

Final Report – Revision 1

White-tailed Deer in Arkansas: Genetic Connectivity and Chronic Wasting Disease susceptibility

Submitted to:

M. Cory Gray and Chris Middaugh
Arkansas Game and Fish Commission
771 Jordan Drive
Monticello, AR 72655

Prepared by:

Marlis R. Douglas
Tyler K. Chafin
Bradley T. Martin
Zachery D. Zbinden
Michael E. Douglas

Arkansas Conservation & Molecular Ecology Laboratory
University of Arkansas
Biological Sciences
850 W Dickson St
Fayetteville, AR 72701

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Table of Contents

Table of Contents	1
Executive Summary	3
<i>Overview</i>	3
<i>Objectives</i>	4
<i>Approach</i>	4
<i>Key Findings</i>	5
I. Introduction	6
<i>Chronic Wasting Disease (CWD)</i>	6
<i>CWD in Arkansas</i>	7
<i>Study Objectives and Approach</i>	8
II. Research Objectives	10
III. Methods	11
<i>Sampling and Tissue Acquisition</i>	11
<i>Lab Work - DNA Extraction</i>	12
<i>Lab Work - SNP Data Generation</i>	12
<i>SNP Analysis - Population Structure</i>	13
<i>SNP Analysis – Estimating Migration</i>	14
<i>SNP Analysis – Examining Relative Dispersal by Sex and Age Class</i>	15
<i>PRNP/ PRNP^{PSG} – Data Generation</i>	16
<i>PRNP Analysis – Haplotype Data</i>	16
<i>PRNP Analysis – Spatial Distribution of PRNP Variants</i>	17
<i>PRNP Analysis – Signatures of Selection on PRNP Variants</i>	18
<i>Landscape Genetics – Spatial Analysis</i>	19
IV. Results	21
<i>Sampling</i>	21
<i>SNP Data, Population Structure and Landscape Genomics</i>	21
<i>Evidence for Age- and Sex- Biased Dispersal</i>	23
<i>PRNP Gene Variants and Frequency of Resistant Genotypes in AR</i>	23
<i>Evidence for Natural Selection on PRNP Gene Variants</i>	25
<i>Spatial and Environmental Components of Migration</i>	26

V. Discussion	28
<i>Key Project Findings</i>	29
<i>Population Connectivity, Dispersal and Disease Spread</i>	30
<i>Genetic Structure and Population Connectivity</i>	31
<i>Effects of Historic Restocking and Translocations on Genetic Structure</i>	32
<i>Sex- and Age- Biased Dispersal in Arkansas</i>	34
<i>PRNP Gene Variants</i>	35
<i>PRNP Selection and Time of Chronic Wasting Disease Exposure in Arkansas</i>	36
<i>Partitioning Spatial Components of Population Structure</i>	37
<i>Management Implications</i>	41
VI. Acknowledgments	43
VII. References Cited	44
VIII. Tables	51
IX. Figures	59
X. Appendices	81
<i>Appendix 1: DNA Extraction</i>	82
<i>Appendix 2: SNP Methods</i>	83
<i>Appendix 3: SNP Analysis</i>	86
<i>Appendix 4: PRNP Methods</i>	88
<i>Appendix 5: Spatial Analysis Methods</i>	90
<i>Appendix 6: Spatial Data – Environmental Maps</i>	93
<i>Appendix 7: Spatial Analysis – 17 Relevant Variables</i>	110
XI. Supplemental Material	128
<i>Table S1: Sample and Data Overview</i>	128
<i>Table S2: PRNP Variants by County</i>	158

Executive Summary

Overview:

This study represents a genetic evaluation of 1,720 white-tailed deer sampled across 75 counties in Arkansas from 2016-2019. It was conducted to better understand the potential risk and spread of Chronic Wasting Disease (CWD) in the state (Fig. 1). The genetic patterns discovered in our study reflect the dispersal of deer through the diverse and complex environments of the state (Figs. 2-4), and help make predictions about the potential spread of CWD from the current Management Zone, but also provide a framework for the adaptive management of both deer and CWD in Arkansas.

Objectives:

1. **We used a genomic approach (SNP genotyping) to infer population connectivity of white-tailed deer in Arkansas.** Population genetic patterns reflect deer dispersal through complex environments and demonstrate levels of population connectivity within an anthropogenically modified landscape (Amaral et al., 2016).
2. **We also assayed levels of polymorphisms at the *PRNP* gene. This allowed us to identify gene variants that are associated with reduced (or elevated) susceptibility to CWD.** The distribution and frequency of *PRNP* gene variants can help identify subpopulations that might be less susceptible to CWD. This, in turn, informs risk assessment and the potential for disease spread (Blanchong et al., 2009; Johnson et al., 2006; Kelly et al., 2014).
3. **We also examined our genetic data within the context of environmental and habitat variables to identify landscape characteristics that can promote or inhibit dispersal of white-tailed deer in Arkansas.** Understanding landscape characteristics conducive to deer dispersal can help management to focus on those areas where CWD might more rapidly spread into deer herds that are currently CWD-free.

Approach:

We used a novel and cutting-edge genomic approach (termed ‘SNP-Genotyping;’ Fig. 5) to analyze our deer samples. This method is more effective than traditional methods (used over the last 20+ years in wildlife management) for detecting subtle population structure, and thus herd connectivity, because it allows hundreds of samples to be screened across thousands of genetic markers. Thus, it is both efficient and cost-effective. We also sequenced a section of the *PRNP* gene to identify variants that might be associated with CWD susceptibility. Given these data, we then determined the spatial distribution of these variants across the landscape. A total of 1,720 samples were evaluated in 75 counties in Arkansas, with the majority taken from the CWD Management Zone (Table 1, Fig. 6).

Key Findings:

1. Analysis of genome-wide genetic variation at ~35,000 SNP loci (genotypes) per individual revealed **eight subpopulations** (gene pools) across Arkansas (Figs. 6-11).
2. Interestingly, our analyses uncovered signatures of **ancestry from earlier** out-of-state **translocation events**, as well as **restocking efforts from within the state** (Fig. 11). These analyses unequivocally demonstrate the power of our analyses to detect genetic traces at both historic and contemporary levels.
3. **Modelling migration rates** (a proxy for **dispersal**) underscored that some areas of the state displayed **reduced connectivity**, suggesting restricted movement of deer between some regions (Fig. 12).
4. Our analyses were able to break down the variability in **migration rates** into spatial and environmental components. This, in turn, revealed the manner by which climate and land-cover influenced deer dispersal across the state, with the strongest signal indicating the **Arkansas River as a major barrier to deer dispersal**.
5. **One variant of the *PRNP* gene** in white-tailed deer from Arkansas appears to be associated with **reduced susceptibility to CWD**; this result is consistent with similar studies from other states (Tables 2-4).

6. We also found that the **distribution and frequencies of *PRNP* variants differed across the state.** Two frequent variants associated with higher (haplotype B) and lower (haplotype C) susceptibility showed distinct distributions (Fig. 18-21). However, sampling density was too low in some areas to support robust statistical analyses (Figs. 16+17).
7. We also found **evidence for natural selection of one *PRNP* gene variant. Haplotype C** (with the 96S mutation) was significantly elevated among **older age classes** and is **consistent with an increased probability of survival in individuals with this variant** (Fig. 21).
8. The signals in our genetic data for white-tailed deer within the focal CWD zone [e.g., selection of haplotype C (above); CWD prevalence rate and distribution] suggests the possibility that the area **was exposed to CWD for at least 20-25 years, possibly longer.** This demonstrates the slow incubation of this disease in wild populations and underscores the necessity for continued monitoring in the state as one aspect of wildlife management.
9. **Additional sampling/analyses are recommended** in areas of the state that are represented in our study at low sampling density. This would allow us to better understand of the distribution of ***PRNP* gene variants associated with low/high susceptibility**, as well as clarify movements of deer within and among subpopulations. It would also increase our resolution with regard to the manner by which the **landscape filters the movements** of deer and CWD spread.

I. Introduction

Chronic Wasting Disease (CWD)

Chronic wasting disease (CWD) is a fatal neurodegenerative disease found in white-tailed deer (*Odocoileus virginianus*) and other cervids (Family Cervidae; Joly et al., 2003, Williams and Young, 1980). The pathogen is a misfolded protein, called prion (Miller and Williams, 2003), which is naturally produced by the deer, but becomes infectious when not folded normally. Because prions are derived from a naturally produced protein, an organism's immune system does not recognize it as alien and hence cannot develop immunity against the disease (Prusiner, 1998). However, certain variants of the *PRNP* gene that produces the prion protein seem to be associated with a lower susceptibility to CWD (Blanchong et al., 2009; Brandt et al., 2015, 2018; Johnson et al., 2003, 2006; Kelly et al., 2008; Wilson et al., 2009).

Transmission of CWD occurs through these prions, either through direct contact among deer, or indirectly through exposure to prions in the environment (Gough and Maddison, 2010; Williams et al., 2002). In North America, CWD has caused economic losses in states where it emerged, primarily due to revenue loss associated with reduced hunting (Arnot et al., 2009) and management of CWD is essential to protect wildlife, as well as local economies. To gather necessary data on CWD occurrence and potential spread, several states have implemented disease surveillance and management plans (e.g., Manjerovic et al., 2014).

One important aspect to proactively manage the disease spread is movement of deer to determine the risk of CWD spread among areas. Behavior of deer facilitates spreading of CWD, such as male dispersal over long distances (e.g., >100 km; Kelly et al., 2010), or philopatry of females that can exacerbate vertical and horizontal transmission within matriarchal groups (Grear et al., 2010).

CWD in Arkansas

CWD in Arkansas was first confirmed in February 2016 in a sample from 2.5-year female elk (*Cervus elaphus*) legally harvested in October of 2015 near Pruitt (Newton County). A few days later, testing also confirmed CWD in a 2.5-year female white-tailed deer found dead at Ponca (also Newton County). During 14-24 March 2016, biologists from the Arkansas Game and Fish Commission (AGFC) and other agencies collected 266 white-tailed deer samples from a 'CWD Focus Area' spanning 125,000-acres in Newton County. Test results indicated 62 individuals (23%) were CWD-positive, with prevalence differing slightly between genders (females= 20%; males=32%). Additional sampling subsequently occurred statewide, to include the collection of road-killed deer. A 2.5-year road-killed male in Pope County (45 miles south of the initial CWD Focus Area) also tested CWD-positive, and prompted a question: Did this individual disperse into the area from another location, or did it indicate that CWD was already established outside the CWD Focal Area? Additional state-wide sampling efforts were initiated in conjunction with hunter harvest and bi-annual surveys to establish a state-wide baseline of CWD occurrence.

As of April 2019, a total of 598 white-tailed deer and 19 elk tested positive for CWD in Arkansas. (Fig. 1). Based on occurrences of confirmed CWD-positive animals, AGFC established a CWD Management Zone (MZ) that include counties within a 10-mile radius of the sampling locations. Currently (June 2019), the MZ in Arkansas encompasses 19 counties located in north-western Arkansas.

Since discovery of CWD in Arkansas, AGFC has made concerted efforts to proactively manage CWD prevalence and potential disease spread. Management actions include relaxed regulations with regards to bag limits and antler size restrictions and focus on additional harvest of the male deer population, one of the best-known management practices to slow disease spread. In addition, restrictions are placed on baiting, feeding, hunting and moving of wildlife within the Management Zone (Fig. 1). Supplemental feeding concentrates animals, increasing the frequency of direct contact between animals and increases the chances of disease transmission. As new CWD+ cases are discovered, the Management Zone is expanded to counties that fall within a 10-mile buffer radius around that location. During the 2018/2019

hunting season, 241 new cases of CWD+ deer and five CWD+ elk were detected. Following this discovery, the CWD Management Zone was expanded to include Baxter, Scott and Stone counties. Arkansas has a compulsory testing requirement for any elk harvested in the state and offers a voluntary program for harvested deer. Testing is facilitated by a system of decentralized drop-off containers, that will be expanded in 2019.

Study Objectives and Approach

The objectives of this study were to assess population connectivity and quantify distribution and frequency of *PRNP* gene variants among deer herds across all 75 counties in Arkansas to (a) determine potential of CWD spread beyond the current Management Zone due to dispersing of infected deer, and (b) evaluate if there were herds in Arkansas that might be more susceptibility or resistant to CWD. We employed a genomic approach (SNP genotyping) to evaluate genetic structure for inference of population connectivity and assessed variation at the *PRNP* gene using sequence analysis. We then compared spatial patterns of genetic diversity and environmental features to identify landscape characteristics that might be either conducive to or inhibit deer dispersal, and hence spread of CWD into other areas.

Population genetic patterns (Figs. 2-4) reflect dispersal of organisms through complex environments and can reveal if population connectivity is indeed present among areas within an anthropogenically-modified landscape (Amaral et al., 2016). Distribution and frequency of *PRNP* gene variants may help identify subpopulations that more or less susceptible to CWD and help inform risk assessment of disease spread. Spatial analysis of genetic and landscape associations can inform pro-active management plans to mitigate future disease spread.

SNP-genotyping is a state-of the art genomic approach for the examination of fine-scale population structure (Fig. 2) and population connectivity (Fig. 3). Admixture analysis (Fig. 4) of SNP-genotypes assays genetic diversity at thousands of genetic markers through a method called RADseq, rather than the 10-20 markers commonly employed in traditional population genetic studies (Fig. 5). This achieves a much higher resolution to detect subtle genetic

structure (Morin et al., 2004), but also allows to distinguish local from dispersed animals (Senn et al., 2013; Tokarska et al., 2009) under the assumption that a resident will significantly associate with a local family, whereas a transient would not.

The **genetic approach developed in this study** and the database established from genotyping SNP polymorphism and *PRNP* gene variation can eventually be used to address a multitude of important questions related to the biology of white-tailed deer in Arkansas and the potential impact of CWD on the state's deer populations. For example, continued SNP and *PRNP* genotyping of white-tailed deer samples could help **monitor deer population dynamics** and their **response to CWD infection** (e.g., selection and adaptation). Comparison of SNP genotypes of Arkansas deer *versus* those from other states could potentially inform our understanding of the **origin of CWD in Arkansas**. And a more a more in-depth evaluation of ***PRNP* gene variation** across the state could increase our understanding of how polymorphisms (different forms) can lead to different prion forms that moderate **individual susceptibility** to and **progression of CWD infection** and help determine how variants of the prion protein influence the natural selection of the *PRNP* gene. The genetic data this project produced constitute the beginning of what we hope will eventually become a **large database** that can be used to address important CWD research objectives, such as those listed above, with Arkansas taking a leading role in adaptive management of CWD in white-tailed deer and other cervids.

II. Research Objectives

Key objectives of this study were to assess:

(1) Population connectivity of white-tailed deer across the entire state of Arkansas

and

(2) Occurrence of *PRNP* gene variants known to be associated with lower or higher CWD susceptibility and spatial distribution across Arkansas

and

(3) Association of landscape features with observed patterns of genetic structure to evaluate potential spread of CWD into other areas in Arkansas.

To infer population connectivity, we assayed genetic population structure using a reduced-representation genomic approach that allows for simultaneous screening of thousands of variable (polymorphic) genetic markers across the genome of each individual deer (Fig. 5). The genetic variation screened comprises Single-Nucleotide-Polymorphisms (SNPs), the most common mutation across the genome. SNP genotyping has several advantages over microsatellite analysis traditionally used in wildlife management and conservation including **better resolution to detect subtle genetic population structure** - as often present amongst populations in wildlife species with moderate to high dispersal rates (such as white-tailed deer) - **higher efficiency** and **lower costs for screening hundreds of samples** (Peterson et al., 2012; Puckett, 2017), and can be more reliably repeated, and thus allows for comparisons amongst studies (Kelly et al., 2011).

III. Methods

Sampling and Tissue Acquisition

Tissue samples were provided by the Arkansas Game and Fish Commission (AGFC) and consisted primarily of earplugs or tongue pieces. Samples either represented road kills, hunter harvested animals submitted for CWD testing, targeted kills by AGFC in response to report of a suspected CWD-positive deer, or as a by-product of other agency efforts (e.g. health surveys).

A total of 1,720 samples were processed for this study. Of these ~500 were obtained during Phase 1+2 of the project (Douglas et al., 2018) and primarily represented white-tailed deer from the CWD Management Zone (MZ) as it was defined during 2017, with the majority collected in two CWD-Focal Areas (FA) located in Newton (N=111) and Pope (N=56) counties.

For Phase 3, an additional 1,207 white-tailed deer were obtained. These represented samples collected from all 75 counties in Arkansas (Fig. 6; Table 1, Supplement Table S1). In addition, 29 white-tailed deer collected from native populations of white-tailed deer in Wisconsin (kindly provided by Dr. Michael D. Samuel) were included as a reference to examine potential retained genetic variation from past agency-conducted translocations of white-tailed deer (Donaldson et al., 1951). Wisconsin samples consisted of extracted genomic DNA or tissue samples.

All samples were compiled into a database and assigned a unique lab-specific number that was used to track samples through all lab procedures and can be cross-referenced with the AGFC field-tag (Supplement Table S1). This provides a quick oversight of genetic data generated for each individual sample and allows to associate genetic with ecological data provided by AGFC, such as gender, age, or GIS coordinates.

Lab Work – DNA Extraction

Lab procedures to generate the genetic data followed standard, published procedures, with slight modifications to optimize each step of data generation for this study. For details see Appendix 1 through 4.

The first step involved obtaining DNA from each individual tissue sample (Table S1) that then was used as DNA template to generate the different types of genetic data (see below). Several DNA extraction methods were tested and a modified version of the QIAamp Fast DNA Tissue Kit extraction protocol was identified as yielding the best quantity of high-quality DNA A kit (Appendix 1).

DNA quality is an important factor in obtaining reliable, reproducible genetic data. DNA can degrade if exposed to the environment, such as is the case for road kills. Degraded DNA can cause spurious results, which in turn can lead to erroneous conclusions. Thus, special efforts were made to ascertain the quality of the DNA used to generate the genetic data for this study (see Figure A1-1A and A1-1B in Appendix 1).

Lab Work - SNP Data Generation

To evaluate population structure and infer population connectivity among white-tailed deer herds in Arkansas, we screened genetic variation at thousands of genetic markers called SNPs (=Single Nucleotide Polymorphism). SNPs are the most common mutations in the genome and are used in wildlife management to infer genetic population structure to identify conservation units (Funk et al., 2012), or detect hybridization across closely related species, including cervids (Russel et al., 2019).

To generate the SNP data for each white-tailed deer sample, we developed protocols for a genomic approach called double-digest restriction site associated DNA sequencing, or ddRAD (Peterson et al., 2012) using a combination of *in silico* (computational) and *in vitro* (wet lab) methods (Chafin et al., 2018). Because sequencing the entire genome for hundreds of

individuals is both cost-prohibitive and would yield an unmanageable amount of data, the intent of the ddRAD approach is to reduce the genome in a consistent and repeatable manner so the same loci (regions of the genome) can be analyzed for each white-tailed deer. Details on protocol optimization, SNP data generation and bioinformatics processing are provided in Appendix 2.

SNP Analysis – Population Structure

The SNP data were used to determine genetic population structure of white-tailed deer across all 75 counties in Arkansas. This information can be used to infer how ‘connected’ deer herds are across the landscape through dispersal of individual deer from one herd to another.

Population structure was inferred from SNP data using an assignment test to determine the most likely number of genetic populations (i.e., gene pools) represented by the current set of samples (for details see Appendix 3). To illustrate spatial extent of inferred populations, results were visualized by plotting each individual as a pie-chart, with colors indicating proportion of the individual’s genome reflecting a particular gene pool (Fig. 7).

In addition to the full dataset (N=1,143 deer from Arkansas and N=29 additional samples from Wisconsin for reference.), we also replicated these analyses across several subsets: (i) partitioned by sex (Fig. 8); and (ii) across 10 down-sampled replicates (20% of individuals), generated using a random sample weighted inversely by spatial sampling density (Fig. 9). The latter was performed so as to evaluate the impact of uneven sampling on our analyses. Sampling density is particularly important to consider with regards to distribution of genetic subpopulations (e.g., Fig. 10), because of the uncertainty associated with areas of low sampling density.

Another approach to visualize distribution of gene pools used a modeling approach called Empirical Bayesian Kriging (EBK) (Gribov and Krivoruchko, 2012). Instead of plotting gene pools represented by each individual, EBK models the **probability of genetic populations across**

the landscape (i.e., EBK probability surfaces; Fig. 11). These were also used as a first-pass qualitative evaluation of landscape features, such as rivers and roads, to inform predictor variable selection for in-depth spatial analyses (described below).

SNP Analysis – Estimating Migration

Natural populations commonly exist as clusters of genetically closely-related individuals (e.g., family clans) within a given area. Populations in geographic proximity are genetically similar, but not as closely related as individuals within a given cluster (Fig. 2). Because individuals are limited in the distance they can move across the landscape, populations commonly exhibit a pattern of ‘isolation by distance’ in which genetic relatedness between populations declines as a function of distance (Wright, 1943).

This pattern of genetic similarity in proximity *versus* genetic differences across distances occurs naturally and is referred to as genetic population structure (Fig. 2). It emerges over generations, as related individuals remain in the same herd (e.g., female fawns generally remain with the maternal herd). Some individuals might move away from the maternal herd (i.e., disperse), as is the case with male fawns once they reach maturity (Fig. 3). Because dispersing individuals carry their unique genetic profile with them, they distribute genetic variation across the landscape (i.e., gene flow). If dispersed animals interbreed with resident individuals, the resulting offspring’s genetic profile reflects admixed ancestry of both parental gene pools (Fig. 4).

When habitats vary (e.g. elevation gradients, vegetation type), some aspects of the landscape will invariably have an effect on the probability of individuals moving through that space – for example the presence of barriers such as rivers or roads, or variation in the suitability of habitat. As individual dispersal declines, so does gene flow (admixture of genetically different populations). As a consequence, those landscape features affecting individual movement accumulate over time as variation in genetic differences over space.

Variation in genetic connectivity (=‘gene flow’) can be estimated by examining spatial patterns

of relatedness, under the general assumption that areas in which genetic relatedness decays very quickly have little gene flow, and areas in which genetic relatedness is retained over large distances have high gene flow. **We visualized this as an ‘effective migration surface’** using the program EEMS (Petkova et al., 2015), as a means to examine underlying landscape resistance (Fig. 12).

These results are complementary to the assignment tests (above), in that they model different, but related, evolutionary processes. EEMS models migration, while assignment tests model a *product* of varied migration over space, namely population structure. The primary purpose of our subsequent analyses was to understand how features of the environment interact as determinants of migration and population structure.

SNP Analysis – Examining Relative Dispersal by Sex and Age Class

A commonly recognized pattern in mammals displaying strong male-male competition is a sex-biased dispersal, with juveniles or young males often moving the longest distances (Dobson, 1982). To examine the potential for a) sex; b) age; and c) age X sex bias in relative dispersal, **we examined how genetic relatedness decays as a function of distance from each individual**. To do so, we randomly sampled 5,000 SNP loci (to reduce computation time) and calculated pairwise genetic dissimilarity. We then partitioned the data by sex, and by age class, and calculated mean genetic dissimilarity of individuals within a variable radius (e.g. 5km, 10km, 50km) (Fig. 13). The primary assumption here is that dispersing individuals (immigrants) will be on average more genetically dissimilar (=less related) to resident individuals than residents are to one another. These calculations were limited to individuals which had neighboring samples within a 5km radius, thus creating an implicit restriction to high-density sampling zones (Fig. 9). We also qualitatively examined sex-bias on population structure.

PRNP/ PRNP^{PSG} – Data Generation

Genomic DNA was also used as a template to evaluate **genetic variability (=polymorphism) of the prion protein *PRNP* gene**. Standard procedures for amplifying and sequencing genes were followed, using modified protocol from previous studies (Brandt et al., 2015, Johnson et al., 2006). For details see Appendix 4. To ascertain if the detected polymorphisms were indeed in the functional *PRNP* gene, presence of the non-coding *PRNP* pseudogene (*PRNP^{PSG}*) was evaluated (O'Rourke et al., 2004).

Sequences were manually verified and compared to a reference database of *PRNP* gene sequences from previous studies in other states (Kelly et al., 2008; Brandt et al., 2015; 2018) that are available from public databases (i.e., NCBI GenBank database). All sequences were compiled into a single database for subsequent data analyses.

PRNP Analysis – Haplotype Data

As diploid organisms, **deer have two alleles for each gene**. Because of the technical methodology of DNA sequencing, these two parental alleles are sequenced *together*, meaning that as an initial step in the analyses of the *PRNP* gene variation, it is first required to distinguish the exact sequence(s) for each allele. To do so, we used a statistical approach called ‘phasing’ (Stephens et al., 2001) that evaluates common associations between mutations along the *PRNP* sequence which may be indicative of them being commonly inherited- that is, they co-occur on the same chromosomal sequence, and were passed as a singular unit (=‘haplotype’) from one parent to an offspring. When data are present from many hundreds of individuals, these associations can be quantified and used to ‘phase’ (separate) the two parental alleles (haplotypes) present in each individual. This is a necessary step, because downstream analyses are based on two distinct alleles (haplotypes) forming the genotype (diplotype) of each individual. For details on the phasing analyses see Appendix 4; scripts to format inputs and parse results of haplotype phasing are available at github.com/tkchafin/haploTools. In order to

mitigate spurious results, we exclusively retained haplotypes that were phased with high confidence (>0.90 posterior probability).

Haplotypes were then categorized (Table 2) according to the nomenclature of Brandt et al. (2015, 2018). To visualize similarity amongst haplotypes, we constructed a haplotype network using the median-joining algorithm employed by POPART (Leigh et al., 2015); a haplotype network reflects numbers of nucleotide substitutions (point mutations) among the different *PRNP* sequences, and can be particularly informative for understanding the genetic differences among haplotypes (Fig. 14). Haplotype frequencies were calculated globally (i.e., state-wide; Fig. 15), by-county (Supplement Table S2), and by CWD status (positive vs. negative) both statewide (Table 3) and Newton County only (Table 4), because our more robust sampling density and higher rate of CWD prevalence in Newton County allows for more robust statistical analyses. Scripts for creating these input files can be found at github.com/tkchafin/scripts.

PRNP Analysis – Spatial Distribution of PRNP Variants

To interpolate ***PRNP* haplotype distributions across the state** and examine **correlation with the spatial distribution of CWD** (see Fig. 16), we first had to compute frequencies. We did so by grouping samples into ‘pseudo-populations’ by dividing the state into a minimum number of non-overlapping polygons, each containing 5-10 sampling localities. This resulted in N=211 polygons (Fig. 17). Haplotype frequencies were then computed within each polygon and interpolated using Empirical Bayesian Kriging. We used this approach rather than computing frequencies by-county in order to take advantage of the increased sampling resolution we have in parts of the state. **Spatial distributions of relative frequencies** for the seven most frequent haplotypes in our data set were then plotted (Fig. 18), with additional details provided for haplotype B (Fig. 19) and haplotype C (Fig. 20), implicated with increased and reduced susceptibility to CWD, respectively.

PRNP Analysis – Signatures of Selection on PRNP Variants

In order to detect **potential biases of specific PRNP haplotypes on the probability of CWD transmission**, we followed Brandt et al. (2015, 2018) in first quantifying effect sizes in the form of an **odds ratio (OR)**. The odds ratio is a common measure of association between an exposure and an outcome. Here, *for each haplotype*, we consider the probability of contracting CWD (=’outcome’), given presence/ absence of the focal haplotype (=’exposure’). The resulting ratio provides information on the **relative risk**, where OR=1 means that individuals with the focal haplotype (e.g. “A”, “B”) are equally represented among CWD-positive and CWD-negative groups, OR>1 means the focal haplotype is over-represented in CWD-positive samples, and OR<1 means the focal haplotype is under-represented in CWD-positive samples. Note that we specifically use terminology referring to their *relative representation*- this is because multiple factors can affect the odds ratio, and thus may not necessarily translate to conclusions regarding the *susceptibility* associated with particular haplotypes. For example, population structure (as above) may create a coincidental bias, when disease prevalence (or detection) is spatially structured. Additionally, an over-representation of a haplotype among CWD-positive individuals could be due to either an increased probability of contraction, or a *survival bias*, wherein individuals having the focal haplotype are more likely to survive with the disease, thus skewing the odds ratio in a random sample. Consequently, it is important to further consider haplotypes that are implicated by the odds ratio (Tables 3 and 4).

To further evaluate **candidate susceptibility variants (CSVs)**, we first asked whether the relative representation of the haplotype shows an **effect among age classes**. Here, our assumption was that if a haplotype affects the probability of survival to adulthood (e.g., by reducing CWD risk), then it should increase or decrease in relative frequency in older age classes. To test this, we first computed the relative representation of CSVs among CWD status groups (CWD+ *versus* CWD- individuals) as an odds ratio within each sampled age class (Table 5). We then tested if this relationship was predicted by age using linear regression (Fig. 21).

To further **test if selection is acting on CSVs showing an age bias**, we computed their relative fitness in the form of a selection coefficient (s). This is a common population genetic

statistic used to quantify fitness differences among genotypes, where $s>0$ means a fitness advantage, and $s<0$ means a fitness disadvantage. In order to calculate s , we first calculated counts of focal and non-focal haplotypes within each age class, and then treated the age class as a *time-series sample*. This was then used to compute s using a statistical model that assumed an idealized population (Mathieson and McVean, 2013).

Landscape Genetics - Spatial Analysis

To identify if landscape features influence dispersal of deer, and consequently population connectivity, genetic data were next evaluated within a spatial context and contrasted against sets of environmental variables describing abiotic (e.g., climatic) and biotic (e.g., vegetations) characteristics (Table 6, Appendix 5 and 6). We first generated a 10 km² hexagonal tessellation grid, overlain across the state of Arkansas. This produced 13,378 tiles (Appendix 5), within which estimates of white-tailed deer migration ($\log M$) were calculated based on genetic information (i.e., SNP differences) among individuals in and around each tile (Fig. 12).

Values for 35 environmental factors from a variety of sources (Table 6, Appendix 6) were also determined for each tile. The goal of the spatial analysis was to 1) determine the **amount of autocorrelation of the estimate of white-tailed deer migration** ($\log M$); 2) determine the **amount of variation in migration** that could be **explained by extrinsic/environmental factors**; 3) create a **list of important explanatory factors**; and 4) draw **inferences about the role of abiotic and biotic processes driving variation in deer dispersal**.

The dataset was first filtered to include tiles with a **migration rate** ($\log M$) generated from a genetic sampling density > 0.01 to overcome heterogeneity of variance among sampling densities (i.e. low densities had high variance). Standard data transformations followed to prepare the data for subsequent analyses, satisfy assumptions, and reduce multiple collinearity (e.g. transforms to fit normality, and Z-score standardization). Then the dataset was reduced to include only factors that significantly related to the migration parameter ($\log M$) via linear regression and t-tests.

Next, we needed to determine how much of the **variation of the migration rate (logM)** **could be explained purely by space** (i.e. autocorrelation). The spatial coordinates of the hexagonal tiles were used to deconstruct the spatial arrangement into various functions representing different combinations of ‘neighborhoods’. These functions result in each tile having a value that in total creates an eigenvector associated with each function. Each eigenvector can be tested for a relationship with migration (logM), and significant relationships are indicative of spatial autocorrelation in the parameter. A set of significant eigenvectors were retained as the spatial dataset for use in variation partitioning.

Finally, partial linear regression was used to partition variation of migration (logM) among spatial and environmental explanatory datasets. This allowed us to determine how much variation of logM could be explained by autocorrelation alone, by environmental factors alone, and by the combination of the two. This step was critical for drawing inferences about the mechanisms driving white-tailed deer dispersal. Additional details on analyses and parameter selection are provided in Appendix 5.

VI. Results

Sampling

A total of 1,720 tissue samples collected in 75 Arkansas counties from 2016-2019 were processed for this study (Fig. 6). Of these, subsets of samples (Supplement Table S1) were subjected to genomic DNA extraction (N=1,720), sequencing of ~800 nucleotides of the *PRNP* gene (N=1,460) and the *PRNP^{psg}* pseudogene (N=1,459), and generation of SNP data (N=1,208). SNP data were generated for an additional 30 samples from Wisconsin (not shown in Table S1). Not all samples yielded data of sufficient quality, and these were excluded from subsequent analyses. Four samples from Miller county were identified as representing elk and were also excluded from subsequent analyses. Sampling density was not evenly distributed across the state (Fig. 9), which needs to be taken into consideration when interpreting results and drawing inferences.

SNP Data, Population Structure and Landscape Genomics

SNP data were successfully obtained for 1,226 white-tailed deer samples, including those from Wisconsin. Sequencing of the ddRAD libraries yielded an average of 25,584 ($s=8,639$) independent genomic loci per sample. Retaining only loci overlapping in a minimum of ~50% of samples yielded a total of 35,642 loci. We then removed loci showing signs of having been overmerged (e.g. individuals with >2 alleles), yielding a final filtered dataset of 35,420 loci, from which 2,655,584 SNPs were discovered. Of these, 54,102 were removed for being only found in a single individual. Further bioinformatic processing randomly selected one SNP per genomic locus (to reduce signal redundancy), yielding a final SNP dataset of 35,099 used for analysis of population structure.

Analysis of population structure performed in ADMIXTURE revealed an optimal number of clusters of K=8, which reflect genetically distinct gene pools ($k=1$ through $k=8$). Samples were

then classified according to their probability of membership to the inferred gene pools (=ancestry) and spatially oriented (Fig. 6). The result shows white-tailed deer to consist of eight weakly differentiated genetic subpopulations that seem to be generally geographically defined (Fig. 10 shows a highly oversimplified version of the spatial distribution of the eight gene pools).

The most apparent pattern is a **north-south division defined by the Arkansas River valley** (Fig. 6). South of the Arkansas River there are two primary genetic subpopulations, loosely geographically bounded by I-30 to the north and the Ouachita River to the south (Fig. 10). Of these, the eastern population is assigned to two gene pools (Fig. 6: $k=1,3$). Note that the latter ($k=3$) is also assigned to individuals in the north-central region of the state (primarily in Baxter, Cleburne, Fulton, Independence, Izard, Lawrence, Randolph, Searcy, Sharp, Stone, Van Buren counties), which may reflect either historical translocations, or is an artefact of weak genetic differentiation, rather than non-random, long-distance dispersal of white-tailed deer between northcentral and southwestern Arkansas (i.e., population connectivity). Coincidentally, the southeastern genetic subpopulation is dominated by gene pool $k=8$ (Fig. 6) that also subsumed all Wisconsin samples, possibly suggesting retention of genetic variation from past translocations.

Populations north of the Arkansas River are more spatially structured, with six main subdivisions (Fig. 6). The most broadly distributed of these genetic subpopulations (defined by gene pool $k=5$) is found in the Mississippi alluvial plains on the eastern side of the state, extending west across the mainstem of the White River and northward to the confluence of the Black and White Rivers, where it grades into several loosely defined, but distinct genetic subpopulations. The northwestern corner of the state is most genetically heterogeneous, being dominated by four primary endemic gene pools ($k=2,3,4$ and 7). The northern-most genetic subpopulations (dominated by gene pool $k=4$) primarily encompasses Boone, Carroll, and Marion counties, is bound loosely on the east by the White River, and grades to the west into an area of high admixture in Benton and Washington counties. Immediately south is a narrowly defined genetic subpopulation, defined by gene pool $k=7$ mainly found in Newton and Madison counties with a southward transition loosely defined by the Buffalo River region into two

remaining genetic subpopulations, defined by gene pools $k=2$ and $k=6$, that are bounded on the south by the Arkansas River. All of these genetic subpopulations display **considerable admixture** (multiple colors in each pie chart) and spatially weak transitions, indicating that while there is some reduction in gene flow, **none of the geographical or environmental barriers** separating genetic subpopulations **are ‘hard’ boundaries** to dispersal of white-tailed deer across Arkansas.

Evidence for Age- and Sex- Biased Dispersal

Restricting population structure analyses to males showed them to generally exhibit less genetic structuring than females (Figs. 8 and 13). Patterns of genetic dissimilarity showed higher distances in age 0 (juvenile) males than females, with a shift towards low dissimilarity in males >5 (Fig. 13A). This suggests that dispersal of male deer in Arkansas has occurred as juveniles (age 0) or yearlings (age 1). By age 5, males have contributed to their local gene pools (i.e., produced offspring with resident females), thereby creating the pattern of lower genetic dissimilarity among neighboring individuals, regardless of distance (Fig. 13C-E). In females, juveniles (age 0) had very low genetic dissimilarity to individuals at low distances (Fig 13B-C), with distances peaking at 1-2 years (Fig. 13B-C).

PRNP Gene Variants and Frequency of Resistant Genotypes in AR

Of the 1,460 samples of white-tailed deer sequenced across the *PRNP* gene, a total of 1,433 yielded useful sequences (>98% success rate). Sequences were trimmed to 720 nucleotides that could be scored unambiguously, with 11 sites showing polymorphism (Table 2). Three sites (nt285, nt299 and nt372) previously reported as polymorphic by Brandt et al. (2015, 2018) were invariable, and one site showed a novel mutation (nt499A/C) that was synonymous (no amino acid change). Variation was also detected at nucleotide position (nt413A/G) known to be associated with a mutation at the *PRNP^{PSG}* pseudogene, a duplicated non-functional copy of the *PRNP* gene; nucleotides at nt413 were all adjusted to reflect the *PRNP* genotype (nt413G/G).

Polymorphism at three sites (nt286, nt367 and nt676) represented non-synonymous substitutions (=NSS) that result in amino acid changes (96S, 122T and 255K, respectively). **The non-synonymous substitution at nt286/A (amino acid 96S) has been associated with reduced susceptibility to CWD in white-tailed deer in other states** (e.g., Brandt et al. 2015, 2018, Johnson et al. 2006, 2011).

The variable sites segregated into **20 distinct haplotypes** (Table 2; Fig. 14), with 16 previously documented in other states (e.g., Kelly et al. 2008, Brandt et al. 2015, 2018) and four novel and potentially unique to Arkansas. Two of the Arkansas haplotypes (AR_2 and AR_3) had the non-synonymous substitution 96S (nt286/A) that has been associated with reduced susceptibility to CWD (i.e., haplotype C of Brandt et al. 2018). Three other haplotypes (I, P and V) also have the 96S amino acid change (Table 2). However, all five haplotypes were at low frequencies (<1% except haplotype I at 1.47%), precluding any statistical associations with CWD susceptibility.

Targeted amplification and sequencing of the *PRNP^{PSG}* pseudogene was successful in 30% of white-tailed deer samples (443 out of 1,459). Comparisons of *PRNP* and *PRNP^{PSG}* haplotypes within these 443 individuals revealed that variation at nucleotide site nt413 appears indeed to be the result of non-targeted amplification of the *PRNP^{PSG}* pseudogene and does not constitute biological variants of the *PRNP* gene.

Haplotype frequencies in our data set (Tables 3 and 4) differ slightly from those reported in other states (e.g., Illinois and Wisconsin; Blanchlong, 2009; Brandt et al. 2015, 2018). Four of the most frequent (<10%) haplotypes in Illinois/Wisconsin deer populations were also common among Arkansas samples (Fig. 15; haplotypes A-D). However, the most common haplotype (A) detected in 30% of samples in Illinois/Wisconsin, was only found in 15% of samples in Arkansas, where haplotype B and D were most common (each at ~ 23% of samples). Haplotype C, potentially associated with reduced CWD susceptibility, was detected at the same frequency in Arkansas (15%) as in Illinois/Wisconsin (17%). In addition, two haplotypes (E and G), were also at high frequencies in Arkansas (7% and 11%, respectively), but were found in <5% of samples in the Brandt et al. (2018) study. Out of the 16 rare haplotypes by Brandt et al.

(2018) with frequencies $\leq 1\%$ (haplotypes K-Z), seven were also present at low frequencies in the Arkansas samples (haplotypes K, L, O, P, R, T, and V). **Haplotype frequencies also differ amongst counties** (Supplement Table S2), although **sample sizes for most counties are too low to statistically quantify a phylogeographic signal.**

With regards to **distribution and frequencies of CSV (Candidate Susceptible Variants) haplotypes between CWD-negative and CWD-positive white-tailed deer in Arkansas** (Fig. 18-20; Table 3, Supplement Table S2), the present results should be considered **preliminary due to limited numbers of CWD positive samples** in some areas of Arkansas (total N=248, Figs. 16 and 17). The seven most common haplotypes were unevenly distributed across Arkansas (Figs. 18-20).

Evidence for Natural Selection on PRNP Gene Variants

Two CSVs (haplotypes) of the PRNP gene showed significant deviations in representation among CWD+ and CWD- individuals: Haplotypes C and B, both also sampled by Brandt et al. (2015, 2018) have been implicated with increased and reduced susceptibility to CWD, respectively. In our data set, haplotype B was significantly over-represented among CWD+ individuals, both when considered state-wide (Odds Ratio $OR= 2.00$; $p=0.000001$; Table 3), and when restricted to Newton County ($OR=1.47$; $p=0.033$; Table 4). Haplotype C was significantly under-represented in CWD+ individuals, also both in state-wide ($OR=0.30$; $p=0.00003$; Table 3) and Newton County comparisons ($OR=0.42$; $p=0.015$; Table 4).

To further test for variability in CWD susceptibility as driving selection on Haplotypes B and C, we hypothesized that, if variants do indeed impact CWD susceptibility, their representation (frequencies) should vary among age classes. Here, a haplotype that confers **reduced CWD risk** should increase the probability of reaching older age classes (=**extended life expectancy**), therefore should increase in relative frequency among older individuals. Haplotype C was found to increase in representation with increasing age (Table 5A), both in terms of relative frequency ($p=0.036$; $R^2=0.635$; Fig. 21A) and odds ratio ($p=0.043$; $R^2=0.601$;

Fig. 21A), supporting the hypothesis that it reduced CWD risk. Haplotype B did not show any significant relationship among age classes (Table 5B, Fig. 21B), and its over-representation in the dataset amongst CWD+ deer (Tables 3 and 4) may be an artefact of population structure. The majority of CWD+ deer in our data set were sampled from NW Arkansas (Figs. 16 and 17) and haplotype B could simply be a common haplotype in deer herds in this area, independent of CWD occurrence.

To track how the frequency of Haplotype C changed across years (=age classes), we computed a selection coefficient (*s*) of 0.1215 for Haplotype C. This corresponds to the strength of selection; where 0.0 means no selection (no impact on survival rate), and 1.0 means total selection (e.g. only individuals having that haplotype would survive). Although it can be difficult to interpret if this selection is direct (=acting on mutations at the *PRNP* gene) or indirect (=acting on mutations elsewhere in the genome that are statistically associated with Haplotype C, or influence *PRNP* gene expression) (Barton and Servedio 2015).

Spatial and Environmental Components of Migration

The 35 environmental factors were distilled into a set of 17 factors that significantly explained white-tailed deer dispersal (Table. 7). Because sampling density was very low in parts of Arkansas, analyses were restricted to areas with sufficient number of samples to conduct statistically meaningful analyses (Fig. 23). The set of 17 meaningful factors included riverine barriers to dispersal (e.g. RIVER_DIST, ECOLYS_LU_Open Water, and SECTION Arkansas River Valley), climatic variables (e.g. BIO8_WETTE), vegetation variables (e.g. West Gulf Coast Mesic Hardwood Forest), and section variables (e.g. Boston Mountains). **The single most explanatory factor was SECTION_Arkansas River Valley** which when present had a mean logM lower than that of non-Arkansas River valley sections by 0.42. For context, logM ranges from -1 to 1 (Fig. 12). This suggests the **Arkansas River is a significant barrier to white-tailed deer dispersal**. Maps and distributions of the 17 environmental factors are provided in Appendix 6 and results of the spatial analyses are detailed in Appendix 7.

Spatial decomposition via dbMEM extracted 81 meaningful eigenvectors, of which 73 were included in the forward selection procedure, and 65 were retained after correcting for multiple tests. These eigenvectors represent spatial autocorrelation in the variable logM (migration rate). Smaller eigenvectors (e.g. V3) represent broad scale spatial structure and larger eigenvectors (e.g. V81) represent relatively finer scale structure (Fig. 24). Prior to variation partitioning, **only the 17 top-ranked eigenvectors were selected so that the environmental and spatial datasets would have the same number of factors.**

A linear model including both spatial eigenvectors and environmental factors explained 67% of the variance in the variable logM ($\text{adj.}R^2 = 0.67$; $p < 0.001$). There was a large proportion of spatial autocorrelation in the variable logM ($\text{adj.}R^2 = 0.64$; $p < 0.001$). However, **only 20% of the variance of logM could be attributed to environmental factors**, the majority of which was **spatially structured environmental variation** (17%). Thus, 47% of the variation of logM was spatially autocorrelated, but could not be explained by the environmental factors presented here (Fig. 25). This suggests that the unexplained autocorrelated structure could be explained by either 1). Unmeasured environmental factors, 2). Biotic factors intrinsic to deer populations (e.g. population size), or 3). A combination of these.

V. Discussion

In this study, we addressed three objectives:

1. **We evaluated genetic structure in white-tailed deer collected in Arkansas from 2016-2019 to infer population connectivity using a genomic (SNP genotyping) approach.** Population genetic patterns reflect dispersal of organisms through complex environments, and hence can reveal if connectivity is indeed present among areas within an anthropogenically modified landscape (Amaral et al., 2016; Kelly et al., 2010).
2. **We also assayed the levels of polymorphisms at the *PRNP* gene using sequencing analysis and to identify gene variants that might be associated with reduced or increased susceptibility to CWD.** Distribution and frequency of *PRNP* gene variants may allow identifying subpopulations less susceptible to CWD and help inform risk assessment of disease spread (Blanchong et al., 2009; Johnson et al., 2006; Kelly et al., 2008).
3. **We analyzed the genetic structure and population connectivity data within a spatial context to examine environmental and habitat variables that promote or inhibit dispersal of white-tailed deer in Arkansas.** Identifying landscape characteristics that are conducive to dispersal of white-tailed deer can help focus management efforts to areas where CWD might spread more rapidly into currently CWD-free herds (Kelly et al., 2014).

Key Project Findings:

1. Analysis of genome-wide genetic variation using a **novel genomic approach** (i.e., genotyping of ~35,000 SNP loci) revealed **eight subtly differentiated subpopulations** (gene pools) among 1,226 white-tailed deer from across Arkansas (Figs. 6-11).
2. These analyses uncovered signatures of **retained ancestry from past out-of-state translocation events**, and of restocking efforts within the state (Fig. 11).
3. Modelling migration rates (a proxy for dispersal) suggested **reduced connectivity in some areas** (Fig. 12).
4. Partitioning variation in **migration rates** into spatial and environmental components revealed roles for climatic and land-cover variables in influencing deer dispersal across the landscape, with the strongest signal being associated with the **Arkansas River as a barrier to dispersal**.
5. **Variants of the prion-coding *PRNP* gene** exist among white-tailed deer in Arkansas, including haplotypes (alleles) identified as being associated in other states with **reduced susceptibility to CWD** (Tables 2-4).
6. **Distribution and frequencies of *PRNP* gene variants differ across the state**; with two frequent variants associated with higher (haplotype B) and lower (haplotype C) **susceptibility showing distinct spatial patterns** (Fig. 18-21). However, sampling density in some areas is too low for robust statistical analyses. (Figs. 16+17).
7. We found **evidence for natural selection on Haplotype C** (96S mutation), with a significant increase in representation among **older age classes** consistent with an **increased survival probability** (Fig. 21). Other *PRNP* variants also share the 96S mutation but were present at too-low frequencies for statistical analysis.
8. Signals in the genetic data (e.g., selection of haplotype C, CWD prevalence rate and distribution) suggests that **the population within the focal CWD zone could have been exposed to the disease for at least 20-25 years, but possibly longer**.
9. **Additional sampling/analyses** in areas of the state with low sampling density would allow to increase understanding of the distribution of the *PRNP* gene variants associated with low/high susceptibility.

Population Connectivity, Dispersal and Disease Spread

‘**Distribution**’ and ‘**abundance**’ are not only natural history attributes of species but also the building blocks of ecology (Andrewartha and Birch, 1954). Yet, their functional integrity is being challenged by anthropogenic habitat alterations (Chen et al., 2011), and traits such as ‘**dispersal**’ and ‘**population connectivity**’ have become paramount (Crooks and Sanjayan, 2006) in that they more appropriately mirror wildlife ecology in the Anthropocene (Corlett, 2015).

They are important ecological characteristics that translate to other aspects, such as the **spread of emerging infectious diseases** (EIDs) and are thus key elements that quantify the availability of and contact rates for host species (Tracey et al., 2014). Population connectivity also plays an important role in the disease ecology of vectors (Gog et al., 2002). A vector is an organism that can transmit the causative agent of a disease, as would be white-tailed deer or elk in the case of CWD, with the prions being the disease-causing agent. Studies that evaluate the mechanisms by which disease vectors disperse through the environment, particularly in the context of contemporary **habitat connectivity**, also provide the **ecological context** necessary for a derivation of broad-scale public health considerations (Park, 2012) - or in the case of CWD, wildlife management.

Landscape genetic tools are often employed to characterize population dynamics, population connectivity (gene flow) and movement pathways of disease vectors across heterogeneous landscapes (Biek and Real, 2010), as well as to ascertain the concurrent spread and persistence of infectious agents associated with these movements (Blanchong et al., 2016). For example, gene flow estimates in white-tailed deer corresponded to the rapid expansion of chronic wasting disease (CWD) in northern Illinois/ southern Wisconsin and served to identify those habitats with an elevated risk for infection (Kelly et al., 2014).

Genetic Structure and Population Connectivity

Single Nucleotide Polymorphisms (SNPs) represent a new generation of genomic markers (Ekblom and Galindo, 2010) and have quickly emerged as the primary approach for **genetic studies into wildlife ecology and management** (Fig 5; Morin et al., 2004). Thousands of loci can be efficiently and cost-effectively screened across hundreds of individuals (Peterson et al., 2012; Puckett, 2017), providing sufficient resolution to track processes at ecological time scales – as in disease ecology (Blanchong et al., 2016) – and to parse out the individual components (e.g. local and landscape-level) driving genetic variation.

Our analysis of thousands of SNP loci successfully revealed eight genetic populations among the 1,226 white-tailed deer collected from 75 counties in Arkansas from 2016-2019 (Fig. 7). Genetic populations were spatially structured suggesting that both **broad-scale landscape-level and local-scale, behavioral processes are shaping genetic structure of white-tailed deer in Arkansas.**

At the **landscape scale**, population structure is primarily shaped by dispersal limitations and likely represents a cumulative effect of environmental heterogeneity (e.g. barriers to dispersal). At the **local scale**, social system may serve to naturally ‘fragment’ metapopulations into social groups (Mussmann et al., 2017), and substructure is often driven by relatedness, including white-tailed deer (Kelly et al., 2011). Hence, kinship in social mammals and its accompanying associations, can be important drivers of disease transmission.

Our analyses suggest both demographic and landscape-level processes are indeed impacting dispersal in white-tailed deer in Arkansas. Weakly differentiated genetic clusters (Fig. 7) seem to be generally geographically defined, and reflect associations with major landscape features, such as the Arkansas River (Figs. 10+11), and broad-scale habitat differences (Table 7, Fig. 25). Elevation is another important factor modulating dispersal of white-tailed deer, although a more comprehensive assessment across the entire state is warranted to statistically evaluate the role of these landscape aspects to dispersal of white-tailed deer in Arkansas; some areas of the state were represented by too few samples (Fig. 9) to conduct statistically robust analyses for spatial association of genetic patterns and landscape

features (Fig. 23, Appendix 7). We also found evidence for age- and sex- biases in dispersal rates (Figs. 8+13), and a strong signal of management interventions (stocking and translocation) on patterns of genetic relatedness (discussed below).

Effects of Historic Restocking and Translocations on Genetic Structure

Following many years of over-hunting and land-use impacts, the Arkansas deer population reached a low ebb of less than 500 individuals (Holder, 1951). Flooding of the Mississippi River in 1927 covered the eastern half of the state and contributed to the decline of deer in this area. Private hunters and AGFC wardens salvaged a small number of individuals, which were used to subsequently re-seed the Delta region. These were distributed in isolated refugia, with known hold-out populations on Caney and Muddy Creeks in the Ouachita Mountains, the Sylamore District of the Ozark Mountains, and the lower bottom lands near the confluence of the Arkansas and Mississippi Rivers. Other isolated groups were known in Pope County, with lesser numbers also found in Woodruff and Cross counties, and a handful of other small remnant populations.

As a mitigation strategy and to bolster population sizes, AGFC implemented a **refuge system**, with restocking of deer playing a major role. Between 1942-1951 a total of 2,343 deer were **translocated across 56 counties** (Donaldson et al., 1951). These supplementations used live-trapped native deer from areas with large deer herds and were intended to reduce crowding in source populations and to boost deer populations in release areas. The majority of these deer were sourced from three areas, with numerous smaller-scale (and poorly documented) translocations by managers and private hunters.

To this end, in 1941 AGFC established the **Howard County Deer Farm** (=720 acres; expanded to 1,305 in 1944) in the southwest corner of the state, within the existing Howard County Refuge (~33,000 acres) provisioned under federal aid to provide a convenient source of individuals for re-stocking (Holder, 1951). Source of the initial Refuge stocks are unknown. Although not all destination records for translocations sourced from the Howard County Farm

are available, it is documented that individuals from the 1945-1946 trapping season were released in Nevada and Little River counties (Holder, 1946), both also located in southwestern Arkansas. The complete extent of stocking from Howard County is unknown.

A second management action was trapping operations initiated in 1942, with the largest source of individuals being the **Sylamore District of the Ozark Mountains** (Hunter, 1952). From 1942-1946, over 900 individuals were trapped in the Sylamore District (Stone and Baxter Counties). Records here are a little more thorough, with known stockings of Sylamore individuals in Baxter, Calhoun, Cleburne, Cleveland, Cross, Hempstead, Howard, Jefferson, Lee, Lincoln, Little River, Logan, Nevada, Newton, Ouachita, Sebastian, Stone, Van Buren, Washington, and White Counties (Holder, 1946). Thus, documented translocations from the Sylamore District in the North-Central Arkansas Ozarks indicate deer have been moved to all corners of the state.

The third major source of individuals were purchased by the Commission from the **Sandhill Game Farm in Babcock**, Wisconsin. The Commission released 107 in 1942, 96 in 1943, and 101 in 1944. We are not aware of any records regarding the destinations and distribution of releases from these purchases. **Several small-scale releases** are also recorded (see Holder, 1951). Arkansas and **Louisiana** deer (unknown origin) were released in Ashley, Franklin, and Washington Counties between 1915-1926, with Ashley County later (~1931) also receiving six individuals from **North Carolina** (and two additional individuals going to Chicot County). An additional 28 deer were imported from the Pisgah National Forest in North Carolina, which were released in Bradley, Drew, Ouachita, and Saline Counties. In 1932-33, 15-18 deer from **Texas** were released in Dallas, Ouachita, and Saline Counties. Additional trapping was also done in the White River National Wildlife Refuge (Hunter, 1952).

Such past translocations often leave some traces of distinct (non-local) genetic diversity in the recipient populations and are likely detected with the high resolution afforded by the SNP approach used in this study, albeit which translocations were indeed successful is highly unpredictable (see Douglas et al., 1999, Douglas and Brunner, 2002). This likely explains some of the anomalous patterns of ancestry seen in our analyses (Figs. 7+11). For example,

common ancestry (=shared gene pools) found in Southwest and Northeast Arkansas ($k=1$ in Fig. 7) likely reflects translocations from the large refuges in the Sylamore District and from the Howard Game Farm. There is also a signature of Wisconsin ancestry ($k=8$ in Fig. 7), most broadly distributed in the southeastern Gulf Coast Plains region, with smaller pockets in Northeast and Northwest Arkansas. Although detailed records of the destination of the Wisconsin Sandhill Game Farm deer are not known, our approach suggests that stocking was likely heavily concentrated in these areas.

All three Arkansas gene pools that lack spatial cohesion can thus be anecdotally connected to the three major stock sources from the 1940's restoration efforts.

Subpopulation $k=1$ has the highest representation in the Howard County region, while $k=3$ is broadly distributed east of the Sylamore area, and $k=8$ likely reflects Wisconsin ancestry (Fig. 11). One genetic subpopulation ($k=5$) is broadly distributed in the Delta region and primarily found in the eastern half of the state north of the Arkansas River and likely reflects re-introduction of salvaged deer after the 1927 Mississippi River flood. The remaining four genetic population clusters ($k=2, 4, 6$, and 7) are 'Ozark endemics'. Although many of the counties in this region were considered to have severely depleted (if not extirpated) populations at the 1930 ebb (Holder, 1951), it is possible that some of this structure reflects genetic variation pre-dating the population crash. At least one such persistent population is documented in Pope County, and which also did not receive any known releases from 1942-1951 (Holder, 1951). **Because severe population bottlenecks (such as this one) can promote large changes in allele frequencies, it can also inflate population structure (e.g. Douglas et al., 2006). This in itself may explain the exceptionally high frequency of PRNP Haplotype B in that region (Fig. 19; discussed below).**

Sex- and Age- Biased Dispersal in Arkansas

The high resolution of SNP data also allowed to examine **age- and sex-related dispersal patterns among white-tailed deer in Arkansas** (Fig. 13). Older males (>5 years) were notably

less genetically dissimilar than younger males, suggesting A) that five-year and above males are contributing substantially more to their local gene pools; and B) that they typically do not move long distances after establishing reproductive success. Local genetic distances peaked for juvenile and yearling males (ages 0 and 1), suggesting that male dispersal likely has already occurred by that age (Fig. 13A). Females, on the other hand, showed notably lower genetic distances as juveniles (Fig. 13B), with local (<10km) genetic distances peaking in the 1-2 year age class (Fig. 13C), suggesting that females move relatively further on average at that age. This is seemingly consistent with the hypothesis of density-dependence driving dispersal in adult females (Lutz et al., 2015), with natal dispersal as a result of mate competition or inbreeding avoidance being dominant in males (Perrin and Mazalov, 2000; Long et al., 2008). The former may explain why 1-2 year females show slightly higher distances at local scales (Fig. 13C), but not long-range scales (Fig. 13D-E).

PRNP Gene Variants

Polymorphism in the *PRNP* gene detected across 1,433 white-tailed deer collected from the 75 counties in Arkansas is comparable to variation reported from other states (Table 2-4). Out of the **20 *PRNP* gene variants** (haplotypes) detected in this study, 16 were previously reported from other states (Blanchlong et al., 2009; Brandt et al. 2015, 2018; Johnson et al., 2006), and generally represent variants found at higher frequencies in these deer populations. **Four novel *PRNP* gene variants** were detected, that to date are unique to Arkansas. Two of these could potentially represent biologically relevant variation at the functional *PRNP* gene (CSV: Candidate Susceptibility Variants), because of the 96S mutation (Table 2) that has been associated with lower susceptibility to CWD (Brandt et al., 2018). However, all four haplotypes unique to Arkansas, as well as six others previously reported, were found at frequencies <1%, preventing statistically robust analyses for association with CWD susceptibility (Table 3+4, Fig. 15). While the **mechanism underlying susceptibility remains unknown**, the mounting evidence that some prion protein (*PrP*) variants are statistically associated with lower number of CWD+ animals suggests that *PrP* amino acid composition - determined by the underlying *PNRP* gene

nucleotide variation - might play a role in disease progression (Johnson et al., 2011, Brandt et al., 2018).

PRNP Selection and Time of Chronic Wasting Disease Exposure in Arkansas

Several aspects can be indicative of **time of exposure to a disease**: (1) **selection** for disease-resistant phenotypes, (2) **prevalence rate** (with higher rates indicating longer time since initial exposure, and (3) **spatial distribution** of disease (initial disease occurrence usually being localized, and extended exposure being more wide-spread).

As in Robinson et al. (2012), we found a signature of selection on the 96S mutation (haplotype C). Given our estimated selection coefficient ($s=0.1215$), **we can yield some insight as to the amount of time the population has been exposed to chronic wasting disease**. In terms of years, in order to reach the level of haplotype C frequency discrepancy in Newton County (the largest CWD prevalence in our sampling) compared to the state-wide average, it would have taken a minimum of 9.78 generations, or 12.78 generations when computing frequencies using only individuals old enough to have reproduced (>2 years old), assuming an idealized population (Crow and Kimura, 1970). Assuming a 2-year minimum generation time (Demarais et al., 2000), which corresponds roughly to the age of sexual maturation for female white-tailed deer, this would correspond to 19.56, or 25.56 years, respectively. However, the real generation time is likely longer, and there are numerous caveats associated with this rudimentary calculation (e.g. the impacts of skewed sex ratios and overlapping generations is ignored). Despite this, **we can posit that the population within the focal CWD zone has likely been exposed to the disease for some time**. A better understanding of chronic wasting disease dynamics and epizootiology (factors controlling CWD presence) in white-tailed deer will likely provide a better estimate of time required to reach the observed prevalence in Arkansas.

