Can Immigration Rescue a White-tailed Deer Population From CWD-induced Declines? A Summary of Tennessee's Endemic Area

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Dedication

I would like to dedicate this thesis to someone who made me believe that I could be more than what I thought was possible. Colonel James K. Cooper II (U.S. Army, Retired) has influenced the lives of every person he has ever encountered. If it were not for him, I would never have come this far and would have missed out on a wondrous world. Secondly, I would like to thank my loving wife, Courtney Wyrick, for her patience and steadfast support. It is not easy being married to a student, but she has been my cornerstone.

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Abstract

During 2021–2025, the Tennessee Wildlife Resources Agency conducted fixed-wing, thermal imaging surveys to assess deer density at Ames AgResearch and Education Center (AmesREC) and the surrounding counties in West Tennessee. Deer density estimates did not significantly decline across the monitoring period despite consistently high prevalence of chronic wasting disease at AmesREC (CWD, >30% positive since 2020). We used deer capture data and stage-structured models to evaluate population-level processes that could promote an apparently stable deer density with high CWD prevalence. From January 2023 – June 2025, we captured adult deer (n = 84) and fitted them with Iridium Satellite GPS collars on AmesREC. We estimated adult survival rates from collared individuals. A subset of 23 females received vaginal implant transmitters to evaluate recruitment. To assess the potential for immigration, we collected hair for genetic analysis using 21 microsatellites. Yearly adult survival probabilities were statistically similar between males and females at 57%. Pregnancy rates were high (89%), including fawn pregnancies. We captured and collared 4 fawns for up to 20 days before collars were lost. Using our estimated vital rates the literature values, we parameterized a stage-structured model at AmesREC. All models predicted growth rates <1 without any immigration. We would have predicted an average of 23.57 – 25.93% annual decline in deer density based on our model. The AmesREC population was relatively genetically heterogeneous, with statistical evidence for contributions from 7 genetic sources, suggesting likely immigration. We found AmesREC was more genetically diverse than a nearby unhunted site Lone Oaks, even after controlling for sample size. Immigration may be acting in a compensatory manner to maintain population density at an apparently stable level in a population that would otherwise be suffering marked declines. As high-quality habitats open from local mortalities, deer dispersed from

nearby locations with lower CWD prevalence are moving in to fill those previously occupied areas. We need to account for all factors affecting population growth rates and the possible contributions from surrounding areas with lower CWD prevalence. Populations should be monitored over time as CWD spreads and limits the possibility for immigration to maintain deer numbers.

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Chapter One Introduction and Background

Chronic wasting disease (CWD) is a transmissible spongiform encephalopathy that affects cervids including white-tailed deer (*Odocoileus virginianus*; hereafter deer), mule deer (*Odocoileus hemionus*), elk (*Cervus canadensis*), and moose (*Alces alces*) (Li et al. 2007). Chronic wasting disease was first found in captive mule deer in Colorado in the 1960s and was first described as a prion disease in the 1970s (Gilch et al. 2011, DeVivo et al. 2017, USDA APHIS 2023). This inevitably fatal disease results from the accumulation of a misfolded variant (PrP^{CWD}) of the regularly occurring cellular prion protein (PrP^{C}) (Prusiner 1998, Haley & Hoover 2015, Mathiason 2015). Population declines have been detected and attributed to direct and indirect mortality from CWD in herds where the disease is present (Dulberger et al. 2010, Edmunds et al. 2016, DeVivo et al. 2017, Gaya et al. 2026), with some researchers suggesting localized extirpation events could be possible (Almberg et al. 2011, DeVivo et al. 2017). However, severe population declines is not necessarily an inevitable outcome following CWD invasion into a population. In other host-pathogen systems, reduced host susceptibility, increased host tolerance, compensatory recruitment, or immigration can dampen or prevent population declines following disease invasion (Brannelly et al. 2021).

A major challenge in disease management is to identify the mechanisms that allow populations to persist at a stable level in the face of ongoing disease pressure and to try to develop management strategies for reducing the negative impacts of disease. This is particularly relevant for CWD because models are often used to assess the benefits of harvest management strategies on disease reduction (e.g., Wehr et al. 2026). Population dynamics, and subsequent models of these dynamics, fundamentally depend on death rates, birth rates, immigration rates,

and emigration rates (Nisbet & Gurney 1982). In populations infected with CWD, there is clear evidence that infection directly impacts per capita death rates.

Chronic wasting disease often presents with emaciation and significant neurological changes in end-stage disease (Williams and Young 1980, Haley et al. 2015, Nemeth et al. 2021). Additionally, CWD has been attributed to increases in per capita death rates from inadequate maternal care, reduced life expectancy, and increased susceptibility to predation (Miller et al. 2008, Dulberger et al. 2010, Blanchong et al. 2012, Schuler et al. 2018). Due to its transmission dynamics CWD can have substantial, continued negative effects on total population mortality rate even as the population declines.

Infective prions are efficiently spread horizontally through direct contact between deer or indirect contact with a contaminated environment (Browning et al. 2004, Miller et al. 2004, Haley et al. 2009, Haley and Hoover 2015, Mathiason 2015). Direct contact with an infected individual's saliva, urine, and feces can lead to infection. Deer social behaviors such as grooming within a family unit likely play a pivotal role in direct contact transmission from infectious excreta (Grear et al. 2010). Indirect transmission results from contact with the CWD prion in a contaminated environment, where it can remain infectious for at least 3 to 5 years (Miller et al. 2004, Mathiason 2015). Importantly, as long-lived infectious prions accumulate in the environment, indirect transmission can start to dominate overall transmission such that changes in host density have little effect on transmission rate (Almberg et al. 2011). Because of this so-called frequency-dependent transmission, high prevalence of CWD can lead to high total mortality rates in the population without any subsequent decreases in infection prevalence. As such, high CWD prevalence in a population may be an indicator that a population is at

substantial risk of CWD-induced declines (Edmunds et al. 2016, National Academy Report 2025).

Less work has focused on how CWD affects birth rates and successful recruitment of cervids. Many diseases can be passed from mother to offspring, including CWD. Nalls et al. (2017) documented CWD prions were found *in utero* and the mechanisms necessary for vertical transmission of CWD were present in asymptomatic mothers. Additionally, *in utero* transmission may be a common feature of CWD (Bravo-Risi 2021, Nalls et al. 2021). Nalls et al. (2021) showed that vertical transmission was possible in free-ranging deer with prion deposition in lymphoid biopsies of offspring born to asymptomatic mothers as early as 42 days post-parturition. While CWD has not been found to be tied to pregnancy probability in deer, CWD's impact on recruitment is still not well understood, mule deer studies have shown variable effects of CWD on recruitment (Dulberger at al. 2010, DeVivo et al. 2017, Mori et al. 2025). Regardless, reduced annual survival from CWD would reduce the number of fawns a female could have over time.

Finally, while CWD does affect fine-scale deer movements, particularly near the end-stage of disease (Barrile et al. 2024) little work is known about how individual CWD infection affects dispersal rates or how deer move into and out of areas with high prevalence of CWD infection. If individuals immigrating cannot detect the presence of CWD in an area, and the area provides other key resources like forage and cover, then this could set-up the opportunity for an "ecological trap" – the process by which an animal mistakenly selects an area with lower fitness (e.g., the presence of novel disease; Hale and Swearer 2016). If animals from outside an area with high CWD prevalence move into an area with high CWD prevalence, then the local negative population-level effects on births and deaths could be compensated for by increased

immigration, at least temporarily. These “ecological trap” and “source-sink” dynamics could lead to the apparent patterns of stable local populations with high CWD prevalence that would otherwise be declining without the consistent input of new immigrants.

In Tennessee, CWD was first detected in Fayette and Hardeman counties in 2018 and as of February 2026 has since spread to 23 counties in the western part of the state (TWRA 2025). In 2023 - 2024, CWD prevalence in Fayette (20.05%) and Hardeman Counties (18.85%) was high. However, prevalence at Ames AgResearch and Education Center (AmesREC), our primary study site, was even higher at 46.6% (female = 27.8%, male = 64.9% (Kosiewska et al. 2024). These high levels of prevalence are suggestive that CWD is having a notable effect on mortality and potentially driving population declines in west Tennessee. Somewhat supporting this hypothesis, Keever et al. (2025) recently found that deer populations were decreasing in west Tennessee more broadly, though this work focused on the entirety of western Tennessee (Unit 1) and not exclusively on areas of high CWD prevalence.

However, in contrast to these large-scale results, five years of local FLIR (forward-looking infrared) aerial surveys over AmesREC and surrounding areas in west Tennessee have shown negative trends but no significant declines in population density, which is not consistent with observed CWD prevalence and high mortality which would drive population declines. Moreover, current models suggest that CWD arrived in west Tennessee at a similar time to Arkansas (~30-40 years ago) with similar trend in prevalence trajectory (National Academy Report 2025, Fig. 5.1.1). Arkansas and AmesREC populations appear at a similar point along the epidemic trajectory. Despite these similarities in CWD dynamics between Arkansas and AmesREC, Gaya et al. (2026) recently reported that CWD has led to on average a 17% decline per year in deer densities in Arkansas. The stark mismatch between observed, local population

trends in west Tennessee and observed CWD prevalence suggests that notable changes in birth rates, death rates, or immigration rates could explain AmesREC's apparently stable local deer density in the face of high CWD prevalence.

