ossabaw Island WMA	Chatham	GA	11/7/1991	F	2.5	+				
H91-149	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	2.5	+				
H91-150	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	5.5	+				
H91-151	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	5.5	+				
H91-152	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	2.5	+				
H91-153	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	2.5	+				
H91-160	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	6.5	+				
H91-161	Ossabaw Island WMA	Chatham	GA	11/7/1991	F	3.5	+				
H91-162	Ossabaw Island WMA	Chatham	GA	11/7/1991	F	0.5	+				
H91-163	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	3.5	+				
H91-167	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	4.5	+				
H91-169	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	3.5	+				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
H91-170	Ossabaw Island WMA	Chatham	GA	11/7/1991	F	5.5	+				
H91-171	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	3.5	+				
H91-172	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	3.5	+				
H91-173	Ossabaw Island WMA	Chatham	GA	11/7/1991	F	4.5	+				
H91-174	Ossabaw Island WMA	Chatham	GA	11/7/1991	F	0.5	+				
H91-175	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	1.5	+				
H91-177	Ossabaw Island WMA	Chatham	GA	11/7/1991	F	0.5	+				
H91-178	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	3.5	+				
H91-179	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	4.5	+				
H91-180	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	2.5	+				
H91-181	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	4.5	+				
487-4	Skidaway Island	Chatham	GA	4/26/1994	F	4	+				2
487-5	Skidaway Island	Chatham	GA	4/26/1994	F	2	+				2
H91-159	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	4.5	-				
H91-164	Ossabaw Island WMA	Chatham	GA	11/7/1991	F	0.5	-				
H91-165	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	1.5	-				
H91-166	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	6.5	-				
H91-168	Ossabaw Island WMA	Chatham	GA	11/7/1991	F	4.5	-				
H91-176	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	2.5	-				
H91-182	Ossabaw Island WMA	Chatham	GA	11/7/1991	M	1.5	-				
487-1	Skidaway Island	Chatham	GA	4/26/1994	F	6	-				2
487-2	Skidaway Island	Chatham	GA	4/26/1994	M	3	-				1
487-3	Skidaway Island	Chatham	GA	4/26/1994	M	2	-				2
416-1	Whitehall Experimental Forest	Clarke	GA	6/27/1991			+				
416-3	Whitehall Experimental Forest	Clarke	GA	6/27/1991			+				
416-5	Whitehall Experimental Forest	Clarke	GA	6/27/1991			+				
451-2	Whitehall Experimental Forest	Clarke	GA	6/29/1992			+				
451-3	Whitehall Experimental Forest	Clarke	GA	6/29/1992			+				
451-4	Whitehall Experimental Forest	Clarke	GA	6/29/1992			+				
451-5	Whitehall Experimental Forest	Clarke	GA	6/29/1992			+				
NIHfawn-12	Mike Dizmanski's	Clarke	GA			0.3	+	+	4 (b,c)	3 (c)	
416-2	Whitehall Experimental Forest	Clarke	GA	6/27/1991			-				
416-4	Whitehall Experimental Forest	Clarke	GA	6/27/1991			-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
451-1	Whitehall Experimental Forest	Clarke	GA	6/29/1992			-				
EHRL-0907		Clinch	GA	10/19/2002	M	2.5	-	-	-		
H00-222		Dooly	GA				+				
H00-224		Dooly	GA				+				
H00-225		Dooly	GA				+				
H00-226		Dooly	GA				+				
H00-227		Dooly	GA				-				
H91-006	Chickasawhatchee WMA	Dougherty	GA	10/18/1991	F	3.5	+				
H91-010	Chickasawhatchee WMA	Dougherty	GA	10/19/1991	F	3.5	+				
H91-096	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	2.5	+				
H91-097	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	M	2.5	+				
H91-098	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	1.5	+				
H91-099	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	1.5	+				
H91-101	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	3.5	+				
H91-103	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	1.5	+				
H91-106	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	1.5	+				
H91-109	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	FM	<4mo.	+				
H91-111	Chickasawhatchee WMA	Dougherty	GA	11/2/1991	F	2.5	+				
H91-001	Chickasawhatchee WMA	Dougherty	GA	10/18/1991	F	3.5	-				
H91-002	Chickasawhatchee WMA	Dougherty	GA	10/18/1991	F	<4 mo	-				
H91-003	Chickasawhatchee WMA	Dougherty	GA	10/18/1991	F	5.5	-				
H91-004	Chickasawhatchee WMA	Dougherty	GA	10/18/1991	M	1.5	-				
H91-005	Chickasawhatchee WMA	Dougherty	GA	10/18/1991	F	3.5	-				
H91-007	Chickasawhatchee WMA	Dougherty	GA	10/18/1991	F	2.5	-				
H91-008	Chickasawhatchee WMA	Dougherty	GA	10/18/1991	F	1.5	-				
H91-009	Chickasawhatchee WMA	Dougherty	GA	10/18/1991	F	2.5	-				
H91-011	Chickasawhatchee WMA	Dougherty	GA	10/19/1991	F	5.5	-				
H91-094	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	M	3.5	-				
H91-095	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	M	4.5	-				
H91-100	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	2.5	-				
H91-102	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	M	2.5	-				
H91-104	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	<4mo.	-				
H91-105	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	3.5	-				
H91-107	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	2.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
H91-108	Chickasawhatchee WMA	Dougherty	GA	11/1/1991	F	3.5	-				
H91-110	Chickasawhatchee WMA	Dougherty	GA	11/2/1991	M	2.5	-				
H91-112	Chickasawhatchee WMA	Dougherty	GA	11/2/1991	F	4.5	-				
EHRL-1125		Echols	GA	12/15/2002	F	2.5	-	-	-		
EHRL-1126		Echols	GA	12/15/2002	F	4.5	-				
EHRL-1127		Echols	GA	12/15/2002	F	3.5	-				
GA Fannin 1	Upper Blue Ridge WMA	Fannin	GA	10/1/1989			-				
GA Fannin 2	Upper Blue Ridge WMA	Fannin	GA	10/1/1989			-				
GA Fannin 3	Upper Blue Ridge WMA	Fannin	GA	10/1/1989			-				
GA Fannin 7	Upper Blue Ridge WMA	Fannin	GA	10/1/1989			-				
GA Fannin 7	Upper Blue Ridge WMA	Fannin	GA	10/1/1989			-				
EHRL-0088	Peachtree City Airport	Fayette	GA	2/21/2001	F	4	+				
EHRL-0089	Peachtree City Airport	Fayette	GA	2/21/2001	F	3	+				
EHRL-0090	Peachtree City Airport	Fayette	GA	2/21/2001	M	0.5	+				
EHRL-0091	Peachtree City Airport	Fayette	GA	2/21/2001	M	3	+				
EHRL-0087	Peachtree City Airport	Fayette	GA	2/21/2001	M	4	-				
H91-451	Berry Farm WMA	Floyd	GA	10/31/1991	M	3.5	-				
H91-452	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-453	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-454	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-455	Berry Farm WMA	Floyd	GA	10/31/1991	M	2.5	-				
H91-457	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-458	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-459	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-460	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-461	Berry Farm WMA	Floyd	GA	10/31/1991	M	2.5	-				
H91-462	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-463	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-465	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-466	Berry Farm WMA	Floyd	GA	11/1/1991	F	0.5	-				
H91-467	Berry Farm WMA	Floyd	GA	11/1/1991	F	4.5	-				
H91-468	Berry Farm WMA	Floyd	GA	11/20/1991	M	1.5	-				
H91-469	Berry Farm WMA	Floyd	GA	11/20/1991	M	3.5	-				
H91-470	Berry Farm WMA	Floyd	GA	11/20/1991	M	1.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
H91-472	Berry Farm WMA	Floyd	GA	11/22/1991	F	0.5	-				
H91-445	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-447	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-448	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H91-449	Berry Farm WMA	Floyd	GA	10/31/1991	M	3.5	-				
H91-450	Berry Farm WMA	Floyd	GA	10/31/1991	M	1.5	-				
H99-080	Berry Farm WMA	Floyd	GA	11/3/1999	M	1.5	-				
H99-081	Berry Farm WMA	Floyd	GA	11/3/1999	M	1.5	-				
H99-083	Berry Farm WMA	Floyd	GA	11/3/1999	M	2.5	-				
H99-087	Berry Farm WMA	Floyd	GA	11/3/1999	M	4.5	-				
H99-088	Berry Farm WMA	Floyd	GA	11/3/1999	M	3.5	-				
Berry 73-1	Berry College	Floyd	GA	3/21/1973			-				
Berry 73-2	Berry College	Floyd	GA	3/21/1973			-				
Berry 73-3	Berry College	Floyd	GA	3/21/1973			-				
Berry 73-4	Berry College	Floyd	GA	3/21/1973			-				
Berry 73-5	Berry College	Floyd	GA	3/21/1973			-				
Berry 79-1	Berry College	Floyd	GA	9/27/1979			-				
Berry 79-2	Berry College	Floyd	GA	9/27/1979			-				
Berry 79-3	Berry College	Floyd	GA	9/27/1979			-				
Berry 79-4	Berry College	Floyd	GA	9/27/1979			-				
Berry 79-5	Berry College	Floyd	GA	9/27/1979			-				
Berry 86-02	Berry College	Floyd	GA	9/9/1986			-				
Berry 86-06	Berry College	Floyd	GA	9/9/1986			-				
Berry 86-08	Berry College	Floyd	GA	9/9/1986			-				
Berry 86-11	Berry College	Floyd	GA	9/9/1986			-				
Berry 86-28	Berry College	Floyd	GA	9/9/1986			-				
H01-074	Berry College	Floyd	GA	11/8/2001	M	4.5	-				0
H01-075	Berry College	Floyd	GA	11/8/2001	M	2.5	-				0
H01-076	Berry College	Floyd	GA	11/8/2001	M	4.5	-				0
H01-077	Berry College	Floyd	GA	11/8/2001	M	3.5	-				0
H01-078	Berry College	Floyd	GA	11/8/2001	M	1.5	-				0
H01-079	Berry College	Floyd	GA	11/8/2001	M	2.5	-				0
H01-080	Berry College	Floyd	GA	11/8/2001	M	2.5	-				0
H01-081	Berry College	Floyd	GA	11/8/2001	M	3.5	-				0

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
H01-083	Berry College	Floyd	GA	11/8/2001	M	3.5	-				0
H01-086	Berry College	Floyd	GA	11/8/2001	M	4.5	-				0
H01-087	Berry College	Floyd	GA	11/8/2001	M	2.5	-				0
H01-088	Berry College	Floyd	GA	11/8/2001	M	1.5	-				0
H01-092	Berry College	Floyd	GA	11/8/2001	M	3.5	-				0
H01-098	Berry College	Floyd	GA	11/9/2001	F	3.5	-				0
H94-398	Lake Russell WMA	Franklin	GA	6/17/1905		6.5	+				
H94-401	Lake Russell WMA	Franklin	GA	6/17/1905		1.5	+				
H94-402	Lake Russell WMA	Franklin	GA	6/17/1905		2.5	-				
H94-403	Lake Russell WMA	Franklin	GA	6/17/1905		3.5	-				
H94-404	Lake Russell WMA	Franklin	GA	6/17/1905		2.5	-				
583-1	Federal Law Enforcement Training Center	Glynn	GA	10/24/1999	F	2.5	+				
583-3	Federal Law Enforcement Training Center	Glynn	GA	10/24/1999	M	3.5	+				
583-4	Federal Law Enforcement Training Center	Glynn	GA	10/24/1999	F	5.5	+				
583-5	Federal Law Enforcement Training Center	Glynn	GA	10/24/1999	F	1.5	+				
583-2	Federal Law Enforcement Training Center	Glynn	GA	10/24/1999	M	2.5	-				
CC24-03		Grady	GA	1/25/2003	F	1.3	-				
EHRL-0036	Reynolds Plantation	Greene	GA	12/20/2000	M	0.5	+				
EHRL-0037	Reynolds Plantation	Greene	GA	12/20/2000	M	1.5	+				
EHRL-0038	Reynolds Plantation	Greene	GA	12/20/2000	F	0.5	-				
EHRL-0039	Reynolds Plantation	Greene	GA	12/20/2000	M	0.5	-				
EHRL-0914		Gwinnett	GA	10/20/2002	M	0.5	+	+	5 (b)	4 (b)	
EHRL-0916		Gwinnett	GA	10/20/2002	M	0.5	+	+	4,5 (b)	4 (b)	
EHRL-0917		Gwinnett	GA	10/20/2002	F	0.5	+	+	4 (b)	4 (b)	
EHRL-0918		Gwinnett	GA	10/27/2002	M	1.5	+	-	-		
EHRL-0919		Gwinnett	GA	10/27/2002	M	0.5	+	-	-		
EHRL-0915		Gwinnett	GA	10/20/2002	F	1.5	-	+	4 (b)	3 (b)	

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
H91-013	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	3.5	-				
H91-014	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	M	2.5	-				
H91-015	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	M	1.5	-				
H91-016	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	2.5	-				
H91-017	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	4.5	-				
H91-018	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	4.5	-				
H91-019	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	0.5	-				
H91-021	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	M	1.5	-				
H91-022	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	2.5	-				
H91-023	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	2.5	-				
H91-024	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	8.5	-				
H91-025	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	M	2.5	-				
H91-026	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	M	2.5	-				
H91-027	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	1.5	-				
H91-028	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	1.5	-				
H91-029	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	M	0.5	-				
H91-030	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	4.5	-				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	 VLPT	 120-kDa	LST
H91-031	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	6.5	-				
H91-032	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	4.5	-				
H91-033	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	M	0.5	-				
H91-034	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	F	0.5	-				
H91-036	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	M	1.5	-				
H91-035	Lake Russell WMA	Habersham/ Stephens	GA	10/18/1991	M	1.5	-				
H00-242		Harris	GA				+				
H00-243		Harris	GA				+				
H00-244		Harris	GA				+				
EHRL-1045	Calloway Gardens	Harris	GA	11/23/2002	F	5.5	+				
EHRL-1046	Calloway Gardens	Harris	GA	11/23/2002	F	3.5	+				
342-01	Callaway Gardens	Harris	GA	7/15/1986	F	2	-				0
342-02	Callaway Gardens	Harris	GA	7/15/1986	F	1	-				0
342-03	Callaway Gardens	Harris	GA	7/15/1986	F	2	-				0
342-04	Callaway Gardens	Harris	GA	7/15/1986	F	4	-				0
342-05	Callaway Gardens	Harris	GA	7/15/1986	F	3	-				0
EHRL-1047	Calloway Gardens	Harris	GA	11/23/2002	M	0.5	-	-	-		
EHRL-1048	Calloway Gardens	Harris	GA	11/23/2002	F	5.5	-				
EHRL-1049	Calloway Gardens	Harris	GA	11/23/2002	F	2.5	-				
GA Houston	Oaky Woods WMA	Houston	GA	10/26/1989			+				
GA Houston	Oaky Woods WMA	Houston	GA	10/26/1989			-				
EHRL-0547	Chateau Elan Winery	Jackson	GA	2/11/2002	F	3.5	-				
EHRL-0548	Chateau Elan Winery	Jackson	GA	2/11/2002	F	2.5	-				
EHRL-0549	Chateau Elan Winery	Jackson	GA	2/11/2002	M	3.5	-				
EHRL-0554	Chateau Elan Winery	Jackson	GA	2/11/2002	M	1.5	-				
EHRL-0556	Chateau Elan Winery	Jackson	GA	2/11/2002	F	1.5	-				
385-2	Piedmont NWR	Jasper/Jones	GA	8/3/1989	M	1	+				3

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	PCR results: VLPT	PCR results: 120-kDa	LST
385-3	Piedmont NWR	Jasper/Jones	GA	8/3/1989	M	1	+				3
385-4	Piedmont NWR	Jasper/Jones	GA	8/3/1989	M	1	+				2
385-5	Piedmont NWR	Jasper/Jones	GA	8/3/1989	F	3	+				2
505-1	Piedmont NWR	Jasper/Jones	GA	9/21/1994	F	1.5	+				1
505-2	Piedmont NWR	Jasper/Jones	GA	9/21/1994	M	1.5	+				1
505-3	Piedmont NWR	Jasper/Jones	GA	9/21/1994	M	1.5	+				2
505-4	Piedmont NWR	Jasper/Jones	GA	9/21/1994	F	3.5	+				1
505-5	Piedmont NWR	Jasper/Jones	GA	9/21/1994	M	1.5	+				3
225-02	Piedmont NWR	Jasper/Jones	GA	9/9/1979			+				
225-03	Piedmont NWR	Jasper/Jones	GA	9/9/1979			+				
225-04	Piedmont NWR	Jasper/Jones	GA	9/9/1979			+				
225-05	Piedmont NWR	Jasper/Jones	GA	9/9/1979			+				
601-1	Piedmont NWR	Jasper/Jones	GA	7/24/2001	F	3.5	+	-	-		1
601-2	Piedmont NWR	Jasper/Jones	GA	7/24/2001	F	2.5	+	-	-		1
601-3	Piedmont NWR	Jasper/Jones	GA	7/24/2001	F	3.5	+	-	-		1
601-4	Piedmont NWR	Jasper/Jones	GA	7/24/2001	F	4.5	+	-	-		1
601-5	Piedmont NWR	Jasper/Jones	GA	7/24/2001	F	1.5	+	-	- (b), 5 (c)	3 (c)	1

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
385-1	Piedmont NWR	Jasper/Jones	GA	8/3/1989	F	2	-				3
225-01	Piedmont NWR	Jasper/Jones	GA	9/9/1979			-				
H91-037	Bullard Creek	Jeff Davis	GA				+				
H91-038	Bullard Creek	Jeff Davis	GA				+				
H91-039	Bullard Creek	Jeff Davis	GA				-				
H91-040	Bullard Creek	Jeff Davis	GA				-				
H91-044	Bullard Creek	Jeff Davis	GA				-				
357-1	Piedmont NWR	Jones	GA	9/10/1987	F	2.5	+				2
357-2	Piedmont NWR	Jones	GA	9/10/1987	F	1.5	+				2
357-4	Piedmont NWR	Jones	GA	9/10/1987	M	1.5	+				2
357-5	Piedmont NWR	Jones	GA	9/10/1987	F	3.5	+				1
295-1	Piedmont NWR	Jones	GA	9/4/1984	M	1.5	+				2
295-2	Piedmont NWR	Jones	GA	9/4/1984	F	2.5	+				3
295-3	Piedmont NWR	Jones	GA	9/4/1984	M	1.5	+				3
295-4	Piedmont NWR	Jones	GA	9/4/1984	F	1.5	+				2
295-5	Piedmont NWR	Jones	GA	9/4/1984	M	2.5	+				2
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	F	4	+				
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	F	3	+				
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	F	4	+				
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	M	.8	+				
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	M	.8	+				
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	F	5	+				
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	F	4	+				
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	F	2	+				
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	F	2	+				
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	M	2	+				
GA Piedmor	Piedmont NWR	Jones	GA	4/3/1989	F	2	+				
357-3	Piedmont NWR	Jones	GA	9/10/1987	M	1.5	-				1
EHRL-0906		Lanier	GA	10/19/2002	M	2.5	-	-	-		
EHRL-1072		Laurens	GA		F	1.5	+	+	4 (b)	3 (b)	
EHRL-1073		Laurens	GA		F	2.5	+	-	4 (b)	-	
EHRL-1074		Laurens	GA		F	1.5	-	-	-		

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-1075		Laurens	GA		M	2.5	-	-	-		
535-1	Wheatley Tract	Lee	GA	4/15/1997	F	3	-				0
535-2	Wheatley Tract	Lee	GA	4/15/1997	M	0.75	-				0
535-3	Wheatley Tract	Lee	GA	4/15/1997	F	5	-				0
535-4	Wheatley Tract	Lee	GA	4/15/1997	M	7	-				1
535-5	Wheatley Tract	Lee	GA	4/15/1997	F	5	-				0
600-1	St. Catherines Island	Liberty	GA	11/13/2000	M	1.5	+	-	-		1
600-2	St. Catherines Island	Liberty	GA	11/13/2000	M	1.5	+	-	-		2
600-3	St. Catherines Island	Liberty	GA	11/13/2000	M	4.5	+	-	-		2
600-4	St. Catherines Island	Liberty	GA	11/13/2000	F	0.5	+	-	-		0
600-5	St. Catherines Island	Liberty	GA	11/13/2000	F	5.5	+	-	-		1
EHRL-0246	Bussey Point	Lincoln	GA	9/24/2001	M	4.5	+				
H01-273	Bussey Point	Lincoln	GA	10/13/2001	F	2.5	+				
EHRL-0905		Lowndes	GA	10/19/2002	F	0.5	+	+	4 (b)	3 (b)	
GA Lumpkin	Blue Ridge	Lumpkin	GA	2/25/1985			-				
GA Lumpkin	Blue Ridge	Lumpkin	GA	2/25/1985			-				
GA Lumpkin	Blue Ridge	Lumpkin	GA	2/25/1985			-				
GA Lumpkin	Blue Ridge	Lumpkin	GA	2/25/1985			-				
GA Lumpkin	Blue Ridge	Lumpkin	GA	2/25/1985			-				
H00-223		Macon	GA				+				
H00-229		Macon	GA				+				
H00-230		Macon	GA				+				
H00-234		Macon	GA				+				
H00-236		Macon	GA				+				
EHRL-0525	Paige Luttrell's Property	Madison	GA	12/16/2001	F	2.5	-				
544-1	Harris Neck NWR	McIntosh	GA	9/23/1997	F	2.5	+	-	-		2
544-2	Harris Neck NWR	McIntosh	GA	9/23/1997	F	5.5	+	-	-		0
544-3	Harris Neck NWR	McIntosh	GA	9/23/1997	F	1.5	+	-	-		1
544-4	Harris Neck NWR	McIntosh	GA	9/23/1997	F	5.5	+	-	-		1
544-5	Harris Neck NWR	McIntosh	GA	9/23/1997	F	0.75	+	-	4 (b)	3 (b)	0
545-1	Blackbeard Island NWR	McIntosh	GA	9/24/1997	F	5.5	+	-	-		2
545-2	Blackbeard Island NWR	McIntosh	GA	9/24/1997	F	5.5	+	-	-		3
545-4	Blackbeard Island NWR	McIntosh	GA	9/24/1997	F	2.5	+	-	-		3
545-5	Blackbeard Island NWR	McIntosh	GA	9/24/1997	F	3.5	+	-	-		2