Prevalence rate can also be indicative of how long a population has been exposed to an infectious disease. For example, Miller et al. (2000) simulated prevalence rates reaching 1% in a 15-20 year span, and 15% in 37 to 50 years, using plausible transmission rates. However, Miller

and Connor (2005) noted variation in prevalence growth rates among sex and age classes, and additionally noted that it is likely non-linear (e.g. growth rate depends on current prevalence). Numerous studies have also found spatial variation in prevalence rate, but association of disease occurrence with landscape features remains unclear.

Almberg et al. (2011) found that prevalence growth rates depend heavily on prion half-life in the environment. Taken together, the above suggest that prevalence growth rate estimates, and hence calendar time predictions for the epidemic, are heavily dependent on the exact model parameterizations. As such, we suggest caution in attempting to apply rate estimates from different contexts to Arkansas. With this in mind, apparent prevalence in the Arkansas CWD Management Zone peaks at 22-30% (C. Middaugh and A. J. Riggs, personal communication), thus it is plausible that CWD exposure in white-tailed deer in Arkansas represents a longer-standing epidemic. The spatial clustering of the disease distribution in Arkansas agrees with a simple spatial epidemic in which prevalence should spread spatially through time (as in Osnas et al., 2009). Given the above, we can posit that endemic CWD in Arkansas could date back potentially as far as the early recovery efforts, e.g. the establishment of Arkansas' refuge system in 1927, or the translocation and restocking efforts starting in 1942 (see below and Holder, 1951 for more information). **However, we once again emphasize that more information regarding population and disease dynamics would be required to make robust estimates.**

Partitioning Spatial Components of Population Structure

Spatial structuring of **biological parameters** (such as genetic population structure or dispersal) can result from extrinsic, **abiotic** determinants which are spatially structured (e.g. rainfall, elevation), or from intrinsic, **biotic** properties (e.g. growth, population size, differential mortality, and competition) (Dray et al., 2006). Our analyses partitioned variation in estimated migration rates (as a proxy for dispersal that cannot be directly measured) into four individual fractions of explained variance (Fig. D1): [a] **non-environmentally explained spatial variance**;

[b] **spatially structured environmental variance**; [c] **non-spatial environmental variance**; and [d] **unexplained variance** (Legendre, 1993). The relative sizes of these fractions of explained variance allow us to infer which mechanisms (e.g., extrinsic/abiotic *versus* intrinsic/biotic) are most likely responsible for the observed structure. Fractions [b+c] represent the total variation explained by the measured abiotic parameters, while fraction [a] represents spatial structure not influenced by environmental variation. Therefore, if [a] > [b+c] then **intrinsic factors, such as population size and differential mortality**, are most important; whereas, if [b+c] > [a] then **extrinsic factors, such as rainfall and elevation**, are most important for the spatial structure of the data. **Understanding these relationships is key for building models that predict the spread of CWD.**

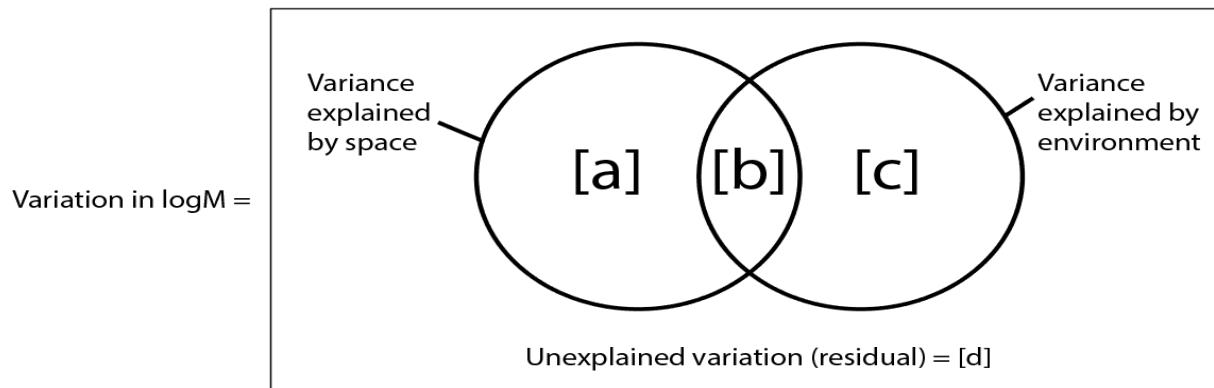


Figure D1: Partitioned components of spatial variation in biological parameters, such as estimated migration rates ($\log M$). [a]= non-environmentally explained spatial variance, [b] spatially structured environmental variance, [c] non-spatial environmental variance, and [d] unexplained variance.

The purpose of developing models of these parameters was to determine how variation in each (migration rate and population structure) is explained by spatial (i.e. autocorrelation) and environmental factors (e.g. elevation or climate.). These analyses provide several pieces of information including: 1) the degree of spatial autocorrelation in the genetic structuring of deer populations, 2) the degree of environmental influence in the genetic structuring of deer populations, 3) a list of powerful explanatory factors, and 4)

inferences about the role of **biotic processes**, internal to populations, versus **abiotic processes**, external to them, in driving overall patterns of population genetic structure. **Although our model explained 67% of the variance in estimated migration rate (logM) across Arkansas, only 17% was attributable to environment- with the remainder relating either to intrinsic biotic or unmeasured abiotic factors.**

Of those environmental variables which did explain variance in migration rate (logM), four were climatic (mean temperature during wettest quarter, mean temperature during driest quarter, precipitation of wettest quarter, and precipitation of wettest quarter). Climatic gradients have been shown to influence forage quality and composition relevant to white-tailed deer (Lesage et al., 2000), with subsequent impacts on deer habitat usage and selection (Shipley and Spalinger, 1995) that could culminate in variable population densities (Roseberry and Woolf, 1998). Deer have also shown inverse density-dependence on rates of population growth (Messier, 1991) and on dispersal (Lutz et al., 2015), thus implicating a potential role for habitat quality on net movement, and thereby gene flow. Six of the remaining variables were categorical assignments to National Vegetation Classification types (Short leaf pine; Gulf Coast mesic hardwood, Crowley's Ridge/ Sand forest, Open water, Large river floodplain forest), again implicating a role for habitat composition on gene flow. The remaining variables related to physical barriers (distance to highway or river), or location within either mountainous regions (Boston and Ouachita mountains) or large river valleys (Mississippi and Arkansas rivers), with the strongest impacts being attributable to the Arkansas River. This result echoes previous studies (e.g., Blanchong et al., 2006) that have found an influence of large rivers in generating landscape genetic patterns and **suggests that rates of CWD expansion to new areas will be slowed by large riverine barriers.**

However, a **large component of spatial variation in the migration rate (logM) was unexplained** (=47%; Fig. 25). We here **hypothesize that local demographic histories likely drive much of this variation**. Two components of the specific history of white-tailed deer in Arkansas could drive variance in migration rate (logM) estimates: 1) the **major population bottleneck**

peaking around 1930, followed by subsequent population expansion; and 2) **artificial ‘gene flow’ facilitated by translocation efforts** (both discussed in more detail above).

Population fluctuations (i.e., bottlenecks followed by rapid population growth) are a well-known mechanism of inflating population genetic structuring and can be commonly observed across deep time scales. For example, population structure in natural populations across much of North America echo genetic effects of Pleistocene ice ages, whereby populations contracted, as individuals retreated into relatively fragmented refugia (Hewitt, 1996, 2004). This isolation has several effects on genetic variation across the landscape, but perhaps foremost are 1) the loss of genetic variation *within* populations, due to the sharp decline in population size; and 2) the increase in genetic variation *among* populations, due to stochastic loss of alleles within each isolated refugium (Nei et al., 1975; Tajima, 1989). The result of population growth after the bottleneck and recolonization of new ranges re-expand is that populations may come into contact again but are much more genetically divergent than before the demographic change. In terms of variants of an individual gene (alleles), many variants will have been lost, and those that remain will have changed drastically in relative frequency among populations (Glenn et al., 2001). The same ‘contraction-expansion’ cycle is likely reflected in the elevated population structure seen in some areas for white-tailed deer in Arkansas. This may suggest that some natural populations persevered through the early 1900s bottleneck.

The second process - facilitated gene flow (i.e., translocations) - is also likely causing anomalous patterns in the migration rate logM estimates. Because the procedure we used to calculate migration rates (i.e., EEMS) models gene flow as occurring step-wise among demes (Petkova et al., 2015), long-range translocations may conflate estimates.

Management Implications

Since the discovery of CWD in Arkansas, AGFC has made concerted efforts to proactively gauge its prevalence and adaptively manage its spread. In this sense, two components must be quantified: **Movement of the disease among populations** (e.g., its penetration across the landscape), and **its prevalence within populations** (e.g. disease growth). As such, hunting regulations and culling strategies should be two-pronged: **Reduce dispersal of deer from CWD areas and decrease population densities**. Below we outline conclusions derived from our genetic analyses and relate how these can be translated within the context of the above two factors. This, in turn, would allow the development of a much broader adaptive management strategy for CWD in white-tailed deer in Arkansas.

<i>Genetic Pattern</i>	<i>Management Implication</i>
<p>Estimated migration patterns indicate that landscape-level features (e.g. Arkansas River) have some impacts on deer movements. However abiotic factors represent a minority of the variance in migration rate.</p>	<p>While landscape features have an impact on deer movement, and thus landscape-level CWD transmission, they are not hard boundaries that will prevent spread of CWD. As such, they offer limited guidance with regards to CWD surveillance or selection of target areas for CWD management. Population dynamics (density) drive disease dynamics at the local scale (see below).</p>
<p>2. Some PRNP gene variants (haplotypes) associate with intrinsic susceptibility to CWD. One variant (haplotype C) persists in older deer and thus shows a strong signature of natural selection. Its presence also impacts the probability of individuals persisting in CWD-prevalent regions.</p>	<p>Selection on haplotype C suggests variation in the susceptibility of deer to CWD. Thus, analysis of haplotype data in deer might support a density reduction strategy wherein individuals with 'low genetic susceptibility' to CWD might be retained, whereas those with 'high genetic susceptibility' might be eliminated through intensive culling. However, the efficacy of differing culling strategies should also be modeled (Wasserberg et al., 2009; Wild et al., 2011). See Potapov et al. (2012) and Uehlinger et al. (2016) for utility of culling in cervids.</p>

3. ***PRNP* haplotypes are structured spatially**, with state-wide variability in frequencies apparent. This in turn suggests state-wide variability in herd-immunity (Brandt et al. 2018).
4. White-tailed deer in Arkansas show a pattern of **age- and sex-biased dispersal**, with greater dispersal by juvenile and sub-adult males (Year 0-1). A slight signal indicates dispersal by young breeding-age females (Year 1-2). However, juvenile females move very little, and the most apparent signal of successful mating is found in older (>= Year 5) males.
5. **Patterns of genetic relatedness across the state** show that genetic ancestry has been retained from historic stockings, with signals reflecting both within-state and out-of state. Again, these data demonstrate how powerful the genomic analyses are to detect genetic patterns in Arkansas deer.
- The rate of CWD spread at the landscape level can be modulated to some degree (but not eliminate) by controlling the frequency of particular haplotypes. However, the long-term consequences of this approach are uncertain and require additional work. Agent-based modelling may provide a means to examine epidemiological and evolutionary host-disease dynamics.
- Sex-biased culling can impact disease spread and prevalence** in two ways: 1) Removing **high-tendency dispersers** can reduce disease spread between populations; and 2) Culling of **reproductive individuals** can reduce rate of growth (or density) within populations. Young males have the highest probability of spreading the disease across space and time. Although females typically do not show natal dispersal, some studies (e.g. Lutz et al., 2015) suggest **density-dependent dispersal** due to competition for fawning habitat, or avoidance of males. This indicates overly high densities as drivers for female migration. Excessive numbers of females can promote large population densities (Holder 1951), thus **female culling should also be considered**.
- Efforts should be harnessed among states to **define translocation histories** of deer so as to track the impacts of historic management actions with regards to the current 'mosaic' distribution of CWD nationwide. Exact translocation sources and destinations would be extremely useful with regards to CWD surveillance.

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VIII. Tables

Table 1: Numbers of white-tailed deer genotyped across ~35,000 SNP loci listed. Samples were collected from 75 counties in Arkansas from 2016-2019. Code indicates standard 2-letter abbreviation for each county.

County	Code	N				
Arkansas	AR	11	Lee	LE	9	
Ashley	AS	1	Lincoln	LI	8	
Baxter	BA	19	Little River	LR	10	
Benton	BE	19	Logan	LO	32	
Boone	BO	34	Lonoke	LN	11	
Bradley	BR	2	Madison	MA	39	
Calhoun	CA	14	Marion	MR	39	
Carroll	CR	50	Miller	MI	8	
Chicot	CH	3	Mississippi	MS	2	
Clark	CL	7	Monroe	MO	10	
Clay	CY	15	Montgomery	MN	2	
Cleburne	CE	8	Nevada	NE	13	
Cleveland	CV	5	Newton	NW	140	
Columbia	CO	4	Ouachita	OU	12	
Conway	CN	11	Perry	PE	8	
Craighead	CG	7	Phillips	PH	9	
Crawford	CW	6	Pike	PI	8	
Crittenden	CT	8	Poinsett	PO	10	
Cross	CS	10	Polk	PL	3	
Dallas	DA	7	Pope	PP	62	
Desha	DE	11	Prairie	PR	10	
Drew	DR	14	Pulaski	PU	11	
Faulkner	FA	14	Randolph	RA	8	
Franklin	FR	20	Saline	SA	11	
Fulton	FU	9	Scott	SC	2	
Garland	GA	14	Searcy	SE	32	
Grant	GR	5	Sebastian	SB	17	
Greene	GE	16	Sevier	SV	12	
Hempstead	HE	9	Sharp	SH	16	
Hot Spring	HS	3	St. Francis	SF	7	
Howard	HO	11	Stone	ST	15	
Independence	IN	7	Union	UN	6	
Izard	IZ	6	Van Buren	VB	23	
Jackson	JA	2	Washington	WA	17	
Jefferson	JE	13	White	WH	10	
Johnson	JO	45	Woodruff	WO	9	
Lafayette	LA	14	Yell	YE	31	
Lawrence	LW	17	Total		1,143	

Table 2: Overview of 20 *PRNP* gene haplotypes detected across 1,433 white-tailed deer collected from 75 counties in Arkansas (2016-2019). Data are based 720 nucleotides and phased haplotypes were derived from genotype data using PHASE2 (only variable nucleotides shown). Haplotype names indicated by letter (A-V) are as in Brandt et al. (2015); haplotypes denoted AR_# are unique to Arkansas and were not previously reported. Mutations differing from haplotype A are shaded, with green indicating synonymous (no amino acid change) and blue non-synonymous substitutions (NSS; amino acid change in protein). Also listed are amino acid position and nucleotide site as referenced in Brandt et al. (2015).

HAP	NSS	Amino Acid Position													
		20	51	81	95	96	99	108	122	124	126	146	166	185	225
Nucleotide Site															
		60	153	243	285	286	299	324	367	372	378	438	499*	555	676
A		C	C	T	A	G	G	A	G	G	G	C	A	C	C
B		C	C	T	A	G	G	A	G	G	G	C	A	T	C
C	96S	C	C	T	A	A	G	A	G	G	G	C	A	T	C
D		C	T	T	A	G	G	A	G	G	G	C	A	C	C
E		C	C	T	A	G	G	A	G	G	G	T	A	C	C
G		T	C	T	A	G	G	A	G	G	G	C	A	C	C
I	96S	C	C	A	A	A	G	A	G	G	G	C	A	T	C
J		C	C	T	A	G	G	G	G	G	G	C	A	C	C
1		C	C	T	A	G	G	G	G	G	A	C	A	C	C
K	225K	T	C	T	A	G	G	A	G	G	G	C	A	C	A
L	122T	C	C	T	A	G	G	A	A	G	G	C	A	C	C
O		T	T	T	A	G	G	A	G	G	G	C	A	C	C
P	96S	C	C	T	A	A	G	A	G	G	G	C	A	C	C
R		C	T	T	A	G	G	A	G	G	G	C	A	T	C
T		C	T	T	A	G	G	A	G	G	A	C	A	C	C
V	96S	C	T	T	A	A	G	A	G	G	G	C	A	C	C
AR_1		C	C	T	A	G	G	G	G	G	A	C	A	C	C
AR_2	96S	C	C	T	A	A	G	A	G	G	G	C	C	T	C
AR_3	96S	T	C	T	A	A	G	A	G	G	G	C	A	T	C
AR_4		C	C	T	A	G	G	A	G	G	G	T	A	T	C

Table 3: PRNP haplotype frequencies and odds ratio for association with CWD status across Arkansas (entire state). Haplotypes were derived from unphased sequences of 720 nucleotides of the *PRNP* gene. Haplotype indicated by letters were also reported by Brandt et al. (2015, 2018), whereas AR_# indicates a haplotype unique to Arkansas. Listed are total numbers (N) and relative frequency f(%), and values for deer that either tested CWD-negative (-), CWD-positive (+) or were not tested (?). Odds Ratio (OR) reflects relative representation of a haplotype in CWD+ deer, with OR>1 indicating over-representation and OR<1 under-representation; SE= standard error, CI= 95% confidence interval, Z(OR)= Z-score and p(OR)= probability. **Values in bold are significant.**

Hap	Counts				Frequency (%)			Odds Ratio					
	N	N(-)	N(+)	N(?)	f%	f%(-)	f%(-)	f(?)	OR	SE	CI	Z(OR)	p(OR)
A	435	367	34	34	15.18	15.17	13.71	17.17	0.89	0.19	[0.61-1.30]	-0.61	0.54
B	657	536	90	31	22.92	22.15	36.29	15.66	2.00	0.14	[1.52-2.64]	4.93	0.00
C	426	376	13	37	14.86	15.54	5.24	18.69	0.30	0.29	[0.17-0.53]	-4.14	0.00
D	657	547	63	47	22.92	22.60	25.40	23.74	1.17	0.15	[0.86-1.58]	1.00	0.32
E	187	160	16	11	6.52	6.61	6.45	5.56	0.97	0.27	[0.57-1.66]	-0.10	0.92
G	309	266	24	19	10.78	10.99	9.68	9.60	0.87	0.22	[0.56-1.35]	-0.63	0.53
I	42	39	1	2	1.47	1.61	0.40	1.01	0.25	1.01	[0.03-1.81]	-1.38	0.17
J	65	59	3	3	2.27	2.44	1.21	1.52	0.49	0.60	[0.15-1.57]	-1.20	0.23
K	10	9	1	0	0.35	0.37	0.40	0.00	1.08	1.06	[0.14-8.60]	0.08	0.94
L	2	2	0	0	0.07	0.08	0.00	0.00	-	-	-	-	-
O	3	2	1	0	0.10	0.08	0.40	0.00	4.89	1.23	[0.44-54.2]	1.29	0.20
P	10	8	0	2	0.35	0.33	0.00	1.01	-	-	-	-	-
R	2	2	0	0	0.07	0.08	0.00	0.00	-	-	-	-	-
T	41	30	1	10	1.43	1.24	0.40	5.05	0.32	1.02	[0.04-2.38]	-1.11	0.27
V	1	1	0	0	0.03	0.04	0.00	0.00	-	-	-	-	-
AR_1	1	0	0	1	0.03	0.00	0.00	0.51	-	-	-	-	-
AR_2	15	14	0	1	0.52	0.58	0.00	0.51	-	-	-	-	-
AR_3	2	2	0	0	0.07	0.08	0.00	0.00	-	-	-	-	-
AR_4	1	0	1	0	0.03	0.00	0.40	0.00	-	-	-	-	-
Total	2,866	2,420	248	198									

Table 4: *PRNP* haplotype frequencies and odds ratio for association with CWD status for Newton County only. Haplotypes were derived from unphased sequences of 720 nucleotides of the *PRNP* gene. Haplotype indicated by letters were also reported by Brandt et al. (2015, 2018), whereas AR_# indicates a haplotype unique to Arkansas. Listed are total numbers (N) and relative frequency f(%), and values for deer that either tested CWD-negative (-), CWD-positive (+) or were not tested (?). Odds Ratio (OR) reflects relative representation of a haplotype in CWD+ deer, with OR>1 indicating over-representation and OR<1 under-representation; SE= standard error, CI= 95% confidence interval, Z(OR)= Z-score and p(OR)= probability. **Values in bold are significant.**

Hap	Counts			Frequency (%)			Odds Ratio				
	N	N(-)	N(+)	f%	f%(-)	f%(-)	OR	SE	CI	Z(OR)	p(OR)
A	95	68	27	15.1	15.7	13.8	0.86	0.25	[053-1.38]	-0.64	0.52
B	197	124	73	31.4	28.7	37.2	1.47	0.18	[1.03-2.11]	2.13	0.03
C	59	49	10	9.39	11.3	5.1	0.42	0.36	[0.21-0.85]	-2.42	0.02
D	158	105	53	25.2	24.3	27	1.15	0.20	[0.79-1.70]	0.73	0.46
E	34	23	11	5.41	5.32	5.61	1.06	0.38	[0.50-2.21]	0.15	0.88
G	65	48	17	10.4	11.1	8.67	0.76	0.30	[0.43-1.35]	-0.93	0.35
I	-	-	-	-	-	-	-	-	-	-	-
J	6	5	1	0.96	1.16	0.51	0.44	1.10	[0.05-3.77]	-0.75	0.45
K	4	3	1	0.64	0.69	0.51	0.73	1.16	[0.08-7.09]	-0.27	0.79
L	-	-	-	-	-	-	-	-	-	-	-
O	3	2	1	0.48	0.46	0.51	1.10	1.23	[0.10-12.23]	0.08	0.94
P	-	-	-	-	-	-	-	-	-	-	-
R	-	-	-	-	-	-	-	-	-	-	-
T	3	2	1	0.48	0.46	0.51	1.10	1.23	[0.10-12.23]	0.08	0.94
V	-	-	-	-	-	-	-	-	-	-	-
AR_1	-	-	-	-	-	-	-	-	-	-	-
AR_2	2	2	-	0.32	0.46	-	-	-	-	-	-
AR_3	1	1	-	0.16	0.23	-	-	-	-	-	-
AR_4	1	-	1	0.16	-	0.51	-	-	-	-	-
Total	628	432	196								

Table 5: PRNP haplotype frequencies and odds ratio for six age classes of white-tailed deer collected in Newton County from 2016-2019. Relative frequencies and odds ratio are shown for (A) **haplotype C** (associated with reduced CWD susceptibility) and (B) **haplotype B** (associated with increased CWD susceptibility. Relative frequency of CWD-negative [f(-)] and CWD-positive [f(+)] samples were calculated by dividing numbers CWD-negatives w/C or B, respectively, divided by negatives w/ other haplotypes.

(A) Haplotype C

Age	N	N(-)	N(+)	f(-)	f(+)	OR
FAWN	9	8	1	0.13	0.04	0.34
Y1	5	5	0	0.08	0.00	0.40
Y2	22	18	4	0.15	0.08	0.53
Y3	16	13	3	0.21	0.09	0.40
Y4	4	3	1	0.07	0.08	1.05
Y5	8	6	2	0.19	0.17	0.89
Total	64	53	11			

(B) Haplotype B

Age	N	N(-)	N(+)	f(-)	f(+)	OR
FAWN	21	14	7	0.25	0.41	1.65
Y1	26	20	6	0.45	0.75	1.65
Y2	73	52	21	0.58	0.60	1.04
Y3	28	15	13	0.25	0.52	2.05
Y4	23	17	6	0.63	0.75	1.19
Y5	11	6	5	0.19	0.56	2.96
Total:	182	124	58			

Table 6: Descriptions of **35 candidate environmental and climatic predictor variables** used in the spatial analysis.

Variable	Description	Source
1. ROAD_DIST	Distance to nearest interstate highway	Arkansas Highway and Transportation Department Road Inventory
2. RIVER_DIST	Distance to nearest stream > stream order 5	Arkansas Department of Environmental Quality
3. DEM	Elevation	Arkansas Digital Orthophotography Program 5m Resolution Digital Elevation Model
4. DENSITY	Sampling density	Point densities calculated in ArcMap
5. HAB	Proportion of area classified as habitable	USGS Gap Analysis Project habitat suitability prediction model for whitetailed deer
6. SLOPE_GRD	Slope gradient	USDA Gridded Soil Survey Geographic database
7. WATER_25CM	Water storage top 25cm soil depth	USDA Gridded Soil Survey Geographic database
8. BIO1_TEMP	Mean annual temperature	WorldClim BioClim database
9. BIO2_DIRAN	Mean diurnal range (mean monthly max-min)	WorldClim BioClim database
10. BIO3_ISOTH	Isothermality (diurnal range/ annual range)	WorldClim BioClim database
11. BIO4_SEASO	Temperature seasonality (std. dev. * 100)	WorldClim BioClim database
12. BIO5_MAXTE	Max temperature of warmest month	WorldClim BioClim database
13. BIO6_MINTE	Min temperature of coldest month	WorldClim BioClim database
14. BIO7_ANRAN	Temperature annual range	WorldClim BioClim database
15. BIO8_WETTE	Mean temp. during wettest quarter	WorldClim BioClim database
16. BIO9_DRYTE	Mean temperature during driest quarter	WorldClim BioClim database
17. BIO10_WQTE	Mean temperature warmest quarter	WorldClim BioClim database
18. BIO11_CQTE	Mean temperature coldest quarter	WorldClim BioClim database
19. BIO12_PREC	Annual precipitation	WorldClim BioClim database
20. BIO13_WMPR	Precipitation of wettest month	WorldClim BioClim database
21. BIO14_DMPR	Precipitation of driest month	WorldClim BioClim database
22. BIO15_PRES	Precipitation seasonality (coef. of variation)	WorldClim BioClim database
23. BIO16_WQPR	Precipitation of wettest quarter	WorldClim BioClim database
24. BIO17_DQPR	Precipitation of driest quarter	WorldClim BioClim database
25. BIO18_WAQP	Precipitation of warmest quarter	WorldClim BioClim database
26. BIO19_COQP	Precipitation of coldest quarter	WorldClim BioClim database
27. NVC_CLASS	NVC Class	U.S. National Vegetation Classification
28. NVC_SUBCL	NVC Subclass	U.S. National Vegetation Classification
29. NVC_FORM	NVC Form	U.S. National Vegetation Classification
30. NVC_DIV	NVC Division	U.S. National Vegetation Classification
31. NVC_GROUP	NVC Group	U.S. National Vegetation Classification
32. ECOLYS_LU	NVC Alliance	U.S. National Vegetation Classification
33. DIVISION	Ecoregion – Division level	Bailey's Ecoregion Classification
34. PROVINCE	Ecoregion – Province level	Bailey's Ecoregion Classification
35. SECTON	Ecoregion – Section level	Bailey's Ecoregion Classification

Table 7. The 17 extrinsic variables that passed through Variation Inflation Factor (VIF) analysis to remove multiple-collinearity, and data reduction procedure. Only those variables with a significant relationship with migration rate (logM) were retained for further analyses. There are two types of variables presented below: continuous and categorical. For continuous variables, linear regression (LR) against migration rate (logM) was performed and the standard results are provided. For categorical variables student's t-test was performed to test for difference in mean migration rate (DMR) between the presence (1) and absence (0) of the given variable.

Variable	Test	Relation w/ logM	R^2	DMR	Statistic	P-value
ROAD_DIST	LR	+	0.02	NA	F = 44.32	< 0.00001
RIVER_DIST	LR	+	0.003	NA	F = 6.73	0.009
HAB	LR	+	0.004	NA	F = 10.62	0.001
BIO8_WETTE	LR	+	0.02	NA	F = 50.59	< 0.00001
BIO9_DRYTE	LR	+	0.004	NA	F = 11.46	0.0007
BIO16_WQPR	LR	+	0.003	NA	F = 8.27	0.004
BIO18_WAQP	LR	+	0.04	NA	F = 109.3	< 0.00001
ECOLYS_LU_Short Leaf Pine/Bluestem Woodland	t-test	Presence is lower	NA	0.15	t = 3.53	0.001
ECOLYS_LU_Gulf Coast Mesic Hardwood	t-test	Presence is higher	NA	0.24	t = -4.06	0.0001
ECOLYS_LU_Managed Tree Plantation	t-test	Presence is higher	NA	0.12	t = -3.56	0.001
ECOLYS_LU_Crowley's Ridge/Sand Forest	t-test	Presence is higher	NA	0.13	t = -12.99	< 0.00001
ECOLYS_LU_Open Water	t-test	Presence is lower	NA	0.15	t = 2.85	0.006
ECOLYS_LU_Large River Floodplain Forest	t-test	Presence is higher	NA	0.28	t = -9.85	< 0.00001
SECTION Boston Mountains	t-test	Presence is lower	NA	0.06	t = 3.90	0.0001
SECTION Mississippi Alluvial Basin	t-test	Presence is higher	NA	0.1	t = -4.24	0.00004
SECTION Arkansas River Valley	t-test	Presence is lower	NA	0.42	t = 26.71	< 0.00001
SECTION Ouachita Mountains	t-test	Presence is higher	NA	0.38	t = -4.14	0.006

IX. Figures

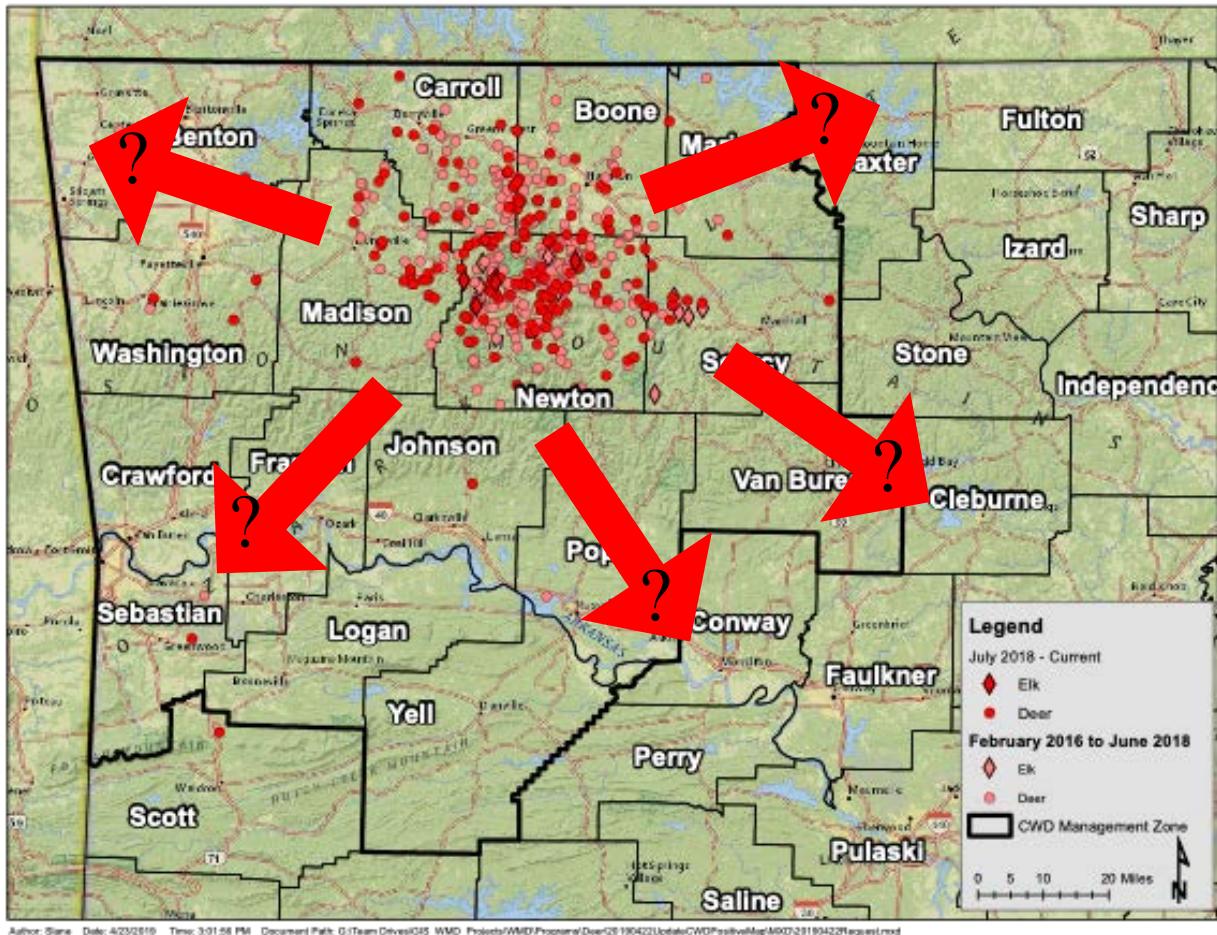


Figure 1. Recorded cases of 598 white-tailed deer (circles) and 19 elk (diamonds) that tested positive for Chronic Wasting Disease (CWD+) in Arkansas as of 24-April-2019. The area enclosed in dark green represents the 16 counties included the 2018 CWD Management Zone. Based on new CWD+ cases in Searcy and Scott counties during the 2018/2019 hunting season, the MZ was expanded to include Scott, Baxter and Stone counties. (source: <https://www.AGFC.com>)

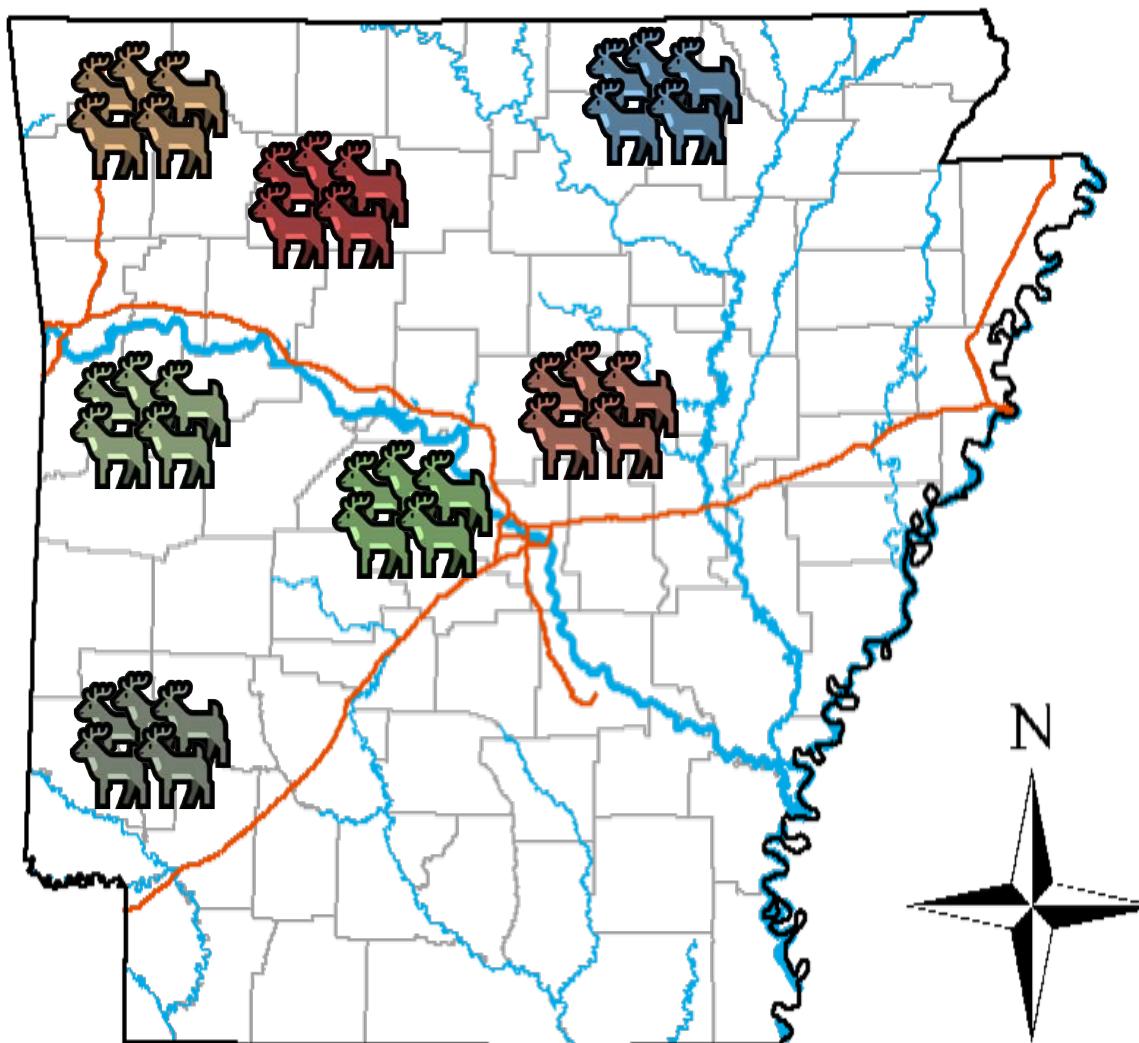


Figure 2. Genetic population structure conceptual graph - colors indicate genetic diversity, with similar colors reflecting genetic similarity. A deer herd comprises of closely related individuals that are genetically similar. This is in part due to female fawns remaining with the mother's herd. Over time, a pattern of genetic similarity and differences across the landscape will emerge that is referred to as genetic population structure. Geographically distant herds will be genetically more distinct (grey *versus* blue deer) than herds in geographic proximity (red and brown deer).

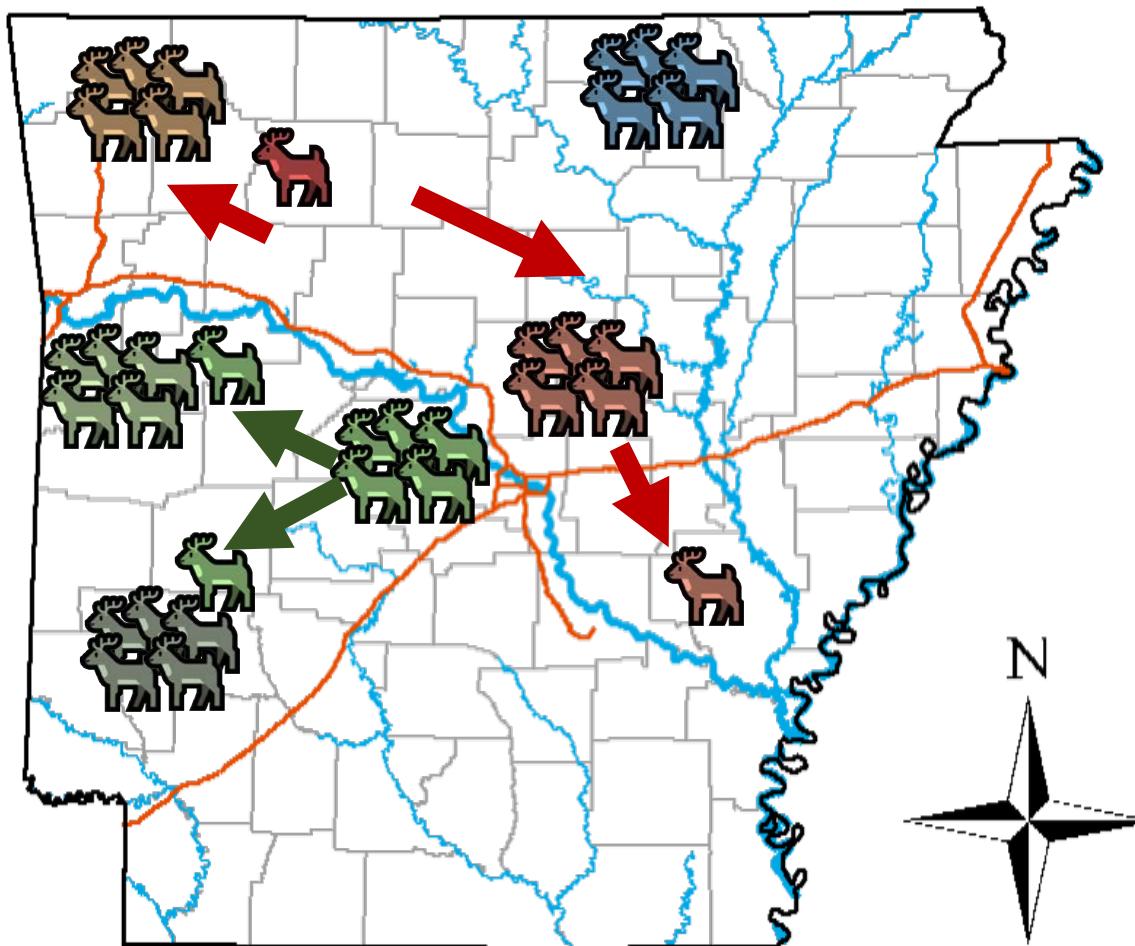


Figure 3. Genetic connectivity conceptual graph – colors indicate genetic diversity, with different colors reflecting genetic differences; arrows indicate dispersal of a deer from one herd to another. In contrast to female fawns, male fawns disperse from the mother's herd and eventually join other herds that are genetically distinct. Such dispersed individuals will show slight genetic differences from local animals. By assessing genetic diversity within and among herds, the rate at which such dispersal occurs can be estimated. This is referred to as population connectivity. Dispersal of a deer is influenced by landscape features, such as rivers and roads being potential barriers; dispersal is more likely to occur over areas that consist of habitat suitable for deer.

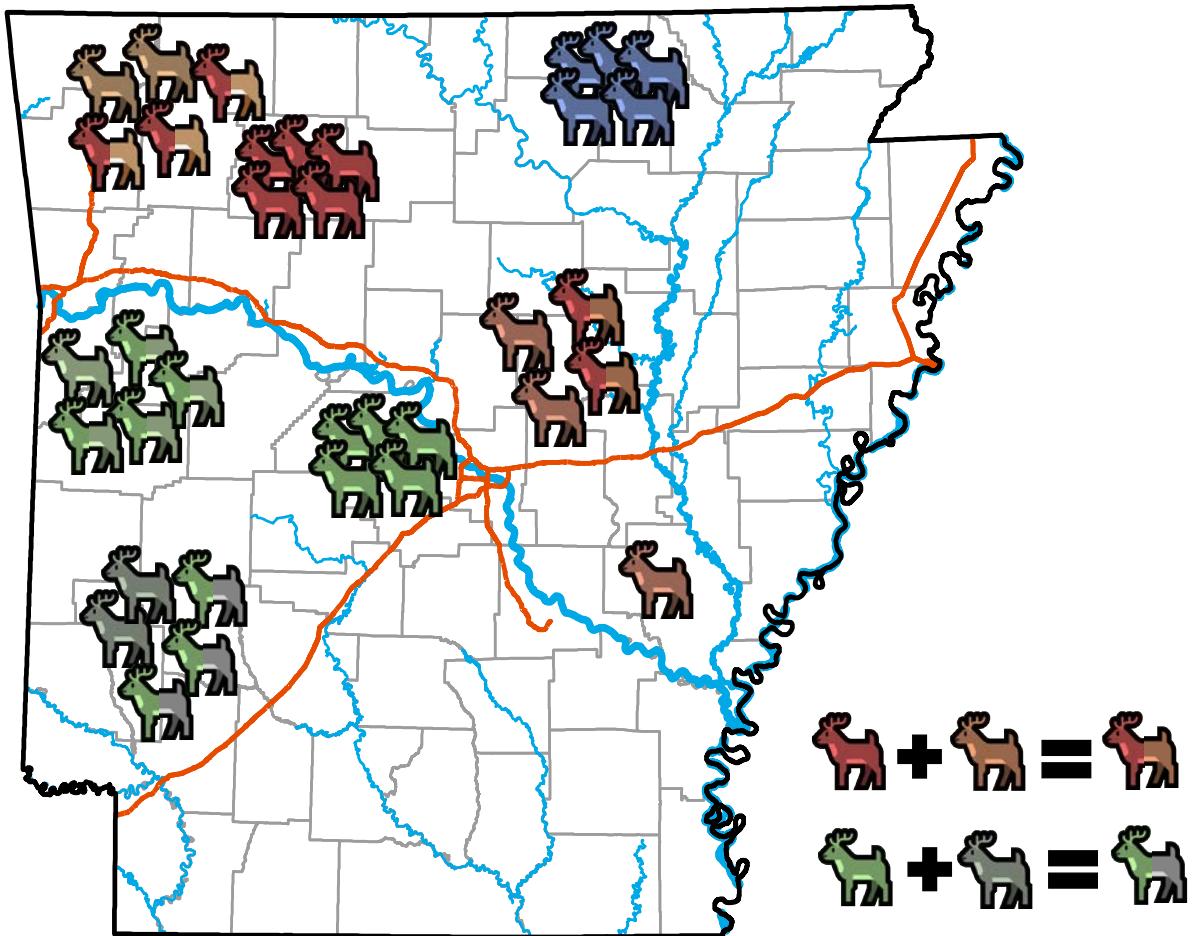


Figure 4. Genetic admixture conceptual graph – colors indicate genetic diversity, with homogenous colors reflecting ancestry in a single genetic group (i.e., gene pool), and bi-colored deer reflecting admixed ancestry. If dispersed and local animals produce offspring, the progeny will show genetic signals (ancestry) of both parental gene pools (i.e., admixed ancestry). By estimating the extent of admixture, population connectivity and migration rates can be inferred.

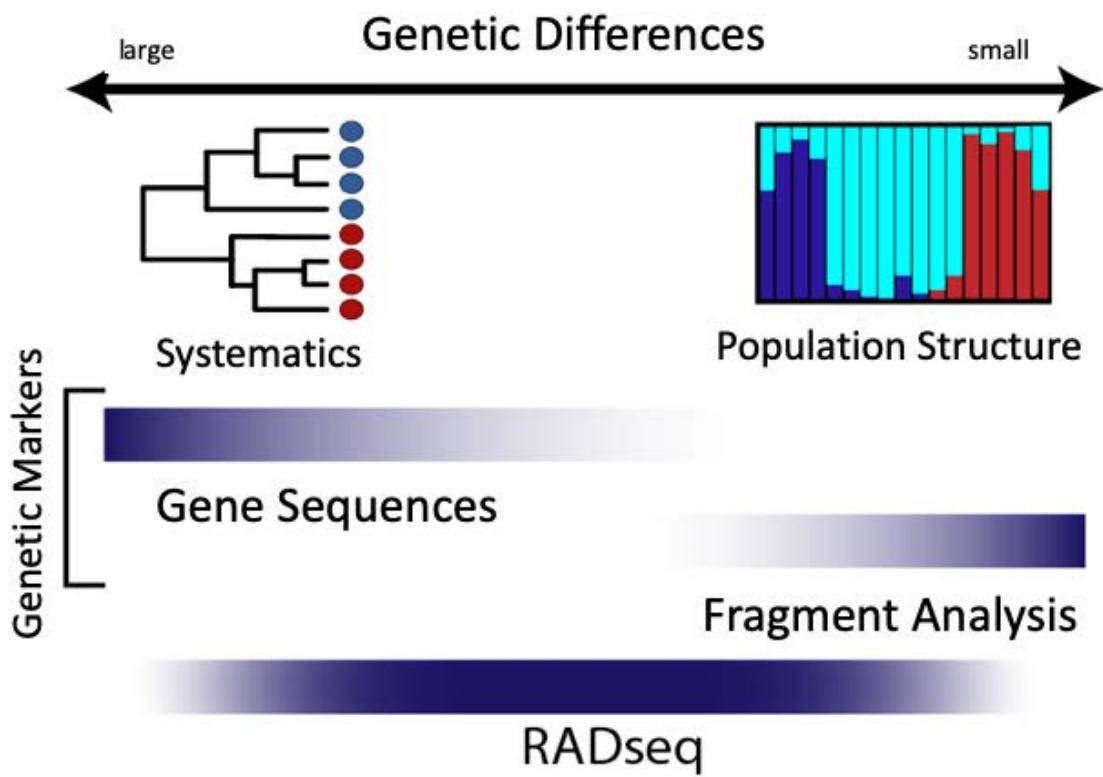


Figure 5. Genomic approach to study genetic structure in white-tailed deer - applicability of RADseq (Restriction-site Associated DNA sequencing). Genetic differences accumulate over hundreds or thousands of generations; large differences reflect evolutionary processes that occurred over long temporal and broad spatial scales (e.g., speciation), whereas small differences reflect more recent, geographically localized processes (e.g., population structure). Genetic markers vary in their capacity to resolve these patterns, with gene sequences generally informative about systematic relationships (Systematics) and fragment analysis (i.e., microsatellite loci) used to infer population structure. RADseq data encapsulate genetic variation at across broad spatial and temporal scales (large and small genetic differences) and thus are suitable to address a variety of research questions, including resolution of taxonomic relationships (Systematics/Phylogeny), geographic patterns of evolutionary lineages (phylogeography), and detailed genetic population structure.

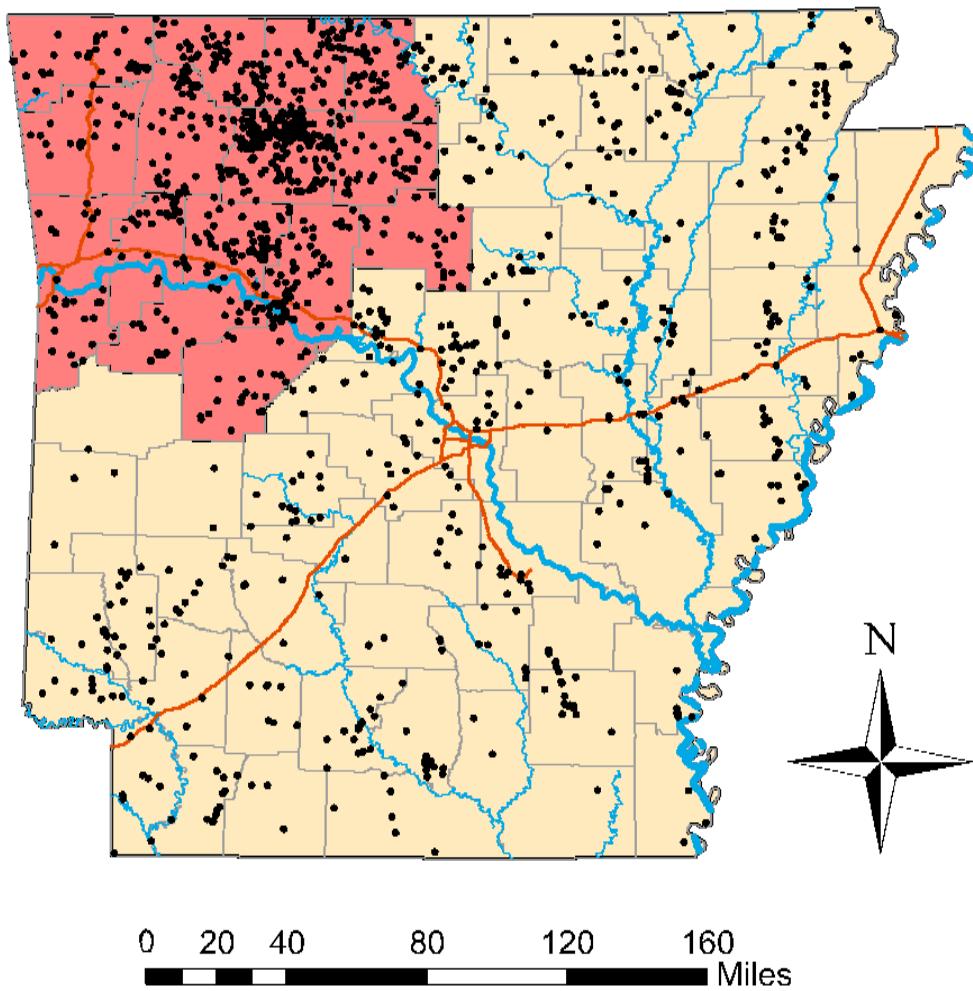


Figure 6: Sampling locations for 1,659 white-tailed deer across Arkansas used in this study. The red shaded area indicates the 16 counties included in the 2018 Chronic Wasting Disease (CWD) Management Zone (MZ), and the points represent collection localities for the individual samples. For details on sample size per county see Table 1. Detailed collection information for each sample provided in Supplements – Table S1.

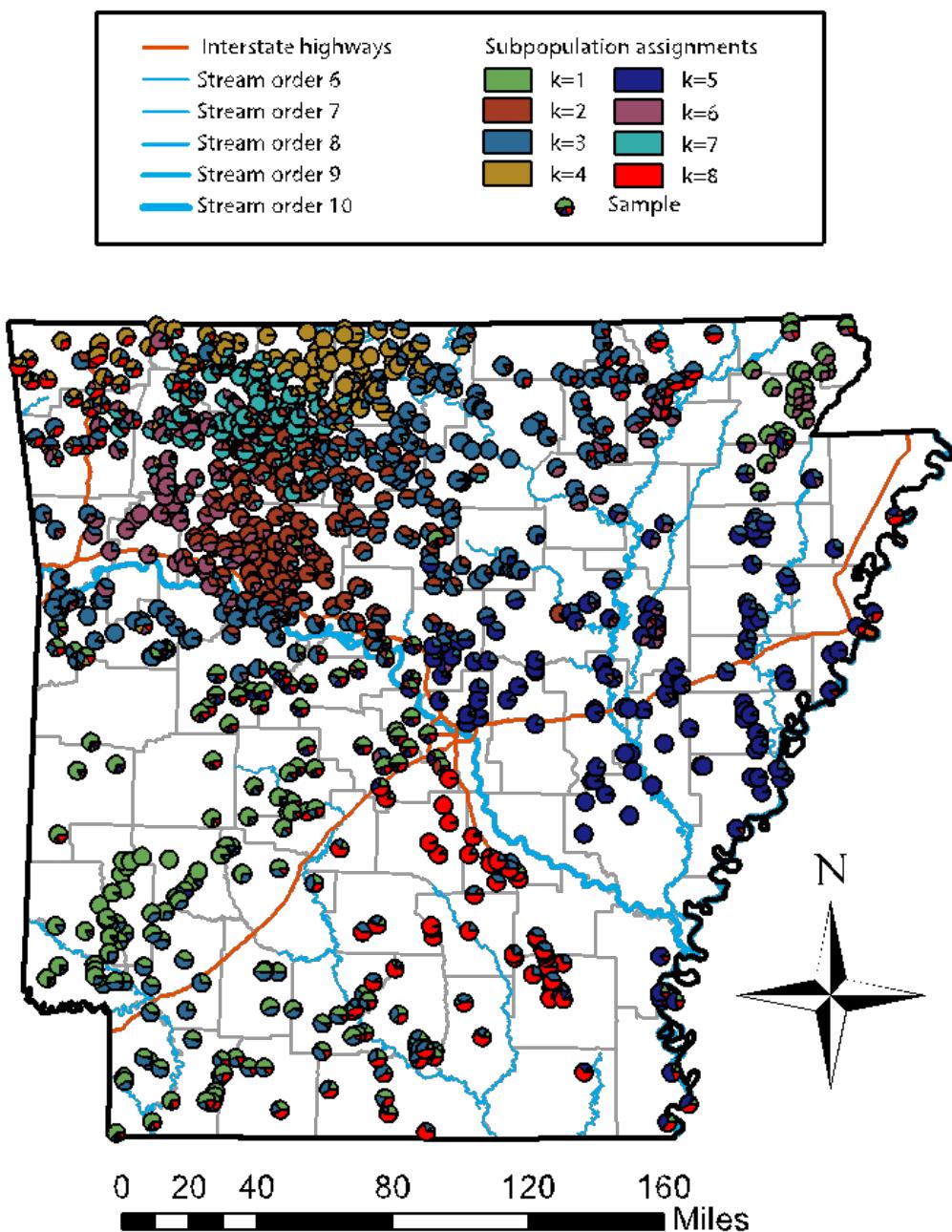


Figure 7: Distribution of eight genetic subpopulations detected across 1,143 white-tailed deer collected in Arkansas from 2016-2019. Subpopulation assignments were inferred using the program ADMIXTURE and are based on 34,214 loci, with one variable site (SNP= Single Nucleotide Polymorphism) retained per locus. Colors represent eight genetic subpopulations ($k=1$ through $k=8$) as identified in the analysis. Each individual sample is represented as a pie chart, with colors proportional to the probability of ancestry assigned to a particular subpopulation.

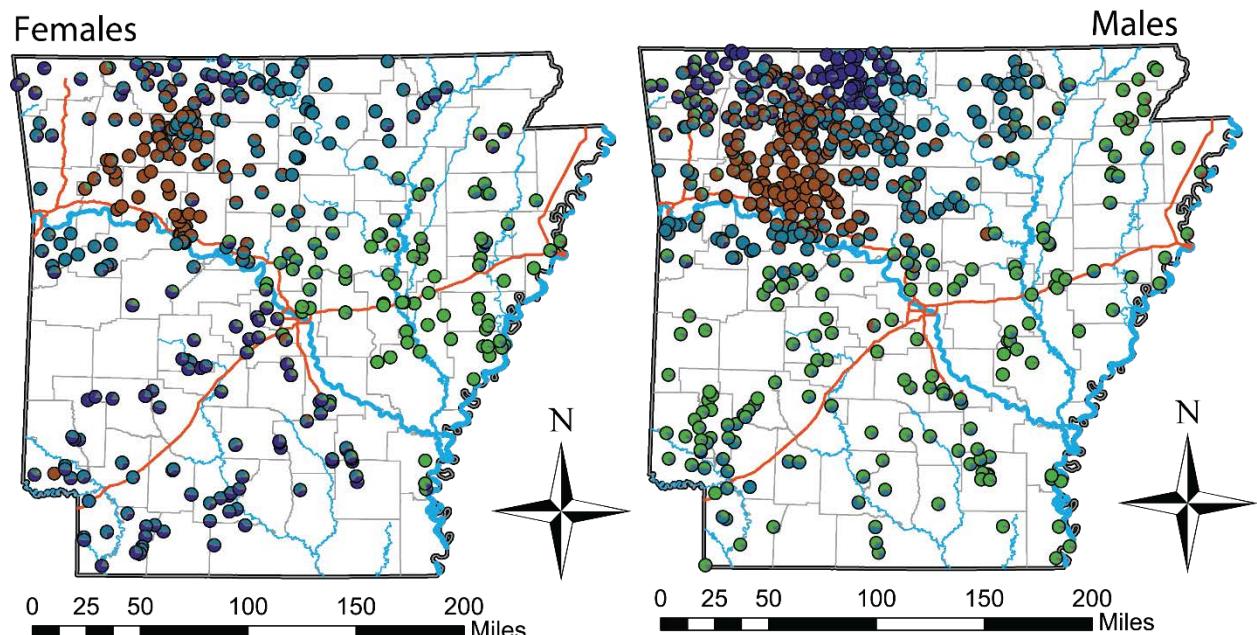
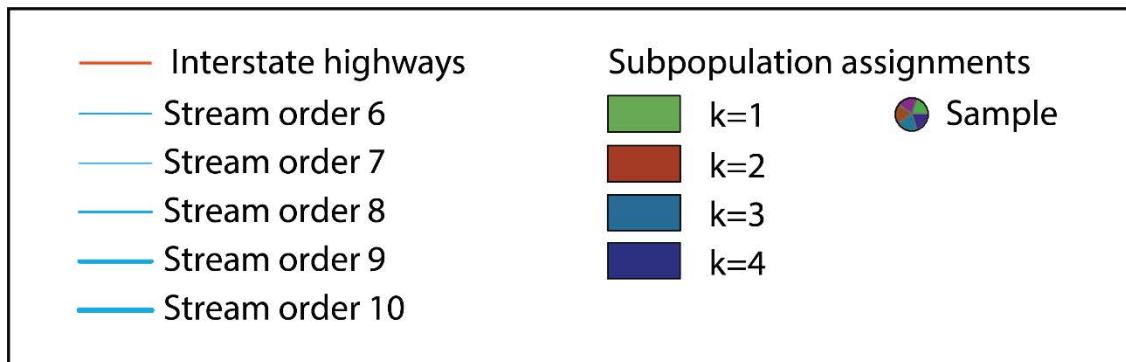


Figure 8: Population ancestry assignments by sex for female (N=414) and male (N=604) white-tailed deer collected in Arkansas from 2016-2019. Assignment was inferred using the program ADMIXTURE and is based on 33,225 loci (females) and 33,886 loci (males), respectively (Note: number of loci are dependent on samples included in a particular analysis). One variable site (SNP= Single Nucleotide Polymorphism) was retained per locus. Colors represent four genetic subpopulations ($K=4$) as identified in this analysis. Each individual sample is represented as a pie chart, with colors proportional to the probability of ancestry assigned to one of the four subpopulations (k_1 through k_4).