We ask three questions. First, are death rates relatively low despite high CWD prevalence, suggesting that some aspect of the population or the environment-population interaction can promote CWD tolerance? Second, can compensatory recruitment or baseline high reproductive output at AmesREC offset the negative effects of CWD on survival, allowing for stable populations? Third, is there any evidence that immigration is occurring into the AmesREC population at a rate higher than other similar populations in west Tennessee, potentially leading to source-sink dynamics at AmesREC and apparently stable densities? We use the vital rates estimated from questions 1 – 2 to parameterize a stage-structured demographic model and test whether measured vital rates in our population are sufficient for population growth rate $\lambda = 1$, indicating a stable population, or whether external immigration is necessary to explain observed patterns of stable deer density despite high levels of CWD prevalence.

Chapter Two Methods

2.1 Study area

The study occurred at two properties affiliated with the University of Tennessee Institute of Agriculture (UTIA) in west Tennessee. AmesREC is on the Fayette and Hardeman County border, approximately 72.5 kilometers south of Jackson, Tennessee, and was 7,446 hectares at the time of the study. The landscape of AmesREC was a mosaic of cultivated crop fields, old field pastures with minimal woody encroachment, upland and bottomland hard-mast producing deciduous forests, woody wetlands, and even aged loblolly pine (*Pinus taeda*) stands. The cultivated crops were primarily corn, soybeans, and cotton. An active beef cattle operation occurs on the property and bird dog field trials occur during the winter. There is also a hunting club on the property that, like other local properties, has promoted near equal male-to-female ratios and allowed males to reach older age classes before harvest.

The other property was Lone Oaks Farm (Lone Oaks) in Hardeman County, TN approximately 26 kilometers east of AmesREC and. Lone Oaks was a 485.6 hectares property comprised of hard-mast-producing deciduous forests and seasonally mowed open pastures. There are multiple ponds and other bodies of water throughout the property. Tornadoes impacted the property in 2 out of 3 years of our study. Lone Oaks primarily functions as a youth 4H camp in the summer months, and no hunting is allowed on the property. However, the northwestern section of the property had a clay shooting range that was active 4 days a week, throughout the year.

2.2 Adult capture

From January through April of 2023, 2024, and 2025, we captured adult deer through a combination of collapsible Clover traps (Industrial Services Group, Watkinsville, Georgia, USA), drop nets (7.62 x 7.62 m) with 15.24 cm mesh; Wildlife Capture Services, Flagstaff, Arizona,

USA), darting with an X-Caliber dart rifle and Pneu darts (Pneu Dart, Williamsport, Pennsylvania, USA), and net gunning from a helicopter (Helicopter Wildlife Services, Austin, TX). Deer captured with ground trapping methods were collared and released on site. All helicopter captured deer were brought back to a central workup site in 2023 and only females were brought back in 2024. Males were helicopter netted and worked up at the site of capture in 2024 without chemical immobilization.

The helicopter transported deer to the workup site where they were immobilized after transport. In 2023, for all capture methods (Clover trap, drop net, and helicopter) we used nalbuphine-medetomidine-azaperone (NalMedA; 40 mg/ml nalbuphine, 10 mg/ml azaperone, 10 mg/ml medetomidine, Wedgewood, Swedesboro, NJ, USA), or butorphanol-azaperone-medetomidine (BAM;17.3 mg/ ml butorphanol tartrate, 9.1 mg/ml azaperone, 10.9 mg/ml medetomidine; Wedgewood). In 2024, we used a combination of medetomidine (0.07 mg/kg, 20 mg/ml, Wedgewood), ketamine (1.5 mg/kg, 100 mg/ml, Covetrus, Ocala, FL, USA) and telazol (MKT, 1.1 mg/kg, 100 mg/ml, Covetrus, Muller et al. 2012), for helicopter-captured females and darting captures and NalMedA or BAM for drop net captures. In 2025 we used MKT for darting and BAM for drop net captures. For all years we estimated age from tooth replacement and wear in the field (Severinghaus 1949), recorded weight and sex, collected hair, collected fecal samples from the anus, and used venipuncture to collect blood. For a subset of 23 female deer in 2024, we assessed pregnancy by visualizing placentomes through transabdominal ultrasound (EVO III portable ultrasound and eCL3 macro convex transducer; Choice Medical Systems, St. Petersburg, FL, USA) and later verified with serum samples analyzed after capture using pregnancy-specific protein B (PSPB, BioPRYN, Pullman, Washington, USA).

We fit adult deer, when possible, with LiteTrack Iridium 420 and 420+ GPS collars with proximity sensor (Lotek Wireless, Newmarket, Ontario, Canada). Collars were programmed to record 30-minute locations, and a subset of 23 pregnant deer in 2024 were fitted with a vaginal implant transmitter (VIT; Lotek Wireless) paired to their collar. After workup and marking, deer were reversed with IM injections of atipamezole (2 ml for every ml of BAM or NalMed-A; 25 mg/ml; Wedgewood) and 0.5 ml naltrexone (50 mg/ml; Wedgewood) for both BAM or NalMedA. Deer immobilized with MKT were reversed with 0.35 mg/kg atipamezole (5 mg/ml, Covetrus).

2.3 Question 1: Survival, cause of death designation, and disease testing

2.3.1 Survival analysis

To assess annual survival in our focal herd we used program R with the survival, ggsurvfit, lubridate, dplyr, and ggplot2 packages (Grolemund and Wickham 2011, Wickham 2016, Wickham et al. 2023, R Core Team 2024, Sjoberg et al. 2024, Therneau 2024). We used a known-fate Kaplan-Meir survival analysis allowing for seasonal variation in survival probabilities of animals in our study (Pollock 1989, Bland and Altman 1998, Delgiudice et al. 2006). We accounted for annual wrapping of those individuals that survived greater than 365 days to appropriately delineate the “at-risk” set when computing our non-parametric survival estimates. We calculated Kaplan–Meier survival estimates for all deer over the project (referred to as overall survival), deer captured only on AmesREC (referred to as AmesREC survival), and deer captured only on Lone Oaks (referred to as Lone Oaks survival). We then used the survdiff function in the survival package in program R to perform log-rank tests to test whether covariates (sex, age class, and capture year) significantly affect our survival curves.

2.3.2 Cause of death designation and disease testing

When a mortality alert was received, we recovered the carcass with remains intact, partially intact, or only bones for all mortalities throughout the study. We performed field assessments to determine whether mortality resulted from a likely predator using the kill site characteristics and procedures defined in Wade and Bowns (2010) guide. Any remains were brought to a Tennessee Wildlife Resources (TWRA) lab in Jackson, Tennessee where we performed necropsies with a licensed veterinarian (D. Grove) to determine cause of death when possible. If available, we collected biological samples for potential disease testing (including retropharyngeal lymph nodes, obex tissue, organ tissues). When possible, we extracted the first incisor for aging using cementum annuli (Matson's Laboratory, Manhattan, Montana; Hamlin et al. 2000).

We combined information from our recovery site evaluations and necropsy findings to categorize mortalities as caused by capture myopathy (n = 9), legal hunter harvest (n = 7), illegal harvest (n = 2), disease associated (n = 7), predation (n = 6), or unknown (n = 9). We defined capture myopathy as death resulting from capture-associated events within 14 days of the capture event (Kreeger et al. 2023). We did not include individuals who died of capture myopathy in our mortality analyses. Hunter harvest included those animals that died because of gunshot wounds or archery equipment from hunters during the regular hunting season and illegal hunter harvest if poached out of season.

If a deer showed clinical signs of disease-associated mortality (either through visual examination of tissues or diagnostic testing), we assigned it to the disease associated mortality category. Due to the challenges associated with determining disease associated mortality from scavenged or autolyzed carcasses we categorized animals that likely died of disease as disease

associated rather than list a specific disease as the cause of death. However, we were able to evaluate for CWD and hemorrhagic disease (HD; which includes epizootic hemorrhagic disease (EHD) and blue tongue virus (BTV)) as outlined below.

We used clinical signs and lab testing to determine that an individual succumbed to end-stage CWD. We determined severe emaciation by examining fat in the femur which had a gelatinous consistency. We evaluated other known complications from CWD such as aspiration pneumonia. For all CWD testing we used either retropharyngeal lymph node or brainstem tissues collected during hunter check-in's or at necropsy (Nemeth et al. 2021). All CWD samples were tested to determine a detected or non-detected result through TWRA using the Mississippi Veterinary Research and Diagnostic Laboratory in accordance with the National Animal Health Laboratory Network standards using Bio-Rad™ CWD ELISA (Bio-Rad Laboratories, Inc., Hercules, CA).

Clinical signs used for the diagnosis of HD included hoof sloughing and hemorrhage around the heart, lungs, or intestines (Nemeth et al. 2021). We submitted serum samples for HD antibody testing. When possible, we also submitted refrigerated samples of spleen, lung, and lymph node tissues to test for HD virus testing using reverse transcriptase polymerase chain reaction (RT-PCR) (Nemeth et al. 2021). All non-CWD disease testing was performed by the Southeastern Cooperative Wildlife Disease Study Group (SCWDS), College of Veterinary Medicine, University of Georgia, Athens, Georgia, USA.