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
545-3	Blackbeard Island NWR	McIntosh	GA	9/24/1997	F	3.5	-	-	-		3
545-6	Blackbeard Island NWR	McIntosh	GA	9/24/1997	M	0.25	-	+	4 (b)	-	NA
545-7	Blackbeard Island NWR	McIntosh	GA	9/24/1997	F	0.25	-	-	-		NA
H00-255		Meriwether	GA				+				
H00-256		Meriwether	GA				+				
H00-257		Meriwether	GA				+				
H00-258		Meriwether	GA				+				
H00-259		Meriwether	GA				+				
H00-271		Miller	GA				+				
H00-272		Miller	GA				+				
H00-273		Miller	GA				-				
H91-145	Central GA WMA	Morgan	GA	11/9/1991	F	2.5	+				
H91-146	Central GA WMA	Morgan	GA	11/9/1991	F	0.5	+				
H91-147	Central GA WMA	Morgan	GA	11/9/1991	F	6.5	+				
H91-237	Central GA WMA	Morgan	GA	11/14/1991	M	2.5	+				
H91-238	Central GA WMA	Morgan	GA	11/14/1991	F	2.5	+				
H91-239	Central GA WMA	Morgan	GA	11/14/1991	M	0.5	+				
H91-241	Central GA WMA	Morgan	GA	11/14/1991	F	2.5	+				
H91-242	Central GA WMA	Morgan	GA	11/14/1991	F	3.5	+				
H91-243	Central GA WMA	Morgan	GA	11/14/1991	F	3.5	+				
H91-244	Central GA WMA	Morgan	GA	11/14/1991	M	0.5	+				
H91-245	Central GA WMA	Morgan	GA	11/14/1991	F	0.5	+				
H91-246	Central GA WMA	Morgan	GA	11/14/1991	F	5.5	+				
H91-249	Central GA WMA	Morgan	GA	11/14/1991	M	0.5	+				
H91-250	Central GA WMA	Morgan	GA	11/14/1991	F	2.5	+				
H91-252	Central GA WMA	Morgan	GA	11/14/1991	F	2.5	+				
H91-253	Central GA WMA	Morgan	GA	11/14/1991	F	3.5	+				
H91-254	Central GA WMA	Morgan	GA	11/14/1991	F	2.5	+				
H91-259	Central GA WMA	Morgan	GA	11/14/1991	M	0.5	+				
H91-260	Central GA WMA	Morgan	GA	11/14/1991	F	4.5	+				
H91-240	Central GA WMA	Morgan	GA	11/14/1991	F	3.5	-				
H91-247	Central GA WMA	Morgan	GA	11/14/1991	F	3.5	-				
H91-248	Central GA WMA	Morgan	GA	11/14/1991	F	3.5	-				
H91-251	Central GA WMA	Morgan	GA	11/14/1991	F	0.5	-				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
H91-255	Central GA WMA	Morgan	GA	11/14/1991	F	1.5	-				
H91-256	Central GA WMA	Morgan	GA	11/14/1991	F	0.5	-				
H91-257	Central GA WMA	Morgan	GA	11/14/1991	M	0.5	-				
H91-258	Central GA WMA	Morgan	GA	11/14/1991	M	0.5	-				
H91-261	Central GA WMA	Morgan	GA	11/14/1991	F	2.5	-				
H91-262	Central GA WMA	Morgan	GA	11/14/1991	F	0.5	-				
H91-263	Central GA WMA	Morgan	GA	11/14/1991	F	2.5	-				
EHRL-0197	Dalton Utilities	Murray	GA	6/20/2001	F	5	-				
EHRL-0198	Dalton Utilities	Murray	GA	6/20/2001	F	4	-				
EHRL-0199	Dalton Utilities	Murray	GA	6/20/2001	F	3	-				
EHRL-0200	Dalton Utilities	Murray	GA	6/20/2001	F	4	-				
EHRL-0202	Dalton Utilities	Murray	GA	6/20/2001	M	2	-				
405-1	Fort Benning	Muscogee/ Chattahoochee	GA	8/29/1990	F	3.5	+				1
405-2	Fort Benning	Muscogee/ Chattahoochee	GA	8/29/1990	M	1.5	+				1
405-4	Fort Benning	Muscogee/ Chattahoochee	GA	8/29/1990	M	1.5	+				1
405-5	Fort Benning	Muscogee/ Chattahoochee	GA	8/29/1990	F	3.5	+				3
405-3	Fort Benning	Muscogee/ Chattahoochee	GA	8/29/1990	F	4.5	-				1
EHRL-0211		Newton	GA	7/19/2001	F	2	+				
EHRL-0212		Newton	GA	7/19/2001	F	1.5	+				
EHRL-0208		Newton	GA	7/19/2001	F	2	+				
EHRL-0209		Newton	GA	7/19/2001	F	3	+				
EHRL-0210		Newton	GA	7/19/2001	M	3	+				
H00-153		Oglethorpe	GA				+				
H00-154		Oglethorpe	GA				+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
H00-155		Oglethorpe	GA				+				
H00-269		Oglethorpe	GA				+				
EHRL-0033		Pike	GA	12/7/2000	F	2.5	+				
EHRL-0084		Pike	GA	1/31/2001	F	2.5	+				
EHRL-0085		Pike	GA	1/31/2001	F	2.5	+				
EHRL-0086		Pike	GA	1/31/2001	M	1.5	+				
EHRL-0034		Pike	GA	12/7/2000	F	2.5	-				
EHRL-0047	Great Waters	Putnam	GA	1/22/2001	F	1.5	+				
EHRL-0049	Great Waters	Putnam	GA	1/22/2001	F	6.5	+				
EHRL-0050	Great Waters	Putnam	GA	1/22/2001	F	0.5	+				
EHRL-0048	Great Waters	Putnam	GA	1/22/2001	F	4.5	-				
EHRL-0051	Great Waters	Putnam	GA	1/22/2001	M	0.5	-				
290-07	Warwoman WMA	Rabun	GA	3/8/1984	M	0.75	-				0
290-09	Warwoman WMA	Rabun	GA	3/8/1984	F	7.5	-				0
290-10	Warwoman WMA	Rabun	GA	3/8/1984	F	3.5	-				0
309-02	Fort Gordon	Richmond	GA	6/19/1985	M	1	+				1
309-03	Fort Gordon	Richmond	GA	6/19/1985	M	2	+				1
309-04	Fort Gordon	Richmond	GA	6/19/1985	F	3	+				1
309-05	Fort Gordon	Richmond	GA	6/19/1985	F	2	+				2
309-01	Fort Gordon	Richmond	GA	6/19/1985	M	1	-				1
H91-482	Tuckahoe WMA	Screven	GA				+				
H91-370	Tuckahoe WMA	Screven	GA				+				
H91-372	Tuckahoe WMA	Screven	GA				+				
H91-500	Tuckahoe WMA	Screven	GA				+				
H91-481	Tuckahoe WMA	Screven	GA				-				
GA Spalding	Griffin Experimental Station	Spalding	GA	10/12/1988			++				
GA Spalding	Griffin Experimental Station	Spalding	GA	10/12/1988			+				
GA Spalding	Griffin Experimental Station	Spalding	GA	10/12/1988			+				
GA Spalding	Griffin Experimental Station	Spalding	GA	10/12/1988			+				
559-2	Eufaula NWR	Stewart	GA	8/11/1998	F	2	+				0
326-06	Eufaula NWR	Stewart	GA	7/17/1986	F	3	-				0
326-07	Eufaula NWR	Stewart	GA	7/17/1986	F	3	-				0
326-08	Eufaula NWR	Stewart	GA	7/17/1986	F	1	-				0
326-09	Eufaula NWR	Stewart	GA	7/17/1986	F	1	-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
326-10	Eufaula NWR	Stewart	GA	7/17/1986	M	1	-				0
559-1	Eufaula NWR	Stewart	GA	8/11/1998	F	3	-				0
559-3	Eufaula NWR	Stewart	GA	8/11/1998	F	3	-				1
559-4	Eufaula NWR	Stewart	GA	8/11/1998	M	1	-				0
559-5	Eufaula NWR	Stewart	GA	8/11/1998	M	1	-				0
EHRL-0891	Big Hammock WMA	Tattnall	GA	10/3/2002	F	0.5	+	-	-	-	
EHRL-0894	Big Hammock WMA	Tattnall	GA	10/3/2002	M	1.5	+	-	-		
EHRL-0895	Big Hammock WMA	Tattnall	GA	10/3/2002	F	1.5	+	-	5 (b)	4 (b)	
EHRL-0892	Big Hammock WMA	Tattnall	GA	10/3/2002	F	2.5	-	-	-		
EHRL-0893	Big Hammock WMA	Tattnall	GA	10/3/2002	M	1.5	-	-	-		
H01-200		Taylor	GA	8/9/2001	M	1.5	-				
H90-157	Horse Creek	Telfair	GA				+				
H90-158	Horse Creek	Telfair	GA				+				
H90-159	Horse Creek	Telfair	GA				+				
H90-200	Horse Creek	Telfair	GA				+				
H90-160	Horse Creek	Telfair	GA				-				
EHRL-0035	D. Hoffman's farm	Troup	GA	12/8/2000	F	1.5	+				
EHRL-0003	D. Hoffman's farm	Troup	GA	11/12/2000	M	2.5	+				
EHRL-0002	D. Hoffman's farm	Troup	GA	11/11/2000	F	1.5	-				
427-1	Chickamauga Battlefield	Walker/ Catoosa	GA	8/28/1991	F	2.5	-				0
427-2	Chickamauga Battlefield	Walker/ Catoosa	GA	8/28/1991	F	2.0	-				0
427-3	Chickamauga Battlefield	Walker/ Catoosa	GA	8/28/1991	F	2.5	-				0
427-4	Chickamauga Battlefield	Walker/ Catoosa	GA	8/28/1991	M	1.5	-				0
427-5	Chickamauga Battlefield	Walker/ Catoosa	GA	8/28/1991	F	2.5	-				0
388-1	Dixon Memorial WMA	Ware	GA	8/15/1989	F	2	+				1
388-2	Dixon Memorial WMA	Ware	GA	8/15/1989	F	2	+				2
388-3	Dixon Memorial WMA	Ware	GA	8/15/1989	F	3	+				1
388-4	Dixon Memorial WMA	Ware	GA	8/15/1989	F	2	+				2
388-5	Dixon Memorial WMA	Ware	GA	8/15/1989	F	4	+				2

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
H91-049	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	2.5	+				
H91-051	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	1.5	+				
H91-052	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	1.5	+				
H91-054	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	1.5	+				
H91-055	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	2.5	+				
H91-056	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	2.5	+				
H91-058	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	2.5	+				
H91-059	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	2.5	+				
H91-060	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	1.5	+				
H91-061	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	3.5	+				
H91-062	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	2.5	+				
H91-063	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	2.5	+				
H91-064	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	0.5	+				
H91-066	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	3.5	+				
H91-067	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	1.5	+				
H91-068	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	1.5	+				
H91-069	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	1.5	+				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	VLPT	120-kDa	LST
H91-070	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	3.5	+				
H91-071	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	3.5	+				
H91-072	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	2.5	+				
H91-050	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	4.5	-				
H91-053	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	1.5	-				
H91-057	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	F	2.5	-				
H91-065	Dixon Memorial WMA	Ware/ Brantley	GA	10/2/1991	M	1.5	-				
EHRL-0901		Washington	GA	10/19/2002	M	3.5	+				
EHRL-0897		Washington	GA	10/19/2002	M	2.5	+	+	4 (b)	4 (b)	
EHRL-0900		Washington	GA	10/19/2002	F	3.5	+				
EHRL-0902		Washington	GA	10/19/2002	M	2.5	-	-	-		
EHRL-0903		Washington	GA	10/19/2002	F	5.5	-				
H91-485	Rayonier WMA	Wayne	GA				+				
H91-486	Rayonier WMA	Wayne	GA				+				
H91-489	Rayonier WMA	Wayne	GA				+				
H91-491	Rayonier WMA	Wayne	GA				+				
H91-492	Rayonier WMA	Wayne	GA				+				
469-1	Dukes Creek Woods (Helen)	White	GA	3/19/1993	F	0.75	-				0
469-2	Dukes Creek Woods (Helen)	White	GA	3/19/1993	F	1.5	-				0
469-3	Dukes Creek Woods (Helen)	White	GA	3/19/1993	M	0.5	-				0
469-4	Dukes Creek Woods (Helen)	White	GA	3/19/1993	F	0.75	-				0
469-5	Dukes Creek Woods (Helen)	White	GA	3/19/1993	F	3.5	-				0
CC436-02		Atchinson	KS	11/18/2002	M	>1.5	+	-	-		
SE98-839		Brown	KS				+				
SE98-824		Butler	KS				+				
SE98-814		Chase	KS				+				
SE98-838		Chase	KS				+				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
SE98-819		Clay	KS				+				
SE98-843		Commanche	KS				-				
EHRL-0522		Elk	KS	12/8/2001	F	2.5	+				
EHRL-0523		Elk	KS	12/8/2001	F	1.5	+	-	-		
EHRL-0524		Elk	KS	12/30/2001	M	4.5	-				
SE98-834		Gove	KS				-				
SE98-835		Graham	KS				-				
SE98-816		Jefferson	KS				+				
EHRL-0497		Jefferson	KS				+	-	-		
EHRL-0496		Jefferson	KS				-	-	-		
EHRL-0498		Jefferson	KS		M		-	-	-		
EHRL-0499		Jefferson	KS	11/29/2001	F	2.5	-				
EHRL-0521		Jefferson	KS	12/11/2001	M	1.5	-	-	5 (b)	4 (b)	
SE98-836		Jewell	KS				-				
SE98-809		Johnson	KS				+				
CC351-02		Lane	KS	10/16/2002			+				
SE98-821		Lincoln	KS				-				
SE98-841		Lincoln	KS				-				
SE98-805		Linn	KS				+				
EHRL-0479	northern part of County	Lyon	KS	12/2/2001	F	2.5+	+				
EHRL-0480	northern part of County	Lyon	KS	12/2/2001	M	1.5	+	-	-		
EHRL-0481		Lyon	KS	12/2/2001			-	-	-		
SE98-810		Marshall	KS				+				
EHRL-0512		Marshall	KS	11/30/2001	M	4	+				
EHRL-0513		Marshall	KS	11/30/2001	M	2.5	+				
EHRL-0514		Marshall	KS	11/30/2001	M	3	+				
EHRL-0509	NE part of county	McPherson	KS	12/11/2001	M	5	+				
EHRL-0510	NE part of county	McPherson	KS	12/11/2001	M	4	+				
EHRL-0511	NE part of county	McPherson	KS	12/11/2001	M	3	+				
EHRL-0508	6 mi N of Galva	McPherson	KS	12/11/2001	M	2.5	-				
SE98-828		Mitchell	KS				-				
SE98-823		Montgomery	KS				+				
EHRL-0482	Elk City WA	Montgomery	KS	11/28/2001	F	4.5	+				
EHRL-0483	Elk City WA	Montgomery	KS	11/28/2001	M	2.5	+				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
EHRL-0485	Elk City WA	Montgomery	KS	11/28/2001	F	2.5	+				
EHRL-0484	Elk City WA	Montgomery	KS	11/28/2001	M	4.5	-				
EHRL-0486	Elk City WA	Montgomery	KS	11/29/2001	F	1.5	-	-	-		
EHRL-0515		Nemaha	KS	12/1/2001	M	1.5	+	-	-		
EHRL-0516		Nemaha	KS	12/9/2001	F	2	+	-	-		
EHRL-0517		Nemaha	KS	12/9/2001	M	2.5	+	-	-		
EHRL-0518		Nemaha	KS	12/9/2001	M	1.5	+	-	-		
EHRL-0478		Ness	KS	12/2/2001	M	2.5+	-				
SE98-830		Norton	KS				-				
EHRL-0456	Pomona SP	Osage	KS	10/28/2001	M	2.5	+	-	-		
EHRL-0505		Osage	KS	12/9/2001	F	1.5	-	-	-		
SE98-806		Osborne	KS				+				
SE98-815		Osborne	KS				-				
SE98-840		Pottawatomie	KS				+				
SE98-827		Pratt	KS				-				
SE98-818		Reno	KS				+				
SE98-820		Republic	KS				-				
SE98-842		Riley	KS				-				
EHRL-0489	Webster WA and surrounding private lands	Rooks	KS	11/28/2001	M	3.5+	-				
EHRL-0490	Webster WA and surrounding private lands	Rooks	KS	11/28/2001	M	3.5	-				
EHRL-0491	Webster WA and surrounding private lands	Rooks	KS	11/28/2001	M	3.5	-				
EHRL-0492	Webster WA and surrounding private lands	Rooks	KS	11/29/2001	M	3.5	-				
EHRL-0495	Webster WA and surrounding private lands	Rooks	KS	11/29/2001	M	1.5	-				
SE98-812		Russell	KS				-				
SE98-822		Russell	KS				-				
SE98-833		Russell	KS				-				
SE98-837		Scott	KS				-				
SE98-813		Stafford	KS				-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0477		Stafford	KS	12/1/2001	F	1.5	-				
SE98-832		Wallace	KS				-				
EHRL-0541		Washington	KS	1/12/2002	F	2.5	+	-	-		
EHRL-0544		Washington	KS	12/27/2001	M	3.5	+				
EHRL-0545		Washington	KS	1/11/2002	F	2.5	+	-	-		
EHRL-0542		Washington	KS	1/12/2002	F	2.5	-	-	-		
EHRL-0543		Washington	KS	1/12/2002	F	2.5	-	-	-		
SE98-811		Wilson	KS				+				
SE98-826		Woodson	KS				+				
SE98-829	Postmark Bell…		KS				-				
EHRL-0401	Green River WMA	Adair	KY	11/1/2000	M	3.5	+				
EHRL-0402	Green River WMA	Adair	KY	11/1/2000	F	2.5	+				
EHRL-0267	Barren River Lake WMA	Allen	KY	4/4/2001	F	5	+				
EHRL-0268	Barren River Lake WMA	Allen	KY	4/4/2001	F	1	-	-	-		
593-1	Ballard WMA	Ballard	KY	7/26/2000	F	3	+	-	-		0
593-2	Ballard WMA	Ballard	KY	7/26/2000	F	3	+	-	-		1
593-3	Ballard WMA	Ballard	KY	7/26/2000	F	5	+	-	-		0
593-4	Ballard WMA	Ballard	KY	7/26/2000	F	2	+	-	-		1
593-5	Ballard WMA	Ballard	KY	7/26/2000	F	2	+	-	-		1
EHRL-0264	Barren River Lake WMA	Barren	KY	3/30/2001	F	2	+				
EHRL-0265	Barren River Lake WMA	Barren	KY	3/30/2001	F	1	-				
EHRL-0266	Barren River Lake WMA	Barren	KY	3/30/2001	F	1	-				
SE99-353	Yellowbank Refuge Area	Breckinridge	KY				+				
SE99-354	Yellowbank Refuge Area	Breckinridge	KY				+				
SE99-355	Yellowbank Refuge Area	Breckinridge	KY				+				
277-1	Bernheim Forest	Bullitt	KY	9/1/1983	F	1	+				0
277-2	Bernheim Forest	Bullitt	KY	9/1/1983	F	3	-				0
277-3	Bernheim Forest	Bullitt	KY	9/1/1983	F	5	-				2
277-4	Bernheim Forest	Bullitt	KY	9/1/1983	F	2	-				0
277-5	Bernheim Forest	Bullitt	KY	9/1/1983	F	1	-				0
EHRL-0307	private home	Calloway	KY	11/1/2000	M	1.5	-				
EHRL-0308	private home	Calloway	KY	11/1/2000	M	0.5	-				
EHRL-0279	Grayson Lake WMA	Carter	KY	4/11/2001	F	2	-				
EHRL-0280	Grayson Lake WMA	Carter	KY	4/11/2001	F	3	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0283	Grayson Lake WMA	Carter	KY	4/11/2001	M	2	-				
SE99-356	Grayson Lake WMA	Carter/Elliott	KY				-				
SE99-357	Grayson Lake WMA	Carter/Elliott	KY				-				
EHRL-0254	Pennyrile SF	Christian	KY	3/21/2001	F	2	+				
EHRL-0257	Pennyrile SF	Christian	KY	3/21/2001	F	6	+				
EHRL-0255	Pennyrile SF	Christian	KY	3/21/2001	F	4	-				
EHRL-0256	Pennyrile SF	Christian	KY	3/21/2001	F	7	-				
EHRL-0258	Pennyrile SF	Christian	KY	9/5/2001	M	1	-				
EHRL-0360	Dale Hollow SRP	Cumberland	KY	12/19/2000	M	0.5	-				
EHRL-0362	Dale Hollow SRP	Cumberland	KY	12/19/2000	F	2.5	-				
EHRL-0363	Dale Hollow SRP	Cumberland	KY	12/19/2000	F	0.5	-				
EHRL-0364	Dale Hollow SRP	Cumberland	KY	12/20/2000	M	1.5	-				
EHRL-0365	Dale Hollow SRP	Cumberland	KY	12/20/2000	M	2.5	-				
296-01	Mammoth Cave National Park (south of Green River)	Edmonson	KY	9/25/1984	M	2.5	+				1
296-03	Mammoth Cave National Park (south of Green River)	Edmonson	KY	9/25/1984	F	1	+				1
296-04	Mammoth Cave National Park (south of Green River)	Edmonson	KY	9/25/1984	M	5.5	+				1
296-05	Mammoth Cave National Park (south of Green River)	Edmonson	KY	9/25/1984	F	8	+				1
296-02	Mammoth Cave National Park (south of Green River)	Edmonson	KY	9/25/1984	F	0.5	-				1
EHRL-0277	Frankfort Airport	Franklin	KY	4/10/2001	F	5	-				
EHRL-0278	Frankfort Airport	Franklin	KY	4/10/2001	F	4	-				
596-1	Fort Knox	Hardin	KY	8/10/2000	F	1.5	+	-	-		2
596-2	Fort Knox	Hardin	KY	8/10/2000	F	3	+	-	-		3
596-3	Fort Knox	Hardin	KY	8/10/2000	F	2	+	-	-		3
596-4	Fort Knox	Hardin	KY	8/10/2000	F	4	+	-	-		3
596-5	Fort Knox	Hardin	KY	8/10/2000	F	2	+	-	-		1
EHRL-0331	Paintsville Lake WMA	Johnson	KY	4/4/2001	F	4	-				
EHRL-0332	Paintsville Lake WMA	Johnson	KY	4/4/2001	F	3	-				
EHRL-0333	Paintsville Lake WMA	Johnson	KY	4/4/2001	F	5	-				
EHRL-0334	Paintsville Lake WMA	Johnson	KY	4/4/2001	M	1	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0325	Addington Resources WMA (AKA Cyprus Amax)	Knott	KY	3/27/2001	F	5	-				
EHRL-0326	Addington Resources WMA (AKA Cyprus Amax)	Knott	KY	4/2/2001	F	4	-				
EHRL-0327	Addington Resources WMA (AKA Cyprus Amax)	Knott	KY	4/2/2001	F	7	-				
EHRL-0386	Redbird	Leslie/Clay	KY	11/11/2000	M	2.5	-				
EHRL-0387	Redbird	Leslie/Clay	KY	11/11/2000	M	1.7	-				
EHRL-0388	Redbird	Leslie/Clay	KY	11/11/2000	M	1.7	-				
EHRL-0390	Redbird	Leslie/Clay	KY	11/11/2000	M	4.5	-				
EHRL-0394	Redbird	Leslie/Clay	KY	11/11/2000	M	3.5	-				
286-01	Land Between the Lakes	Lyon/Trigg	KY	8/29/1983	F	1	+				2
286-02	Land Between the Lakes	Lyon/Trigg	KY	8/29/1983	F	2	+				2
286-03	Land Between the Lakes	Lyon/Trigg	KY	8/29/1983	F	2	+				2
286-04	Land Between the Lakes	Lyon/Trigg	KY	8/29/1983	M	1	+				2
286-05	Land Between the Lakes	Lyon/Trigg	KY	8/29/1983	F	2	+				2
SE91-001	Bluegrass Army Depot	Madison	KY	11/2/1991	M	1.5	-				
SE91-002	Bluegrass Army Depot	Madison	KY	11/2/1991	F	2.5	-				
SE91-003	Bluegrass Army Depot	Madison	KY	11/2/1991	M	2.5	-				
SE91-004	Bluegrass Army Depot	Madison	KY	11/2/1991	M	2.5	-				
SE91-007	Bluegrass Army Depot	Madison	KY	11/2/1991	M	2.5	-				
SE91-008	Bluegrass Army Depot	Madison	KY	11/2/1991	M	2.5	-				
SE91-009	Bluegrass Army Depot	Madison	KY	11/2/1991	M	4.5	-				
SE91-011	Bluegrass Army Depot	Madison	KY	11/2/1991	F	1.5	-				
SE91-012	Bluegrass Army Depot	Madison	KY	11/2/1991	M	2.5	-				
SE91-013	Bluegrass Army Depot	Madison	KY	11/2/1991	M	1.5	-				
SE91-014	Bluegrass Army Depot	Madison	KY	11/2/1991	M	1.5	-				
SE91-015	Bluegrass Army Depot	Madison	KY	11/2/1991	M	1.5	-				
SE91-016	Bluegrass Army Depot	Madison	KY	11/2/1991	M	1.5	-				
SE91-017	Bluegrass Army Depot	Madison	KY	11/2/1991	F	2.5	-				
SE91-018	Bluegrass Army Depot	Madison	KY	11/2/1991	M	3.5	-				
SE91-019	Bluegrass Army Depot	Madison	KY	11/2/1991	M	2.5	-				
SE91-020	Bluegrass Army Depot	Madison	KY	11/2/1991	M	0.5	-				
SE91-021	Bluegrass Army Depot	Madison	KY	11/2/1991	M	2.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE91-022	Bluegrass Army Depot	Madison	KY	11/2/1991	M	1.5	-				
SE91-023	Bluegrass Army Depot	Madison	KY	11/2/1991	M	2.5	-				
SE91-024	Bluegrass Army Depot	Madison	KY	11/2/1991	M	3.5	-				
SE91-025	Bluegrass Army Depot	Madison	KY	11/2/1991	F	2.5	-				
SE91-026	Bluegrass Army Depot	Madison	KY	11/2/1991	F	2.5	-				
SE91-027	Bluegrass Army Depot	Madison	KY	11/2/1991	F	3.5	-				
SE91-028	Bluegrass Army Depot	Madison	KY	11/2/1991	F	2.5	-				
SE91-029	Bluegrass Army Depot	Madison	KY	11/2/1991	F	2.5	-				
SE91-030	Bluegrass Army Depot	Madison	KY	11/2/1991	F	3.5	-				
SE91-031	Bluegrass Army Depot	Madison	KY	11/2/1991	M	2.5	-				
SE91-032	Bluegrass Army Depot	Madison	KY	11/2/1991	F	4.5	-				
SE91-005	Bluegrass Army Depot	Madison	KY	11/2/1991	M	2.5	-				
594-1	Bluegrass Army Depot	Madison	KY	8/8/2000	F	3.5	-				0
594-2	Bluegrass Army Depot	Madison	KY	8/8/2000	F	4.5	-				0
594-3	Bluegrass Army Depot	Madison	KY	8/8/2000	M	1.5	-				1
594-4	Bluegrass Army Depot	Madison	KY	8/8/2000	M	1.5	-				1
594-5	Bluegrass Army Depot	Madison	KY	8/8/2000	F	2.5	-				0
592-1	West Kentucky WMA	McCracken	KY	7/25/2000	F	2	+	-	-		3
592-2	West Kentucky WMA	McCracken	KY	7/25/2000	F	4	+	-	-		3
592-3	West Kentucky WMA	McCracken	KY	7/25/2000	F	2	+	-	-		3
592-5	West Kentucky WMA	McCracken	KY	7/25/2000	M	1	+	-	-		3
592-6	West Kentucky WMA	McCracken	KY	7/25/2000	F	1	+	+	5 (b)	4 (b)	3
EHRL-0328	Beaver Creek WMA	McCreary	KY	3/20/2001	F	7	+				
EHRL-0329	Beaver Creek WMA	McCreary	KY	3/20/2001	F	4	-				
EHRL-0330	Beaver Creek WMA	McCreary	KY	3/20/2001	F	6	-				
EHRL-0378	WHF Training Center	Muhlenberg	KY	11/4/2000	M	2.5	++				
EHRL-0376	WHF Training Center	Muhlenberg	KY	11/4/2000	M	2.5	+				
EHRL-0377	WHF Training Center	Muhlenberg	KY	11/4/2000	M	2.5	+				
EHRL-0379	WHF Training Center	Muhlenberg	KY	11/4/2000	F	2.5	+				
EHRL-0381	WHF Training Center	Muhlenberg	KY	11/4/2000	M	1.5	+				
436-2	Nolan Boone Farm	Nelson	KY	10/26/1991			+				0
436-3	Nolan Boone Farm	Nelson	KY	10/26/1991			+				0
436-4	Nolan Boone Farm	Nelson	KY	10/26/1991			+				0
436-1	Nolan Boone Farm	Nelson	KY	10/26/1991			-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
436-5	Nolan Boone Farm	Nelson	KY	10/26/1991			-				0
EHRL-0309	Clay WMA	Nicholas	KY	11/4/2000	M	1.5	-				
EHRL-0310	Clay WMA	Nicholas	KY	11/4/2000	M	1.5	-				
EHRL-0311	Clay WMA	Nicholas	KY	11/4/2000	F	2.5	-				
EHRL-0313	Clay WMA	Nicholas	KY	11/4/2000	M	1.5	-				
EHRL-0314	Clay WMA	Nicholas	KY	11/4/2000	F	2.5	-				
EHRL-0259	Peabody WMA - Ken Unit	Ohio	KY	3/28/2001	F	3	+				
EHRL-0260	Peabody WMA - Ken Unit	Ohio	KY	3/28/2001	F	4	+				
EHRL-0261	Peabody WMA - Ken Unit	Ohio	KY	3/28/2001	F	3	-				
EHRL-0262	Peabody WMA - Ken Unit	Ohio	KY	3/28/2001	F	5	-				
EHRL-0263	Peabody WMA - Ken Unit	Ohio	KY	3/28/2001	F	5	-				
595-1	Kleber WMA	Owen	KY	8/9/2000	F	3	-				0
595-2	Kleber WMA	Owen	KY	8/9/2000	F	5	-				0
595-3	Kleber WMA	Owen	KY	8/9/2000	F	5	-				0
595-4	Kleber WMA	Owen	KY	8/9/2000	M	2	-				0
595-5	Kleber WMA	Owen	KY	8/9/2000	F	2	-				0
EHRL-0366	Fishtrap Lake	Pike	KY	11/19/2000	F	2.5	-				
EHRL-0367	Fishtrap Lake	Pike	KY	11/19/2000	M	1.7	-				
EHRL-0368	Fishtrap Lake	Pike	KY	11/19/2000	M	2.5	-				
EHRL-0372	Fishtrap Lake	Pike	KY	11/19/2000	M	4.5+	-				
EHRL-0375	Fishtrap Lake	Pike	KY	11/19/2000	M	1.6	-				
EHRL-0385	LCSRP	Russell	KY	12/19/2000	F	2.5	+				
SE98-556	Lake Cumberland	Russell	KY	1/5/1999			-				
SE98-558	Lake Cumberland	Russell	KY	1/5/1999			-				
SE98-560	Lake Cumberland	Russell	KY	1/5/1999			-				
EHRL-0384	LCSRP	Russell	KY	12/19/2000	M	2.5	-				
EHRL-0345	Taylorsville Lake WMA	Spencer/ Anderson	KY	4/4/2001	F	4	-				
EHRL-0346	Taylorsville Lake WMA	Spencer/ Anderson	KY	4/4/2001	M	>1.5	-				
EHRL-0347	Taylorsville Lake WMA	Spencer/ Anderson	KY	4/4/2001	F	0.6	-				
EHRL-0348	Taylorsville Lake WMA	Spencer/ Anderson	KY	4/4/2001	M	4	-				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
EHRL-0349	Taylorsville Lake WMA	Spencer/ Anderson	KY	4/4/2001	M	4	-				
EHRL-0400	Green River WMA	Taylor	KY	11/1/2000	F	2.5	++				
EHRL-0397	Green River WMA	Taylor	KY	11/1/2000	M	0.5	+				
EHRL-0398	Green River WMA	Taylor	KY	11/1/2000	M	2.5	+				
EHRL-0399	Green River WMA	Taylor	KY	11/1/2000	M	2.5	+				
EHRL-0396	Green River WMA	Taylor	KY	11/1/2000	F	2.5	-				
SE91-086	Higginson-Henry WMA	Union	KY	12/7/1991	F	1.5	+				
SE91-090	Higginson-Henry WMA	Union	KY	12/7/1991	F	1.5	+				
SE91-091	Higginson-Henry WMA	Union	KY	12/7/1991	F	0.5	+				
SE91-092	Higginson-Henry WMA	Union	KY	12/7/1991	M	0.5	+				
SE91-097	Higginson-Henry WMA	Union	KY	12/7/1991	F	0.5	+				
SE91-098	Higginson-Henry WMA	Union	KY	12/7/1991	F	0.5	+				
SE91-099	Higginson-Henry WMA	Union	KY	12/7/1991	F	3.5	+				
SE91-100	Higginson-Henry WMA	Union	KY	12/7/1991	F	2.5	+				
SE91-102	Higginson-Henry WMA	Union	KY	12/7/1991	F	2.5	+				
SE91-105	Higginson-Henry WMA	Union	KY	12/7/1991	M	1.5	+				
SE91-107	Higginson-Henry WMA	Union	KY	12/8/1991	F	2.5	+				
SE95-0390	West Bay WMA	Allen	LA	6/17/1905		1.5	-				
SE95-0391	West Bay WMA	Allen	LA	6/17/1905		2.5	-				
SE95-0392	West Bay WMA	Allen	LA	6/17/1905		2.5	-				
SE95-0393	West Bay WMA	Allen	LA	6/17/1905		2.5	-				
SE95-0395	West Bay WMA	Allen	LA	6/17/1905		2.5	-				
SE02-068	Maurepas Swamp Area	Ascension	LA				+				
SE02-067	Maurepas Swamp Area	Ascension	LA				-				
SE02-069	Maurepas Swamp Area	Ascension	LA				-				
SE02-073	Maurepas Swamp Area	Ascension	LA				-				
SE02-075	Maurepas Swamp Area	Ascension	LA				-				
454-1	Lake Ophelia NWR	Avoyelles	LA	9/23/1992	M	1	-				0
454-2	Lake Ophelia NWR	Avoyelles	LA	9/23/1992	F	1.5	-				0
454-3	Lake Ophelia NWR	Avoyelles	LA	9/23/1992	F	2	-				0
454-4	Lake Ophelia NWR	Avoyelles	LA	9/23/1992	F	2.5	-				0
454-5	Lake Ophelia NWR	Avoyelles	LA	9/23/1992	F	2	-				0
581-1	Lake Ophelia NWR	Avoyelles	LA	9/22/1999	F	4.5	-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
581-2	Lake Ophelia NWR	Avoyelles	LA	9/22/1999	M	1.5	-				0
581-3	Lake Ophelia NWR	Avoyelles	LA	9/22/1999	F	1.5	-				0
581-4	Lake Ophelia NWR	Avoyelles	LA	9/22/1999	F	1	-				0
581-5	Lake Ophelia NWR	Avoyelles	LA	9/22/1999	F	3.5	-				0
SE98-788	DeKidder Airport	Beauregard	LA				-				
SE98-789	DeKidder Airport	Beauregard	LA				-				
SE95-0332	Jackson Bienville WMA	Bienville	LA	6/17/1905		3.5	+				
SE95-0337	Jackson Bienville WMA	Bienville	LA	6/17/1905		2.5	+				
SE95-0334	Jackson Bienville WMA	Bienville	LA	6/17/1905		0.5	-				
SE95-0335	Jackson Bienville WMA	Bienville	LA	6/17/1905		4.5	-				
SE95-0336	Jackson Bienville WMA	Bienville	LA	6/17/1905		0.5	-				
410-11	Private Property	Bossier	LA	9/23/1990	F	3.5	+				1
410-12	Private Property	Bossier	LA	9/23/1990	F	1.5	+				1
410-13	Private Property	Bossier	LA	9/23/1990	M	1.5	+				1
410-15	Private Property	Bossier	LA	9/23/1990	M	1.5	+				1
410-14	Private Property	Bossier	LA	9/23/1990	M	1.5	-				1
466-1	Lawton Property	Calcasieu	LA	10/19/1992	F	4.5	-				0
466-2	Lawton Property	Calcasieu	LA	10/19/1992	F	3.5	-				0
466-3	Lawton Property	Calcasieu	LA	10/19/1992	F	3.5	-				0
466-4	Lawton Property	Calcasieu	LA	10/19/1992	M	0.5	-				0
466-5	Lawton Property	Calcasieu	LA	10/19/1992	F	0.5	-				0
SE91-084	Boeuf River WMA	Caldwell	LA	11/29/1991	F	2.5	+				
SE91-085	Boeuf River WMA	Caldwell	LA	11/29/1991	F	2.5	+				
SE91-078	Boeuf River WMA	Caldwell	LA	11/29/1991	F	2.5	-				
SE91-083	Boeuf River WMA	Caldwell	LA	11/29/1991	M	1.5	-				
310-01	Lacassine NWR	Cameron	LA	7/14/1985	M	3	-				0
310-02	Lacassine NWR	Cameron	LA	7/14/1985	M	2	-				0
310-03	Lacassine NWR	Cameron	LA	7/14/1985	M	1	-				0
310-04	Lacassine NWR	Cameron	LA	7/14/1985	M	1	-				0
310-05	Lacassine NWR	Cameron	LA	7/14/1985	M	2	-				0
351-1	Weldon Area	Claiborne	LA	9/16/1987	M	1.5	+				1
351-2	Weldon Area	Claiborne	LA	9/16/1987	F	3	+				2
351-4	Weldon Area	Claiborne	LA	9/16/1987	M	1.5	+				1
351-3	Weldon Area	Claiborne	LA	9/16/1987	M	1.5	-				1

