Population estimation, harvest management, and landscape-scale spatial ecology of wild turkeys in Maine

Year 3 Progress Report

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Disclaimer: The findings contained in this report represent preliminary results of ongoing research, and they should be cited as unpublished data until they have undergone peer review and publication. We expect that estimated values and interpretation of results could change as additional years of data are collected. These changes will be incorporated into future reports and final published products.

Summary

1) The reintroduction of wild turkeys to Maine has been extremely successful, with the species now established and breeding in all counties of the state. The Maine Department of Inland Fisheries and Wildlife is now challenged with managing an abundant and popular game species that also lives at the human/wildlife interface.
2) In this report we summarize data collection and preliminary results from three years of research. Our major objectives are to develop tools for wild turkey population and harvest estimation, assess demographic rates and seasonal movements under varying landscape conditions, and evaluate prevalence and ecology of wild turkey diseases in Maine. We have also taken the opportunity to address a number of methodological questions related to wild turkey research in general.
3) Using rocket and drop nets, we captured and banded 890 unique wild turkeys; 124 in 2018, 395 in 2019, and 371 in 2020. We fitted 121 females with VHF backpack transmitters, 30 females with VHF necklace transmitters, and 59 females with GPS transmitters. We fitted 57 males with VHF necklace transmitters (Table 2). We collected blood and cloacal swabs from 627 turkeys for pathogen diagnostics; 89 in 2018, 280 in 2019, and 258 in 2020.
4) We modeled harvest rates for male turkeys during the spring hunting season using a band recovery model that integrated band recovery data with survival information from radio-marked individuals. In 2019, we estimated the adult male harvest rate to be 0.261 (0.168–0.371 95% CI) compared to a harvest rate of 0.107 (0.058–0.169 95% CI) for juvenile male turkeys. In 2020, we estimated adult male harvest rate to be 0.244 (0.165–0.345

95% CI) compared to a harvest rate of 0.099 (0.052–0.164 95% CI) for juvenile male turkeys.

5) We developed an integrated population model that combined harvest rate estimates (*h*) and total harvest numbers (*H*) provided by MDIFW to estimate statewide population size (*N*) using a Lincoln Estimator ($N = \frac{H}{h}$). We estimated Maine's total male turkey population to be 31,677 (95% Credible Intervals: 21,331-53,347) prior to the spring 2018 hunting season, 32,512 (22,011-54,274) prior to the spring 2019 season, and 33,500 (21,063-58,726) prior to the spring 2020 season. We provide age-specific estimates by Wildlife Management District (WMD).
6) From the integrated population model, we estimated the risk of mortality outside of the spring hunting season for adult and juvenile male turkeys, where non-harvest survival is the probability of surviving from the end of one spring hunting season to the beginning of the next. We estimated a mean non-harvest survival of 0.716 (0.341 – 0.927, 95% CI) for adult males and 0.721 (0.346 – 0.932, 95% CI) for juvenile males. Adult male non-harvest survival ranged from 0.432 (0.0 – 1.0, 95% CI) in WMD 16 to 0.985 (0.807 – 0.1.0, 95% CI) in WMD 27. Juvenile male non-harvest survival ranged from 0.435 (0.0 – 1.0, 95% CI) in WMD 6 to 0.986 (0.812 – 1.0, 95% CI) in WMD 27.
7) Molecular methods were used across all age and sex classes to detect individual infection with lymphoproliferative disease virus (LPDV) and reticuloendotheliosis virus (REV), while serological methods were used to detect previous exposure to *Mycoplasma gallisepticum* (*Mycoplasma*) and *Salmonella pullorum* (*Salmonella*) from blood collected during turkey capture. We found an overall prevalence of 56.5% (354/627) for LPDV infection, 17.2% (108/627) for REV infection, 74.5% (175/235) for *Mycoplasma*

exposure, and 3.4% (8/235) for *Salmonella* exposure. *Salmonella* was not included in any statistical analysis due to the low number of positive individuals.