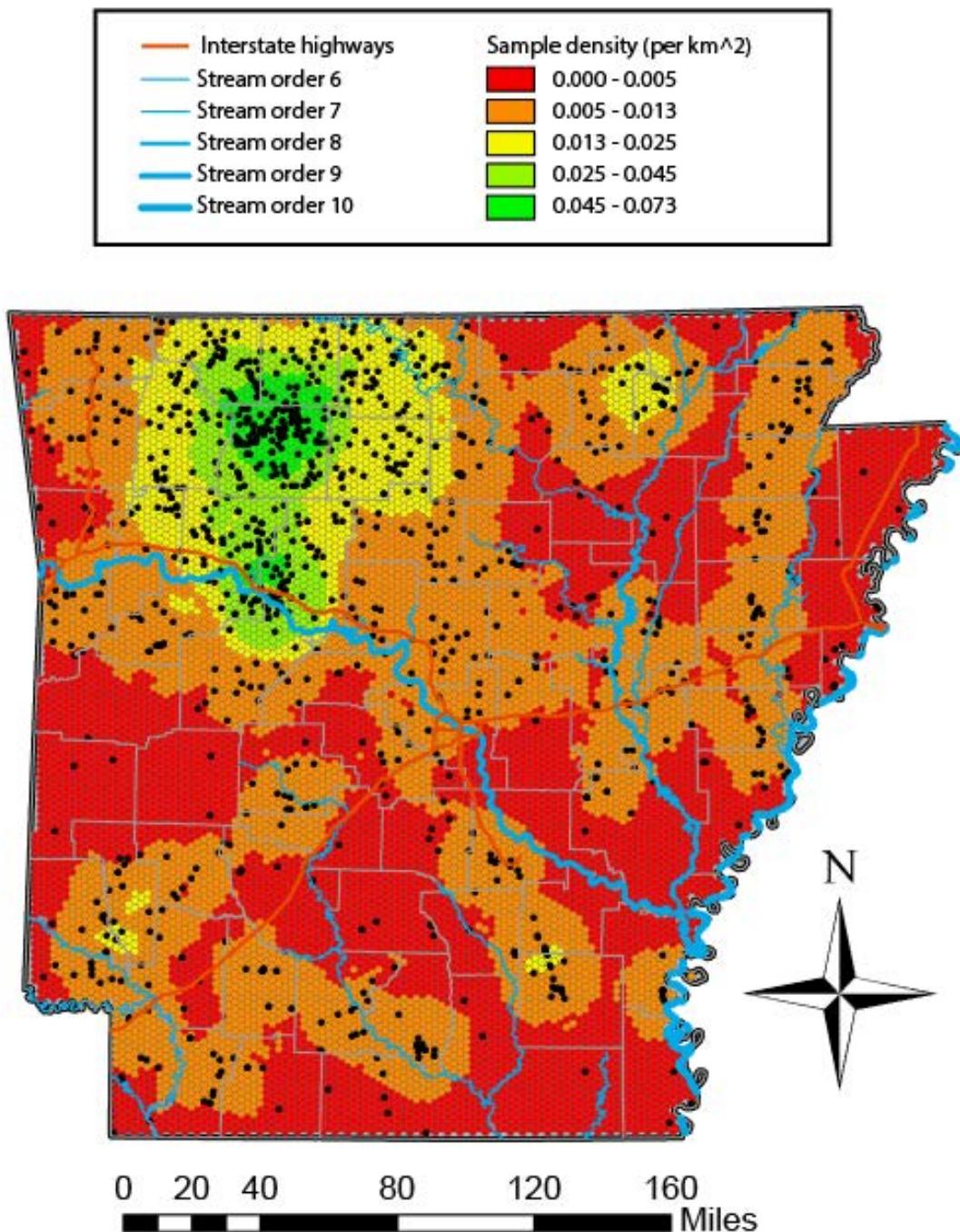


Figure 9: Sample density (=individuals per unit area) for 1,143 white-tailed deer included in genetic population structure analyses. Deer were collected by AGFC in Arkansas in 2016-2019 and individual samples are shown as black dots. Densities are reported as averaged values within a tessellated grid of 10 km² hexagonal tiles, with red reflecting low densities, and green indicating high density.

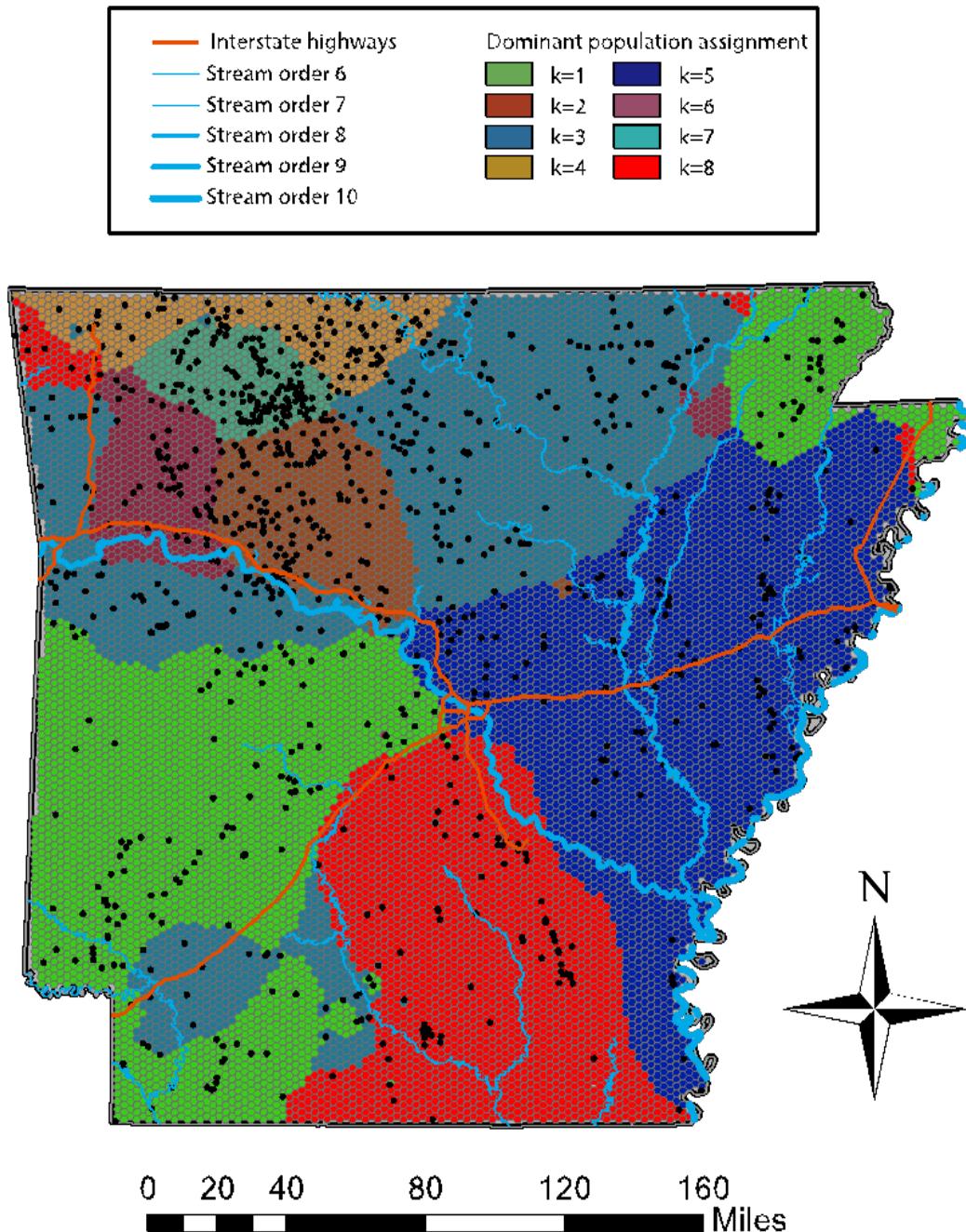


Figure 10: Oversimplified distribution of eight genetic subpopulations identified across 1,143 white-tailed deer collected in Arkansas from 2016-2019. Loci and sample sizes are identical to Figure 7, but data are presented as dominant ADMIXTURE assignment for each hexagonal tile ($N=13,378$), defined as the genetic population k with the largest mean ancestry assignment within each tile.

Assignment

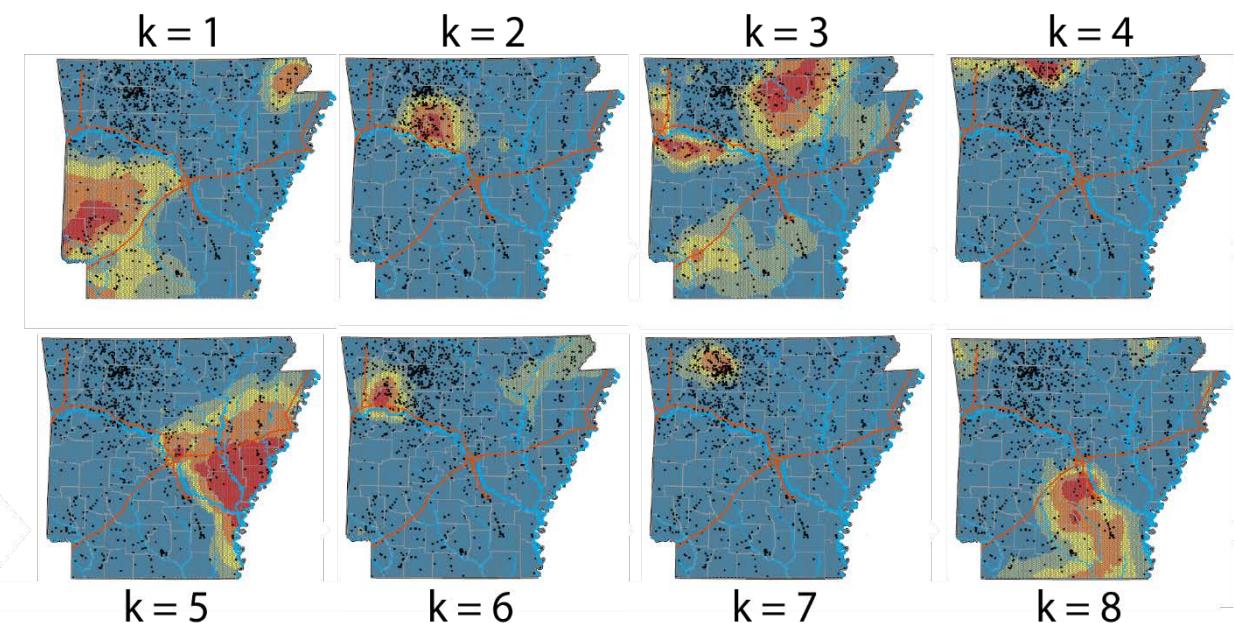
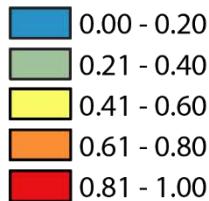


Figure 11: Probabilistic distribution of eight genetic subpopulations identified in 1,143 white-tailed deer collected in Arkansas from 2016-2019. For each subpopulation ($k=1$ through $k=8$) ADMIXTURE assignment probability was interpolated across the landscape (partitioned into 13,378 hexagonal tiles), where $P(k)=1$ corresponds to a 100% probability of a tile having ancestry of subpopulation k , and $P(k)=0$ corresponds to a 0% probability of subpopulation k ancestry. Loci and sample sizes are identical to Figure 7, but ancestry probabilities were interpolated from point data using Empirical Bayesian Kriging.

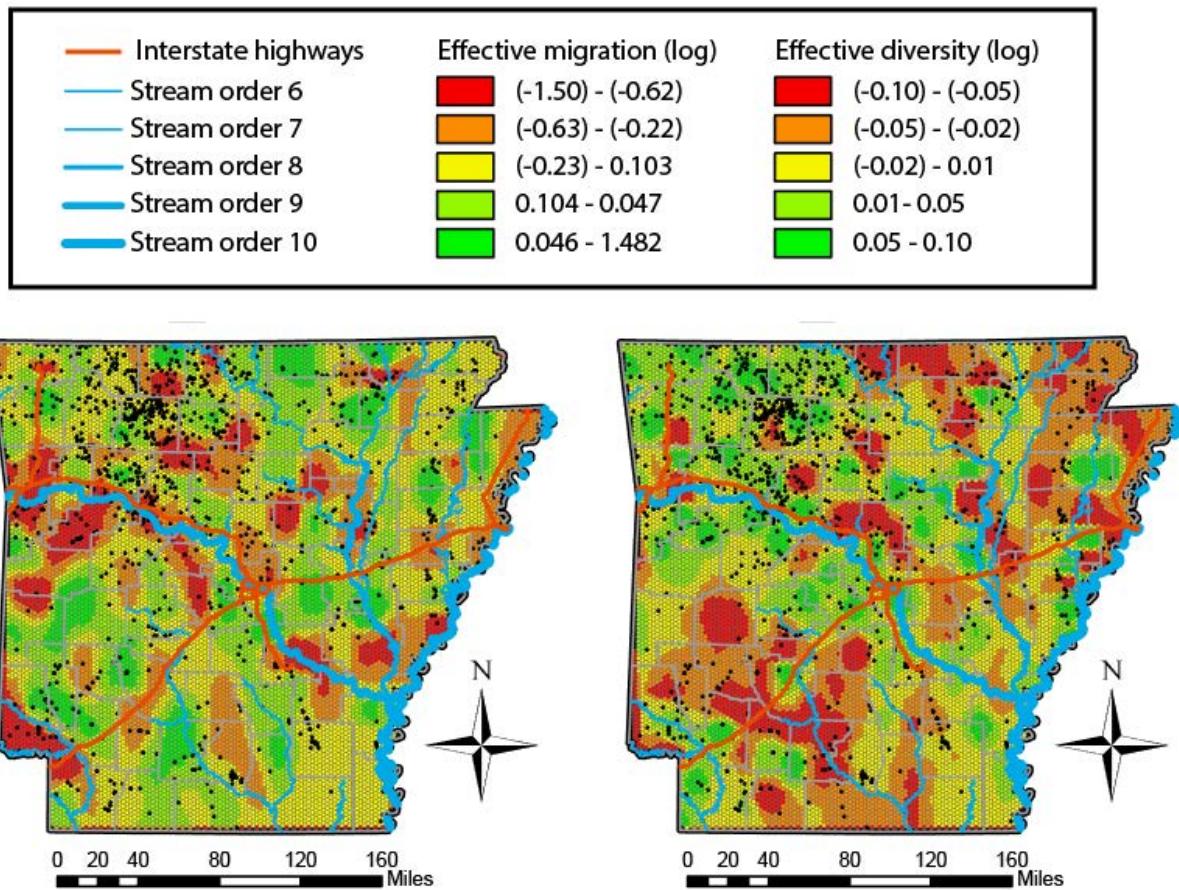


Figure 12: Visualization of population connectivity among white-tailed deer collected in Arkansas from 2016-2019. Population connectivity was estimated as effective migration rates (left) and intra-population diversity (\log_{10} scale; right), calculated using the program EEMS. Analysis was based on 1,143 samples (black dots) evaluated for genetic diversity across 34,214 loci, with one variable site (SNP= Single Nucleotide Polymorphism) retained per locus. Rates were estimated across 13,378 hexagonal tiles and are plotted by colored bin, with bin divisions calculated as natural breaks using the Jenks algorithm in ARCMAP.

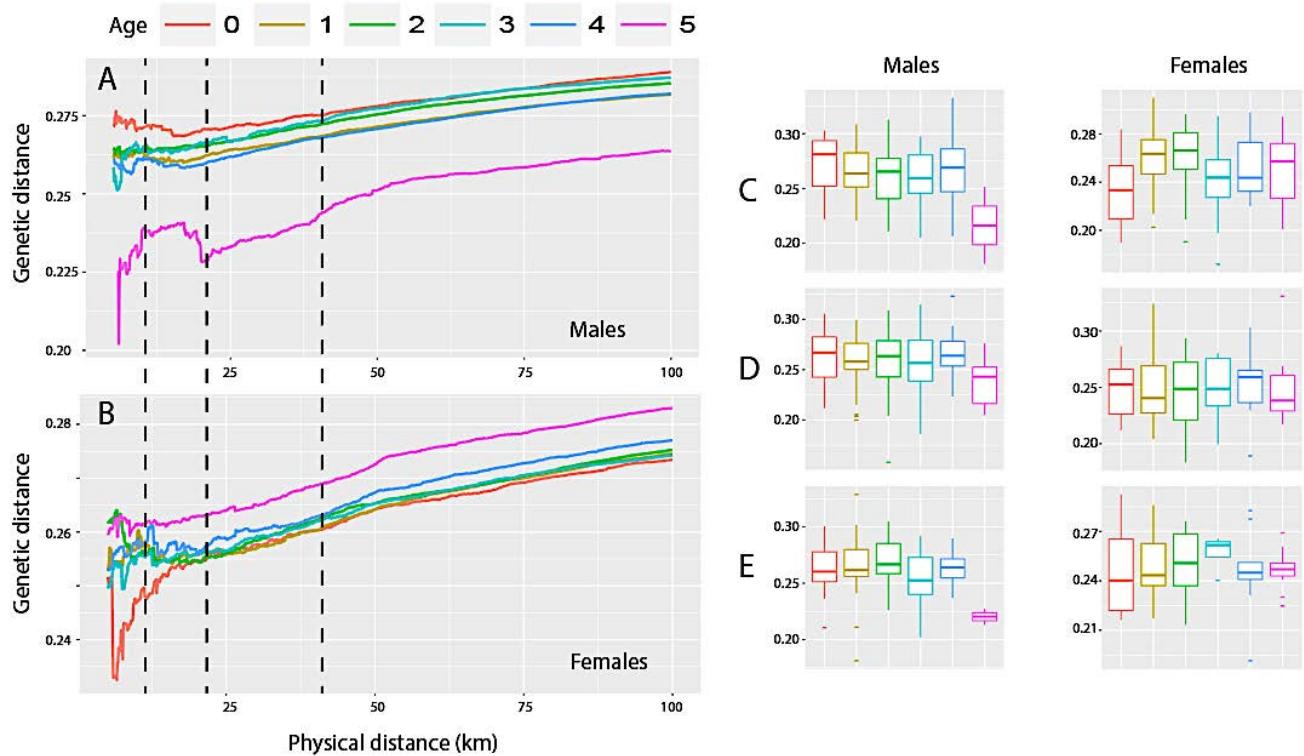


Figure 13: Spatial patterns of genetic dissimilarity among deer partitioned by age and sex. Genetic distances between individuals and their neighbors was calculated from 5,000 randomly sampled variable sites (SNP= Single Nucleotide Polymorphism), using different physical distances (x-axis). Results are shown for age classes of males (A) and females (B), with histograms shown for distance slices at 10km (C), 20km (D), and 40km (E).

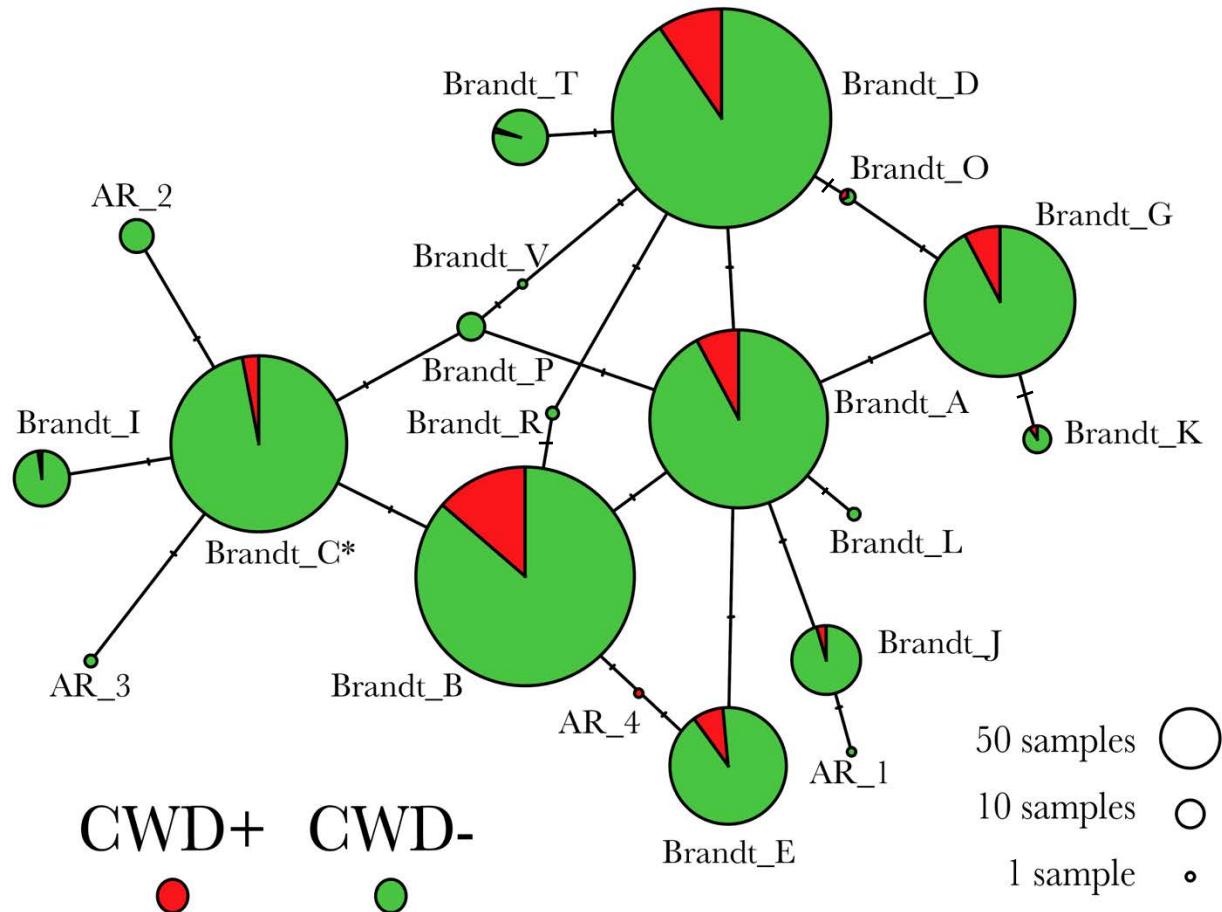


Figure 14: Haplotype network showing relationship of *PRNP* gene variants detected across 1,433 white-tailed deer collected from 75 counties in Arkansas (2016-2019). Data are based on sequence analysis of 720 nucleotides. Circles represent 20 haplotypes with size reflecting frequency of occurrence in entire data set (Table 3) and tick marks number of mutations (nucleotide substitutions) distinguishing one from another (Table 2). Color codes reflect relative frequency among CWD-positive (red) and CWD-negative (green) animals. Letters correspond to haplotype names in Brandt et al. (2015), with haplotypes unique to Arkansas indicated with numbers (AR_#).

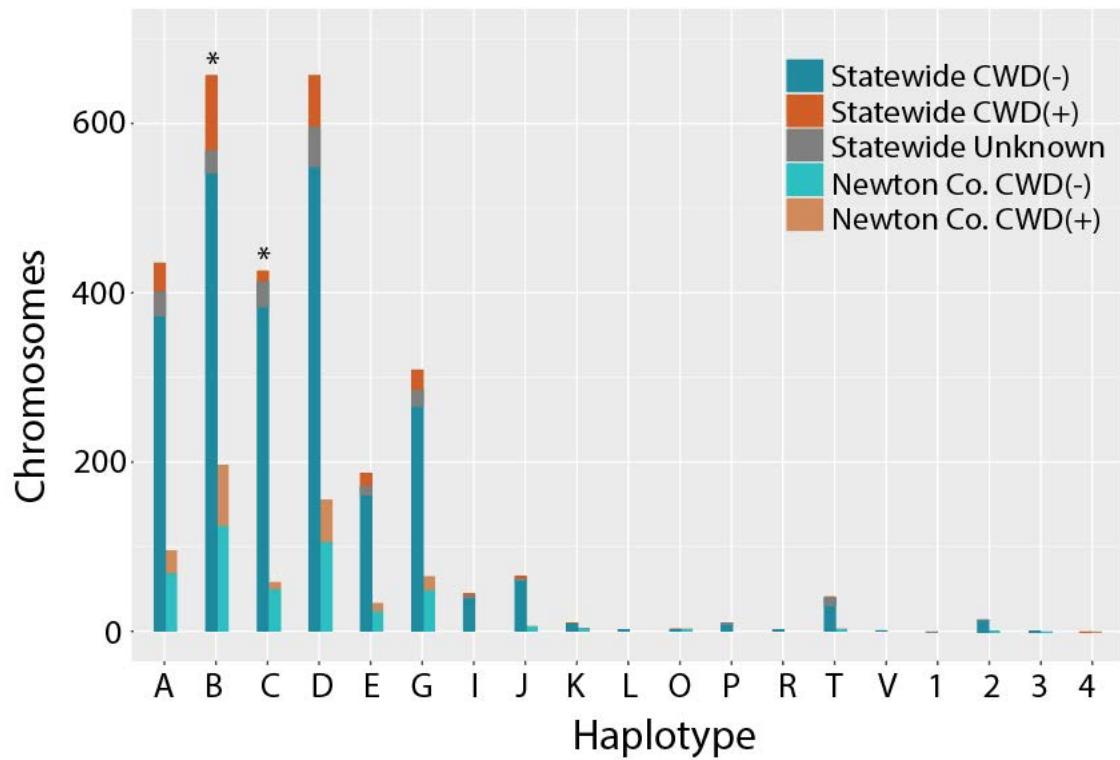


Figure 15: Frequency distribution of 2,866 *PRNP* haplotypes detected in white-tailed deer collected in Arkansas 2016-2019. Haplotypes were determined by phasing individual genotypes derived from sequencing 1,433 deer across 720 bp of the *PRNP* gene. Letters (A through V) refer to haplotypes identified by Brandt et al. (2015), whereas numbers (1-4) are haplotypes unique to Arkansas, not previously detected in other states. Frequencies are plotted for all 1,433 samples (=statewide) and a subset of 314 samples from Newton County (N=628 chromosomes). Color codes reflect frequency among CWD-positive (CWD+) and CWD-negative (CWD-) samples; unknown indicates sample was not tested for CWD.

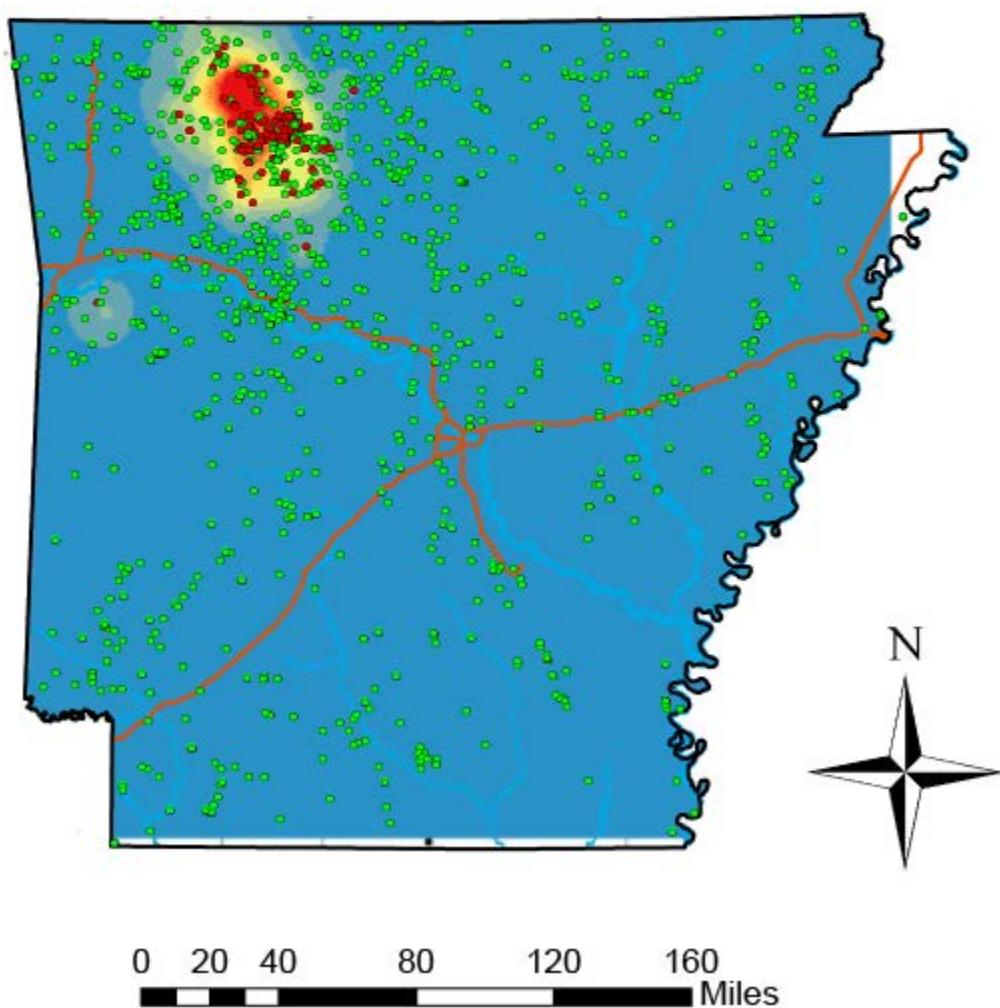
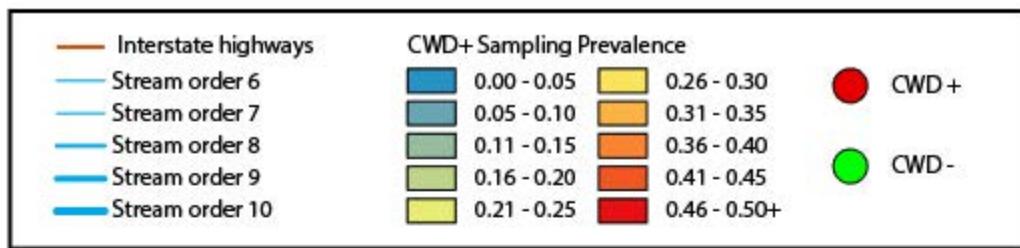


Figure 16: Spatial distribution of 1,433 white-tailed deer samples included in the *PRNP* gene polymorphism analyses. Green dots represent samples that tested negative for CWD (CWD-), whereas red dots represent CWD-positive (CWD+) samples collected in Arkansas 2016-2019. NOTE: Proportion of CWD- vs CWD+ do not necessarily reflect absolute CWD prevalence.

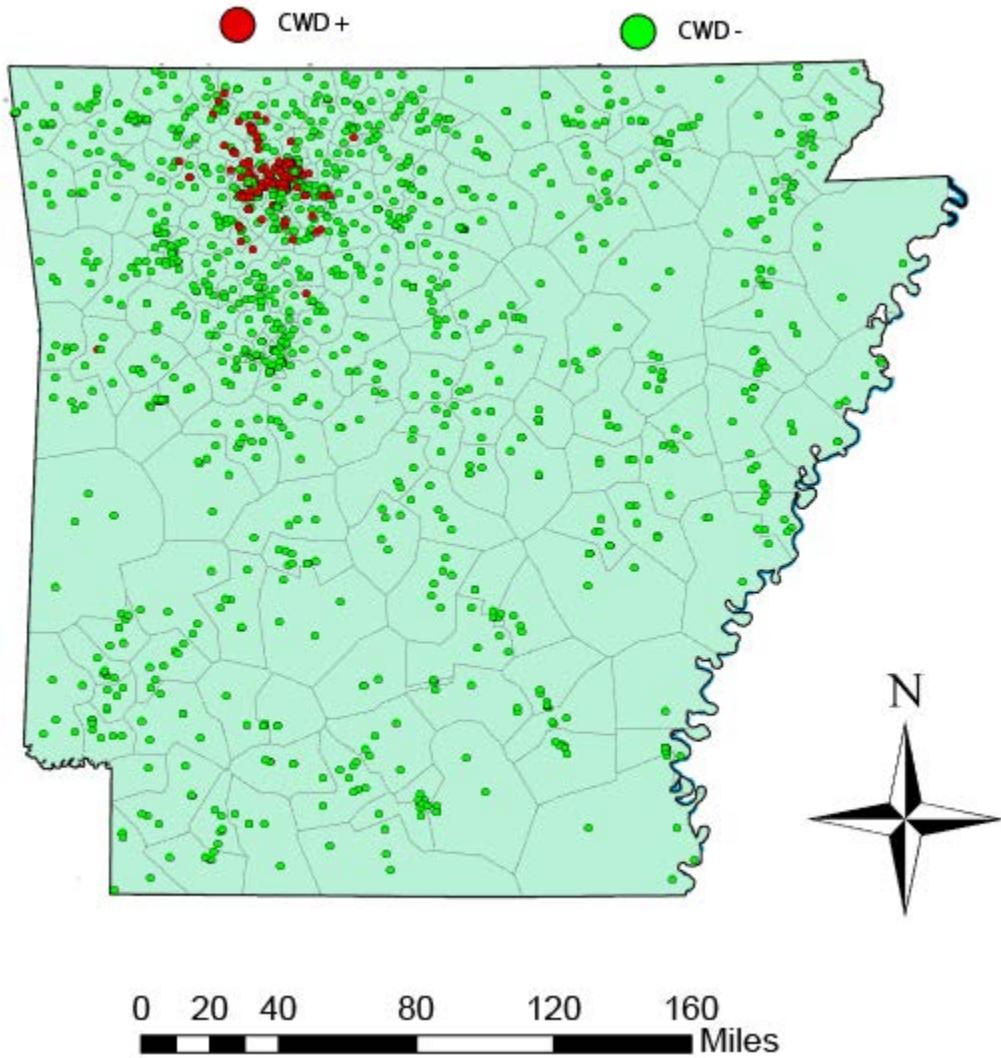


Figure 17: Spatial distribution of 211 non-overlapping polygons, each encapsulating 5-10 sampling locations, derived from 1,433 white-tailed deer samples (shown as green that were used to compute *PRNP* haplotype frequencies for interpolation.

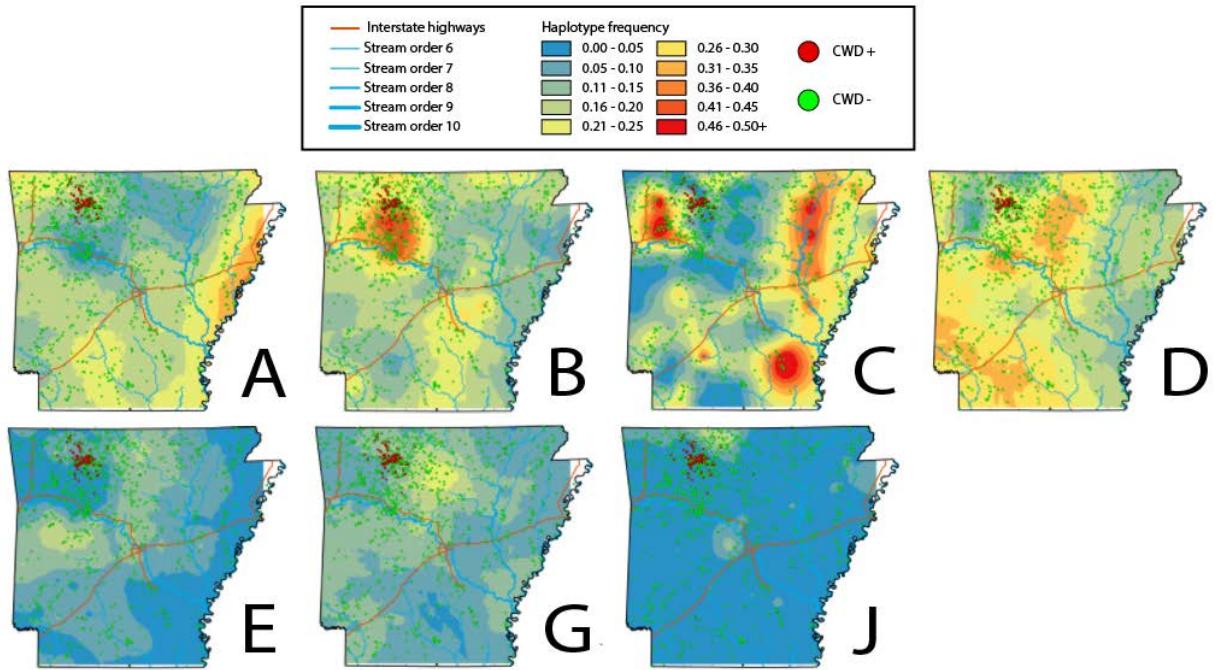


Figure 18: Spatial distribution of relative frequency of seven common *PRNP* gene haplotypes. Data are based on 720 nucleotides sequenced across 1,433 white-tailed deer collected in Arkansas from 2016-2019. Frequencies were first calculated within arbitrarily defined non-overlapping groupings of 5-10 samples (Figure 17), then interpolated using empirical Bayesian kriging. Frequency is depicted by color, with blue reflecting low occurrence (0-5%) whereas red indicating 46-50% of haplotypes were of this type.

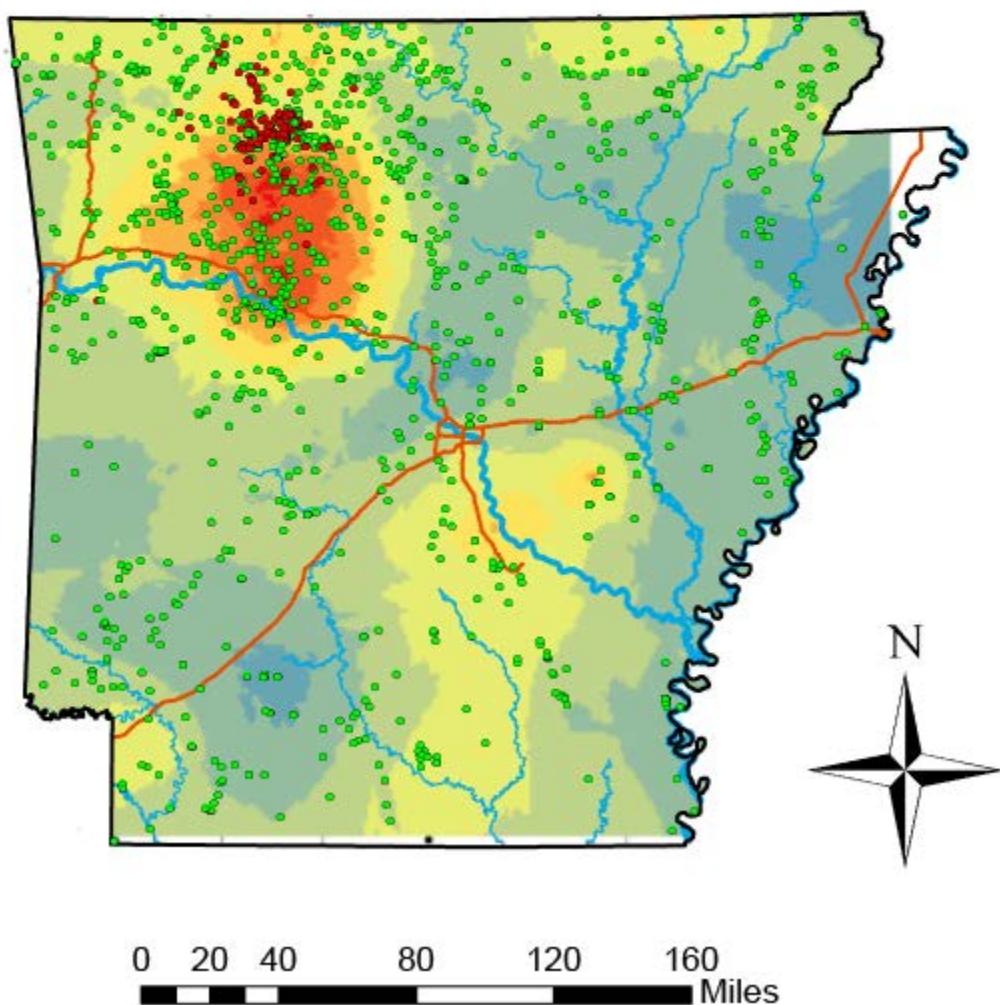
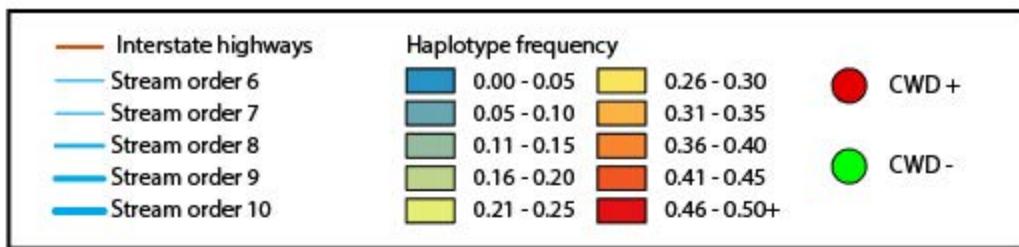


Figure 19: Spatial distribution of *PRNP* haplotype B, presented as relative frequency. Data are based on 720 nucleotides sequenced across 1,433 white-tailed deer collected in Arkansas from 2016-2019. Frequencies were first calculated within arbitrarily defined non-overlapping groupings of 5-10 samples (Figure 17), then interpolated using empirical Bayesian kriging. Frequency is depicted by color, with blue reflecting low occurrence (0-5%) whereas red indicating 46-50% of haplotypes were of this type.

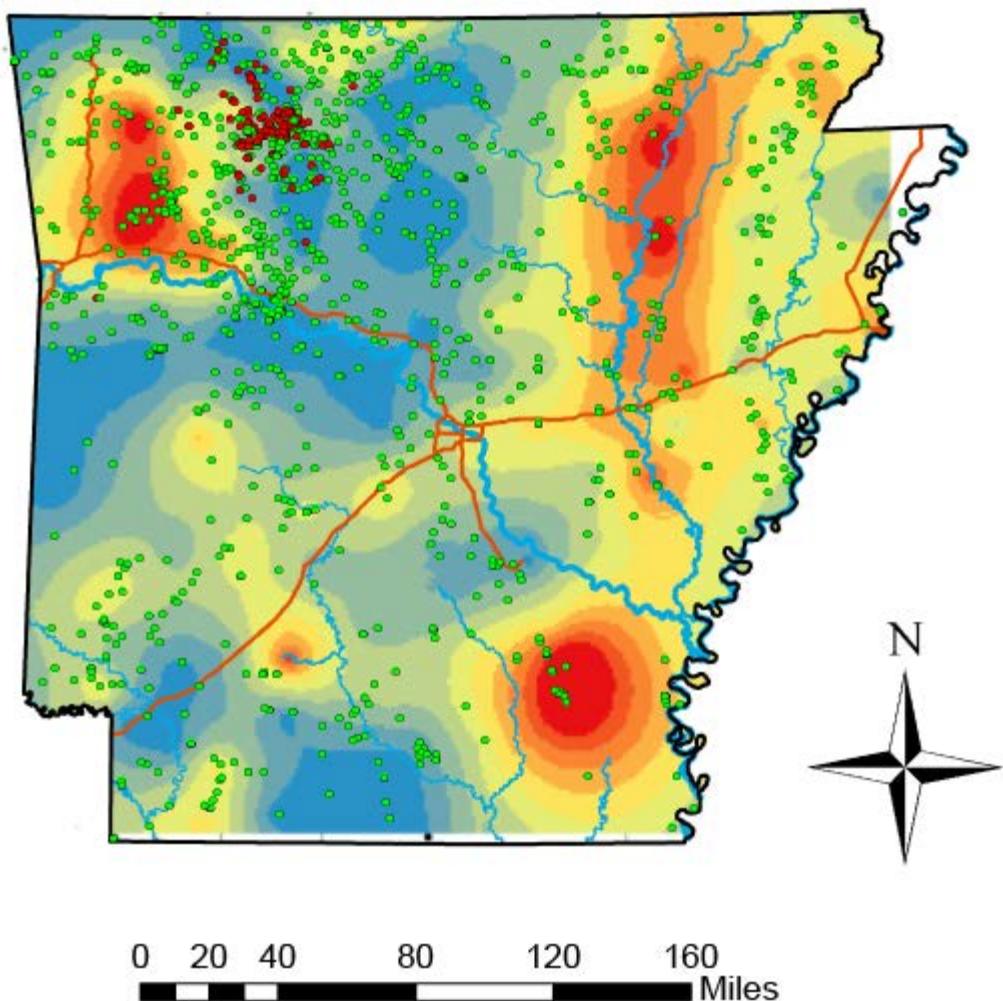
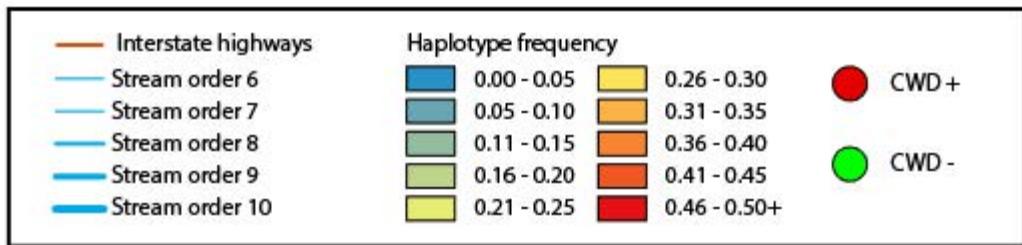


Figure 20: Spatial distribution of *PRNP* haplotype C, presented as relative frequency. Data are based on 720 nucleotides sequenced across 1,433 white-tailed deer collected in Arkansas from 2016-2019. Frequencies were first calculated within arbitrarily defined non-overlapping groupings of 5-10 samples (Figure 17), then interpolated using empirical Bayesian kriging. Frequency is depicted by color, with blue reflecting low occurrence (0-5%) whereas red indicating 46-50% of haplotypes were of this type.

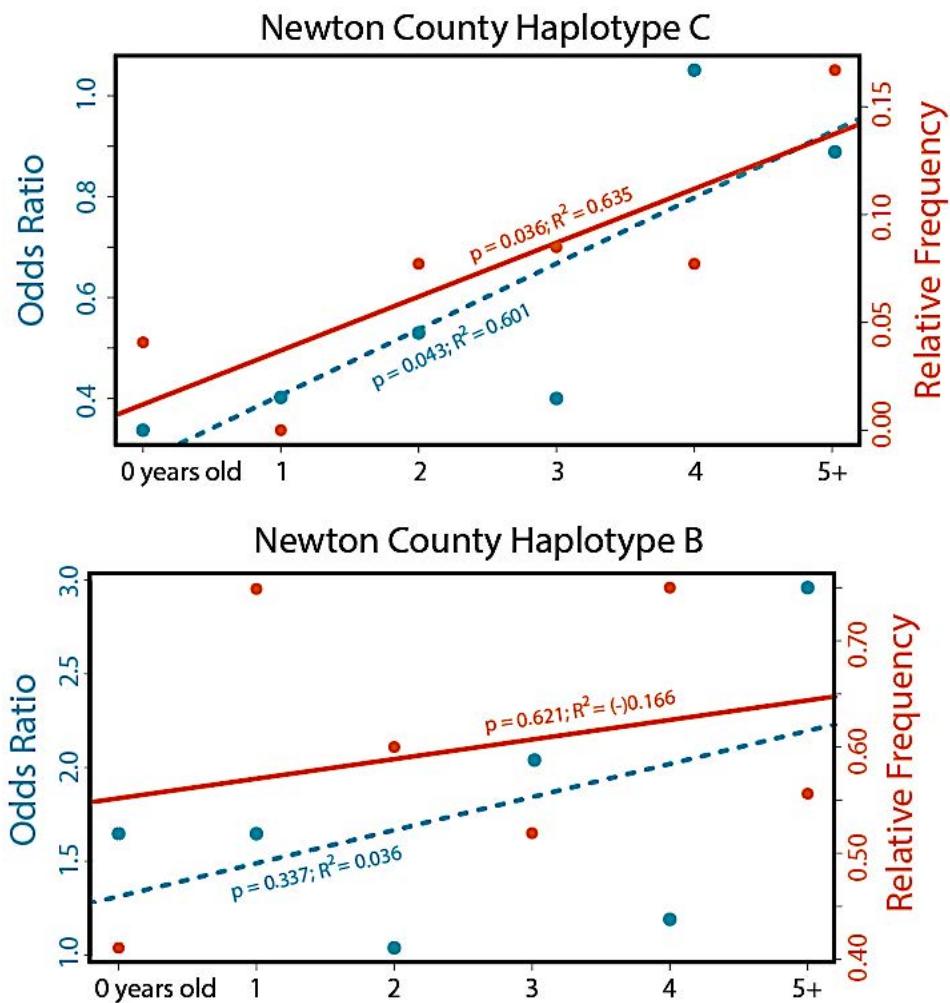


Figure 21: Relative frequency and odds ratio for two candidate susceptibility variants (CSV) of *PRNP* gene haplotypes detected in white-tailed deer age cohorts (<1 year to 5+ years) sampled in Arkansas from 2016-2019. Haplotype_C (top panel) has been associated with reduced susceptibility to CWD, whereas Haplotype_B (lower panel) has been associated with higher susceptibility (Brandt et al. 2018). Data are based on phased haplotypes derived from 720 nucleotides of the *PRNP* gene sequenced across 1,433 deer.

X. Appendices

Appendix 1: DNA Extraction

DNA Extraction and Quantification

Genomic DNA was extracted from all tissues following the QIAamp Fast DNA Tissue Kit protocol (QIAGEN[®] Corporation, Maryland, USA). To maximize DNA yield from the samples, several DNA extraction methods were tested and a modified version of the QIAamp Fast DNA Tissue Kit extraction protocol was identified as yielding the best quantity of high-quality DNA. Concentration of DNA from each sample was quantified with a Qubit 2.0 Fluorometer (Invitrogen, Inc.) following the standard manufacturer's protocol.

To ascertain the presence of high-quality genomic DNA (i.e., molecular weight >10kb), a 5 μ l aliquot of the DNA extract was separated on a 2% agarose gel and visualized using GelGreen on a blue-light transiluminator (Gel Doc[™] EZ Imager; Bio-Rad). Large DNA fragments migrate more slowly than small fragments in a gel, and high-quality DNA forms a distinct band (Fig. A1-1A), whereas degraded or fragmented DNA forms of a 'smear' of small fragments (Fig. A1-1B).

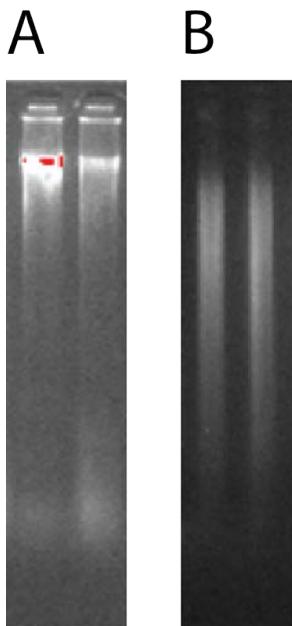
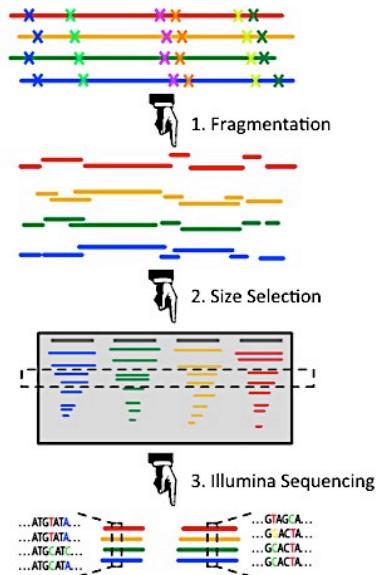


Figure A1-1: Visualization of DNA fragments (white band or smudge) on an agarose gel (dark) based on four samples (each lane represents a sample). (A) High-quality, non-fragmented genomic DNA visible as a distinct bright band in the upper section of the gel. (B) Degraded, fragmented genomic DNA visible as a smear across the gel. Genomic DNA digested with restriction enzymes for ddRAD sequencing would look similar to samples in B.

Appendix 2: SNP Methods

SNP Data Generation – ddRAD Library Preparation

To assay SNP variation across thousands of loci for each white-tailed deer sample, we developed protocols for a genomic approach called double-digest restriction site associated DNA sequencing, or ddRAD (Peterson et al., 2012) using a combination of *in silico* and *in vitro* methods (Chafin et al., 2018). RADseq methods (Fig. A2-1) use restriction enzymes to perform a targeted fragmentation of DNA (i.e., cut the genome into smaller pieces), followed by a size selection to reduce the genome down to some specified number of fragments (i.e., subsample of pieces). Because the fragments selected from this process, and ultimately the fraction of the genome which will be sequenced, depends on 1) where the genome is cleaved (e.g. cut by the restriction enzymes) and 2) which fragments are chosen for sequencing (e.g. by the ‘bounds’ of the size selection), it is necessary to tailor both of these parameters to a specific target organism.



ddRADseq = Double-digest Restriction-site Associated sequencing

1. Targeted fragmentation of genome with restriction enzymes
2. Selection of specific-sized fragments from each individual
3. Next-Generation-Sequencing (Illumina) of selected fragments

Figure A2-1: Schematic of ddRADseq approach. Genomes of different individuals are represented in colors. The first step involves targeted fragmentation of genomic DNA with restriction enzymes resulting in similar fragments across individuals. The next step represents size-selection of fragments from each individual to subsample the genome in a consistent and comparable manner. Selected fragments are then barcoded for individual identification and prepared for massive-parallel Next-Generation Sequencing (Illumina Sequencing). The digital output consists of millions of short sequences (reads) that are then bioinformatically processed to identify genetically variable loci.

To select enzymes, we performed simulated digests on multiple reference genomes for cervids and bovids, using the software FRAGMATIC (Chafin et al., 2018). Simulated digests were performed for enzyme combinations *PstI/MspI*, *PstI/BsaHI*, *PstI/NarI*, *NsiI/MspI*, *SbfI/MspI*, and *NsiI/HpyCHIV*, using reference genomes for *Capreolus capreolus*, *Capra hircus*, *Bos taurus*, *Bison bison*, and *Odocoileus virginianus*.

From these results, we selected candidate enzyme pairings for *in vitro* digestion of an exploratory set of white-tailed deer samples (N=8), followed by fragment analysis on the Agilent Tapestation (Agilent, Santa Clara, CA). This allowed quantification of DNA fragments occupying ranges within the distribution of fragments resulting from the restriction digest. We averaged estimates across samples and estimated the distinct number of loci within each region using the following equation, where Γ is the expected haploid genome size, \bar{y} is the mean fragment length for the size range in question (e.g. 250-350 base pairs), \hat{c} is the proportion of DNA mass contained within the fragment length range, and \hat{p} is the expected proportion of sequence-able fragments, as estimated using the *in silico* approach described above.

$$n \text{ loci} = \frac{2\Gamma * \hat{c} * \hat{p}}{\bar{y}}$$

This was calculated for each sample for a variety of potential size selection ranges, for each candidate restriction enzyme. Enzyme pairings and size selection parameters were then selected to optimize a) sequencing coverage across individuals, b) number of individuals which could be multiplexed per lane of sequencing (e.g. cost efficiency), and c) number of sampled loci.

We then performed restriction digests using the selected enzymes (*NsiI* and *MspI*) as the first step in a modified ddRAD protocol, using 1 μ g of template DNA per sample. These digests were purified using Ampure XP magnetic bead-based separation (Beckman Coulter, Inc., France). Purified digests were then ligated with individually barcoded adaptor sequences using T4 DNA ligase (New England Biolabs, Inc.) and manufacturer-supplied buffer with a 60min incubation at 37°C, followed by heat-inactivation of enzymes at 65°C. Adapter oligonucleotide fragments were annealed prior to ligation, and diluted to create a 5-10X excess concentration relative to the template DNA.

Individual uniquely-barcoded samples were then pooled, Ampure XP purified, and size-selected using a PippinPrep for automated gel extraction (Sage Science, Inc.). This is advantageous over manual

gel-based methods in that it significantly increases replicability across libraries and diminishes ‘small fragment carryover’ (DaCosta and Sorenson, 2016).

Adaptors were then extended to include indices for a dual-indexing strategy (Peterson et al., 2012) as well as sequences for anchoring to the Illumina flowcell (Illumina, Inc.) via PCR with the following conditions: initial denaturation at 98°C; 10 cycles of 98°C for 15s, 62°C for 30s, and 72°C for 30s; followed by a terminating extension period at 72°C for 7min. Samples were then submitted for sequencing (N=96 per lane) on the Illumina HiSeq 4000 (single-end; 1x100bp) at the University of Oregon Genomics and Cell Characterization Facility (Eugene, OR).

SNP Data Generation – ddRAD Loci Assembly and Filtering

The digital output of Illumina sequencing consists of millions of short sequences (=reads) that need to be bioinformatically processed to assemble the SNP loci used for analyses. The Illumina data of the ddRAD library was processed and filtered in the assembly pipeline PYRAD (Eaton, 2014). We first demultiplexed reads into per-individual sets, allowing zero barcode mismatches, and deleting any reads with >4 bases falling below a quality threshold of 99% accuracy. Reads were then clustered within individuals to find those representing the same genomic regions (=loci) using a distance threshold of 15% via the VSEARCH algorithm (Rognes et al., 2016), allowing a maximum of 3 indels, and deleting any loci with coverage greater than $\text{max}(500, \text{mean}+2\text{sd})X$ or less than 20X. PYRAD then performs global alignment within each locus (Edgar, 2004) and distinguishes biological signal (i.e., true SNP variation) from sequencing errors using a maximum likelihood estimation of genotypes (Li et al., 2008). Finally, loci of all samples were then clustered among individuals to identify homology, with any locus present in fewer than 50% of the individuals being removed.

Appendix 3: SNP Analysis

SNP Analysis - Population Structure

Population structure was inferred from SNP data using the program ADMIXTURE (Alexander et al., 2009) with the admixturePipeline (github.com/smussmann82/admixturePipeline). In addition to the full dataset (N=1,183), we also replicated these analyses across several subsets: (i) partitioned by sex; and (ii) across ten down-sampled replicates (20% of individuals), generated using a random sample weighted inversely by spatial sampling density. The latter was performed so as to evaluate the impact of uneven sampling on our ADMIXTURE results.

Results were parsed in CLUMPAK (Kopelman et al., 2015). Model selection (for value of K , i.e., number of populations) was performed by cross-validation, and results for the best models were re-created using DISTRUCT (github.com/smussmann82/distruct-rerun) (Rosenberg, 2004). To visualize the spatial extent of inferred populations, samples were plotted as pie charts representing probability of assignment to gene pools in ARCMAP (Environmental Systems Research Institute, Inc.). Assignment probabilities were also interpolated using Empirical Bayesian Kriging (EBK) (Gribov and Krivoruchko, 2012). EBK probability surfaces were used as a first-pass qualitative evaluation of landscape features, such as rivers and roads, to inform predictor variable selection for in-depth spatial analyses (described below).

SNP Analysis – Estimating migration

Natural populations commonly exhibit a pattern of ‘isolation by distance’ in which genetic relatedness declines as a function of distance (Wright, 1943). When habitats vary (e.g. elevation gradients, vegetation type), some aspects of the landscape will invariably have an effect on the probability of individuals moving through that space – for example the presence of barriers such as rivers or roads, or variation in the suitability of habitat. As individual dispersal declines, so does gene flow. As a consequence, those landscape features effecting individual movement accumulate over time as variation in genetic differences over space. Variation in genetic connectivity (=‘gene flow’) can be

estimated by examining spatial patterns of relatedness, under the general assumption that areas in which genetic relatedness decays very quickly have little gene flow, and areas in which genetic relatedness is retained over large distances have high gene flow. We visualized this as an ‘effective migration surface’ using the program EEMS (Petkova et al., 2015), as a means to examine underlying landscape resistance.

These results are complementary to the ADMIXTURE results (above), in that they model different, but related, evolutionary processes. EEMS models migration, while ADMIXTURE models a *product* of varied migration over space, namely population structure. The primary purpose of our subsequent analyses was to understand how features of the environment interact as determinants of migration and population structure.

Appendix 4: *PRNP* Methods

PRNP/PRNP^{PSG} Amplification and Sequencing

Genomic DNA was used as template to amplify a coding section of the *PRNP* gene following a modified protocol from previous studies (Brandt et al., 2015, Johnson et al., 2003). For the functional *PRNP* gene, the forward primer (CWD-13) straddles Intron 2 and Exon 3, with the reverse primer (CWD-LA) located 850bp downstream (Johnson et al., 2003). To ascertain if the detected polymorphisms were indeed in the functional *PRNP* gene, presence of the non-coding *PRNP* pseudogene (*PRNP^{PSG}*) was evaluated by using pseudogene primers 223 and 224 from O'Rourke et al. (2004).