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
351-5	Weldon Area	Claiborne	LA	9/16/1987	F	3	-				3
SE91-056	Red River/Three River WMA	Concordia	LA	11/29/1991	M	2.5	+				
SE91-060	Red River/Three River WMA	Concordia	LA	11/29/1991	M	1.5	+				
SE91-063	Red River/Three River WMA	Concordia	LA	11/29/1991	F	2.5	+				
SE91-064	Red River/Three River WMA	Concordia	LA	11/29/1991	M	1.5	+				
SE91-065	Red River/Three River WMA	Concordia	LA	11/29/1991	F	2.5	+				
580-3	Bayou Cocodrie NWR	Concordia	LA	9/21/1999	F	6.5	+				1
580-4	Bayou Cocodrie NWR	Concordia	LA	9/21/1999	F	3.5	+				1
580-5	Bayou Cocodrie NWR	Concordia	LA	9/21/1999	M	2.5	+				1
SE91-054	Red River/Three River WMA	Concordia	LA	11/29/1991	M	1.5	-				
SE91-055	Red River/Three River WMA	Concordia	LA	11/29/1991	M	1.5	-				
SE91-057	Red River/Three River WMA	Concordia	LA	11/29/1991	F	2.5	-				
SE91-058	Red River/Three River WMA	Concordia	LA	11/29/1991	F	2.5	-				
SE91-059	Red River/Three River WMA	Concordia	LA	11/29/1991	M	0.5	-				
SE91-061	Red River/Three River WMA	Concordia	LA	11/29/1991	M	1.5	-				
SE91-062	Red River/Three River WMA	Concordia	LA	11/29/1991	F	2.5	-				
336-06	Red River WMA	Concordia	LA	9/9/1986	F	2	-				0
336-07	Red River WMA	Concordia	LA	9/9/1986	F	2	-				0
336-08	Red River WMA	Concordia	LA	9/9/1986	F	1	-				0
336-09	Red River WMA	Concordia	LA	9/9/1986	M	1	-				0
336-10	Red River WMA	Concordia	LA	9/9/1986	F	2	-				0
580-1	Bayou Cocodrie NWR	Concordia	LA	9/21/1999	M	1.5	-				1
580-2	Bayou Cocodrie NWR	Concordia	LA	9/21/1999	F	2.5	-				1
EHRL-0138	Ascantia Plantation	E. Baton Rouge	LA	12/27/2000	M	2.5	+				
EHRL-0140	Ascantia Plantation	E. Baton Rouge	LA	1/6/2001	F	3.5	+				
EHRL-0137	Ascantia Plantation	E. Baton Rouge	LA	12/24/2000	M	3.5	-				
EHRL-0139	Ascantia Plantation	E. Baton Rouge	LA	12/30/2000	F	1.5	-				
420-2	Oak Grove Swamp WMA	E. Carroll	LA	7/25/1991	F	2	+				1
420-3	Oak Grove Swamp WMA	E. Carroll	LA	7/25/1991	F	5	+				1
420-4	Oak Grove Swamp WMA	E. Carroll	LA	7/25/1991	F	8	+				1

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
420-1	Oak Grove Swamp WMA	E. Carroll	LA	7/25/1991	F	3	-				1
420-5	Oak Grove Swamp WMA	E. Carroll	LA	7/25/1991	F	3	-				0
SE96-374	Beechgrove Plantation	E. Feliciana	LA	2/7/1996	M	3.5	+				
SE96-375	Beechgrove Plantation	E. Feliciana	LA	2/7/1996	F	2.5	+				
SE96-376	Beechgrove Plantation	E. Feliciana	LA	2/7/1996	F	4.5	+				
SE96-377	Beechgrove Plantation	E. Feliciana	LA	2/7/1996	F	2.5	+				
SE96-373	Beechgrove Plantation	E. Feliciana	LA	2/7/1996	M	1.5	-				
355-08	St. Landry	Evangeline	LA	8/25/1987	M	1	-				
355-09	St. Landry	Evangeline	LA	8/25/1987	M	2	-				
355-10	St. Landry	Evangeline	LA	8/25/1987	F	5	-				
355-11	St. Landry	Evangeline	LA	8/25/1987	F	2	-				
SE91-066	Big Lake WMA	Franklin/ Tensas	LA	11/29/1991	M	1.5	+				
SE91-068	Big Lake WMA	Franklin/ Tensas	LA	11/29/1991	F	3.5	+				
SE91-069	Big Lake WMA	Franklin/ Tensas	LA	11/29/1991	M	3.5	+				
SE91-070	Big Lake WMA	Franklin/ Tensas	LA	11/29/1991	F	2.5	+				
SE91-071	Big Lake WMA	Franklin/ Tensas	LA	11/29/1991	M	1.5	+				
SE91-072	Big Lake WMA	Franklin/ Tensas	LA	11/29/1991	M	1.5	+				
SE91-076	Big Lake WMA	Franklin/ Tensas	LA	11/29/1991	M	1.5	+				
391-2	Avery Island	Iberia	LA	9/21/1989	F	5.5	+				1
391-4	Avery Island	Iberia	LA	9/21/1989	F	1	+				1
250-09	Avery Island	Iberia	LA	8/18/1981	F	5	+				1
391-1	Avery Island	Iberia	LA	9/21/1989	F	6.5	-				1
391-3	Avery Island	Iberia	LA	9/21/1989	F	10	-				1
391-5	Avery Island	Iberia	LA	9/21/1989	F	3.5	-				1
250-06	Avery Island	Iberia	LA	8/18/1981	M	2	-				1
250-07	Avery Island	Iberia	LA	8/18/1981	F	4	-				1
250-08	Avery Island	Iberia	LA	8/18/1981	F	3	-				1

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
250-10	Avery Island	Iberia	LA	8/18/1981	F	8	-				1
SE00-540	Sherburne South and Red Diamond HC	Iberville	LA	6/11/2001	F	6	-				
SE00-542	Sherburne South and Red Diamond HC	Iberville	LA	6/11/2001	F	1	-				
SE00-543	Sherburne South and Red Diamond HC	Iberville	LA	6/11/2001	F	1	-				
SE00-544	Sherburne South and Red Diamond HC	Iberville	LA	6/11/2001	F	3	-				
SE00-545	Sherburne South and Red Diamond HC	Iberville	LA	6/11/2001	M	1.5	-				
384-06	Big Thicket HC	Jackson	LA	9/1/1988	F	4	+				
384-07	Big Thicket HC	Jackson	LA	9/1/1988	F	1	+				
384-08	Big Thicket HC	Jackson	LA	9/1/1988	M	1	+				
384-09	Big Thicket HC	Jackson	LA	9/1/1988	F	3	+				
384-10	Big Thicket HC	Jackson	LA	9/1/1988	F	4	+				
SE93-015	Golden Ranch	LaFourche	LA	7/12/1993		.75	-				
SE93-016	Golden Ranch	LaFourche	LA	7/12/1993		.75	-				
SE93-017	Golden Ranch	LaFourche	LA	7/12/1993		.75	-				
SE93-018	Golden Ranch	LaFourche	LA	7/12/1993		4	-				
SE93-019	Golden Ranch	LaFourche	LA	7/12/1993		3	-				
431-1	Saline WMA	LaSalle	LA	9/19/1991	F	3.5	-				0
431-2	Saline WMA	LaSalle	LA	9/19/1991	F	2.5	-				0
431-3	Saline WMA	LaSalle	LA	9/19/1991	M	0.75	-				0
431-4	Saline WMA	LaSalle	LA	9/19/1991	M	3.5	-				0
431-5	Saline WMA	LaSalle	LA	9/19/1991	M	3.5	-				0
SE94-546	Bear Creek HC	Livingston	LA	6/16/1905		2.5	+				
SE94-548	Bear Creek HC	Livingston	LA	6/16/1905		4.5	+				
SE94-547	Bear Creek HC	Livingston	LA	6/16/1905		2.5	-				
529-2	Tensas River NWR	Madison	LA	8/19/1996	F	2	+	-	-		0
529-3	Tensas River NWR	Madison	LA	8/19/1996	M	1.5	+	-	5 (b)	-	0
529-4	Tensas River NWR	Madison	LA	8/19/1996	M	1.5	+	-	-		0
529-5	Tensas River NWR	Madison	LA	8/19/1996	F	2.5	+	-	-		1
529-1	Tensas River NWR	Madison	LA	8/19/1996	F	1	-	-	-		0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE98-880		Morehouse	LA				-				
SE98-883		Morehouse	LA				-				
SE98-885		Morehouse	LA				-				
SE98-886		Morehouse	LA				-				
SE98-887		Morehouse	LA				-				
375-1	Red Dirt Wildlife Preserve	Natchitoches	LA	9/14/1988	F	2	+				1
375-2	Red Dirt Wildlife Preserve	Natchitoches	LA	9/14/1988	F	3	+				1
375-4	Red Dirt Wildlife Preserve	Natchitoches	LA	9/14/1988	M	1	+				0
375-5	Red Dirt Wildlife Preserve	Natchitoches	LA	9/14/1988	M	1	+				1
375-3	Red Dirt Wildlife Preserve	Natchitoches	LA	9/14/1988	F	4	-				1
EHRL-0244	Little Rock HC	Ouachita	LA	8/27/2001	F	2	+	-	-		
EHRL-0245	Little Rock HC	Ouachita	LA	8/27/2001	F	6	+				
SE95-0422	Russell Sage WMA	Ouachita	LA	6/17/1905		1.5	-				
SE95-0423	Russell Sage WMA	Ouachita	LA	6/17/1905		1.5	-				
SE95-0424	Russell Sage WMA	Ouachita	LA	6/17/1905		0.5	-				
SE95-0425	Russell Sage WMA	Ouachita	LA	6/17/1905		2.5	-				
SE95-0426	Russell Sage WMA	Ouachita	LA	6/17/1905		1.5	-				
307-01	Delta NWR	Plaquemines	LA	7/10/1985	M	1	-				0
307-02	Delta NWR	Plaquemines	LA	7/10/1985	M	2	-				0
307-03	Delta NWR	Plaquemines	LA	7/10/1985	M	1	-				0
307-04	Delta NWR	Plaquemines	LA	7/10/1985	M	5	-				0
307-05	Delta NWR	Plaquemines	LA	7/10/1985	M	1	-				0
SE95-0361	Sherburne WMA	Pointe Coupee	LA	6/17/1905		2.5	-				
SE95-0362	Sherburne WMA	Pointe Coupee	LA	6/17/1905		2.5	-				
SE95-0363	Sherburne WMA	Pointe Coupee	LA	6/17/1905		2.5	-				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	VLPT	120-kDa	LST
SE95-0365	Sherburne WMA	Pointe Coupee	LA	6/17/1905		4.5	-				
SE95-0366	Sherburne WMA	Pointe Coupee	LA	6/17/1905		3.5	-				
SE96-378	Lottie Wildlife	Pointe Coupee	LA	8/26/1996	F	1	-				
SE96-379	Lottie Wildlife	Pointe Coupee	LA	8/26/1996	F	1	-				
SE96-380	Lottie Wildlife	Pointe Coupee	LA	8/26/1996	F	3	-				
SE96-381	Lottie Wildlife	Pointe Coupee	LA	8/26/1996	M	1	-				
SE96-382	Lottie Wildlife	Pointe Coupee	LA	8/26/1996	F	1	-				
355-04	Oliver Farms	Richland	LA	9/3/1987	F	2	+				
355-01	Oliver Farms	Richland	LA	9/3/1987	F	3	-				
355-02	Oliver Farms	Richland	LA	9/3/1987	F	5	-				
355-03	Oliver Farms	Richland	LA	9/3/1987	F	3	-				
355-05	Oliver Farms	Richland	LA	9/3/1987	F	2	-				
441-2	Louisiana Land and Exploration Company	St. Charles	LA	9/24/1991	F	2.5	-				
441-3	Louisiana Land and Exploration Company	St. Charles	LA	9/24/1991	F	1.5	-				
441-5	Louisiana Land and Exploration Company	St. Charles	LA	9/24/1991	F	3.5	-				
SE95-0375	Thistlewaite	St. Landry	LA	6/17/1905		2.5	+				
SE95-0376	Thistlewaite	St. Landry	LA	6/17/1905		4.5	+				
SE95-0377	Thistlewaite	St. Landry	LA	6/17/1905		1.5	+				
SE95-0378	Thistlewaite	St. Landry	LA	6/17/1905		1.5	+				
SE95-0379	Thistlewaite	St. Landry	LA	6/17/1905		4.5	+				
SE02-084	Attakapas WMA	St. Martin	LA				-				
SE99-381	Atchafalaya Delta WMA	St. Mary	LA	9/7/1999	F	0.5	-				
SE99-383	Atchafalaya Delta WMA	St. Mary	LA	9/7/1999	F		-				
SE99-384	Atchafalaya Delta WMA	St. Mary	LA	9/7/1999	M	1	-				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
SE99-385	Atchafalaya Delta WMA	St. Mary	LA	9/8/1999	M	2	-				
SE99-391	Atchafalaya Delta WMA	St. Mary	LA				-				
SE95-0371	PRWMA	St. Tammany	LA	6/17/1905		1.5	-				
SE95-0372	PRWMA	St. Tammany	LA	6/17/1905		3.5	-				
SE95-0373	PRWMA	St. Tammany	LA	6/17/1905		6.5	-				
SE95-0374	PRWMA	St. Tammany	LA	6/17/1905		1.5	-				
CC340-02		St. Tammany	LA				-				
SE98-784	Zemurray Park	Tangipahoa	LA				+				
SE98-785	Zemurray Park	Tangipahoa	LA				+				
SE98-783	Zemurray Park	Tangipahoa	LA				-				
SE98-786	Zemurray Park	Tangipahoa	LA				-				
SE98-787	Zemurray Park	Tangipahoa	LA				-				
291-1	Big Lake WMA	Tensas	LA	8/18/1984	F	2	+				1
291-2	Big Lake WMA	Tensas	LA	8/18/1984	F	3	+				1
291-4	Big Lake WMA	Tensas	LA	8/18/1984	F	3	+				1
291-3	Big Lake WMA	Tensas	LA	8/18/1984	F	3	-				1
291-5	Big Lake WMA	Tensas	LA	8/18/1984	F	3	-				1
495-1	D'Arbonne NWR	Union	LA	8/27/1994	M	1.5	+				1
495-2	D'Arbonne NWR	Union	LA	8/27/1994	F	3.5	+				1
495-3	D'Arbonne NWR	Union	LA	8/27/1994	M	1.5	+				0
495-5	D'Arbonne NWR	Union	LA	8/27/1994	F	3.5	+				1
495-4	D'Arbonne NWR	Union	LA	8/27/1994	F	2.5	-				1
SE92-014	Bercham HC	W. Baton Rouge	LA	9/21/1992	F	2.5	+				
SE92-015	Bercham HC	W. Baton Rouge	LA	9/21/1992	F	3.5	+				
SE92-011	Bercham HC	W. Baton Rouge	LA	9/23/1992	M	1.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE92-012	Bercham HC	W. Baton Rouge	LA	9/21/1992	F	1.5	-				
SE92-013	Bercham HC	W. Baton Rouge	LA	9/23/1992	F	1.5	-				
SE99-376	River Bend	W. Feliciana	LA	8/25/1999	F		+				
SE99-377	River Bend	W. Feliciana	LA	8/25/1999	F		+				
SE99-378	River Bend	W. Feliciana	LA	8/25/1999	F		+				
SE99-379	River Bend	W. Feliciana	LA	8/25/1999	F		+				
SE99-380	River Bend, West Feliciana, LA	W. Feliciana	LA	8/25/1999	F		+				
SE95-0409	Bens Creek WMA	Washington	LA	6/17/1905		0.5	-				
SE95-0410	Bens Creek WMA	Washington	LA	6/17/1905		2.5	-				
SE95-0411	Bens Creek WMA	Washington	LA	6/17/1905		0.5	-				
SE95-0412	Bens Creek WMA	Washington	LA	6/17/1905		1.5	-				
SE95-0413	Bens Creek WMA	Washington	LA	6/17/1905		5.5	-				
410-08	Manville Property	Winn	LA	9/22/1990	F	4.5	+				1
410-09	Manville Property	Winn	LA	9/22/1990	M	1.5	+				1
410-06	Manville Property	Winn	LA	9/22/1990	M	1.5	-				1
410-07	Manville Property	Winn	LA	9/22/1990	M	6.5	-				1
410-10	Manville Property	Winn	LA	9/22/1990	M	0.5	-				0
SE99-369	Fair Hill WMA	Cecil	MD	1/3/2000	F	2	+				
SE99-367	Fair Hill WMA	Cecil	MD	1/3/2000	M	0.5	-				
SE99-368	Fair Hill WMA	Cecil	MD	1/3/2000	F	2	-				
SE99-370	Fair Hill WMA	Cecil	MD	1/3/2000	F	2	-				
SE99-375	Fair Hill WMA	Cecil	MD	1/3/2000	M		-				
SE99-031	Checkstation	Charles	MD	11/27/1999	M	3.5	+				
SE99-032	Checkstation	Charles	MD	11/27/1999	M	1.5	+				
SE99-033	Checkstation	Charles	MD	11/27/1999	M	2.5	+				
SE99-034	Checkstation	Charles	MD	11/27/1999	F	2.5	+				
SE99-035	Checkstation	Charles	MD	11/27/1999	F	2.5	+				
SE99-039	Blossom Pt. ARF	Charles	MD	12/2/1999	M	1.5	+				
SE99-040	Blossom Pt. ARF	Charles	MD	12/2/1999	M	1.5	+				
SE99-041	Blossom Pt. ARF	Charles	MD	12/2/1999	M	0.5	+				
380-01	Blackwater NWR	Dorchester	MD	8/17/1988	F	1	+				1
380-02	Blackwater NWR	Dorchester	MD	8/17/1988	F	5	+				1