We assigned deer to the predation category if the carcass showed signs of predation, such as puncture wounds and subcutaneous hemorrhaging, in conjunction with kill site characteristics such as carcass caching, moving of carcasses, and multiple carcasses present (Wade and Bowns 2010). We did not determine the species responsible for predation events through puncture swabs

due to the limited success of the technique and CWD contamination concerns. Finally, for all deer where the remains were too degraded to definitively determine a cause of death we assigned them to the unknown category.

2.2 Question 2: Reproduction and recruitment

2.2.1 Reproduction

We assessed reproductive rates at capture as outlined above using PSPB and ultrasound. We examined fetal number and development at necropsy for females that died during the study. We determined age using measurements compared to a fetal scale developed by Hamilton (1985).

2.2.2 Neonate capture

In 2024, we monitored a subset of deer (n = 23) for birthing using the VITs. We received a possible birth event notification from Iridium once the VIT was expelled and there was a change in temperature (≥1.7ºC (3º F)) and lack of movement for 1 hour. We would only approach the birth site ≥ 2 hours after notification to allow the doe time to groom, feed, and bond with her offspring (hereafter referred to as fawn/s) (Haskell et al. 2007). We chose the 2-hour timing for searches because fawns stand 20-30 minutes after birth and the mother may move them within 3 hours (Townsend and Bailey 1975, Bartush and Lewis 1978). Once we approached the birth site, if we did not find fawns at the VIT or mother's location, we searched the area with a 100-meter radius from where the VIT was discovered (Edge et al. 2023).

When we located fawns, we immediately blindfolded them to reduce stress, placed them in a mesh bag, and weighed them using a handheld scale (Chitwood et al. 2015, Clevinger et. al 2024). We determined sex, collected hair, and fit them with proximity-enabled expandable drop-off very high frequency (VHF) collars (MCFT3 collar; Lotek Wireless) paired with the mother's

collar. We then placed the fawn back where it was found, tried to place the vegetation around it, and left the same way we came in to reduce any visual cues for predators. Fawns were monitored via the proximity sensor on the doe's collar and additionally with VHF telemetry at least twice a day. During the peak of fawning, we performed transect searches daily through areas of likely birth site or fawn cover and doe location clusters. Fawns found through these transects (henceforth opportunistic fawns) were handled similarly. We estimated age through hoof growth (Haugen and Speake 1958, Sams et al. 1996, Brinkman et al. 2004).

2.3 Question 3: Stage-structure demographic model and immigration

2.3.1 Stage-structured population model

Using our estimated demographic rates, we built a stage-structure matrix model to assess population growth rates. Our model assumed three primary stages of males and females: Fawns (0-10 months, Yearlings (1-2 years old), and Adults (> 2 years old). We did not consider a finer partitioning of stages (e.g., Ketz et al. 2023) because we did not have data to estimate stage-specific survival at a finer scale. Our model projects deer population dynamics on yearly time steps.

Our model of these state variables is given by Equations 1 through 6, where Equations 1 and 2 give the number of fawns in the system, Equations 3 and 4 give the number of yearlings in the system, and Equations 5 and 6 give the number of adults in the system.

$$F_f(t+1) = \left(A_f(t) + Y_f(t)\right) p_A r \sigma_N \pi + F_f(t) p_F r\, \sigma_N \pi + \phi_{F_f} \quad (1)$$

$$F_m(t+1) = \left(A_f(t) + Y_f(t)\right) p_A r \sigma_N (1 - \pi) + F_f(t) p_F r\, \sigma_N (1 - \pi) + \phi_{F_m} \quad (2)$$

Equation 1-2 gives the number of female and male fawns, respectively, added to the system from year t to year t + 1. A fawn is produced over a year if adult or yearling females breed with some probability p_A, produce an average of r neonates with a neonate having a probability π of being

female, and a neonate having a probability σ_N of surviving 12 weeks and recruiting as a fawn. There is also some probability that fawns reproduce p_F and produce new fawns. Finally, we allow for some constant immigration rate (female or male fawns per year) into the population ϕ_{F_f}, ϕ_{F_m} even though we do not typically expect fawns to immigrate. Equation 2 is the same as equation 1, but male fawns are produced with probability $1 - \pi$. We make two key assumptions. First, we assume that probability of a female breeding is independent of male density. Second, we assume that the per capita number of neonates produced and the probability of neonates surviving and recruiting to fawns does not depend on deer density (i.e. is density-independent).

We modeled the change in yearling female and male density over a year time step as:

$$Y_f(t+1) = F_f(t)\sigma_{F_f} + \phi_{Y_f} \quad (3)$$

$$Y_m(t+1) = F_m(t)\sigma_{F_m} + \phi_{Y_m} \quad (4)$$

For Equation 3, yearling female density at time t + 1 depends on the female fawns that survive and age into the yearling class with probability σ_{F_f}, where this probability is a 9-10 month probability given that neonate survival lasts 12 weeks. We also allow for some immigration $\phi_{Y_f}$of yearling fawns from outside the population. Equation 4 is similar but with male-specific vital rates.

Finally, we modeled the change in adult female and male density over a year time step as:

$$A_f(t+1) = Y_f(t)\sigma_{Y_f} + A_f(t)\sigma_{A_f} + \phi_{A_f} \quad (5)$$

$$A_m(t+1) = Y_m(t)\sigma_{Y_m} + A_m(t)\sigma_{A_m} + \phi_{A_m} \quad (6)$$

For Equation 5, adult female density at time t + 1 depends on how yearling females survive and age into adults with probability σ_{Y_f} and how adult females in time t survive over a

year with probability σ_{A_f}. Moreover, we allow for some immigration of adult females per year ϕ_{A_f}. Equation 6 is similar but with male-specific vital rates.

We did not include CWD transmission in the model as we assumed that transmission was largely frequency-dependent or environmentally driven and did not depend on host density. Moreover, this also means that we assume CWD prevalence remains constant in the population. Given that CWD prevalence is likely still increasing at AmesREC, our estimates of population growth rate are likely optimistically high. Thus, we are giving our model the best possible chance to predict stable population densities consistent with observations.

We parameterized our model using the parameters given in Table 1. Nearly all of these parameters we were able to estimate or calculate directly from our field study as described above. Additionally, we used two reproductive rates for the number of neonates per birth event. In an effort to be as conservative as possible by allowing for maximum reproduction in our modeled system we assumed r = 2. Our second model rate was r = 1.67 which was based on our field data and the Southeastern literature to give a more biologically realistic component to the model (Jones et al. 2010, Chitwood et al. 2015, Turner et al. 2019). These systems will be referred to as the high reproduction system (where r = 2) and a real-world system (where r = 1.67).

There were two primary outputs from our model. First, we calculated the population growth rate (λ) from our parameterized model under various assumptions about other unknown parameters as described in Table 1. We tested whether there was any evidence that λ = 1 when there was no immigration, consistent with the observed stable trend in the deer population. Second, we used our model to assess what the necessary immigration rate would be in order to produce approximately stable population dynamics.

2.3.2 Immigration potential

We collected hair samples from captured deer from 2023 - 2024 and hunter-harvested deer in 2024 from AmesREC and captured deer from Lone Oaks in 2024 and 2025. Wildlife Genetics International (WGI: Nelson, British Columbia Canada) analyzed plucked hair samples for 21 microsatellite markers optimized for white-tailed deer (Table 2). We used program CERVUS (3.0.7; Kalinowski et al. 2007) to assess observed and expected heterozygosity, frequency of alleles, polymorphic information content (PIC), estimate of any null allele that might be present (F(Null)), and test for Hardy-Weinberg (HW) Equilibrium using chi-square test with Bonferoni correction in CERVUS by microsatellite locus and study site. To assess general possible population structure, we used program STRUCTURE (2.3.4; Prichard et al. 2000) which is a Bayesian clustering algorithm used to assign genetic cluster without prior information on group membership. We used the delta K (ΔK) method of Evanno et al. (2005) to determine the correct number of population clusters using data from both study sites. We ran K from 1-10 using a burn-in of 100,000 and a run length of 100,000 with admixture. All runs were repeated 15 times. We evaluated the change in mean likelihood values and divided it by the mean standard deviation for each run to determine best fit for the cluster model (ΔK). Once the value of K was determined we ran the final analysis at 1,000,000 burn-in and run length with admixture. We compared overall genetic diversity at each study site by comparing pairwise relatedness from the microsatellite data using 7 different methods in the program COANCESTRY (1.0.2.0; Wang 2011). We tested differences in relatedness between the 2 study sites using the relatedness test with the Wang estimator with 1,000,000 bootstrapping samples.

We know there are landscape and spatial differences between AmesREC and Lone Oaks. To attempt to account for this we used ArcGIS (ESRI, Redlands, California, USA) to generate a

95% minimum convex polygon (MCP) of all deer locations at Lone Oaks with a 1km buffer. We centered the generated polygon on AmesREC where the majority of capture locations were found to standardized size and sample numbers between the 2 locations.