8) We estimated weekly survival rates for VHF- and GPS-marked female wild turkeys using nest survival models. Our top performing model of weekly survival probability was based on the Month of the year (ΔAIC = 0.0; Table 6). The lowest weekly survival probability occurred during the month of May (0.948; 0.927 – 0.963, 95% CI) and the highest was in January (.996; 0.975-1.000, 95% CI). Additional support was found for a model based on MDIFW Region. No strong support was found for year of the study, WMD or study area of capture, age classes, sex, or transmitter type.
9) We also included models of survival based on disease status for wild turkey hens at capture. Our second-best supported model for survival was based on REV infection status (ΔAIC = 15.327; Table 6). The weekly survival probability was 0.983 (0.979–0.987, 95% CI) for uninfected turkeys and 0.967 (0.936–0.983, 95% CI) for REV-infected turkeys. These estimates correspond to annual survival rates of 0.413 (0.330–0.495 95% CI) for uninfected turkeys compared to 0.176 (0.033–0.417 95% CI) for infected turkeys. Additional support was found for a model based on LPDV infection status. No strong support was found for *Mycoplasma* infection status.
10) To assess the potential for mortalities related to capture and handling up to 30 days post capture, we modeled daily survival rate with a log-log link function. Our best performing model was based on the total amount of time the bird was held prior to release (ΔAIC = 0.0; Table 7), with birds experiencing longer handling times having a higher probability of survival to 30 days post capture. The second ranked model showed that birds fit with backpack style transmitters had a lower survival rate of 0.962 (0.929–0.979 95% CI) one

day post capture compared to a survival rate of 0.997 (0.963–1.000 95% CI) for birds with necklace transmitters (Figure 8). The cumulative survival rate during the first 14 days post-release for birds fit with backpack-style transmitters was 0.836 (0.758–0.890 95% CI), compared to 0.960 (0.862–0.986 95% CI) for birds fit with necklaces. There was additional support for models based on age of the bird at capture, REV infection status at capture, and both the mean temperature on day of capture and averaged across the week post capture. We did not find strong support for precipitation, LPDV and *Mycoplasma* infection status, sex, or location. We modified field protocols during years 2 and 3 of the project in response to these findings.

11) We monitored 120 nests from radio-marked hens. The average dates of initiation (first egg laid) for first, second, and third nests (Figure 15) were April 30, May 31, and June 23 (single nest). We estimated daily nest survival rates for these nests and found the top model was based on a linear relationship with age of the nest (ΔAIC = 0.0; Table 10). As nest age increased, the probability of daily survival decreased (β = -0.050; -0.075 – -0.024, 85% CI). The probability a nest survived a 38-day exposure period was 0.310 (0.192-0.432 95% CI; Figure 14). We did not find strong support for models based on nest initiation date, disease status, transmitter type, study area, or year.
12) We compared nest initiation dates and the number of hens nesting with reported harvests to identify potential conflict between turkey nesting ecology and current management practices. In 2018, 32.0% of harvests occurred before the median date of nest initiation compared to 65.7% of harvests in 2019. In general, peak hunter effort occurred immediately following (2018) or concurrent with (2019) the peak of nest initiation (Figure 15).

13) We compared nest initiation dates to identify potential sources of variation in wild turkey breeding phenology. Variation in nest initiation date was best described by the percentage of developed and agricultural land cover surrounding the nest as well as year (ΔAIC = 0, Table 11). For every 1 standard deviation (14.5%) increase in developed land cover, nest initiation dates shifted 3.274 (SE = 1.713) days earlier. For every 1 standard deviation (13.2%) increase in agricultural land cover, nest initiation dates shifted 2.928 (SE = 1.559) days later. Additionally, nests were initiated 10.035 (SE = 4.110) days earlier on average in 2018 compared with 2019 and there was no significant difference in mean nest initiation dates for first nests between 2018 and 2020. To detect differences in the distribution of nest initiations between years, we performed a chi squared analysis which determined that the distribution of nests in 2018 and 2019 differed from 2020.
14) We compared hen and nest characteristics to identify sources of variation in clutch size. Average clutch size of VHF-marked hens across three years of the study was 11.38 eggs (range = 6 to 20). Clutch size was greater for nests initiated earlier in the year, with a predicted value of 14.91 eggs (13.80-16.02 95% CI) for a nest initiated on April 10th, compared with 8.64 eggs (6.82-10.46 95% CI; Figure 16) for a nest initiated on June 22nd. Hens that were infected with LPDV at capture had an average clutch size of 11.08 (10.53-11.62 95% CI) compared to 12.27 (11.41-13.14 95% CI) for uninfected hens (Figure 17).
15) We used dynamic Brownian Bridge Movement Models to create seasonal home ranges based on shifts in movement behaviors of wild turkey hens. Average area of use (95% UD) for GPS-marked females that survived from capture until August 1 was 6.81 km^2 (1.61 km^2 – 21.42 km^2, Figure 18, 19, 20). The average seasonal movement distance