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
380-04	Blackwater NWR	Dorchester	MD	8/17/1988	F	2	+				1
380-03	Blackwater NWR	Dorchester	MD	8/17/1988	F	2	-				1
380-05	Blackwater NWR	Dorchester	MD	8/17/1988	F	1	-				0
369-1	Catoctin Mountain NP	Frederick	MD	8/21/1988	M	2	-				0
369-2	Catoctin Mountain NP	Frederick	MD	8/21/1988	F	3	-				0
369-3	Catoctin Mountain NP	Frederick	MD	8/21/1988	F	7	-				0
369-4	Catoctin Mountain NP	Frederick	MD	8/21/1988	F	5	-				0
369-5	Catoctin Mountain NP	Frederick	MD	8/21/1988	F	6	-				0
SE00-005	Middle Patuxent Env. Area	Howard	MD	10/30/2000	M	0.5	+				
SE00-001	Middle Patuxent Env. Area	Howard	MD	10/30/2000	F	1.5	-				
SE00-002	Middle Patuxent Env. Area	Howard	MD	10/30/2000	F	1.5	-				
SE00-003	Middle Patuxent Env. Area	Howard	MD	10/30/2000	F	1.5	-				
SE00-004	Middle Patuxent Env. Area	Howard	MD	10/30/2000	F	2.5	-				
EHRL-0887	Chesapeake Farms	Kent	MD		F	3.5	+	-	-	-	
EHRL-0889	Chesapeake Farms	Kent	MD		F	3.5	+	-	-	-	
366-1	White Oak Naval Surface Weapons Center	Montgomery/ Prince George's	MD	8/18/1988	F	3	-				0
366-2	White Oak Naval Surface Weapons Center	Montgomery/ Prince George's	MD	8/18/1988	M	2	-				0
366-3	White Oak Naval Surface Weapons Center	Montgomery/ Prince George's	MD	8/18/1988	M	1	-				0
366-4	White Oak Naval Surface Weapons Center	Montgomery/ Prince George's	MD	8/18/1988	M	3	-				0
366-5	White Oak Naval Surface Weapons Center	Montgomery/ Prince George's	MD	8/18/1988	M	1	-				0
624-4	Antietam NBP	Washington	MD	8/26/2002	F	4.5	-				0
624-5	Antietam NBP	Washington	MD	8/26/2002	F	1.5	-				0
624-1	Antietam NBP	Washington	MD	8/26/2002	F	3	-				0
624-2	Antietam NBP	Washington	MD	8/26/2002	M	1.5	-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
624-3	Antietam NBP	Washington	MD	8/26/2002	F	2.5	-				0
SE01-264	Savannah	Andrew	MO				+	-	-		
SE01-266	Savannah	Andrew	MO				+				
SE01-268	Savannah	Andrew	MO				-				
SE01-265	Savannah	Andrew	MO				-				
SE01-267	Savannah	Andrew	MO				-	-	-		
SE01-407		Bollinger	MO		F	1.5	+				
SE01-410		Bollinger	MO		F	1.5	+				
SE01-411		Bollinger	MO		M	1.5	+				
EHRL-0531		Boone	MO		F	1.5	+				
SE01-190		Camden	MO		F	2+	+				
SE01-186		Camden	MO		F	2+	+				
SE01-188		Camden	MO		F	2+	+				
SE01-370		Camden	MO	11/15/2001	M	1.5	+				
SE01-369		Camden	MO	11/15/2001	F	1.5	-				
SE01-412		Cape Girardeau	MO		M	1.5	+				
SE01-414		Cape Girardeau	MO		M	1.5	+				
SE01-416		Cape Girardeau	MO		M	1.5	+				
SE01-418		Cape Girardeau	MO		M	1.5	+				
SE01-420		Cape Girardeau	MO		M	1.5	+				
502-1	Peck Ranch Conservation Area	Carter	MO	9/28/1994	F	1.5	+				3
502-4	Peck Ranch Conservation Area	Carter	MO	9/28/1994	F	2.5	+				2
502-5	Peck Ranch Conservation Area	Carter	MO	9/28/1994	F	1.5	+				2
502-2	Peck Ranch Conservation Area	Carter	MO	9/28/1994	F	1.5	-				3
502-3	Peck Ranch Conservation Area	Carter	MO	9/28/1994	F	6.5	-				2
EHRL-0553	Kansas City Downtown (MKC) Airport	Clay	MO	1/9/2002			+				
EHRL-0550	Kansas City Downtown (MKC) Airport	Clay	MO	1/9/2002			+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0551	Kansas City Downtown (MKC) Airport	Clay	MO	1/9/2002			+				
EHRL-0552	Kansas City Downtown (MKC) Airport	Clay	MO	1/9/2002			+				
EHRL-0350		Crawford	MO	1/14/1994			+				
EHRL-0352		Crawford	MO	2/1/1994			+				
EHRL-0353		Crawford	MO	2/7/1994			+				
EHRL-0351		Crawford	MO	1/29/1994			-				
EHRL-0354		Crawford	MO	3/2/1994			-				
SE91-190	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-191	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-192	Squaw Creek NWR	Holt	MO	1/4/1991	F	1.5	-				
SE91-194	Squaw Creek NWR	Holt	MO	1/4/1991	M	0.5	-				
SE91-196	Squaw Creek NWR	Holt	MO	1/4/1991	F	1.5	-				
SE91-197	Squaw Creek NWR	Holt	MO	1/4/1991	M	0.5	-				
SE91-199	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-200	Squaw Creek NWR	Holt	MO	1/4/1991	F	1.5	-				
SE91-203	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-204	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-205	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-207	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-209	Squaw Creek NWR	Holt	MO	1/4/1991	M	1.5	-				
SE91-210	Squaw Creek NWR	Holt	MO	1/4/1991	M	1.5	-				
SE91-211	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-213	Squaw Creek NWR	Holt	MO	1/4/1991	F	1.5	-				
SE91-214	Squaw Creek NWR	Holt	MO	1/4/1991	F	0.5	-				
SE91-216	Squaw Creek NWR	Holt	MO	1/4/1991	M	1.5	-				
SE91-217	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-219	Squaw Creek NWR	Holt	MO	1/4/1991	M	0.5	-				
SE91-220	Squaw Creek NWR	Holt	MO	1/4/1991	M	A	-				
SE91-223	Squaw Creek NWR	Holt	MO	1/4/1991	F	1.5	-				
SE91-224	Squaw Creek NWR	Holt	MO	1/4/1991	M	1.5	-				
SE91-225	Squaw Creek NWR	Holt	MO	1/4/1991	F	0.5	-				
SE91-226	Squaw Creek NWR	Holt	MO	1/4/1991	M	A	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE91-227	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-228	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
SE91-229	Squaw Creek NWR	Holt	MO	1/4/1991	F	A	-				
448-1	Squaw Creek NWR	Holt	MO	9/1/1992	F	1.5	-				0
448-2	Squaw Creek NWR	Holt	MO	9/1/1992	F	1.5	-				0
448-3	Squaw Creek NWR	Holt	MO	9/1/1992	F	1.5	-				0
448-4	Squaw Creek NWR	Holt	MO	9/1/1992	F	2.5	-				0
448-5	Squaw Creek NWR	Holt	MO	9/1/1992	F	4.5	-				0
EHRL-0528		Howard	MO		F	1.5	+				
SE01-037		Howell	MO		M	0.5	+				
SE01-038		Howell	MO		F	0.5	+				
SE01-042		Howell	MO		M	0.5	+				
SE01-044		Howell	MO		F	0.5	+				
SE01-039		Howell	MO		F	0.5	-				
SE01-041		Howell	MO		M	0.5	-				
501-1	Fleming Park	Jackson	MO	9/27/1994	F	2.5	++				1
501-2	Fleming Park	Jackson	MO	9/27/1994	F	2.5	+				1
501-3	Fleming Park	Jackson	MO	9/27/1994	F	3.5	+				1
501-4	Fleming Park	Jackson	MO	9/27/1994	F	4.5	+				1
501-5	Fleming Park	Jackson	MO	9/27/1994	F	5.5	+				1
450-1	Knob Nobster WMA	Johnson	MO	9/3/1992	M	2.5	+				2
450-2	Knob Nobster WMA	Johnson	MO	9/3/1992	F	3.5	+				2
450-3	Knob Nobster WMA	Johnson	MO	9/3/1992	F	2.5	+				2
450-4	Knob Nobster WMA	Johnson	MO	9/3/1992	F	1.5	+				2
450-5	Knob Nobster WMA	Johnson	MO	9/3/1992	M	1.5	+				2
EHRL-0526		Lewis	MO		M	1.5	+				
EHRL-0527		Lewis	MO		F	0.5	+				
EHRL-0529		Lewis	MO		M	1.5	+				
EHRL-0530		Lewis	MO		F	0.5	+				
SE01-191		Macon	MO		F	1.5	+				
SE01-192		Macon	MO		F	1.5	+				
SE01-194		Macon	MO		M	1.5	+				
SE01-196		Macon	MO		M	1.5	+				
SE01-385	Unit 45	Newton	MO	11/11/2001	M	0.5	+				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
SE01-387	Unit 45	Newton	MO	11/11/2001	M	0.5	+				
SE01-389	Unit 45	Newton	MO	11/11/2001	M	0.5	+				
SE01-393	Unit 45	Newton	MO	11/11/2001	M	0.5	+				
SE01-395	Unit 45	Newton	MO	11/11/2001	M	0.5	-				
EHRL-0538	Kansas City International Airport	Platte	MO		M	0.5	+				
EHRL-0539	Kansas City International Airport	Platte	MO		F	2.5	+				
EHRL-0535	Kansas City International Airport	Platte	MO		F	2.5	-				
EHRL-0536	Kansas City International Airport	Platte	MO		F	5.5	-				
EHRL-0537	Kansas City International Airport	Platte	MO		F	2.5	-				
EHRL-1121	Unionville	Putnam	MO	12/21/2002	M	0.5	+	+	-	-	
EHRL-1122	Unionville	Putnam	MO	12/21/2002	F	0.5	+	+	4 (b)	3 (b)	
EHRL-1124	Unionville	Putnam	MO	12/21/2002	F	1.5	+	-	-		
EHRL-1123	Unionville	Putnam	MO	12/21/2002	M	0.5	-	+	5 (b)	4 (b)	
SE91-231	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	0.5	+				
SE91-232	Busch Wildlife Area	St. Charles	MO	1/4/1991	M	1.5	+				
SE91-233	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	0.5	+				
SE91-234	Busch Wildlife Area	St. Charles	MO	1/4/1991	M	0.5	+				
SE91-236	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	0.5	+				
SE91-237	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	0.5	+				
SE91-238	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	0.5	+				
SE91-239	Busch Wildlife Area	St. Charles	MO	1/4/1991	M	1.5	+				
SE91-240	Busch Wildlife Area	St. Charles	MO	1/4/1991	M	2.5	+				
SE91-241	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	0.5	+				
SE91-242	Busch Wildlife Area	St. Charles	MO	1/4/1991	M	0.5	+				
SE91-243	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	2.5	+				
SE91-244	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	2.5	+				
SE91-245	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	2.5	+				
SE91-230	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	1.5	-				
SE91-235	Busch Wildlife Area	St. Charles	MO	1/4/1991	F	0.5	-				
SE01-168		St. Clair	MO				+				
SE01-170		St. Clair	MO				+				
SE01-166		St. Clair	MO				-	-	-		
SE01-169		St. Clair	MO				-	-	-		
SE01-165		St. Clair	MO				-				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
EHRL-0359		St. Louis	MO	2/19/1998			+				
EHRL-0355		St. Louis	MO	12/23/1997			-				
EHRL-0356		St. Louis	MO	1/15/1998			-				
EHRL-0357		St. Louis	MO	2/10/1998			-				
EHRL-0358		St. Louis	MO	2/24/1998			-				
SE01-159		Vernon	MO	11/16/2001	M	1.5	+				
SE01-160		Vernon	MO	11/16/2001	M	1.5	+				
515-1	St. Catherine's Creek NWR	Adams	MS	9/12/1995	F	1	+				1
515-2	St. Catherine's Creek NWR	Adams	MS	9/12/1995	F	1	+				0
515-4	St. Catherine's Creek NWR	Adams	MS	9/12/1995	F	3	+				0
579-1	St. Catherine's Creek NWR	Adams	MS	9/20/1999	F	3.5	+				0
579-2	St. Catherine's Creek NWR	Adams	MS	9/20/1999	F	1.5	+				0
579-3	St. Catherine's Creek NWR	Adams	MS	9/20/1999	F	7.5	+				1
579-4	St. Catherine's Creek NWR	Adams	MS	9/20/1999	F	1	+				1
515-3	St. Catherine's Creek NWR	Adams	MS	9/12/1995	F	1	-				0
515-5	St. Catherine's Creek NWR	Adams	MS	9/12/1995	F	1	-				0
579-5	St. Catherine's Creek NWR	Adams	MS	9/20/1999	M	2.5	-				0
SE99-584		Alcorn/ Prentiss	MS				-				
SE99-585		Alcorn/ Prentiss	MS				-				
SE99-588		Alcorn/ Prentiss	MS				-				
SE99-589		Alcorn/ Prentiss	MS				-				
SE99-590		Alcorn/ Prentiss	MS				-				
SE95-0734	Longleaf Farms	Amite	MS	6/17/1905		2.5	+				
SE95-0735	Longleaf Farms	Amite	MS	6/17/1905		1.5	+				
SE95-0736	Longleaf Farms	Amite	MS	6/17/1905		1.5	+				
SE95-0732	Longleaf Farms	Amite	MS	6/17/1905		1.5	-				
SE95-0733	Longleaf Farms	Amite	MS	6/17/1905		1.5	-				
456-1	Dahomey NWR	Bolivar	MS	9/24/1992	F	4.5	+				0
456-4	Dahomey NWR	Bolivar	MS	9/24/1992	F	4.5	+				0

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
456-5	Dahomey NWR	Bolivar	MS	9/24/1992	F	3.5	+				0
540-1	Dahomey NWR	Bolivar	MS	9/4/1997	F	4	+	-	-		0
540-2	Dahomey NWR	Bolivar	MS	9/4/1997	F	7	+	-	-		1
540-3	Dahomey NWR	Bolivar	MS	9/4/1997	F	6	+	-	-		1
456-2	Dahomey NWR	Bolivar	MS	9/24/1992	F	3.5	-				0
456-3	Dahomey NWR	Bolivar	MS	9/24/1992	M	3.5	-				0
540-4	Dahomey NWR	Bolivar	MS	9/4/1997	F	2.5	-	-	-		1
540-5	Dahomey NWR	Bolivar	MS	9/4/1997	F	2.5	-	-			0
SE99-539	Box B	Carroll	MS				+				
SE99-542	Box B	Carroll	MS				+				
SE99-544	Box B	Carroll	MS				+				
SE99-545	Box B	Carroll	MS				+				
SE99-540	Box B	Carroll	MS				-				
SE00-654	Chickasaw WMA	Chickasaw/ Pontotoc	MS	3/15/2001	F	4.5	+				
SE00-655	Chickasaw WMA	Chickasaw/ Pontotoc	MS	3/15/2001	F	3.5	+				
SE00-657	Chickasaw WMA	Chickasaw/ Pontotoc	MS	3/15/2001	F	3.5	+				
SE00-656	Chickasaw WMA	Chickasaw/ Pontotoc	MS	3/15/2001	F	2.5	-				
SE00-792	Choctaw WMA	Choctaw/ Winston	MS	2/28/2001	F	6.5	+				
SE00-793	Choctaw WMA	Choctaw/ Winston	MS	2/28/2001	F	4.5	+				
SE00-794	Choctaw WMA	Choctaw/ Winston	MS	2/28/2001	F	5.5	+				
SE00-795	Choctaw WMA	Choctaw/ Winston	MS	2/28/2001	F	2.5	+				
SE00-796	Choctaw WMA	Choctaw/ Winston	MS	2/28/2001	F	2.5	+				
SE99-568	Canemount Plantation	Claiborne	MS				+				
SE99-569	Canemount Plantation	Claiborne	MS				+				
SE99-571	Canemount Plantation	Claiborne	MS				+				

							PCR results					
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE99-572	Canemount Plantation	Claiborne	MS				-				
SE99-573	Canemount Plantation	Claiborne	MS				-				
SE99-601	Deviney	Copiah	MS				+				
SE99-604	Deviney	Copiah	MS				+				
SE99-609	Deviney	Copiah	MS				+				
SE99-610	Deviney	Copiah	MS				+				
SE99-611	Deviney	Copiah	MS				+				
SE99-629	Camp Shelby Contonement	Forrest	MS				+				
SE99-633	Camp Shelby Contonement	Forrest	MS				+				
SE99-636	Camp Shelby Contonement	Forrest	MS				+				
SE99-631	Camp Shelby Contonement	Forrest	MS				-				
SE99-635	Camp Shelby Contonement	Forrest	MS				-				
SE95-0934	Pascagoula WMA	George	MS	6/17/1905		2.5	-				
SE95-0935	Pascagoula WMA	George	MS	6/17/1905		7.5+	-				
SE95-0936	Pascagoula WMA	George	MS	6/17/1905		0.5	-				
SE95-0937	Pascagoula WMA	George	MS	6/17/1905		0.5	-				
SE95-0938	Pascagoula WMA	George	MS	6/17/1905		0.5	-				
SE99-553	Malmaison WMA	Grenada	MS				+				
SE99-554	Malmaison WMA	Grenada	MS				+				
SE99-555	Malmaison WMA	Grenada	MS				+				
SE99-552	Malmaison WMA	Grenada	MS				-				
SE99-556	Malmaison WMA	Grenada	MS				-				
SE00-688	Army Ammo Plant	Hancock	MS	3/19/2001	F	2.5	-				
SE00-690	Army Ammo Plant	Hancock	MS	3/19/2001	F	4.5	-				
SE00-691	Army Ammo Plant	Hancock	MS	3/19/2001	F	6.5	-				
SE00-692	Army Ammo Plant	Hancock	MS	3/19/2001	F	5.5	-				
SE00-693	Army Ammo Plant	Hancock	MS	3/19/2001	F	2.5	-				
538-3	Hillside NWR	Holmes	MS	9/3/1997	F	2.5	+	-	-		1
538-5	Hillside NWR	Holmes	MS	9/3/1997	F	2.5	+	-	-		0
538-1	Hillside NWR	Holmes	MS	9/3/1997	F	2.5	-	-	-		1
538-2	Hillside NWR	Holmes	MS	9/3/1997	F	2.5	-	-	-		1
538-4	Hillside NWR	Holmes	MS	9/3/1997	M	1.5	-	-	-		0
SE00-667	Black Bear Plantation	Issaquena	MS	2/28/2001	F	2.5	-				
SE00-670	Black Bear Plantation	Issaquena	MS	2/28/2001	F	4.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE00-671	Black Bear Plantation	Issaquena	MS	2/28/2001	F	2.5	-				
SE00-672	Black Bear Plantation	Issaquena	MS	2/28/2001	F	2.5	-				
457-1	Mississippi Sandhill Crane NWR	Jackson	MS	9/21/1992	F	3.5	-				0
457-2	Mississippi Sandhill Crane NWR	Jackson	MS	9/21/1992	M	1	-				0
457-3	Mississippi Sandhill Crane NWR	Jackson	MS	9/21/1992	M	1	-				0
457-4	Mississippi Sandhill Crane NWR	Jackson	MS	9/21/1992	F	4	-				0
457-5	Mississippi Sandhill Crane NWR	Jackson	MS	9/21/1992	F	2	-				0
SE99-421	Tallahala WMA	Jasper	MS				+				
SE99-424	Tallahala WMA	Jasper	MS				+				
SE99-432	Tallahala WMA	Jasper	MS				+				
SE99-423	Tallahala WMA	Jasper	MS				-				
SE99-431	Tallahala WMA	Jasper	MS				-				
SE00-595	Chickasawhay WMA	Jones/ Wayne/ Greene	MS	3/7/2001	F	3.5	+				
SE00-596	Chickasawhay WMA	Jones/ Wayne/ Greene	MS	3/7/2001	F	2.5	+				
SE00-597	Chickasawhay WMA	Jones/ Wayne/ Greene	MS	3/7/2001	F	1.5	+				
SE00-598	Chickasawhay WMA	Jones/ Wayne/ Greene	MS	3/7/2001	F	5.5	+				
SE00-599	Chickasawhay WMA	Jones/ Wayne/ Greene	MS	3/7/2001	F	3.5	+				
SE99-439	Sardis WMA	Lafayette	MS				+				
SE99-440	Sardis WMA	Lafayette	MS				+				
SE99-441	Sardis WMA	Lafayette	MS				+				
SE99-442	Sardis WMA	Lafayette	MS				+				
SE99-443	Sardis WMA	Lafayette	MS				+				
SE00-634	Black Prairie WMA	Lowndes	MS	2/26/2001	F	3.5	+				
SE00-636	Black Prairie WMA	Lowndes	MS	2/26/2001	F	5.5	+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE00-639	Black Prairie WMA	Lowndes	MS	2/26/2001	F	4.5	+				
SE00-641	Black Prairie WMA	Lowndes	MS	2/26/2001	F	2.5	+				
SE00-640	Black Prairie WMA	Lowndes	MS	2/26/2001	F	1.5	-				
SE91-336	Marion Co. WMA	Marion	MS	10/1/1991	M	1.5	+				
SE91-337	Marion Co. WMA	Marion	MS	11/2/1991	M	1.5	+				
SE91-338	Marion Co. WMA	Marion	MS	11/2/1991	F	3.5	+				
SE91-339	Marion Co. WMA	Marion	MS	11/9/1991	F	3.5	+				
SE91-340	Marion Co. WMA	Marion	MS	11/19/1991	F	5.5	+				
SE00-766	Audobon Society	Marshall	MS	3/2/2001	F	5	++				
SE00-762	Audobon Society	Marshall	MS	3/2/2001	F	3	+				
SE00-763	Audobon Society	Marshall	MS	3/2/2001	F	3	+				
SE00-764	Audobon Society	Marshall	MS	3/2/2001	F	5	+				
SE00-765	Audobon Society	Marshall	MS	3/2/2001	F	3	+				
417-1	Noxubee NWR	Noxubee	MS	7/10/1991	F	2	+				1
417-2	Noxubee NWR	Noxubee	MS	7/10/1991	F	5	+				1
417-3	Noxubee NWR	Noxubee	MS	7/10/1991	M	1	+				1
417-4	Noxubee NWR	Noxubee	MS	7/10/1991	F	3	+				0
417-5	Noxubee NWR	Noxubee	MS	7/10/1991	M	1	+				1
SE99-470	Leaf River WMA	Perry	MS				+				
SE99-471	Leaf River WMA	Perry	MS				+				
SE99-473	Leaf River WMA	Perry	MS				+				
SE99-469	Leaf River WMA	Perry	MS				-				
SE99-472	Leaf River WMA	Perry	MS				-				
SE99-497	Canal Section WMA	Prentiss/ Itawamba/ Monroe	MS				+				
SE99-494	Canal Section WMA	Prentiss/ Itawamba/ Monroe	MS				-				
SE99-496	Canal Section WMA	Prentiss/ Itawamba/ Monroe	MS				-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE99-498	Canal Section WMA	Prentiss/ Itawamba/ Monroe	MS				-				
SE99-500	Canal Section WMA	Prentiss/ Itawamba/ Monroe	MS				-				
SE00-769	Okeefe WMA	Quitman	MS	3/22/2001	F	3	+				
SE00-770	Okeefe WMA	Quitman	MS	3/22/2001	F	4	-				
SE00-771	Okeefe WMA	Quitman	MS	3/22/2001	F	1	-				
SE99-399	Caney Creek WMA	Scott	MS				+				
SE99-397	Caney Creek WMA	Scott	MS				+				
SE99-398	Caney Creek WMA	Scott	MS				+				
SE99-400	Caney Creek WMA	Scott	MS				-				
SE99-401	Caney Creek WMA	Scott	MS				-				
SE00-619	Sunflower WMA (South)	Sharkey	MS	2/20/2001	F	3.5	-				
SE00-620	Sunflower WMA (South)	Sharkey	MS	2/20/2001	M	2.5	-				
SE00-621	Sunflower WMA (South)	Sharkey	MS	2/20/2001	F	4.5	-				
SE00-629	Sunflower WMA (North)	Sharkey	MS	2/20/2001	F	5.5	-				
SE00-630	Sunflower WMA (North)	Sharkey	MS	2/21/2001	F	5.5	-				
SE00-659	Little Biloxi WMA	Stone/ Harrison	MS	3/27/2001	F	3.5	-				
SE00-660	Little Biloxi WMA	Stone/ Harrison	MS	3/27/2001	F	2.5	-				
SE00-662	Little Biloxi WMA	Stone/ Harrison	MS	3/27/2001	F	1.5	-				
SE00-663	Little Biloxi WMA	Stone/ Harrison	MS	3/27/2001	F	1.5	-				
SE00-842	Tallahatchie/Pinhook	Tippah	MS	2/26/2001	F	1	+				
SE00-844	Tallahatchie/Pinhook	Tippah	MS	2/26/2001	F	1	+				
SE00-846	Tallahatchie/Pinhook	Tippah	MS	2/26/2001	F	5	+				
SE00-848	Tallahatchie/Pinhook	Tippah	MS	2/26/2001	F	3	+				
SE00-847	Tallahatchie/Pinhook	Tippah	MS	2/26/2001	F	3	-				
SE99-591	Divide Section WMA	Tishomingo	MS				+				
SE99-592	Divide Section WMA	Tishomingo	MS				+				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	PCR results: VLPT	PCR results: 120-kDa	LST
SE99-593	Divide Section WMA	Tishomingo	MS				+				
SE99-596	Divide Section WMA	Tishomingo	MS				+				
SE99-597	Divide Section WMA	Tishomingo	MS				+				
SE00-723	Sandfield HC	Warren	MS	3/22/2001	F	5.5	-				
SE00-724	Sandfield HC	Warren	MS	3/22/2001	F	1.5	-				
SE00-726	Sandfield HC	Warren	MS	3/22/2001	F	2.5	-				
SE00-727	Sandfield HC	Warren	MS	3/22/2001	F	3.5	-				
SE00-728	Sandfield HC	Warren	MS	3/22/2001	F	4.5	-				
332-12	Yazoo NWR	Washington	MS	9/12/1986	F	3.5	-				0
332-13	Yazoo NWR	Washington	MS	9/12/1986	F	1.5	-				0
332-14	Yazoo NWR	Washington	MS	9/12/1986	M	1.5	-				0
332-15	Yazoo NWR	Washington	MS	9/12/1986	F	3.5	-				0
332-16	Yazoo NWR	Washington	MS	9/12/1986	F	3.5	-				0
539-1	Yazoo NWR	Washington	MS	9/4/1997	F	2.5	-	-	-		0
539-2	Yazoo NWR	Washington	MS	9/4/1997	F	3.5	-	-	-		0
539-3	Yazoo NWR	Washington	MS	9/4/1997	F	1.5	-	-	-		0
539-4	Yazoo NWR	Washington	MS	9/4/1997	F	3.5	-	-	-		0
539-5	Yazoo NWR	Washington	MS	9/4/1997	F	2.5	-	-	-		0
606-1	Panther Swamp NWR	Yazoo	MS	8/20/2001	F	0.75	+	+	5 (b)	4 (b)	0
606-2	Panther Swamp NWR	Yazoo	MS	8/20/2001	F	4.5	+				0
606-4	Panther Swamp NWR	Yazoo	MS	8/20/2001	F	2.5	+				0
332-06	Panther Swamp NWR	Yazoo	MS	9/10/1986	F	3.5	-				0
332-07	Panther Swamp NWR	Yazoo	MS	9/10/1986	F	4.5	-				0
332-08	Panther Swamp NWR	Yazoo	MS	9/10/1986	F	3.5	-				0
332-09	Panther Swamp NWR	Yazoo	MS	9/10/1986	F	1.5	-				0
332-10	Panther Swamp NWR	Yazoo	MS	9/10/1986	F	3.5	-				0
606-3	Panther Swamp NWR	Yazoo	MS	8/20/2001	F	1.5	-	-	-		0
606-5	Panther Swamp NWR	Yazoo	MS	8/20/2001	M	1.0	-	-	-		0
CC222-02		Alamance	NC	8/31/2002	F	1.5	+	-	-		
EHRL-1050		Alamance	NC	11/20/2002	F	3.5	-				
EHRL-1051		Alamance	NC	11/20/2002	M	2.5	-				
CC365-02		Alheghany	NC	10/18/2002			-				
349-1	Pee Dee NWR	Anson	NC	7/23/1987	F	4	-				0
349-2	Pee Dee NWR	Anson	NC	7/23/1987	M	1	-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
349-3	Pee Dee NWR	Anson	NC	7/23/1987	F	2	-				0
349-4	Pee Dee NWR	Anson	NC	7/23/1987	F	1	-				0
349-5	Pee Dee NWR	Anson	NC	7/23/1987	F	2	-				0
623-3	Pee Dee NWR	Anson/ Richmond	NC	8/21/2002	F	1.5	+	-	-		1
623-5	Pee Dee NWR	Anson/ Richmond	NC	8/21/2002	F	1.5	+	-	-		2
623-1	Pee Dee NWR	Anson/ Richmond	NC	8/21/2002	M	1.5	-	-	-		1
623-2	Pee Dee NWR	Anson/ Richmond	NC	8/21/2002	F	7.5	-	-	-		1
623-4	Pee Dee NWR	Anson/ Richmond	NC	8/21/2002	F	1.25	-	- (b)	- (b), 5 (c)	3 (c)	1
CC294-02		Beaufort	NC	9/25/2002			-	-	-	-	
622-6	Roanoke River NWR	Bertie	NC	8/19/2002			+	-	-		
CC269-02C	southern part of county	Bertie	NC				+	-	-		
622-1	Roanoke River NWR	Bertie	NC	8/19/2002		2.5	-	-	-		0
622-2	Roanoke River NWR	Bertie	NC	8/19/2002		0.75	-	-	-		0
622-3	Roanoke River NWR	Bertie	NC	8/19/2002		0.75	-	-	-		1
622-4	Roanoke River NWR	Bertie	NC	8/19/2002		0.9	-	-	-		0
622-5	Roanoke River NWR	Bertie	NC	8/19/2002		3.5	-	-	-		0
CC269-02A	central part of county	Bertie	NC		M	0.5	-	+	4,5 (b)	3 (b)	
EHRL-1087	Sunny Point, US Army Base, Southport	Brunswick	NC	12/8/2002	F	3.5	+				
EHRL-1088	Sunny Point, US Army Base, Southport	Brunswick	NC	11/16/2002	F	4.5	+				
EHRL-1089	Sunny Point, US Army Base, Southport	Brunswick	NC	11/8/2002	F	0.5	+	-	-		
EHRL-1090	Sunny Point, US Army Base, Southport	Brunswick	NC	11/9/2002		3.5	+				
EHRL-1091	Sunny Point, US Army Base, Southport	Brunswick	NC	11/15/2002	M	1.5	-	-	4 (b)	3 (b)	
260-3	Biltmore Estates	Buncombe	NC	7/27/1982	F	4	+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
260-4	Biltmore Estates	Buncombe	NC	7/27/1982	F	2	+				
260-1	Biltmore Estates	Buncombe	NC	7/27/1982	F	2	-				
260-2	Biltmore Estates	Buncombe	NC	7/27/1982	F	0.66	-				
260-5	Biltmore Estates	Buncombe	NC	7/27/1982	F	4	-				
EHRL-1100	Hwy 181 Perry's Store	Burke	NC	12/9/2002	M	2.5	-				
EHRL-1101	Hwy 181 Perry's Store	Burke	NC	12/9/2002	F	0.5	-				
EHRL-1097	Hwy 181 Perry's Store	Burke	NC	12/9/2002	M	5.5	-				
EHRL-1098	Hwy 181 Perry's Store	Burke	NC	12/9/2002	M	1.5	-				
EHRL-1099	Hwy 181 Perry's Store	Burke	NC	12/9/2002	M	2.5	-				
CC217-02	north of Mt. Pleasant	Cabarrus	NC	9/1/2002	F	1.5	-	-	-		0
EHRL-1106	Lakens Island	Carteret	NC		F	1.5	+	-	-	-	
EHRL-1110	Lakens Island	Carteret	NC		F	5.5	+	-	-		
EHRL-1111	Lakens Island	Carteret	NC		F	0.5	+	+	4 (b)	4 (b)	
EHRL-1112	Lakens Island	Carteret	NC		F	2.5	+	-	-		
EHRL-1113	Lakens Island	Carteret	NC		F	1.5	+	-	-	-	
CC244-02A		Caswell	NC				+	-	-		
CC223-02		Caswell	NC	8/31/2002	M	1.5	-	-	-		
SE99-342	Ft. Bragg	Cumberland/ Hoke/Moore/ Harnett	NC	11/20/1999	F	1.5	+				
SE99-343	Ft. Bragg	Cumberland/ Hoke/Moore/ Harnett	NC	11/20/1999	M	1.5	+				
SE99-344	Ft. Bragg	Cumberland/ Hoke/Moore/ Harnett	NC	11/20/1999	M	1.5	+				
SE99-346	Ft. Bragg	Cumberland/ Hoke/Moore/ Harnett	NC	11/25/1999	M	2.5	+				
SE99-345	Ft. Bragg	Cumberland/ Hoke/Moore/ Harnett	NC	11/20/1999	F	3.5	-				
368-1	MacKay Island NWR	Currituck	NC	8/15/1988	F	3	+				1
368-3	MacKay Island NWR	Currituck	NC	8/15/1988	M	1	+				1