Chapter Three Results

From 1 January 2023 to 1 June 2025, we captured 84 adult deer (Ames: 44 females, 19 males; Lone Oaks: 13 females, 8 males) with 3 recaptures at Lone Oaks. A total of 72 adult deer were fitted with Iridium satellite collars (52 females, 20 males). We captured and collared four fawns (2 female, 2 male) at AmesREC. However, likely due to battery failure, we lost contact with 11 adult collars and one fawn collar. Additionally, 1 adult collar slipped off the deer.

3.1 Question 1: Survival, cause of death designation, and disease testing

3.1.1 Survival analysis

The annual survival for the AmesREC population including hunter harvest was 0.570 (SE = 0.069, 95% CI = 0.449 - 0.723) without hunter harvest was 0.649 (SE = 0.066 95% CI = 0.531-0.793) and the annual survival for the Lones Oaks population was 0.716 (SE = 0.149, 95% CI = 0.475 -1.0; Table 3). As shown in Table 3, survival did not differ by sex or age class regardless of population. Although survival was generally higher for females in both populations. Using an alpha value of 0.05 we did not find a difference between capture years (AmesREC $P = 0.7$) or Lone Oaks ($P = 0.5$). Focusing on AmesREC and combining years by month, we saw 3 distinct periods on the survival curve with drops in survival during February - April, July - October, and November – December as shown in Figure 1.

3.1.2 Cause of death designation and disease testing

We removed 10 deer (4 in 2023, 5 in 2024, and 1 in 2025) that died within 14 days of capture from the analysis. These deer were presumed to have died of capture myopathy except for 1 which was harvested by a hunter in 2024. Four of the 10 deer were CWD positive. For all dead deer throughout the project Table 4 shows individual ID, sex, age , capture location, CWD results, available EHD and BTV antibody results, and cause of death category. Our cause of

death analysis included 30 deer that lived greater than 14 days from capture (Ames: 17 females, 9 males; Lone Oaks: 1 females, 2 males).

We observed 8/22 mortality events from 1 January 2023 to 31 December 2023, 16/55 mortality events from 1 January 2024 to 31 December 2024, and 6/35 mortality events from 1 January 2025 to 1 June 2025. From 2023 to 2024, cause of death included 38% legal harvest (3/8), 12% illegal harvest (1/8), 25% predation (2/8), 25% unknown (2/8), and 7 collars lost communication. From 2024 to 2025, cause of death was 19% legal harvest (3/16), 6% illegal harvest (1/16), 31% disease-associated mortality (5/16), 13% predation (2/16), and 31% unknown (5/16). From 1 January 2025 to 1 June 2025 our observed causes of death were 33% disease associated mortality (2/6), 33% predation (2/6), and 33% unknown (2/6). Of the total 7 deer determined to be disease-associated mortalities 6/7 were positive for CWD, and 2/7 were also positive for EHD via RT-PCR at necropsy (neither had HD antibodies at capture).

Approximately half of all mortalities (15/30, 50%) occurred during the local gestation period (January - May, Wilber et al. 2026, J. Kosiewska, University of Tennessee, unpublished data). There was a total of 7 deer that died of disease-associated events. Of those 7 deer that died of disease-associated events there were 3 that died during the gestation window. All 3 of these deer (1 females, 2 males) were captured at AmesREC and were CWD positive at necropsy. Of these 3 deer, 2 had antibodies to EHD, indicating previous exposure. The next highest period for overall mortality was consistent with local HD outbreaks and of the 7 total disease-associated mortalities 2 died during this window. Out of these 2 deer 1 was positive for CWD at necropsy. While the other was not detected for CWD but tested positive for EHD antibodies at necropsy while being negative at capture. One deer died during the period consistent with the local ruts

from November – January (Wilber et al. 2026, J. Kosiewska, University of Tennessee, unpublished data) and was positive for HD antibodies at capture and CWD at necropsy.

We sampled 31 deer for CWD and found 17 were CWD positive, 10 were not detected, and 4 were unknown. At capture, 43 out of 84 total deer had antibodies to HD. Of those 43 individuals 31 had exposure to more than one virus with 27 of them testing positive for both EHD and BTV antibodies. At the time of death, 10 individuals tested positive for CWD and had EHD antibodies. Six of those 10 individuals that tested positive for CWD had both EHD and BTV antibodies as shown in Table 4. Additionally, there was evidence of a HD outbreak reported in 2024 (SCWDS 2024).

3.2 Question 2: Reproduction and recruitment

3.2.1 Reproduction

Reproduction was high each year with 87% (13/15) pregnant in 2023 and 91% (30/33) in 2024. We recorded 67% (2/3) pregnancy rate for fawns (2/3 in 2023, 1/3 in 2024) over 2 years of sampling. We estimated peak fawning time using 6 deer necropsied in 2023 and 2024, with estimated fawning to be between June 15-30 and all were carrying at least 2 fetuses. One of these necropsied individuals had 5 similarly developed fetuses (Kosiewska et al. 2024). In 2024, a subset of 23 pregnant deer received VITs that were paired with their collars. Unfortunately, 35% (8/23) females died before peak fawning, and 4% (1/23) died before the typical end of lactation, approximately 10-12 weeks after birth (DeYoung and Miller 2011). The most observed cause of death category of these 9 mothers was predation 44% (4/9), followed by unknown 33% (3/9).

We lost communication with 10 of the placed VITS. We received our earliest birth alert from the remaining 5 VIT/collars on 6 June 2024, and the final birth alert received was on 17 June 2024. We recovered 60% (3/5) of the VITS and placed 4 fawn collars (3 from VITs and 1

opportunistic). We used a mean search radius of 115.4 m (min = 60m, max = 200m) to find these fawns. One fawn was captured and collared opportunistically from random encounter transect searches of likely fawn cover. We collared 2 female fawns (3.3 kg and 2.8 kg) and 2 males (3.3 kg and 2.7 kg). The average fawn collar retention time was 11.25 days (min = 3 days, max = 20 days). We were unable to monitor fawn recruitment due to a collar malfunction 3 days after placement and the remaining 3 collars were either removed from maternal grooming or possible predation events with no carcass.

3.3 Question 3: Stage-structure demographic model and immigration potential

3.3.1 Stage-structured population model

We only used the AmesREC population for annual survival estimates since the Lone Oaks population's estimate of survival has an upper 95% CI of 1. We modeled the high reproduction system and real-world systems, as defined above, using the values shown in Table 1. Modeling of our high reproduction system and real-world system yielded λ values below 1, with the highest at 0.878 (95% CI 0.708 – 0.967). Through sensitivity analysis, 12-week neonate survival would need to be greater than 0.468 in our high reproduction system or greater than 0.649 in our real-world system to maintain a population ($\lambda = 1$). Table 5 shows the output of our high reproduction system and real-world system in the absence of immigration.

Additionally, we allowed for uncertainty within our parameters by simulating 10,000 growth curves using the lowest declining projection, the highest population growth rate (λ = 0.878). We found that even when we allowed for uncertainty our credible intervals were still below λ = 1 (95% CI 0.695 – 0.936). The projection is shown in Figure 2 along with the reported 5 years of FLIR survey densities. The confidence intervals for the final year of FLIR densities were unavailable at the time of writing. Using the lowest and highest population growth outputs

regardless of system modeled we found that for the population to be stable we would need an annual immigration rate of between 3 – 8 females per square mile.

3.3.2 Immigration potential

We sampled 85 individuals at AmesREC (53 adult captures, 4 fawn captures, and 28 hunter harvested individuals) and 21 at Lone Oaks (21 adult captures) for full genetic analysis for AmesREC (2023-2024) and Lone Oaks (2024-2025) (Table 2). The mean expected heterozygosity (He) was higher at AmesREC (0.77; 9.49 alleles/locus) compared to Lone Oaks (0.74; 6.86 alleles/locus). CERVUS was not able to conduct a HW test for 13 loci due to limited minimum expected frequency for some alleles. The other loci all tested negative and so were within HW equilibrium. According to the ΔK analysis for samples taken in 2023 and 2024 using STRUCTURE, the correct number of populations was 3 (Figure 3). However, there was a second peak at 7 indicating potential substructure in one of the populations (Balkenhol et al. 2014). At K = 3 no individuals had > 0.8 for a q value indicating majority of one population (Figure 4). Therefore, we used K=7 (Figure 5) to evaluate potential structuring within the 2 study sites and found 2 individuals at AmesREC had > 0.9 contributions of population 4 and overall, more varied contributions of the other populations.

Using COANCESTRY with the Wang estimator for relatedness a value of 0 would indicate both groups were equally related within the population compared to what you would expect for the average. Using all genetic data for the full analysis (2023-2025), AmesREC was −0.00399 (n = 85 deer; variance = 0.0113) and Lone Oaks was 0.0340 (n = 21 deer; variance = 0.0126). Therefore, AmesREC deer with a negative number were less related than what you would expect and Lone Oaks deer had a positive value indicating higher genetic relatedness. Using the bootstrapping permutation test between the 2 groups in COANCESTRY, AmesREC

relatedness minus Lone Oaks relatedness was significantly different. The observed value for the difference between sites (-0.0380) was outside of the 1-99% quantile values obtained by bootstrapping (Figure 6). We found a significant negative value indicating AmesREC deer were less related than average compared to deer at Lone Oaks which follows the pattern seen in program STRUCTURE. We also performed a reduced analysis looking at only those individuals within the 95% MCP with buffer and found the trend was the same in the 1% quantile (AmesREC: n = 18 deer, 0.00609, variance 0.0162; Lone Oaks: n= 21 deer, 0.0340, variance 0.0126).