between wintering home range and nesting home range was 4.981 km. Individual female movements between winter and nesting home ranges varied from 0.238 km to 23.216 km. Variation in pre-nesting home range size was best explained by *Mycoplasma* infection status, study area best explained variation in distance traveled between winter and pre-nesting home ranges, and no models for winter home range size performed better than the null model.

16) We examined the relationship between any two pathogen infections using a Pearson's chi-squared test. We found that infection with REV and *Mycoplasma* were not independent of each other ($\chi^2_1 = 5.585$, $n = 235$, $p = 0.018$). An individual exposed to *Mycoplasma* was less likely to be infected with REV ($\beta = -0.81 \pm 0.32$, $p = 0.012$; Figure 24). Infection with all other pairs of pathogens (LPDV and REV; LPDV and *Mycoplasma*) were considered independent of each other.

17) We assessed 10 individual and spatial risk factors for LPDV infection using AIC model selection ($n = 627$). Age, sex, year, and region of collection were considered significant in the final model (Table 18 and 19, Figures 25–28). Adults had a higher prevalence of 71.1% (95% CI: 66.3–75.5%) compared with juveniles (34.8%; 95% CI: 29.2–40.8%; Table 20, Figure 25) and females had a higher prevalence of 64.1% (95% CI: 56.0–68.9%) compared with males (46.7%; 95% CI: 40.9–52.6%; Table 20, Figure 26). Variation in prevalence across the three years ranged from 51.6 to 77.5% and variation in prevalence by region ranged from 20.0 to 68.4% (Table 20, and Figure 27 and 28, respectively). There was also model support (performed better than the null model), for infection with REV, percent agriculture cover, and percent forested cover, though these

variables were not considered significant (Table 18). There was no model support for percent developed cover.

18) We assessed 10 individual and spatial risk factors for REV infection using AIC model selection (n = 627). Year of collection, region of collection, and infection with LPDV were considered significant in the final model (Tables 21 and 22, Figures 27–29). Variation in prevalence across the three years ranged from 9.0 to 22.9% and variation in prevalence by region ranged from 4.2 to 31.9% (Table 23, Figures 27 and 28, respectively). Infection with LPDV increased the probability of infection with REV (β= 0.503 ± 0.257, p = 0.0499; Table 22, Figure 29). This varies from the results mentioned from the chi-squared analysis above because this model considers other risk factors in predicting REV infection, rather than just the direct assessment of the relationship between the two pathogens. There was also model support for percent developed cover and age, but these variables were not considered significant (Table 21). There was no model support for percent agriculture cover, percent forested cover, or sex.

19) We assessed 11 individual and spatial risk factors for *Mycoplasma* exposure using AIC model selection (n = 235). Year of collection was the only significant factor in the final model, which also included infection with REV and percent forested cover (Tables 24 and 25, Figure 27). However, this model did not perform better than year of collection alone, suggesting year of collection is the only variable important for *Mycoplasma* infection. Prevalence of *Mycoplasma* decreased from 87.6% (95% CI: 79.2–93.0%) in 2018 to 21.4% (95% CI: 17.0–26.6%) in 2019 to 14.3% (95% CI: 10.6–19.1%) in 2020 (Table 26, Figure 27). There was no model support for age, sex, infection with LPDV,

WMD of collection, region of collection, percent developed cover, percent agriculture cover, or density (Table 24).