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
368-4	MacKay Island NWR	Currituck	NC	8/15/1988	F	2	+				1
368-5	MacKay Island NWR	Currituck	NC	8/15/1988	F	3	+				2
474-1	MacKay Island NWR	Currituck	NC	7/28/1993	M	2.5	+				1
474-2	MacKay Island NWR	Currituck	NC	7/28/1993	F	6.5	+				1
474-3	MacKay Island NWR	Currituck	NC	7/28/1993	F	3.5	+				0
474-4	MacKay Island NWR	Currituck	NC	7/28/1993	F	1.5	+				2
474-5	MacKay Island NWR	Currituck	NC	7/28/1993	F	5.5	+				1
610-1	MacKay Island NWR	Currituck	NC	9/7/2001	F	2.5	+				1
610-2	MacKay Island NWR	Currituck	NC	9/7/2001	M	1	+	-	-		1
610-3	MacKay Island NWR	Currituck	NC	9/7/2001	F	1	+	-	-		1
610-4	MacKay Island NWR	Currituck	NC	9/7/2001	F	2.5	+				1
610-5	MacKay Island NWR	Currituck	NC	9/7/2001	F	5.5	+				1
368-2	MacKay Island NWR	Currituck	NC	8/15/1988	M	2	-				1
320-01	Alligator River NWR	Dare	NC	9/5/1985	F	3	+				2
320-02	Alligator River NWR	Dare	NC	9/5/1985	M	3	+				2
320-03	Alligator River NWR	Dare	NC	9/5/1985	F	2	+				2
320-04	Alligator River NWR	Dare	NC	9/5/1985	M	2	+				2
320-05	Alligator River NWR	Dare	NC	9/5/1985	M	4	+				1
506-1	Nags Head Woods	Dare	NC	10/3/1994	F	3	+				NA
569-2	Alligator River NWR	Dare	NC	9/16/1998	M	2.5	+				2
569-3	Alligator River NWR	Dare	NC	9/16/1998	M	6.5	+				3
569-4	Alligator River NWR	Dare	NC	9/16/1998	M	2.5	+				1
569-5	Alligator River NWR	Dare	NC	9/16/1998	M	1.5	+				1
590-2	Wright Brothers Memorial/Nagshead Woods, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	F	1.5	+	-	-		2
590-3	Wright Brothers Memorial/Nagshead Woods, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	M	3.5	+	-	-		3
590-4	Wright Brothers Memorial/Nagshead Woods, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	F	1.5	+	+	4 (b)	-	1

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	VLPT	120-kDa	LST
590-5	Wright Brothers Memorial/Nagshead Woods, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	F	1.5	+	+	-	-	2
590-6	Wright Brothers Memorial/Nagshead Woods, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	F	1.5	+	-	-		1
591-1	Bodie Island, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	M	1.5	+	+	4 (b)	-	3
591-2	Bodie Island, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	F	2.5	+	-	-		3
591-3	Bodie Island, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	F	1	+	-	-		2
591-4	Bodie Island, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	F	2.5	+	-	-		3
591-5	Bodie Island, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	F	3.5	+				3
506-2	Nags Head Woods	Dare	NC	10/3/1994	F	1	-				NA
506-3	Nags Head Woods	Dare	NC	10/3/1994	F	3	-				NA
506-4	Nags Head Woods	Dare	NC	10/3/1994	M	2	-				NA
506-5	Nags Head Woods	Dare	NC	10/3/1994	F	4	-				NA
569-1	Alligator River NWR	Dare	NC	9/16/1998	M	1.5	-				1
590-1	Wright Brothers Memorial/Nagshead Woods, Cape Hatteras Nat'l Seashore	Dare	NC	10/2/2000	F	0.3	-	+	4 (b)	4 (b)	0
EHRL-0977	Denton check station	Davidson	NC	11/9/2002	M	1.5	+	-	-		
EHRL-0978	Denton check station	Davidson	NC	11/9/2002	M	2.5	+				
EHRL-0979	Denton check station	Davidson	NC	11/9/2002	M	1.5	+	-	-		
EHRL-0980	Denton check station	Davidson	NC	11/9/2002	M	2.5	+				
CC242-02	Salsbury	Davidson	NC	9/9/2002			-	-	-		
EHRL-0981	Denton check station	Davidson	NC	11/9/2002	M	1.5	-	-	-		
EHRL-0951	Drum Hill	Gates	NC	10/24/2002	M	>1.5	+				
EHRL-0953	Corapeake	Gates	NC	10/26/2002	F	0.5	+	-	-		
EHRL-0954	Gatesville	Gates	NC	10/26/2002	M	>1.5	+				
EHRL-0955	Gatesville	Gates	NC	11/1/2002	M	>1.5	+				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
433-1	Granville	Granville	NC	9/11/1991	F	2.5	+				1
433-2	Granville	Granville	NC	9/11/1991	F	3.5	+				1
433-3	Granville	Granville	NC	9/11/1991	M	1.5	+				1
433-4	Granville	Granville	NC	9/11/1991	F	1.5	+				1
433-5	Granville	Granville	NC	9/11/1991	F	5.5	+				1
CC244-02B		Granville	NC		M	2.5	+	+	4 (b)	4 (b)	
CC225-02	Glenview	Halifax	NC	8/29/2002			-	-	-		
354-1	Cameron Property	Hyde	NC	7/28/1987	F	2	+				2
354-2	Cameron Property	Hyde	NC	7/28/1987	F	2	+				2
354-3	Cameron Property	Hyde	NC	7/28/1987	F	5	+				1
354-4	Cameron Property	Hyde	NC	7/28/1987	F	4	+				2
354-5	Cameron Property	Hyde	NC	7/28/1987	F	5	+				3
599-1	Mattamukseet NWR	Hyde	NC	10/4/2000	M	2.5	+	-	-		2
599-2	Mattamukseet NWR	Hyde	NC	10/4/2000	F	1.5	+	-	4 (b)	-	2
599-3	Mattamukseet NWR	Hyde	NC	10/4/2000	F	7.5	+	-	-		1
599-4	Mattamukseet NWR	Hyde	NC	10/4/2000	F	1.5	+	+	4 (b)	4 (b)	1
599-5	Mattamukseet NWR	Hyde	NC	10/4/2000	F	8.5	-	-	-		1
CC377-02	Blackman Cross Road	Johnston	NC	10/23/2002			+	-	4 (b)	-	
587-1	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	8/24/2000	F	3.5	+	-	-		0
587-2	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	8/24/2000	F	1	+	-	-		0
504-02	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	9/12/1994	F	5	-				
504-03	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	9/12/1994	F	4	-				
504-04	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	9/12/1994	F	4	-				
504-05	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	9/12/1994	F	6	-				
504-06	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	9/12/1994	F	2	-				
504-08	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	9/12/1994	F	3	-				
573-1	Latta Plantation Nature Preserve	Mecklenburg	NC	8/20/1998	F	3.5	-				
573-2	Latta Plantation Nature Preserve	Mecklenburg	NC	8/20/1998	F	4.5	-				
573-3	Latta Plantation Nature Preserve	Mecklenburg	NC	8/20/1998	F	2.5	-				
573-4	Latta Plantation Nature Preserve	Mecklenburg	NC	8/20/1998	F	3.5	-				
573-5	Latta Plantation Nature Preserve	Mecklenburg	NC	8/20/1998	F	1.5	-				
587-3	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	8/24/2000	M	1	-				0
587-4	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	8/24/2000	F	2	-				0
587-5	Cowan's Ford Wildlife Refuge	Mecklenburg	NC	8/24/2000	F	2	-				0