Chapter Four Discussion

High CWD prevalence has previously led to notable declines in cervid populations in different areas of the United States. However, despite high levels of CWD prevalence in some areas of West Tennessee, 5 years of deer density surveys have shown that a population with high CWD prevalence is not showing notable population declines. Our study shows that some level of immigration is almost certainly needed to describe this observed pattern. Using both the mean values, as well as values with measures of uncertainty, even our highest estimates of lambda (λ) were below what is required for a stable population ($\lambda = 1$). In the absence of immigration, our model outputs showed that we should be seeing average population declines of 23.57% (the high reproduction system) and 25.93% (the real-world system) annually.

We believe that these expected population declines are being driven by low annual survival of adult deer and the potential for low neonate survival rates at AmesREC. In the Southeast, annual survival for deer is generally high with female survival being the driver of population viability (Chitwood et al. 2015, Kilgo et al. 2016, Peters et al. 2020). Female survival in the Southeast is often 80% or greater (Chitwood et al. 2015, Kilgo et al. 2016, Haymes et al. 2018). In Arkansas, Collier and Krementz (2007) parameterized sub-adult/adult survival as 0.7 – 0.99 which was uniformly distributed. Our mean annual survival for adult deer ranged from 0.404 – 0.681, depending on age class and sex. These values are well below what has been reported in the Southeast but are consistent with the reduced annual survival seen in high prevalence CWD areas (Miller et. al 2008, Edmunds et. al 2016). Even with high wolf (*Canis lupus*) mortality in northeastern Minnesota, annual survival rates were similar but still higher than our observed rates (0.31 – 0.80, depending on age and sex) (Nelson and Mech 1986).

We observed a nearly 50% mortality rate (47.6%) for all collared deer during the three time periods of the study. We had a high rate of mortality during our first year of helicopter captures with four deer dying of capture myopathy; 75% (3/4) were CWD positive. These mortality events for the CWD positive deer may have been facilitated by elevated cortisol which likely contributed to overall poor body condition (Mitchell et al., in prep). We also observed a high mortality for females monitored for birthing events where ~33.3% of the does that received VITs died before they would have given birth. Our highest observed mortality (50%, 15/30) of females was during the gestation period.

We found that observed mortality strongly reduced population growth, but we also wanted to know if compensatory recruitment or baseline high reproductive output at AmesREC could offset the negative effects of CWD on survival. Overall reproductive output was high for the study (89%) with some fawn breeding occurring regardless of the CWD prevalence. Mori et al. (2025) also found that CWD infection did not impact pregnancy probabilities. Because of the high female mortality leading to loss of VITs, the low fawn recovery, and the fact that the longest a fawn retained their collar was 20 days, we were unable to estimate recruitment. However, even when we assumed relatively high recruitment rates consistent with other areas in the southeast, (λ) still remained below 1, indicating that it was highly unlikely that recruitment could compensate for the high mortality rates in the population.

Even after accounting for uncertainty in our parameters, the most optimistic values of λ (upper 95% CI = 0.936) were less than 1 and the final projected density (23 deer/sqmi) slightly below the observed 2025 FLIR density (24 deer/sqmi), as shown in Figure 2. Gaya et. al (2026) reported an average of 17% annual decline in deer density across study sites in Arkansas where CWD county-level prevalence ranged from 11 – 49%, during the study. The absolute values of

CWD prevalence and rate of change in CWD prevalence appear similar for Arkansas and Tennessee (National Academy Report 2025, Fig. 5.1.1). At our study site as of 14 March 2025, CWD prevalence in Fayette (28.76%) and Hardeman (21.72%) counties are similar to what was found in Arkansas (Gaya et al. 2026). However, the local prevalence of AmesREC has been greater than 30% since the 2020 – 2021 hunting season. Our modeled results of 23.57 – 25.93% annual decline were higher than what was reported from Arkansas (Gaya et al. 2026). Keever et al. (2025) showed that deer abundance across the West Tennessee area (which included our study site) declined overall since 2010 although for areas with low CWD prevalences these declines are likely due to loss of hunter engagement.

With the reduced survival from high mortality that is not offset by reproduction, it appears immigration may be allowing for an apparently stable population. AmesREC was more genetically diverse than Lone Oaks at both a total and similar-sized comparison. While we cannot quantify the level of which immigration is occurring, we do have strong evidence that it is occurring. For the AmesREC population to have a stable population with the observed vital rates, our model showed that 3 – 8 females per square mile needed to immigrate into the population annually. Typical female dispersal is between 2 – 20% annually (DeYoung and Miller 2011) and the deer density at AmesREC fluctuates around 30.6 deer per square mile with higher deer densities in the surrounding areas. Thus, it is biologically plausible that this number of immigrating females could be sustaining the AmesREC population.

Chapter Five Management Implications

This result has important implications for our understanding and managing disease dynamics and population impacts on heterogeneous landscapes. We are potentially seeing evidence of an ecological trap: an area that is of low fitness – likely due to the high prevalence of CWD – but is not yet perceived as an area of low fitness by individuals moving into the area. During the time of our study and for many years before, AmesREC was actively managed for deer habitat. Higher quality forage and resources could become attractive for deer on the periphery to immigrate into the AmesREC population even though it may serve as a sink with high mortality. The contrasting relationship between the spatial gradient in disease risk (high at AmesREC and lower outside of AmesREC) and the spatial gradient of deer resources (high at AmesREC and lower outside) could set up the ideal conditions for transient source-sink dynamics where the negative impacts of a pathogen on a host population are temporarily masked. However, as the spatial distribution of CWD continues to slowly expand in Tennessee with corresponding increases in CWD prevalence at the current edge, we would expect this source-sink dynamic to be disrupted as sources near the current edge of CWD spread begin to suffer high CWD-induced mortality and can no longer stabilize deer populations at the core. At this point, we would expect to see population declines in white-tail deer similar to what has been observed in other high prevalence CWD areas with significant implications for an already declining deer harvest in West Tennessee.

Ethics statement

All research was conducted in accordance with federal, state, local, and University regulations. All animal procedures were approved by University of Tennessee Institutional Animal Care and Use Committee (UT IACUC 2850). We received a scientific collection permit from Tennessee Wildlife Resources Agency (3059).

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Appendix

Table 1. Estimated demographic rates used to build a stage-structure matrix model to assess population growth rates for white-tailed deer at Ames Research and Education Center, Tennessee during 2023-2025. Age classes were considered as Neonates (0 – 12 weeks), Fawns (13 weeks - 1 year), Yearlings (>1-2 years), and Adults (2+ years). Survival probabilities with more than one value reflects non-sex specific, sex specific, age specific, and sex plus age specific survival values derived from our annual survival analysis as shown in Table 3.

Parameter	Description	Value	Source
p_A	Probability of an adult or yearling breeding	0.89	Calculated from field data
p_F	Probability of fawn breeding	0.67	Calculated from field data
π	Probability of a fawn being born female	0.50	Estimated from field data
$1-\pi$	Probability of a fawn being born male	0.50	Estimated from field data
r	Number of neonates per birth event.	2, 1.67	Maximum value expected, mean based on field data and literature for deer in the Southeastern US (Jones et al. 2010[a], Chitwood et al. 2015[b], Turner et al. 2019[c)]

Table 1. Continued

σ_N	12-week neonate survival probability	0.141[d], 0.196[e], 0.310[f]	Chitwood et al. 2015[b], Edge et al. 2023[d], Clevinger er al. 2024[e]
σ_{F_f}	Probability a female fawn survives to yearling	0.57, 0.622, 0.51	Estimated from field data
σ_{F_m}	Probability a male fawn survives to yearling	0.57, 0.404, 0.51	Estimated from field data
σ_{Y_f}	Probability a female yearling survives to adult class	0.57, 0.622, 0.359, 0.356	Estimated from field data
σ_{Y_m}	Probability a male yearling survives to adult class	0.57, 0.404, 0.359, 0.375	Estimated from field data
σ_{A_f}	Probability a female adult survives another year	0.57, 0.622, 0.624, 0.681	Estimated from field data

Table 1. Continued

σ_{A_m}	Probability a male adult survives another year	0.57, 0.404, 0.624, 0.415	Estimated from field data
ϕ_{F_f}	Annual number of female fawn immigration	0	Calculated from model
ϕ_{F_m}	Annual number of male fawn immigration	0	Calculated from model
ϕ_{Y_f}	Annual number of female yearling immigration	0	Calculated from model
ϕ_{Y_m}	Annual number of male yearling immigration	0	Calculated from model
ϕ_{A_f}	Annual number of female adult immigration	3,8	Calculated from model
ϕ_{A_m}	Annual number of male adult immigration	0	Calculated from model

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Table 2. Microsatellites used to analyze genetic variation for deer at Ames Research and Education Center (AmesREC) and Lone Oaks in West Tennessee during 2023-2025. There were 85 individuals from AmesREC (53 adult captures, 4 fawn captures, and 28 from 2024 hunter harvest) and 21 individuals from Lone Oaks (21 adult captures) used in this analysis.