Amplifications for both the functional *PRNP* gene and the *PRNP^{PSG}* pseudogene were performed in 20μl reactions consisting of 10μl Qiagen HotStart Master Mix (1unit HotStartTaq DNA Polymerase, PCR Buffer with 3mM MgCl₂, and 400μM of each dNTP), 8μM each of the forward and reverse primer, 7.4μl RNase-free water, and 1μl of template DNA (~50-100ng). Thermocycling protocols consisted of an initial denaturation step of 15min at 95°C, followed by 10 cycles of 45s denaturation at 95°C, 45s annealing at 57°C, and 75s extension at 72°C, 25 cycles of 30s denaturation at 95°C, 30s annealing at 55°C and 60s extension at 72°C, completed with a final extension step of 5min at 72°C.

Samples where the *PRNP* and *PRNP^{PSG}* amplified were sequenced across both to identify the true polymorphism in the functional *PRNP* gene. Amplicons were enzymatically purified, sequenced using BigDye v. 3.1 (Applied Biosystem Inc., Forest City CA) dye-terminator chemistry and resolved on an ABI 3730XL GeneAnalyzer at the University of Illinois Keck Center for Functional and Comparative Genomics. Sequences were manually edited using SEQUENCER (v 5.4, Gene Codes, Ann Arbor MI) and aligned against a reference database of *PRNP* gene sequences obtained from the NCBI GenBank database (Accession # AF156185.1, AY360089.1, AY3600091.1).

PRNP Analysis – Haplotype Data

Following alignment, sequences were phased to haplotypes (paired nuclear alleles) using the program PHASE2 (Stephens et al., 2001), which reconstructs haplotypes using a probabilistic model of

linkage disequilibrium. Only haplotypes assigned with >90% posterior probability (N=1,433) were retained. Scripts to format inputs and parse results of haplotype phasing are available at github.com/tkchafin/fasta2phase2. Haplotypes were then categorized according to the nomenclature of Brandt et al. (2015), and haplotype frequencies were calculated globally, by-county, and by CWD status (positive *vs.* negative). To visualize similarity amongst haplotype, we constructed a haplotype network using the median-joining algorithm employed by POPART (Leigh et al., 2015); a haplotype network reflects numbers of nucleotide substitutions (point mutations) among the different *PRNP* sequences. Scripts for creating these input files can be found at github.com/tkchafin/scripts.

Appendix 5 – Spatial Analyses Methods

Spatial Analysis Parameters

All of the following analyses were computed in R version 3.6.0, and all of the code are provided as online supplementary material (<https://github.com/zdzbinden>). An outline of the spatial analyses is provided in Fig 22. The initial data for the spatial analysis was composed of 35 environmental factors (Table 6, Figs. A6-1 through A6-16) plus the variable of interest, log M (Fig. 12), which were all associated with the 13,378 hexagonal grid nodes. Exploratory analyses revealed higher variance in log M at lower genetic sampling densities, so a threshold of sampling density (>0.01) was found in order to remove heteroscedasticity in the variable. This reduced the number of spatial nodes from 13,378 to 2,665.

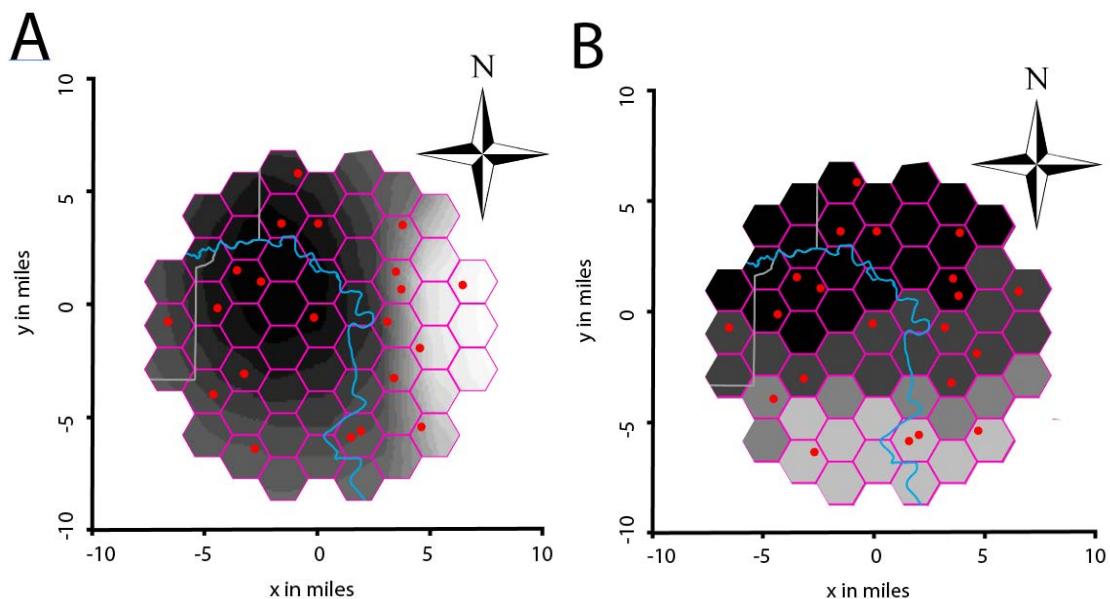


Figure A5-1: Schematic of hexagonal network with reference cells in space before (A) and after (B) grid averaging. Lines show tessellation grid and dots represent spatial distribution of genetic samples in a spatial framework.

Spatial Analysis – Analytical Steps

The analyses consisted of two parts: (1) transforming the environmental data to fit assumptions of the subsequent analyses and reducing the set of candidate environmental variables into a more meaningful and explanatory set of environmental factors, and (2) estimating spatial autocorrelation of the data.

The **data transformation and standardization** included: (a) categorical variables were transformed into ‘dummy’ binary variables, (b) all variables were checked for deviations from normality and, if non-normal, were corrected using standard transformations, and (c) data were standardized using Z-score scaling.

Reduction of the 35 environmental variables (Table 6) to an explanatory set of 17 factors (Table 7) was accomplished using a variety of methods. First, *Variation Inflation Factors* (*VIF*) were calculated for each variable as a means to determine **how correlated each variable** was with others in the set. Variables with a $VIF > 10$ were removed from the set (Dorman et al., 2012). Next, the remaining variables were each tested individually for a **relationship/effect on the variable of interest**, the migration rate (logM). Continuous variables were tested using linear regression and categorical, binary variables were tested for differences in means between the presence and absence of a factor using Student’s t-test.

The second part of the analysis involved estimating the **spatial component or autocorrelation of the data**. This was done using *distance-based Moran’s Eigenvector Mapping* (dbMEM) (Dray et al., 2006), which is also referred to as eigenvector spatial filtering (ESF) (Murakami and Griffith, 2019) and principal coordinates of neighbor matrices (PCNM) (Borcard and Legendre, 2002). Briefly, this analysis involves decomposing the spatial position of samples (i.e. coordinates) into n-1 eigenvectors by generating more and more complex eigenfunctions that explain ‘neighborhoods’ of sites based on, in this case, an exponential kernel. The set of eigenvectors is then used in a forward selection procedure to determine **which eigenvectors explain autocorrelation in the parameter of interest**, in this case the migration rate (logM). The forward selection calculates *VIF* and *Akaike Information Criterion* (*AIC*) to select the best set of eigenvectors for explaining/representing the spatial component of the data. The final spatial model lists factors by rank decrease in AIC (i.e. degree the variable made the model better) so that the top number of spatial eigenvectors equal to the number of environmental factors could be

selected. This was done so that the environmental and spatial datasets would have equal number of variables for the variation partitioning procedure.

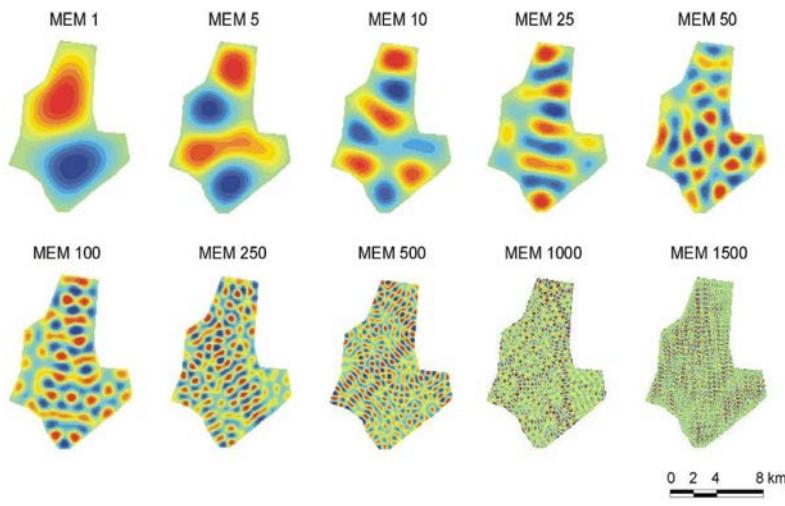


Figure A5-2: Illustration of Moran's Eigenvector Maps (MEM). Given the overall region sampled (green shape in background) the Moran's Eigenvector Maps ($n-1$) decompose the spatial structure of the data into eigenfunctions that range from relatively broad scale structure ($\text{MEM}=1$) to relatively fine scale structure ($\text{MEM}=1500$). Figure after Fig S1 in Vandam and Vanschoenwinkel (2013).

The final step of the analysis was **partitioning the variation of the migration rate ($\log M$) among the two datasets: environmental** (17 factors) and **spatial** (17 eigenvectors). This process is done using partial multiple linear regression to determine the proportion of variation of $\log M$ explained by each set separately (Legendre et al., 2005). Significance of the model and the partitions were tested via permutation procedure with 999 randomizations (Oksanen et al., 2016).

Appendix 6 – Spatial Data – Environmental Maps

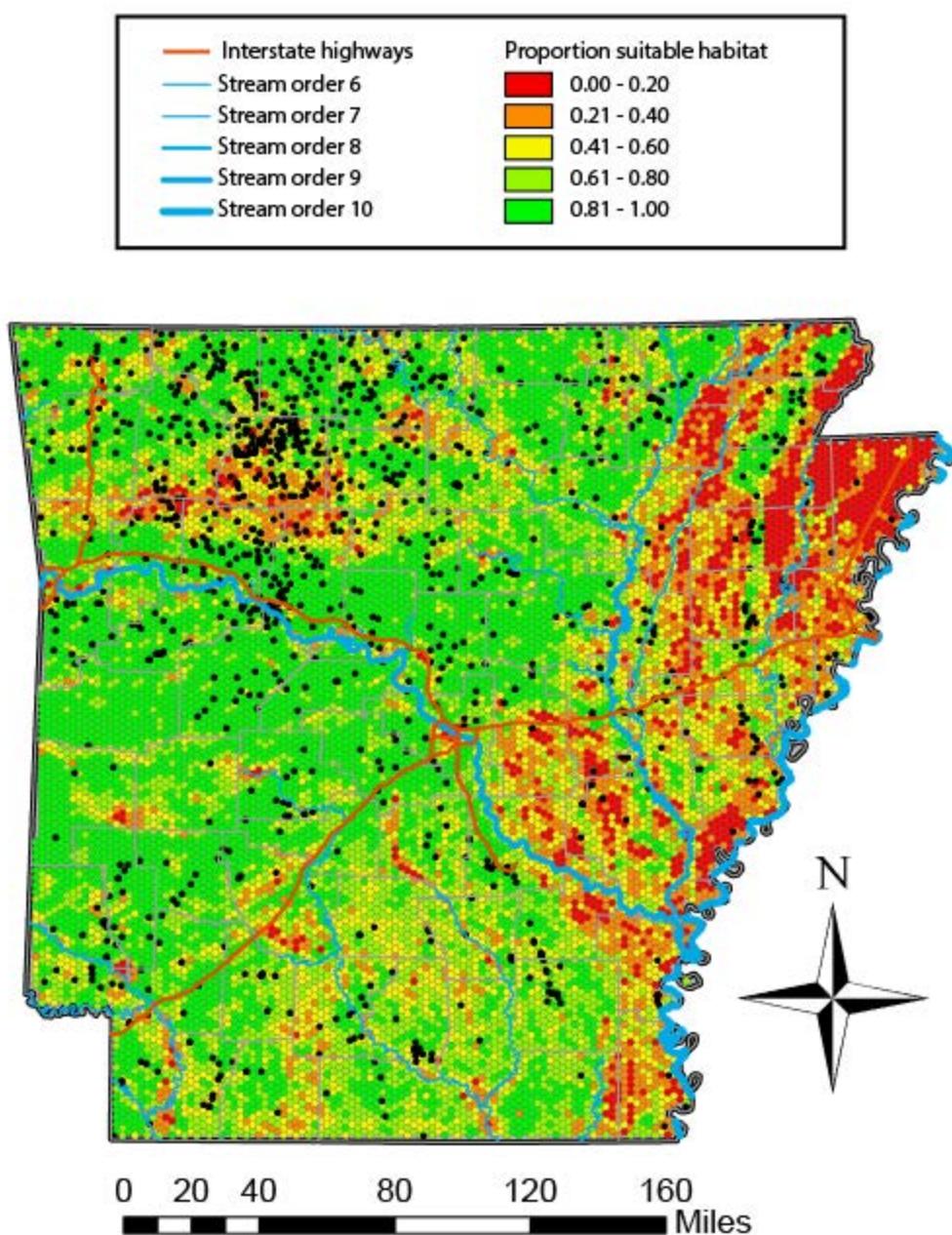


Figure A6-1: Habitat suitability, reported as the proportion of each tile classified as 'predicted habitat' by the USGS Gap Analysis projections for white-tailed deer.

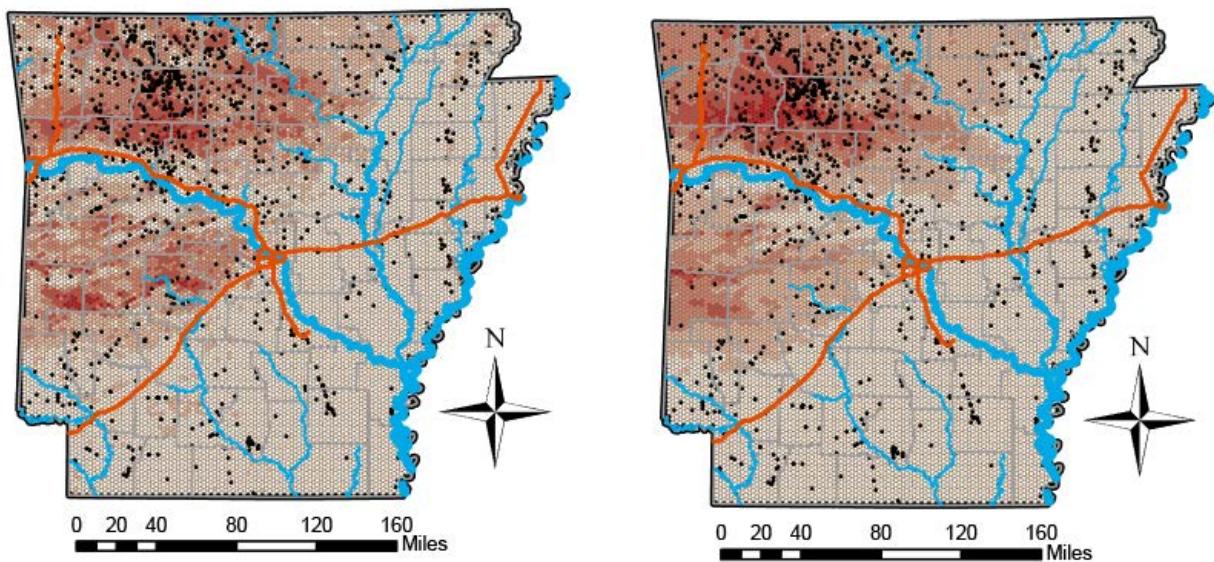
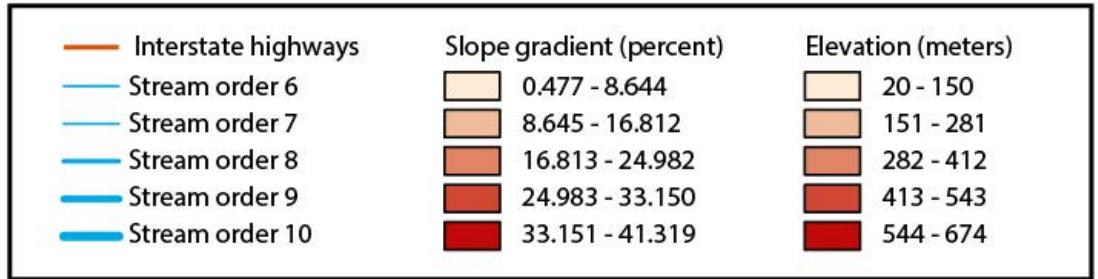


Figure A6-2: Slope gradient (rise as a percentage of run; left) and elevation (meters; right) averaged within a 10 km² hexagonal grid. Slope gradients were derived from the Gridded Soil Survey Geographic (gSSURGO) database, and elevation from a five-meter resolution digital elevation model (DEM) published by the Arkansas GIS Office.

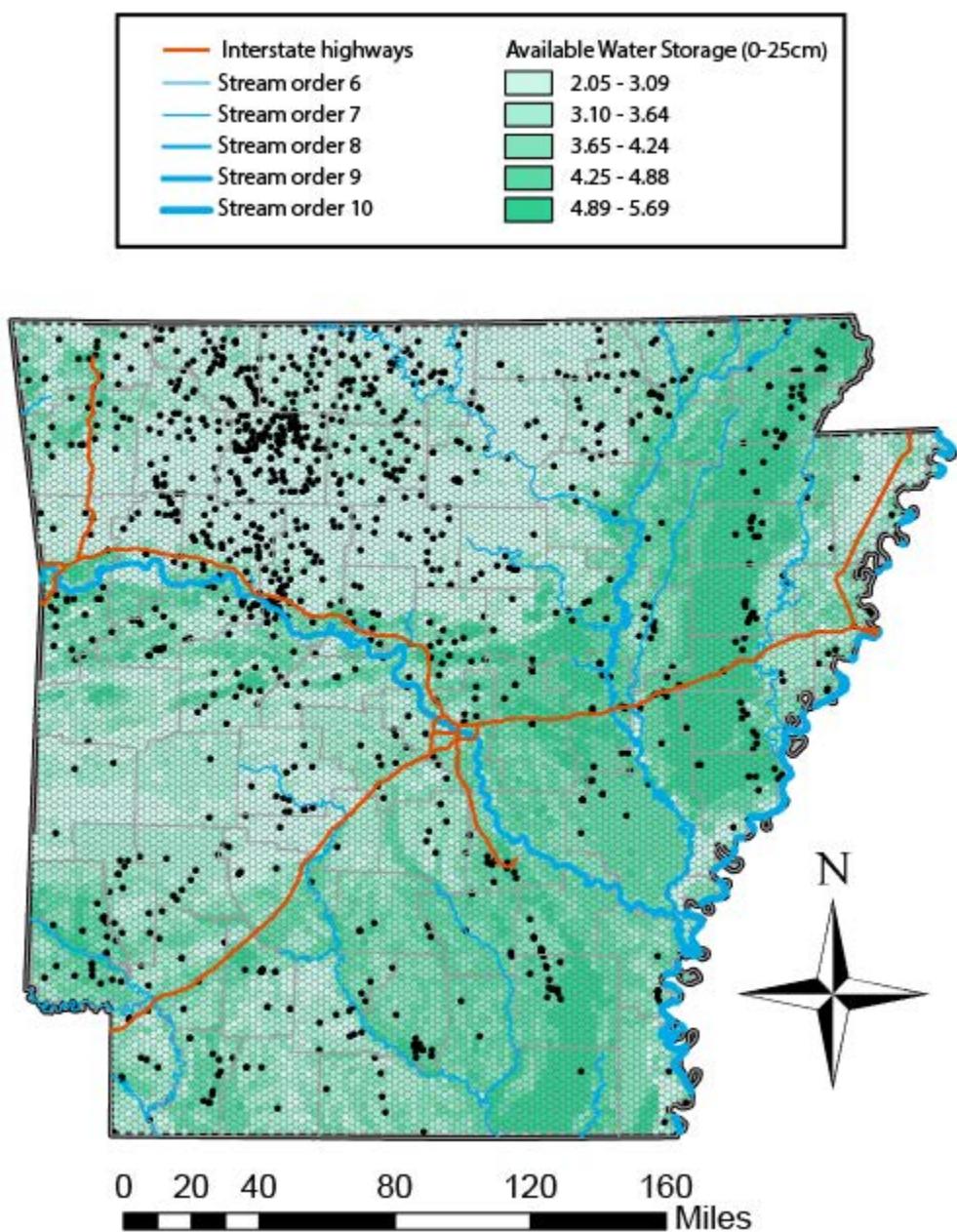


Figure A6-3: Available soil water storage (0-25cm depth) measured in centimeters, taken from the from the Gridded Soil Survey Geographic (gSSURGO) database maintained by the U.S. Department of Agriculture Natural Resources Conservation Service (USDA NRCS).

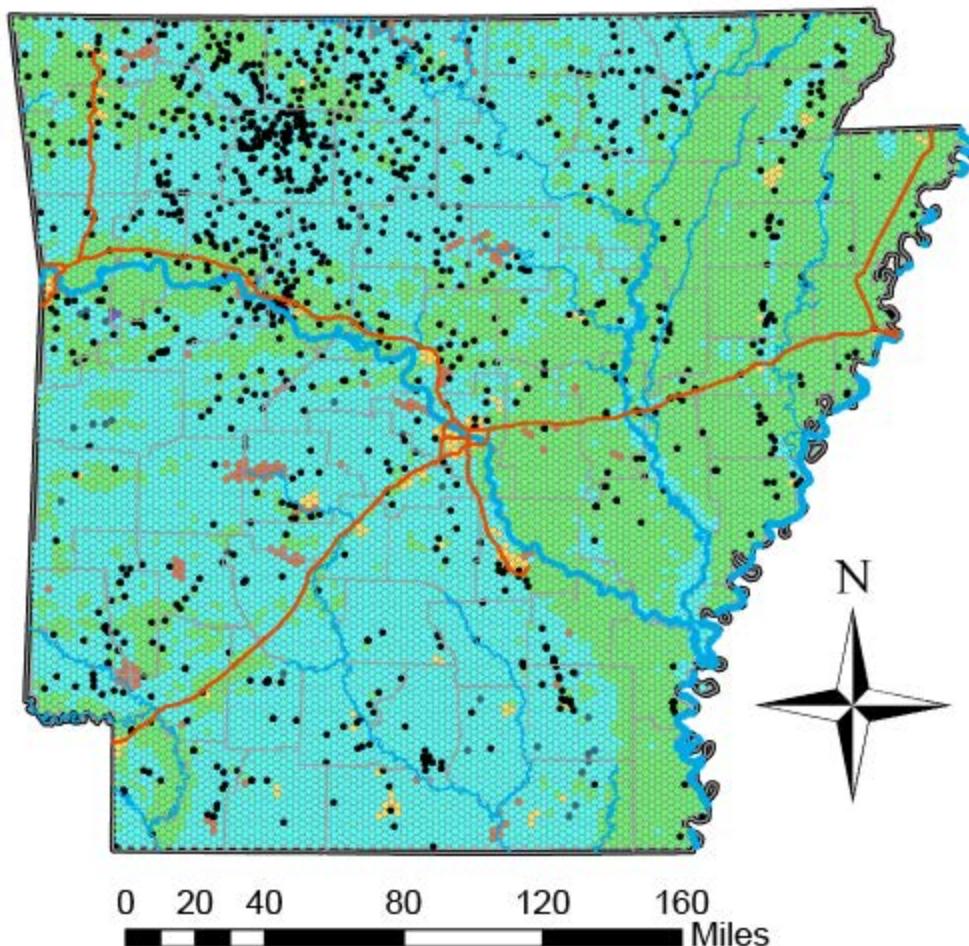
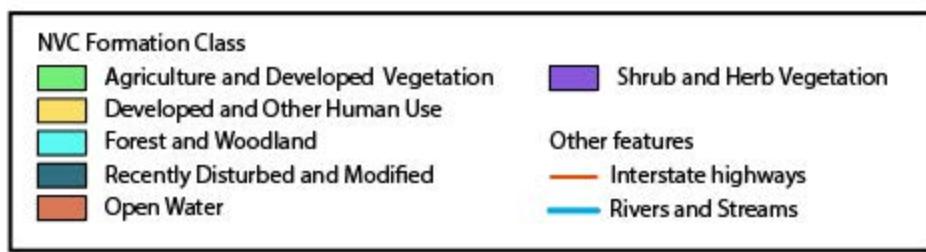


Figure A6-4: Dominant National Vegetation Classification (NVC) Formation Class of each hexagonal tile. NVC Formation Class represents broad combinations of general dominant growth forms and reflects broad-scale variation in climate and substrate conditions.

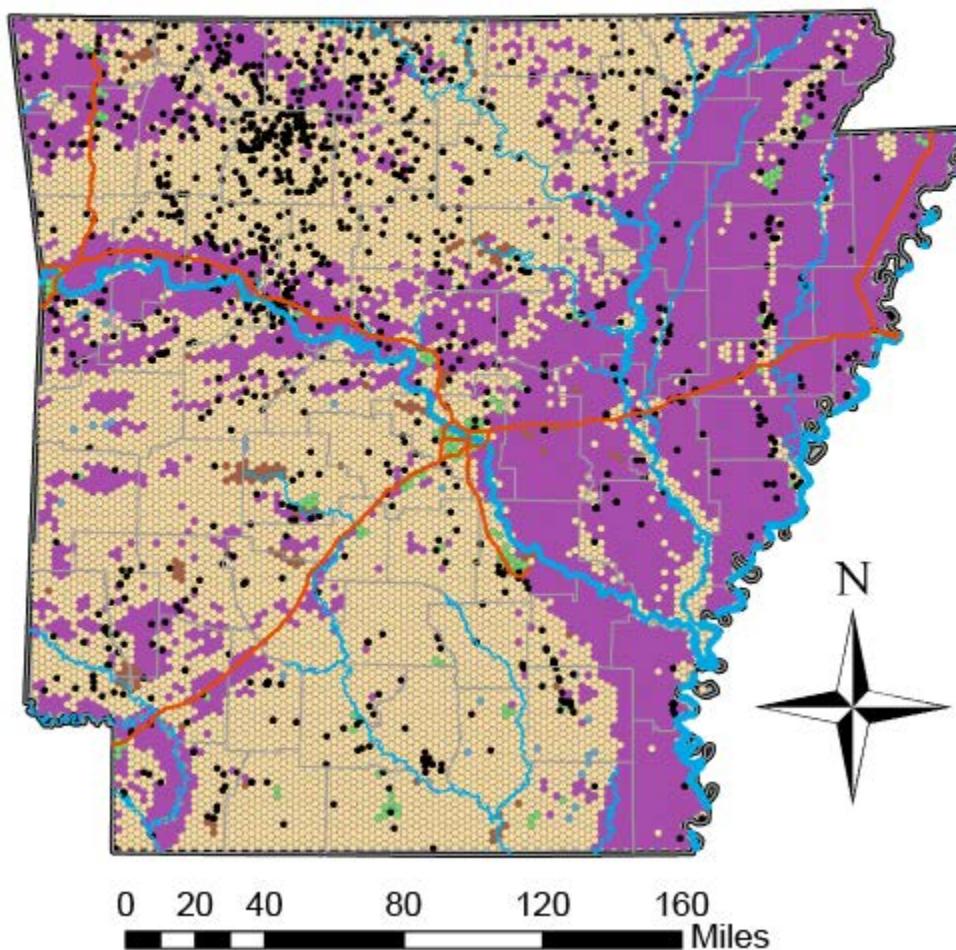


Figure A6-5: Dominant National Vegetation Classification (NVC) Formation Subclass of each hexagonal tile. NVC Formation Subclass represents combinations of general dominant and diagnostic growth forms and reflects macroclimatic variation primarily due to latitude and continental position.

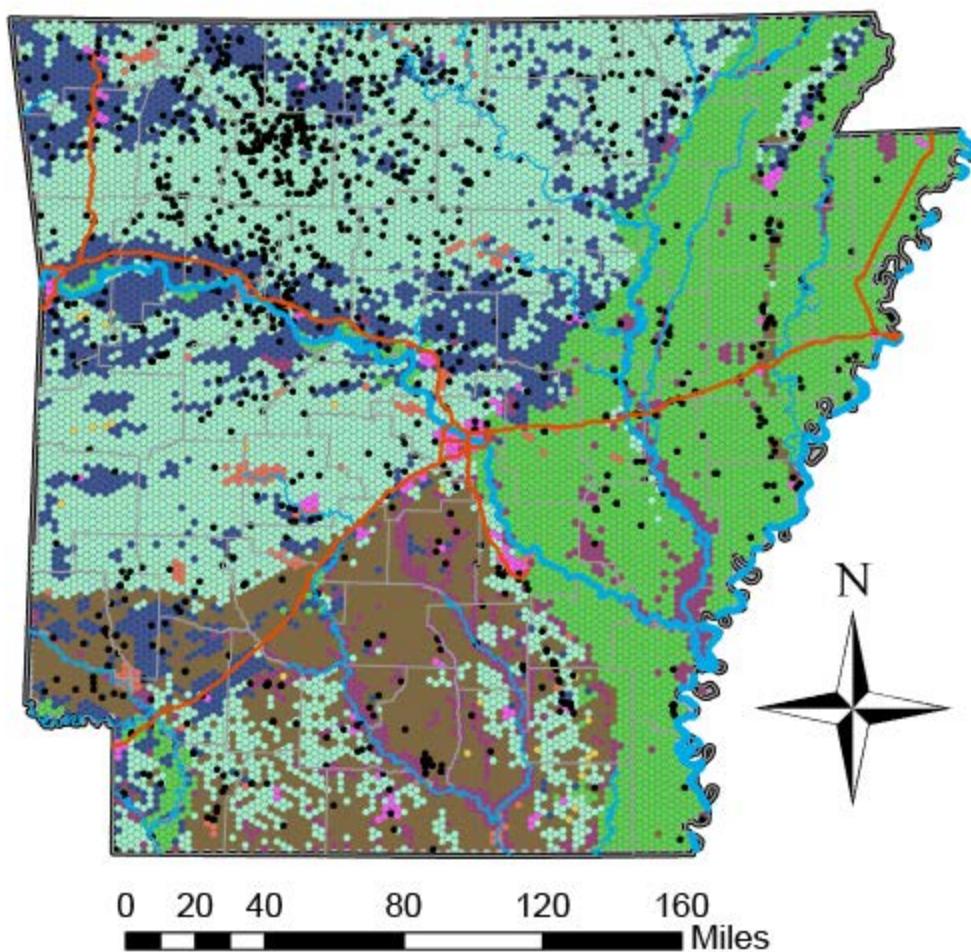
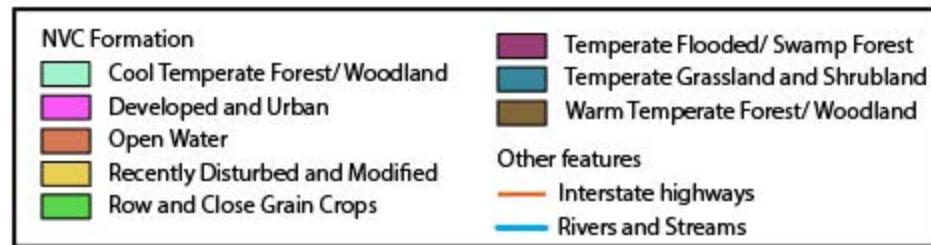


Figure A6-6: Dominant National Vegetation Classification (NVC) Formation type of each hexagonal tile. NVC Formation type represents a finer scale categorization of the NVC Formation Subclass.

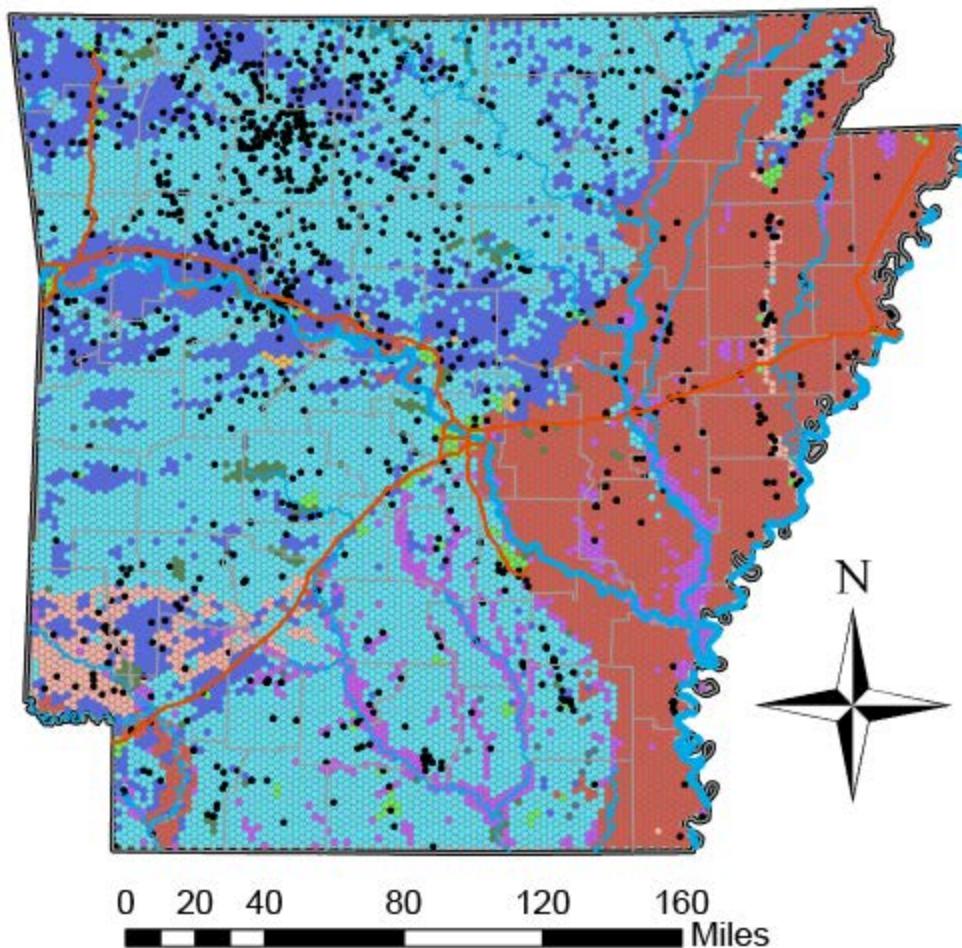
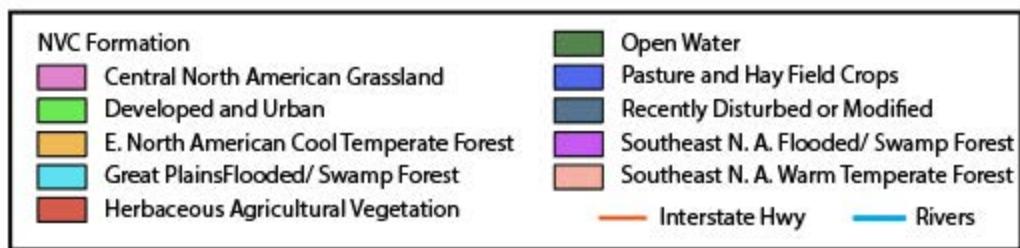


Figure A6-7: Dominant National Vegetation Classification (NVC) Division classification of each hexagonal tile. NVC Division represents dominant growth forms and a broad set of diagnostic plant species representing broad-scale biogeographic differences. N. A. = North America; E. = Eastern.

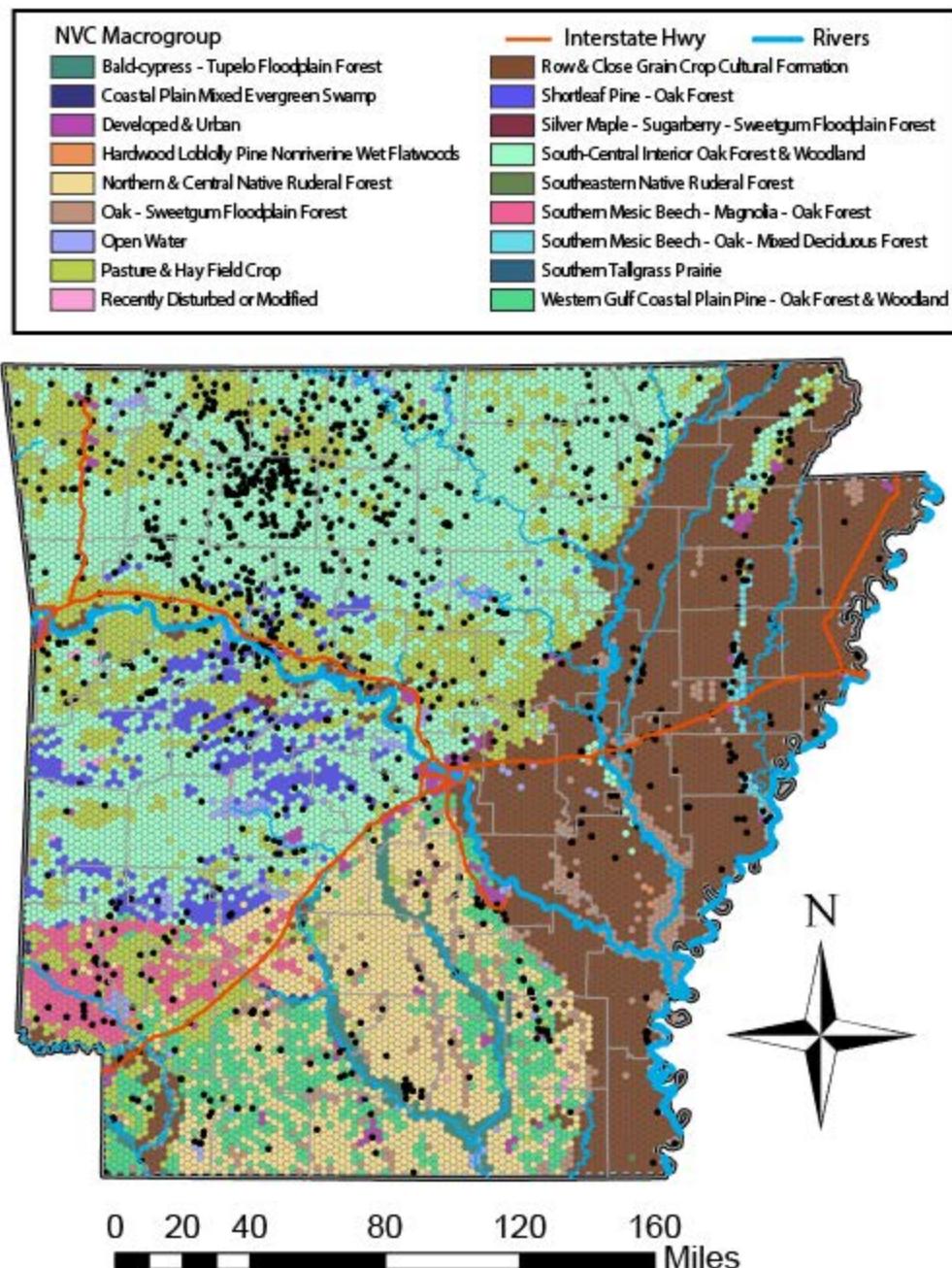


Figure A6-8: Dominant National Vegetation Classification (NVC) Macrogroup classification of each hexagonal tile. NVC Macrogroup represents sub-continental to regional differences in mesoclimate, substrate, and disturbance regimes and is a finer-scale version of the NVC Division class.

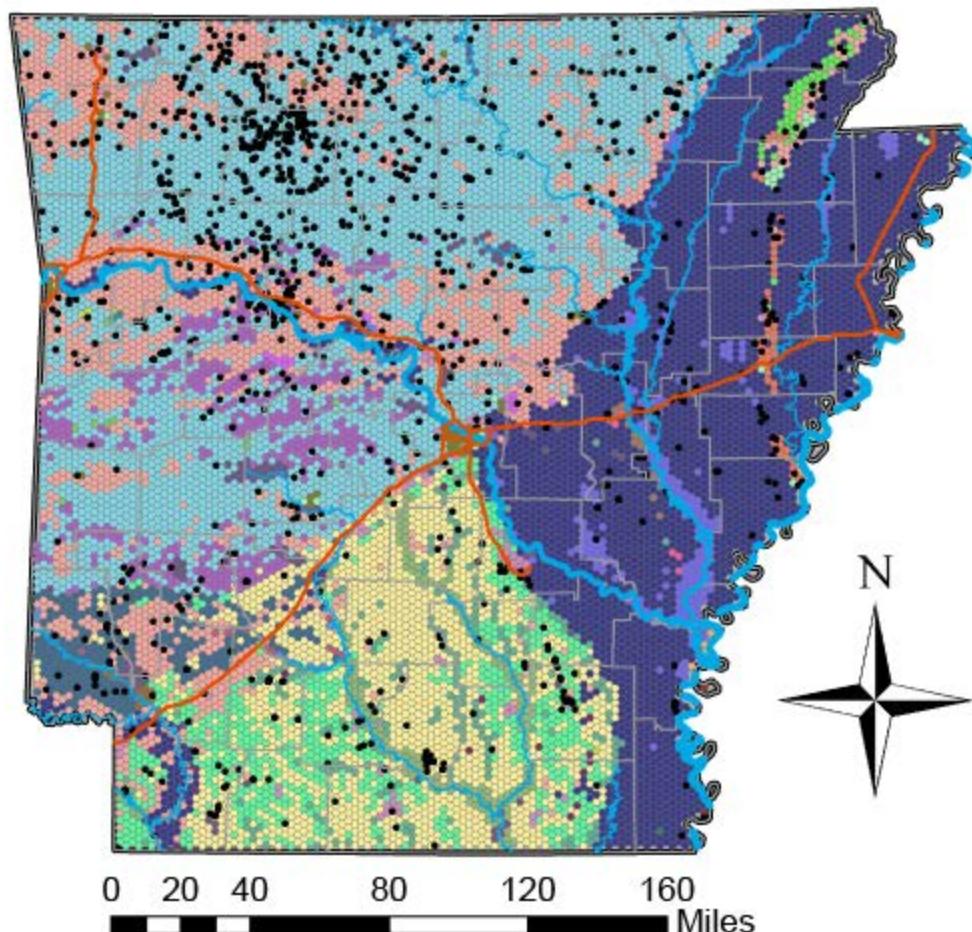
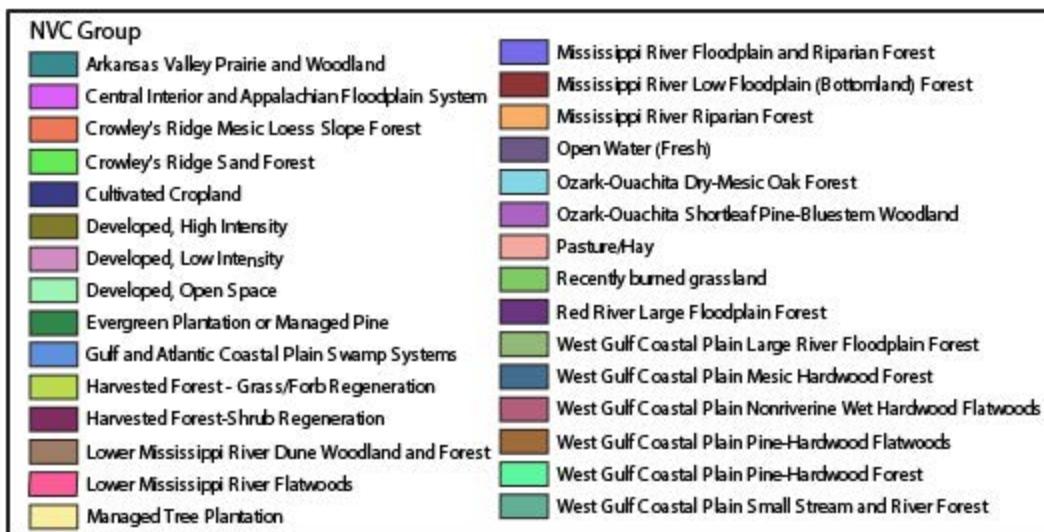


Figure A6-9: Dominant National Vegetation Classification (NVC) Group classification of each hexagonal tile. NVC ecological Group represents finer-scale regional divisions within NVC Macrogroup categories.

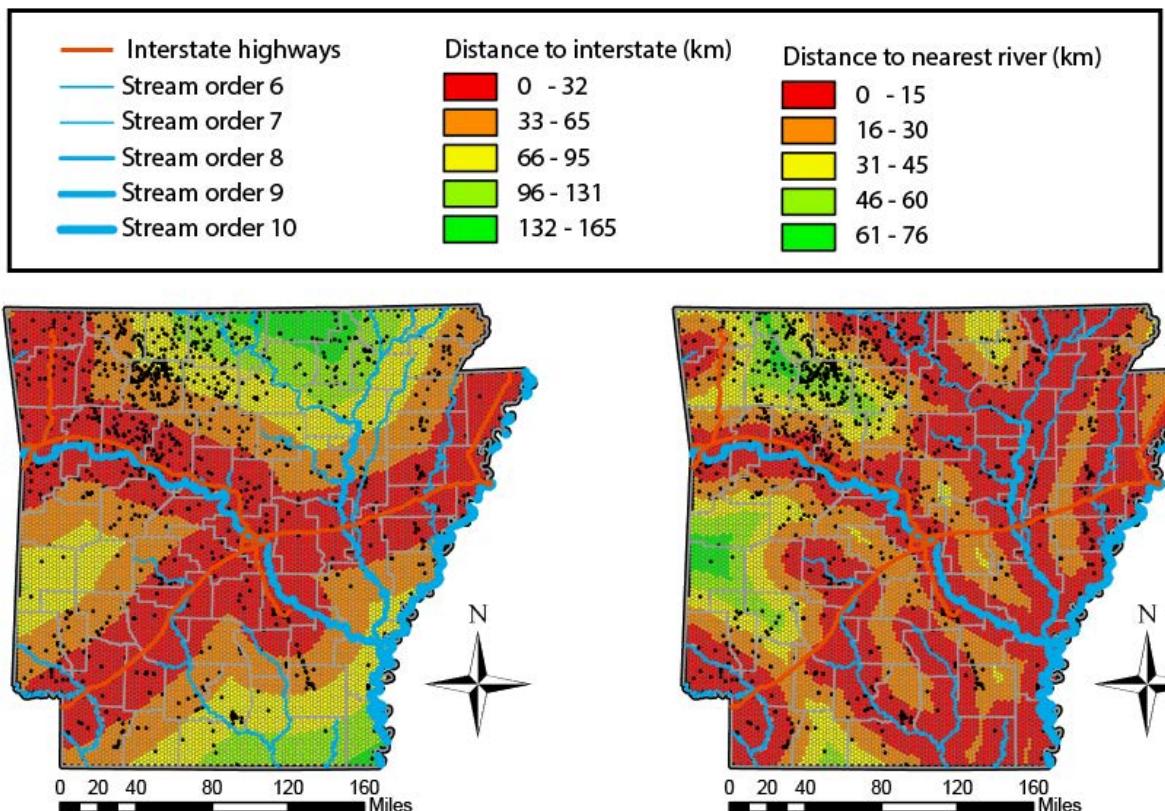


Figure A6-10: Distance of tile to nearest interstate (left) or river larger than order 5 (right), measured in kilometers.

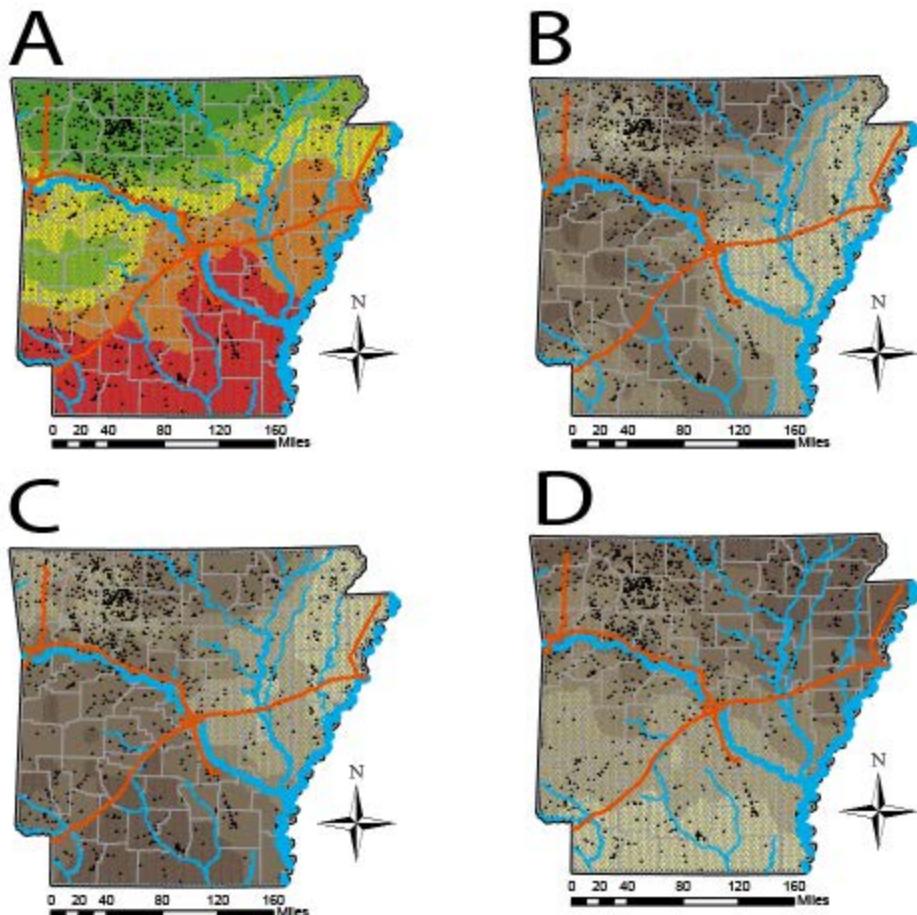
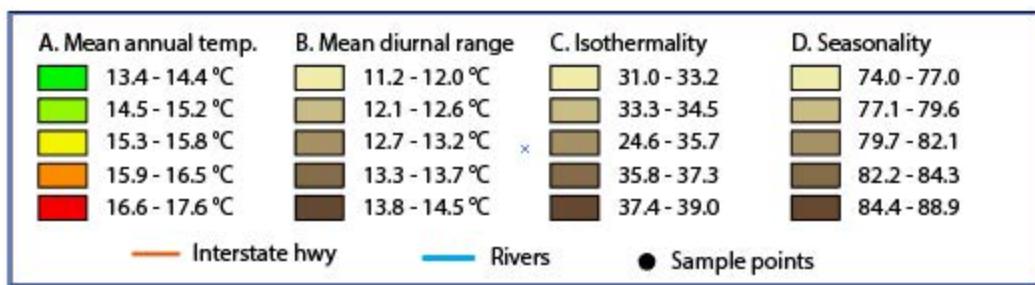


Figure A6-11: BioClim temperature variables 1 through 4: (A) Mean annual range; (B) Mean diurnal range, defined as the mean of monthly ranges; (C) Isothermality, or the annual range divided by the diurnal range; and (D) Temperature seasonality (standard deviation * 100). Results shown are the mean values for each hexagonal cell, after resampling BioClim rasters.

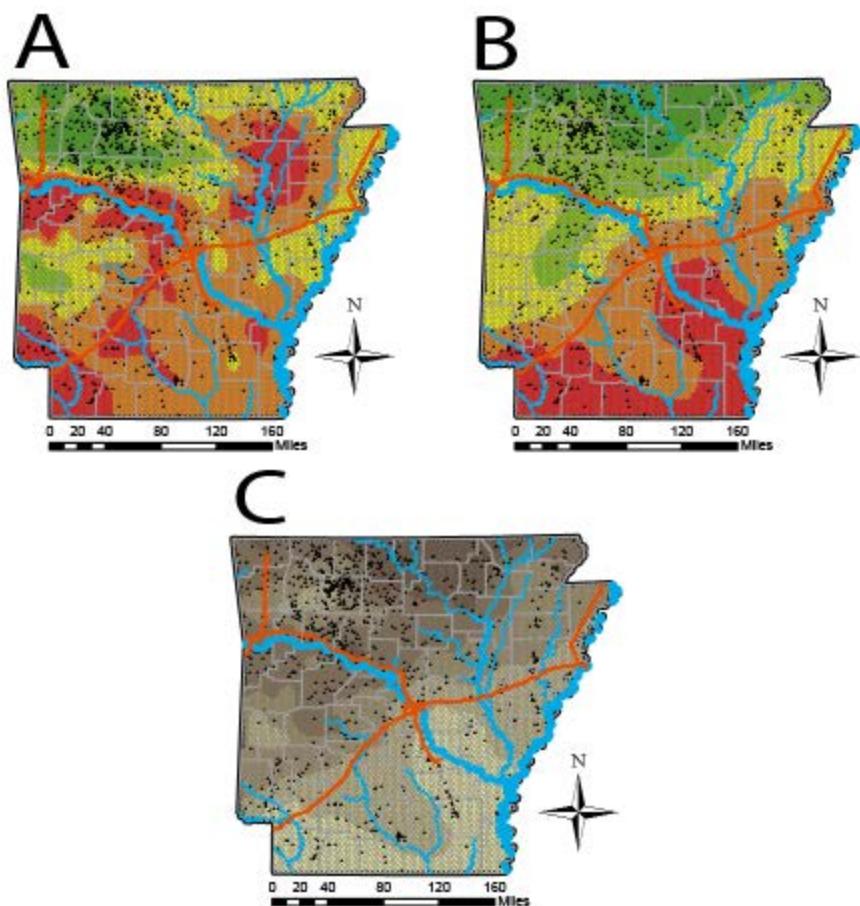
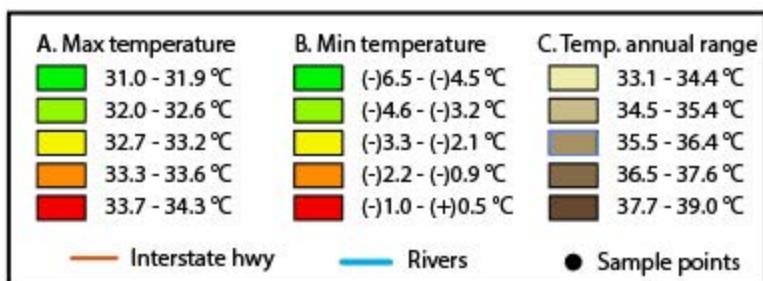


Figure A6-12: BioClim temperature variables 5 through 7: (A) Maximum temperature during warmest month; (B) Minimum temperature during coldest month; and (C) Temperature annual range. Results shown are the mean values for each hexagonal cell, after resampling BioClim rasters.

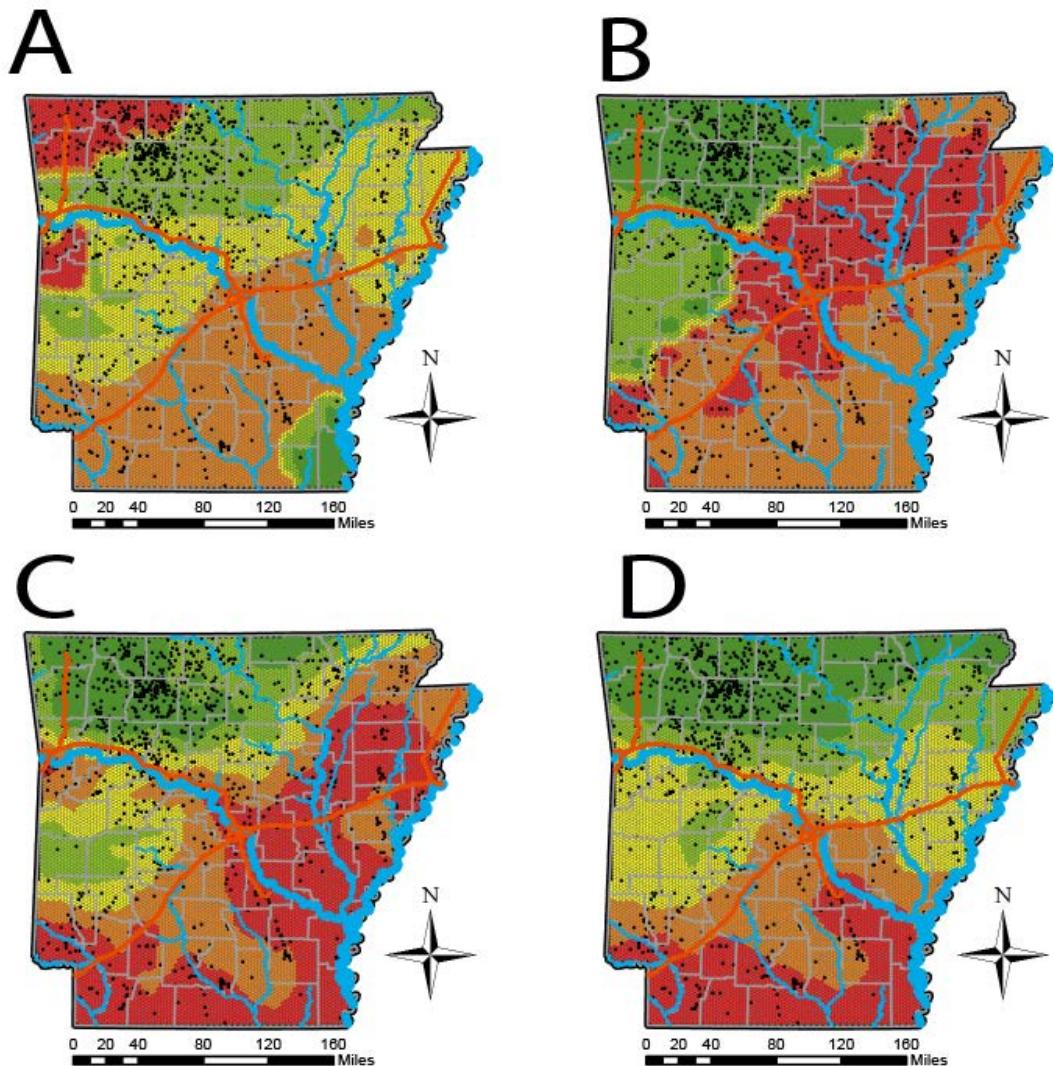
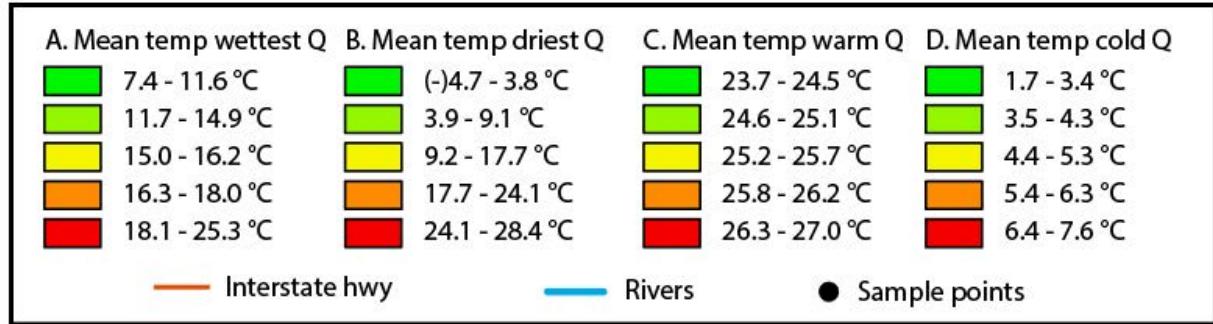


Figure A6-13: BioClim temperature variables 8 through 11: (A) Mean temperature of wettest quarter (=Q); (B) Mean temperature of driest quarter; (C) Mean temperature of warmest quarter; and (D) Mean temperature of coldest quarter. Results shown are the mean values for each hexagonal cell, after resampling BioClim rasters.