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
SE91-164	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	1.5	+				
SE91-165	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	1.5	+				
SE91-167	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	2.5	+				
SE91-170	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	1.5	+				
SE91-173	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	2.5	+				
SE91-178	Uwharrie Game Lands	Montgomery	NC	12/4/1991	M	1.5	+				
SE91-179	Uwharrie Game Lands	Montgomery	NC	12/4/1991	F	2.5	+				
SE91-180	Uwharrie Game Lands	Montgomery	NC	12/4/1991	F	2.5	+				
SE91-181	Uwharrie Game Lands	Montgomery	NC	12/4/1991	F	2.5	+				
SE91-182	Uwharrie Game Lands	Montgomery	NC	12/7/1991	F	2.5	+				
SE91-183	Uwharrie Game Lands	Montgomery	NC	12/4/1991	M	1.5	+				
SE91-186	Uwharrie Game Lands	Montgomery	NC	12/5/1991	M	2.5	+				
SE91-187	Uwharrie Game Lands	Montgomery	NC	12/6/1991	F	1.5	+				
SE91-166	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	1.5	-				
SE91-168	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	1.5	-				
SE91-169	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	1.5	-				
SE91-171	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	1.5	-				
SE91-172	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	1.5	-				
SE91-174	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	1.5	-				
SE91-175	Uwharrie Game Lands	Montgomery	NC	11/18/1991	M	1.5	-				
SE91-185	Uwharrie Game Lands	Montgomery	NC	12/4/1991	F	2.5	-				
SE91-188	Uwharrie Game Lands	Montgomery	NC	12/7/1991	F	2.5	-				
CC359-02		Northampton	NC	10/17/2002			+	-	-		
CC326-02		Onslow	NC				+	-	-	-	
CC224-02		Orange	NC	9/1/2002	F	2.5	-	-	-		
EHRL-1138		Pitt	NC	1/8/2003	F	0.5	+	-	5 (b)	2 (b)	
EHRL-1139		Pitt	NC	1/8/2003	F	3.5	+				
EHRL-1137		Pitt	NC	1/8/2003	F	1.5	-	-	-		
EHRL-1140		Pitt	NC	1/8/2003	F	5.5	-				
EHRL-1081	Big Buck HC (6mi S of Alleton, Hwy 211)	Robeson	NC	11/2/2002	M	1.5	+	-	-		
EHRL-1082	Big Buck HC (6mi S of Alleton, Hwy 211)	Robeson	NC	11/8/2002	F	2.5	+				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	 VLPT	 120-kDa	 LST
EHRL-1083	Big Buck HC (6mi S of Alleton, Hwy 211)	Robeson	NC	10/28/2002	F	1.5	+	-	-		
EHRL-1085	Big Buck HC (6mi S of Alleton, Hwy 211)	Robeson	NC	11/5/2002	F	2.5	+				
EHRL-1086	Big Buck HC (6mi S of Alleton, Hwy 211)	Robeson	NC	11/1/2002	M	1.5	+	-	-		
CC216-02	near Spenser (eastern part of Co.)	Rowan	NC	8/30/2002	F	2.5	-	-	-		0
EHRL-0789	near New Hill	Wake	NC	3/30/2002	F	>1	+	-	-		
EHRL-0790	near New Hill	Wake	NC	3/30/2002	M	1	+	-	4 (b)	4 (b)	
568-1	Pocosin Lakes NWR	Washington/ Tyrrell/Hyde	NC	9/15/1998	F	4.5	+				2
568-2	Pocosin Lakes NWR	Washington/ Tyrrell/Hyde	NC	9/15/1998	F	1.5	+				2
568-3	Pocosin Lakes NWR	Washington/ Tyrrell/Hyde	NC	9/15/1998	F	3.5	+				2
568-4	Pocosin Lakes NWR	Washington/ Tyrrell/Hyde	NC	9/15/1998	F	0.5	+				2
568-5	Pocosin Lakes NWR	Washington/ Tyrrell/Hyde	NC	9/15/1998	F	7.5	+				3
EHRL-1104		Wilkes	NC	11/18/2002	F	1.5	-				
EHRL-1108		Wilkes	NC	11/18/2002	F	4.5	-				
EHRL-1109		Wilkes	NC	11/18/2002	F	2.5	-				
CC220-02		Wilkes	NC	9/3/2002			-				
EHRL-0834		Cumberland	NJ	12/3/2001	M	1.5	+	-	-		
EHRL-0840		Cumberland	NJ	12/3/2001	M	2.5	+				
EHRL-0841		Cumberland	NJ	12/3/2001	M	1.5	+	-	-		
EHRL-0842		Cumberland	NJ	12/3/2001	M	1.5	-	-	-		
EHRL-0843		Cumberland	NJ	12/3/2001	M	2.5	-				
EHRL-0844		Cumberland	NJ	12/3/2001	M	2.5	-				
EHRL-0830		Salem	NJ	12/3/2001	M	1.5	+	-	-		
EHRL-0831		Salem	NJ	12/3/2001	M	3.5	+				
EHRL-0833		Salem	NJ	12/3/2001	M	2.5	+				
EHRL-0832		Salem	NJ	12/3/2001	M	2.5	-				
EHRL-0869		Adair	OK		F		+				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	VLPT	120-kDa	LST
EHRL-0870		Adair	OK		F		+				
EHRL-0871		Adair	OK		F		+				
EHRL-0855		Blain	OK		F		-				
EHRL-0791	Cherokee GMA	Cherokee	OK	8/7/1985			+				
EHRL-0792	Cherokee GMA	Cherokee	OK	8/7/1985			+				
EHRL-0793	Cherokee GMA	Cherokee	OK	8/7/1985			+				
EHRL-0795	Cookson	Cherokee	OK	8/3/1989			+				
EHRL-0794	Cherokee GMA	Cherokee	OK	8/7/1985			-				
EHRL-0856		Comanche	OK		F		+				
EHRL-0857		Comanche	OK		F		+				
SE02-004		Hughes	OK				+				
SE02-008		Hughes	OK				+				
SE02-001		Hughes	OK				-				
SE02-007		Hughes	OK				-				
SE02-013		Hughes	OK				-				
EHRL-0852		Major	OK		F		+				
EHRL-0853		Major	OK		F		+				
EHRL-0850		Major	OK		F		-				
EHRL-0851		Major	OK		F		-				
EHRL-0854		Major	OK		F		-				
EHRL-0797	Spavinaw	Mayes	OK	7/23/1985			+				
EHRL-0798	Spavinaw	Mayes	OK	9/11/1987			+				
EHRL-0799	Spavinaw	Mayes	OK	7/23/1985			+				
EHRL-0214	Ft. Gibson	Muskogee	OK	9/8/2001	F	3.5	+				
EHRL-0215	Ft. Gibson	Muskogee	OK	9/8/2001	F	1.5	+	-	-		
EHRL-0216	Ft. Gibson	Muskogee	OK	9/8/2001	M	1.5	+	-	-		
EHRL-0217	Ft. Gibson	Muskogee	OK	9/8/2001	F	2.5	+				
EHRL-0213	Ft. Gibson	Muskogee	OK	9/8/2001	F	2.5	-	-	-		
EHRL-0804	Airport	Oklahoma	OK	3/10/1982			-				
EHRL-0805	Airport	Oklahoma	OK	3/10/1982			-				
EHRL-0806	Airport	Oklahoma	OK	3/10/1982			-				
EHRL-0807	Airport	Oklahoma	OK	3/10/1982			-				
EHRL-0808	Airport	Oklahoma	OK	3/10/1982			-				
EHRL-0818		Osage	OK				+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0819		Osage	OK				+				
EHRL-0820		Osage	OK				+				
EHRL-0821		Osage	OK				+				
EHRL-0822		Osage	OK				+				
EHRL-0811		Payne	OK	6/27/1990		3	+				
EHRL-0812		Payne	OK	6/27/1990		1	+				
SE02-002		Pontotoc	OK				+				
SE02-005		Pontotoc	OK				+				
SE02-006		Pontotoc	OK				+				
SE02-003		Pontotoc	OK				-				
SE02-009		Pontotoc	OK				-				
EHRL-0864		Woodward	OK		F		-				
EHRL-0865		Woodward	OK		F		-				
EHRL-0866		Woodward	OK		F		-				
EHRL-0867		Woodward	OK		F		-				
EHRL-0410		Abbeville	SC		F	1.5	+	-	-		
EHRL-0411		Abbeville	SC		M	1.5	+	-	-		
EHRL-0412		Abbeville	SC		F	1.5	+	-	-		
EHRL-0065	near Eden Hall	Abbeville	SC	10/22/1999	M	1.5	-				
EHRL-0066	near Eden Hall	Abbeville	SC	11/19/1999	M	3.5	-				
EHRL-0005	Savannah River Site	Aiken	SC	11/8/2000	M	1.5	-				
EHRL-0006	Savannah River Site	Aiken	SC	11/8/2000	M	3.5	-				
EHRL-0007	Savannah River Site	Aiken	SC	11/8/2000	M	3.5	-				
EHRL-0008	Savannah River Site	Aiken	SC	11/18/2000	M	4.5	-				
EHRL-0004	Savannah River Site	Aiken	SC	11/8/2000	M	2.5	-				
EHRL-0016	Savannah River Site	Allendale	SC	11/1/2000	M	.5	-				
EHRL-0017	Savannah River Site	Allendale	SC	11/1/2000	M	1.5	-				
EHRL-0018	Savannah River Site	Allendale	SC	11/1/2000	M	1.5	-				
EHRL-0019	Savannah River Site	Allendale	SC	11/1/2000	M	1.5	-				
EHRL-0020	Savannah River Site	Allendale	SC	11/1/2000	M	3.5	-				
EHRL-0067	Fants Grove WMA	Anderson	SC	12/12/2000	F	1.5	-				
EHRL-0068	Fants Grove WMA	Anderson	SC	12/12/2000	F	3.5	-				
EHRL-0070	Fants Grove WMA	Anderson	SC	12/12/2000	F	3.5	-				
EHRL-0071	Fants Grove WMA	Anderson	SC	12/14/2000	F	3.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0025	Savannah River Site	Barnwell	SC	11/4/2000	M	0.5	+				
EHRL-0022	Savannah River Site	Barnwell	SC	11/4/2000	M	1.5	-				
EHRL-0023	Savannah River Site	Barnwell	SC	11/4/2000	M	2.5	-				
EHRL-0024	Savannah River Site	Barnwell	SC	11/4/2000	F	5.5	-				
EHRL-0026	Savannah River Site	Barnwell	SC	11/4/2000	M	1.5	-				
SP-033	Sea Pines	Beaufort	SC	9/22/1996	F	2.6	+	-	-		
SP-034	Sea Pines	Beaufort	SC	9/23/1996	F	5.6	+	-	-		
SP-036	Sea Pines	Beaufort	SC	9/23/1996	F	2.6	+	-	-		
SP-037	Sea Pines	Beaufort	SC	9/23/1996	F	1.6	+	-	-		
SP-039	Sea Pines	Beaufort	SC	9/23/1996	M	1.6	+	-	-		
SP-040	Sea Pines	Beaufort	SC	9/24/1996	F	1.6	+	-	-		
SP-041	Sea Pines	Beaufort	SC	9/24/1996	F	0.5	+	-			
SP-060	Sea Pines	Beaufort	SC	9/14/1997	F	2.5	+	-	-		
SP-061	Sea Pines	Beaufort	SC	9/15/1997	M	1.6	+	-	-		
SP-062	Sea Pines	Beaufort	SC	9/15/1997	F	3.6	+	-	-		
SP-063	Sea Pines	Beaufort	SC	9/16/1997	F	1.6	+	-	-		
SP-064	Sea Pines	Beaufort	SC	9/18/1997	F	3.6	+	-	-		
SP-065	Sea Pines	Beaufort	SC	9/18/1997	F	1.6	+	-	-		
SP-524	Sea Pines	Beaufort	SC	9/18/1997	F	6.6	+	-	-		
SP-531	Sea Pines	Beaufort	SC	9/16/1997	F	8.6	+	-	-		
SP-550	Sea Pines	Beaufort	SC	9/16/1997	M	3.6	+	-	-		
SP-554	Sea Pines	Beaufort	SC	9/17/1997	F	4.6	+	-	-		
613-1	Fripp Island	Beaufort	SC	11/5/2001	F	4.5	+				0
613-2	Fripp Island	Beaufort	SC	11/5/2001	M	6.5	+				0
613-3	Fripp Island	Beaufort	SC	11/5/2001	F	7.5	+				0
613-4	Fripp Island	Beaufort	SC	11/5/2001	F	5.5	+				1
613-5	Fripp Island	Beaufort	SC	11/5/2001	F	1.5	+				1
SP-035	Sea Pines	Beaufort	SC	9/22/1996	F	3.6	-	-	-		
SP-038	Sea Pines	Beaufort	SC	9/23/1996	F	3.6	-	-	-		
SE99-359	Santee WMA	Berkeley	SC	11/13/1999	F	3.5	+				
SE99-360	Santee WMA	Berkeley	SC	11/13/1999	M	2.5	+				
SE99-361	Santee WMA	Berkeley	SC	11/13/1999	F	2.5	+				
SE99-362	Hellhole WMA	Berkeley	SC	12/17/1999	M	2.5	+				
SE99-363	Hellhole WMA	Berkeley	SC	12/17/1999	F	2.5	+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE99-366	Santee WMA	Berkeley	SC	12/4/1999	F	3.5	+				
SE99-358	Santee WMA	Berkeley	SC	11/13/1999	F	4.5	-				
SE99-364	Hellhole WMA	Berkeley	SC	12/17/1999	F	4.5	-				
348-2	Cape Romain NWR	Charleston	SC	7/21/1987	M	1	+				2
348-3	Cape Romain NWR	Charleston	SC	7/21/1987	F	5	+				1
348-5	Cape Romain NWR	Charleston	SC	7/21/1987	M	2	+				2
KI-33	Kiawah Island	Charleston	SC	9/3/1997	F	8	+	-	-		
KI-34	Kiawah Island	Charleston	SC	9/4/1997	F	1.6	+	-	-		
KI-37	Kiawah Island	Charleston	SC	9/5/1997	F	2.6	+	-	-		
KI-29	Kiawah Island	Charleston	SC	8/31/1997	F	2	+	-	-		
KI-32	Kiawah Island	Charleston	SC	9/2/1997	M	1.6	+	-	-		
348-1	Cape Romain NWR	Charleston	SC	7/21/1987	F	2	-				2
348-4	Cape Romain NWR	Charleston	SC	7/21/1987	F	1	-				2
564-1	Ace Basin NWR	Charleston	SC	8/31/1998	F	3.5	-				2
564-2	Ace Basin NWR	Charleston	SC	8/31/1998	M	1.5	-				2
KI-35	Kiawah Island	Charleston	SC	9/5/1997	F	<.3	-	-			
KI-36	Kiawah Island	Charleston	SC	9/5/1997	F	1.6	-	-	-		
KI-30	Kiawah Island	Charleston	SC	8/31/1997	M	1	-	-	-		
KI-31	Kiawah Island	Charleston	SC	9/2/1997	M	3.6	-	-	-		
429-4	Johnson Farm	Cherokee	SC	9/5/1991	M	1.5	+				0
429-1	Johnson Farm	Cherokee	SC	9/5/1991	F	4.5	-				0
429-2	Johnson Farm	Cherokee	SC	9/5/1991	F	1.5	-				0
429-3	Johnson Farm	Cherokee	SC	9/5/1991	F	1.5	-				1
429-5	Johnson Farm	Cherokee	SC	9/5/1991	F	0.5	-				0
EHRL-0475		Chester	SC	11/15/2001	M	0.5	+	-	-	-	
EHRL-0431		Chester	SC				-				
428-3	Carolina Sandhills NWR	Chesterfield	SC	9/4/1991	F	5.5	+				1
428-1	Carolina Sandhills NWR	Chesterfield	SC	9/4/1991	F	6.5	-				0
428-2	Carolina Sandhills NWR	Chesterfield	SC	9/4/1991	M	1.5	-				0
428-4	Carolina Sandhills NWR	Chesterfield	SC	9/4/1991	F	8.5	-				0
428-5	Carolina Sandhills NWR	Chesterfield	SC	9/4/1991	F	5.5	-				0
565-6	Santee NWR	Clarendon	SC	9/1/1998			-				0
325-01	Santee NWR	Clarendon	SC	7/22/1986	F	1	-				0
325-02	Santee NWR	Clarendon	SC	7/22/1986	F	5	-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
325-03	Santee NWR	Clarendon	SC	7/22/1986	F	1	-				0
325-04	Santee NWR	Clarendon	SC	7/22/1986	M	3	-				0
325-05	Santee NWR	Clarendon	SC	7/22/1986	F	6	-				0
565-1	Santee NWR	Clarendon	SC	9/1/1998	M	1.5	-				0
565-2	Santee NWR	Clarendon	SC	9/1/1998	F	5.5	-				0
565-3	Santee NWR	Clarendon	SC	9/1/1998	M	1.5	-				0
565-4	Santee NWR	Clarendon	SC	9/1/1998	F	4.5	-				0
565-5	Santee NWR	Clarendon	SC	9/1/1998	F	4.5	-				0
EHRL-0458	Lower Pee Dee HC	Dillon	SC	11/3/2001	M	2.5	+				
EHRL-0460	Lower Pee Dee HC	Dillon	SC	11/3/2001	F	5.5	+				
EHRL-0461	Lower Pee Dee HC	Dillon	SC	11/3/2001	F	4.5	+				
EHRL-0459	Lower Pee Dee HC	Dillon	SC	11/3/2001	M	3.5	-				
EHRL-0462	Lower Pee Dee HC	Dillon	SC	11/3/2001	F	3.5	-				
EHRL-0473		Fairfield	SC	11/15/2001	F	4.5	+				
EHRL-0474		Fairfield	SC	11/15/2001	M	1.5	+	-	-	-	
EHRL-0076	Dutchman WMA	Fairfield	SC	12/15/2000	M	0.5	-				
EHRL-0476		Fairfield	SC	11/15/2001	M	4.5	-				
EHRL-0449	Pinewood Game Club	Florence	SC	10/30/2001	M	2.5	+				
EHRL-0450	Pinewood Game Club	Florence	SC	10/30/2001	M	2.5	+				
EHRL-0451	Pinewood Game Club	Florence	SC	10/30/2001	M	1.5	+	-	-		
EHRL-0452	Pinewood Game Club	Florence	SC	10/30/2001	F	2.5	+				
EHRL-0454	Willow Creek HC	Florence	SC	10/31/2001	M	2.5	+				
EHRL-0432	SE Cty, "The Pond", IPCO, Just S of airport	Georgetown	SC	10/20/2001	M	2.5	+				
EHRL-0434	SW Cty, Sampit HC	Georgetown	SC	10/20/2001	M	2.5	+				
EHRL-0435	Ncentral Cty, Blacu R. Plantation	Georgetown	SC	10/20/2001	F	2.5	+				
EHRL-0437	Ncentral Cty, Blacu R. Plantation	Georgetown	SC	10/21/2001	F	1.5	+	-	4 (b)	-	
EHRL-0433	central Cty, Friendfold Plantation	Georgetown	SC	10/20/2001	M	3.5	-				
SE91-365	Webb Wildlife Center	Hampton	SC	12/13/1991	F	0.5	+				
SE91-371	Webb Wildlife Center	Hampton	SC	12/14/1991	F	5.5	+				
SE91-375	Webb Wildlife Center	Hampton	SC	11/15/1991	M	1.5	+				
SE91-376	Webb Wildlife Center	Hampton	SC	11/23/1991	F	6.5	+				
SE91-386	Webb Wildlife Center	Hampton	SC	11/26/1991	F	7.5	+				
SE91-366	Webb Wildlife Center	Hampton	SC	11/22/1991	F	0.5	-				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
SE91-370	Webb Wildlife Center	Hampton	SC	12/6/1991	F	1.5	-				
SE91-380	Webb Wildlife Center	Hampton	SC	11/22/1991	F	3.5	-				
SE91-381	Webb Wildlife Center	Hampton	SC	11/22/1991	F	1.5	-				
SE91-382	Webb Wildlife Center	Hampton	SC	11/18/1991	F	5.5	-				
EHRL-0439	Wcentral Cty, Jordanville, Everett Brown Farm	Horry	SC	10/20/2001	M	2.5	+				
EHRL-0440	SE Cty, Oregon HC, near Murrells Inlet	Horry	SC	10/20/2001	M	1.5	+	-	-		
EHRL-0441	Scentral Cty, Jackson Bluff HC, below Conway	Horry	SC	10/20/2001	M	3.5	+				
EHRL-0442	SE Cty, near Bucksville	Horry	SC	10/21/2001	M	1.5	-	-	-		
EHRL-0443	NE Cty, near Red Bluff	Horry	SC	10/21/2001	M	1.5	-	-	-		
481-1	Savannah NWR	Jasper	SC	9/21/1993	M	1.5	-				0
481-2	Savannah NWR	Jasper	SC	9/21/1993	F	1.5	-				0
481-3	Savannah NWR	Jasper	SC	9/21/1993	F	3.5	-				0
481-4	Savannah NWR	Jasper	SC	9/21/1993	F	2.5	-				0
481-5	Savannah NWR	Jasper	SC	9/21/1993	M	2.5	-				0
EHRL-0075		Lancaster	SC	11/29/2000	M	2.5	-				
EHRL-0072		Laurens	SC	12/15/2000	F	2.5	-				
EHRL-0073		Laurens	SC	12/15/2000	F	2.5	-				
EHRL-0422		Laurens	SC				-				
EHRL-0423		Laurens	SC				-				
EHRL-0424		Laurens	SC				-				
EHRL-0463	1 mile ne of schtsville very close to Sumter Co. line	Lee	SC	11/5/2001	F	3.5	-				
EHRL-0464	SE Lee Co. near Atkins	Lee	SC	11/6/2001	F	2.5	-				
EHRL-0465	SE Lee Co. 1.4 miles NNW of Atkins	Lee	SC	11/6/2001	F	0.6	-				
EHRL-0466	SE Lee Co. at Atkins drainage district off CCC rd. (Sr 327 - NW of Atkins)	Lee	SC	11/7/2001	F	4.5	-				
EHRL-0052	Eden Hall HC	McCormick	SC	11/6/1999	F	2.5	+				
EHRL-0053	Eden Hall HC	McCormick	SC	11/6/1999	M	1.5	+				
EHRL-0054	Eden Hall HC	McCormick	SC	11/12/1999	F	1.5	+				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	VLPT	120-kDa	LST
EHRL-0055	Eden Hall HC	McCormick	SC	11/13/1999	M	3.5	+				
EHRL-0056	Eden Hall HC	McCormick	SC	11/5/1999	M	0.5	-				
EHRL-0069	Fants Grove WMA	Oconee	SC	12/14/2000	F	1.5	-				
611-4	Santee WMA	Orangeburg	SC	10/16/2001	F	4.5	+				0
611-1	Santee WMA	Orangeburg	SC	10/16/2001	F	8+	+				1
611-2	Santee WMA	Orangeburg	SC	10/16/2001	F	2.5	+				1
611-5	Santee WMA	Orangeburg	SC	10/16/2001	F	1.1	+	-	-		1
611-3	Santee WMA	Orangeburg	SC	10/16/2001	F	8+	+				1
SE91-341	Millacre HC	Richland	SC	11/30/1990	F	3.5	-				
SE91-342	Millacre HC	Richland	SC	11/30/1990	M	0.5	-				
SE91-344	Millacre HC	Richland	SC	11/30/1990	F	1.5	-				
SE91-350	Millacre HC	Richland	SC	11/30/1990	F	3.5	-				
SE91-351	Millacre HC	Richland	SC	11/30/1990	F	1.5	-				
SE91-353	Millacre HC	Richland	SC	11/30/1990	M	4.5	-				
SE91-356	Millacre HC	Richland	SC	11/30/1990	M	3.5	-				
SE91-357	Millacre HC	Richland	SC	11/30/1990	F	1.5	-				
SE91-359	Millacre HC	Richland	SC	11/30/1990	F	5.5	-				
SE91-361	Millacre HC	Richland	SC	11/30/1990	F	1.5	-				
SE91-362	Millacre HC	Richland	SC	11/30/1990	F	5.5	-				
SE91-363	Millacre HC	Richland	SC	11/30/1990	F	2.5	-				
SE91-364	Millacre HC	Richland	SC	11/30/1990	F	3.5	-				
EHRL-0408		Saluda	SC		F	1.5	+				
EHRL-0407		Saluda	SC		F	3.5	+				
EHRL-0409		Saluda	SC		M	2.5	-				
EHRL-0406		Saluda	SC		M	1.5	-				
EHRL-0403		Saluda	SC		M	1.5	-				
386-1	Croft State Park	Spartanburg	SC	8/9/1989	F	3.5	-				0
386-2	Croft State Park	Spartanburg	SC	8/9/1989	F	7.5	-				0
386-3	Croft State Park	Spartanburg	SC	8/9/1989	F	4.5	-				0
386-4	Croft State Park	Spartanburg	SC	8/9/1989	F	3.5	-				0
386-5	Croft State Park	Spartanburg	SC	8/9/1989	F	3.5	-				0
EHRL-0415		Union	SC				-				
EHRL-0416		Union	SC				-				
EHRL-0417		Union	SC				-				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
EHRL-0418		Union	SC				-				
EHRL-0419		Union	SC				-				
EHRL-0467	collected at Nichols store	York	SC	11/15/2001	F	3.5	+				
EHRL-0468	collected at Nichols store	York	SC	11/15/2001	M	0.5	+	-	-	-	
EHRL-0469	collected at Nichols store	York	SC	11/15/2001	F	2.5	+				
EHRL-0074		York	SC	11/29/2000	M	3.5	-				
EHRL-0429		York	SC				-				
EHRL-0430		York	SC				-				
EHRL-0470	collected at Nichols store	York	SC	11/15/2001	F	2.5	-				
SE94-400	Cheatham	Cheatham	TN	12/17/1994		0.5	+				
SE94-401	Cheatham	Cheatham	TN	12/17/1994		1.5	+				
SE94-403	Cheatham	Cheatham	TN	12/17/1994		3.5	+				
SE94-402	Cheatham	Cheatham	TN	12/17/1994		1.5	-				
SE94-406	Cheatham	Cheatham	TN	12/17/1994		3.5	-				
EHRL-0561	Chickasaw SP	Chester	TN	8/16/2001	F	3.5	+				
EHRL-0563	Chickasaw SP	Chester	TN	8/16/2001	F	7.5	+				
EHRL-0564	Chickasaw SP	Chester	TN	8/16/2001	F	2.5	+				
EHRL-0565	Chickasaw SP	Chester	TN	8/16/2001	M	1.5	+				
EHRL-0562	Chickasaw SP	Chester	TN	8/16/2001	F	1.5	-				
EHRL-0575	Arnold Engineering Devolpment Center, Arnold ARB	Coffee	TN	8/21/2001	F	4.5	++				
EHRL-0571	Arnold Engineering Devolpment Center, Arnold ARB	Coffee	TN	8/21/2001	F	2.5	+				
EHRL-0572	Arnold Engineering Devolpment Center, Arnold ARB	Coffee	TN	8/21/2001	F	1.5	+				
EHRL-0573	Arnold Engineering Devolpment Center, Arnold ARB	Coffee	TN	8/21/2001	F	3.5	+				
EHRL-0574	Arnold Engineering Devolpment Center, Arnold ARB	Coffee	TN	8/21/2001	F	2.5	+				
EHRL-0591	Catoosa WMA	Cumberland/ Morgan	TN	8/9/2001	F	3.5	+				
EHRL-0592	Catoosa WMA	Cumberland/ Morgan	TN	8/9/2001	F	1.5	+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0593	Catoosa WMA	Cumberland/ Morgan	TN	8/9/2001	F	2.5	+				
EHRL-0594	Catoosa WMA	Cumberland/ Morgan	TN	8/9/2001	F	1.5	+				
363-1	Carter Mountain Property	Franklin	TN	7/21/1988	F	2	+				1
363-2	Carter Mountain Property	Franklin	TN	7/21/1988	F	2	+				1
363-4	Carter Mountain Property	Franklin	TN	7/21/1988	M	1	+				1
363-5	Carter Mountain Property	Franklin	TN	7/21/1988	F	2	+				1
363-3	Carter Mountain Property	Franklin	TN	7/21/1988	F	2	-				1
EHRL-0576	NW	Giles	TN	8/15/2001	F	3.5	++				
EHRL-0579	central	Giles	TN	8/15/2001	F	2.5	++				
EHRL-0577	SE	Giles	TN	8/15/2001	F	3.5	+				
EHRL-0578	E-central	Giles	TN	8/15/2001	F	2.5	+				
EHRL-0580	SE	Giles	TN	8/15/2001	F	1.5	+				
EHRL-0567	Chickasaw SP	Hardeman	TN	8/16/2001	F	3.5	+				
EHRL-0569	Chickasaw SP	Hardeman	TN	8/16/2001	F	6.5	-				
EHRL-0570	Chickasaw SP	Hardeman	TN	8/16/2001	F	1.5	-				
EHRL-0566	Chickasaw SP	Hardeman	TN	8/16/2001	F	3.5	-				
EHRL-0568	Chickasaw SP	Hardeman	TN	8/16/2001	F	1.5	-				
EHRL-0600	Central	Hawkins	TN	8/30/2001	F	3.5	-				
EHRL-0601	NW	Hawkins	TN	8/30/2001	F	8.5	-				
EHRL-0602	SW	Hawkins	TN	8/30/2001	M	1.5	-				
EHRL-0604	NE	Hawkins	TN	8/30/2001	F	3.5	-				
EHRL-0605		Hawkins	TN	8/30/2001	F	0.5	-				
563-4	Hatchie NWR	Haywood	TN	8/20/1998	F	2.5	+				1
394-1	Hatchie NWR	Haywood	TN	9/14/1989	F	4.5	-				0
394-2	Hatchie NWR	Haywood	TN	9/14/1989	F	2.5	-				0
394-3	Hatchie NWR	Haywood	TN	9/14/1989	F	3.5	-				0
394-4	Hatchie NWR	Haywood	TN	9/14/1989	F	3.5	-				0
394-5	Hatchie NWR	Haywood	TN	9/14/1989	F	2.5	-				0
503-1	Hatchie NWR	Haywood	TN	9/29/1994	F	2.5	-				0
503-2	Hatchie NWR	Haywood	TN	9/29/1994	F	1.5	-				0
503-3	Hatchie NWR	Haywood	TN	9/29/1994	M	1.5	-				0
503-4	Hatchie NWR	Haywood	TN	9/29/1994	F	2.5	-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
503-5	Hatchie NWR	Haywood	TN	9/29/1994	M	1.5	-				0
503-6	Hatchie NWR	Haywood	TN	9/29/1994	F	0.5	-				
563-1	Hatchie NWR	Haywood	TN	8/20/1998	F	4	-				0
563-2	Hatchie NWR	Haywood	TN	8/20/1998	F	4	-				0
563-3	Hatchie NWR	Haywood	TN	8/20/1998	F	1.5	-				1
563-5	Hatchie NWR	Haywood	TN	8/20/1998	F	5.5	-				1
SE91-246	Natchez Trace WMA	Henderson	TN	10/4/1991	F	4.5	+				
SE91-250	Natchez Trace WMA	Henderson	TN	10/4/1991	F	7.5+	+				
SE91-252	Natchez Trace WMA	Henderson	TN	10/4/1991	F	7.5+	+				
SE91-255	Natchez Trace WMA	Henderson	TN	10/4/1991	F	3.5	+				
SE91-259	Natchez Trace WMA	Henderson	TN	10/4/1991	F	3.5	+				
SE91-260	Natchez Trace WMA	Henderson	TN	10/4/1991	F	7.5+	+				
SE91-261	Natchez Trace WMA	Henderson	TN	10/4/1991	F	1.5	+				
SE91-247	Natchez Trace WMA	Henderson	TN	10/4/1991	F	2.5	-				
SE91-249	Natchez Trace WMA	Henderson	TN	10/4/1991	F	3.5	-				
SE91-251	Natchez Trace WMA	Henderson	TN	10/4/1991	F	4.5	-				
SE91-253	Natchez Trace WMA	Henderson	TN	10/4/1991	F	5.5	-				
SE91-254	Natchez Trace WMA	Henderson	TN	10/4/1991	F	2.5	-				
SE91-256	Natchez Trace WMA	Henderson	TN	10/4/1991	F	3.5	-				
SE91-258	Natchez Trace WMA	Henderson	TN	10/4/1991	F	0	-				
SE91-263	Natchez Trace WMA	Henderson	TN	10/4/1991	F	4.5	-				
SE91-264	Natchez Trace WMA	Henderson	TN	10/4/1991	F	2.5	-				
424-2	Tennessee NWR, Big Sandy Unit	Henry	TN	8/21/1991	M	1	+				1
424-3	Tennessee NWR, Big Sandy Unit	Henry	TN	8/21/1991	F	1	+				1
424-4	Tennessee NWR, Big Sandy Unit	Henry	TN	8/21/1991	F	1	+				1
424-5	Tennessee NWR, Big Sandy Unit	Henry	TN	8/21/1991	F	3	+				1
561-1	Tennessee NWR, Duck River Unit	Henry	TN	8/17/1998	F	3.5	+				2
561-3	Tennessee NWR, Duck River Unit	Henry	TN	8/17/1998	F	4.5	+				1
424-1	Tennessee NWR, Big Sandy Unit	Henry	TN	8/21/1991	F	1	-				1
561-2	Tennessee NWR, Duck River Unit	Henry	TN	8/17/1998	F	5.5	-				1
561-4	Tennessee NWR, Duck River Unit	Henry	TN	8/17/1998	F	5	-				1
561-5	Tennessee NWR, Duck River Unit	Henry	TN	8/17/1998	F		-				1
560-1	Tennessee NWR, Big Sandy Unit	Humphreys	TN	8/18/1998	F	2.5	+				1
560-2	Tennessee NWR, Big Sandy Unit	Humphreys	TN	8/18/1998	F	4.5	+				1