20) Flock size was assessed separately as a risk factor, using only a subset of live-captured individuals with associated flock size data. We performed AIC model selection on this data subset with the same variables as above, in addition to flock size, to determine if flock size is an important predictor of LPDV (n = 511) infection, REV (n = 511) infection, or *Mycoplasma* (n = 150) exposure. While flock size was not found to be a significant predictor of pathogen infection, it did perform better than both the LPDV and REV null models (Table 27, 28). There was no model support for flock size predicting *Mycoplasma* exposure (Table 29).

21) Overall sero-prevalence of *Salmonella* was 3.4%. While too low to include in statistical analysis, observed prevalence was greater in adults (7/159, 4.4%) than juveniles (1/76, 1.3%) and greater in females (8/150, 5.3%) than males (0/85, 0%). Adult females comprised 87.5% (7/8) of those infected while juvenile females comprised 12.5% (1/8) of those infected. Prevalence decreased by year from 5.9% (5/85) in 2018 to 3.3% (3/91) in 2019 to 0% (0/59) in 2020.

22) We evaluated the use of cloacal swabs as a minimally invasive detection method for LPDV in live-captured individuals and found an overall sensitivity (true positives) of 88% (57/65) and specificity (true negatives) of 75% (15/20) compared with the current method of blood collection, using samples only from January–March 2018 (Table 30). We compared this to cloacal swabs collected from 54 hunter-harvested turkeys in May of 2017 and 2018 coupled with bone marrow samples and found a significantly lower sensitivity (12/39, 31%; $\chi_1^2 = 32.87$, $n = 139$, $p < 0.001$), but the specificities were not

different (12/15; 80%; χ^2_1 < 0.001, n = 139, p = 1.00; Table 30). Additionally, there was no significant difference in prevalence estimated from cloacal swab samples (73%) versus blood samples (76%) from paired live-captured individuals (McNemar = 0.69, P = 0.41; Table 30). However, there was a difference in prevalence estimated from cloacal swab samples (28%) versus bone marrow samples (72%) from paired hunter-harvested individuals (McNemar = 19.20, P < 0.001; Table 30).

Conclusions and Future Directions

1) We used our estimates of adult and juvenile harvest rates in combination with the number of harvested and reported turkeys provided by MDIFW to estimate statewide population size. These methods account for mortality of individuals between capture and harvest, which may bias abundance estimates high. Additionally, by accounting for spatial variation of harvest, we were better able to estimate harvest rates by WMD, especially where we had few or no banded individuals, which in turn allowed us to derive more precise WMD-specific estimates of abundance and density. Moving forward, these models can be incorporated into a more sophisticated adaptive harvest management tool that is tailored to deal with the localized management needs across Maine.
2) Out GPS tracking efforts indicate that wild turkeys often make regular, directional movements among seasonal home ranges. Sometimes these movements can be substantial, with turkeys covering dozens of miles and traversing diverse landscapes. Future analyses will seek to understand the role of landcover in affecting wild turkey seasonal space use and movements, as well as their consequences for nest site selection and success.

3) Post-release mortality is commonly observed in wild turkey research, and we found multiple factors affected this in our data The most significant difference in post-release survival was related to handling time, where turkeys that experienced longer handling times had lower post-release mortality rates. We also found that style of transmitter impacted post-release survival, with backpack transmitters showing lower survival than necklaces. If there is a period following capture during which flight abilities are compromised, turkeys may be more susceptible to predation as they acclimate to their transmitters. Comparatively, necklace style transmitters are much smaller and less obtrusive to turkeys, which may explain the lower mortalities rates post-release. By adjusting our field methods during our second and third field season, we were able to substantially reduce post-release mortality.
4) We plan to assess genetic sequence data from LPDV-infected birds that will enable us to distinguish between LPDV strains and examine spatial clustering. These data may be used to describe potential transmission pathways that would improve our understanding of transmission dynamics.
5) The prevalence of each pathogen (REV, LPDV, *Mycoplasm a*, and *Salmonella*) varied significantly by year, which warrants continued surveillance of these pathogens and the incorporation of their annual variability into turkey population models for AHM.