	Ames						Lone Oaks					
Locus	Number different alleles	HObs	HExp	PIC	HW	F(Null)	Number different alleles	HObs	HExp	PIC	HW	F(Null)

Table 2. Continued

BM4107	11	0.847	0.84	0.818	NS	-0.0042		10	1	0.895	0.861	ND	-0.0688
BM6506	11	0.859	0.881	0.864	ND	0.0109		9	0.905	0.839	0.795	ND	-0.0567
Inra11	4	0.553	0.561	0.472	NS	0.0045		5	0.667	0.664	0.603	ND	-0.0063
OhemD	6	0.788	0.813	0.78	NS	0.0112		6	0.81	0.776	0.718	ND	-0.0363
OvirH	9	0.729	0.807	0.776	NS	0.0535		7	0.667	0.799	0.747	ND	0.0731
OhemL	9	0.824	0.81	0.779	NS	-0.0117		7	0.762	0.683	0.632	ND	-0.0682
OhemN	13	0.847	0.878	0.86	ND	0.0148		9	0.857	0.826	0.786	ND	-0.0255
OhemP	9	0.788	0.797	0.766	NS	0.001		6	0.81	0.748	0.693	ND	-0.0437
OvirA	11	0.835	0.872	0.852	ND	0.0192		9	0.81	0.889	0.853	ND	0.0351
Rt5	12	0.894	0.879	0.862	ND	-0.0125		8	0.952	0.843	0.799	ND	-0.0741
Rt7	13	0.906	0.857	0.836	ND	-0.0321		9	0.905	0.811	0.764	ND	-0.0672

Table 2. Continued

Rt13	9	0.6	0.811	0.783	NS	0.1476		9	0.476	0.796	0.754	ND	0.2189
Rt24	12	0.929	0.858	0.837	NS	-0.0439		12	0.905	0.884	0.849	ND	-0.021
BL25	3	0.435	0.44	0.38	NS	0.0009		4	0.476	0.53	0.482	ND	0.0547
BL42	11	0.824	0.859	0.836	ND	0.0184		11	0.857	0.862	0.823	ND	-0.0164
BM6438	12	0.812	0.877	0.858	ND	0.0346		10	1	0.88	0.844	ND	-0.079
OFCB193	9	0.776	0.783	0.759	NS	0.0099		8	0.905	0.84	0.796	ND	-0.047
OhemK	4	0.388	0.423	0.387	NS	0.0714		3	0.238	0.22	0.199	ND	-0.0567
OhemzO	2	0.165	0.209	0.186	ND	0.1152		3	0.095	0.094	0.09	ND	-0.0149
OhemQ	14	0.929	0.886	0.871	ND	-0.0286		14	0.905	0.919	0.888	ND	-0.0046
OhemS	21	0.859	0.918	0.907	ND	0.0329		14	0.762	0.904	0.871	ND	0.0793

Table 3. Annual survival for white-tailed deer calculated for deer at Ames Research and Education Center (AmesREC) and Loan Oaks in West Tennessee during 2023-2025. Age classes were considered as Neonates (0 – 12 weeks), Fawns (13 weeks - 1 year), Yearlings (>1-2 years), and Adults (2+ years).

	Mean	Lower 95% CI	Upper 95% CI	Standard error	*p*-value
Overall:	0.592	0.481	0.730	0.063	NA
Female	0.662	0.541	0.811	0.068	0.20
Male	0.389	0.202	0.750	0.130	0.20
Fawn	0.510	-	-	-	-
Yearling	0.397	0.136	0.203	0.777	0.10
Adult	0.652	0.068	0.533	0.799	0.10
Ames:	0.570	0.449	0.723	0.069	NA
Female	0.622	0.489	0.791	0.076	0.30
Male	0.404	0.198	0.824	0.147	0.30
Fawn	0.510	-	-	-	-
Yearling	0.359	0.153	0.845	0.157	0.20
Adult	0.624	0.494	0.788	0.074	0.20
Lone oaks:	0.716	0.475	1.00	0.149	NA
Female	0.933	0.815	1.00	0.064	0.20
Male	0.333	0.067	1.00	0.272	0.20
Fawn	0.510	-	-	-	-
Yearling	0.667	0.272	1.00	0.272	1.00

Table 3. Continued

Adult	0.750	0.475	1.00	0.175	1.00

Table 4. All project deer that died from 2023-2025 with their ID, sex, age, capture location, disease results, and cause of death (COD) category. Cause of death categories are: capture myopathy (CM), legal hunter harvest (HH), illegal harvest (IH), diseased assocaited (Dz), predation (P), and unknown (U). For those individuals with multiple COD categories the first is the primary COD and the second could not be ruled out. .

Deer ID	Sex	Age	Location	CWD status	EHD antibodies at capture	EHD antibodies at necropsy	BTV antibodies at capture	COD
1	F	2	Ames	-	negative	-	negative	IH
2	F	5	Ames	-	negative	-	positive	P
6	M	1	Ames	detect	-	-	-	U
7	M	2	Ames	-	negative	-	negative	HH
9	F	5	Ames	-	positive	-	positive	P
10	M	2	Ames	detect	positive	-	positive	HH
13	F	NA	Ames	detect	-	-	-	CM
14	F	4	Ames	unknown	negative	-	negative	U
15	M	3	Ames	detect	negative	-	negative	CM
16	F	2	Ames	detect	positive	-	positive	U
17	F	4	Ames	non-detect	positive	-	negative	HH

Table 4. Continued

19	F	3	Ames	detect	positive	-	positive	CM
23	M	5	Ames	detect	positive	-	negative	HH
24	F	4	Ames	unknown	positive	-	positive	U
27	F	3	Ames	non-detect	negative	-	negative	CM
28	F	2	Ames	detect	negative	-	negative	HH
29	F	3	Ames	-	negative	-	negative	P
33	F	5	Ames	non-detect	positive	-	positive	HH
34	M	3	Ames	-	-	-	-	IH
35	F	3	Ames	non-detect	negative	-	negative	P, CM
36	F	4	Ames	detect	positive	-	positive	P
38	F	14	Ames	detect	positive	-	negative	P, CM
39	F	5	Ames	non-detect	negative	positive	negative	Dz
40	M	4	Ames	detect	positive	-	negative	Dz
43	M	3	Ames	detect	negative	-	negative	Dz
47	M	3	Ames	detect	positive	-	positive	Dz
48	F	5	Ames	-	negative	-	negative	U
51	F	2	Ames	detect	positive	-	negative	Dz
52	F	5+	Ames	-	positive	-	positive	P

Table 4. Continued

53	F	2	Ames	detect	negative	-	negative	Dz
54	M	2	Ames	detect	negative	positive	negative	Dz
57	F	3	Ames	unknown	positive	-	positive	U
60	M	5	Ames	detect	positive	-	positive	P
61	F	5	Ames	unknown	positive	-	positive	U
62	F	4	Ames	-	positive	-	positive	U, CM
68	F	5+	Lone oaks	non-detect	positive	-	positive	P, CM
71	M	2.5	Lone oaks	non-detect	negative	-	negative	U
72	F	5+	Lone oaks	non-detect	positive	-	positive	U
73	M	2	Lone oaks	non-detect	positive	-	negative	HH
77	M	3	Lone oaks	non-detect	-	-	-	CM

Table 5. The projected population growth rates (λ) for the AmesREC population without immigration by modeled system and annual survival rate. The annual survival rates, shown in Table 3, were combined with our low, medium, and high 12-week neonate survival values to project the population growth rates. Along side these rates there is percent annual decline (% decline) and the 12-week neonate survival required for the population to be stable (λ=1).).

	High Reproduction System	Real-world System

Table 5. Continued

Survival rate used	λ	% decline	12-week survival for λ=1	λ	% decline	12-week survival for λ=1
Non-sex specific:						
Low 12-week neonate survival	0.6901	30.99	-	0.6709	32.91	-
Medium 12-week neonate survival	0.7348	26.52	-	0.7086	29.14	-
High 12-week neonate survival	0.8248	17.52	0.541	0.7848	21.52	0.649
Sex specific:						
Low 12-week neonate survival	0.7425	25.75	-	0.7232	27.68	-
Medium 12-week neonate survival	0.7874	21.26	-	0.7611	23.89	-
High 12-week neonate survival	0.878	12.2	0.4689	0.8377	16.23	0.562
Age specific:						
Low 12-week neonate survival	0.6902	30.98	-	0.6783	32.17	-

Table 5. Continued

Medium 12-week neonate survival	0.7195	28.05	-	0.7021	29.79	-
High 12-week neonate survival	0.7854	21.46	0.645	0.7551	24.49	0.772
Sex+Age specific:						
Low 12-week neonate survival	0.7367	26.33	-	0.7266	27.34	-
Medium 12-week neonate survival	0.7619	23.81	-	0.7468	25.32	-
High 12-week neonate survival	0.8198	18.02	0.62	0.7929	20.71	0.738
Average	0.7643	23.57		0.7407	25.93	