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
560-3	Tennessee NWR, Big Sandy Unit	Humphreys	TN	8/18/1998	F	2.5	+				1
560-4	Tennessee NWR, Big Sandy Unit	Humphreys	TN	8/18/1998	F	3.5	+				0
560-5	Tennessee NWR, Big Sandy Unit	Humphreys	TN	8/18/1998	M	1.5	+				0
EHRL-0609	SE	Jefferson	TN	8/29/2001	F	2.5	-				
EHRL-0610	NE	Jefferson	TN	8/29/2001	F	3.5	-				
EHRL-0611	NE	Jefferson	TN	8/29/2001	F	1.5	-				
EHRL-0612	NE	Jefferson	TN	8/29/2001	F	3.5	-				
EHRL-0613	NE	Jefferson	TN	8/29/2001	F	4.5	-				
547-1	Lake Isom NWR	Lake	TN	7/29/1997	M	1.5	-	-	-		
547-2	Lake Isom NWR	Lake	TN	7/29/1997	M	1.5	-	-	-		0
547-3	Lake Isom NWR	Lake	TN	7/29/1997	F	2.5	-	-	-		0
547-4	Lake Isom NWR	Lake	TN	7/29/1997	F	2.5	-	-	-		0
547-5	Lake Isom NWR	Lake	TN	7/29/1997	F	2.5	-	-	-		0
464-1	Chickasaw NWR	Lauderdale	TN	9/21/1992	F	2.5	-				0
464-2	Chickasaw NWR	Lauderdale	TN	9/21/1992	F	3.5	-				0
464-3	Chickasaw NWR	Lauderdale	TN	9/21/1992	M	1.5	-				0
464-4	Chickasaw NWR	Lauderdale	TN	9/21/1992	M	2.5	-				0
464-5	Chickasaw NWR	Lauderdale	TN	9/21/1992	F	1	-				0
426-2		Marion	TN				+				0
426-3		Marion	TN				+				0
426-5		Marion	TN				+				0
426-1		Marion	TN				-				0
426-4		Marion	TN				-				0
393-1	Reelfoot NWR	Obion	TN	9/13/1989	M	3.5	-				0
393-2	Reelfoot NWR	Obion	TN	9/13/1989	M	3.5	-				0
393-3	Reelfoot NWR	Obion	TN	9/13/1989	F	2.5	-				0
393-4	Reelfoot NWR	Obion	TN	9/13/1989	F	3.5	-				0
393-5	Reelfoot NWR	Obion	TN	9/13/1989	M	1.5	-				0
546-1	Reelfoot NWR	Obion	TN	7/29/1997	M	1.5	-	-	-		0
546-2	Reelfoot NWR	Obion	TN	7/29/1997	F	3.5	-	-	-		0
546-3	Reelfoot NWR	Obion	TN	7/29/1997	F	2.5	-	-	-		0
546-4	Reelfoot NWR	Obion	TN	7/29/1997	F	4.5	-	-	-		0
546-5	Reelfoot NWR	Obion	TN	7/29/1997	F	1	-	-	-		0
EHRL-0595	Smith Bend Refuge	Rhea	TN	8/20/2001	F	1.5	+				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
EHRL-0596	Smith Bend Refuge	Rhea	TN	8/20/2001	F	3.5	+				
EHRL-0597	Smith Bend Refuge	Rhea	TN	8/20/2001	F	4.5	+				
EHRL-0598	Smith Bend Refuge	Rhea	TN	8/20/2001	F	1.5	+				
EHRL-0599	Smith Bend Refuge	Rhea	TN	8/20/2001	F	7.5	+				
249-1	Shelby Forest	Shelby	TN	8/25/1981	M	3	+				1
249-2	Shelby Forest	Shelby	TN	8/25/1981	M	1	+				1
249-3	Shelby Forest	Shelby	TN	8/25/1981	F	2	+				1
249-4	Shelby Forest	Shelby	TN	8/25/1981	F	2	-				0
249-5	Shelby Forest	Shelby	TN	8/25/1981	F	3	-				0
EHRL-0581	NW	Smith	TN	8/13/2001	F	1.5	+				
EHRL-0582	NW	Smith	TN	8/13/2001	F	1.5	+				
EHRL-0583	NW	Smith	TN	8/13/2001	F	4.5	+				
EHRL-0584	NW	Smith	TN	8/13/2001	F	4.5	+				
EHRL-0590	W-central	Smith	TN	8/13/2001	F	1.5	+				
562-3	Cross Creeks NWR	Stewart	TN	8/19/1998	F	2.5	+				1
562-4	Cross Creeks NWR	Stewart	TN	8/19/1998	M	1.5	+				0
562-5	Cross Creeks NWR	Stewart	TN	8/19/1998	F	2.5	+				1
562-1	Cross Creeks NWR	Stewart	TN	8/19/1998	M	1.5	-				1
562-2	Cross Creeks NWR	Stewart	TN	8/19/1998	F	3.5	-				1
EHRL-0585	Hartsville Nuclear Plant	Trousdale	TN	8/13/2001	F	3.5	+				
EHRL-0586	Hartsville Nuclear Plant	Trousdale	TN	8/13/2001	F	3.5	+				
EHRL-0587	Hartsville Nuclear Plant	Trousdale	TN	8/13/2001	F	2.5	+				
EHRL-0588	Hartsville Nuclear Plant	Trousdale	TN	8/13/2001	F	2.5	+				
EHRL-0589	Hartsville Nuclear Plant	Trousdale	TN	8/13/2001	F	6.5	+				
SE91-265	Chuck Swan WMA	Union	TN	1/10/1991	F	5.5	+				
SE91-268	Chuck Swan WMA	Union	TN	1/10/1991	F	3.5	+				
SE91-273	Chuck Swan WMA	Union	TN	1/10/1991	F	4.5	+				
SE91-287	Chuck Swan WMA	Union	TN	1/10/1991	F	2.5	-				
SE91-289	Chuck Swan WMA	Union	TN	1/10/1991	F	2.5	-				
TX-92-047		Anderson	TX	1992	F	5.5	+				
TX-92-048		Anderson	TX	1992	F	3.5	+				
TX-92-049		Anderson	TX	1992	F	4.5	+				
TX-92-050		Anderson	TX	1992	F	5.5	-				
TX-92-051		Anderson	TX	1992	F	4.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
TX-92-052		Anderson	TX	1992	F	3.5	-				
SE95-0513		Angelina	TX	1992		4.5	+				
TX-92-531		Angelina	TX	1992	F	3.5	-				
TX-92-532		Angelina	TX	1992	F	6.5	-				
TX-92-534		Angelina	TX	1992	F	6.5	-				
TX-92-535		Angelina	TX	1992	F	5.5	-				
TX-92-299		Bandera	TX	1992	F	3.5	+				
TX-92-300		Bandera	TX	1992	F	1.5	+				
TX-92-302		Bandera	TX	1992	F	3.5	+				
TX-92-304		Bandera	TX	1992	F	3.5	+				
TX-92-305		Bandera	TX	1992	F	1.5	-				
TX-92-461		Brazoria	TX	1992	F	3.5	-				
TX-92-462		Brazoria	TX	1992	F	1.5	-				
TX-92-463		Brazoria	TX	1992	F	4.5	-				
TX-92-464		Brazoria	TX	1992	F	3.5	-				
TX-92-468		Brazoria	TX	1992	F	8.5	-				
TX-92-469		Brazoria	TX	1992	F	5.5	-				
TX-92-471		Brazoria	TX	1992	F	3.5	-				
TX-92-241		Brewster	TX	1992	F	4.5	-				
TX-92-135	Lake Brownwood SP	Brown	TX	1992	F	5.5	+				
TX-92-136	Lake Brownwood SP	Brown	TX	1992	F	1.5	+				
TX-92-128	Lake Brownwood SP	Brown	TX	1992	F	7.5	+				
TX-92-130	Lake Brownwood SP	Brown	TX	1992	F	3.5	+				
TX-92-131	Lake Brownwood SP	Brown	TX	1992	F	4.5	+				
TX-92-132	Lake Brownwood SP	Brown	TX	1992	F	2.5	+				
TX-92-133	Lake Brownwood SP	Brown	TX	1992	F		+				
TX-92-134	Lake Brownwood SP	Brown	TX	1992	F	3.5	-				
TX-92-137	Lake Brownwood SP	Brown	TX	1992	F	6.5	-				
TX-92-077		Burleson	TX	1992	F	4.5	-				
TX-92-086		Burleson	TX	1992	F	5.5	-				
TX-92-089		Burleson	TX	1992	F	3.5	-				
TX-92-090		Burleson	TX	1992	F	3.5	-				
TX-92-091		Burleson	TX	1992	F	5.5	-				
TX-92-092		Burleson	TX	1992	F	5.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
TX-92-430	Powderhorn and Welder	Calhoun	TX	1992	F	1.5	+				
TX-92-431	Powderhorn and Welder	Calhoun	TX	1992	F	3.5	+				
TX-92-433	Powderhorn and Welder	Calhoun	TX	1992	F	5.5	+				
TX-92-435	Powderhorn and Welder	Calhoun	TX	1992	F	7.5	+				
TX-92-432	Powderhorn and Welder	Calhoun	TX	1992	F	6.5	-				
SE95-0507	Cass	Cass	TX	6/17/1995		4.5	+				
SE95-0508	Cass	Cass	TX	6/17/1995		2.5	+				
SE95-0509	Cass	Cass	TX	6/17/1995		7.5	+				
TX-92-525		Cass	TX	1992	F	1.5	+				
TX-92-524		Cass	TX	1992	F	1.5	-				
TX-92-537		Cherokee	TX	1992	F	2.5	+				
TX-92-536		Cherokee	TX	1992	F	2.5	-				
TX-92-538		Cherokee	TX	1992	F	5.5	-				
TX-92-539		Cherokee	TX	1992	F	3.5	-				
TX-92-540		Cherokee	TX	1992	F	1.5	-				
TX-92-231		Clay	TX	1992	F	6.5	+				
TX-92-232		Clay	TX	1992	F	3.5	+				
TX-92-233		Clay	TX	1992	F	2.5	+				
TX-92-234		Clay	TX	1992	F	3.5	+				
TX-92-235		Clay	TX	1992	F	6.5	+				
TX-92-506		Colorado	TX	1992	F	4.5	+				
TX-92-507		Colorado	TX	1992	F	2.5	+				
TX-92-504		Colorado	TX	1992	F	6.5	-				
TX-92-505		Colorado	TX	1992	F	7.5	-				
TX-92-508		Colorado	TX	1992	F	3.5	-				
TX-92-349		Coryell	TX	1992	F	5.5	+				
TX-92-351		Coryell	TX	1992	F	3.5	+				
TX-92-352		Coryell	TX	1992	F	4.5	+				
TX-92-353		Coryell	TX	1992	F	2.5	+				
TX-92-354		Coryell	TX	1992	F	4.5	+				
TX-92-350		Coryell	TX	1992	F	1.2	-				
TX-92-001		Cottle	TX	1992	F	6.5	-				
TX-92-002		Cottle	TX	1992	F	2.5	-				
TX-92-003		Cottle	TX	1992	F	2.5	-				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	VLPT	120-kDa	LST
TX-92-005		Cottle	TX	1992	F	2.5	-				
TX-92-006		Cottle	TX	1992	F	2.5	-				
TX-92-007		Cottle	TX	1992	F	5.5	-				
TX-92-008		Cottle	TX	1992	F	4.5	-				
TX-92-009		Cottle	TX	1992	F	5.5	-				
TX-92-024		Cottle	TX	1992	F	0.5	-				
TX-92-379		Crockett	TX	1992	F	2.5	+				
TX-92-380		Crockett	TX	1992	F	2.5	+				
TX-92-381		Crockett	TX	1992	F	6.5	+				
TX-92-383		Crockett	TX	1992	F	2.5	+				
TX-92-382		Crockett	TX	1992	F	3.5	-				
TX-92-622		Dimmit	TX	1992	F	4.5	-				
TX-92-623		Dimmit	TX	1992	F	3.5	-				
TX-92-624		Dimmit	TX	1992	F	4.5	-				
TX-92-625		Dimmit	TX	1992	F	3.5	-				
TX-92-628		Dimmit	TX	1992	F	1.5	-				
TX-92-629		Dimmit	TX	1992	F	3.5	-				
TX-92-630		Dimmit	TX	1992	F	1.5	-				
TX-92-631		Dimmit	TX	1992	F	4.5	-				
TX-92-632		Dimmit	TX	1992	F	4.5	-				
TX-92-480		Fort Bend	TX	1992	F	2.5	+				
TX-92-484		Fort Bend	TX	1992	F	5.5	+				
TX-92-476		Fort Bend	TX	1992	F	3.5	-				
TX-92-477		Fort Bend	TX	1992	F	2.5	-				
TX-92-478		Fort Bend	TX	1992	F	3.5	-				
TX-92-071		Freestone	TX	1992	F	2.5	+				
TX-92-064		Freestone	TX	1992	F	2.5	-				
TX-92-065		Freestone	TX	1992	F	4.5	-				
TX-92-066		Freestone	TX	1992	F	1.5	-				
TX-92-068		Freestone	TX	1992	F	3.5	-				
EHRL-1094	Eckert Ranch	Gillespie	TX	12/17/2002	F	2.5	+	-	-		
EHRL-1095	Eckert Ranch	Gillespie	TX	12/17/2002	F	5.5	-				
TX-92-451	Lazy F. Ranch	Goliad	TX	1992	F	5.5	+				
TX-92-450	Lazy F. Ranch	Goliad	TX	1992	F	1.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
TX-92-457		Gonzales	TX	1992	F	5.5	+				
TX-92-458		Gonzales	TX	1992	F	3.5	+				
TX-92-454		Gonzales	TX	1992	F	2.5	-				
TX-92-455		Gonzales	TX	1992	F	6.5	-				
TX-92-456		Gonzales	TX	1992	F	4.5	-				
SE93-737	Post Oak Savannah	Grimes	TX	2/25/1994		3.5	-				
SE93-738	Post Oak Savannah	Grimes	TX	2/25/1994		6.5	-				
SE93-739	Post Oak Savannah	Grimes	TX	2/25/1994		5.5	-				
TX-92-094		Grimes	TX	1992	F	5.5	-				
TX-92-095		Grimes	TX	1992	F	4.5	-				
SE95-0505	Harrison	Harrison	TX	6/17/1995		2.5	+				
SE95-0506	Harrison	Harrison	TX	6/17/1995		1.5	+				
TX-92-528		Harrison	TX	1992	F	2.5	+				
TX-92-529		Harrison	TX	1992	F	2.5	-				
TX-92-530		Harrison	TX	1992	F	2.5	-				
TX-92-342		Hays	TX	1992	F	3.5	+				
TX-92-343		Hays	TX	1992	F	8.5	+				
TX-92-344		Hays	TX	1992	F	2.5	+				
TX-92-345		Hays	TX	1992	F	6.5	-				
TX-92-010		Hemphill	TX	1992	F	3.5	-				
TX-92-012		Hemphill	TX	1992	F	4.5	-				
TX-92-013		Hemphill	TX	1992	F	3.5	-				
TX-92-015		Hemphill	TX	1992	F	2.2	-				
TX-92-016		Hemphill	TX	1992	F	1.5	-				
TX-92-017		Hemphill	TX	1992	F	5.5	-				
TX-92-018		Hemphill	TX	1992	F	2.5	-				
SE93-709	Post Oak Savannah	Henderson	TX	1/5/1994		2.5	+				
SE93-710	Post Oak Savannah	Henderson	TX	1/6/1994		8.5+	+				
TX-92-053		Henderson	TX	1992	F	3.5	+				
TX-92-061		Henderson	TX	1992	F	7.5	+				
TX-92-057		Henderson	TX	1992	F	5.5	-				
SE94-082		Hopkins	TX	11/5/1994		3.5	+				
SE94-083		Hopkins	TX	11/5/1994		1.5	+				
SE94-084		Hopkins	TX	11/5/1994		1.5	+				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	VLPT	120-kDa	LST
SE94-086		Hopkins	TX	11/5/1994		1.5	+				
SE94-088		Hopkins	TX	11/5/1994		3.5	+				
SE94-252	Houston	Houston	TX	11/22/1994		7.5	+				
SE94-253	Houston	Houston	TX	11/22/1994		3.5	+				
TX-92-542		Houston	TX	1992	F	5.5	+				
TX-92-543		Houston	TX	1992	F	1.5	+				
TX-92-541		Houston	TX	1992	F	6.5	-				
TX-92-019		Hutchinson	TX	1992	F	6.5	-				
TX-92-020		Hutchinson	TX	1992	F	6.5	-				
TX-92-021		Hutchinson	TX	1992	F	5.5	-				
TX-92-022		Hutchinson	TX	1992	F	7.5	-				
TX-92-023		Hutchinson	TX	1992	F	3.5	-				
TX-92-199		Irion	TX	1992	F	6.5	+				
TX-92-200		Irion	TX	1992	F	1.5	+				
TX-92-201		Irion	TX	1992	F	7.5	-				
TX-92-202		Irion	TX	1992	F	4.5	-				
TX-92-203		Irion	TX	1992	F	2.5	-				
TX-92-601		Kenedy	TX	1992	F	7.5	+				
TX-92-603		Kenedy	TX	1992	F	4.5	+				
TX-92-606		Kenedy	TX	1992	F	7.5	+				
TX-92-609		Kenedy	TX	1992	F	3.5	+				
TX-92-610		Kenedy	TX	1992	F	5.5	+				
TX-92-613		Kenedy	TX	1992	F	5.5	+				
TX-92-615		Kenedy	TX	1992	F	5.5	+				
TX-92-616		Kenedy	TX	1992	F	7.5	+				
TX-92-621		Kenedy	TX	1992	F	5.5	+				
TX-92-605		Kenedy	TX	1992	F	6.5	-				
TX-92-619		Kenedy	TX	1992	F	8.5+	-				
TX-92-096		Lee	TX	1992	F	5.5	-				
TX-92-097		Lee	TX	1992	F	4.5	-				
TX-92-098		Lee	TX	1992	F	5.5	-				
TX-92-099		Lee	TX	1992	F	1.5	-				
TX-92-100		Lee	TX	1992	F	4.5	-				
TX-92-101		Leon	TX	1992	F	7.5	+				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
TX-92-102		Leon	TX	1992	F	2.5	+				
TX-92-105		Leon	TX	1992	F	5.5	+				
TX-92-103		Leon	TX	1992	F	6.5	-				
TX-92-104		Leon	TX	1992	F	4.5	-				
TX-92-106		Limestone	TX	1992	F	5.5	+				
TX-92-108		Limestone	TX	1992	F	2.5	+				
TX-92-109		Limestone	TX	1992	F	5.5	+				
TX-92-107		Limestone	TX	1992	F	4.5	-				
TX-92-027		Lipscomb	TX	1992	F	2.5	-				
TX-92-028		Lipscomb	TX	1992	F	3.5	-				
TX-92-029		Lipscomb	TX	1992	F	1.5	-				
SE92-764	Piney Woods North	Marion	TX	2/25/1992	F	5.5	+				
SE92-765	Piney Woods North	Marion	TX	2/25/1992	F	3.5	+				
TX-92-527		Marion	TX	1992	F	7.5	+				
SE92-763	Piney Woods North	Marion	TX	2/9/1992	F	7.5	-				
TX-92-526		Marion	TX	1992	F	2.5	-				
TX-92-321		Mason	TX	1992	F	4.5	+				
TX-92-322		Mason	TX	1992	F	4.5	+				
TX-92-324		Mason	TX	1992	F	3.5	+				
TX-92-325		Mason	TX	1992	F	6.5	+				
TX-92-323		Mason	TX	1992	F	6.5	-				
TX-92-491		Matagorda	TX	1992	F	2.5	+				
TX-92-488		Matagorda	TX	1992	F	4.5	-				
TX-92-489		Matagorda	TX	1992	F	2.5	-				
TX-92-490		Matagorda	TX	1992	F	5.5	-				
TX-92-492		Matagorda	TX	1992	F	2.5	-				
TX-92-494		Matagorda	TX	1992	F	1.5	-				
TX-92-495		Matagorda	TX	1992	F	1.5	-				
TX-92-498		Matagorda	TX	1992	F	2.5	-				
TX-92-499		Matagorda	TX	1992	F	3.5	-				
TX-92-586		Maverick	TX	1992	F	5.5	+				
TX-92-587		Maverick	TX	1992	F	2.5	+				
TX-92-585		Maverick	TX	1992	F	3.5	-				
TX-92-588		Maverick	TX	1992	F	1.5	-				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
TX-92-589		Maverick	TX	1992	F	3.5	-				
TX-92-590		Maverick	TX	1992	F	4.5	-				
TX-92-591		Maverick	TX	1992	F	4.5	-				
TX-92-592		Maverick	TX	1992	F	4.5	-				
TX-92-647		McMullen	TX	1992	F	7.5	+				
TX-92-648		McMullen	TX	1992	F	4.5	+				
TX-92-649		McMullen	TX	1992	F	5.5	+				
TX-92-650		McMullen	TX	1992	F	4.5	+				
TX-92-651		McMullen	TX	1992	F	6.5	+				
TX-92-546		Nacogdoches	TX	1992	F	5.5	+				
TX-92-544		Nacogdoches	TX	1992	F	3.5	-				
TX-92-545		Nacogdoches	TX	1992	F	5.5	-				
TX-92-547		Nacogdoches	TX	1992	F	4.5	-				
TX-92-548		Nacogdoches	TX	1992	F	3.5	-				
TX-92-549		Nacogdoches	TX	1992	F	2.5	-				
TX-92-550		Nacogdoches	TX	1992	F	6.5	-				
TX-92-139	Posssum Kingdom Lake State Park	Palo Pinto	TX	1992	F	6.5	+				
TX-92-140	Posssum Kingdom Lake State Park	Palo Pinto	TX	1992	F	3.5	+				
TX-92-141	Posssum Kingdom Lake State Park	Palo Pinto	TX	1992	F	4.5	+				
TX-92-145	Posssum Kingdom Lake State Park	Palo Pinto	TX	1992	F	8.5	+				
TX-92-147	Posssum Kingdom Lake State Park	Palo Pinto	TX	1992	F	4.5	+				
TX-92-148	Posssum Kingdom Lake State Park	Palo Pinto	TX	1992	F	4.5	+				
TX-92-149	Posssum Kingdom Lake State Park	Palo Pinto	TX	1992	F	6.5	+				
TX-92-142	Posssum Kingdom Lake State Park	Palo Pinto	TX	1992	F	4.5	-				
TX-92-143	Posssum Kingdom Lake State Park	Palo Pinto	TX	1992	F	7.5	-				
TX-92-144	Posssum Kingdom Lake State Park	Palo Pinto	TX	1992	F	2.5	-				
TX-92-246		Pecos	TX	1992	F	2.5	-				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
TX-92-248		Pecos	TX	1992	F	3.5	-				
TX-92-254		Pecos	TX	1992	F	4.5	-				
TX-92-255		Pecos	TX	1992	F	3.5	-				
TX-92-258		Pecos	TX	1992	F	4.5	-				
TX-92-259		Pecos	TX	1992	F	2.5	-				
TX-92-264		Pecos	TX	1992	F	3.5	-				
TX-92-267		Pecos	TX	1992	F	1.5	-				
TX-92-270		Pecos	TX	1992	F	1.5	-				
TX-92-273		Pecos	TX	1992	F	4.5	-				
TX-92-274		Pecos	TX	1992	F	5.5	-				
TX-92-275		Pecos	TX	1992	F	6.5	-				
TX-92-276		Pecos	TX	1992	F	4.5	-				
TX-92-278		Pecos	TX	1992	F	5.5	-				
TX-92-281		Pecos	TX	1992	F	2.5	-				
TX-92-283		Pecos	TX	1992	F	3.5	-				
TX-92-030		Potter	TX	1992	F	6.5	-				
TX-92-031		Potter	TX	1992	F	7.5	-				
TX-92-032		Potter	TX	1992	F	4.5	-				
TX-92-033		Potter	TX	1992	F	5.5	-				
TX-92-034		Potter	TX	1992	F	7.5	-				
TX-92-046		Red River	TX	1992	F	5.5	+				
TX-92-044		Red River	TX	1992	F	4.5	-				
TX-92-045		Red River	TX	1992	F	8.5+	-				
TX-92-035		Roberts	TX	1992	F	3.5	-				
TX-92-036		Roberts	TX	1992	F	2.5	-				
TX-92-037		Roberts	TX	1992	F	3.5	-				
TX-92-038		Roberts	TX	1992	F	6.5	-				
TX-92-183		Runnels	TX	1992	F	7.5	+				
TX-92-187		Runnels	TX	1992	F	4.5	+				
TX-92-188		Runnels	TX	1992	F	1.5	+				
TX-92-185		Runnels	TX	1992	F	4.5	-				
TX-92-186		Runnels	TX	1992	F	4.5	-				
SE95-0473	Sabine	Sabine	TX	6/17/1995		1.5	+				
SE95-0475	Sabine	Sabine	TX	6/17/1995		3.5	+				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
SE95-0477	Sabine	Sabine	TX	6/17/1995		2.5	+				
SE95-0474	Sabine	Sabine	TX	6/17/1995		1.5	-				
SE95-0476	Sabine	Sabine	TX	6/17/1995		2.5	-				
TX-92-375		Schleicher	TX	1992	F	4.5	+				
EHRL-1119	Thompson Ranch	Schleicher	TX	12/13/2002	F	1.5	+	-	-		
EHRL-1120	Thompson Ranch	Schleicher	TX	12/13/2002	F	1.5	+	-	-		
TX-92-374		Schleicher	TX	1992	F	4.5	-				
TX-92-376		Schleicher	TX	1992	F	6.5	-				
TX-92-377		Schleicher	TX	1992	F	2.5	-				
TX-92-378		Schleicher	TX	1992	F	3.5	-				
EHRL-1116	Pfluger Ranch	Schleicher	TX	12/13/2002	M	5.5	-				
EHRL-1117	Pfluger Ranch	Schleicher	TX	12/13/2002	M	5.5	-				
EHRL-1118	Pfluger Ranch	Schleicher	TX	12/13/2002	M	5.5	-				
TX-92-043		Scurry	TX	1992	F	3.5	-				
TX-92-153		Shackelford	TX	1992	F	6.5	+				
TX-92-154		Shackelford	TX	1992	F	6.5	+				
TX-92-157		Shackelford	TX	1992	F	1.5	+				
TX-92-155		Shackelford	TX	1992	F	4.5	-				
TX-92-156		Shackelford	TX	1992	F	3.5	-				
TX-92-158		Shackelford	TX	1992	F	1.5	-				
TX-92-159		Shackelford	TX	1992	F	3.5	-				
TX-92-160		Shackelford	TX	1992	F	0.5	-				
TX-92-285		Terrell	TX	1992	F	3.5	-				
TX-92-287		Terrell	TX	1992	F	1.5	-				
TX-92-288		Terrell	TX	1992	F	3.5	-				
TX-92-289		Terrell	TX	1992	F	2.5	-				
TX-92-290		Terrell	TX	1992	F	1.5	-				
TX-92-296		Terrell	TX	1992	F	3.5	-				
TX-92-365		Travis	TX	1992	F	7.5	+				
TX-92-366		Travis	TX	1992	F	7.5	+				
TX-92-368		Travis	TX	1992	F	3.5	+				
TX-92-369		Travis	TX	1992	F	3.5	+				
TX-92-372		Travis	TX	1992	F	5.5	+				
TX-92-367		Travis	TX	1992	F	3.5	-				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
TX-92-371		Travis	TX	1992	F	8.5	-				
EHRL-0920		Travis	TX	10/26/2002	F	6.5	-	-	-		
EHRL-0921		Travis	TX	10/26/2002	M	3.5	-	-	-		
EHRL-0922		Travis	TX	10/26/2002	F	0.5	-	-	-		
EHRL-0923		Travis	TX	10/26/2002	M	0.5	-	-	-		
EHRL-0924		Travis	TX	10/26/2002	M	0.5	-	-	-		
TX-92-552		Trinity	TX	1992	F	3.5	+				
TX-92-551		Trinity	TX	1992	F	1.5	-				
TX-92-553		Trinity	TX	1992	F	5.5	-				
TX-92-554		Trinity	TX	1992	F	5.5	-				
TX-92-555		Trinity	TX	1992	F	6.5	-				
TX-92-571		Tyler	TX	1992	F	4.5	+				
TX-92-572		Tyler	TX	1992	F	5.5	-				
TX-92-573		Tyler	TX	1992	F	3.5	-				
TX-92-574		Tyler	TX	1992	F	2.5	-				
TX-92-575		Tyler	TX	1992	F	1.5	-				
TX-92-422		Val Verde	TX	1992	F	5.5	+				
TX-92-419		Val Verde	TX	1992	F	3.5	-				
TX-92-421		Val Verde	TX	1992	F	4.5	-				
TX-92-423		Val Verde	TX	1992	F	4.5	-				
TX-92-424		Val Verde	TX	1992	F	4.5	-				
TX-92-637		Webb	TX	1992	F	3.5	+				
TX-92-640		Webb	TX	1992	F	1.5	+				
TX-92-644		Webb	TX	1992	F	6.5	+				
TX-92-636		Webb	TX	1992	F	6.5	-				
TX-92-638		Webb	TX	1992	F	5.5	-				
TX-92-639		Webb	TX	1992	F	5.5	-				
TX-92-641		Webb	TX	1992	F	7.5	-				
TX-92-642		Webb	TX	1992	F	3.5	-				
TX-92-643		Webb	TX	1992	F	4.5	-				
TX-92-645		Webb	TX	1992	F	2.5	-				
TX-92-646		Webb	TX	1992	F		-				
TX-92-357		Williamson	TX	1992	F	4.5	+				
TX-92-358		Williamson	TX	1992	F	2.5	+				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results 16rRNA	VLPT	120-kDa	LST
TX-92-360		Williamson	TX	1992	F	1.5	+				
TX-92-361		Williamson	TX	1992	F	3.5	+				
TX-92-362		Williamson	TX	1992	F	4.5	+				
TX-92-355		Williamson	TX	1992	F	4.5	-				
TX-92-359		Williamson	TX	1992	F	3.5	-				
TX-92-363		Williamson	TX	1992	F	2.5	-				
TX-92-364		Williamson	TX	1992	F	5.5	-				
TX-92-218		Wise	TX	1992	F	3.5	+				
TX-92-219		Wise	TX	1992	F	6.5	+				
TX-92-221		Wise	TX	1992	F	7.5	+				
TX-92-222		Wise	TX	1992	F	6.5	+				
TX-92-223		Wise	TX	1992	F	3.5	+				
TX-92-238		Young	TX	1992	F	5.5	+				
TX-92-239		Young	TX	1992	F	6.5	+				
TX-92-240		Young	TX	1992	F	6.5	+				
TX-92-152	Cross Timbers and Prairies Eco. Area	Young	TX	1992	F	4.5	+				
TX-92-150	Cross Timbers and Prairies Eco. Area	Young	TX	1992	F	3.5	-				
EHRL-0041	NASA/Wallops Flight Facility	Accomack	VA	11/16/2000	M	0.5	+				
EHRL-0042	NASA/Wallops Flight Facility	Accomack	VA	11/16/2000	F	0.5	+				
EHRL-0043	NASA/Wallops Flight Facility	Accomack	VA	11/16/2000	F	2.5	+				
401-01	Chincoteague NWR	Accomack	VA	9/7/1990	F	3.5	+				2
401-02	Chincoteague NWR	Accomack	VA	9/7/1990	F	6.5	+				2
401-03	Chincoteague NWR	Accomack	VA	9/7/1990	F	5.5	+				3
401-04	Chincoteague NWR	Accomack	VA	9/7/1990	F	5.5	+				2
401-05	Chincoteague NWR	Accomack	VA	9/7/1990	M	2.5	+				1
EHRL-0040	NASA/Wallops Flight Facility	Accomack	VA	11/16/2000	M	1.5	-				
EHRL-0044	NASA/Wallops Flight Facility	Accomack	VA	11/16/2000	M	0.5	-				
EHRL-0146		Albemarle	VA	4/25/2001	M		+				
EHRL-0147		Albemarle	VA	4/25/2001	M		+				
EHRL-0148		Albemarle	VA	4/25/2001	F		+				
EHRL-1064		Albemarle	VA	11/30/2002	M	1.5	+				
EHRL-1070		Albemarle	VA	11/30/2002	M	0.5	+	-	4 (b)	4 (b)	

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-1069		Albemarle	VA	11/30/2002	M	0.5	-	+	4 (b)	4 (b)	
EHRL-0643		Alleghany	VA		F	2.5	-				
EHRL-0644		Alleghany	VA		M	2.5	-				
EHRL-0645		Alleghany	VA		M	2.5	-				
EHRL-0646		Alleghany	VA		F	2.5	-				
EHRL-0647		Alleghany	VA		F	1.5	-				
EHRL-0748		Amherst	VA		F	2.5	+				
EHRL-0746		Amherst	VA		F	5.5	-				
EHRL-0747		Amherst	VA		F	2.5	-				
EHRL-0749		Amherst	VA		M	0.5	-				
EHRL-0750		Amherst	VA		F	1.5	-				
EHRL-0739		Brunswick	VA		M	2.5	+				
EHRL-0740		Brunswick	VA		F	3.5	+				
EHRL-0741		Brunswick	VA		F	2.5	+				
EHRL-0742		Brunswick	VA		M	2.5	+				
EHRL-0743		Brunswick	VA		M	2.5	+				
EHRL-0622		Buckingham	VA		M	1+	+				
EHRL-0623		Buckingham	VA		F	1.5	+				
EHRL-0624		Buckingham	VA		M	1.5	+				
EHRL-0625		Buckingham	VA		F	4.5	+				
EHRL-0621		Buckingham	VA		M	1+	-				
CC237-02		Campbell	VA	9/1/2002			-	-	-		
EHRL-0769		Caroline	VA				+				
EHRL-0770		Caroline	VA				+				
EHRL-0772		Caroline	VA				+				
EHRL-0773		Caroline	VA				+				
EHRL-0774		Caroline	VA				+				
EHRL-0615		Charlotte	VA		F	1.5	+				
EHRL-0617		Charlotte	VA		F	3.5	+				
EHRL-0619		Charlotte	VA		F	1+	+				
EHRL-0614		Charlotte	VA		M	0.5	-				
EHRL-0620		Charlotte	VA		F	4.5	-				
SE94-023	Colonial Heights	Chesterfield	VA	8/29/1994		2.5	+				
SE94-024	Colonial Heights	Chesterfield	VA	9/19/1994		4.5	+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE94-025	Colonial Heights	Chesterfield	VA	9/19/1994		1.5	+				
SE94-026	Colonial Heights	Chesterfield	VA	9/19/1994		2.5	+				
SE94-027	Colonial Heights	Chesterfield	VA	9/19/1994		2.5	+				
EHRL-0776		Culpeper	VA				+				
EHRL-0778		Culpeper	VA				+				
EHRL-0779		Culpeper	VA				+				
EHRL-0775		Culpeper	VA				-				
EHRL-0777		Culpeper	VA				-				
CC343-02		Cumberland	VA	10/10/2002	M	1.5	+	+	-	4 (b)	
EHRL-1008	Spring Hill HC	Dinwiddie	VA	11/20/2002			+	+	4 (b)	4 (b)	
EHRL-1011	Spring Hill HC	Dinwiddie	VA	11/20/2002			+	-	-		
EHRL-1012	Spring Hill HC	Dinwiddie	VA	11/20/2002			+	-	-		
EHRL-1013	Spring Hill HC	Dinwiddie	VA	11/20/2002			-	-	-		
EHRL-1014	Spring Hill HC	Dinwiddie	VA	11/20/2002			-	-	-		
443-1	Mason Neck NWR	Fairfax	VA	7/27/1992	M	4	+				3
443-4	Mason Neck NWR	Fairfax	VA	7/27/1992	F	3	+				2
443-2	Mason Neck NWR	Fairfax	VA	7/27/1992	M	2	-				3
443-3	Mason Neck NWR	Fairfax	VA	7/27/1992	M	4	-				3
443-5	Mason Neck NWR	Fairfax	VA	7/27/1992	F	2	-				2
EHRL-0727		Goochland	VA				+				
EHRL-0728		Goochland	VA		M		+				
EHRL-0729		Goochland	VA				+				
EHRL-0730		Goochland	VA				+				
EHRL-0731		Goochland	VA				+				
EHRL-0695		Grayson	VA		F	6.5	-				
EHRL-0697		Grayson	VA		F	2.5	-				
EHRL-0699		Grayson	VA		F	1.5	-				
EHRL-0700		Grayson	VA		F	2.5	-				
EHRL-0701		Grayson	VA		F	3.5	-				
EHRL-0673		Highland	VA		F	3.5	-				
EHRL-0674		Highland	VA		F	3.5	-				
EHRL-0675		Highland	VA		F	4.5	-				
EHRL-0676		Highland	VA		F	6.5	-				
EHRL-0677		Highland	VA		M	1.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE95-0092	Xerox Corporation Property	Loudoun	VA	6/17/1905		3.5	+				
SE95-0093	Xerox Corporation Property	Loudoun	VA	6/17/1905		3.5	+				
SE95-0094	Xerox Corporation Property	Loudoun	VA	6/17/1905		2.5	+				
SE95-0095	Xerox Corporation Property	Loudoun	VA	6/17/1905		4.5	-				
SE95-0096	Xerox Corporation Property	Loudoun	VA	6/17/1905		3.5	-				
EHRL-1016	Swamp Boys HC	Lunenburg	VA	11/20/2002			+	-	-		
EHRL-1017	Swamp Boys HC	Lunenburg	VA	11/20/2002			+	-	-		
EHRL-1018	Swamp Boys HC	Lunenburg	VA	11/20/2002			-	-	-		
EHRL-1019	Swamp Boys HC	Lunenburg	VA	11/20/2002			-	+	4 (b)	3 (b)	
EHRL-0717		Middlesex	VA		M	2.5	+				
EHRL-0718		Middlesex	VA		F	0.5	+				
EHRL-0719		Middlesex	VA		F	0.5	+				
EHRL-0716		Middlesex	VA		M	2.5	-				
EHRL-0709		Montgomery	VA		F	1.5	-				
EHRL-0710		Montgomery	VA		M	1.5	-				
EHRL-0711		Montgomery	VA		M	0.5	-				
EHRL-0712		Montgomery	VA		M	0.5	-				
EHRL-0713		Montgomery	VA		M	1.5	-				
CC287-02		Montgomery	VA				-				
VA 1		Nansemond (now Suffolk)	VA	1/1/1983			+				
VA 2		Nansemond (now Suffolk)	VA	1/1/1983			+				
VA 3		Nansemond (now Suffolk)	VA	1/1/1983			+				
VA 5		Nansemond (now Suffolk)	VA	1/1/1983			+				
VA 4		Nansemond (now Suffolk)	VA	1/1/1983			-				
EHRL-1134		Nelson	VA	11/19/2002	M		+	-	-		
EHRL-1135		Nelson	VA	11/19/2002	F		+	+	-	3 (b)	
EHRL-1136		Nelson	VA	11/19/2002	F		+	-	-		
EHRL-0720		Northumber-land	VA		M	1.5	+				