Introduction

The restoration of wild turkeys to Maine has been very successful, as evidenced by a robust population throughout their historical range within the state, and viable populations that now extend into areas that likely lacked turkeys prior to European settlement. Wild turkeys are now established and successfully reproducing in all Maine counties. Over the last 30 years the wild turkey program has grown from one focused on re-establishment and very limited harvest to

one that allows for relatively liberal spring and fall hunting seasons. The first spring season in 1986 was limited to 500 hunters resulting in a harvest of 9 birds. Presently both spring and fall seasons are open to all interested participants, and the program supports around 20,000 wild turkey hunters, including an estimated 2,500 youth. In recent years Maine hunters have averaged a spring harvest of 6,000 bearded turkeys, and a fall harvest of 2,000 turkeys of either sex (MDIFW 2017). A recent assessment of wild turkey populations across the country suggests that Maine's wild turkey population is increasing at one of the greatest rates among all states (Erikson et al 2016).

With the success of this reestablished population, MDIFW is now faced with the challenges of managing for a viable turkey population and a successful hunting program, while simultaneously addressing social and ecological issues associated with an abundant wildlife species that often lives at the human/wildlife interface. Maine's wild turkey population continues to increase and expand into nearly all corners of the state. This is an obvious benefit to wild turkey hunters by providing opportunities for quality hunting, and recent surveys suggest that 78% of Maine turkey hunters are satisfied with their wild turkey hunting experience in the state (Responsive Management 2020). However, increases in wild turkey abundance also inherently increase the potential for human-turkey conflicts (Miller et al. 2000), and a survey of Maine residents performed in 2016 revealed that approximately 30% believe the abundance of wild turkeys should be reduced in the state (Responsive Management 2016). Thus, MDIFW is likely to face societal pressures in coming years to manage Maine turkey populations based on competing objectives.

Greater densities of wildlife are often associated with heightened risk of disease transmission, as well as increased potential for interaction with domestic poultry resulting in a

higher risk of pathogen spillover. Information on pathogen prevalence and distribution in Maine wild turkeys is scarce, and little is known about the effects of disease on individual and population health, the potential for disease transmission across the state, or transmission to humans, other wildlife, or domestic animals. In other wild turkey populations, greater than 25% of morbidity or mortality cases have been attributed to infectious diseases (MacDonald et al. 2016). We evaluated the prevalence, risk factors, and coinfection status of four infectious diseases in Maine wild turkeys: lymphoproliferative disease virus (LPDV), reticuloendotheliosis virus (REV), and the bacteria *Mycoplasma gallisepticum* (*Mycoplasma*) and *Salmonella pullorum* (*Salmonella*). Each of these qualify as pathogens that should be monitored in wild turkeys for several reasons: there are diagnostic tests readily available, they are a threat to poultry and occur at the domestic-wildlife interface, they can infect (or have the potential to infect) other wild birds, they have been found to be immunosuppressive and/or their pathogenicity is increased with stress or secondary infection, and there is a knowledge gap regarding their impact on wild turkeys at the individual and population level.

Our project began in 2018 as a component of MDIFW's implementation of the Big Game Management Plan. In this new management plan, goals and objectives were established through a thorough public input process to guide the Department's wild turkey management over the next 10 to 15 years. In modern wildlife management, a number of toolkits exist for addressing complex management challenges in the face of uncertainty. Adaptive harvest management and structured decision making are two examples, and these tools clearly have high potential for addressing management questions that are unique to wild turkeys (e.g. Robinson et al. 2017). However, nearly all comprehensive approaches to management require adequate data to inform

decisions, and much of the information necessary for informed decisions about wild turkey management is currently lacking in Maine.