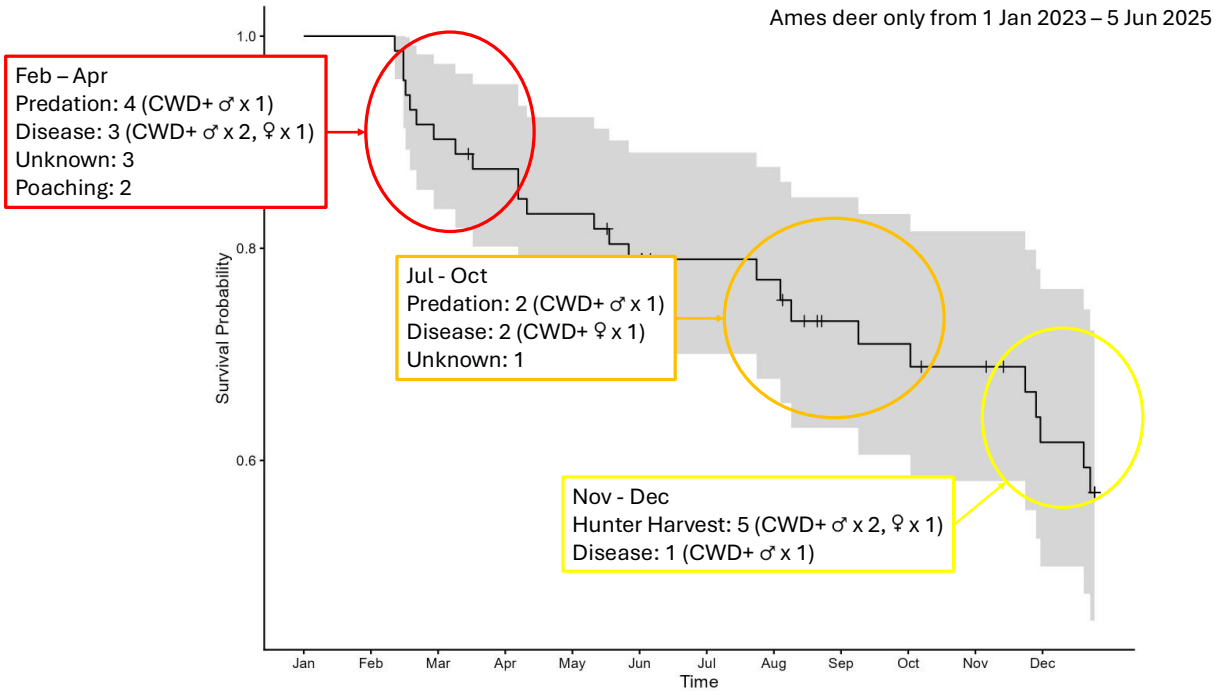

Figure 1. Survival of white-tailed deer at Ames Research and Education Center (AmesREC) in West Tennessee from deer monitored between 2023-2025. We combined capture years by month since year did not differ. We found 3 distinct periods on the survival curve with drops in survival during February - April, July - October, and November – December.

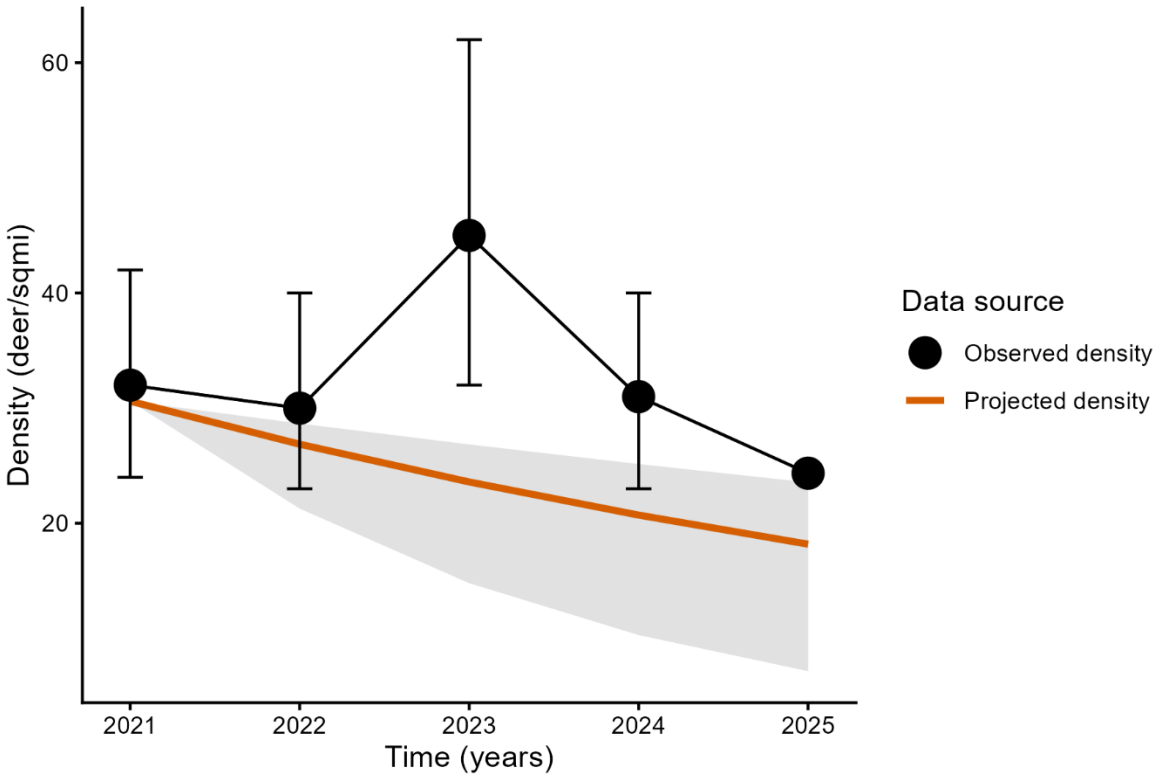

Figure 2. Observed versus projected densities of white-tailed deer at Ames Research and Education Center (AmesREC) in West Tennessee from deer monitored between 2023-2025. The observed densities are those from the 5 years of forward-looking infrared (FLIR) surveys. The projected densities are the result of uncertainty within our parameters after 10,000 simulations (grey area) and the projection for our lowest declining population growth value.

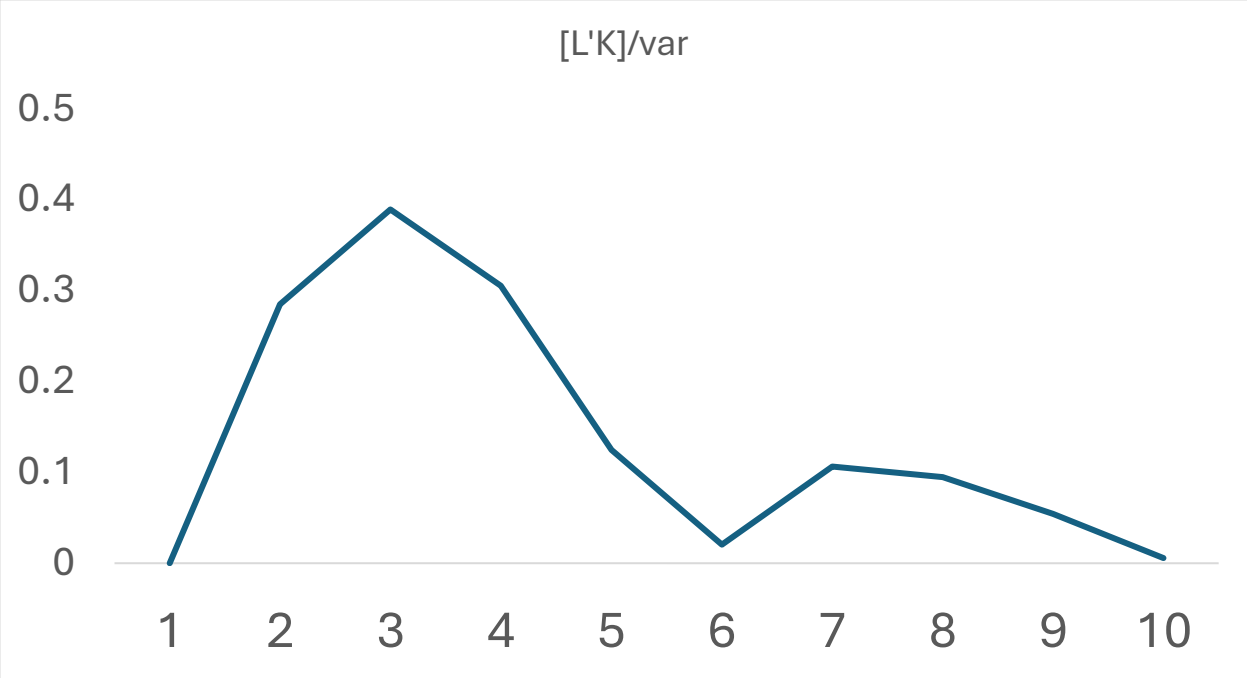

Figure 3. Analysis of change in likelihood (Delta K) with different values for population clusters (K) using STRUCTURE and microsatellite data for white-tailed deer in West Tennessee from 2023-2024.