Number	Location	County	State	Date	Sex	Age	IFA	PCR results: 16rRNA	VLPT	120-kDa	LST
EHRL-0721		Northumber-land	VA		M	0.5	+				
EHRL-0722		Northumber-land	VA		F	1.5	+				
EHRL-0723		Northumber-land	VA		F	1.5	+				
EHRL-0724		Northumber-land	VA		F	0.5	+				
EHRL-0702		Patrick	VA		F	5.5	-				
EHRL-0703		Patrick	VA		F	1.5	-				
EHRL-0705		Patrick	VA		F	2.5	-				
EHRL-0706		Patrick	VA		F	3.5	-				
EHRL-0707		Patrick	VA		F	1.5	-				
EHRL-0733		Pittsylvania	VA				+				
EHRL-0734		Pittsylvania	VA				+				
EHRL-0735		Pittsylvania	VA				+				
EHRL-0736		Pittsylvania	VA				+				
EHRL-0737		Pittsylvania	VA				+				
365-1	Prince William Forest Park	Prince William	VA	8/18/1988	F	3	+				1
365-2	Prince William Forest Park	Prince William	VA	8/18/1988	F	1	+				1
365-4	Prince William Forest Park	Prince William	VA	8/18/1988	F	4	+				1
365-5	Prince William Forest Park	Prince William	VA	8/18/1988	F	5	+				1
365-3	Prince William Forest Park	Prince William	VA	8/18/1988	F	2	-				1
SE94-109	Radford Army Ammun. Plant	Pulaski	VA	10/22/1994		2.5	-				
SE94-110	Radford Army Ammun. Plant	Pulaski	VA	10/22/1994		0.5	-				
SE94-111	Radford Army Ammun. Plant	Pulaski	VA	10/22/1994		0.5	-				
SE94-112	Radford Army Ammun. Plant	Pulaski	VA	10/22/1994		4.5	-				
SE94-113	Radford Army Ammun. Plant	Pulaski	VA	10/22/1994		1.5	-				
EHRL-0687		Scott	VA		M	2.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0688		Scott	VA		M	1.5	-				
EHRL-0689		Scott	VA		M	2.5	-				
EHRL-0690		Scott	VA		M	2.5	-				
EHRL-0692		Scott	VA		M	1.5	-				
EHRL-0628		Shenandoah	VA		F	3.5	-				
EHRL-0630		Shenandoah	VA		F	1.5	-				
EHRL-0631		Shenandoah	VA		F	0.5	-				
EHRL-0632		Shenandoah	VA		F	4.5	-				
EHRL-0633		Shenandoah	VA		M	0.5	-				
EHRL-0667		Southampton	VA		F	2.5	+				
EHRL-0668		Southampton	VA		F	1.5	+				
EHRL-0669		Southampton	VA		F	2.5	+				
EHRL-0672		Southampton	VA		M	3.5	+				
EHRL-0671		Southampton	VA		M	2.5	-				
SE95-0098	Lake Anna SP	Spotslvania	VA	6/17/1905		2.5	+				
SE95-0099	Lake Anna SP	Spotslvania	VA	6/17/1905		5.5	+				
SE95-0100	Lake Anna SP	Spotslvania	VA	6/17/1905		2.5	+				
SE95-0101	Lake Anna SP	Spotslvania	VA	6/17/1905		1.5	+				
EHRL-1026	Quantico	Stafford	VA	11/23/2002	M	1.6	-	-	-		
EHRL-1028	Quantico	Stafford	VA	11/23/2002	M	1.5	-	-	-		
EHRL-0763		Surry	VA		M	1.5	+				
EHRL-0764		Surry	VA		F	2.5	+				
EHRL-0765		Surry	VA		M	2.5	+				
EHRL-0766		Surry	VA		M	1+	+				
EHRL-0767		Surry	VA				+				
EHRL-0756		Sussex	VA		M	3.5	+				
EHRL-0757		Sussex	VA		F	2.5	+				
EHRL-0760		Sussex	VA		F	4.5	+				
EHRL-0758		Sussex	VA		F	2.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0759		Sussex	VA		F	3.5	-				
EHRL-0680		Tazewell	VA		F	15.5	-				
EHRL-0681		Tazewell	VA		F	2.5	-				
EHRL-0684		Tazewell	VA		F	4.5	-				
EHRL-0685		Tazewell	VA		F	2.5	-				
EHRL-0686		Tazewell	VA		F	3.5	-				
EHRL-0636		Virginia Beach	VA		M	1.5	+				
EHRL-0637		Virginia Beach	VA		M	0.5	+				
EHRL-0639		Virginia Beach	VA		F	3.5	+				
EHRL-0640		Virginia Beach	VA		M	1.5	+				
EHRL-0642		Virginia Beach	VA		M	1.5	+				
316-01	The Smithsonian Conservation and Research Center	Warren	VA	9/24/1985	M	1.5	-				0
316-02	The Smithsonian Conservation and Research Center	Warren	VA	9/24/1985	F	2.5	-				0
316-03	The Smithsonian Conservation and Research Center	Warren	VA	9/24/1985	F	3.5	-				0
316-04	The Smithsonian Conservation and Research Center	Warren	VA	9/24/1985	F	3.5	-				0
316-05	The Smithsonian Conservation and Research Center	Warren	VA	9/24/1985	M	2.5	-				0
EHRL-0648		Westmore-land	VA		F	0.5	+				
EHRL-0649		Westmore-land	VA		F	2.5	+				
EHRL-0650		Westmore-land	VA		F	2.5	+				
EHRL-0653		Westmore-land	VA		F	3.5	+				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0654		Westmore-land	VA		F	0.5	+				
CC235-02		Wythe	VA	9/6/2002			-	-	-		
CC288-02		Wythe	VA				-				
SE91-133	Camp Perry	York	VA	3/13/1992	M	1.5	+				
SE91-134	Camp Perry	York	VA	12/18/1991	M	0.5	+				
SE91-135	Camp Perry	York	VA	12/18/1991	F	1.5	+				
SE91-136	Camp Perry	York	VA	12/18/1991	M	0.5	+				
SE91-137	Camp Perry	York	VA	12/18/1991	F	3.5	+				
SE91-138	Camp Perry	York	VA	12/19/1991	F	2.5	+				
SE91-139	Camp Perry	York	VA	12/26/1991	F	2.5	+				
SE91-140	Camp Perry	York	VA	12/26/1991	F	1.5	+				
SE91-141	Camp Perry	York	VA	12/26/1991	F	2.5	+				
SE91-142	Camp Perry	York	VA	12/26/1991	F	2.5	+				
SE91-143	Camp Perry	York	VA	12/26/1991	F	2.5	+				
SE91-144	Camp Perry	York	VA	12/30/1991	F	1.5	+				
SE91-145	Camp Perry	York	VA	12/30/1991	F	1.5	+				
SE91-146	Camp Perry	York	VA	12/30/1991	F	2.5	+				
SE91-147	Camp Perry	York	VA	12/30/1991	F	1.5	+				
SE91-148	Camp Perry	York	VA	12/31/1991	F	0.5	+				
SE91-149	Camp Perry	York	VA	12/31/1991	F	0.5	+				
SE91-150	Camp Perry	York	VA	1/1/1991	M	0.5	+				
SE91-151	Camp Perry	York	VA	1/1/1991	F	2.5	+				
SE91-152	Camp Perry	York	VA	1/1/1991	F	1.5	+				
SE91-153	Camp Perry	York	VA	1/1/1991	F	3.5	+				
SE91-154	Camp Perry	York	VA	1/1/1991	F	3.5	+				
SE91-155	Camp Perry	York	VA	1/2/1991	F	2.5	+				
SE91-156	Camp Perry	York	VA	1/2/1991	F	0.5	+				
SE91-157	Camp Perry	York	VA	1/2/1991	F	1.5	+				
SE91-158	Camp Perry	York	VA	1/3/1991	F	2.5	+				
SE91-159	Camp Perry	York	VA	1/3/1991	M	0.5	+				
SE91-160	Camp Perry	York	VA	1/3/1991	M	0.5	+				
SE91-161	Camp Perry	York	VA	1/3/1991	M	0.5	+				
SE91-162	Camp Perry	York	VA	1/3/1991	M	1.5	+				

								PCR results			
Number	**Location**	**County**	**State**	**Date**	**Sex**	**Age**	**IFA**	**16rRNA**	**VLPT**	**120-kDa**	**LST**
SE91-163	Camp Perry	York	VA	1/3/1991	M	1.5	+				
SE93-654		Grant	WV	12/9/1993			-				
SE93-655		Grant	WV	12/9/1993			-				
SE93-577		Hampshire	WV	11/22/1993		3.5	-				
SE93-587		Hampshire	WV	11/22/1993		2.5	-				
SE93-588		Hampshire	WV	11/22/1993		0	-				
SE93-589		Hampshire	WV	11/22/1993		0	-				
SE93-590		Hampshire	WV	11/22/1993		0	-				
SE93-598		Hampshire	WV	11/22/1993		0	-				
SE93-599		Hampshire	WV	11/22/1993		0	-				
SE93-601		Hampshire	WV	11/22/1993		0	-				
SE93-597		Hardy	WV	11/22/1993		0	-				
SE93-600		Hardy	WV	11/22/1993		2.5	-				
SE93-638		Hardy	WV	12/10/1993			-				
SE93-639		Hardy	WV	12/10/1993			-				
SE93-640		Hardy	WV	12/10/1993			-				
SE93-643		Hardy	WV	12/10/1993			-				
SE93-651		Hardy	WV	12/10/1993			-				
389-11	Sloan Parson Farm	Hardy	WV	8/29/1989	F	6	-				0
389-12	Sloan Parson Farm	Hardy	WV	8/29/1989	M	2	-				0
389-13	Sloan Parson Farm	Hardy	WV	8/29/1989	F	7	-				0
389-14	Sloan Parson Farm	Hardy	WV	8/29/1989	F	3	-				0
389-15	Sloan Parson Farm	Hardy	WV	8/29/1989	F	5	-				0
499-1	Sloan Parson Farm	Hardy	WV	9/9/1994	F	1.5	-				0
499-2	Sloan Parson Farm	Hardy	WV	9/9/1994	F	1.5	-				0
499-3	Sloan Parson Farm	Hardy	WV	9/9/1994	M	1.5	-				0
499-4	Sloan Parson Farm	Hardy	WV	9/9/1994	F	4.5	-				0
499-5	Sloan Parson Farm	Hardy	WV	9/9/1994	M	1.5	-				0
574-1	Sloan Parson Farm	Hardy	WV	8/18/1999	M	3	-				0
574-2	Sloan Parson Farm	Hardy	WV	8/18/1999	F	1	-				0
574-3	Sloan Parson Farm	Hardy	WV	8/18/1999	F	5	-				0
574-4	Sloan Parson Farm	Hardy	WV	8/18/1999	F	2	-				0
574-5	Sloan Parson Farm	Hardy	WV	8/18/1999	M	0.75	-				0
247-01	Sloan Parson Farm	Hardy	WV	9/9/1981	M	1.5	-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
247-02	Sloan Parson Farm	Hardy	WV	9/9/1981	F	1.5	-				0
247-03	Sloan Parson Farm	Hardy	WV	9/9/1981	F	1.5	-				0
247-04	Sloan Parson Farm	Hardy	WV	9/9/1981	F	1.5	-				0
247-05	Sloan Parson Farm	Hardy	WV	9/9/1981	M	1.5	-				0
300-01	Sloan Parson Farm	Hardy	WV	9/21/1984	F	2.5	-				0
300-02	Sloan Parson Farm	Hardy	WV	9/21/1984	F	3.5	-				0
300-03	Sloan Parson Farm	Hardy	WV	9/21/1984	M	1.5	-				0
300-04	Sloan Parson Farm	Hardy	WV	9/21/1984	F	2.5	-				0
300-05	Sloan Parson Farm	Hardy	WV	9/21/1984	F	4.5	-				0
200-2	Sloan Parson Farm South Fork	Hardy	WV	7/26/1977			-				
200-3	Sloan Parson Farm South Fork	Hardy	WV	7/26/1977			-				
200-4	Sloan Parson Farm South Fork	Hardy	WV	7/26/1977			-				
200-5	Sloan Parson Farm South Fork	Hardy	WV	7/26/1977			-				
200-1	Sloan Parson Farm South Fork	Hardy	WV	7/26/1977			-				
572-1	Garrett-Hall Farms	Lewis	WV	8/31/1998	F	4.5	-				0
572-2	Garrett-Hall Farms	Lewis	WV	8/31/1998	M	1.2	-				0
572-3	Garrett-Hall Farms	Lewis	WV	8/31/1998	F	2.5	-				0
572-4	Garrett-Hall Farms	Lewis	WV	8/31/1998	F	1.2	-				0
572-5	Garrett-Hall Farms	Lewis	WV	8/31/1998	F	3.5	-				0
EHRL-0153		Lincoln	WV	11/21/2000	M		-				
EHRL-0154		Lincoln	WV	11/21/2000	M		-				
EHRL-0155		Lincoln	WV	11/21/2000	M		-				
EHRL-0156		Lincoln	WV	11/21/2000	M		-				
EHRL-0157		Lincoln	WV	11/21/2000	M		-				
571-1	Fish Creek/Route 250 vicinity	Marshall	WV	8/26/1998	F	7.5	-				0
571-2	Fish Creek/Route 250 vicinity	Marshall	WV	8/26/1998	F	1.2	-				0
571-3	Fish Creek/Route 250 vicinity	Marshall	WV	8/26/1998	F	1.25	-				0
571-4	Fish Creek/Route 250 vicinity	Marshall	WV	8/26/1998	F	5.5	-				0
571-5	Fish Creek/Route 250 vicinity	Marshall	WV	8/26/1998	F	3.5	-				0
549-1	McClintic WMA	Mason	WV	8/26/1997	F	3.5	-				
549-2	McClintic WMA	Mason	WV	8/26/1997	F	4.5	-				
549-3	McClintic WMA	Mason	WV	8/26/1997	M	1.5	-				
549-4	McClintic WMA	Mason	WV	8/26/1997	F	2.5	-				
549-5	McClintic WMA	Mason	WV	8/26/1997	F	3.5	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
EHRL-0077	Brogan Property	Mercer	WV	1/8/2001	M	3.5	-				
EHRL-0078	Brogan Property	Mercer	WV	1/8/2001	M	.5	-				
EHRL-0079	Brogan Property	Mercer	WV	1/8/2001	F	3.5	-				
EHRL-0080	Brogan Property	Mercer	WV	1/8/2001	F	4.5	-				
EHRL-0081	Brogan Property	Mercer	WV	1/8/2001	F	.5	-				
498-1	Patterson Creek	Mineral	WV	9/8/1994	M	2.5	-				0
498-2	Patterson Creek	Mineral	WV	9/8/1994	F	2.5	-				0
498-3	Patterson Creek	Mineral	WV	9/8/1994	F	7.5	-				0
498-4	Patterson Creek	Mineral	WV	9/8/1994	M	1.5	-				0
498-5	Patterson Creek	Mineral	WV	9/8/1994	F	2.5	-				0
575-1	Margaret Welch Farm	Mineral	WV	8/18/1999	F	6	-				0
575-2	Margaret Welch Farm	Mineral	WV	8/18/1999	F	4	-				0
575-3	Margaret Welch Farm	Mineral	WV	8/18/1999	F	4	-				0
575-4	Margaret Welch Farm	Mineral	WV	8/18/1999	F	4.5	-				0
575-5	Margaret Welch Farm	Mineral	WV	8/18/1999	F	2.5	-				0
353-1	Bluestone Farm	Monroe	WV	8/25/1987	M	1.25	-				0
353-2	Bluestone Farm	Monroe	WV	8/25/1987	F	1.25	-				0
353-3	Bluestone Farm	Monroe	WV	8/25/1987	F	2.25	-				0
353-4	Bluestone Farm	Monroe	WV	8/25/1987	F	1.25	-				0
353-5	Bluestone Farm	Monroe	WV	8/25/1987	M	1.25	-				0
496-1	Little Mountain	Monroe	WV	9/7/1994	F	2.5	-				0
496-2	Little Mountain	Monroe	WV	9/7/1994	M	1.5	-				0
496-3	Little Mountain	Monroe	WV	9/7/1994	F	2.5	-				0
496-4	Little Mountain	Monroe	WV	9/7/1994	F	2.5	-				0
496-5	Little Mountain	Monroe	WV	9/7/1994	F	3.5	-				0
576-1	Little Mountain	Monroe	WV	8/19/1999	M	1.5	-				0
576-2	Little Mountain	Monroe	WV	8/19/1999	M	1.5	-				0
576-3	Little Mountain	Monroe	WV	8/19/1999	F	3.5	-				0
576-4	Little Mountain	Monroe	WV	8/19/1999	F	1.5	-				0
576-5	Little Mountain	Monroe	WV	8/19/1999	F	3.5	-				0
SE93-608		Pendleton	WV	11/22/1993		9.5+	-				
SE93-609		Pendleton	WV	11/22/1993		A	-				
SE93-610		Pendleton	WV	11/22/1993		9.5+	-				
SE93-611		Pendleton	WV	11/22/1993		A	-				

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
SE93-612		Pendleton	WV	11/22/1993		A	-				
500-1	National Radio Astronomy Lab	Pocahontas	WV	9/8/1994	F	4.5	-				0
500-2	National Radio Astronomy Lab	Pocahontas	WV	9/8/1994	F	3.5	-				0
500-3	National Radio Astronomy Lab	Pocahontas	WV	9/8/1994	M	1.5	-				0
500-4	National Radio Astronomy Lab	Pocahontas	WV	9/8/1994	F	3.5	-				0
500-5	National Radio Astronomy Lab	Pocahontas	WV	9/8/1994	F	1.5	-				0
577-1	National Radio Astronomy Lab	Pocahontas	WV	8/19/1999	F	4	-				0
577-2	National Radio Astronomy Lab	Pocahontas	WV	8/19/1999	F	3	-				0
577-3	National Radio Astronomy Lab	Pocahontas	WV	8/19/1999	F	2	-				0
577-4	National Radio Astronomy Lab	Pocahontas	WV	8/19/1999	F	0.75	-				0
577-5	National Radio Astronomy Lab	Pocahontas	WV	8/19/1999	F		-				0
EHRL-0168	Bolt	Raleigh	WV	11/20/2000	M	2.5	-				
EHRL-0169	Bolt	Raleigh	WV	11/20/2000	M	1.5	-				
EHRL-0170	Bolt	Raleigh	WV	11/20/2000	M	2.5	-				
EHRL-0171	Bolt	Raleigh	WV	11/20/2000	M	3.5	-				
EHRL-0172	Bolt	Raleigh	WV	11/20/2000	M	2.5	-				
548-1	State Farm Commission	Taylor	WV	8/26/1997	M	1.5	-				
548-2	State Farm Commission	Taylor	WV	8/26/1997	F	3.5	-				
548-3	State Farm Commission	Taylor	WV	8/26/1997	F	2.5	-				
548-4	State Farm Commission	Taylor	WV	8/26/1997	F	3.5	-				
548-5	State Farm Commission	Taylor	WV	8/26/1997	F	2.5	-				
522-1		Tucker	WV	8/30/1995	F	2.5	-	-			0
522-2		Tucker	WV	8/30/1995	F	1.5	-	-			0
522-3		Tucker	WV	8/30/1995	F	3.5	-	-			0
522-4		Tucker	WV	8/30/1995	F	1.5	-	-			0
522-5		Tucker	WV	8/30/1995	F	2.5	-	-			0
317-01	Loren Bagley and Carl Nolan Farms	Tyler	WV	9/10/1985	F	3.5	-				0
317-02	Loren Bagley and Carl Nolan Farms	Tyler	WV	9/10/1985	F	4.5	-				0
317-03	Loren Bagley and Carl Nolan Farms	Tyler	WV	9/10/1985	F	3.5	-				0
317-04	Loren Bagley and Carl Nolan Farms	Tyler	WV	9/10/1985	M	1.5	-				0
317-05	Loren Bagley and Carl Nolan Farms	Tyler	WV	9/10/1985	F	5.5	-				0
317-06	Loren Bagley and Carl Nolan Farms	Tyler	WV	9/10/1985	F	0.5	-				0
408-06	Loren Bagley and Carl Nolan Farms	Tyler	WV	8/28/1990	F	3.25	-				0
408-07	Loren Bagley and Carl Nolan Farms	Tyler	WV	8/28/1990	F	4.25	-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
408-08	Loren Bagley and Carl Nolan Farms	Tyler	WV	8/28/1990	F	1.25	-				0
408-09	Loren Bagley and Carl Nolan Farms	Tyler	WV	8/28/1990	F	3.25	-				0
408-10	Loren Bagley and Carl Nolan Farms	Tyler	WV	8/28/1990	M	1.25	-				0
597-1		Tyler	WV	9/7/2000			-				
597-2		Tyler	WV	9/7/2000			-				
597-3		Tyler	WV	9/7/2000			-				
597-4		Tyler	WV	9/7/2000			-				
521-1		Tyler	WV	8/28/1995	F	1.2	-	-			0
521-2		Tyler	WV	8/28/1995	M	1.2	-	-			0
521-3		Tyler	WV	8/28/1995	F	3.25	-	-			0
521-4		Tyler	WV	8/28/1995	F	2.25	-	-			0
521-5		Tyler	WV	8/28/1995	F	2.5	-	-			0
597-5		Tyler	WV	9/7/2000			-				
389-26	French Creek	Upshur	WV	8/22/1989	F	2.5	-				0
389-27	French Creek	Upshur	WV	8/22/1989	M	1.5	-				0
389-28	French Creek	Upshur	WV	8/22/1989	M	1.5	-				0
389-29	French Creek	Upshur	WV	8/22/1989	F	2.5	-				0
389-30	French Creek	Upshur	WV	8/22/1989	F	1.5	-				0
497-1	French Creek	Upshur	WV	9/10/1994	F	2.5	-				0
497-2	French Creek	Upshur	WV	9/10/1994	F	3.5	-				0
497-3	French Creek	Upshur	WV	9/10/1994	M	1.5	-				0
497-4	French Creek	Upshur	WV	9/10/1994	F	2.5	-				0
497-5	French Creek	Upshur	WV	9/10/1994	F	2.5	-				0
578-1	French Creek	Upshur	WV	8/13/1999	F	4	-				0
578-2	French Creek	Upshur	WV	8/13/1999	F	1	-				0
578-3	French Creek	Upshur	WV	8/13/1999	M	1	-				0
578-4	French Creek	Upshur	WV	8/13/1999	F	3	-				0
578-5	French Creek	Upshur	WV	8/13/1999	F	3	-				0
CC280-02		Wayne	WV				-				
CC293-02A		Wayne	WV				-				
CC293-02C		Wayne	WV				-				
389-21	Somerville Fork	Wirt	WV	8/30/1989	M	1.5	-				0
389-22	Somerville Fork	Wirt	WV	8/30/1989	M	1.5	-				0
389-23	Somerville Fork	Wirt	WV	8/30/1989	M	1.5	-				0

								PCR results			
Number	Location	County	State	Date	Sex	Age	IFA	16rRNA	VLPT	120-kDa	LST
389-24	Somerville Fork	Wirt	WV	8/30/1989	F	1.5	-				0
389-25	Somerville Fork	Wirt	WV	8/30/1989	F	2.5	-				0
570-1	Somerville Fork	Wirt	WV	9/2/1998	F	2.5	-				0
570-2	Somerville Fork	Wirt	WV	9/2/1998	M	1.2	-				0
570-3	Somerville Fork	Wirt	WV	9/2/1998	F	3.5	-				0
570-4	Somerville Fork	Wirt	WV	9/2/1998	F	2.5	-				0
570-5	Somerville Fork	Wirt	WV	9/2/1998	F	1.2	-				0
SE91-410	Blennerhassett Island	Wood	WV	1/27/1991	F	.6	-				
SE91-390	Blennerhassett Island	Wood	WV	1/27/1991	F	2.5	-				
SE91-391	Blennerhassett Island	Wood	WV	1/27/1991	M	.6	-				
SE91-392	Blennerhassett Island	Wood	WV	1/27/1991	F	1.5	-				
SE91-393	Blennerhassett Island	Wood	WV	1/27/1991	F	1.5	-				
SE91-394	Blennerhassett Island	Wood	WV	1/27/1991	M	.6	-				
SE91-395	Blennerhassett Island	Wood	WV	1/27/1991	M	2.5	-				
SE91-396	Blennerhassett Island	Wood	WV	1/27/1991	M	1.5	-				
SE91-397	Blennerhassett Island	Wood	WV	1/27/1991	F	.6	-				
SE91-398	Blennerhassett Island	Wood	WV	1/27/1991	F	.6	-				
SE91-399	Blennerhassett Island	Wood	WV	1/27/1991	F	3.5	-				
SE91-400	Blennerhassett Island	Wood	WV	1/27/1991	M	1.5	-				