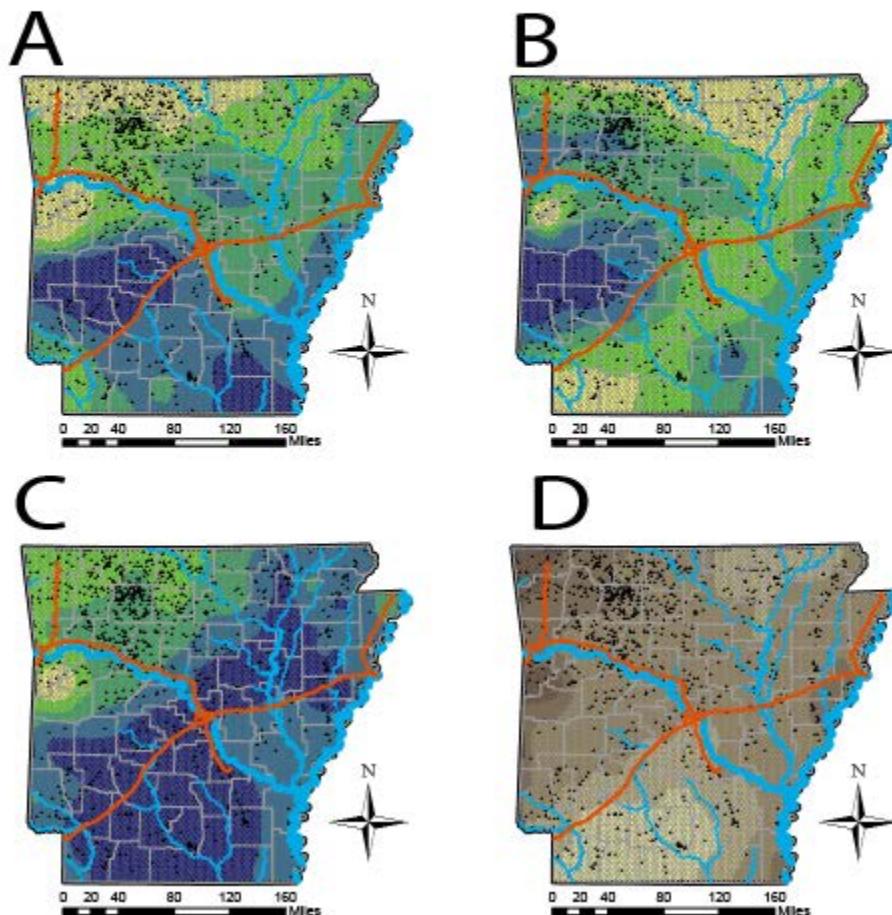
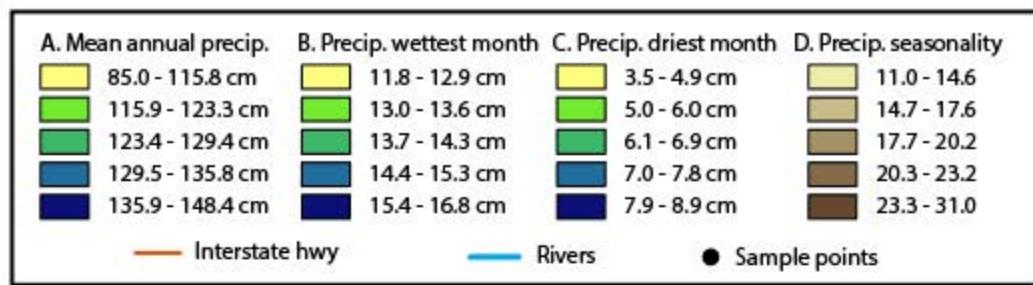


Figure A6-14: BioClim precipitation variables 12 through 15: (A) Mean annual precipitation; (B) Mean precipitation during wettest month; (C) Mean precipitation during driest month; and (D) Precipitation seasonality (coefficient of variation). Results shown are the mean values for each hexagonal cell, after resampling BioClim rasters.

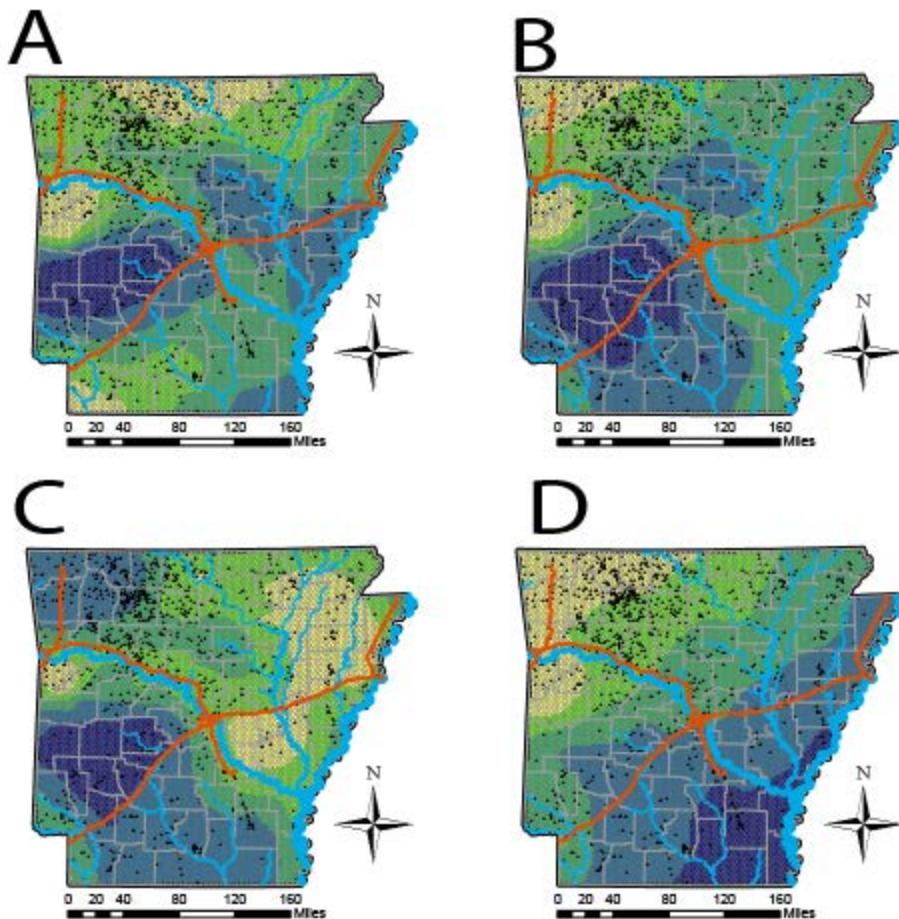
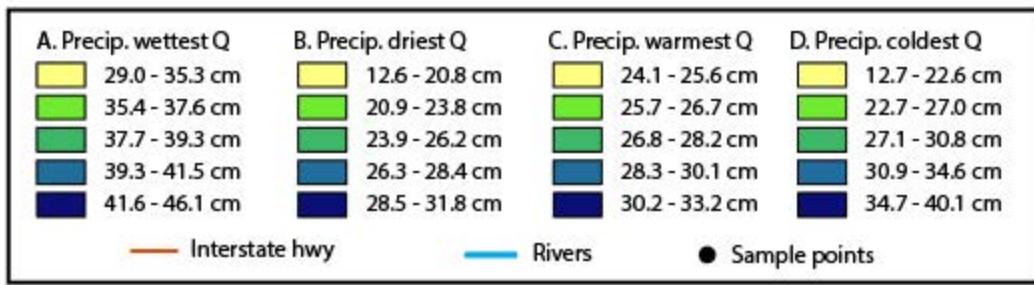


Figure A6-15: BioClim precipitation variables 16 through 19: (A) Precipitation during wettest quarter; (B) Precipitation during driest quarter; (C) Precipitation during warmest quarter; and (D) Precipitation during coldest quarter. Results shown are the mean values for each hexagonal cell, after resampling BioClim rasters.

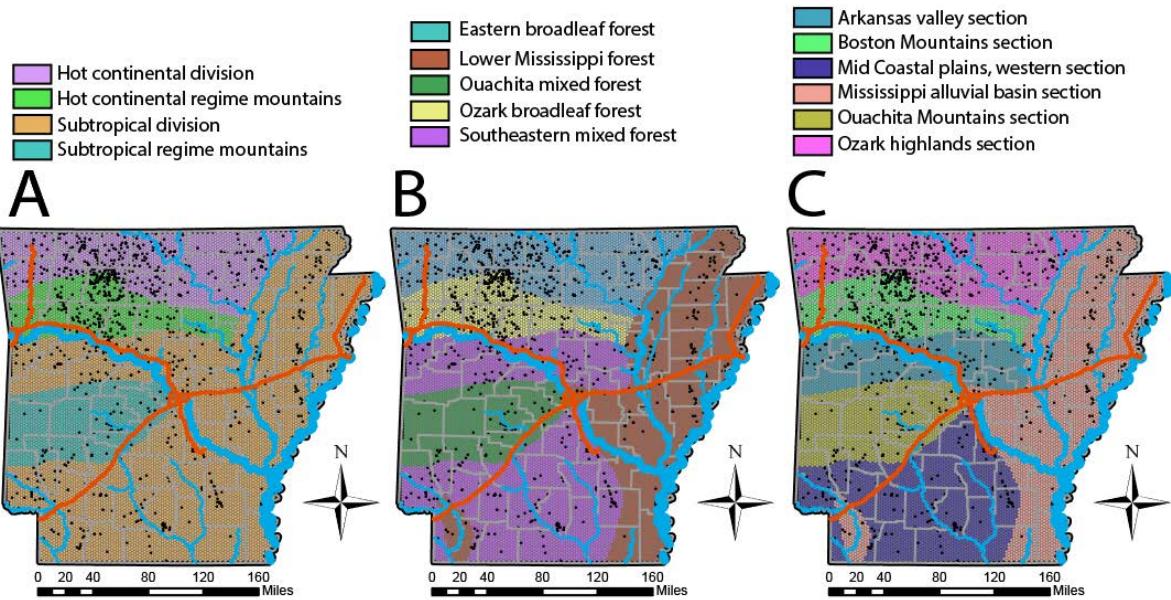


Figure A6-16: Bailey's ecoregion classifications at hierarchical levels of: (A) Division; (B) Province; and (C) Section.

Appendix 7 – Spatial Analysis: 17 Relevant Variables

Spatial Analysis Results (In-depth)

The 35 environmental factors were distilled into a set of 17 factors that significantly explained white-tailed deer dispersal (Table 7). This set of meaningful factors included riverine barriers to dispersal (e.g. RIVER_DIST, ECOLYS_LU_Open Water, and SECTION Arkansas River Valley), climatic variables (e.g. BIO8_WETTE), vegetation variables (e.g. West Gulf Coast Mesic Hardwood Forest), and section variables (e.g. Boston Mountains). The single most explanatory factor was SECTION_Arkansas River Valley which when present had a mean logM lower than that of non-Arkansas River valley sections by 0.42. For context logM ranges from -1 to 1 (Fig. 12). This suggests the Arkansas River is a significant barrier to white-tailed deer dispersal. Maps and distributions of the 17 environmental factors and associated results of spatial analyses are provided in Figs. A1-A17).

Spatial decomposition via dbMEM extracted 81 meaningful eigenvectors, of which 73 were included in the forward selection procedure, and 65 were retained after correcting for multiple tests. These eigenvectors represent spatial autocorrelation in the variable logM. Smaller eigenvectors (e.g. V3) represent broad scale spatial structure and larger eigenvectors (e.g. V81) represent relatively finer scale structure (Fig. 24). Prior to variation partitioning, only the 17 top-ranked eigenvectors were selected so that the environmental and spatial datasets would have the same number of factors.

A linear model including both spatial eigenvectors and environmental factors explained 67% of the variance in the variable logM ($\text{adj.R}^2 = 0.67; p < 0.001$). There was a large proportion of spatial autocorrelation in the variable logM ($\text{adj.R}^2 = 0.64; p < 0.001$). However, only 20% of the variance of logM could be attributed to environmental factors, the majority of which was spatially structured environmental variation (17%). Thus, 47% of the variation of logM was spatially autocorrelated, but could not be explained by the environmental factors presented here (Fig. 25). This suggests that the unexplained autocorrelated structure could be explained by either 1) unmeasured environmental factors, 2) biotic factors intrinsic to deer populations (e.g. population size), or 3) a combination of these.

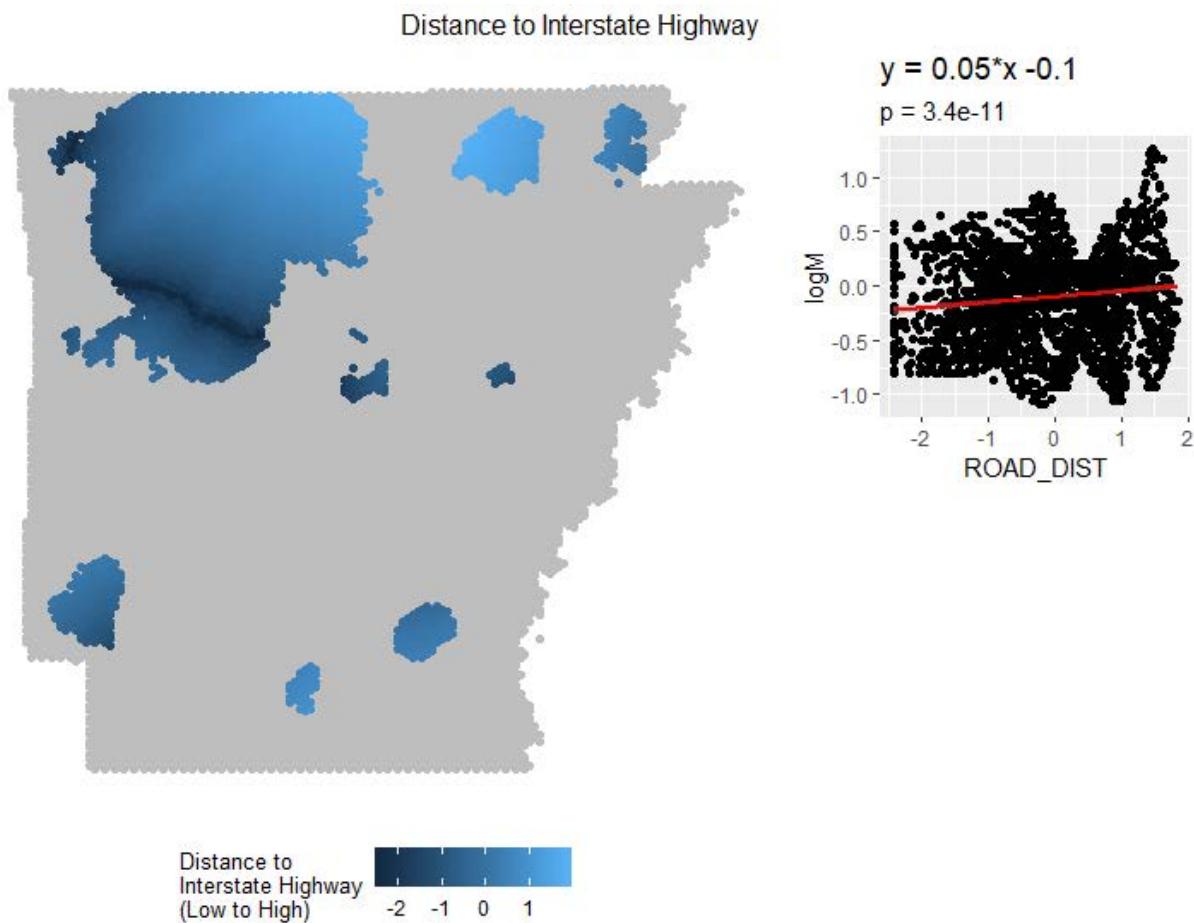


Figure A7-1: Distribution of the variable **ROAD_DIST** across the state. This variable represents the distance to the nearest interstate highway. The relationship between **ROAD_DIST** and **logM** is illustrated in the top right corner.

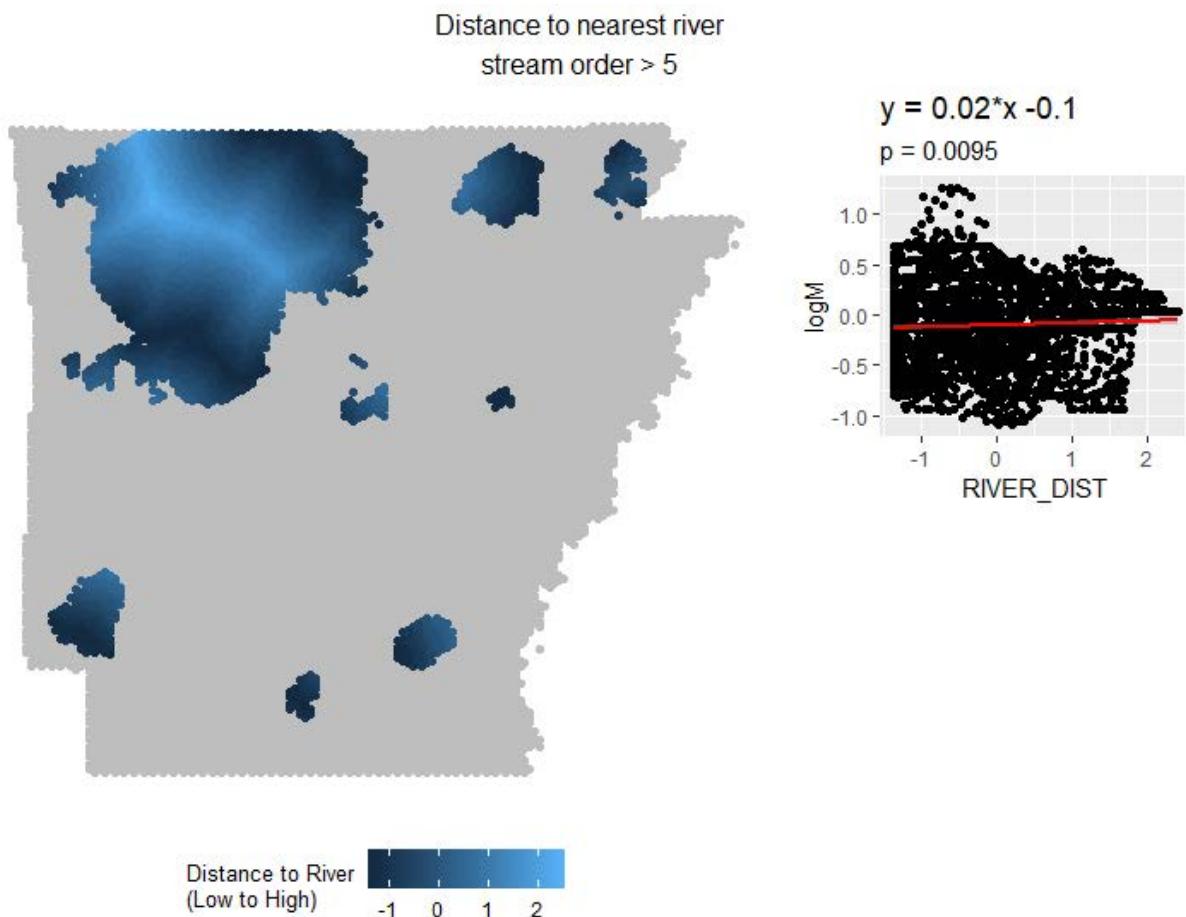


Figure A7-2: Distribution of the variable **RIVER_DIST** across the state. This variable represents the distance to the nearest river (stream order > 5). The relationship between **RIVER_DIST** and **logM** is illustrated in the top right corner.

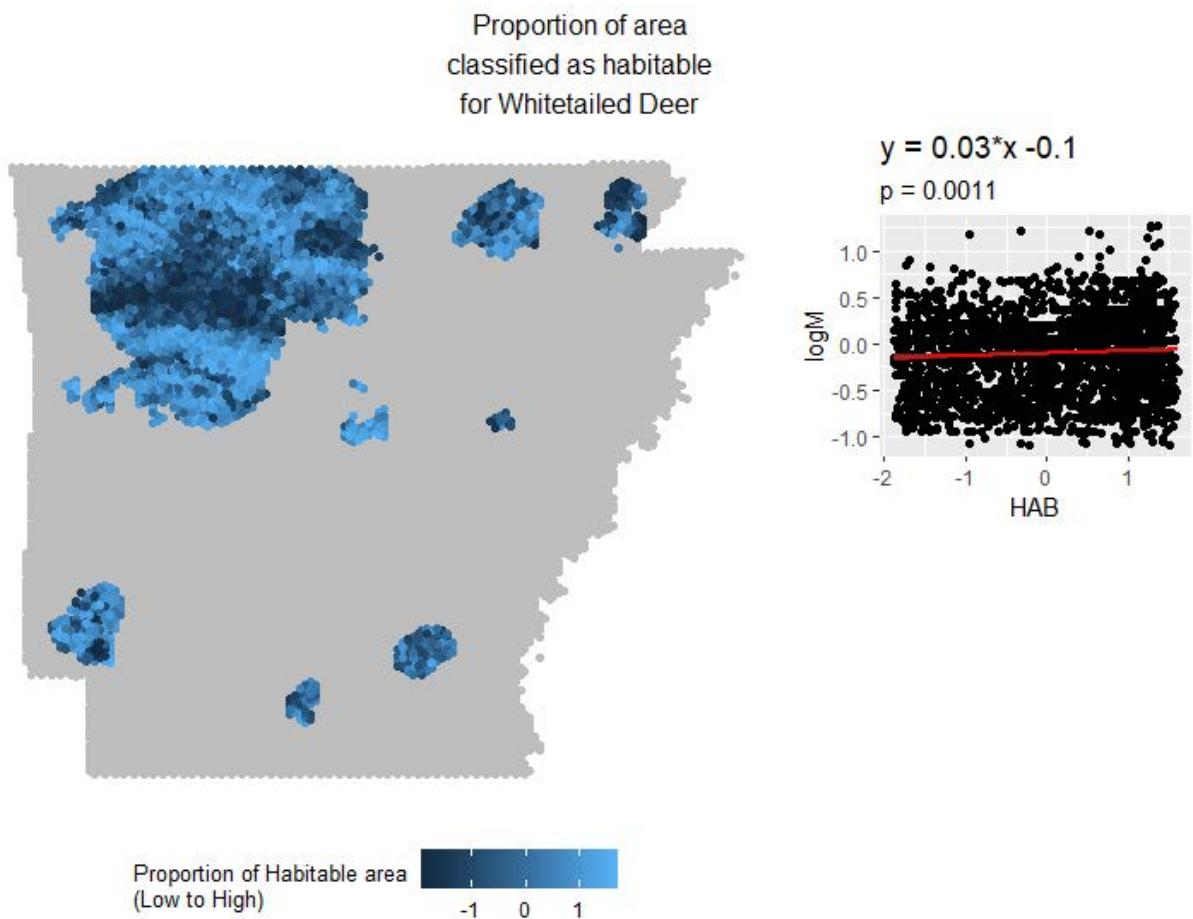


Figure A7-3: Distribution of the variable **HAB** across the state. This variable represents the proportion of an area classified as habitable by white-tailed deer. The relationship between HAB and logM is illustrated in the top right corner.

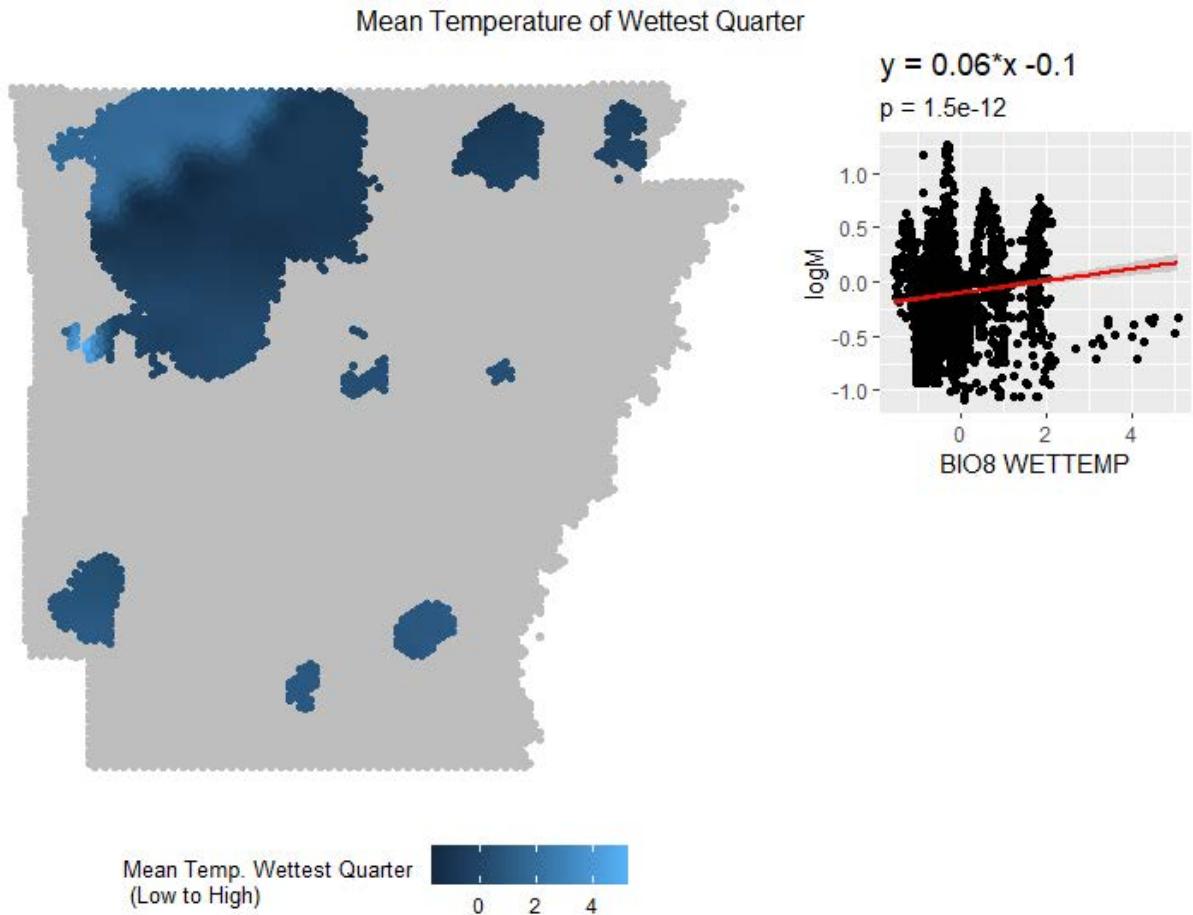


Figure A7-4: Distribution of the variable **BIO_WETTEMP** across the state. This variable represents the mean temperature during the wettest quarter of the year. The relationship between **BIO8_WETTEMP** and **logM** is illustrated in the top right corner.

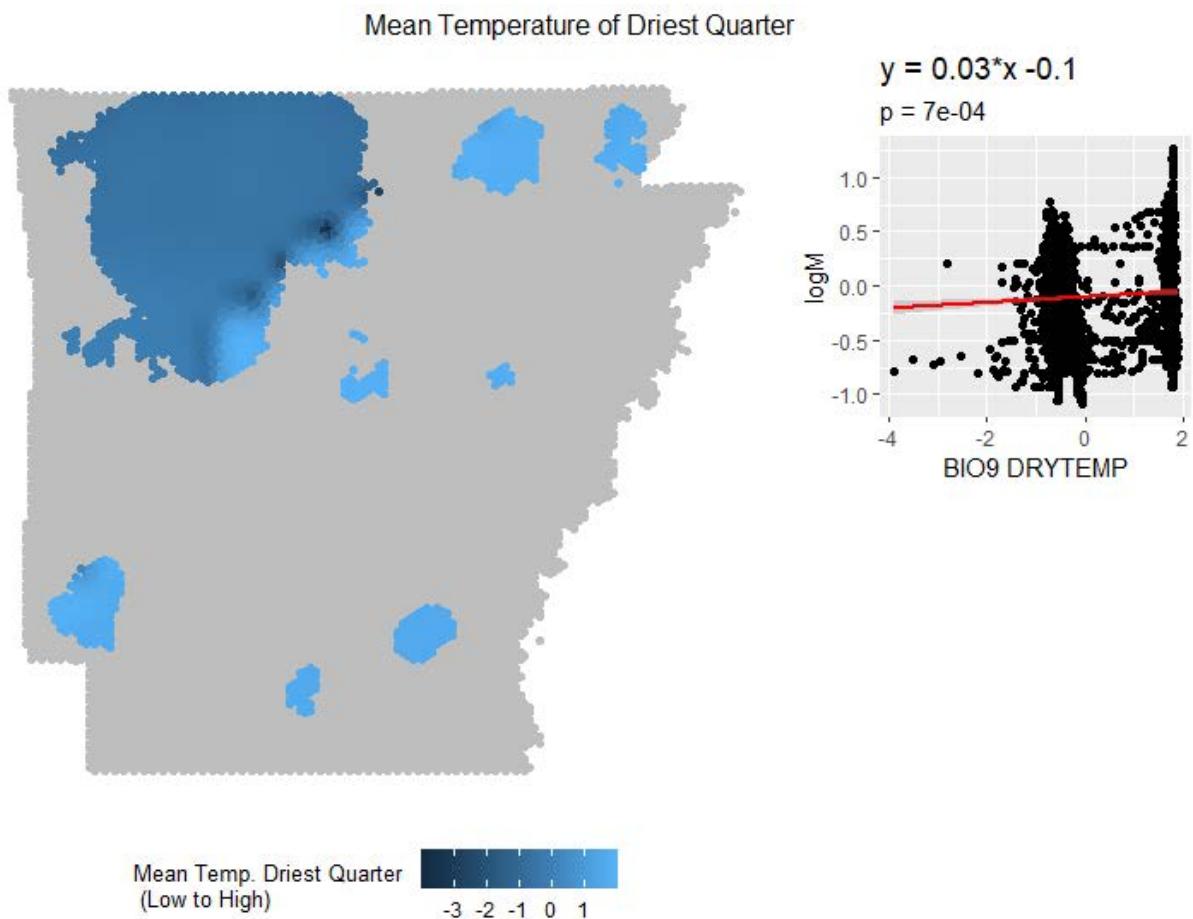


Figure A7-5: Distribution of the variable **BIO9_DRYTEMP** across the state. This variable represents the mean temperature during the driest quarter of the year. The relationship between **BIO9_DRYTEMP** and **logM** is illustrated in the top right corner.

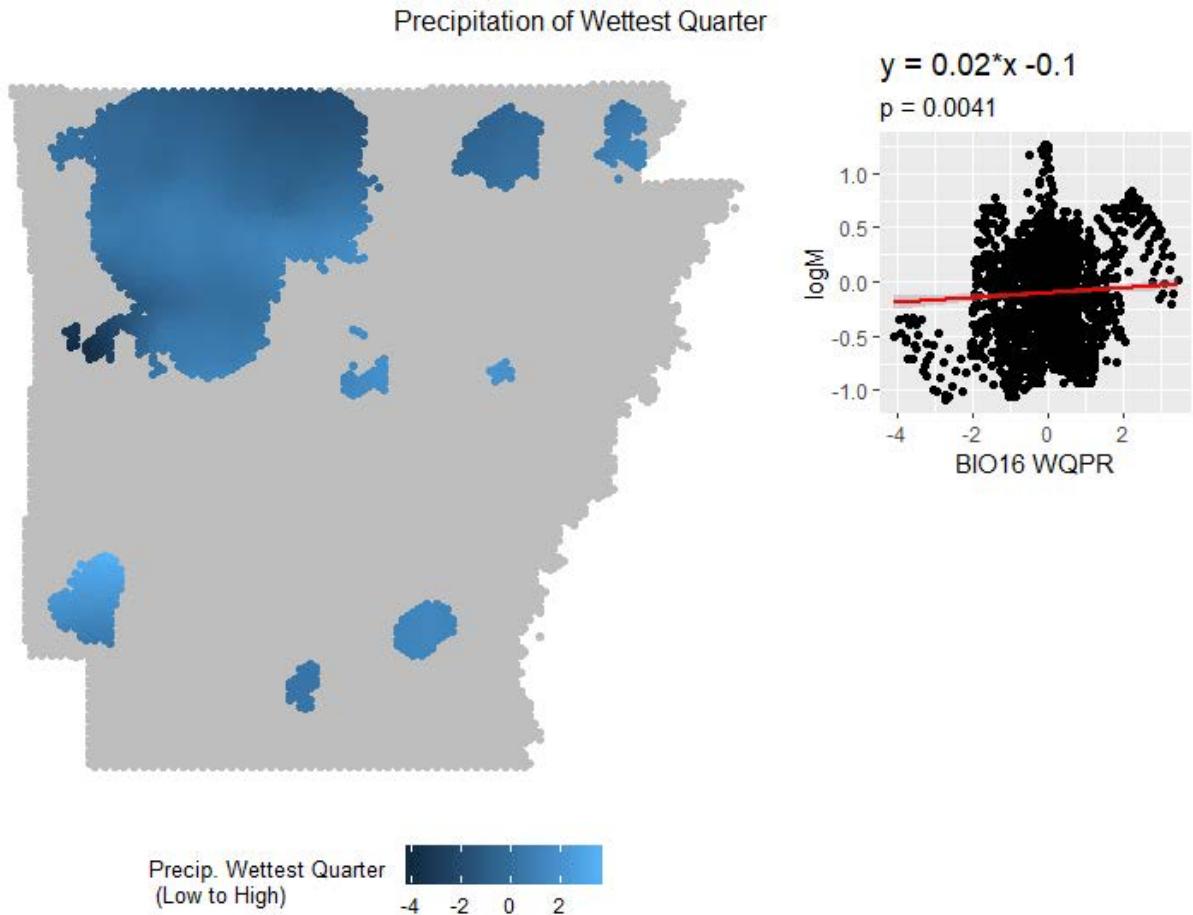


Figure A7-6: Distribution of the variable **BIO16WQPR** across the state. This variable represents the precipitation of the wettest quarter of the year. The relationship between BIO16WQPR and logM is illustrated in the top right corner.

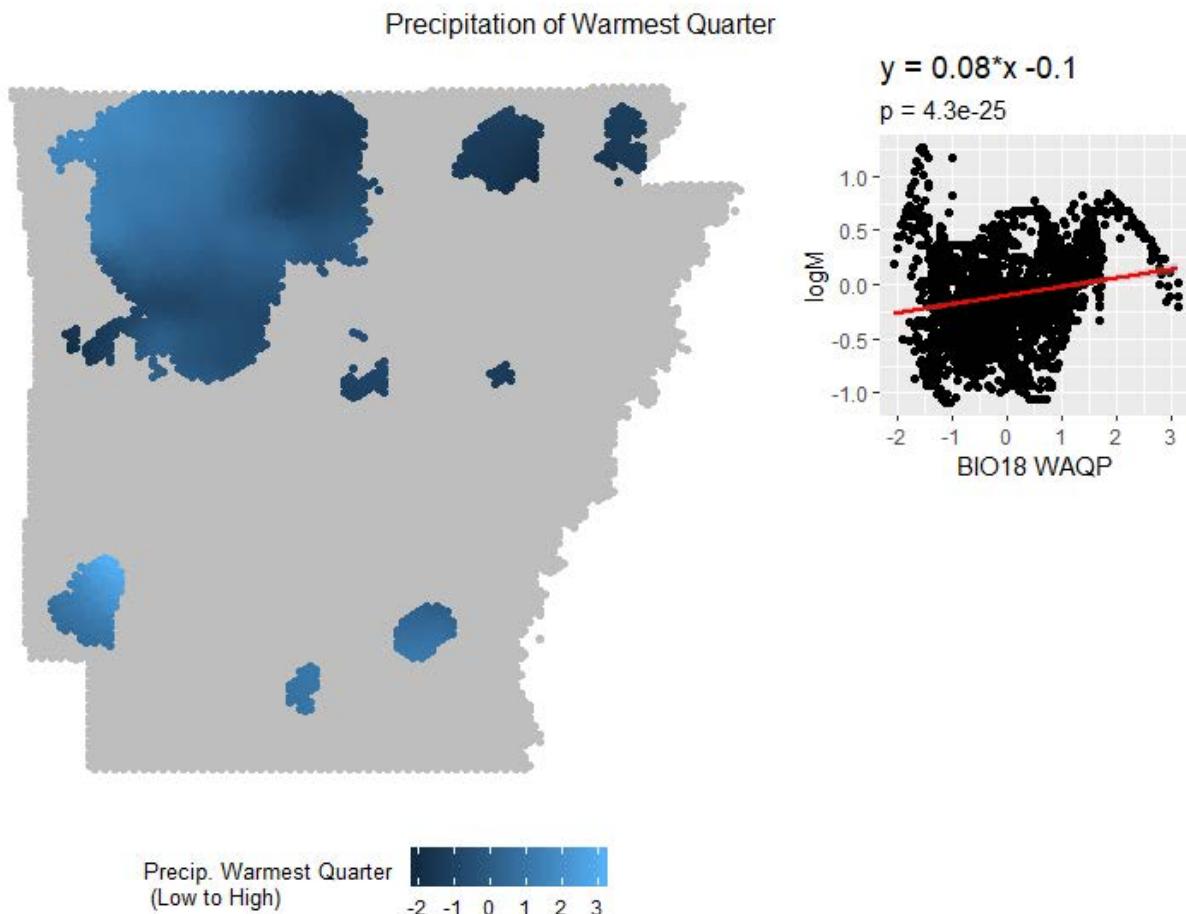


Figure A7-7: Distribution of the variable **BIO18WAQP** across the state. This variable represents the precipitation of the warmest quarter of the year. The relationship between **BIO18WAQP** and **logM** is illustrated in the top right corner.

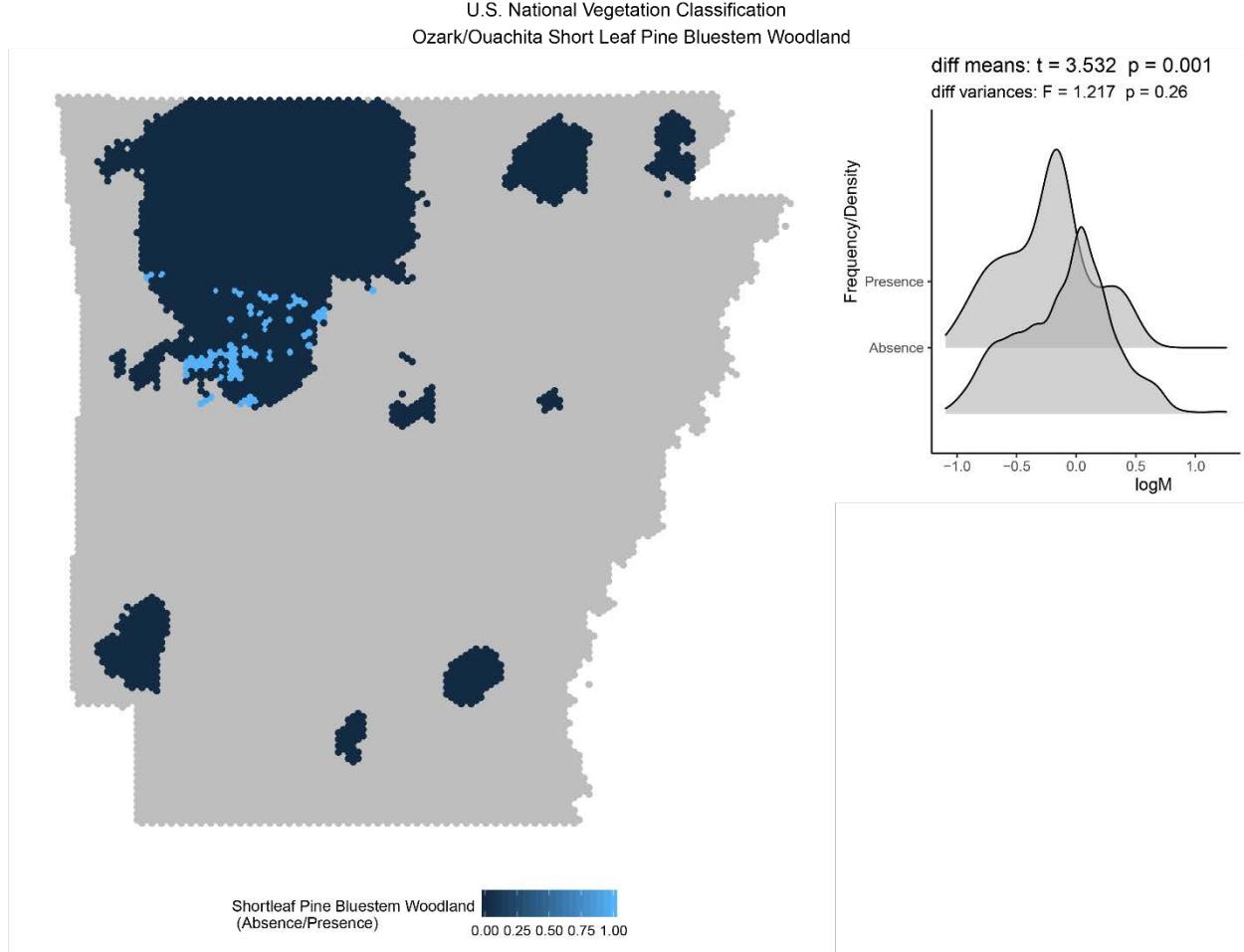


Figure A7-8: Distribution of Ozark/Ouachita Short Leaf Pine Bluestem Woodlands across the state. The distributions of $\log M$ when this variable is present and absent are illustrated in the top right corner.

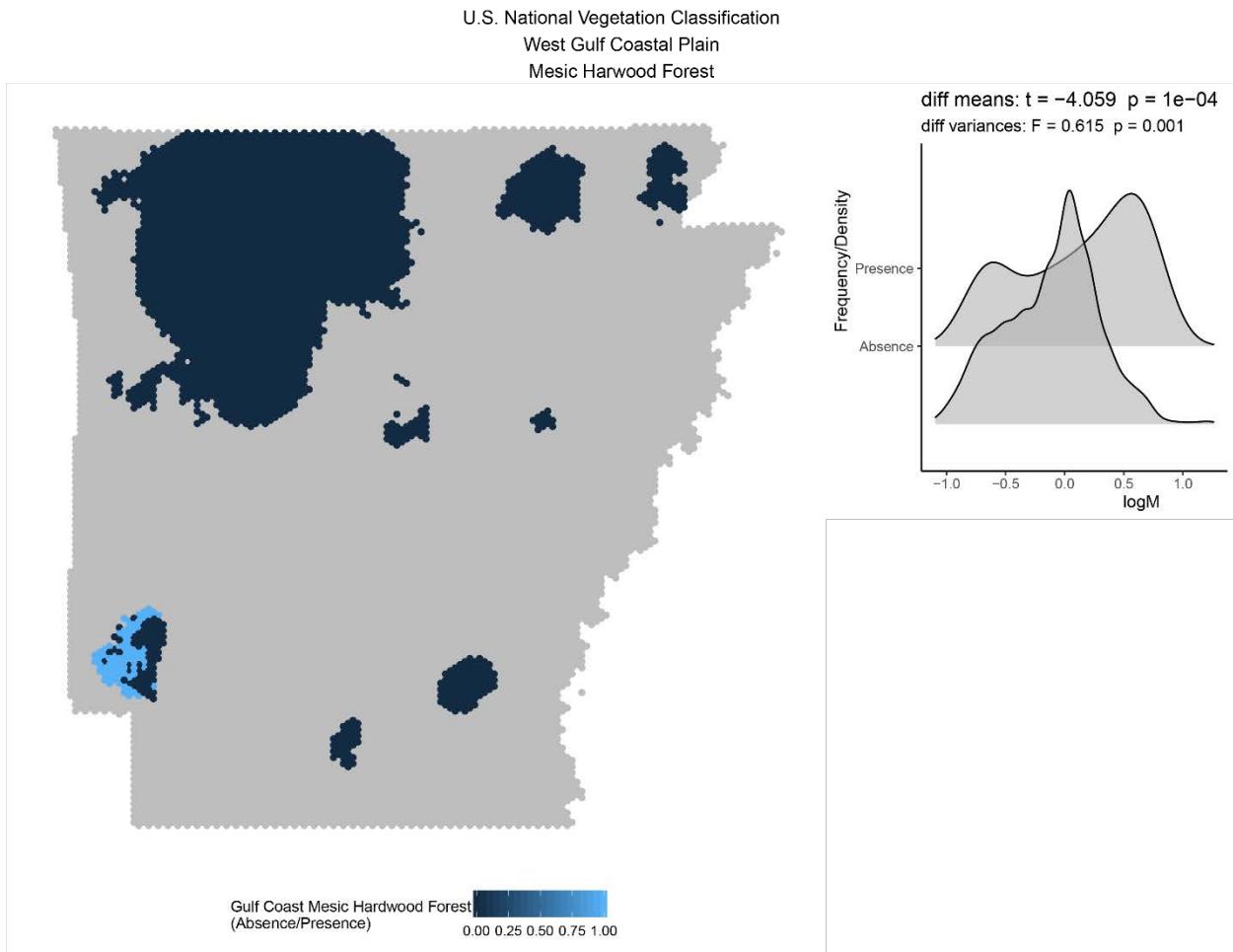


Figure A7-9: Distribution of **West Gulf Coastal Plain Mesic Hardwood Forest** across the state. The distributions of $\log M$ when this variable is present and absent are illustrated in the top right corner.

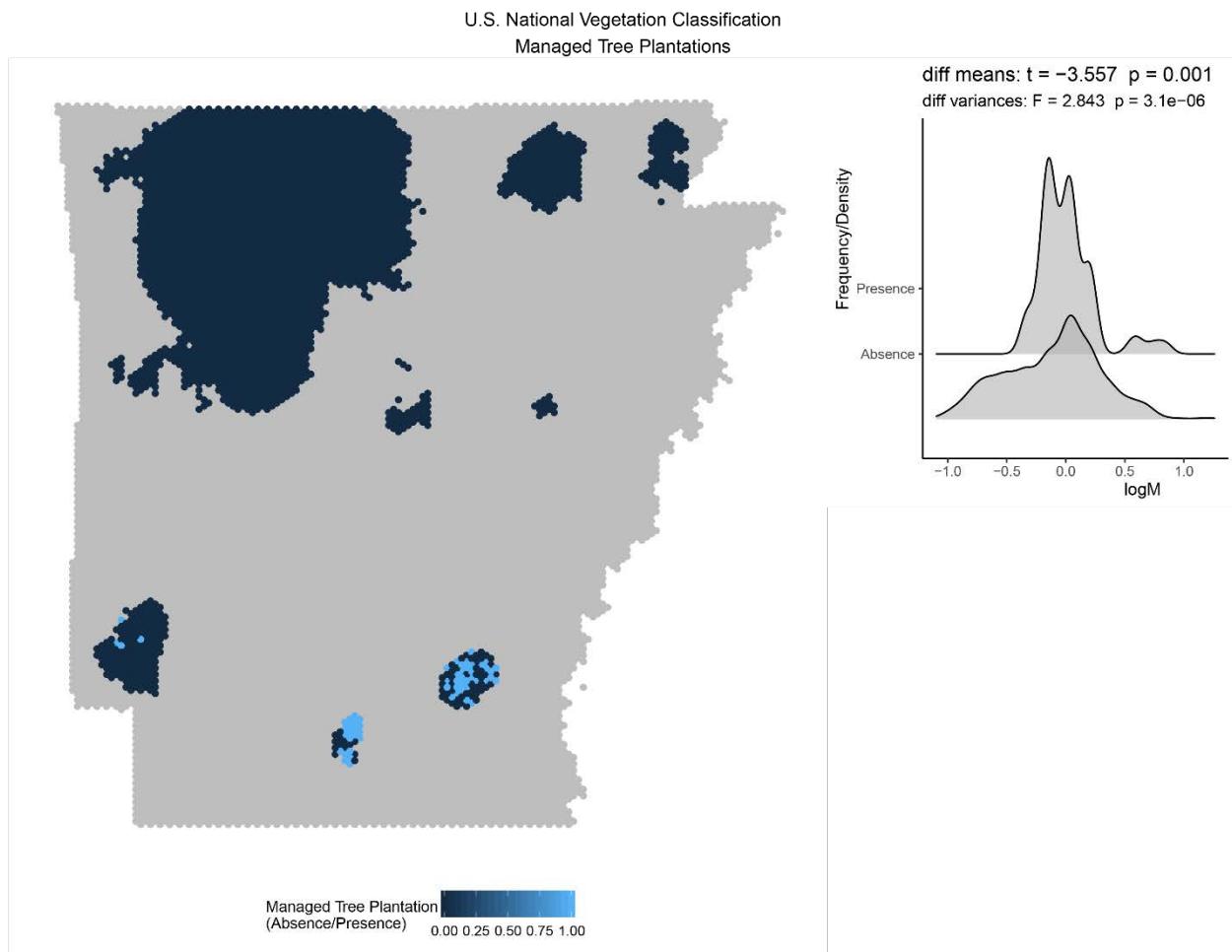


Figure A7-10: Distribution of **Managed Tree Plantations** across the state. The distributions of $\log M$ when this variable is present and absent are illustrated in the top right corner.

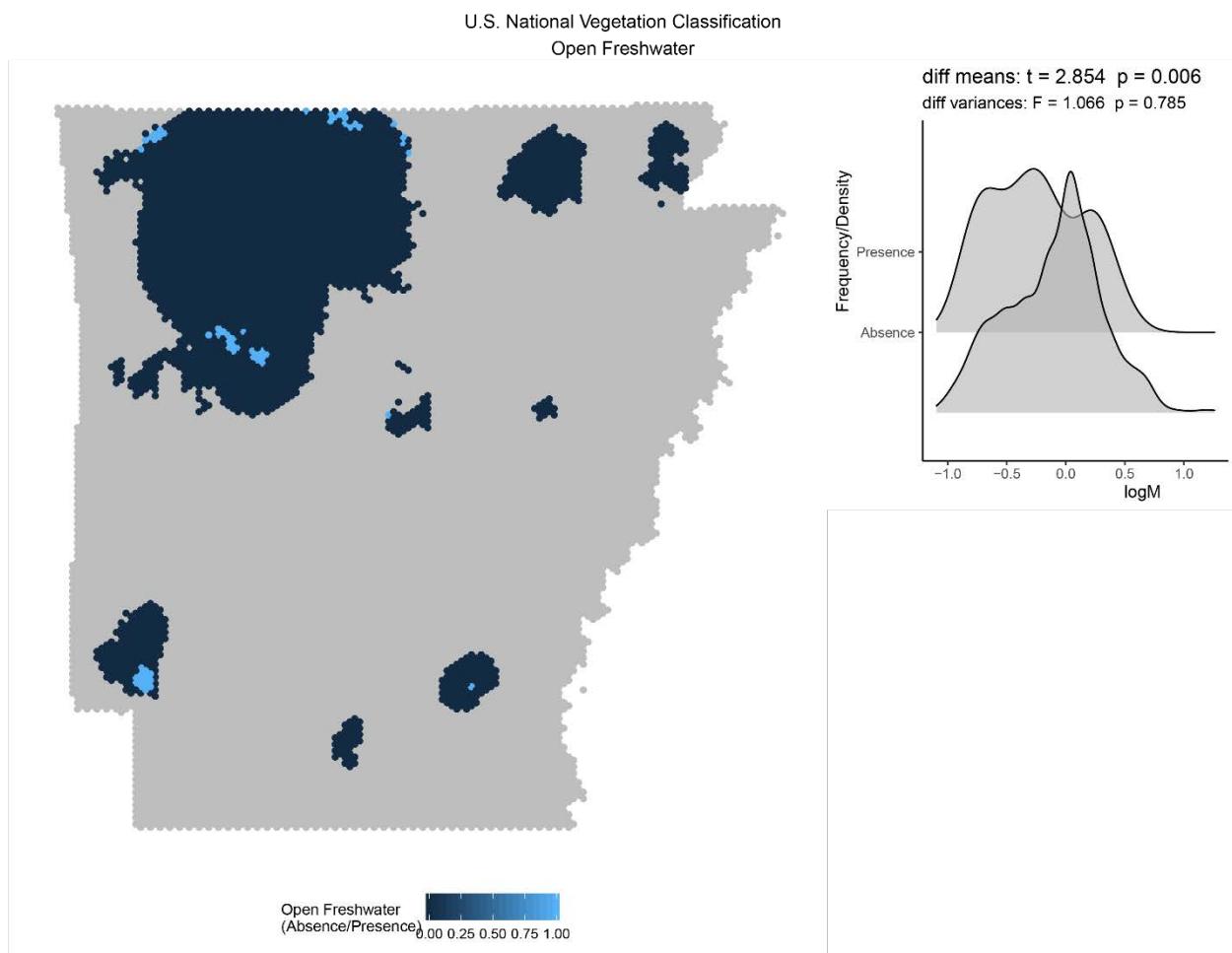


Figure A7-11: Distribution of Open Freshwater (majority of 10 km² area) across the state. The distributions of logM when this variable is present and absent are illustrated in the top right corner.

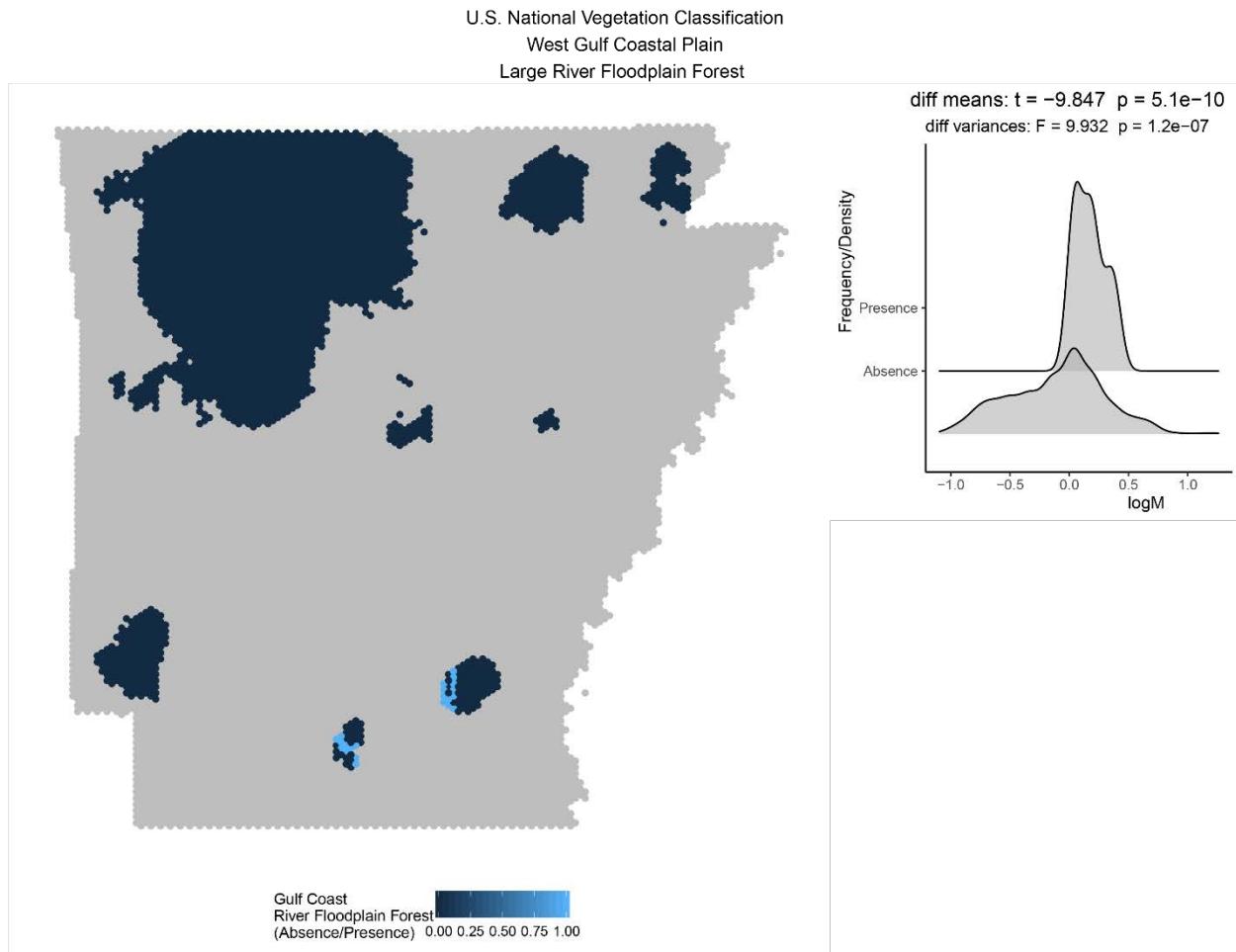


Figure A7-12: Distribution of **West Gulf Coastal Plain Large River Floodplain Forest** across the state. The distributions of $\log M$ when this variable is present and absent are illustrated in the top right corner.

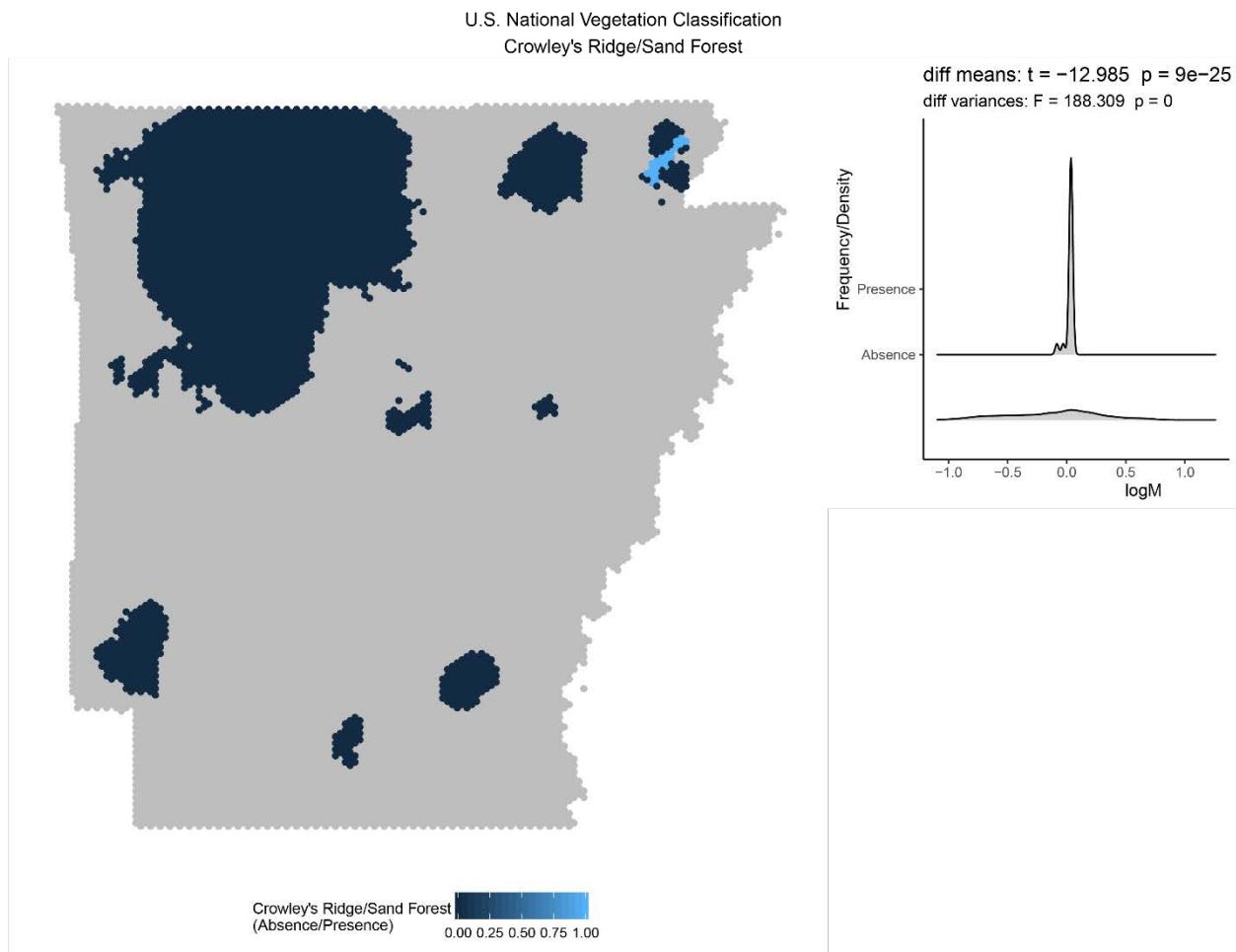


Figure A7-13: Distribution of **Crowley's Ridge/Sand Forest** across the state. The distributions of $\log M$ when this variable is present and absent are illustrated in the top right corner.