The overall goal of our project is to produce rigorous information on a host of biological processes for turkeys in Maine, including population dynamics, survival and harvest rates, habitat use and reproductive success, seasonal movements, and disease prevalence and transmission. This information can then be used to develop tools that address MDIFW's population and habitat goal to "maintain a healthy turkey population below biological carrying capacity while providing hunting and viewing opportunity." Our specific objectives are to 1) improve MDIFW's ability to monitor wild turkey population trends by exploring population models that incorporate variables such as weather, productivity, harvest, sex, age, natural mortality, pathogen infection and other factors; 2) improve the quality and availability of wild turkey harvest data; 3) inform management that can be used to stabilize wild turkey populations in portions of southern and central Maine and increase the size and distribution of turkey populations in portions of northern, eastern, and western Maine; and 4) identify the prevalence and individual risk factors of LPDV, *Mycoplasma*, and REV infection and evaluate if there is a correlation between coinfection of these pathogens within an individual. Given the large amount of data collection required to achieve objectives 1-4, we are also 5) taking every opportunity to address methodological and ecological questions that will improve our ability to study wild turkeys and increase our knowledge of the species in general. In this report we detail results from three years of data collection, which provide preliminary insights to some of these objectives.

Field and Laboratory Methods

Study Areas

In the first year of the project, wild turkey captures took place in 4 study areas located in Wildlife Management Districts (WMD) 17, 18, 21, and 26 (Figure 1). In an effort to increase the sample size of banded individuals during our second and third year, we expanded banding efforts

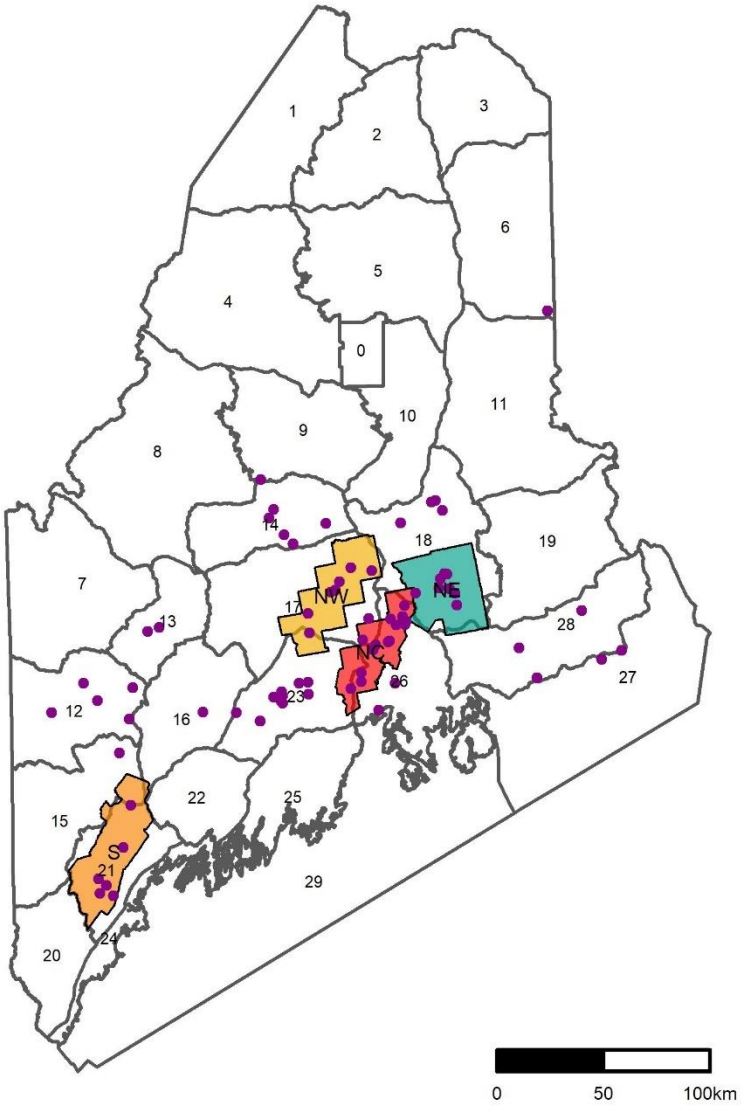


Figure 1. Map of Maine, USA, depicting Wildlife Management District boundaries (numbered) and approximate study area boundaries for Exeter/Corinth (NW, Orange), Orono/Old Town (NC, Blue), Greenfield/Stud Mill Road (NE, Green), Gray/Gorham (S, Purple)). Trapping sites are shown as pink dots.

throughout Maine to sites that were monitored and operated by MDIFW regional staff. We banded captured turkey at these additional sites and collected morphometrics and blood, but only a small number of transmitters were deployed at select sites.