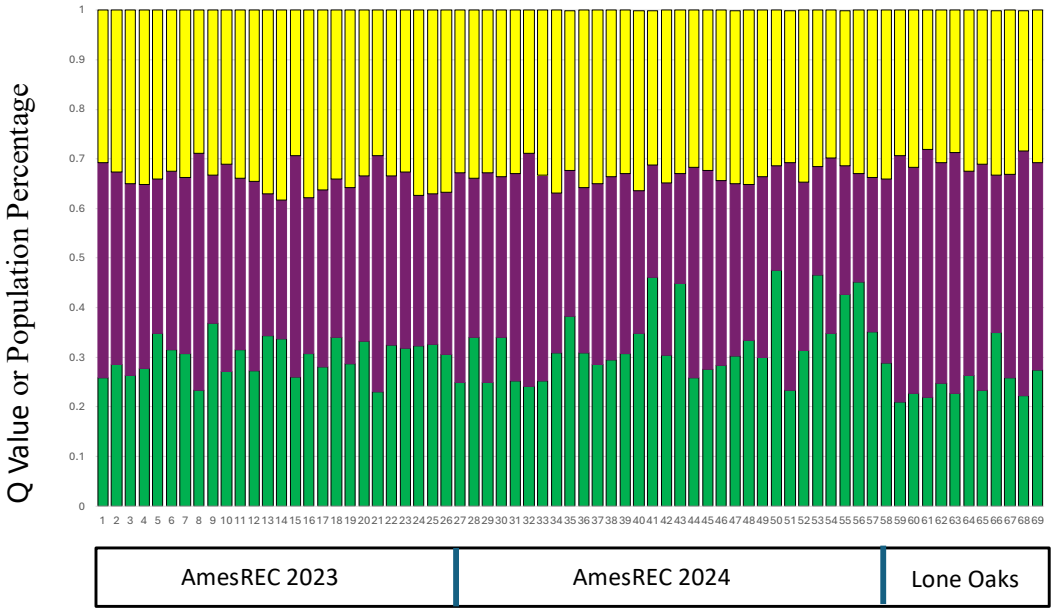

Figure 4. Population structure of white-tailed deer in West Tennessee from Program STRUCTURE using microsatellite data collected in 2023 and 2024 using 3 populations.

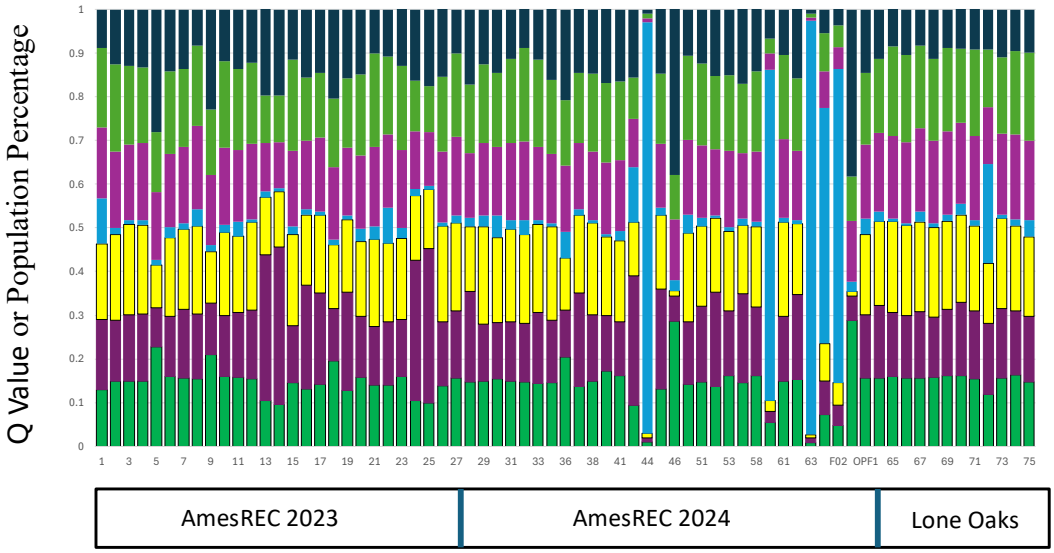

Figure 5. Population structure of white-tailed deer in West Tennessee from Program STRUCTURE using microsatellite data collected in 2023 and 2024 using 7 populations.

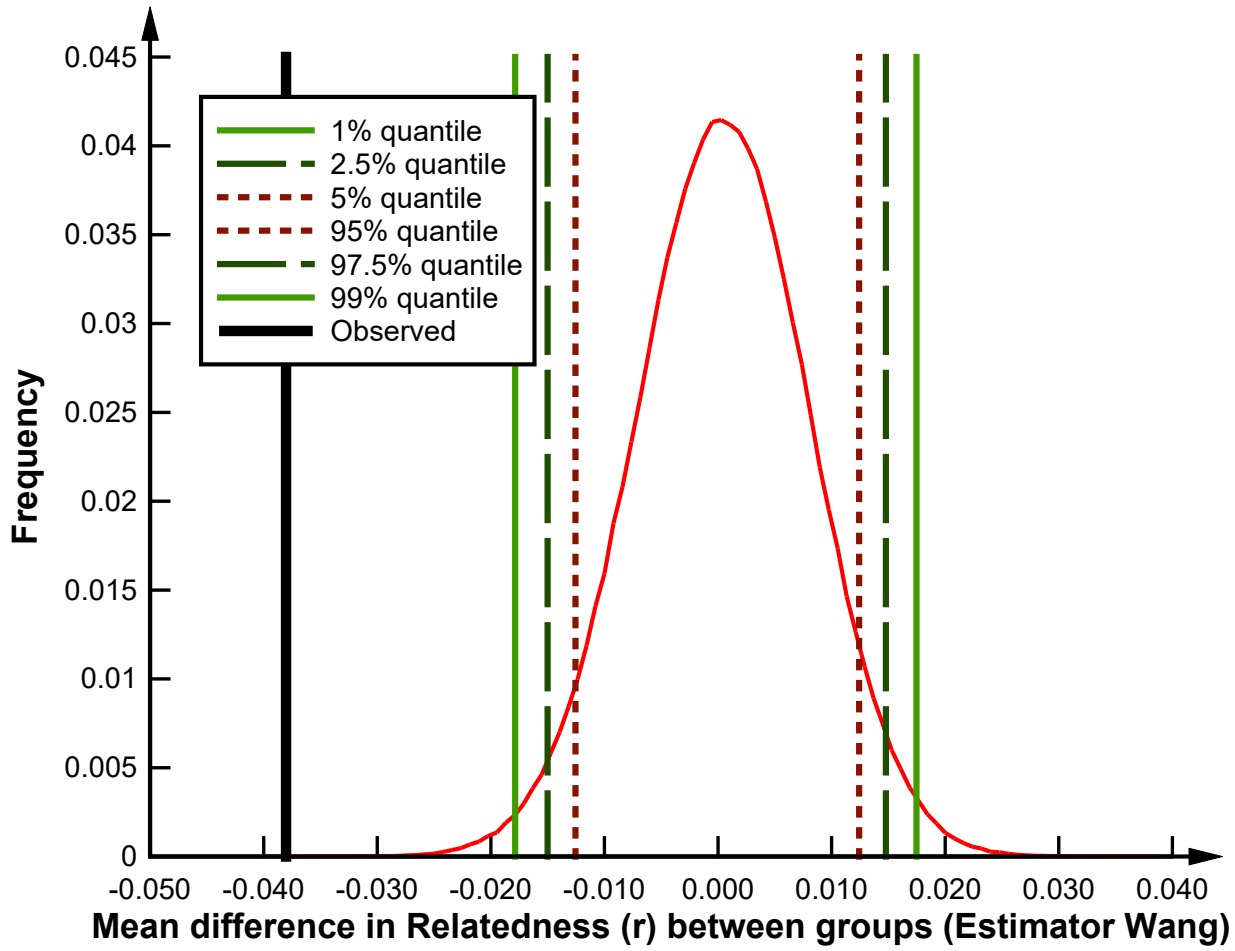

Figure 6. We compared overall genetic diversity of white-tailed deer at Ames Research and Education Center (AmesREC) and Lone Oaks in West Tennessee (2023-2025) by comparing pairwise relatedness from microsatellite data using program COANCESTRY (1.0.2.0) We tested differences in relatedness between the 2 study sites using the relatedness test with the Wang estimator with 1,000,000 bootstrapping samples and found AmesREC was less genetically related compared to Lone Oaks.

Vita

Jacob Wyrick was raised in Corryton, Tennessee. After high school, he joined the Tennessee Army National Guard as a medic. It was during his time in the military that his mentor encouraged him to pursue higher education. Following the honorable completion of his military service, he received an Associate of Science degree with cum laude honors from Pellissippi State Community College in December 2021 and a Bachelor of Science in Wildlife and Fisheries Management with summa cum laude honors from the University of Tennessee at Knoxville in May 2024. Jacob is currently pursuing a Master of Science in Wildlife and Fisheries Management at the University of Tennessee at Knoxville under the supervision of Drs. Lisa Muller, Mark Wilber, and Dan Grove. His research investigates the impacts of chronic wasting disease on white-tailed deer in Tennessee's endemic area. More specifically, Jacob is interested in the population dynamics that are currently preventing white-tailed deer population declines and maintaining an apparently stable population.