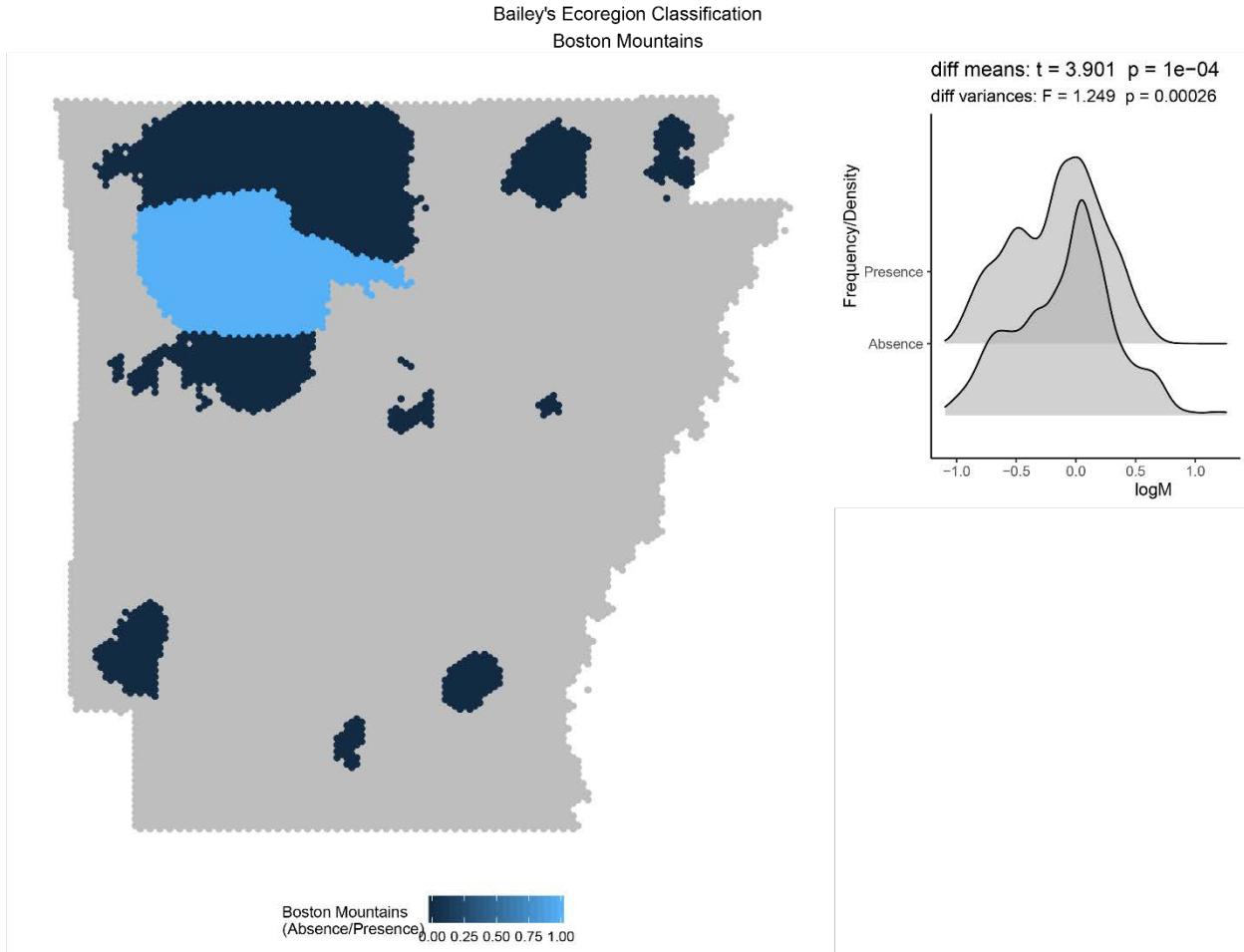


Figure A7-14: Distribution of the **Boston Mountains** across the state. The distributions of logM when this variable is present and absent are illustrated in the top right corner.

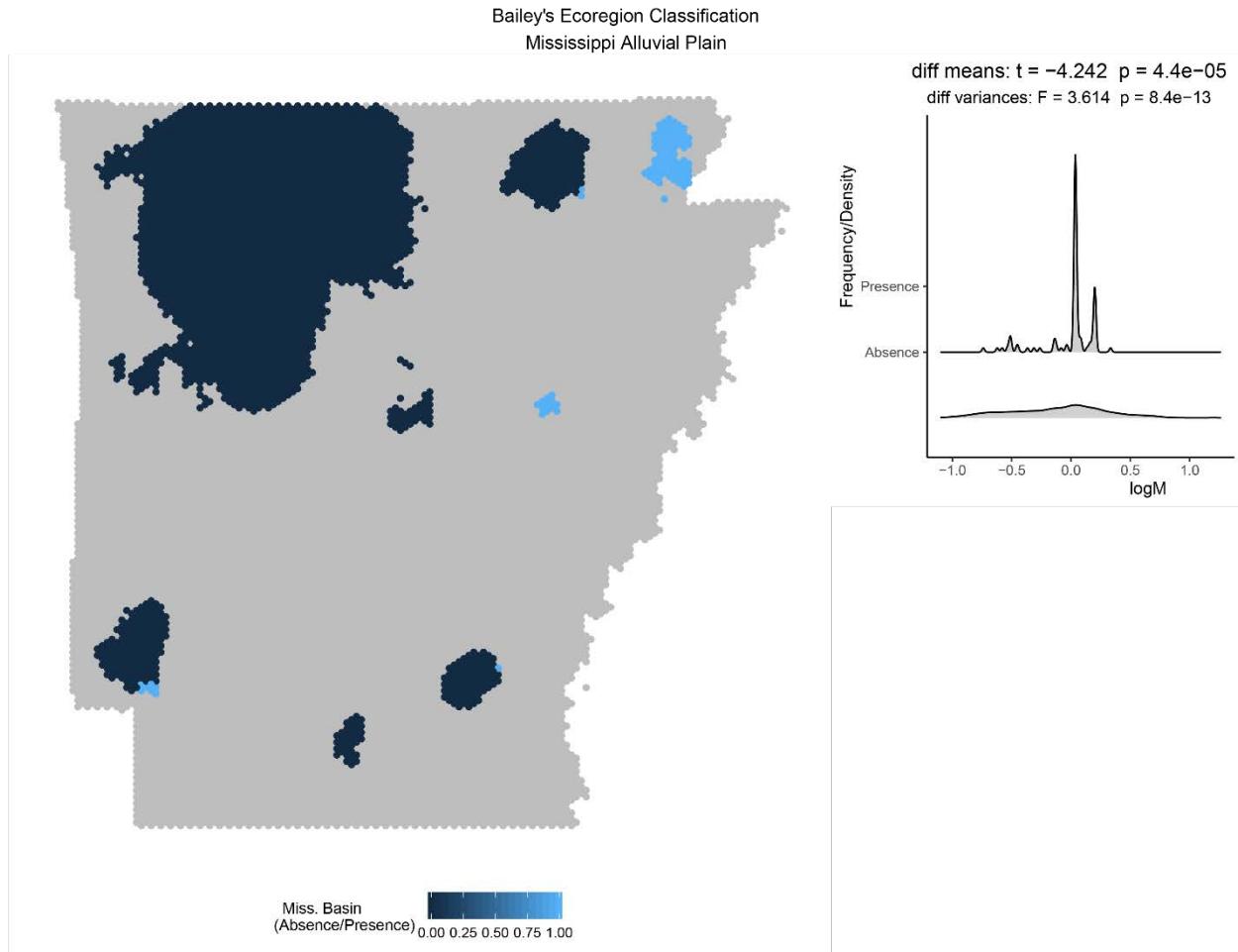


Figure A7-15: Distribution of the **Mississippi Alluvial Basin** across the state. The distributions of $\log M$ when this variable is present and absent are illustrated in the top right corner.

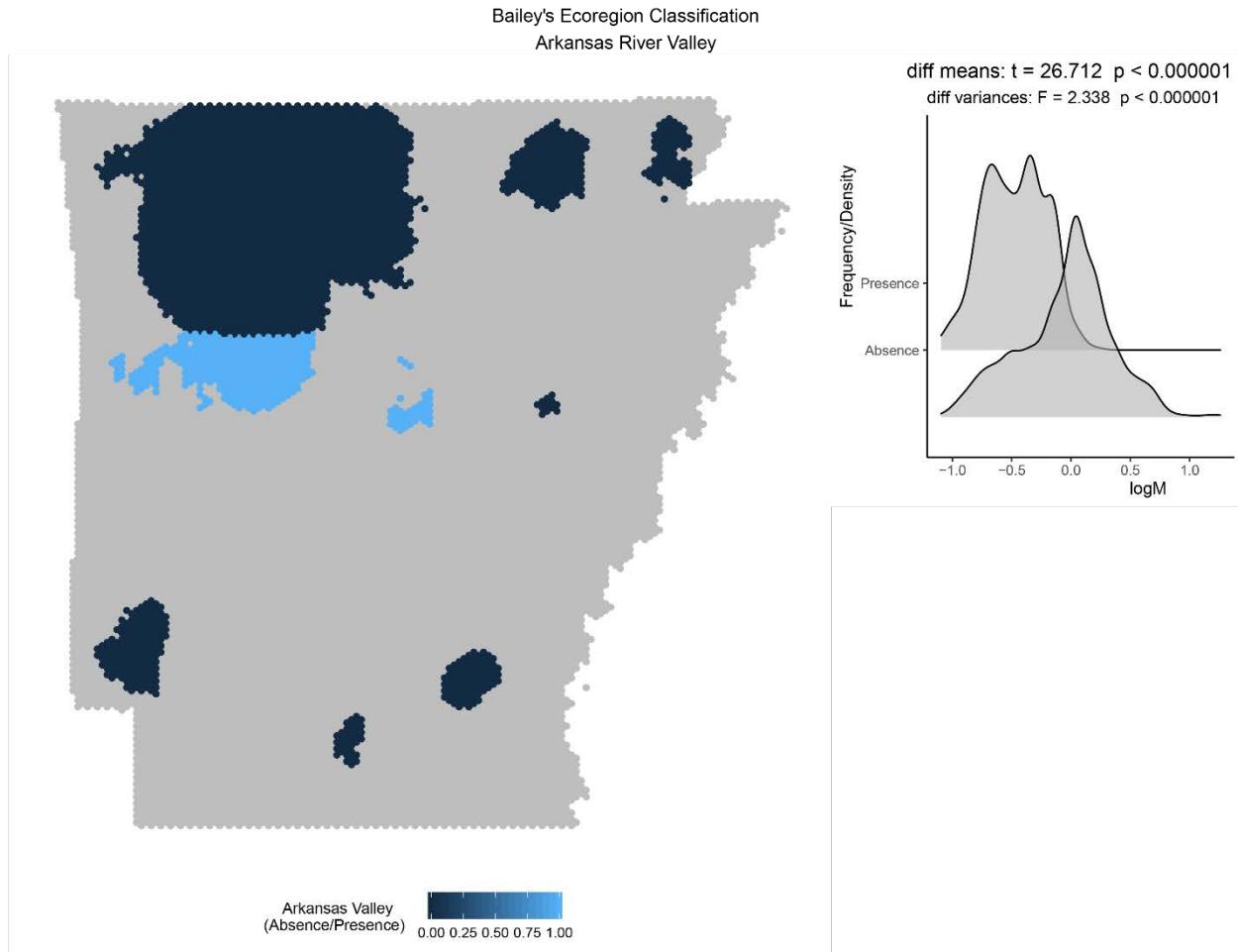


Figure A7-16: Distribution of the **Arkansas River Valley** across the state. The distributions of $\log M$ when this variable is present and absent are illustrated in the top right corner.

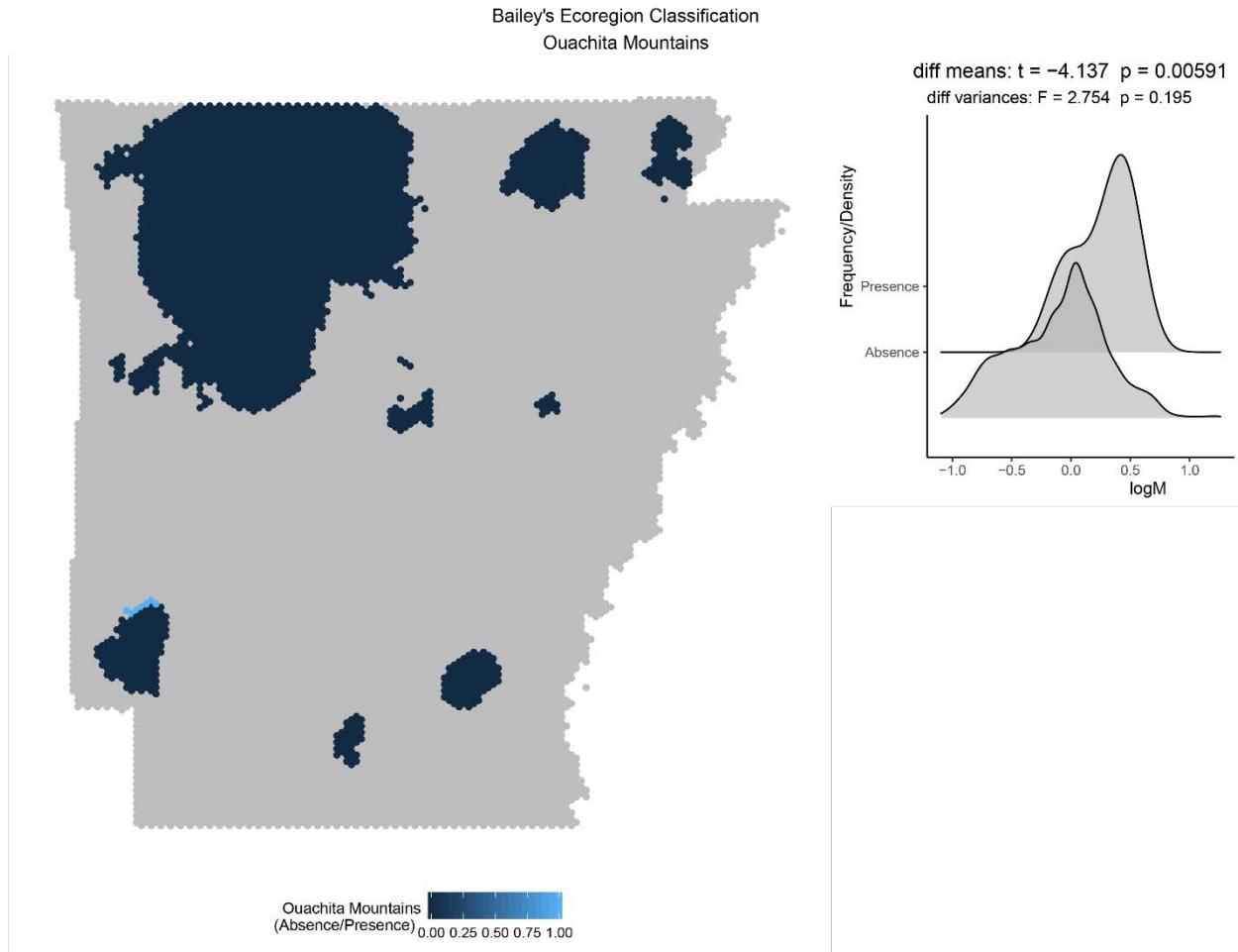


Figure A7-17: Distribution of the **Ouachita Mountains** across the state. The distributions of $\log M$ when this variable is present and absent are illustrated in the top right corner.

Supplemental Material

Table S1: Overview of 1,720 white-tailed deer tissue samples collected in 75 Arkansas counties from 2016-2019. Samples are listed alpha-numerically by DNA code (=DNA), and corresponding collection information is provided by referencing AGFC field/tissue number (=field.ID) and county. Listed is also the DNA extraction protocol number (=DNAex). Data columns indicate if samples was extracted (=Dx), and type of data generated: PRNP = sequences for *PRNP* gene, PSG = sequences for *PRNP^{PSG}* pseudogene; SNP = SNP/ddRAD data. '+' = data generation successful; '-' = data generation attempted, but unsuccessful. Samples without field.ID either lack a reference number or are cross-referenced with UTM coordinates in the original AGFC database.

AGFC field.ID	county	DNAex	DNA		Data			comments
			sp	loc	num	Dx	PRNP	
CWD-AR-18-0407	Arkansas	D1805-22	83	AR2N	001	+	+	+
CWD-AR-18-408	Arkansas	D1805-22	83	AR2N	002	+	+	-
CWD-AR-18-0409	Arkansas	D1805-22	83	AR2N	003	+	+	-
CWD-AR-18-411	Arkansas	D1805-22	83	AR2N	004	+	+	-
CWD-AR-18-0241B	Arkansas	D1805-22	83	AR2N	005	+	+	-
CWD-AR-000422	Arkansas	D1901-01	83	AR3N	006	+	+	-
CWD-AR-000324	Arkansas	D1901-01	83	AR3N	007	+	+	-
CWD-AR-18-01085	Arkansas	D1902-25	83	AR3U	008	+	+	-
CWD-AR-18-01086	Arkansas	D1902-25	83	AR3U	009	+	+	-
CWD-AR-18-01087	Arkansas	D1902-25	83	AR3U	010	+	+	+
CWD-AR-18-01217	Arkansas	D1902-25	83	AR3U	011	+	+	-
CWD-AR-18-164	Ashley	D1805-23	83	AS3N	001	+	+	+
CWD-AR-16-01585	Baxter	D1802-03	83	BA1N	001	+	+	-
CWD-AR-16-01571	Baxter	D1802-03	83	BA1N	002	+	+	-
CWD-AR-17-731	Baxter	D1805-24	83	BA2N	003	+	+	-
CWD-AR-17-15249	Baxter	D1805-24	83	BA2N	004	+	+	-
CWD-AR-17-15316	Baxter	D1805-24	83	BA2N	005	+	+	-
CWD-AR-17-15964	Baxter	D1805-24	83	BA2N	006	+	+	+
CWD-AR-17-15965	Baxter	D1805-24	83	BA2N	007	+	+	-
CWD-AR-18-239	Baxter	D1805-24	83	BA2N	008	+	+	-
CWD-AR-00-8476	Baxter	D1901-02	83	BA3N	009	+	+	-
CWD-AR-00-9016	Baxter	D1901-02	83	BA3N	010	+	+	+
CWD-AR-00-1503	Baxter	D1901-02	83	BA3N	011	+	+	+
CWD-AR-00-1528	Baxter	D1901-02	83	BA3N	012	+	+	+
CWD-AR-00-1536	Baxter	D1901-02	83	BA3N	013	+	+	+
CWD-AR-00-1537	Baxter	D1901-02	83	BA3N	014	+	+	-
CWD-AR-00-1539	Baxter	D1901-02	83	BA3N	015	+	+	-
CWD-AR-00-9001	Baxter	D1901-02	83	BA3N	016	+	+	-
CWD-AR-00-1526	Baxter	D1902-26	83	BA3N	017	+	+	+
CWD-AR-16-4532	Benton	D1802-03	83	BE1N	001	+	+	-
CWD-AR-16-5250	Benton	D1802-03	83	BE1N	002	+	+	-
CWD-AR-16-4528	Benton	D1802-03	83	BE1N	003	+	+	-
CWD-AR-16-00532	Benton	D1802-03	83	BE1N	004	+	+	+
CWD-AR-16-6925	Benton	D1802-03	83	BE1N	005	+	+	-
CWD-AR-16-5079	Benton	D1805-25	83	BE2N	006	+	+	+
CWD-AR-16-6935	Benton	D1805-25	83	BE2N	007	+	+	-
CWD-AR-16-6936	Benton	D1805-25	83	BE2N	008	+	+	-
CWD-AR-17-826	Benton	D1805-25	83	BE2N	009	+	+	-
CWD-AR-17-828	Benton	D1805-25	83	BE2N	010	+	+	+
CWD-AR-17-829	Benton	D1805-25	83	BE2N	011	+	+	+

CWD-AR-17-830	Benton	D1805-25	83	BE2N	012	+	+	+
CWD-AR-17-831	Benton	D1805-25	83	BE2N	013	+	+	-
CWD-AR-17-832	Benton	D1805-25	83	BE2N	014	+	+	+
CWD-AR-17-833	Benton	D1805-25	83	BE2N	015	+	+	+
CWD-AR-17-834	Benton	D1805-25	83	BE2N	016	+	+	-
CWD-AR-17-835	Benton	D1805-25	83	BE2N	017	+	+	+
CWD-AR-17-838	Benton	D1805-26	83	BE2N	018	+	+	-
CWD-AR-17-839	Benton	D1805-26	83	BE2N	019	+	+	-
CWD-AR-17-1342	Benton	D1805-26	83	BE2N	020	+	+	+
CWD-AR-17-1343	Benton	D1805-26	83	BE2N	021	+	+	-
CWD-AR-17-1344	Benton	D1805-26	83	BE2N	022	+	+	-
CWD-AR-17-1345	Benton	D1805-26	83	BE2N	023	+	+	-
CWD-AR-17-18638	Benton	D1805-26	83	BE2N	024	+	+	-
CWD-AR-17-4085	Benton	D1805-26	83	BE2N	025	+	+	+
CWD-AR-17-4086	Benton	D1805-26	83	BE2N	026	+	+	
CWD-AR-17-4114	Benton	D1805-26	83	BE2N	027	+	+	-
CWD-AR-17-4115	Benton	D1805-26	83	BE2N	028	+	+	-
CWD-AR-17-4117	Benton	D1805-26	83	BE2N	029	+	+	-
CWD-AR-17-4118	Benton	D1805-26	83	BE2N	030	+	+	-
CWD-AR-17-4120	Benton	D1805-26	83	BE2N	031	+		-
CWD-AR-17-4121	Benton	D1805-26	83	BE2N	032	+	+	-
CWD-AR-17-4122	Benton	D1805-26	83	BE2N	033	+	+	-
CWD-AR-17-4123	Benton	D1805-26	83	BE2N	034	+	+	-
CWD-AR-17-4492	Benton	D1805-26	83	BE2N	035	+	+	+
CWD-AR-17-4494	Benton	D1805-26	83	BE2N	036	+	+	-
CWD-AR-17-4497	Benton	D1805-26	83	BE2N	037	+	+	-
CWD-AR-17-4532	Benton	D1805-26	83	BE2N	038	+	+	-
CWD-AR-17-4533	Benton	D1805-26	83	BE2N	039	+		
CWD-AR-17-4534	Benton	D1805-26	83	BE2N	040	+		
CWD-AR-18-351	Benton	D1805-26	83	BE2N	041	+		
CWD-AR-18-352	Benton	D1805-27	83	BE2N	042	+	+	-
CWD-AR-18-320	Benton	D1805-28	83	BE3N	043	+		
CWD-AR-18-323	Benton	D1805-28	83	BE3N	044	+		
CWD-AR-18-324	Benton	D1805-28	83	BE3N	045	+		
CWD-AR-18-326	Benton	D1805-28	83	BE3N	046	+		
CWD-AR-18-327	Benton	D1805-28	83	BE3N	047	+		
CWD-AR-18-328	Benton	D1805-28	83	BE3N	048	+		
CWD-AR-18-332	Benton	D1805-28	83	BE3N	049	+	+	+
CWD-AR-18-333	Benton	D1805-28	83	BE3N	050	+		
CWD-AR-16-0066	Boone	D1701-02	83	BO1N	001	+	+	-
CWD-AR-16-0781	Boone	D1701-02	83	BO1N	002	+		
CWD-AR-16-0022	Boone	D1610-16	83	BO1N	003	+	+	+
CWD-AR-16-0024	Boone	D1610-16	83	BO1N	004	+	+	+
CWD-AR-16-0427	Boone	D1712-08	83	BO1N	005	+	+	+
CWD-AR-16-0591	Boone	D1712-08	83	BO1N	006	+	+	-
CWD-AR-16-0701	Boone	D1712-08	83	BO1N	007	+	+	+
CWD-AR-16-00004	Boone	D1712-08	83	BO1N	008	+	+	+
CWD-AR-16-01044	Boone	D1712-08	83	BO1N	009	+	+	-
CWD-AR-16-01305	Boone	D1712-08	83	BO1N	011	+	+	-
CWD-AR-16-01308	Boone	D1712-08	83	BO1N	012	+	+	+
CWD-AR-16-01311	Boone	D1712-08	83	BO1N	013	+	+	-
CWD-AR-16-01316	Boone	D1712-08	83	BO1N	014	+	+	+
CWD-AR-16-01317	Boone	D1712-08	83	BO1N	015	+	+	-
CWD-AR-16-01319	Boone	D1712-08	83	BO1N	016	+	+	-
CWD-AR-16-01573	Boone	D1712-08	83	BO1N	017	+	+	+
CWD-AR-16-01574	Boone	D1712-08	83	BO1N	018	+	+	-
CWD-AR-16-02344	Boone	D1712-08	83	BO1N	019	+	+	-
CWD-AR-16-02346	Boone	D1712-08	83	BO1N	020	+	+	-
CWD-AR-16-02629	Boone	D1712-08	83	BO1N	021	+	+	+

CWD-AR-16-00000	Boone	D1712-08	83	BO1N	022	+	+	+	+
CWD-AR-16-02343	Boone	D1712-08	83	BO1N	023	+	+	-	+
CWD-AR-17-12650	Boone	D1805-29	83	BO2N	024	+			
CWD-AR-17-12651	Boone	D1805-29	83	BO2N	025	+	+	+	+
CWD-AR-17-12657	Boone	D1805-29	83	BO2N	026	+	+	-	+
CWD-AR-17-12658	Boone	D1805-29	83	BO2N	027	+			
CWD-AR-17-14541	Boone	D1805-29	83	BO2N	028	+	+	-	+
CWD-AR-17-14844	Boone	D1805-29	83	BO2N	029	+	+	+	+
CWD-AR-17-14847	Boone	D1805-29	83	BO2N	030	+	+	-	+
CWD-AR-17-14848	Boone	D1805-29	83	BO2N	031	+			
CWD-AR-17-14849	Boone	D1805-29	83	BO2N	032	+			
CWD-AR-17-14850	Boone	D1805-29	83	BO2N	033	+	+	-	+
CWD-AR-17-14864	Boone	D1805-29	83	BO2N	034	+	+	-	+
CWD-AR-17-15940	Boone	D1805-29	83	BO2N	035	+			
CWD-AR-17-15942	Boone	D1805-29	83	BO2N	036	+			
CWD-AR-17-15946	Boone	D1805-29	83	BO2N	037	+			
CWD-AR-17-15947	Boone	D1805-29	83	BO2N	038	+			
CWD-AR-17-15950	Boone	D1806-01	83	BO2N	039	+			
CWD-AR-17-15952	Boone	D1806-01	83	BO2N	040	+	+	-	+
CWD-AR-17-15953	Boone	D1806-01	83	BO2N	041	+			
CWD-AR-17-15954	Boone	D1806-01	83	BO2N	042	+			
CWD-AR-17-15955	Boone	D1806-01	83	BO2N	043	+			
CWD-AR-17-15956	Boone	D1806-01	83	BO2N	044	+			
CWD-AR-17-15957	Boone	D1806-01	83	BO2N	045	+			
CWD-AR-17-15958	Boone	D1806-01	83	BO2N	046	+			
CWD-AR-17-15962	Boone	D1806-01	83	BO2N	047	+			
CWD-AR-17-15963	Boone	D1806-01	83	BO2N	048	+			
CWD-AR-17-15967	Boone	D1806-01	83	BO2N	049	+			
CWD-AR-17-15968	Boone	D1806-01	83	BO2N	050	+			
CWD-AR-17-15970	Boone	D1806-01	83	BO2N	051	+			
CWD-AR-17-15971	Boone	D1806-01	83	BO2N	052	+			
CWD-AR-17-15972	Boone	D1806-01	83	BO2N	053	+	+	+	+
CWD-AR-17-15974	Boone	D1806-01	83	BO2N	054	+			
CWD-AR-17-15976	Boone	D1806-01	83	BO2N	055	+			
CWD-AR-17-15978	Boone	D1806-01	83	BO2N	056	+			
CWD-AR-17-15979	Boone	D1806-01	83	BO2N	057	+			
CWD-AR-17-15989	Boone	D1806-01	83	BO2N	058	+			
CWD-AR-17-15990	Boone	D1806-01	83	BO2N	059	+			
CWD-AR-17-15996	Boone	D1806-01	83	BO2N	060	+			
CWD-AR-17-15997	Boone	D1806-01	83	BO2N	061	+			
CWD-AR-17-15999	Boone	D1806-01	83	BO2N	062	+	+	-	+
CWD-AR-17-16000	Boone	D1806-02	83	BO2N	063	+	+	-	+
CWD-AR-17-16001	Boone	D1806-02	83	BO2N	064	+			
CWD-AR-17-16016	Boone	D1806-02	83	BO2N	065	+			
CWD-AR-17-12463	Boone	D1807-07	83	BO2P	066	+	+	-	+
CWD-AR-17-14545	Boone	D1807-07	83	BO2P	067	+	+	+	+
CWD-AR-18-0430	Bradley	D1901-04	83	BR3N	001	+	+	-	+
CWD-AR-18-0431	Bradley	D1901-04	83	BR3N	002	+	+	+	+
CWD-AR-16-0064	Carroll	D1701-01	83	CA1N	001	+	+	-	+
CWD-AR-16-0065	Carroll	D1701-01	83	CA1N	002	+	+	-	+
CWD-AR-16-7226	Carroll	D1712-08	83	CA1N	003	+	+	-	+
CWD-AR-16-00001	Carroll	D1712-08	83	CA1N	004	+	+	+	+
CWD-AR-16-00008	Carroll	D1712-08	83	CA1N	005	+	+	-	+
CWD-AR-16-00260	Carroll	D1712-08	83	CA1N	006	+	+	+	+
CWD-AR-16-00262	Carroll	D1712-08	83	CA1N	007	+	+	-	+
CWD-AR-16-00264	Carroll	D1712-09	83	CA1N	008	+	+	-	+
CWD-AR-16-00265	Carroll	D1712-09	83	CA1N	009	+	+	+	+
CWD-AR-16-00266	Carroll	D1712-09	83	CA1N	010	+	+	-	+
CWD-AR-16-00268	Carroll	D1712-09	83	CA1N	011	+	+	+	+

CWD-AR-16-00269	Carroll	D1712-09	83	CA1N	012	+	+	+	+
CWD-AR-16-00270	Carroll	D1712-09	83	CA1N	013	+	+	-	+
CWD-AR-16-00271	Carroll	D1712-09	83	CA1N	014	+	+	-	+
CWD-AR-16-00272	Carroll	D1712-09	83	CA1N	015	+	+	+	+
CWD-AR-16-00273	Carroll	D1712-09	83	CA1N	016	+	+	-	+
CWD-AR-16-00274	Carroll	D1712-09	83	CA1N	017	+	+	-	+
CWD-AR-16-4539	Carroll	D1712-09	83	CA1N	018	+	+	-	+
CWD-AR-16-4540	Carroll	D1712-09	83	CA1N	019	+	+	-	+
CWD-AR-16-4541	Carroll	D1712-09	83	CA1N	020	+	+	-	+
CWD-AR-16-00261	Carroll	D1712-09	83	CA1N	021	+	+	-	+
CWD-AR-16-00275	Carroll	D1712-09	83	CA1N	022	+	+	-	+
CWD-AR-16-00276	Carroll	D1712-09	83	CA1N	023	+	+	-	+
CWD-AR-16-00263	Carroll	D1712-09	83	CA1N	024	+	+	-	+
CWD-AR-16-00002	Carroll	D1712-07	83	CA1P	001	+	+	-	+
CWD-AR-16-00003	Carroll	D1712-07	83	CA1P	002	+	+	+	+
CWD-AR-16-00006	Carroll	D1712-07	83	CA1P	003	+	+	-	+
CWD-AR-16-00007	Carroll	D1712-07	83	CA1P	004	+	+	-	+
CWD-AR-16-00009	Carroll	D1712-07	83	CA1P	005	+	+	+	+
CWD-AR-16-00267	Carroll	D1712-07	83	CA1P	006	+	+	+	+
CWD-AR-16-00277	Carroll	D1712-07	83	CA1P	007	+	+	+	+
CWD-AR-16-00278	Carroll	D1712-07	83	CA1P	008	+	+	-	+
CWD-AR-17-12459	Carroll	D1806-03	83	CA2N	025	+			
CWD-AR-17-12461	Carroll	D1806-03	83	CA2N	026	+			
CWD-AR-17-12478	Carroll	D1806-03	83	CA2N	027	+			
CWD-AR-17-12479	Carroll	D1806-03	83	CA2N	028	+			
CWD-AR-17-12541	Carroll	D1806-03	83	CA2N	029	+			
CWD-AR-17-12640	Carroll	D1806-03	83	CA2N	030	+			
CWD-AR-17-12641	Carroll	D1806-03	83	CA2N	031	+			
CWD-AR-17-12642	Carroll	D1806-03	83	CA2N	032	+	+	-	+
CWD-AR-17-12643	Carroll	D1806-03	83	CA2N	033	+			
CWD-AR-17-12644	Carroll	D1806-03	83	CA2N	034	+			
CWD-AR-17-12645	Carroll	D1806-03	83	CA2N	035	+			
CWD-AR-17-12646	Carroll	D1806-03	83	CA2N	036	+	+	-	+
CWD-AR-17-12647	Carroll	D1806-03	83	CA2N	037	+			
CWD-AR-17-12648	Carroll	D1806-03	83	CA2N	038	+			
CWD-AR-17-12649	Carroll	D1806-03	83	CA2N	039	+	+	-	+
CWD-AR-17-12652	Carroll	D1806-03	83	CA2N	040	+	+	-	+
CWD-AR-17-12653	Carroll	D1806-03	83	CA2N	041	+	+	-	+
CWD-AR-17-12655	Carroll	D1806-03	83	CA2N	042	+	+	-	+
CWD-AR-17-12656	Carroll	D1806-03	83	CA2N	043	+			
CWD-AR-17-12659	Carroll	D1806-03	83	CA2N	044	+			
CWD-AR-17-12662	Carroll	D1806-03	83	CA2N	045	+	+	+	+
CWD-AR-17-12663	Carroll	D1806-04	83	CA2N	046	+	+	+	+
CWD-AR-17-12667	Carroll	D1806-04	83	CA2N	047	+			
CWD-AR-17-12978	Carroll	D1806-04	83	CA2N	048	+			
CWD-AR-17-13196	Carroll	D1806-04	83	CA2N	049	+	+	+	+
CWD-AR-17-12441	Carroll	D1807-11	83	CA2N	052	+			
CWD-AR-17-12442	Carroll	D1807-11	83	CA2N	053	+			
CWD-AR-17-12654	Carroll	D1807-11	83	CA2N	054	+			
CWD-AR-17-12445	Carroll	D1807-08	83	CA2P	051	+	+	-	+
CWD-AR-17-12455	Carroll	D1807-08	83	CA2P	055	+	+	-	+
CWD-AR-17-12457	Carroll	D1807-08	83	CA2P	056	+	+	-	+
CWD-AR-17-12458	Carroll	D1807-08	83	CA2P	057	+	+	-	+
CWD-AR-17-12462	Carroll	D1807-08	83	CA2P	058	+	+	+	+
CWD-AR-17-12665	Carroll	D1807-08	83	CA2P	059	+	+	-	+
CWD-AR-17-14855	Carroll	D1807-08	83	CA2P	060	+	+	+	+
CWD-AR-17-15975	Carroll	D1807-08	83	CA2P	061	+	+	+	+
CWD-AR-18-321	Carroll	D1806-05	83	CA3N	050	+			
	Calhoun	D1901-05	83	CA3U	062	+	+	-	+

	Calhoun	D1901-05	83	CA3U	063	+	+	-	+
	Calhoun	D1901-05	83	CA3U	064	+			
	Calhoun	D1901-05	83	CA3U	065	+	+	+	+
CWD-AR-18-01469	Calhoun	D1901-05	83	CA3U	066	+	+	-	+
	Calhoun	D1901-05	83	CA3U	067	+	+	+	+
	Calhoun	D1901-05	83	CA3U	068	+	+	-	+
	Calhoun	D1901-05	83	CA3U	069	+	+	-	+
	Calhoun	D1901-05	83	CA3U	070	+	+	-	+
	Calhoun	D1901-05	83	CA3U	071	+	+	-	+
	Calhoun	D1901-05	83	CA3U	072	+	+	-	+
	Calhoun	D1901-05	83	CA3U	073	+	+	-	+
	Calhoun	D1901-06	83	CA3U	074	+	+	-	+
	Calhoun	D1901-06	83	CA3U	075	+	+	-	+
	Calhoun	D1901-06	83	CA3U	076	+	+	-	+
CWD-AR-17-18598	Cleburne	D1806-08a	83	CB2N	001	+	+	+	+
CWD-AR-18-8	Cleburne	D1806-08a	83	CB2N	002	+	+	-	+
CWD-AR-18-9	Cleburne	D1806-08a	83	CB2N	003	+	+	-	+
CWD-AR-18-12	Cleburne	D1806-08a	83	CB2N	004	+	+	-	+
CWD-AR-18-14	Cleburne	D1806-08a	83	CB2N	005	+	+	+	+
CWD-AR-18-15	Cleburne	D1806-08a	83	CB2N	006	+	+	-	+
CWD-AR-18-16	Cleburne	D1806-08a	83	CB2N	007	+	+	-	+
CWD-AR-18-646	Cleburne	D1806-08a	83	CB2N	008	+	+	+	+
CWD-AR-18-0207HC	Cleburne	D1807-03	83	CB2N	009	+			
CWD-AR-18-0208HC	Cleburne	D1807-03	83	CB2N	010	+			
CWD-AR-17-426	Chicot	D1806-06	83	CH2N	001	+	+	+	+
CWD-AR-17-0028	Chicot	D1806-06	83	CH2N	002	+	+	-	+
CWD-AR-18-165	Chicot	D1806-07	83	CH3N	003	+	+	-	+
CWD-AR-18-166	Chicot	D1806-07	83	CH3N	004	+	+	-	+
CWD-AR-18-0526HC	Clark	D1807-04	83	CK2N	001	+		+	should be CL
CWD-AR-18-453	Cleveland	D1806-08b	83	CL2N	001	+	+	-	+
CWD-AR-18-455	Cleveland	D1806-08b	83	CL2N	002	+	-	-	+
CWD-AR-18-456	Cleveland	D1806-08b	83	CL2N	003	+	+	+	should be CV
CWD-AR-18-245HC	Cleveland	D1807-05	83	CL2N	007	+			should be CV
CWD-AR-18-15998	Cleveland	D1807-05	83	CL2N	008	+			should be CV
CWD-AR-18-84	Cleveland	D1806-09	83	CL3N	004	+	+	+	should be CV
CWD-AR-18-161	Cleveland	D1806-09	83	CL3N	005	+	+		should be CV
CWD-AR-18-162	Cleveland	D1806-09	83	CL3N	006	+	+	+	should be CV
CWD-AR-00-0884	Clark	D1901-08	83	CL3N	010	+	+	-	+
CWD-AR-00-1280	Clark	D1901-08	83	CL3N	011	+	+	-	+
CWD-AR-00-1336	Clark	D1901-08	83	CL3N	012	+	+	-	+
UTM	Clark	D1901-08	83	CL3N	013	+	+	-	should be CL3U?
UTM	Clark	D1901-08	83	CL3N	014	+	+	-	should be CL3U?
UTM	Clark	D1901-07	83	CL3U	009	+	+	-	+
CWD-AR-00-0862	Clark	D1902-14	83	CL3U	015	+	+	-	+
CWD-AR-00-0862	Clark	D1902-30	83	CL3U	016	+	+	-	+
CWD-AR-16-06285	Conway	D1802-03	83	CN1N	001	+	+	-	+
CWD-AR-16-05253	Conway	D1802-03	83	CN1N	002	+	+	-	+
CWD-AR-16-6731	Conway	D1802-03	83	CN1N	003	+	+	-	+
CWD-AR-17-19691	Conway	D1806-10	83	CN2N	004	+	+	-	+
CWD-AR-17-19973	Conway	D1806-11	83	CN2N	005	+	+	-	+
CWD-AR-18-106	Conway	D1806-11	83	CN2N	006	+	+	-	+
CWD-AR-18-203B	Conway	D1807-06	83	CN2N	011	+			
CWD-AR-18-204B	Conway	D1807-06	83	CN2N	012	+			
CWD-AR-18-205B	Conway	D1807-06	83	CN2N	013	+			
CWD-AR-18-206B	Conway	D1807-06	83	CN2N	014	+			
CWD-AR-18-207B	Conway	D1807-12	83	CN2N	015	+			
CWD-AR-18-208B	Conway	D1807-12	83	CN2N	016	+			
CWD-AR-18-209B	Conway	D1807-12	83	CN2N	017	+			
CWD-AR-18-210B	Conway	D1807-12	83	CN2N	018	+			

CWD-AR-18-501B	Conway	D1807-12	83	CN2N	019	+				
CWD-AR-18-200	Conway	D1806-12	83	CN3N	007	+	+	+	+	+
CWD-AR-18-486	Conway	D1806-12	83	CN3N	008	+	+	+	+	+
CWD-AR-18-497	Conway	D1806-12	83	CN3N	009	+	+	+	+	+
CWD-AR-18-500	Conway	D1806-12	83	CN3N	010	+	+	-	+	+
CWD-AR-00-0845	Columbia	D1901-11	83	CO3N	001	+	+	-	+	+
CWD-AR-00-0846	Columbia	D1901-11	83	CO3N	002	+	+	-	+	+
	Columbia	D1902-27	83	CO3U	003	+	+	-	+	+
	Columbia	D1902-27	83	CO3U	004	+	+	-	+	+
CWD-AR-16-6821	Craighead		83	CR1N	001					
CWD-AR-18-581	Craighead	D1806-13	83	CR2N	002	+	+	-	+	+
CWD-AR-18-01347	Craighead	D1901-13	83	CR3N	003	+	+	+	+	+
CWD-AR-00-0583	Craighead	D1901-13	83	CR3N	004	+	+	+	+	+
CWD-AR-00-0584	Craighead	D1901-13	83	CR3N	005	+	+	-	+	+
CWD-AR-00-0621	Craighead	D1901-13	83	CR3N	006	+	+	-	+	+
CWD-AR-00-0622	Craighead	D1901-13	83	CR3N	007	+	+	-	+	+
CWD-AR-18-01343	Craighead	D1901-13	83	CR3N	009	+	+	-	+	+
CWD-AR-18-01344	Craighead	D1901-13	83	CR3N	010	+	+	-	+	+
CWD-AR-18-01346	Craighead	D1901-13	83	CR3N	011	+	+	-	+	+
CWD-AR-00-0661	Craighead	D1902-29	83	CR3N	013	+	+	-	+	+
CWD-AR-00-0772	Craighead	D1902-29	83	CR3N	014	+	+	-	+	+
	Craighead	D1902-31	83	CR3U	015	+	+	-	+	+
CWD-AR-18-633	Cross	D1806-14	83	CS2N	001	+	+	+	+	+
CWD-AR-18-655	Cross	D1806-14	83	CS2N	002	+	+	+	+	+
CWD-AR-18-700	Cross	D1806-14	83	CS2N	003	+	+	-	+	+
	Cross	D1901-15	83	CS3N	004	+	+	-	+	+
CWD-AR-00-0582	Cross	D1901-15	83	CS3N	005	+	+	-	+	+
	Cross	D1901-15	83	CS3N	006	+	+	+	+	+
	Cross	D1901-15	83	CS3N	007	+	+	-	+	+
	Cross	D1901-15	83	CS3N	008	+	+	-	+	+
CWD-AR-1801350	Cross	D1902-22	83	CS3U	009	+	+	+	+	+
CWD-AR-18-662	Crittenden	D1806-15	83	CT2N	001	+	+	-	+	+
CWD-AR-18-674	Crittenden	D1806-15	83	CT2N	002	+	+	-	+	+
CWD-AR-18-675	Crittenden	D1806-15	83	CT2N	003	+	+	+	+	+
CWD-AR-18-676	Crittenden	D1806-15	83	CT2N	004	+	+	-	+	+
CWD-AR-18-699	Crittenden	D1806-15	83	CT2N	005	+	+	-	+	+
CWD-AR-000302	Crittenden	D1902-32	83	CT3N	006	+	+	-	+	+
CWD-AR-000303	Crittenden	D1902-32	83	CT3N	007	+	+	-	+	+
CWD-AR-007686	Crittenden	D1902-32	83	CT3N	008	+	+	-	+	+
CWD-AR-18-827	Crawford	D1806-16	83	CW2N	001	+	+	-	+	+
CWD-AR-18-829	Crawford	D1806-16	83	CW2N	002	+	+	+	+	+
CWD-AR-18-902	Crawford	D1806-16	83	CW2N	003	+	+	-	+	+
CWD-AR-18-903	Crawford	D1806-16	83	CW2N	004	+	+	+	+	+
CWD-AR-18-907	Crawford	D1806-16	83	CW2N	005	+	+	-	+	+
CWD-AR-18-909	Crawford	D1806-16	83	CW2N	006	+	+	+	+	+
CWD-AR-00-1461	Crawford	D1901-14	83	CW3N	007	+	+	+	+	+
CWD-AR-00-1464	Crawford	D1901-14	83	CW3N	008	+	+	-	+	+
CWD-AR-00-1468	Crawford	D1901-14	83	CW3N	009	+	+	+	+	+
CWD-AR-00-0641	Clay	D1901-10	83	CY3N	002	+	+	-	+	+
CWD-AR-00-0642	Clay	D1902-28	83	CY3N	003	+	+	+	+	+
UTM	Clay	D1901-09	83	CY3U	001	+	+	+	+	+
UTM	Clay	D1902-28	83	CY3U	004	+	+	-	+	+
UTM	Clay	D1902-28	83	CY3U	005	+	+	+	+	+
UTM	Clay	D1902-28	83	CY3U	006	+	+	+	+	+
UTM	Clay	D1902-28	83	CY3U	007	+	+	-	+	+
UTM	Clay	D1902-28	83	CY3U	008	+	+	+	+	+
UTM	Clay	D1902-28	83	CY3U	009	+	+	+	+	+
UTM	Clay	D1902-28	83	CY3U	010	+	+	+	+	+
UTM	Clay	D1902-28	83	CY3U	011	+	+	-	+	+

UTM	Clay	D1902-28	83	CY3U	012	+	+	+	+
UTM	Clay	D1902-28	83	CY3U	013	+	+	-	+
UTM	Clay	D1902-28	83	CY3U	014	+	+	+	+
CWD-AR-18-86	Dallas	D1806-17	83	DL3N	001	+	+	-	+
CWD-AR-18-87	Dallas	D1806-17	83	DL3N	002	+	+	+	+
CWD-AR-18-88	Dallas	D1806-17	83	DL3N	003	+	+	-	+
CWD-AR-18-89	Dallas	D1806-18	83	DL3N	004	+	+	-	+
	Dallas	D1901-16	83	DL3N	005	+	+	-	+
CWD-AR-18-	Dallas	D1901-16	83	DL3N	006	+	+	-	+
CWD-AR-00-0851	Dallas	D1902-16	83	DL3N	007	+	+	-	+
CWD-AR-00-0852	Dallas	D1902-33	83	DL3N	008	+	+	+	+
CWD-AR-18-01533	Dallas	D1902-33	83	DL3N	009	+	+	-	+
CWD-AR-16-4440	Drew	D1802-04	83	DR1N	001	+	+	+	+
CWD-AR-16-4443	Drew	D1802-04	83	DR1N	002	+	+	+	+
CWD-AR-18-427	Drew	D1806-19	83	DR2N	003	+	+	-	+
CWD-AR-18-428	Drew	D1806-19	83	DR2N	004	+	+	+	+
CWD-AR-18-429	Drew	D1806-19	83	DR2N	005	+	+	-	+
CWD-AR-18-454	Drew	D1806-19	83	DR2N	006	+	+	-	+
CWD-AR-18-160	Drew	D1806-20	83	DR3N	007	+	+	+	+
CWD-AR-18-163	Drew	D1806-20	83	DR3N	008	+	+	-	+
CWD-AR-18-243	Drew	D1806-20	83	DR3N	009	+	+	-	+
CWD-AR-18-240B	Drew	D1807-13	83	DR3N	010	+			
CWD-AR-18-242B	Drew	D1807-13	83	DR3N	011	+			
CWD-AR-18-01083	Drew	D1901-18	83	DR3N	012	+	+	-	+
CWD-AR-00-0402	Drew	D1901-18	83	DR3N	013	+	+	-	+
CWD-AR-00-6902	Drew	D1902-11	83	DR3N	016	+	+	-	+
CWD-AR-18-1828	Drew	D1901-18	83	DR3U	014	+	+	-	+
CWD-AR-18-1829	Drew	D1901-18	83	DR3U	015	+	+	-	+
CWD-AR-18-376	Desha	D1806-21	83	DS2N	001	+	+	-	+
CWD-AR-18-391	Desha	D1806-21	83	DS2N	002	+	+	-	+
CWD-AR-18-392	Desha	D1806-21	83	DS2N	003	+	+	-	+
CWD-AR-18-0393	Desha	D1901-17	83	DS3N	004	+	+	-	+
CWD-AR-00-7041	Desha	D1902-34	83	DS3N	012	+	+	+	+
CWD-AR-00-0405	Desha	D1902-13	83	DS3U	005	+	+	-	+
CWD-AR-00-0406	Desha	D1902-13	83	DS3U	006	+	+	-	+
CWD-AR-00-0404	Desha	D1902-13	83	DS3U	007	+	+	-	+
CWD-AR-00-0408	Desha	D1902-13	83	DS3U	008	+	+	+	+
CWD-AR-00-0407	Desha	D1902-13	83	DS3U	009	+	+	-	+
CWD-AR-00-0410	Desha	D1902-13	83	DS3U	010	+	+	-	+
CWD-AR-00-0409	Desha	D1902-13	83	DS3U	011	+	+	-	+
CWD-AR-17-18545	Faulkner	D1806-22	83	FA2N	001	+			
CWD-AR-18-3	Faulkner	D1806-22	83	FA2N	002	+	+	-	+
CWD-AR-18-4	Faulkner	D1806-22	83	FA2N	003	+			
CWD-AR-18-5	Faulkner	D1806-22	83	FA2N	004	+	+	-	+
CWD-AR-18-7	Faulkner	D1806-22	83	FA2N	005	+	+	+	+
CWD-AR-18-10	Faulkner	D1806-22	83	FA2N	006	+			
CWD-AR-18-11	Faulkner	D1806-22	83	FA2N	007	+	+	-	+
CWD-AR-18-13	Faulkner	D1806-22	83	FA2N	008	+	+	-	+
CWD-AR-18-17	Faulkner	D1806-22	83	FA2N	009	+	+	+	+
CWD-AR-18-0201HC	Faulkner	D1806-22	83	FA2N	010	+			
CWD-AR-18-0202HC	Faulkner	D1806-22	83	FA2N	011	+	+	-	+
CWD-AR-18-0209HC	Faulkner	D1806-22	83	FA2N	012	+	+	-	+
CWD-AR-18-0211HC	Faulkner	D1806-22	83	FA2N	013	+	+	-	+
CWD-AR-18-0526B	Faulkner	D1807-14	83	FA2N	021	+			
CWD-AR-18-0644B	Faulkner	D1807-14	83	FA2N	022	+			
CWD-AR-18-483	Faulkner	D1806-23	83	FA3N	014	+	+	+	+
CWD-AR-18-487	Faulkner	D1806-23	83	FA3N	015	+	+	-	+
CWD-AR-18-488	Faulkner	D1806-23	83	FA3N	016	+	+	-	+
CWD-AR-18-492	Faulkner	D1806-23	83	FA3N	017	+	+	-	+

CWD-AR-18-496	Faulkner	D1806-23	83	FA3N	018	+				
CWD-AR-18-498	Faulkner	D1806-23	83	FA3N	019	+				
CWD-AR-18-499	Faulkner	D1806-23	83	FA3N	020	+	+	+	+	+
CWD-AR-16-03951	Franklin	D1802-04	83	FR1N	001	+	+	+	+	+
CWD-AR-16-03950	Franklin	D1802-04	83	FR1N	002	+	+	-	+	
CWD-AR-16-03952	Franklin	D1802-04	83	FR1N	003	+	+	-	+	
CWD-AR-17-1347	Franklin	D1806-24	83	FR2N	004	+	+	+	+	+
CWD-AR-17-23900	Franklin	D1806-24	83	FR2N	005	+	+	+		
CWD-AR-17-23901	Franklin	D1806-24	83	FR2N	006	+	+	+	+	
CWD-AR-17-23903	Franklin	D1806-24	83	FR2N	007	+	+	-		
CWD-AR-17-23904	Franklin	D1806-24	83	FR2N	008	+	+	-	+	
CWD-AR-17-23905	Franklin	D1806-24	83	FR2N	009	+	+	-		
CWD-AR-17-23906	Franklin	D1806-24	83	FR2N	010	+	+	-	+	
CWD-AR-17-23907	Franklin	D1806-24	83	FR2N	011	+	+	-	+	
CWD-AR-17-23909	Franklin	D1806-24	83	FR2N	012	+	+	-		
CWD-AR-17-23910	Franklin	D1806-24	83	FR2N	013	+	+	+		
CWD-AR-17-23911	Franklin	D1806-24	83	FR2N	014	+	+	-	+	
CWD-AR-17-23912	Franklin	D1806-24	83	FR2N	015	+	+	+	+	
CWD-AR-17-23913	Franklin	D1806-24	83	FR2N	016	+	+	+	+	
CWD-AR-17-23915	Franklin	D1806-24	83	FR2N	017	+	+	-	+	
CWD-AR-17-23918	Franklin	D1806-24	83	FR2N	018	+	+	-	+	
CWD-AR-17-24040	Franklin	D1806-24	83	FR2N	019	+	+	-	+	
CWD-AR-17-24041	Franklin	D1806-24	83	FR2N	020	+	+	+	+	
CWD-AR-17-24042	Franklin	D1806-25	83	FR2N	021	+	+	-	+	
CWD-AR-17-24043	Franklin	D1806-25	83	FR2N	022	+	+	+		
CWD-AR-17-24044	Franklin	D1806-25	83	FR2N	023	+	+	-		
CWD-AR-17-24045	Franklin	D1806-25	83	FR2N	024	+	+	-	+	
CWD-AR-17-24046	Franklin	D1806-25	83	FR2N	025	+	+	-		
CWD-AR-17-24047	Franklin	D1806-25	83	FR2N	026	+	+	-	+	
CWD-AR-17-24048	Franklin	D1806-25	83	FR2N	027	+	+	-		
CWD-AR-17-24049	Franklin	D1806-25	83	FR2N	028	+	+	-	+	
CWD-AR-17-24050	Franklin	D1806-25	83	FR2N	029	+	+	-		
CWD-AR-18-828	Franklin	D1806-25	83	FR2N	030	+	+	-		
CWD-AR-18-834	Franklin	D1806-25	83	FR2N	031	+	+	-		
CWD-AR-18-904	Franklin	D1806-25	83	FR2N	032	+	+	-		
CWD-AR-18-1076	Franklin	D1806-25	83	FR2N	033	+	+	-	+	
CWD-T021-AR-170015	Franklin	D1806-25	83	FR2N	034	+	-	-		
CWD-AR-17-19700	Fulton	D1806-26	83	FU2N	001	+	+	+	+	
CWD-AR-17-19703	Fulton	D1806-26	83	FU2N	002	+	+	-	+	
CWD-AR-18-154	Fulton	D1806-26	83	FU2N	003	+	-	-	+	
CWD-AR-18-155	Fulton	D1806-26	83	FU2N	004	+	+	+	+	
CWD-AR-18-177	Fulton	D1806-26	83	FU2N	005	+	+	-	+	
CWD-AR-18-179	Fulton	D1806-26	83	FU2N	006	+	+	-	+	
CWD-AR-00-1342	Fulton	D1901-19	83	FU3N	007	+	+	-	+	
CWD-AR-18-01345	Fulton	D1901-19	83	FU3N	008	+	+	-	+	
CWD-AR-00-1353	Fulton	D1901-19	83	FU3N	009	+	+	-	+	
CWD-AR-00-1403	Fulton	D1902-09	83	FU3N	010	+	+	+	+	
CWD-AR-00-1405	Fulton	D1902-09	83	FU3N	011	+	+	-	+	
CWD-AR-00-1404	Fulton	D1902-09	83	FU3N	012	+	+	-	+	
CWD-AR-00-1402	Fulton	D1902-24	83	FU3N	013	+	+	-	+	
CWD-AR-18-01357	Fulton	D1902-35	83	FU3N	014	+	+	+	+	
CWD-AR-00-1357	Fulton	D1902-35	83	FU3N	015	+	+	-	+	
CWD-AR-00-1407	Fulton	D1902-35	83	FU3N	016	+	+	+	+	
CWD-AR-00-1408	Fulton	D1902-35	83	FU3N	017	+	+	+	+	
CWD-AR-00-1409	Fulton	D1902-35	83	FU3N	018	+	+	-	+	
CWD-AR-00-1411	Fulton	D1902-35	83	FU3N	019	+	+	-	+	
CWD-AR-00-1412	Fulton	D1902-35	83	FU3N	020	+	+	+	+	
CWD-AR-00-1414	Fulton	D1902-35	83	FU3N	022	+	+	-	+	
CWD-AR-00-1413	Fulton	D1902-35	83	FU3U	021	+	+	-	+	

CWD-AR-18-0127B	Garland	D1807-15	83	GA2N	004	+			
CWD-AR-18-125	Garland	D1806-27	83	GA3N	001	+	+	-	+
CWD-AR-18-126	Garland	D1806-27	83	GA3N	002	+	+	-	+
CWD-AR-18-131	Garland	D1806-27	83	GA3N	003	+	+	-	+
CWD-AR-18-01044	Garland	D1901-20	83	GA3N	005	+	+	-	+
CWD-AR-18-01046	Garland	D1901-20	83	GA3N	006	+	+	-	+
CWD-AR-18-01047	Garland	D1901-20	83	GA3N	007	+	+	-	+
CWD-AR-18-01048	Garland	D1901-20	83	GA3N	008	+	+	+	+
CWD-AR-18-01049	Garland	D1901-20	83	GA3N	009	+	+	-	+
CWD-AR-18-01051	Garland	D1901-20	83	GA3N	010	+	+	-	+
CWD-AR-18-01052	Garland	D1901-21	83	GA3N	011	+	+	-	+
CWD-AR-18-01053	Garland	D1901-21	83	GA3N	012	+	+	-	+
CWD-AR-18-01057	Garland	D1901-21	83	GA3N	013	+	+	-	+
CWD-AR-18-01076	Garland	D1901-21	83	GA3N	014	+	+	-	+
CWD-AR-18-01513	Garland	D1901-21	83	GA3N	015	+	+	-	+
CWD-AR-18-01649	Garland	D1901-21	83	GA3N	016	+	+	-	+
CWD-AR-18-01535	Garland	D1902-36	83	GA3N	017	+	+	+	+
CWD-AR-00-0626	Greene	D1901-23	83	GE3N	001	+	+	-	+
CWD-AR-18-01348	Greene	D1901-23	83	GE3N	002	+	+	-	+
CWD-AR-00-0624	Greene	D1901-23	83	GE3N	003	+	+	-	+
CWD-AR-00-0721	Greene	D1901-23	83	GE3N	004	+	+	-	+
CWD-AR-00-0722	Greene	D1901-23	83	GE3N	005	+	+	-	+
CWD-AR-00-0723	Greene	D1901-23	83	GE3N	006	+	+	-	+
CWD-AR-18-01355	Greene	D1901-37	83	GE3N	012	+	+	-	+
	Greene	D1901-37	83	GE3N	013	+	+	-	+
	Greene	D1901-37	83	GE3N	014	+	+	+	+
	Greene	D1901-37	83	GE3N	015	+	+	-	+
	Greene	D1901-37	83	GE3N	016	+	+	-	+
	Greene	D1901-37	83	GE3N	017	+	+	-	+
CWD-AR-16-6550	Greene	D1806-28	83	GR2N	001	+	+	-	+
CWD-AR-18-576	Greene	D1806-29	83	GR2N	002	+	-	-	+
CWD-AR-18-577	Greene	D1806-28	83	GR2N	003	+	+	-	+
CWD-AR-18-578	Greene	D1806-29	83	GR2N	004	+	+	-	+
CWD-AR-18-580	Greene	D1806-29	83	GR2N	005	+	+	+	+
CWD-AR-18-01464	Grant	D1901-22	83	GR3N	006	+	+	-	+
CWD-AR-18-01462	Grant	D1901-23	83	GR3N	007	+	+	-	+
CWD-AR-18-01466	Grant	D1901-24	83	GR3N	008	+	+	-	+
CWD-AR-18-01467	Grant	D1901-25	83	GR3N	009	+	+	-	+
CWD-AR-18-01471	Grant	D1901-26	83	GR3N	010	+	+	-	+
CWD-AR-00-0922	Grant	D1902-21	83	GR3N	011	+	+	-	+
CWD-AR-00-0981	Hampstead	D1901-24	83	HE3N	007	+	+	-	+
CWD-AR-00-0982	Hampstead	D1901-24	83	HE3N	008	+	+	-	+
CWD-AR-00-0989	Hampstead	D1901-24	83	HE3N	009	+	+	-	+
CWD-AR-00-983	Hampstead	D1901-24	83	HE3N	010	+	+	-	+
CWD-AR-17-4360	Hempstead	D1806-30	83	HM2N	001	+	+	-	+
CWD-AR-18-979	Hempstead	D1806-30	83	HM2N	002	+	+	-	+
CWD-AR-18-983	Hempstead	D1806-30	83	HM2N	003	+	+	-	+
CWD-AR-18-1054	Hempstead	D1806-30	83	HM2N	004	+	+	-	+
CWD-AR-18-1057	Hempstead	D1806-30	83	HM2N	005	+	+	-	+
CWD-AR-18-1059	Hempstead	D1806-30	83	HM2N	006	+	+	+	+
CWD-AR-00-0985	Howard	D1901-27	83	HO3N	002	+	+	-	+
CWD-AR-00-0988	Howard	D1901-27	83	HO3N	003	+	+	-	+
CWD-AR-00-0990	Howard	D1901-27	83	HO3N	004	+	+	-	+
CWD-AR-00-1101	Howard	D1902-38	83	HO3N	013	+	+	-	+
CWD-AR-00-1102	Howard	D1902-38	83	HO3N	014	+	+	-	+
CWD-AR-00-0975	Howard	D1901-27	83	HO3U	005	+	+	-	+
CWD-AR-00-0977	Howard	D1901-27	83	HO3U	006	+	+	+	+
CWD-AR-00-0978	Howard	D1901-27	83	HO3U	007	+	+	+	+
CWD-AR-00-1081	Howard	D1901-27	83	HO3U	008	+	+	-	+