Our north-western study area (NW) is located in Penobscot County, Maine, USA (44.98912°N, 69.07784°W). NW is within WMD 17 and encompasses the towns of Exeter, Corinth, Charleston, and Bradford. Property within NW is primarily privately owned and its land use is characterized by rural agricultural and pasture fields intermixed with forested areas. Human population density within NW ranges from fewer than 50 up to 100 individuals per sq. mile (USDC 2012) and the landscape has moderate road coverage with both paved, gravel, and dirt roads. NW is in central Maine and experiences moderate winters compared to more Northern regions of the state, but more severe winter weather than more southern regions.

Our north-central study area (NC) is also located in Penobscot County (44.91855°N, 68.66162°W). NC is primarily in the northern part of WMD 26, with some overlap of WMD 17 and 18. Research takes place within the towns of Orono, Old Town, Veazie, Bangor and Hampden. This area is primarily characterized by suburban and urban human residential areas with population density ranging from 100 to greater than 500 individuals per sq. mile (USDC 2012). Road density and residential development is higher in NC compared to our other study areas; however, forested area and agricultural lands are still present in the study area, albeit far more sparse and isolated compared to the other study areas. NC is in the same climatic zone as NW and experiences comparable weather.

Our north-eastern study area (NE) is located in both Penobscot and Hancock Counties, Maine, USA (45.01749°N, 68.39635°W) within WMD 18 between the towns of Greenfield and Amherst. Human population density in NE is very low with fewer than 50 individuals per sq

mile (USDC 2012), and includes large expanses that are completely uninhabited and undeveloped. Despite this, substantial human activity occurs in the form of forestry operations within privately-owned commercial forests that dominate the area. Moderate cover of maintained gravel and dirt roads are also present, although many of these roads become inaccessible in the winter after considerable snowfall. NE is in the same climatic zone as NW and NC, and experiences similar weather patterns.

Our southern study area (S) is in Cumberland County, Maine, USA (43.71543°N, 70.39268°W), and was chosen to represent a distinctly different region of the state than the previous three study areas. S is within WMD 21 and located between the towns of Gorham and Gray. The landscape within S spans a gradient between rural areas and the suburban edge of the greater Portland metropolitan area. This gradient of land use leads to mixed landcover and human activity levels. The landscape is a mix of residential areas, agricultural fields, and fragmented forests. Human population density in this area is greater than 200 individuals per sq. mile (USDC 2012). Being farther south and closer to the coast, S is in a separate climactic zone compared to the other 3 study areas and experiences generally milder weather compared to NW, NC, and NE.

Wild Turkey Capture and Sample Collection/Storage

Capture of wild turkeys took place from January through March 2018 (Year-1), December 2018 through March 2019 (Year-2), and December 2019 through March 2020 (Year-3). During this time of year, wild turkeys form large flocks and are more likely to frequent bait sites due to snow obscuring normal food sources. We trapped both male and female wild turkeys using either drop nets (Glazener et al. 1964) or rocket nets (Grubb 1988). Turkeys were weighed (+/- 0.5 lbs) using a spring scale. The sex and age of each bird was assessed based on its plumage

and presence of a beard and spurs (Dickson 1992). The flock size was recorded, which we defined as the number of birds observed gathering at the bait, whether captured under the net or not. Each turkey received either a size 22 (female) or 28 (male) butt-end aluminum leg band (National Band and Tag Co., Newport, Kentucky, USA) with an identification number for the bird as well as contact information for reporting the bird if harvested or otherwise discovered dead. During Year-1, each turkey also received an additional mark in the form of an aluminum rivet band, patagial wing tag, or color leg band. During Year-2 and Year-3, only a combination of aluminum and rivet bands was used. Tarsus length was measured for all birds as well as spur and beard length, if present.