CWD-AR-00-1082	Howard	D1901-27	83	HO3U	009	+	+	-	+
CWD-AR-00-1083	Howard	D1901-27	83	HO3U	010	+	+	+	+
CWD-AR-00-1084	Howard	D1901-27	83	HO3U	011	+	+	-	+
CWD-AR-00-1085	Howard	D1901-27	83	HO3U	012	+	+	-	+
CWD-AR-18-563	Hot Springs	D1806-31	83	HS2N	001	+	+	-	+
CWD-AR-00-0885	Hot Springs	D1901-26	83	HS3N	005	+	+	-	+
	Hot Springs	D1901-25	83	HS3U	002	+	+	-	+
CWD-AR-00-882	Hot Springs	D1901-25	83	HS3U	003	+	+	-	+
CWD-AR-00-883	Hot Springs	D1901-25	83	HS3U	004	+	+	-	+
CWD-AR-18-0686B	Howard	D1807-16	83	HW2N	005	+	-	-	+
CWD-AR-18-151	Independence	D1806-32	83	IN2N	001	+	+	+	+
CWD-AR-18-152	Independence	D1806-32	83	IN2N	002	+	+	-	+
CWD-AR-18-153	Independence	D1806-32	83	IN2N	003	+	+	+	+
CWD-AR-18-156	Independence	D1806-32	83	IN2N	004	+	+	-	+
CWD-AR-18-159	Independence	D1806-32	83	IN2N	005	+	+	+	+
CWD-AR-18-178	Independence	D1806-32	83	IN2N	006	+	+	+	+
CWD-AR-00-1352	Independence	D1901-28	83	IN3N	007	+	+	-	+
CWD-AR-17-0005	Independence	D1901-28	83	IN3N	008	+	+	-	+
CWD-AR-18-52	Izard	D1806-33	83	IZ2N	001	+	+	-	+
CWD-AR-18-53	Izard	D1806-33	83	IZ2N	002	+	+	+	+
CWD-AR-18-0241HC	Izard	D1806-33	83	IZ2N	003	+	+	-	+
CWD-AR-00-8984	Izard	D1901-29	83	IZ3N	004	+	+	+	+
CWD-AR-00-9017	Izard	D1901-29	83	IZ3N	005	+	+	-	+
CWD-AR-00-1521	Izard	D1901-29	83	IZ3N	006	+	+	-	+
CWD-AR-00-8962	Izard	D1902-39	83	IZ3N	007	+	+	-	+
CWD-AR-00-8963	Izard	D1902-39	83	IZ3N	008	+	+	-	+
CWD-AR-00-8966	Izard	D1902-39	83	IZ3N	009	+	+	-	+
CWD-AR-18-586	Jackson	D1806-34	83	JA2N	001	+	+	-	+
CWD-AR-00-0603	Jackson	D1901-30	83	JA3N	002	+	+	-	+
CWD-AR-16-3810	Jefferson	D1802-04	83	JE1N	001	+	+	+	+
CWD-AR-16-4436	Jefferson	D1802-04	83	JE1N	002	+	+	-	+
CWD-AR-18-451	Jefferson	D1806-35	83	JE2N	003	+	+	-	+
CWD-AR-18-452	Jefferson	D1806-35	83	JE2N	004	+	+	+	+
CWD-AR-18-01121	Jefferson	D1901-31	83	JE3N	005	+	+	+	+
CWD-AR-00-0401	Jefferson	D1901-31	83	JE3N	006	+	+	-	+
CWD-AR-00-0403	Jefferson	D1901-31	83	JE3N	007	+	+	+	+
CWD-AR-18-01081	Jefferson	D1901-31	83	JE3N	008	+	+	-	+
CWD-AR-18-01082	Jefferson	D1901-31	83	JE3N	009	+	+	-	+
CWD-AR-18-01120	Jefferson	D1901-31	83	JE3N	010	+	+	-	+
CWD-AR-18-01124	Jefferson	D1902-18	83	JE3U	011	+	+	-	+
CWD-AR-00-0412	Jefferson	D1902-23	83	JE3U	012	+	+	-	+
CWD-AR-00-0413	Jefferson	D1902-23	83	JE3U	013	+	+	+	+
CWD-AR-16-03663	Johnson	D1712-09	83	JO1N	001	+	+	-	+
CWD-AR-16-03665	Johnson	D1712-09	83	JO1N	002	+	+	-	+
CWD-AR-16-03667	Johnson	D1712-09	83	JO1N	003	+	+	-	+
CWD-AR-16-03670	Johnson	D1712-09	83	JO1N	004	+	+	-	+
CWD-AR-16-03671	Johnson	D1712-09	83	JO1N	005	+	+	-	+
CWD-AR-16-03675	Johnson	D1712-09	83	JO1N	006	+	+	-	+
CWD-AR-16-03676	Johnson	D1712-09	83	JO1N	007	+	+	+	+
CWD-AR-16-03679	Johnson	D1801-01	83	JO1N	008	+	+	-	+
CWD-AR-16-03685	Johnson	D1801-01	83	JO1N	009	+	+	-	+
CWD-AR-16-03689	Johnson	D1801-01	83	JO1N	010	+	+	+	+
CWD-AR-16-03690	Johnson	D1801-01	83	JO1N	011	+	+	-	+
CWD-AR-16-03694	Johnson	D1801-01	83	JO1N	012	+	+	-	+
CWD-AR-16-03696	Johnson	D1801-01	83	JO1N	013	+	+	-	+
CWD-AR-16-03698	Johnson	D1801-01	83	JO1N	014	+	+	-	+
CWD-AR-16-03942	Johnson	D1801-01	83	JO1N	015	+	+	-	+
CWD-AR-16-03947	Johnson	D1801-01	83	JO1N	016	+	+	+	+
CWD-AR-16-03949	Johnson	D1801-01	83	JO1N	017	+	+	-	+

CWD-AR-16-04180	Johnson	D1801-01	83	JO1N	018	+	+	-	+
CWD-AR-16-04188	Johnson	D1801-01	83	JO1N	019	+	+	-	+
CWD-AR-16-04193	Johnson	D1801-01	83	JO1N	020	+	+	+	+
CWD-AR-16-04194	Johnson	D1801-01	83	JO1N	021	+	+	-	+
CWD-AR-16-04202	Johnson	D1801-01	83	JO1N	022	+	+	-	+
CWD-AR-16-04204	Johnson	D1801-01	83	JO1N	023	+	+	-	+
CWD-AR-16-04205	Johnson	D1801-01	83	JO1N	024	+	+	-	+
CWD-AR-16-04207	Johnson	D1801-01	83	JO1N	025	+	+	+	+
CWD-AR-16-04209	Johnson	D1801-01	83	JO1N	026	+	+	-	+
CWD-AR-16-04212	Johnson	D1801-01	83	JO1N	027	+	+	-	+
CWD-AR-16-04213	Johnson	D1801-01	83	JO1N	028	+	+	-	+
CWD-AR-16-04215	Johnson	D1801-01	83	JO1N	029	+	+	+	+
CWD-AR-16-04216	Johnson	D1801-01	83	JO1N	030	+	+	-	+
CWD-AR-16-04222	Johnson	D1801-01	83	JO1N	031	+	+	-	+
CWD-AR-16-04223	Johnson	D1801-02	83	JO1N	032	+	+	+	+
CWD-AR-16-04224	Johnson	D1801-02	83	JO1N	033	+	+	-	+
CWD-AR-16-04225	Johnson	D1801-02	83	JO1N	034	+	+	-	+
CWD-AR-16-04228	Johnson	D1801-02	83	JO1N	035	+	+	-	+
CWD-AR-16-04235	Johnson	D1801-02	83	JO1N	036	+	+	+	+
CWD-AR-17-12592	Johnson	D1806-36	83	JO2N	037	+	+	+	+
CWD-AR-17-13356	Johnson	D1806-36	83	JO2N	038	+			
CWD-AR-17-23784	Johnson	D1806-37	83	JO2N	039	+			
CWD-AR-17-23792	Johnson	D1806-37	83	JO2N	040	+			
CWD-AR-17-23796	Johnson	D1806-37	83	JO2N	041	+			
CWD-AR-17-23797	Johnson	D1806-37	83	JO2N	042	+	+	+	+
CWD-AR-17-23798	Johnson	D1806-37	83	JO2N	043	+	+	-	+
CWD-AR-17-23825	Johnson	D1806-37	83	JO2N	044	+			
CWD-AR-17-23826	Johnson	D1806-37	83	JO2N	045	+			
CWD-AR-17-23829	Johnson	D1806-37	83	JO2N	046	+			
CWD-AR-17-23830	Johnson	D1806-37	83	JO2N	047	+	+	-	+
CWD-AR-17-23831	Johnson	D1806-37	83	JO2N	048	+	+	+	+
CWD-AR-17-23832	Johnson	D1806-37	83	JO2N	049	+			
CWD-AR-17-23833	Johnson	D1806-37	83	JO2N	050	+			
CWD-AR-17-23834	Johnson	D1806-37	83	JO2N	051	+			
CWD-AR-17-23836	Johnson	D1806-37	83	JO2N	052	+			
CWD-AR-17-23838	Johnson	D1806-37	83	JO2N	053	+	+	-	+
CWD-AR-17-23839	Johnson	D1806-37	83	JO2N	054	+	+	-	+
CWD-AR-18-826	Johnson	D1806-37	83	JO2N	055	+			
CWD-AR-18-830	Johnson	D1806-37	83	JO2N	056	+			
CWD-AR-18-831	Johnson	D1806-37	83	JO2N	057	+			
CWD-AR-18-832	Johnson	D1806-37	83	JO2N	058	+			
CWD-AR-18-833	Johnson	D1806-37	83	JO2N	059	+			
CWD-T060-AR-17001	Johnson	D1806-37	83	JO2N	060	+			
CWD-T060-AR-17002	Johnson	D1806-37	83	JO2N	061	+			
CWD-AR-17-23786	Johnson	D1806-37	83	JO2N	062	+			
CWD-AR-17-23787	Johnson	D1806-38	83	JO2N	063	+			
CWD-AR-17-23788	Johnson	D1806-38	83	JO2N	064	+			
CWD-AR-17-23789	Johnson	D1806-38	83	JO2N	065	+			
CWD-AR-17-23790	Johnson	D1806-38	83	JO2N	066	+			
CWD-AR-17-23791	Johnson	D1806-38	83	JO2N	067	+	+	-	+
CWD-AR-17-23793	Johnson	D1806-38	83	JO2N	068	+			
CWD-AR-17-23794	Johnson	D1806-38	83	JO2N	069	+	+	+	+
CWD-AR-17-23795	Johnson	D1806-38	83	JO2N	070	+			
CWD-AR-17-23828	Johnson	D1806-38	83	JO2N	071	+			
CWD-T060-AR-17-003	Johnson	D1806-38	83	JO2N	072	+			
CWD-T060-AR-17-004	Johnson	D1806-38	83	JO2N	073	+			
CWD-T060-AR-17-005	Johnson	D1806-38	83	JO2N	074	+			
CWD-AR-18-976	Lafayette	D1806-39	83	LA2N	001	+	+	-	+
CWD-AR-18-982	Lafayette	D1806-39	83	LA2N	002	+	+	+	+

CWD-AR-18-984	Lafayette	D1806-39	83	LA2N	003	+	+	+	+
CWD-AR-00-0961	Lafayette	D1901-40	83	LA3U	004	+	+	-	+
CWD-AR-00-0969	Lafayette	D1901-40	83	LA3U	005	+	+	-	+
CWD-AR-00-0970	Lafayette	D1901-40	83	LA3U	006	+	+	+	+
CWD-AR-00-0971	Lafayette	D1901-40	83	LA3U	007	+	+	-	+
CWD-AR-00-0972	Lafayette	D1901-40	83	LA3U	008	+	+	-	+
CWD-AR-00-0973	Lafayette	D1901-40	83	LA3U	009	+	+	+	+
CWD-AR-00-0974	Lafayette	D1901-40	83	LA3U	010	+	+	-	+
CWD-AR-00-1087	Lafayette	D1901-40	83	LA3U	011	+	+	-	+
CWD-AR-00-1088	Lafayette	D1901-40	83	LA3U	012	+	+	-	+
CWD-AR-00-1089	Lafayette	D1901-40	83	LA3U	013	+	+	-	+
CWD-AR-00-1090	Lafayette	D1901-40	83	LA3U	014	+	+	-	+
CWD-AR-00-1091	Lafayette	D1901-40	83	LA3U	015	+	+	-	+
CWD-AR-18-244	Lincoln	D1806-40	83	LC3N	001	+	+	-	+
CWD-AR-16-7136	Lee	D1806-41	83	LE2N	001	+	+	-	+
CWD-AR-17-3526	Lee	D1806-41	83	LE2N	002	+	+	+	+
CWD-AR-17-3529	Lee	D1806-41	83	LE2N	003	+	+	-	+
	Lee	D1901-42	83	LE3N	004	+	+	-	+
	Lee	D1901-42	83	LE3N	005	+	+	+	+
CWD-AR-00-7682	Lee	D1902-10	83	LE3N	006	+	+	+	+
CWD-AR-00-7683	Lee	D1902-10	83	LE3N	007	+	+	-	+
CWD-AR-00-7681	Lee	D1902-10	83	LE3N	008	+	+	-	+
CWD-AR-00-0301	Lee	D1902-41	83	LE3N	009	+	+	-	+
CWD-AR-18-01091	Lincoln	D1902-42	83	LI3N	009	+	+	-	+
CWD-AR-18-1826	Lincoln	D1901-43	83	LI3U	002	+	+	+	+
CWD-AR-00-0411	Lincoln	D1901-78	83	LI3U	004	+	+	-	+
CWD-AR-18-01123	Lincoln	D1902-17	83	LI3U	005	+	+	-	+
CWD-AR-18-01088	Lincoln	D1902-42	83	LI3U	006	+	+	-	+
CWD-AR-18-01089	Lincoln	D1902-42	83	LI3U	007	+	+	-	+
CWD-AR-18-01090	Lincoln	D1902-42	83	LI3U	008	+	+	-	+
CWD-AR-17-4254	Lonoke	D1806-42	83	LN2N	001	+	+	-	+
CWD-AR-18-0203HC	Lonoke	D1806-42	83	LN2N	002	+	+	+	+
CWD-AR-18-0210HC	Lonoke	D1806-42	83	LN2N	003	+	+	-	+
CWD-AR-18-628	Lonoke	D1806-42	83	LN2N	004	+	+	-	+
CWD-AR-18-0681HC	Lonoke	D1806-42	83	LN2N	005	+	+	-	+
CWD-AR-18-0682HC	Lonoke	D1806-43	83	LN2N	006	+	+	-	+
CWD-AR-18-0683HC	Lonoke	D1806-43	83	LN2N	007	+	+	-	+
CWD-AR-18-0684HC	Lonoke	D1806-43	83	LN2N	008	+	+	-	+
CWD-AR-18-681	Lonoke	D1806-43	83	LN3N	009	+	+	+	+
CWD-AR-18-682	Lonoke	D1806-43	83	LN3N	010	+	+	-	+
CWD-AR-18-683	Lonoke	D1806-43	83	LN3N	011	+	+	-	+
CWD-AR-18-684	Lonoke	D1806-43	83	LN3N	012	+	+	-	+
CWD-AR-18-01207	Lonoke	D1901-51	83	LN3N	013	+	+	-	+
CWD-AR-16-04189	Logan	D1801-02	83	LO1N	001	+	+	-	+
CWD-AR-16-04190	Logan	D1801-02	83	LO1N	002	+	+	-	+
CWD-AR-16-04441	Logan	D1801-02	83	LO1N	003	+	+	+	+
CWD-AR-16-04446	Logan	D1801-02	83	LO1N	004	+	+	-	+
CWD-AR-16-04449	Logan	D1801-02	83	LO1N	005	+	+	+	+
CWD-AR-16-04450	Logan	D1801-02	83	LO1N	006	+	+	-	+
CWD-AR-16-04451	Logan	D1801-02	83	LO1N	007	+	+	-	+
CWD-AR-16-04456	Logan	D1801-02	83	LO1N	008	+	+	+	+
CWD-AR-16-04457	Logan	D1801-02	83	LO1N	009	+	+	+	+
CWD-AR-16-04458	Logan	D1801-02	83	LO1N	010	+	+	-	+
CWD-AR-16-04460	Logan	D1801-02	83	LO1N	011	+	+	+	+
CWD-AR-16-04462	Logan	D1801-02	83	LO1N	012	+	+	-	+
CWD-AR-16-06281	Logan	D1801-02	83	LO1N	013	+	+	+	+
CWD-AR-16-06282	Logan	D1801-02	83	LO1N	014	+	+	-	+
CWD-AR-16-06283	Logan	D1801-02	83	LO1N	015	+	+	-	+
CWD-AR-16-06293	Logan	D1801-02	83	LO1N	016	+	+	-	+

CWD-AR-16-5636	Logan	D1801-02	83	LO1N	017	+	+	+	+
CWD-AR-16-5637	Logan	D1801-02	83	LO1N	018	+	+	-	+
CWD-AR-16-5638	Logan	D1801-02	83	LO1N	019	+	+	+	+
CWD-AR-16-5639	Logan	D1801-03	83	LO1N	020	+	+	+	+
CWD-AR-16-5640	Logan	D1801-03	83	LO1N	021	+	+	-	+
CWD-AR-16-5641	Logan	D1801-03	83	LO1N	022	+	+	+	+
CWD-AR-16-5642	Logan	D1801-03	83	LO1N	023	+	+	+	+
CWD-AR-16-04440	Logan	D1802-04	83	LO1N	024	+	+	-	+
CWD-AR-16-04444	Logan	D1802-04	83	LO1N	025	+	+	-	+
CWD-AR-16-04443	Logan	D1802-04	83	LO1N	026	+	+	-	+
CWD-A+3:1469R-17-856	Logan	D1806-44	83	LO2N	027	+	+	-	
CWD-AR-17-857	Logan	D1806-44	83	LO2N	028	+	+	+	
CWD-AR-17-858	Logan	D1806-44	83	LO2N	029	+	+	-	
CWD-AR-17-859	Logan	D1806-44	83	LO2N	030	+	+	+	
CWD-AR-17-861	Logan	D1806-44	83	LO2N	031	+	+	-	
CWD-AR-17-862	Logan	D1806-44	83	LO2N	032	+	+	-	+
CWD-AR-17-863	Logan	D1806-44	83	LO2N	033	+	+	+	+
CWD-AR-18-1078	Logan	D1806-44	83	LO2N	034	+	+	-	+
CWD-T060-AR-17021	Logan	D1806-44	83	LO2N	035	+	+	-	
CWD-T060-AR-17022	Logan	D1806-44	83	LO2N	036	+	+	-	
CWD-T060-AR-17023	Logan	D1806-44	83	LO2N	037	+	+	-	
CWD-T060-AR-17024	Logan	D1806-44	83	LO2N	038	+	+	-	+
CWD-T060-AR-17025	Logan	D1806-44	83	LO2N	039	+	+	+	+
CWD-T060-AR-17026	Logan	D1806-44	83	LO2N	040	+	+	-	+
CWD-T060-AR-17027	Logan	D1806-44	83	LO2N	041	+	+	+	+
CWD-T060-AR-17028	Logan?	D1806-44	83	LO2N	042	+			*no record in field data
CWD-AR-17-23837	Little River	D1806-45	83	LR2N	001	+	+	+	+
CWD-AR-18-977	Little River	D1806-46	83	LR2N	002	+	+	-	+
CWD-AR-18-978	Little River	D1806-46	83	LR2N	003	+	+	-	+
CWD-AR-18-981	Little River	D1806-46	83	LR2N	004	+	+	-	+
CWD-AR-18-1051	Little River	D1806-46	83	LR2N	005	+	+	-	+
CWD-AR-18-1052	Little River	D1806-46	83	LR2N	006	+	+	-	+
CWD-AR-18-1053	Little River	D1806-46	83	LR2N	007	+	+	-	+
CWD-AR-18-1055	Little River	D1806-46	83	LR2N	008	+	+	+	+
CWD-AR-18-1056	Little River	D1806-46	83	LR2N	009	+	+	+	+
CWD-AR-18-1058	Little River	D1806-46	83	LR2N	010	+	+	+	+
CWD-AR-00-0601	Lawrence	D1901-41	83	LW3N	001	+	+	+	+
CWD-AR-00-0625	Lawrence	D1901-41	83	LW3N	002	+	+	-	+
CWD-AR-00-1347	Lawrence	D1901-41	83	LW3N	003	+	+	-	+
CWD-AR-00-0640	Lawrence	D1902-12	83	LW3N	004	+	+	-	+
	Lawrence	D1902-40	83	LW3N	005	+	+	-	+
	Lawrence	D1902-40	83	LW3N	006	+	+	-	+
	Lawrence	D1902-40	83	LW3N	007	+	+	-	+
	Lawrence	D1902-40	83	LW3N	008	+	+	+	+
	Lawrence	D1902-40	83	LW3N	009	+	+	-	+
	Lawrence	D1902-40	83	LW3N	010	+	+	-	+
	Lawrence	D1902-40	83	LW3N	011	+	+	+	+
	Lawrence	D1902-40	83	LW3N	012	+	+	-	+
	Lawrence	D1902-40	83	LW3N	013	+	+	-	+
	Lawrence	D1902-40	83	LW3N	014	+	+	-	+
	Lawrence	D1902-40	83	LW3N	015	+	+	-	+
	Lawrence	D1902-40	83	LW3N	016	+	+	-	+
	Lawrence	D1902-40	83	LW3N	017	+	+	-	+
CWD-AR-16-00521	Madison	D1801-03	83	MA1N	001	+	+	-	+
CWD-AR-16-00525	Madison	D1801-03	83	MA1N	002	+	+	-	+
CWD-AR-16-00526	Madison	D1801-03	83	MA1N	003	+	+	-	+
CWD-AR-16-00527	Madison	D1801-03	83	MA1N	004	+	+	-	+
CWD-AR-16-00529	Madison	D1801-03	83	MA1N	005	+	+	-	+
CWD-AR-16-00530	Madison	D1801-03	83	MA1N	006	+	+	+	+

CWD-AR-16-00531	Madison	D1801-03	83	MA1N	007	+	+	-	+
CWD-AR-16-00784	Madison	D1801-03	83	MA1N	008	+	+	-	+
CWD-AR-16-00785	Madison	D1801-03	83	MA1N	009	+	+	-	+
CWD-AR-16-00786	Madison	D1801-03	83	MA1N	010	+	+	-	+
CWD-AR-16-00790	Madison	D1801-03	83	MA1N	011	+	+	-	+
CWD-AR-16-00791	Madison	D1801-03	83	MA1N	012	+	+	+	+
CWD-AR-16-00792	Madison	D1801-03	83	MA1N	013	+	+	-	+
CWD-AR-16-00794	Madison	D1801-03	83	MA1N	014	+	+	+	+
CWD-AR-16-00796	Madison	D1801-03	83	MA1N	015	+	+	-	+
CWD-AR-16-00797	Madison	D1801-03	83	MA1N	016	+	+	-	+
CWD-AR-16-00799	Madison	D1801-03	83	MA1N	017	+	+	-	+
CWD-AR-16-02080	Madison	D1801-03	83	MA1N	018	+	+	+	+
CWD-AR-16-02083	Madison	D1801-03	83	MA1N	019	+	+	-	+
CWD-AR-16-00523	Madison	D1801-03	83	MA1N	020	+	+	-	+
CWD-AR-16-00524	Madison	D1801-04	83	MA1N	021	+	+	+	+
CWD-AR-16-00528	Madison	D1801-04	83	MA1N	022	+	+	+	+
CWD-AR-16-00522	Madison	D1801-04	83	MA1N	023	+	+	-	+
CWD-AR-16-00520	Madison	D1801-04	83	MA1N	024	+	+	+	+
CWD-AR-16-01825	Madison	D1712-07	83	MA1P	001	+	+	-	+
CWD-AR-17-12450	Madison	D1806-47	83	MA2N	022	+	+	-	+
CWD-AR-17-12465	Madison	D1806-47	83	MA2N	023	+	+	+	+
CWD-AR-17-12466	Madison	D1806-47	83	MA2N	024	+			
CWD-AR-17-12540	Madison	D1806-47	83	MA2N	025	+			
CWD-AR-17-12542	Madison	D1806-47	83	MA2N	026	+	+	-	+
CWD-AR-17-12543	Madison	D1806-47	83	MA2N	027	+	+	+	+
CWD-AR-17-12544	Madison	D1806-47	83	MA2N	028	+			
CWD-AR-17-12546	Madison	D1806-47	83	MA2N	029	+	+	+	+
CWD-AR-17-12560	Madison	D1806-47	83	MA2N	030	+			
CWD-AR-17-12561	Madison	D1806-47	83	MA2N	031	+			
CWD-AR-17-12562	Madison	D1806-47	83	MA2N	032	+			
CWD-AR-17-12563	Madison	D1806-47	83	MA2N	033	+			
CWD-AR-17-12564	Madison	D1806-47	83	MA2N	034	+			
CWD-AR-17-12565	Madison	D1806-47	83	MA2N	035	+			
CWD-AR-17-12588	Madison	D1806-47	83	MA2N	036	+	+	-	+
CWD-AR-17-12589	Madison	D1806-48	83	MA2N	037	+	+	+	+
CWD-AR-17-12591	Madison	D1806-48	83	MA2N	038	+	+	+	+
CWD-AR-17-12608	Madison	D1806-48	83	MA2N	039	+			
CWD-AR-17-12979	Madison	D1806-48	83	MA2N	040	+			
CWD-AR-17-12980	Madison	D1806-48	83	MA2N	041	+			
CWD-AR-17-13106	Madison	D1806-48	83	MA2N	042	+			
CWD-AR-17-13116	Madison	D1806-48	83	MA2N	043	+			
CWD-AR-17-13120	Madison	D1806-48	83	MA2N	044	+			
CWD-AR-17-13121	Madison	D1806-48	83	MA2N	045	+	+	+	+
CWD-AR-17-13133	Madison	D1806-48	83	MA2N	046	+			
CWD-AR-17-13140	Madison	D1806-48	83	MA2N	047	+			
CWD-AR-17-13191	Madison	D1806-48	83	MA2N	048	+			
CWD-AR-17-13192	Madison	D1806-48	83	MA2N	049	+			
CWD-AR-17-19502	Madison	D1806-48	83	MA2N	050	+	+	+	+
CWD-AR-17-19702	Madison	D1806-48	83	MA2N	051	+			
CWD-AR-17-23902	Madison	D1806-48	83	MA2N	052	+			
CWD-AR-17-23914	Madison	D1806-48	83	MA2N	053	+			
CWD-AR-17-23916	Madison	D1806-48	83	MA2N	054	+			
CWD-AR-17-23917	Madison	D1806-48	83	MA2N	055	+	+	+	+
CWD-AR-17-4116	Madison	D1806-48	83	MA2N	056	+	+	-	+
CWD-AR-17-12440	Madison	D1807-25	83	MA2P	058	+	+	-	+
CWD-AR-17-12444	Madison	D1807-25	83	MA2P	059	+	+	-	+
CWD-AR-17-12545	Madison	D1807-25	83	MA2P	060	+	+	+	+
CWD-AR-18-322	Madison	D1806-49	83	MA3N	057	+			
CWD-AR-00-0962	Miller	D1901-53	83	MI3U	006	+	+	-	+

CWD-AR-00-0963	Miller	D1901-53	83	MI3U	007	+	+	-	+
CWD-AR-00-0964	Miller	D1901-53	83	MI3U	008	+	+	-	+
CWD-AR-00-0965	Miller	D1901-54	83	MI3U	009	+	+	-	+
CWD-AR-00-0966	Miller	D1901-54	83	MI3U	010	+	+	-	+
CWD-AR-00-0967	Miller	D1901-54	83	MI3U	011	+	+	-	+
CWD-AR-00-0968	Miller	D1901-54	83	MI3U	012	+	+	-	+
CWD-AR-18-980	Miller	D1806-50	83	ML2N	001	+	+	-	+
CWD-AR-18-0688B	Miller	D1806-50	83	ML2N	002	+	-	-	+
CWD-AR-18-0689B	Miller	D1806-50	83	ML2N	003	+	+	-	+
CWD-AR-18-0690B	Miller	D1806-51	83	ML2N	004	+	+	-	+
CWD-AR-18-0691B	Miller	D1806-51	83	ML2N	005	+	-	-	+
CWD-AR-16-7138	Monroe	D1806-52	83	MN2N	001	+	+	-	+
CWD-AR-16-7141	Monroe	D1806-52	83	MN2N	002	+			
CWD-AR-16-7142	Monroe	D1806-52	83	MN2N	003	+			
CWD-AR-16-7143	Monroe	D1806-52	83	MN2N	004	+	+	-	+
CWD-AR-16-7144	Monroe	D1806-52	83	MN2N	005	+	+	-	+
CWD-AR-17-3528	Monroe	D1806-52	83	MN2N	006	+	+	-	+
CWD-AR-17-3705	Monroe	D1806-52	83	MN2N	007	+	+	-	+
CWD-AR-17-3854	Monroe	D1806-52	83	MN2N	008	+	+	-	+
CWD-AR-17-3856	Monroe	D1806-52	83	MN2N	009	+	-	-	+
CWD-AR-18-650	Monroe	D1806-52	83	MN2N	010	+	+	+	+
CWD-AR-18-652	Monroe	D1806-52	83	MN2N	011	+	+	-	+
CWD-AR-18-668	Monroe	D1806-52	83	MN2N	012	+	+	+	+
CWD-AR-00-7685	Monroe	D1902-48	83	MN3N	013	+	+	-	+
	Montgomery	D1902-46	83	MO3N	001	+	+	-	+
	Montgomery	D1902-46	83	MO3N	002	+	+	-	+
CWD-AR-16-01563	Marion	D1801-04	83	MR1N	001	+	+	-	+
CWD-AR-16-01569	Marion	D1801-04	83	MR1N	002	+	+	+	+
CWD-AR-16-01570	Marion	D1801-04	83	MR1N	003	+	+	+	+
CWD-AR-16-01572	Marion	D1801-04	83	MR1N	004	+	+	+	+
CWD-AR-16-01579	Marion	D1801-04	83	MR1N	005	+	+	+	+
CWD-AR-16-01580	Marion	D1801-04	83	MR1N	006	+	+	-	+
CWD-AR-16-01583	Marion	D1801-04	83	MR1N	007	+	+	-	+
CWD-AR-16-01823	Marion	D1801-04	83	MR1N	008	+	+	-	+
CWD-AR-16-01824	Marion	D1801-04	83	MR1N	009	+	+	-	+
CWD-AR-16-01827	Marion	D1801-04	83	MR1N	010	+	+	+	+
CWD-AR-16-01830	Marion	D1801-04	83	MR1N	011	+	+	+	+
CWD-AR-16-01831	Marion	D1801-04	83	MR1N	012	+	+	+	+
CWD-AR-16-01832	Marion	D1801-04	83	MR1N	013	+	+	-	+
CWD-AR-16-01834	Marion	D1801-04	83	MR1N	014	+	+	-	+
CWD-AR-16-02345	Marion	D1801-04	83	MR1N	015	+	+	-	+
CWD-AR-16-05795	Marion	D1801-04	83	MR1N	016	+	+	+	+
CWD-AR-16-0279	Marion	D1801-04	83	MR1N	017	+	+	-	+
CWD-AR-17-14872	Marion	D1806-53	83	MR2N	018	+	+	+	+
CWD-AR-17-15250	Marion	D1806-53	83	MR2N	019	+			
CWD-AR-17-15252	Marion	D1806-53	83	MR2N	020	+	+	-	+
CWD-AR-17-15253	Marion	D1806-53	83	MR2N	021	+			
CWD-AR-17-15254	Marion	D1806-53	83	MR2N	022	+	+	+	+
CWD-AR-17-15255	Marion	D1806-53	83	MR2N	023	+			
CWD-AR-17-15256	Marion	D1806-53	83	MR2N	024	+			
CWD-AR-17-15259	Marion	D1806-53	83	MR2N	025	+			
CWD-AR-17-15260	Marion	D1806-53	83	MR2N	026	+			
CWD-AR-17-15261	Marion	D1806-53	83	MR2N	027	+	+	-	+
CWD-AR-17-15262	Marion	D1806-62	83	MR2N	028	+	+	-	+
CWD-AR-17-15263	Marion	D1806-62	83	MR2N	029	+	+	+	+
CWD-AR-17-15280	Marion	D1806-62	83	MR2N	030	+			
CWD-AR-17-15282	Marion	D1806-62	83	MR2N	031	+			
CWD-AR-17-15300	Marion	D1806-62	83	MR2N	032	+			
CWD-AR-17-15302	Marion	D1806-62	83	MR2N	033	+			

CWD-AR-17-15303	Marion	D1806-62	83	MR2N	034	+				
CWD-AR-17-15304	Marion	D1806-62	83	MR2N	035	+				
CWD-AR-17-15305	Marion	D1806-62	83	MR2N	036	+				
CWD-AR-17-15307	Marion	D1806-62	83	MR2N	037	+	+	+	+	+
CWD-AR-17-15312	Marion	D1806-62	83	MR2N	038	+				
CWD-AR-17-15313	Marion	D1806-62	83	MR2N	039	+				
CWD-AR-17-15314	Marion	D1806-62	83	MR2N	040	+				
CWD-AR-17-15315	Marion	D1806-62	83	MR2N	041	+	+	-	+	
CWD-AR-17-15317	Marion	D1806-62	83	MR2N	042	+				
CWD-AR-17-15318	Marion	D1806-62	83	MR2N	043	+				
CWD-AR-17-15319	Marion	D1806-62	83	MR2N	044	+	+	-	+	
CWD-AR-17-15320	Marion	D1806-62	83	MR2N	045	+				
CWD-AR-17-15321	Marion	D1806-62	83	MR2N	046	+				
CWD-AR-17-15325	Marion	D1806-62	83	MR2N	047	+				
CWD-AR-17-15335	Marion	D1806-62	83	MR2N	048	+				
CWD-AR-17-15338	Marion	D1806-62	83	MR2N	049	+				
CWD-AR-17-15339	Marion	D1806-62	83	MR2N	050	+	+	+	+	+
CWD-AR-17-15949	Marion	D1806-62	83	MR2N	051	+	+	-	+	
CWD-AR-17-15959	Marion	D1806-62	83	MR2N	052	+	+	-	+	
CWD-AR-17-15960	Marion	D1806-93	83	MR2N	053	+	+	-	+	
CWD-AR-17-15966	Marion	D1806-93	83	MR2N	054	+	+	-	+	
CWD-AR-17-15991	Marion	D1806-93	83	MR2N	055	+				
CWD-AR-17-15992	Marion	D1806-93	83	MR2N	056	+				
CWD-AR-17-15993	Marion	D1806-93	83	MR2N	057	+				
CWD-AR-17-15994	Marion	D1806-93	83	MR2N	058	+				
CWD-AR-17-15995	Marion	D1806-93	83	MR2N	059	+				
CWD-AR-17-16004	Marion	D1806-93	83	MR2N	060	+	+	+	+	+
CWD-AR-17-19025	Marion	D1806-93	83	MR2N	061	+	+	+	+	+
CWD-AR-17-19026	Marion	D1806-93	83	MR2N	062	+				
CWD-AR-17-19027	Marion	D1806-93	83	MR2N	063	+	-	+		
CWD-AR-17-19030	Marion	D1806-93	83	MR2N	064	+	+	-		
CWD-AR-17-19031	Marion	D1806-93	83	MR2N	065	+	-	+		
CWD-AR-17-19032	Marion	D1806-93	83	MR2N	066	+	-	-		
CWD-AR-18-228	Marion	D1806-93	83	MR2N	067	+	-	-		
CWD-AR-18-401	Marion	D1806-94	83	MR3N	068	+	+	-	+	
CWD-AR-00-1527	Marion	D1901-52	83	MR3N	069	+	+	-	+	
CWD-AR-00-8469	Marion	D1902-43	83	MR3N	070	+	+	+	+	
CWD-AR-00-8470	Marion	D1902-44	83	MR3N	071	+	+	-	+	
CWD-AR-00-8471	Marion	D1902-44	83	MR3N	072	+	+	+	+	
CWD-AR-18-579	Mississippi	D1806-95	83	MS2N	001	+	+	-	+	
CWD-AR-18-01358	Mississippi	D1902-45	83	MS3N	002	+	+	-	+	
CWD-AR-18-01470	Nevada	D1901-55	83	NE3N	001	+	+	+	+	
	Nevada	D1901-55	83	NE3U	002	+	+	+	+	
	Nevada	D1901-55	83	NE3U	003	+	+	+	+	
	Nevada	D1901-55	83	NE3U	004	+	+	+	+	
	Nevada	D1901-60	83	NE3U	005	+	+	-	+	
	Nevada	D1902-20	83	NE3U	006	+	+	+	+	
CWD-AR-00-1093	Nevada	D1902-47	83	NE3U	007	+	+	+	+	
CWD-AR-00-1094	Nevada	D1902-47	83	NE3U	008	+	+	-	+	
CWD-AR-00-1095	Nevada	D1902-47	83	NE3U	009	+	+	-	+	
CWD-AR-00-1096	Nevada	D1902-47	83	NE3U	010	+	+	-	+	
CWD-AR-00-1097	Nevada	D1902-47	83	NE3U	011	+	+	+	+	
CWD-AR-00-1098	Nevada	D1902-47	83	NE3U	012	+	+	-	+	
CWD-AR-00-1099	Nevada	D1902-47	83	NE3U	013	+	+	-	+	
CWD-AR-00-1100	Nevada	D1902-47	83	NE3U	014	+	+	-	+	
CWD-AR-16-0002	Newton	D1610-15	83	NW1N	001	+	+	+	+	
CWD-AR-16-0004	Newton	D1610-15	83	NW1N	002	+	+	-	+	
CWD-AR-16-0006	Newton	D1610-15	83	NW1N	003	+	+	+	+	
CWD-AR-16-0007	Newton	D1610-15	83	NW1N	004	+	+	+	+	

CWD-AR-16-0008	Newton	D1610-15	83	NW1N	005	+	+	+	+
CWD-AR-16-0010	Newton	D1610-15	83	NW1N	006	+	+	-	+
CWD-AR-16-0011	Newton	D1610-15	83	NW1N	007	+	+	-	+
CWD-AR-16-0012	Newton	D1610-15	83	NW1N	008	+	+	-	+
CWD-AR-16-0013	Newton	D1610-15	83	NW1N	009	+	+	-	+
CWD-AR-16-0014	Newton	D1610-15	83	NW1N	010	+	+	+	+
CWD-AR-16-0015	Newton	D1610-15	83	NW1N	011	+	+	+	+
CWD-AR-16-0016	Newton	D1610-15	83	NW1N	012	+	+	-	
CWD-AR-16-0017	Newton	D1610-15	83	NW1N	013	+	+	+	+
CWD-AR-16-0018	Newton	D1610-15	83	NW1N	014	+	+	+	+
CWD-AR-16-0019	Newton	D1610-15	83	NW1N	015	+	+	+	+
CWD-AR-16-0021	Newton	D1610-15	83	NW1N	016	+	+	+	
CWD-AR-16-0137	Newton	D1701-14	83	NW1N	017	+	+	+	+
CWD-AR-16-0023	Newton	D1610-15	83	NW1N	018	+	+	+	
CWD-AR-16-0134	Newton	D1701-14	83	NW1N	019	+	+	+	
CWD-AR-16-0025	Newton	D1610-15	83	NW1N	020	+	+	-	
CWD-AR-16-0026	Newton	D1612-11	83	NW1N	021	+	+	-	+
CWD-AR-16-0027	Newton	D1612-11	83	NW1N	022	+	+	-	
CWD-AR-16-0029	Newton	D1612-11	83	NW1N	023	+	+	+	+
CWD-AR-16-0030	Newton	D1612-11	83	NW1N	024	+	+	-	+
CWD-AR-16-0031	Newton	D1612-11	83	NW1N	025	+	+	-	
CWD-AR-16-0033	Newton	D1612-11	83	NW1N	026	+	+	-	+
CWD-AR-16-0034	Newton	D1612-11	83	NW1N	027	+	+	-	+
CWD-AR-16-0040	Newton	D1612-11	83	NW1N	028	+	+	-	
CWD-AR-16-0043	Newton	D1612-11	83	NW1N	029	+	+	-	+
CWD-AR-16-0044	Newton	D1612-11	83	NW1N	030	+	+	+	
CWD-AR-16-0047	Newton	D1612-11	83	NW1N	031	+	+	-	
CWD-AR-16-0048	Newton	D1612-11	83	NW1N	032	+	+	-	+
CWD-AR-16-0049	Newton	D1612-11	83	NW1N	033	+	+	+	
CWD-AR-16-0051	Newton	D1612-11	83	NW1N	034	+	+	+	
CWD-AR-16-0053	Newton	D1612-11	83	NW1N	035	+	+	+	
CWD-AR-16-0054	Newton	D1612-11	83	NW1N	036	+	+	-	
CWD-AR-16-0055	Newton	D1612-11	83	NW1N	037	+	+	+	
CWD-AR-16-0056	Newton	D1612-11	83	NW1N	038	+	+	-	
CWD-AR-16-0057	Newton	D1612-11	83	NW1N	039	+	+	+	
CWD-AR-16-0058	Newton	D1612-11	83	NW1N	040	+	+	+	+
CWD-AR-16-0126	Newton	D1701-11	83	NW1N	041	+	+	+	+
CWD-AR-16-0060	Newton	D1701-14	83	NW1N	042	+	+	-	+
CWD-AR-16-0061	Newton	D1701-14	83	NW1N	043	+	+	+	+
CWD-AR-16-0062	Newton	D1701-14	83	NW1N	044	+	+	-	+
CWD-AR-16-0063	Newton	D1701-14	83	NW1N	045	+	+	-	
CWD-AR-16-0076	Newton	D1701-14	83	NW1N	046	+	+	-	
CWD-AR-16-0077	Newton	D1701-14	83	NW1N	047	+	+	-	
CWD-AR-16-0078	Newton	D1701-14	83	NW1N	048	+	+	+	+
CWD-AR-16-0079	Newton	D1701-14	83	NW1N	049	+	+	-	+
CWD-AR-16-0081	Newton	D1701-14	83	NW1N	050	+	+	-	+
CWD-AR-16-0084	Newton	D1701-14	83	NW1N	051	+	+	+	+
CWD-AR-16-0085	Newton	D1701-14	83	NW1N	052	+	+	-	
CWD-AR-16-0086	Newton	D1701-14	83	NW1N	053	+	+	-	+
CWD-AR-16-0088	Newton	D1701-14	83	NW1N	054	+	+	+	
CWD-AR-16-0089	Newton	D1701-14	83	NW1N	055	+	+	-	
CWD-AR-16-0094	Newton	D1701-14	83	NW1N	056	+	+	-	
CWD-AR-16-0101	Newton	D1701-14	83	NW1N	057	+	+	-	
CWD-AR-16-0102	Newton	D1701-14	83	NW1N	058	+	+	+	+
CWD-AR-16-0103	Newton	D1701-14	83	NW1N	059	+	+	-	
CWD-AR-16-0106	Newton	D1701-14	83	NW1N	060	+	+	-	
CWD-AR-16-0128	Newton	D1701-14	83	NW1N	061	+	-	-	
CWD-AR-16-0131	Newton	D1701-14	83	NW1N	062	+	+	-	
CWD-AR-16-0132	Newton	D1701-14	83	NW1N	063	+	+	-	

CWD-AR-16-0378	Newton	D1701-11	83	NW1N	064	+	+	-	
CWD-AR-16-01047	Newton	D1801-04	83	NW1N	065	+	+	-	+
CWD-AR-16-01826	Newton	D1801-04	83	NW1N	066	+	+	-	+
CWD-AR-16-02086	Newton	D1801-04	83	NW1N	067	+	+	-	+
CWD-AR-16-02087	Newton	D1801-05	83	NW1N	068	+	+	+	+
CWD-AR-16-02088	Newton	D1801-05	83	NW1N	069	+	+	-	+
CWD-AR-16-02090	Newton	D1801-05	83	NW1N	070	+	+	-	+
CWD-AR-16-02096	Newton	D1801-05	83	NW1N	071	+	+	+	+
CWD-AR-16-02340	Newton	D1801-05	83	NW1N	072	+	+	-	+
CWD-AR-16-02350	Newton	D1801-05	83	NW1N	073	+	+	+	+
CWD-AR-16-02624	Newton	D1801-05	83	NW1N	074	+	+	-	+
CWD-AR-16-02625	Newton	D1801-05	83	NW1N	075	+	+	+	+
CWD-AR-16-02628	Newton	D1801-05	83	NW1N	076	+	+	-	+
CWD-AR-16-02883	Newton	D1801-05	83	NW1N	077	+	+	-	+
CWD-AR-16-02884	Newton	D1801-05	83	NW1N	078	+	+	+	+
CWD-AR-16-02886	Newton	D1801-05	83	NW1N	079	+	+	-	+
CWD-AR-16-02887	Newton	D1801-05	83	NW1N	080	+	+	-	+
CWD-AR-16-02890	Newton	D1801-05	83	NW1N	081	+	+	-	+
CWD-AR-16-02891	Newton	D1801-05	83	NW1N	082	+	+	+	+
CWD-AR-16-02893	Newton	D1801-05	83	NW1N	083	+	+	-	+
CWD-AR-16-02895	Newton	D1801-05	83	NW1N	084	+	+	+	+
CWD-AR-16-02899	Newton	D1801-05	83	NW1N	085	+	+	-	+
CWD-AR-16-03955	Newton	D1801-05	83	NW1N	086	+	+	+	+
CWD-AR-16-04709	Newton	D1801-05	83	NW1N	087	+	+	+	+
CWD-AR-16-04711	Newton	D1801-05	83	NW1N	088	+	+	-	+
CWD-AR-16-04712	Newton	D1801-05	83	NW1N	089	+	+	-	+
CWD-AR-16-04713	Newton	D1801-05	83	NW1N	090	+	+	-	+
CWD-AR-16-05792	Newton	D1801-06	83	NW1N	091	+	+	-	+
CWD-AR-16-02881	Newton	D1801-06	83	NW1N	092	+	+	-	+
CWD-AR-16-02880	Newton	D1801-06	83	NW1N	093	+	+	-	+
CWD-AR-16-02885	Newton	D1801-06	83	NW1N	094	+	+	-	+
CWD-AR-16-02898	Newton	D1801-06	83	NW1N	095	+	+	+	+
CWD-AR-16-02897	Newton	D1801-06	83	NW1N	096	+	+	+	+
CWD-AR-16-02888	Newton	D1801-06	83	NW1N	097	+	+	-	+
CWD-AR-16-02081	Newton	D1801-06	83	NW1N	098	+	+	-	+
CWD-AR-16-0138	Newton	D1804-51	83	NW1N	099	+	+	-	
CWD-AR-16-0141	Newton	D1804-51	83	NW1N	100	+	+	+	
CWD-AR-16-0142	Newton	D1804-51	83	NW1N	101	+	-	-	
CWD-AR-16-0151	Newton	D1804-51	83	NW1N	102	+	+	-	
CWD-AR-16-0152	Newton	D1804-51	83	NW1N	103	+	+	-	
CWD-AR-16-0153	Newton	D1804-51	83	NW1N	104	+	+	-	
CWD-AR-16-0154	Newton	D1804-51	83	NW1N	105	+	+	-	
CWD-AR-16-0155	Newton	D1804-51	83	NW1N	106	+	+	-	
CWD-AR-16-0156	Newton	D1804-51	83	NW1N	107	+	+	-	
CWD-AR-16-0157	Newton	D1804-51	83	NW1N	108	+	+	-	
CWD-AR-16-0159	Newton	D1804-51	83	NW1N	109	+	+	-	
CWD-AR-16-0160	Newton	D1804-51	83	NW1N	110	+	+	-	
CWD-AR-16-0161	Newton	D1804-51	83	NW1N	111	+	+	-	
CWD-AR-16-0162	Newton	D1804-51	83	NW1N	112	+	+	-	
CWD-AR-16-0163	Newton	D1804-51	83	NW1N	113	+	+	-	
CWD-AR-16-0164	Newton	D1804-51	83	NW1N	114	+	+	-	
CWD-AR-16-0165	Newton	D1804-51	83	NW1N	115	+	+	+	
CWD-AR-16-0166	Newton	D1804-51	83	NW1N	116	+	+	-	
CWD-AR-16-0167	Newton	D1804-51	83	NW1N	117	+	+	-	
CWD-AR-16-0168	Newton	D1804-51	83	NW1N	118	+	+	-	
CWD-AR-16-0170	Newton	D1804-51	83	NW1N	119	+	+	-	
CWD-AR-16-0171	Newton	D1804-51	83	NW1N	120	+	+	-	
CWD-AR-16-0172	Newton	D1804-51	83	NW1N	121	+	+	+	
CWD-AR-16-0174	Newton	D1804-51	83	NW1N	122	+	+	-	

CWD-AR-16-0178	Newton	D1804-52	83	NW1N	123	+	+	-
CWD-AR-16-0179	Newton	D1804-52	83	NW1N	124	+	+	-
CWD-AR-16-0181	Newton	D1804-52	83	NW1N	125	+	+	-
CWD-AR-16-0183	Newton	D1804-52	83	NW1N	126	+	+	-
CWD-AR-16-0185	Newton	D1804-52	83	NW1N	127	+	+	-
CWD-AR-16-0187	Newton	D1804-52	83	NW1N	128	+	+	-
CWD-AR-16-0188	Newton	D1804-52	83	NW1N	129	+	+	-
CWD-AR-16-0189	Newton	D1804-52	83	NW1N	130	+	+	-
CWD-AR-16-0190	Newton	D1804-52	83	NW1N	131	+	+	-
CWD-AR-16-0191	Newton	D1804-52	83	NW1N	132	+	+	-
CWD-AR-16-0192	Newton	D1804-52	83	NW1N	133	+	+	-
CWD-AR-16-0193	Newton	D1804-52	83	NW1N	134	+	+	-
CWD-AR-16-0194	Newton	D1804-52	83	NW1N	135	+	+	-
CWD-AR-16-0195	Newton	D1804-52	83	NW1N	136	+	+	-
CWD-AR-16-0196	Newton	D1804-52	83	NW1N	137	+	+	-
CWD-AR-16-0197	Newton	D1804-52	83	NW1N	138	+	+	-
CWD-AR-16-0198	Newton	D1804-52	83	NW1N	139	+	+	-
CWD-AR-16-0199	Newton	D1804-52	83	NW1N	140	+	+	-
CWD-AR-16-0200	Newton	D1804-52	83	NW1N	141	+	+	-
CWD-AR-16-0201	Newton	D1804-52	83	NW1N	142	+	+	-
CWD-AR-16-0251	Newton	D1804-52	83	NW1N	143	+	+	-
CWD-AR-16-0252	Newton	D1804-52	83	NW1N	144	+	+	-
CWD-AR-16-0253	Newton	D1804-52	83	NW1N	145	+	+	-
CWD-AR-16-0276	Newton	D1804-52	83	NW1N	146	+	+	-
CWD-AR-16-0001	Newton	D1612-10	83	NW1P	001	+	+	-
CWD-AR-16-0003	Newton	D1612-10	83	NW1P	002	+	+	-
CWD-AR-16-0005	Newton	D1612-10	83	NW1P	003	+	+	+
CWD-AR-16-0009	Newton	D1612-10	83	NW1P	004	+	+	-
CWD-AR-16-0020	Newton	D1612-10	83	NW1P	005	+	+	-
CWD-AR-16-0028	Newton	D1612-10	83	NW1P	006	+	+	-
CWD-AR-16-0032	Newton	D1612-10	83	NW1P	007	+	+	-
CWD-AR-16-0035	Newton	D1612-10	83	NW1P	008	+	+	-
CWD-AR-16-0036	Newton	D1612-10	83	NW1P	009	+	+	-
CWD-AR-16-0038	Newton	D1612-10	83	NW1P	010	+	+	-
CWD-AR-16-0059	Newton	D1701-08	83	NW1P	011	+	+	+
CWD-AR-16-0080	Newton	D1701-08	83	NW1P	012	+	+	-
CWD-AR-16-0083	Newton	D1701-08	83	NW1P	013	+	+	+
CWD-AR-16-0104	Newton	D1701-08	83	NW1P	014	+	+	+
CWD-AR-16-0105	Newton	D1701-08	83	NW1P	015	+	-	-
CWD-AR-16-0182	Newton	D1701-10	83	NW1P	016	+	+	+
CWD-AR-16-0133	Newton	D1701-08	83	NW1P	017	+	+	-
CWD-AR-16-0135	Newton	D1701-08	83	NW1P	018	+	+	-
CWD-AR-16-0176	Newton	D1701-08	83	NW1P	019	+	+	+
CWD-AR-16-0379	Newton	D1804-20	83	NW1P	020	+	+	-
CWD-AR-16-0401	Newton	D1701-08	83	NW1P	021	+	+	-
CWD-AR-16-0402	Newton	D1701-08	83	NW1P	022	+	+	-
CWD-AR-16-0426	Newton	D1701-08	83	NW1P	023	+	+	-
CWD-AR-16-0428	Newton	D1701-08	83	NW1P	024	+	+	-
CWD-AR-16-0460	Newton	D1701-08	83	NW1P	025	+	+	-
CWD-AR-16-0501	Newton	D1701-08	83	NW1P	026	+	+	-
CWD-AR-16-0507	Newton	D1701-08	83	NW1P	027	+	+	+
CWD-AR-16-0526	Newton	D1701-08	83	NW1P	028	+	+	-
CWD-AR-16-0595	Newton	D1701-08	83	NW1P	029	+	+	-
CWD-AR-16-0727	Newton	D1701-08	83	NW1P	030	+	+	-
CWD-AR-16-0732	Newton	D1701-08	83	NW1P	031	+	+	-
CWD-AR-16-0779	Newton	D1701-08	83	NW1P	032	+	+	-
CWD-AR-16-0039	Newton	D1701-10	83	NW1P	033	+	+	-
CWD-AR-16-0041	Newton	D1701-10	83	NW1P	034	+	+	+
CWD-AR-16-0042	Newton	D1701-10	83	NW1P	035	+	+	+

CWD-AR-16-0045	Newton	D1701-10	83	NW1P	036	+	+	+	+
CWD-AR-16-0046	Newton	D1701-10	83	NW1P	037	+	+	+	+
CWD-AR-16-0052	Newton	D1701-10	83	NW1P	038	+	-	-	-
CWD-AR-16-0082	Newton	D1701-10	83	NW1P	039	+	+	-	-
CWD-AR-16-0087	Newton	D1701-10	83	NW1P	040	+	+	-	-
CWD-AR-16-0090	Newton	D1701-10	83	NW1P	041	+	+	+	+
CWD-AR-16-0091	Newton	D1701-10	83	NW1P	042	+	+	-	+
CWD-AR-16-0093	Newton	D1701-10	83	NW1P	043	+	+	-	-
CWD-AR-16-0127	Newton	D1701-10	83	NW1P	044	+	+	-	-
CWD-AR-16-0129	Newton	D1701-10	83	NW1P	045	+	+	-	+
CWD-AR-16-0130	Newton	D1701-10	83	NW1P	046	+	+	+	+
CWD-AR-16-0136	Newton	D1701-10	83	NW1P	047	+	+	-	-
CWD-AR-16-0139	Newton	D1701-10	83	NW1P	048	+	+	-	+
CWD-AR-16-0140	Newton	D1701-10	83	NW1P	049	+	+	-	+
CWD-AR-16-0158	Newton	D1701-10	83	NW1P	050	+	+	-	+
CWD-AR-16-0169	Newton	D1701-10	83	NW1P	051	+	+	-	+
CWD-AR-16-0173	Newton	D1701-10	83	NW1P	052	+	+	+	+
CWD-AR-16-0175	Newton	D1701-10	83	NW1P	053	+	+	+	+
CWD-AR-16-0177	Newton	D1701-10	83	NW1P	054	+	+	+	-
CWD-AR-16-0180	Newton	D1701-10	83	NW1P	055	+	+	+	-
CWD-AR-16-0184	Newton	D1804-20	83	NW1P	056	+	+	-	-
CWD-AR-16-0186	Newton	D1804-20	83	NW1P	057	+	+	-	-
CWD-AR-16-0454	Newton	D1804-20	83	NW1P	058	+	+	-	-
CWD-AR-16-0462	Newton	D1804-20	83	NW1P	059	+	+	-	-
CWD-AR-16-0470	Newton	D1804-20	83	NW1P	060	+	+	+	-
CWD-AR-16-0472	Newton	D1804-20	83	NW1P	061	+	+	-	-
CWD-AR-16-0502	Newton	D1804-20	83	NW1P	062	+	+	+	-
CWD-AR-16-0508	Newton	D1804-20	83	NW1P	063	+	+	-	-
CWD-AR-16-0578	Newton	D1804-20	83	NW1P	064	+	+	-	-
CWD-AR-16-0590	Newton	D1804-20	83	NW1P	065	+	+	-	-
CWD-AR-16-0713	Newton	D1804-20	83	NW1P	066	+	+	-	-
CWD-AR-16-0782	Newton	D1804-20	83	NW1P	067	+	+	+	-
CWD-AR-16-02896	Newton	D1712-07	83	NW1P	068	+	+	+	+
CWD-AR-16-0314	Newton	D1712-07	83	NW1P	069	+	+	-	+
CWD-AR-16-02082	Newton	D1712-07	83	NW1P	070	+	+	-	+
CWD-AR-16-02084	Newton	D1712-07	83	NW1P	071	+	+	-	+
CWD-AR-16-02085	Newton	D1712-07	83	NW1P	072	+	+	+	+
CWD-AR-16-02089	Newton	D1712-07	83	NW1P	073	+	+	-	+
CWD-AR-16-02091	Newton	D1712-07	83	NW1P	074	+	+	+	+
CWD-AR-16-02092	Newton	D1712-07	83	NW1P	075	+	+	-	+
CWD-AR-16-02341	Newton	D1712-07	83	NW1P	076	+	+	-	+
CWD-AR-16-02342	Newton	D1712-07	83	NW1P	077	+	+	+	+
CWD-AR-16-02626	Newton	D1712-07	83	NW1P	078	+	+	-	+
CWD-AR-16-02889	Newton	D1712-07	83	NW1P	079	+	+	-	+
CWD-AR-16-02892	Newton	D1712-07	83	NW1P	080	+	+	-	+
CWD-AR-16-02894	Newton	D1712-07	83	NW1P	081	+	+	-	+
CWD-AR-17-392	Newton	D1806-96	83	NW2N	147	+	+	-	-
CWD-AR-17-393	Newton	D1806-96	83	NW2N	148	+	+	-	+
CWD-AR-17-400	Newton	D1806-96	83	NW2N	149	+	+	+	-
CWD-AR-17-428	Newton	D1806-96	83	NW2N	150	+	+	-	-
CWD-AR-17-429	Newton	D1806-96	83	NW2N	151	+	+	-	-
CWD-AR-17-430	Newton	D1806-96	83	NW2N	152	+	+	-	+
CWD-AR-17-431	Newton	D1806-96	83	NW2N	153	+	+	-	-
CWD-AR-17-434	Newton	D1806-98	83	NW2N	154	+	+	-	-
CWD-AR-17-435	Newton	D1806-98	83	NW2N	155	+	-	-	-
CWD-AR-17-12110	Newton	D1806-98	83	NW2N	156	+	+	-	-
CWD-AR-17-12443	Newton	D1806-98	83	NW2N	157	+	+	-	-
CWD-AR-17-12456	Newton	D1806-98	83	NW2N	158	+	+	-	-
CWD-AR-17-14242	Newton	D1806-98	83	NW2N	159	+	-	-	-

CWD-AR-17-14244	Newton	D1806-98	83	NW2N	160	+	+	-	
CWD-AR-17-14245	Newton	D1806-98	83	NW2N	161	+	+	-	
CWD-AR-17-14246	Newton	D1806-98	83	NW2N	162	+	+	+	+
CWD-AR-17-14248	Newton	D1806-98	83	NW2N	163	+	+	+	
CWD-AR-17-14251	Newton	D1806-98	83	NW2N	164	+	+	-	+
CWD-AR-17-14253	Newton	D1806-98	83	NW2N	165	+	+	+	
CWD-AR-17-14254	Newton	D1806-98	83	NW2N	166	+	+	-	
CWD-AR-17-14255	Newton	D1806-98	83	NW2N	167	+	+	-	
CWD-AR-17-14256	Newton	D1806-98	83	NW2N	168	+	+	-	
CWD-AR-17-14542	Newton	D1806-98	83	NW2N	169	+	+	-	
CWD-AR-17-14546	Newton	D1806-98	83	NW2N	170	+	+	+	
CWD-AR-17-14547	Newton	D1806-98	83	NW2N	171	+	+	+	
CWD-AR-17-14548	Newton	D1806-98	83	NW2N	172	+	+	-	
CWD-AR-17-14550	Newton	D1806-98	83	NW2N	173	+	+	-	
CWD-AR-17-14551	Newton	D1806-98	83	NW2N	174	+	+	-	
CWD-AR-17-14841	Newton	D1806-98	83	NW2N	175	+	+	-	+
CWD-AR-17-14842	Newton	D1806-98	83	NW2N	176	+	+	+	
CWD-AR-17-14845	Newton	D1806-98	83	NW2N	177	+	+	-	+
CWD-AR-17-14846	Newton	D1806-100	83	NW2N	178	+	+	+	
CWD-AR-17-14852	Newton	D1806-100	83	NW2N	179	+	+	+	
CWD-AR-17-14853	Newton	D1806-100	83	NW2N	180	+	+	+	
CWD-AR-17-14857	Newton	D1806-100	83	NW2N	181	+	+	+	
CWD-AR-17-14862	Newton	D1806-100	83	NW2N	182	+	+	-	
CWD-AR-17-14866	Newton	D1806-100	83	NW2N	183	+	+	-	
CWD-AR-17-14867	Newton	D1806-100	83	NW2N	184	+	+	-	
CWD-AR-17-14869	Newton	D1806-100	83	NW2N	185	+	+	+	
CWD-AR-17-14871	Newton	D1806-100	83	NW2N	186	+	+	-	
CWD-AR-17-14878	Newton	D1806-100	83	NW2N	187	+	+	-	
CWD-AR-17-14880	Newton	D1806-100	83	NW2N	188	+	+	+	
CWD-AR-17-14881	Newton	D1806-100	83	NW2N	189	+	+	-	
CWD-AR-17-14882	Newton	D1806-100	83	NW2N	190	+	+	-	
CWD-AR-17-19501	Newton	D1806-100	83	NW2N	191	+	+	-	+
CWD-AR-17-19503	Newton	D1806-100	83	NW2N	192	+	+	+	
CWD-AR-17-19504	Newton	D1806-100	83	NW2N	193	+	+	+	+
CWD-AR-17-19505	Newton	D1806-100	83	NW2N	194	+	+	-	
CWD-AR-17-19506	Newton	D1806-100	83	NW2N	195	+	+	-	
CWD-AR-17-19507	Newton	D1806-100	83	NW2N	196	+	+	-	
CWD-AR-17-19508	Newton	D1806-100	83	NW2N	197	+	+	-	
CWD-AR-17-19509	Newton	D1806-100	83	NW2N	198	+	+	-	
CWD-AR-17-19621	Newton	D1806-100	83	NW2N	199	+	+	-	
CWD-AR-17-19622	Newton	D1806-100	83	NW2N	200	+	+	-	
CWD-AR-17-19623	Newton	D1806-100	83	NW2N	201	+	+	+	
CWD-AR-17-19624	Newton	D1806-101	83	NW2N	202	+	+	+	
CWD-AR-17-19625	Newton	D1806-101	83	NW2N	203	+	+	+	
CWD-AR-17-19627	Newton	D1806-101	83	NW2N	204	+	+	+	
CWD-AR-17-19628	Newton	D1806-101	83	NW2N	205	+	+	+	
CWD-AR-17-19629	Newton	D1806-101	83	NW2N	206	+	+	-	
CWD-AR-17-19630	Newton	D1806-101	83	NW2N	207	+	+	+	
CWD-AR-17-19631	Newton	D1806-101	83	NW2N	208	+	+	-	
CWD-AR-17-19632	Newton	D1806-101	83	NW2N	209	+	+	+	+
CWD-AR-17-19633	Newton	D1806-101	83	NW2N	210	+	+	+	
CWD-AR-17-19634	Newton	D1806-101	83	NW2N	211	+	+	-	
CWD-AR-17-19636	Newton	D1806-101	83	NW2N	212	+	+	-	+
CWD-AR-17-19638	Newton	D1806-101	83	NW2N	213	+	+	-	+
CWD-AR-17-19640	Newton	D1806-101	83	NW2N	214	+	+	+	
CWD-AR-17-19641	Newton	D1806-101	83	NW2N	215	+	+	+	
CWD-AR-17-19926	Newton	D1806-101	83	NW2N	216	+	+	-	
CWD-AR-17-14240	Newton	D1807-17	83	NW2N	224	+	+	+	
CWD-AR-17-14241	Newton	D1807-17	83	NW2N	225	+	+	-	

CWD-AR-17-14861	Newton	D1807-17	83	NW2N	226	+	+	-	+
CWD-AR-17-19500	Newton	D1807-17	83	NW2N	227	+	+	+	
CWD-AR-17-394	Newton	D1807-09	83	NW2P	217	+	+	+	+
CWD-AR-17-397	Newton	D1807-09	83	NW2P	218	+	+	-	+
CWD-AR-17-398	Newton	D1807-09	83	NW2P	219	+	+	-	+
CWD-AR-17-399	Newton	D1807-09	83	NW2P	220	+	+	-	+
CWD-AR-17-12012	Newton	D1807-09	83	NW2P	221	+	+	-	+
CWD-T060-AR-17-094	Newton	D1807-09	83	NW2P	222	+	+	-	+
CWD-AR-17-433	Newton	D1807-09	83	NW2P	223	+	+	-	+
CWD-AR-17-12448	Newton	D1807-09	83	NW2P	228	+	+	-	+
CWD-AR-17-12449	Newton	D1807-09	83	NW2P	229	+	+	+	+
CWD-AR-17-12460	Newton	D1807-09	83	NW2P	230	+	+	-	+
CWD-AR-17-14249	Newton	D1807-09	83	NW2P	231	+	+	-	+
CWD-AR-17-14250	Newton	D1807-09	83	NW2P	232	+	+	-	+
CWD-AR-17-14252	Newton	D1807-09	83	NW2P	233	+	+	-	+
CWD-AR-17-14544	Newton	D1807-09	83	NW2P	234	+	+	+	+
CWD-AR-17-14851	Newton	D1807-09	83	NW2P	235	+	+	+	+
CWD-AR-17-14856	Newton	D1807-09	83	NW2P	236	+	+	+	+
CWD-AR-17-14868	Newton	D1807-09	83	NW2P	237	+	+	-	+
CWD-AR-17-14870	Newton	D1807-09	83	NW2P	238	+	+	-	+
CWD-AR-17-19637	Newton	D1807-09	83	NW2P	239	+	+	-	+
CWD-AR-17-19639	Newton	D1807-09	83	NW2P	240	+	+	-	+
CWD-AR-17-23835	Newton	D1807-09	83	NW2P	241	+	+	-	+
CWD-AR-17-1153	Ouachita	D1806-102	83	OU2N	001	+	+	-	+
CWD-AR-18-476	Ouachita	D1806-102	83	OU2N	002	+	+	-	+
CWD-AR-18-477	Ouachita	D1806-102	83	OU2N	003	+			
CWD-AR-18-0501HC	Ouachita	D1806-102	83	OU2N	004	+	+	+	+
CWD-AR-18-0502HC	Ouachita	D1806-102	83	OU2N	005	+	+	-	+
CWD-AR-18-0503HC	Ouachita	D1806-102	83	OU2N	006	+			
CWD-AR-18-504	Ouachita	D1806-102	83	OU2N	007	+	+	-	+
CWD-AR-18-505	Ouachita	D1806-102	83	OU2N	008	+	+	+	+
CWD-AR-18-506	Ouachita	D1806-102	83	OU2N	009	+	+	+	+
CWD-AR-18-551	Ouachita	D1806-103	83	OU2N	010	+	+	-	+
CWD-AR-18-80	Ouachita	D1806-104	83	OU3N	011	+			
CWD-AR-18-82	Ouachita	D1806-104	83	OU3N	012	+			
CWD-AR-18-83	Ouachita	D1806-104	83	OU3N	013	+			
CWD-AR-18-85	Ouachita	D1806-104	83	OU3N	014	+	+	-	+
CWD-AR-18-90	Ouachita	D1806-104	83	OU3N	015	+	+	-	+
CWD-AR-18-91	Ouachita	D1806-104	83	OU3N	016	+			
CWD-AR-00-0842	Ouachita	D1901-56	83	OU3N	017	+	+	-	+
CWD-AR-18-01465	Ouachita	D1901-56	83	OU3N	018	+	+	-	+
CWD-AR-00-0844	Ouachita	D1901-56	83	OU3N	019	+	+	-	+
CWD-AR-00-0861	Ouachita	D1902-15	83	OU3U	021	+	+	-	+
CWD-AR-17-1010	Perry	D1806-105	83	PE2N	017	+	+	-	+
CWD-AR-17-1012	Perry	D1806-105	83	PE2N	018	+	+	-	+
CWD-AR-17-1013	Perry	D1806-105	83	PE2N	19	+			
CWD-AR-18-751	Perry	D1806-105	83	PE2N	020	+	+	-	+
CWD-AR-18-120	Perry	D1806-106	83	PE3N	021	+	+	+	+
CWD-AR-18-122	Perry	D1806-106	83	PE3N	022	+	+	+	+
CWD-AR-18-0129B	Perry	D1807-18	83	PE3N	023	+	+	+	+
CWD-AR-18-01050	Perry	D1901-57	83	PE3N	024	+	+	+	+
CWD-AR-00-0122	Perry	D1901-57	83	PE3N	025	+	+	-	+
CWD-AR-16-7139	Phillips	D1806-107	83	PH2N	001	+	+	+	+
CWD-AR-16-7140	Phillips	D1806-107	83	PH2N	002	+	+	+	+
CWD-AR-17-3527	Phillips	D1806-107	83	PH2N	003	+	+	-	+
CWD-AR-17-3852	Phillips	D1806-107	83	PH2N	004	+	+	+	+
CWD-AR-17-3855	Phillips	D1806-107	83	PH2N	005	+	+	+	+
CWD-AR-18-663	Phillips	D1806-107	83	PH2N	006	+	+	+	+
CWD-AR-00-0321	Phillips	D1901-58	83	PH3N	007	+	+	+	+

CWD-AR-00-0322	Phillips	D1901-58	83	PH3N	008	+	+	-	+
CWD-AR-00-0328	Phillips	D1901-58	83	PH3N	009	+	+	-	+
CWD-AR-00-0886	Pike	D1901-59	83	PI3N	002	+	+	-	+
CWD-AR-00-0984	Pike	D1901-59	83	PI3N	003	+	+	+	+
CWD-AR-00-0986	Pike	D1901-59	83	PI3N	004	+	+	-	+
CWD-AR-00-0991	Pike	D1901-59	83	PI3N	005	+	+	-	+
CWD-AR-00-0992	Pike	D1901-59	83	PI3N	006	+	+	-	+
CWD-AR-00-0993	Pike	D1901-59	83	PI3N	007	+	+	+	+
CWD-AR-00-1092	Pike	D1901-59	83	PI3N	008	+	+	+	+
CWD-AR-18-0680B	Pike	D1806-108	83	PK2N	001	+	+	-	+
CWD-AR-18-801	Polk	D1806-109	83	PL2N	001	+	+	-	+
CWD-AR-00-8767	Polk	D1901-64	83	PL3N	002	+	+	+	+
CWD-AR-00-8769	Polk	D1901-64	83	PL3N	003	+	+	-	+
CWD-AR-18-591	Poinsett	D1806-110	83	PN2N	001	+	+	-	+
CWD-AR-18-592	Poinsett	D1806-110	83	PN2N	002	+	+	-	+
CWD-AR-18-593	Poinsett	D1806-110	83	PN2N	003	+	+	-	+
CWD-AR-00-0623	Poinsett	D1901-61	83	PO3N	004	+	+	-	+
CWD-AR-00-0742	Poinsett	D1901-63	83	PO3N	005	+	+	+	+
CWD-AR-00-0761	Poinsett	D1901-63	83	PO3N	006	+	+	-	+
CWD-AR-00-0768	Poinsett	D1901-63	83	PO3N	007	+	+	-	+
UTM	Poinsett	D1901-63	83	PO3N	008	+	+	+	+
CWD-AR-00-0741	Poinsett	D1901-63	83	PO3N	009	+	+	-	+
CWD-AR-00-0767	Poinsett	D1901-63	83	PO3N	010	+	+	-	+
CWD-AR-00-0766	Poinsett	D1901-63	83	PO3N	011	+	+	-	+
CWD-AR-00-0769	Poinsett	D1902-19	83	PO3N	012	+	+	-	+
CWD-AR-00-0770	Poinsett	D1902-50	83	PO3N	013	+	+	-	+
CWD-AR-18-01359	Poinsett	D1902-50	83	PO3N	014	+	+	-	+
CWD-AR-16-4403	Pope	D1701-03	83	PP1N	002	+	-	-	+
CWD-AR-16-4551	Pope	D1701-03	83	PP1N	003	+	-	+	+
CWD-AR-16-4552	Pope	D1701-03	83	PP1N	004	+	+	+	+
CWD-AR-16-4553	Pope	D1701-03	83	PP1N	005	+	+	+	+
CWD-AR-16-4554	Pope	D1701-03	83	PP1N	006	+	+	-	+
CWD-AR-16-4555	Pope	D1701-03	83	PP1N	007	+	+	-	+
CWD-AR-16-4556	Pope	D1701-03	83	PP1N	008	+	+	-	+
CWD-AR-16-4557	Pope	D1701-03	83	PP1N	009	+	+	-	+
CWD-AR-16-4576	Pope	D1701-03	83	PP1N	010	+	+	-	+
CWD-AR-16-4577	Pope	D1701-05	83	PP1N	011	+	+	+	+
CWD-AR-16-4578	Pope	D1701-05	83	PP1N	012	+	+	-	+
CWD-AR-16-4579	Pope	D1701-05	83	PP1N	013	+	+	-	+
CWD-AR-16-4580	Pope	D1701-05	83	PP1N	014	+	+	+	+
CWD-AR-16-4581	Pope	D1701-05	83	PP1N	015	+	+	-	+
CWD-AR-16-4582	Pope	D1701-05	83	PP1N	016	+	+	+	+
CWD-AR-16-4583	Pope	D1701-05	83	PP1N	017	+	+	-	+
CWD-AR-16-4584	Pope	D1701-05	83	PP1N	018	+	+	+	+
CWD-AR-16-4585	Pope	D1701-05	83	PP1N	019	+	+	-	+
CWD-AR-16-4586	Pope	D1701-05	83	PP1N	020	+	+	-	+
CWD-AR-16-04993	Pope	D1801-06	83	PP1N	021	+	+	+	+
CWD-AR-16-04994	Pope	D1801-06	83	PP1N	022	+	+	+	+
CWD-AR-16-05001	Pope	D1801-06	83	PP1N	023	+	+	-	+
CWD-AR-16-05240	Pope	D1801-06	83	PP1N	024	+	+	-	+
CWD-AR-16-05242	Pope	D1801-06	83	PP1N	025	+	+	-	+
CWD-AR-16-05245	Pope	D1801-06	83	PP1N	026	+	+	-	+
CWD-AR-16-05247	Pope	D1801-06	83	PP1N	027	+	+	-	+
CWD-AR-16-05248	Pope	D1801-06	83	PP1N	028	+	+	+	+
CWD-AR-16-05249	Pope	D1801-06	83	PP1N	029	+	+	-	+
CWD-AR-16-05251	Pope	D1801-06	83	PP1N	030	+	+	+	+
CWD-AR-16-05256	Pope	D1801-06	83	PP1N	031	+	+	-	+
CWD-AR-16-05257	Pope	D1801-06	83	PP1N	032	+	+	-	+
CWD-AR-16-05258	Pope	D1801-06	83	PP1N	033	+	+	+	+

CWD-AR-16-05501	Pope	D1801-06	83	PP1N	034	+	+	-	+
CWD-AR-16-05504	Pope	D1801-06	83	PP1N	035	+	+	-	+
CWD-AR-16-05505	Pope	D1801-06	83	PP1N	036	+	+	-	+
CWD-AR-16-05507	Pope	D1801-08	83	PP1N	037	+	+	-	+
CWD-AR-16-05509	Pope	D1801-08	83	PP1N	038	+	+	-	+
CWD-AR-16-05511	Pope	D1801-08	83	PP1N	039	+	+	-	+
CWD-AR-16-05780	Pope	D1801-08	83	PP1N	040	+	+	-	+
CWD-AR-16-05782	Pope	D1801-08	83	PP1N	041	+	+	+	+
CWD-AR-16-05784	Pope	D1801-08	83	PP1N	042	+	+	+	+
CWD-AR-16-05785	Pope	D1801-08	83	PP1N	043	+	+	-	+
CWD-AR-16-05787	Pope	D1801-08	83	PP1N	044	+	+	-	+
CWD-AR-16-05798	Pope	D1801-08	83	PP1N	045	+	+	+	+
CWD-AR-16-05799	Pope	D1801-08	83	PP1N	046	+	+	-	+
CWD-AR-16-05800	Pope	D1801-08	83	PP1N	047	+	+	-	+
CWD-AR-16-06729	Pope	D1801-08	83	PP1N	048	+	+	-	+
CWD-AR-16-06730	Pope	D1801-08	83	PP1N	049	+	+	-	+
CWD-AR-16-06738	Pope	D1801-08	83	PP1N	050	+	+	-	+
CWD-AR-16-02882	Pope	D1801-08	83	PP1N	051	+	+	-	+
CWD-AR-16-5002	Pope	D1802-04	83	PP1N	052	+	+	-	+
CWD-AR-16-7228	Pope	D1802-04	83	PP1N	053	+	+	-	+
CWD-AR-16-7229	Pope	D1802-04	83	PP1N	054	+	+	-	+
CWD-AR-16-7251	Pope	D1802-04	83	PP1N	055	+	+	-	+
CWD-AR-16-7252	Pope	D1802-04	83	PP1N	056	+	+	-	+
bone marrow & skin	Pope	D1701-07	83	PP1P	001	+	-	-	+
CWD-AR-16-05790	Pope	D1712-07	83	PP1P	002	+	+	-	+
CWD-AR-16-2101	Pope	D1806-111	83	PP2N	057	+			
CWD-AR-16-2102	Pope	D1806-111	83	PP2N	058	+			
CWD-AR-16-2103	Pope	D1806-111	83	PP2N	059	+			
CWD-AR-16-2104	Pope	D1806-111	83	PP2N	060	+			
CWD-AR-16-2105	Pope	D1806-111	83	PP2N	061	+			
CWD-AR-16-2106	Pope	D1806-111	83	PP2N	062	+			
CWD-AR-16-2107	Pope	D1806-111	83	PP2N	063	+			
CWD-AR-16-2108	Pope	D1806-111	83	PP2N	064	+			
CWD-AR-16-2109	Pope	D1806-111	83	PP2N	065	+			
CWD-AR-16-3957	Pope	D1806-111	83	PP2N	066	+			
CWD-AR-16-3958	Pope	D1806-111	83	PP2N	067	+			
CWD-AR-16-3959	Pope	D1806-111	83	PP2N	068	+			
CWD-AR-17-19680	Pope	D1806-111	83	PP2N	069	+			
CWD-AR-17-19681	Pope	D1806-111	83	PP2N	070	+			
CWD-AR-17-19682	Pope	D1806-111	83	PP2N	071	+			
CWD-AR-17-19683	Pope	D1806-111	83	PP2N	072	+			
CWD-AR-17-19684	Pope	D1806-111	83	PP2N	073	+			
CWD-AR-17-19685	Pope	D1806-111	83	PP2N	074	+			
CWD-AR-17-19686	Pope	D1806-111	83	PP2N	075	+			
CWD-AR-17-19687	Pope	D1806-111	83	PP2N	076	+			
CWD-AR-17-19688	Pope	D1806-111	83	PP2N	077	+			
CWD-AR-17-19689	Pope	D1806-111	83	PP2N	078	+			
CWD-AR-17-19709	Pope	D1806-111	83	PP2N	079	+			
CWD-AR-17-19860	Pope	D1806-111	83	PP2N	080	+			
CWD-AR-17-19861	Pope	D1806-112	83	PP2N	081	+			
CWD-AR-17-19862	Pope	D1806-112	83	PP2N	082	+	+	+	+
CWD-AR-17-19920	Pope	D1806-112	83	PP2N	083	+	+	-	+
CWD-AR-17-19923	Pope	D1806-112	83	PP2N	084	+	+	+	+
CWD-AR-17-19924	Pope	D1806-112	83	PP2N	085	+			
CWD-AR-17-19969	Pope	D1806-112	83	PP2N	086	+			
CWD-AR-17-19970	Pope	D1806-112	83	PP2N	087	+			
CWD-AR-17-19972	Pope	D1806-112	83	PP2N	088	+	+	-	+
CWD-AR-17-19974	Pope	D1806-112	83	PP2N	089	+			
CWD-AR-17-19975	Pope	D1806-112	83	PP2N	090	+	+	-	+

CWD-AR-17-19978	Pope	D1806-112	83	PP2N	091	+	+	-	+
CWD-AR-17-20004	Pope	D1806-112	83	PP2N	092	+			
CWD-AR-17-20005	Pope	D1806-112	83	PP2N	093	+			
CWD-AR-17-19922	Pope	D1807-19	83	PP2N	095	+			
CWD-AR-17-19927	Pope	D1807-19	83	PP2N	096	+			
CWD-AR-17-19921	Pope	D1807-19	83	PP2N	097	+			
CWD-AR-18-491	Pope	D1806-113	83	PP3N	094	+	+	+	+
CWD-AR-00-8739	Pope	D1902-51	83	PP3N	098	+	-	+	+
CWD-AR-17-3704	Prairie	D1806-114	83	PR2N	001	+	+	-	+
CWD-AR-18-410	Prairie	D1806-114	83	PR2N	002	+	+	-	+
CWD-AR-18-626	Prairie	D1806-114	83	PR2N	003	+	+	-	+
CWD-AR-18-627	Prairie	D1806-114	83	PR2N	004	+	+	-	+
CWD-AR-18-634	Prairie	D1806-114	83	PR2N	005	+	+	-	+
CWD-AR-18-0685HC	Prairie	D1806-114	83	PR2N	006	+	+	-	+
CWD-AR-18-0686HC	Prairie	D1806-114	83	PR2N	007	+	+	-	+
CWD-AR-18-0687HC	Prairie	D1806-114	83	PR2N	008	+	+	-	+
CWD-AR-18-0688HC	Prairie	D1806-114	83	PR2N	009	+	+	-	+
CWD-AR-18-0689HC	Prairie	D1806-114	83	PR2N	010	+	+	-	+
CWD-AR-18-694	Prairie	D1806-115	83	PR2N	011	+	+	-	+
CWD-AR-18-685	Prairie	D1806-116	83	PR3N	012	+			
CWD-AR-18-687	Prairie	D1806-116	83	PR3N	013	+			
CWD-AR-18-0204HC	Pulaski	D1806-117	83	PU2N	001	+	+	-	+
CWD-AR-18-0205HC	Pulaski	D1806-117	83	PU2N	002	+	+	-	+
CWD-AR-18-520	Pulaski	D1806-118	83	PU3N	003	+			
CWD-AR-18-521	Pulaski	D1806-118	83	PU3N	004	+			
CWD-AR-18-522	Pulaski	D1806-118	83	PU3N	005	+			
CWD-AR-18-523	Pulaski	D1806-118	83	PU3N	006	+	+	+	+
CWD-AR-18-524	Pulaski	D1806-118	83	PU3N	007	+			
CWD-AR-18-525	Pulaski	D1806-118	83	PU3N	008	+	+	+	+
CWD-AR-18-527	Pulaski	D1806-118	83	PU3N	009	+	+	-	+
CWD-AR-18-528	Pulaski	D1806-118	83	PU3N	010	+	+	-	+
CWD-AR-18-529	Pulaski	D1806-118	83	PU3N	011	+	+	-	+
CWD-AR-18-530	Pulaski	D1806-118	83	PU3N	012	+	+	-	+
CWD-AR-18-640	Pulaski	D1806-118	83	PU3N	013	+	+	-	+
CWD-AR-18-642	Pulaski	D1806-118	83	PU3N	014	+	-	-	+
CWD-AR-18-643	Pulaski	D1806-118	83	PU3N	015	+	+	-	+
CWD-AR-18-0645B	Pulaski	D1807-21	83	PU3N	016	+	+	-	+
CWD-AR-16-4201	Randolph	D1806-119	83	RA2N	001	+	+	-	+
CWD-AR-18-176	Randolph	D1806-119	83	RA2N	002	+	+	+	+
CWD-AR-18-182	Randolph	D1806-119	83	RA2N	003	+	+	-	+
CWD-AR-18-183	Randolph	D1806-119	83	RA2N	004	+	+	-	+
CWD-AR-00-1343	Randolph	D1901-65	83	RA3N	005	+	+	+	+
CWD-AR-00-1344	Randolph	D1901-65	83	RA3N	006	+	+	-	+
	Randolph	D1902-52	83	RA3N	007	+	+	+	+
	Randolph	D1902-52	83	RA3N	008	+	+	+	+
	Randolph	D1902-52	83	RA3N	009	+	+	-	+
CWD-AR-17-19925	Saline	D1806-120	83	SA2N	001	+	+	+	+
CWD-AR-18-121	Saline	D1806-121	83	SA3N	002	+	+	-	+
CWD-AR-18-123	Saline	D1806-126	83	SA3N	003	+	+	-	+
CWD-AR-18-124	Saline	D1806-126	83	SA3N	004	+	+	-	+
CWD-AR-18-136	Saline	D1806-126	83	SA3N	005	+	+	-	+
CWD-AR-18-531	Saline	D1806-126	83	SA3N	006	+	+	-	+
CWD-AR-18-0130B	Saline	D1807-20	83	SA3N	007	+	+	-	+
CWD-AR-18-0132B	Saline	D1807-20	83	SA3N	008	+	+	-	+
CWD-AR-18-01054	Saline	D1901-66	83	SA3N	009	+	+	-	+
CWD-AR-00-1242	Saline	D1901-66	83	SA3N	010	+	+	-	+
CWD-AR-18-01534	Saline	D1902-53	83	SA3N	011	+	+	+	+
CWD-AR-18-01536	Saline	D1902-53	83	SA3N	012	+	+	-	+
CWD-AR-17-884	Sebastian	D1806-127	83	SB2N	001	+	+	+	+

CWD-AR-17-1348	Sebastian	D1806-127	83	SB2N	002	+	+	+	+
CWD-AR-17-1350	Sebastian	D1806-127	83	SB2N	003	+	+	-	+
CWD-AR-18-726	Sebastian	D1806-127	83	SB2N	004	+	+	-	+
CWD-AR-18-776	Sebastian	D1806-127	83	SB2N	005	+	+	+	+
CWD-AR-18-901	Sebastian	D1806-127	83	SB2N	006	+	+	+	+
CWD-AR-18-905	Sebastian	D1806-127	83	SB2N	007	+	+	+	+
CWD-AR-18-906	Sebastian	D1806-127	83	SB2N	008	+	+	+	+
CWD-AR-18-908	Sebastian	D1806-127	83	SB2N	009	+	+	-	+
CWD-AR-18-1077	Sebastian	D1806-127	83	SB2N	010	+	+	+	+
CWD-AR-01-3434	Sebastian	D1902-54	83	SB3N	019	+	+	+	+
CWD-T021-AR-170019	Sebastian	D1807-10	83	SB2P	017	+	+	-	+
CWD-AR-17-23920	Sebastian	D1806-128	83	SB3N	011	+	+	-	+
CWD-AR-17-23921	Sebastian	D1806-128	83	SB3N	012	+			
CWD-AR-17-23922	Sebastian	D1806-128	83	SB3N	013	+			
CWD-AR-17-23925	Sebastian	D1806-128	83	SB3N	014	+	+	+	+
CWD-AR-18-361	Sebastian	D1806-128	83	SB3N	015	+	+	+	+
CWD-AR-18-362	Sebastian	D1806-128	83	SB3N	016	+	+	+	
CWD-AR-18-01426	Sebastian	D1901-69	83	SB3N	018	+	+	-	+
CWD-AR-18-01427	Scott	D1901-67	83	SC3N	001	+	+	+	+
CWD-AR-00-1335	Scott	D1901-67	83	SC3N	002	+	+	+	+
CWD-AR-16-02347	Searcy	D1801-08	83	SE1N	001	+	+	-	+
CWD-AR-16-03142	Searcy	D1801-08	83	SE1N	002	+	+	+	+
CWD-AR-16-03143	Searcy	D1801-08	83	SE1N	003	+	+	-	+
CWD-AR-16-03145	Searcy	D1801-08	83	SE1N	004	+	+	-	+
CWD-AR-16-03148	Searcy	D1801-08	83	SE1N	005	+	+	-	+
CWD-AR-16-03152	Searcy	D1801-08	83	SE1N	006	+	+	+	+
CWD-AR-16-03154	Searcy	D1801-08	83	SE1N	007	+	+	-	+
CWD-AR-16-03160	Searcy	D1801-08	83	SE1N	008	+	+	-	+
CWD-AR-16-03406	Searcy	D1801-08	83	SE1N	009	+	+	+	+
CWD-AR-16-04983	Searcy	D1802-03	83	SE1N	010	+	+	+	+
CWD-AR-16-04986	Searcy	D1802-03	83	SE1N	011	+	+	-	+
CWD-AR-16-04989	Searcy	D1802-03	83	SE1N	012	+	+	-	+
CWD-AR-17-13642	Searcy	D1806-129	83	SE2N	013	+			
CWD-AR-17-13645	Searcy	D1806-129	83	SE2N	014	+	+	-	+
CWD-AR-17-13646	Searcy	D1806-129	83	SE2N	015	+			
CWD-AR-17-13647	Searcy	D1806-129	83	SE2N	016	+			
CWD-AR-17-13648	Searcy	D1806-130	83	SE2N	017	+			
CWD-AR-17-13649	Searcy	D1806-130	83	SE2N	018	+			
CWD-AR-17-13673	Searcy	D1806-130	83	SE2N	019	+	+	+	+
CWD-AR-17-13674	Searcy	D1806-130	83	SE2N	020	+			
CWD-AR-17-13675	Searcy	D1806-130	83	SE2N	021	+	+	+	+
CWD-AR-17-13676	Searcy	D1806-130	83	SE2N	022	+			
CWD-AR-17-13677	Searcy	D1806-130	83	SE2N	023	+	+	-	+
CWD-AR-17-13678	Searcy	D1806-130	83	SE2N	024	+			
CWD-AR-17-13679	Searcy	D1806-130	83	SE2N	025	+			
CWD-AR-17-13698	Searcy	D1806-130	83	SE2N	026	+	+	+	+
CWD-AR-17-14840	Searcy	D1806-130	83	SE2N	027	+			
CWD-AR-17-14854	Searcy	D1806-130	83	SE2N	028	+	+	-	+
CWD-AR-17-14858	Searcy	D1806-130	83	SE2N	029	+	+	-	
CWD-AR-17-14859	Searcy	D1806-130	83	SE2N	030	+	+	+	+
CWD-AR-17-14860	Searcy	D1806-130	83	SE2N	031	+	+	-	
CWD-AR-17-14863	Searcy	D1806-130	83	SE2N	032	+	+	+	
CWD-AR-17-14879	Searcy	D1806-130	83	SE2N	033	+	+	-	
CWD-AR-17-15306	Searcy	D1806-130	83	SE2N	034	+	+	-	+
CWD-AR-17-19021	Searcy	D1806-130	83	SE2N	035	+	+	-	
CWD-AR-17-19022	Searcy	D1806-130	83	SE2N	036	+	+	+	+
CWD-AR-17-19024	Searcy	D1806-130	83	SE2N	037	+	+	+	
CWD-AR-17-19028	Searcy	D1806-130	83	SE2N	038	+	+	-	
CWD-AR-17-19029	Searcy	D1806-130	83	SE2N	039	+	+	-	

CWD-AR-17-19033	Searcy	D1806-130	83	SE2N	040	+	+	+	+
CWD-AR-17-19034	Searcy	D1806-131	83	SE2N	041	+	+	-	
CWD-AR-17-19035	Searcy	D1806-131	83	SE2N	042	+	+	-	+
CWD-AR-17-19626	Searcy	D1806-131	83	SE2N	043	+	+	-	+
CWD-AR-17-19635	Searcy	D1806-131	83	SE2N	044	+	+	+	+
CWD-AR-17-13640	Searcy	D1807-22	83	SE2N	045	+	+	-	+
CWD-AR-17-13641	Searcy	D1807-22	83	SE2N	046	+	+	+	+
CWD-AR-17-13643	Searcy	D1807-22	83	SE2N	047	+	+	-	+
CWD-AR-17-16344	Searcy	D1807-22	83	SE2N	048	+	+	-	+
CWD-AR-17-19020	Searcy	D1807-22	83	SE2N	049	+	+	-	+
CWD-AR-00-8474	Searcy	D1901-68	83	SE3N	050	+	+	+	+
CWD-AR-00-8475	Searcy	D1901-68	83	SE3N	051	+	+	-	+
CWD-AR-00-8441	Searcy	D1901-68	83	SE3N	052	+	+	+	+
CWD-AR-16-7137	St. Francis	D1806-132	83	SF2N	001	+	+	-	+
CWD-AR-17-3851	St. Francis	D1806-132	83	SF2N	002	+	+	+	+
CWD-AR-17-3853	St. Francis	D1806-132	83	SF2N	003	+	+	-	+
CWD-AR-18-654	St. Francis	D1806-132	83	SF2N	004	+	+	+	+
CWD-AR-18-664	St. Francis	D1806-132	83	SF2N	005	+	-	-	+
CWD-AR-18-698	St. Francis	D1806-132	83	SF2N	006	+	+	-	+
CWD-AR-00-0323	St. Francis	D1901-73	83	SF3N	007	+	+	-	+
CWD-AR-00-0329	St. Francis	D1901-73	83	SF3N	008	+	+	+	+
CWD-AR-17-3862	St. Francis	D1901-73	83	SF3N	009	+	+	-	+
CWD-AR-18-110	Sharp	D1806-133	83	SH2N	001	+	+	-	+
CWD-AR-18-157	Sharp	D1806-133	83	SH2N	002	+	+	-	+
CWD-AR-18-158	Sharp	D1806-133	83	SH2N	003	+			
CWD-AR-18-180	Sharp	D1806-133	83	SH2N	004	+	+	-	+
CWD-AR-18-181	Sharp	D1806-133	83	SH2N	005	+	+	-	+
CWD-AR-00-0602	Sharp	D1901-71	83	SH3N	006	+	+	-	+
CWD-AR-00-1341	Sharp	D1901-71	83	SH3N	007	+	+	+	+
CWD-AR-00-1346	Sharp	D1901-71	83	SH3N	008	+	+	+	+
CWD-AR-00-1348	Sharp	D1901-71	83	SH3N	009	+	-	-	+
CWD-AR-00-1350	Sharp	D1901-71	83	SH3N	010	+	-	-	+
CWD-AR-00-1351	Sharp	D1901-71	83	SH3N	011	+	+	+	+
CWD-AR-00-1354	Sharp	D1901-72	83	SH3N	012	+	+	-	+
CWD-AR-00-1356	Sharp	D1901-72	83	SH3N	013	+	+	+	+
CWD-AR-00-1401	Sharp	D1901-72	83	SH3N	014	+	+	+	+
CWD-AR-00-1406	Sharp	D1901-72	83	SH3N	015	+	+	-	+
CWD-AR-00-9254	Sharp	D1901-72	83	SH3N	016	+	+	-	+
CWD-AR-18-0184	Sharp	D1901-72	83	SH3N	017	+	+	+	+
CWD-AR-00-1410	Sharp	D1902-56	83	SH3N	018	+	+	+	+
CWD-AR-16-03404	Stone	D1802-04	83	ST1N	001	+	+	-	+
CWD-AR-16-03159	Stone	D1802-04	83	ST1N	002	+	+	-	+
CWD-AR-17-14247	Stone	D1806-134	83	ST2N	003	+	+	+	+
CWD-AR-17-19023	stone	D1806-134	83	ST2N	004	+	+	+	+
CWD-AR-18-0240HC	Stone	D1806-134	83	ST2N	005	+	+	+	+
CWD-AR-18-0242HC	Stone	D1806-134	83	ST2N	006	+	+	-	+
CWD-AR-00-1522	Stone	D1901-74	83	ST3N	007	+	+	-	+
CWD-AR-00-9002	Stone	D1901-74	83	ST3N	008	+	+	-	+
CWD-AR-00-8467	Stone	D1902-57	83	ST3N	009	+	+	-	+
CWD-AR-00-8468	Stone	D1902-57	83	ST3N	010	+	+	-	+
CWD-AR-01-0461	Stone	D1902-57	83	ST3N	011	+	+	-	+
CWD-AR-01-0462	Stone	D1902-57	83	ST3N	012	+	+	-	+
CWD-AR-01-0463	Stone	D1902-57	83	ST3N	013	+	+	+	+
CWD-AR-01-0464	Stone	D1902-57	83	ST3N	014	+	+	+	+
CWD-AR-01-0465	Stone	D1902-57	83	ST3N	015	+	+	+	+
CWD-AR-00-0996	Sevier	D1902-55	83	SV3N	004	+	+	-	+
CWD-AR-00-0997	Sevier	D1902-55	83	SV3N	005	+	+	+	+
CWD-AR-00-0998	Sevier	D1902-55	83	SV3N	006	+	+	-	+
CWD-AR-00-0999	Sevier	D1902-55	83	SV3N	007	+	+	+	+

CWD-AR-00-1000	Sevier	D1902-55	83	SV3N	008	+	+	+	+
CWD-AR-00-1001	Sevier	D1902-55	83	SV3N	009	+	+	-	+
CWD-AR-00-1002	Sevier	D1902-55	83	SV3N	010	+	+	-	+
CWD-AR-00-1003	Sevier	D1902-55	83	SV3N	011	+	+	-	+
CWD-AR-00-0979	Sevier	D1901-70	83	SV3U	001	+	+	-	+
CWD-AR-00-0994	Sevier	D1901-70	83	SV3U	002	+	+	-	+
CWD-AR-00-0995	Sevier	D1901-70	83	SV3U	003	+	+	+	+
CWD-AR-00-0822	Union	D1901-75	83	UN3N	001	+	+	-	+
CWD-AR-00-0843	Union	D1901-75	83	UN3N	002	+	+	-	+
CWD-AR-00-0823	Union	D1901-75	83	UN3N	003	+	+	+	+
CWD-AR-00-0924	Union	D1901-75	83	UN3N	004	+	+	-	+
CWD-AR-00-0848	Union	D1901-75	83	UN3N	005	+	+	-	+
CWD-AR-18-0552	Union	D1901-75	83	UN3N	006	+	+	+	+
UTM	Union	D1902-58	83	UN3U	007	+	+	-	+
CWD-AR-16-03140	Van Buren	D1802-03	83	VB1N	001	+	+	+	+
CWD-AR-16-03146	Van Buren	D1802-03	83	VB1N	002	+	+	-	+
CWD-AR-16-04985	Van Buren	D1802-03	83	VB1N	003	+	+	-	+
CWD-AR-16-05002	Van Buren	D1802-04	83	VB1N	004	+	+	-	
CWD-AR-17-18541	Van Buren	D1806-135	83	VB2N	005	+	+	-	+
CWD-AR-17-18544	Van Buren	D1806-135	83	VB2N	006	+	+	-	+
CWD-AR-17-18546	Van Buren	D1806-135	83	VB2N	007	+	+	-	+
CWD-AR-17-18547	Van Buren	D1806-135	83	VB2N	008	+	+	+	
CWD-AR-17-18548	Van Buren	D1806-135	83	VB2N	009	+	+	+	
CWD-AR-17-18588	Van Buren	D1806-136	83	VB2N	010	+	+	-	+
CWD-AR-17-18599	Van Buren	D1806-136	83	VB2N	011	+	+	+	+
CWD-AR-17-18607	Van Buren	D1806-136	83	VB2N	012	+	+	-	
CWD-AR-17-18608	Van Buren	D1806-136	83	VB2N	013	+	+	+	+
CWD-AR-17-18609	Van Buren	D1806-136	83	VB2N	014	+	+	+	
CWD-AR-17-18612	Van Buren	D1806-136	83	VB2N	015	+	+	+	+
CWD-AR-17-18613	Van Buren	D1806-136	83	VB2N	016	+	+	-	+
CWD-AR-17-18616	Van Buren	D1807-02	83	VB2N	017	+	+	-	+
CWD-AR-17-18617	Van Buren	D1807-02	83	VB2N	018	+	+	-	
CWD-AR-17-18618	Van Buren	D1807-02	83	VB2N	019	+	+	-	+
CWD-AR-17-18619	Van Buren	D1807-02	83	VB2N	020	+	+	-	
CWD-AR-17-18620	Van Buren	D1807-02	83	VB2N	021	+	+	-	+
CWD-AR-17-18621	Van Buren	D1807-02	83	VB2N	022	+	+	+	+
CWD-AR-17-18622	Van Buren	D1807-02	83	VB2N	023	+	+	+	+
CWD-AR-17-18623	Van Buren	D1807-02	83	VB2N	024	+	+	-	+
CWD-AR-17-19706	Van Buren	D1807-02	83	VB2N	025	+	+	-	
CWD-AR-18-212	Van Buren	D1807-02	83	VB2N	026	+	+	-	+
CWD-AR-18-213	Van Buren	D1807-02	83	VB2N	027	+	+	-	+
CWD-AR-18-214	Van Buren	D1807-02	83	VB2N	028	+	+	-	
CWD-AR-18-215	Van Buren	D1807-02	83	VB2N	029	+		-	
CWD-AR-17-18549	Van Buren	D1807-23	83	VB2N	033	+	+	+	+
CWD-AR-17-18550	Van Buren	D1807-23	83	VB2N	034	+	+	-	+
CWD-AR-18-133	Van Buren	D1806-137	83	VB3N	030	+	+	+	
CWD-AR-18-134	Van Buren	D1806-137	83	VB3N	031	+	+	-	
CWD-AR-18-135	Van Buren	D1806-137	83	VB3N	032	+	+	-	+
CWD-AR-16-00783	Washington	D1802-04	83	WA1N	001	+	+	-	+
CWD-AR-16-4538	Washington	D1802-04	83	WA1N	002	+	+	-	+
CWD-AR-16-4531	Washington	D1802-04	83	WA1N	003	+	+	-	+
CWD-AR-16-5300	Washington	D1802-04	83	WA1N	004	+	+	-	+
CWD-AR-16-4537	Washington	D1802-04	83	WA1N	005	+	+	-	+
CWD-AR-16-4536	Washington	D1802-04	83	WA1N	006	+	+	+	+
CWD-AR-16-5053	Washington	D1806-138	83	WA2N	007	+	+	-	+
CWD-AR-16-5077	Washington	D1806-138	83	WA2N	008	+	+	-	+
CWD-AR-16-6937	Washington	D1806-138	83	WA2N	009	+	+	+	+
CWD-AR-17-6938	Washington	D1806-138	83	WA2N	010	+	+	-	+
CWD-AR-17-12590	Washington	D1806-138	83	WA2N	011	+	+	-	+

CWD-AR-17-4082	Washington	D1806-138	83	WA2N	012	+			
CWD-AR-17-4083	Washington	D1806-138	83	WA2N	013	+	+	-	+
CWD-AR-17-4087	Washington	D1806-138	83	WA2N	014	+			
CWD-AR-17-4119	Washington	D1806-138	83	WA2N	015	+	+	-	+
CWD-AR-18-355	Washington	D1806-138	83	WA2N	016	+	+	-	+
CWD-AR-18-356	Washington	D1806-138	83	WA2N	017	+	+	-	+
CWD-AR-18-325	Washington	D1806-139	83	WA3N	018	+	+	-	+
CWD-AR-18-329	Washington	D1806-139	83	WA3N	019	+			
CWD-AR-18-330	Washington	D1806-139	83	WA3N	020	+			
CWD-AR-00-6659	Washington	D1901-76	83	WA3n	021	+	+	-	+
CWD-AR-01-5452	Washington	D1902-59	83	WA3n	023	+	+	-	+
CWD-AR-18-632	Woodruff	D1806-140	83	WD2N	001	+	+	-	+
CWD-AR-18-651	Woodruff	D1806-140	83	WD2N	002	+	+	-	+
CWD-AR-18-653	Woodruff	D1806-140	83	WD2N	003	+	+	-	+
CWD-AR-00-0326	Woodruff	D1901-77	83	WD3N	004	+	+	-	+
CWD-AR-18-01349	Woodruff	D1901-77	83	WD3N	005	+	+	+	+
CWD-AR-00-0327	Woodruff	D1901-77	83	WD3N	006	+	+	-	+
CWD-AR-17-3863	Woodruff	D1901-77	83	WD3N	007	+	+	-	+
CWD-AR-00-7688	Woodruff	D1902-60	83	WD3N	008	+	+	-	+
CWD-AR-00-0340	Woodruff	D1902-60	83	WD3N	009	+	+	+	+
CWD-AR-17-19690	White	D1806-141	83	WH2N	001	+	+	-	+
CWD-AR-18-6	White	D1806-141	83	WH2N	002	+	+	-	+
CWD-AR-18-280	White	D1806-141	83	WH2N	003	+			
CWD-AR-18-0644HC	White	D1806-141	83	WH2N	004	+	+	+	+
CWD-AR-18-0645HC	White	D1806-141	83	WH2N	005	+	+	-	+
CWD-AR-18-656	White	D1806-141	83	WH2N	006	+			
CWD-AR-18-657	White	D1806-141	83	WH2N	007	+	+	-	+
CWD-AR-18-0692HC	White	D1806-141	83	WH2N	008	+	+	-	+
CWD-AR-18-0693HC	White	D1806-141	83	WH2N	009	+			
CWD-AR-18-695	White	D1806-141	83	WH2N	010	+	+	-	+
CWD-AR-18-696	White	D1806-141	83	WH2N	011	+	+	-	+
CWD-AR-18-402	White	D1806-142	83	WH3N	012	+	-	-	+
CWD-AR-18-692	White	D1806-142	83	WH3N	013	+			
CWD-AR-18-693	White	D1806-142	83	WH3N	014	+			
CWD-AR-16-3128	Yell	D1701-04	83	YE1N	001	+	+	-	
CWD-AR-16-3129	Yell	D1701-04	83	YE1N	002	+			
CWD-AR-16-3130	Yell	D1701-04	83	YE1N	003	+	+	-	+
CWD-AR-16-3131	Yell	D1701-04	83	YE1N	004	+	+	-	+
CWD-AR-16-3132	Yell	D1701-04	83	YE1N	005	+	+	+	+
CWD-AR-16-3133	Yell	D1701-04	83	YE1N	006	+	+	+	+
CWD-AR-16-3134	Yell	D1701-04	83	YE1N	007	+	+	+	+
CWD-AR-16-3135	Yell	D1701-04	83	YE1N	008	+	+	+	+
CWD-AR-16-3136	Yell	D1701-04	83	YE1N	009	+	+	+	+
CWD-AR-16-5805	Yell	D1701-04	83	YE1N	010	+	+	+	+
CWD-AR-16-3138	Yell	D1701-04	83	YE1N	011	+			
CWD-AR-16-05503	Yell	D1802-03	83	YE1N	012	+	+	-	+
CWD-AR-16-06032	Yell	D1802-03	83	YE1N	013	+	+	-	+
CWD-AR-16-06033	Yell	D1802-03	83	YE1N	014	+	+	-	+
CWD-AR-16-06038	Yell	D1802-03	83	YE1N	015	+	+	+	+
CWD-AR-16-06039	Yell	D1802-03	83	YE1N	016	+	+	-	+
CWD-AR-16-06284	Yell	D1802-03	83	YE1N	017	+	x	+	+
CWD-AR-16-06286	Yell	D1802-03	83	YE1N	018	+	+	+	+
CWD-AR-16-06287	Yell	D1802-03	83	YE1N	019	+	+	-	+
CWD-AR-16-06294	Yell	D1801-05	83	YE1N	020	+	+		+
CWD-AR-16-1876	Yell	D1806-143	83	YE2N	021	+	+	+	+
CWD-AR-16-1877	Yell	D1806-143	83	YE2N	022	+	+	-	+
.	Yell	D1806-143	83	YE2N	023	+	+	+	+
CWD-AR-16-1879	Yell	D1806-143	83	YE2N	024	+			
CWD-AR-16-1880	Yell	D1806-143	83	YE2N	025	+			

CWD-AR-16-3964	Yell	D1806-143	83	YE2N	026	+			
CWD-AR-16-3965	Yell	D1806-143	83	YE2N	027	+			
CWD-AR-16-3966	Yell	D1806-144	83	YE2N	028	+			
CWD-AR-16-3967	Yell	D1806-144	83	YE2N	029	+			
CWD-AR-16-3968	Yell	D1806-144	83	YE2N	030	+			
CWD-AR-16-3969	Yell	D1806-144	83	YE2N	031	+			
CWD-AR-16-3970	Yell	D1806-144	83	YE2N	032	+			
CWD-AR-16-3971	Yell	D1806-144	83	YE2N	033	+			
CWD-AR-16-3972	Yell	D1806-144	83	YE2N	034	+			
CWD-AR-16-3973	Yell	D1806-144	83	YE2N	035	+			
CWD-AR-16-3975	Yell	D1806-144	83	YE2N	036	+	+	+	+
CWD-AR-17-1009	Yell	D1806-144	83	YE2N	037	+	+	+	+
CWD-AR-17-1014	Yell	D1806-144	83	YE2N	038	+	+	-	
CWD-AR-17-1015	Yell	D1806-144	83	YE2N	039	+	+	-	
CWD-AR-17-16440	Yell	D1806-144	83	YE2N	040	+	+	-	
CWD-AR-17-16442	Yell	D1806-144	83	YE2N	041	+	+	-	+
CWD-AR-17-16443	Yell	D1806-144	83	YE2N	042	+	+	-	
CWD-AR-17-16444	Yell	D1806-144	83	YE2N	043	+	+	-	+
CWD-AR-17-16445	Yell	D1806-144	83	YE2N	044	+	+	-	+
CWD-AR-17-16446	Yell	D1806-144	83	YE2N	045	+	+	-	
CWD-AR-17-16447	Yell	D1806-144	83	YE2N	046	+	+	-	+
CWD-AR-17-16448	Yell	D1806-144	83	YE2N	047	+	+	-	+
CWD-AR-17-16449	Yell	D1806-144	83	YE2N	048	+	+	-	+
CWD-AR-17-16450	Yell	D1806-144	83	YE2N	049	+	+	-	+
CWD-AR-17-19971	Yell	D1806-144	83	YE2N	050	+	+	-	
CWD-AR-17-19976	Yell	D1806-144	83	YE2N	051	+	+	+	+
CWD-AR-17-19977	Yell	D1807-01	83	YE2N	052	+	+	-	
CWD-AR-17-20020	Yell	D1807-01	83	YE2N	053	+	+	-	+
CWD-AR-17-16441	Yell	D1807-24	83	YE2N	054	+	+	-	

Table S2: Frequency of 20 *PRNP* haplotypes detected in 1,433 white-tailed deer collected in 75 counties in Arkansas from 2016-2019. Phased haplotypes were derived from sequence analysis of 720 nucleotides of the *PRNP* gene. Letters indicate haplotypes previously detected in other states, whereas numbers (1-4) indicate haplotypes unique to Arkansas. Variable sites of haplotypes are listed in Table 2. Samples that tested positive for CWD (+) are listed separately for those counties where CWD was detected.

County	Haplotype																	
	A	B	C	D	E	G	I	J	K	L	O	P	R	T	V	1	2	3
Arkansas	4	5	5	4	-	3	-	-	-	-	-	-	-	-	1	-	-	-
Ashley	1	-	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-
Baxter	3	7	3	8	4	6	-	1	-	-	-	-	-	-	-	-	-	-
Benton	25	19	3	16	5	5	1	4	-	-	-	-	1	-	1	-	-	-
Boone	6	24	8	7	5	8	-	7	-	1	-	-	-	-	-	-	-	-
Boone(+)	-	-	-	3	-	1	-	-	-	-	-	-	-	-	-	-	-	-
Bradley	1	-	2	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-
Carroll	18	13	4	11	4	7	-	6	-	-	-	-	-	-	3	-	-	-
Carroll(+)	5	12	2	5	3	5	-	-	-	-	-	-	-	-	-	-	-	-
Calhoun	4	9	1	6	3	2	-	1	-	-	-	1	-	1	-	-	-	-
Cleburne	2	2	2	4	2	4	-	-	-	-	-	-	-	-	-	-	-	-
Chicot	3	-	1	2	-	1	1	-	-	-	-	-	-	-	-	-	-	-
Clark	2	5	6	6	1	1	3	1	-	-	-	1	-	-	-	-	-	-
Conway	1	4	1	6	3	5	-	-	-	-	-	-	-	-	-	-	-	-
Columbia	1	1	-	4	-	2	-	-	-	-	-	-	-	-	-	-	-	-
Craighead	5	1	5	7	1	3	-	1	-	-	-	-	-	1	-	-	-	-
Cross	4	4	3	5	-	1	1	-	-	-	-	-	-	-	-	-	-	-
Crittenden	5	1	5	4	-	1	-	-	-	-	-	-	-	-	-	-	-	-
Crawford	1	3	5	6	-	1	-	-	2	-	-	-	-	-	-	-	-	-
Clay	7	4	7	3	1	2	1	-	-	-	-	1	-	2	-	-	-	-
Dallas	6	3	1	3	3	1	1	-	-	-	-	-	-	-	-	-	-	-
Drew	4	2	16	3	1	2	-	-	-	-	-	-	-	-	-	-	-	-
Desha	8	4	5	4	-	1	-	-	-	-	-	-	-	1	-	1	-	-
Faulkner	5	1	2	11	4	1	-	1	-	-	-	1	2	-	-	-	-	-
Franklin	6	23	29	1	-	5	-	-	-	-	-	-	-	-	-	2	-	-
Fulton	3	8	4	12	4	5	-	1	-	-	-	-	-	5	-	-	-	-
Garland	6	5	6	5	4	1	3	-	-	-	-	-	-	-	-	2	-	-
Greene	1	8	7	-	-	2	2	1	-	-	-	-	-	3	-	-	-	-
Grant	4	3	3	7	-	2	-	-	-	-	-	-	-	1	-	-	-	-
Hampstead	6	3	-	5	2	1	3	-	-	-	-	-	-	-	-	-	-	-
Howard	-	3	6	11	2	2	1	-	-	-	-	-	-	1	-	-	-	-
Hot Springs	2	2	2	1	1	2	-	-	-	-	-	-	-	-	-	-	-	-
Independence	-	3	5	4	1	4	-	-	-	-	-	-	-	1	-	2	-	-
Izard	-	2	-	7	6	2	-	-	-	-	-	-	-	-	-	1	-	-
Jackson	-	-	3	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Jefferson	6	7	2	5	1	4	-	1	-	-	-	-	-	-	-	-	-	-
Johnson	10	33	19	20	1	4	1	-	-	-	-	1	-	-	-	1	-	-

Lafayette	5	3	7	5	1	4	1	-	-	-	-	-	-	3	-	-	1	-	-
Lincoln	3	3	5	4	-	1	-	2	-	-	-	-	-	-	-	-	-	-	-
Lee	4	6	3	1	-	1	-	-	1	-	-	-	-	-	-	-	-	-	-
Lonoke	6	4	5	7	3	1	-	-	-	-	-	-	-	-	-	-	-	-	-
Logan	12	15	3	26	12	13	-	1	-	-	-	-	-	-	-	-	-	-	-
Little River	1	4	5	8	1	1	-	-	-	-	-	-	-	-	-	-	-	-	-
Lawrence	1	3	16	2	4	3	-	-	-	-	-	-	-	3	-	-	-	-	-
Madison	9	18	24	6	3	6	1	2	-	-	-	-	-	2	-	-	1	-	-
Madison(+)	1	1	1	-	2	-	1	2	-	-	-	-	-	-	-	-	-	-	-
Marion	10	12	11	12	10	7	-	14	1	-	-	2	-	1	-	-	-	-	-
Miller	3	5	2	1	1	2	-	-	-	-	-	-	-	2	-	-	-	-	-
Monroe	4	1	5	3	4	1	-	-	-	-	-	-	-	-	-	-	-	-	-
Montgomery	1	1	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mississippi	2	-	1	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
Nevada	7	-	6	10	2	3	-	-	-	-	-	-	-	-	-	-	-	-	-
Newton	68	124	49	105	23	48	-	5	3	-	2	-	-	2	-	-	2	1	-
Newton(+)	28	75	10	54	11	17	-	1	1	-	1	-	-	1	-	-	-	-	1
Ouachita	4	3	3	13	3	1	1	-	-	-	-	-	-	-	-	-	-	-	-
Perry	4	3	2	2	-	2	2	1	-	-	-	-	-	-	-	-	-	-	-
Phillips	8	1	1	1	-	5	-	1	-	-	-	-	-	-	-	-	-	1	-
Pike	2	3	2	5	-	2	2	-	-	-	-	-	-	-	-	-	-	-	-
Polk	2	-	-	-	2	1	1	-	-	-	-	-	-	-	-	-	-	-	-
Poinsett	7	1	5	6	2	3	-	1	-	-	-	-	-	-	-	-	1	-	-
Pope	3	48	9	41	3	15	3	-	-	-	-	-	-	-	-	-	-	-	-
Pope(+)	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-
Prairie	3	5	7	3	-	1	1	-	2	-	-	-	-	-	-	-	-	-	-
Pulaski	3	3	4	5	3	3	1	-	-	-	-	-	-	-	-	-	-	-	-
Randolph	3	3	5	3	-	-	-	1	-	-	-	-	-	1	-	-	-	-	-
Saline	4	4	4	1	3	3	1	2	-	-	-	-	-	2	-	-	-	-	-
Sebastian	6	3	2	12	3	5	1	-	-	-	-	-	-	-	-	-	-	-	-
Sebastian(+)	-	1	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Scott	1	2	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Searcy	8	15	7	31	5	16	-	1	-	-	-	1	-	-	-	-	-	-	-
St Francis	4	4	3	5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Sharp	3	6	7	8	1	1	-	1	-	-	-	-	-	3	-	-	-	-	-
Stone	6	5	3	6	1	9	-	-	-	-	-	-	-	-	-	-	-	-	-
Sevier	5	1	2	5	1	4	2	-	-	-	-	-	-	-	-	-	-	-	-
Union	3	3	1	4	1	1	-	-	-	-	-	-	-	-	-	-	1	-	-
VanBuren	7	10	2	21	8	14	2	-	-	1	-	-	-	1	-	-	-	-	-
Washington	7	5	11	9	-	2	1	1	-	-	-	-	-	-	-	-	-	-	-
Woodruff	1	2	7	2	1	4	-	-	-	-	-	-	-	-	-	-	1	-	-
White	2	4	6	-	1	2	-	1	-	-	-	-	-	-	-	-	-	-	-
Yell	9	22	5	21	10	9	3	1	-	-	-	-	-	-	-	-	-	-	-
TOTAL	435	657	426	657	187	309	42	65	10	2	3	10	2	41	1	1	15	2	1