Wild turkeys were fitted with a VHF or GPS transmitter, or banded only, based on trap site location, sex and age, and status of deployed transmitters. We deployed transmitters to disperse them within and among the four primary study areas, with a goal of maintaining a 50:50 ratio between adult and juvenile females when possible. We deployed three unique transmitter models; a VHF backpack, a GPS backpack, and a VHF necklace. VHF backpack packages consisted of an 80g transmitter from Advanced Telemetry Systems (Isanti, Minnesota, USA) attached using a backpack-style harness. GPS packages were 90g Litetrack GPS transmitters with a built in VHF component (Lotek Wireless Fish and Wildlife Monitoring, Newmarket, Ontario, CA), also attached with a similar backpack-style harness. The VHF necklace packages consisted of a 12g transmitter from Advanced Telemetry Systems (Isanti, Minnesota, USA) attached around the neck using wire, crimps, and plastic tubing. We only deployed GPS transmitters in the three northern study areas (NW, NC, NE) as these study areas were located within the same climatic zone and represented the major landcover types (agricultural, suburban-urban, forested) relevant to our objectives on movement and space use of wild turkey hens.

Backpack-style transmitters were secured to each bird using elastic cord tied around the base of both wings. Any transmitters that were recovered and still functioning were reserved so they could be redeployed at a later capture. Transmitters did not exceed 4% body mass, and all capture and handling of wild turkeys was approved by the University of Maine Institutional Animal Care and Use Committee (IACUC Protocol # A2017_11_03).

When possible, we collected blood from the brachial vein and cloacal swabs from turkeys during capture for pathogen analysis. Within 24-hr post-capture, we processed the blood (see below) and archived additional aliquots in a -80°F freezer. Blood tubes with no anticoagulant (red-top) were centrifuged to separate the serum layer, which was collected and stored to test for *Mycoplasma* and *Salmonella* exposure (see below). Anticoagulant-treated (purple-top) tubes were also centrifuged to enable the collection of the buffy coat layer (concentrated white blood cells), the preferred sample type for LPDV detection (Alger et al. 2015). If the buffy coat layer could not be obtained due to low blood collection volume, we used whole blood, which has also been found to be reliable for LPDV diagnostics (Alger et al. 2015). When we were unable to draw blood from the brachial vein or when birds were trapped specifically for banding only, we alternatively pricked the foot vein with a needle and used a heparin-treated capillary tube to collect whole blood, which was immediately transferred to a vial containing queen's lysis buffer for long-term storage. We stored cloacal swabs at -80°F until processing. Additionally, we collected the leg bone from one turkey postmortem (to extract bone marrow, the preferred sample type for LPDV diagnostics postmortem; Thomas et al. 2015), which was stored at -20°F until processing.

Furthermore, we collected leg bones and cloacal swabs from hunter-harvested turkeys during the hunting season (April–May 2017 and 2018) for pathogen diagnostics. Samples were stored as described above.

GPS Transmitter Programming and Monitoring

GPS transmitters were programmed to take locations every hour during daylight from November through July, along with a single overnight location to document roosting sites. To extend the battery life of the transmitters to collect data over two nesting seasons per bird, the number of daytime points collected were reduced from August through October to only a morning (9am), afternoon (3pm), and roost location. This model of GPS transmitter requires downloading data remotely from the transmitter using a Pin Point Commander unit and ultra-high frequency (UHF) connection. We located birds approximately once weekly to download waypoint files from the transmitters as needed to preserve battery life. We uploaded waypoint files to Movebank.org (Wikelski and Kays 2018) to ensure a backup and to easily convert them for viewing and analysis.

Adult Survival Monitoring

At least once a week, we recorded a signal from each bird with a VHF or GPS transmitter using a hand-held three element directional antenna and receiver. When a VHF-marked bird was located, the Live-Dead status was recorded based on the speed of the transmitter signal. Status of GPS-marked birds was determined from downloaded locations where sequential points at the same location indicated a potential death. For two weeks following a trapping event, birds were monitored with increased frequency to more accurately detect any trapping-related mortality. If a bird was suspected dead, the transmitter was approached to determine fate and record a plausible cause of death.

Band Reporting

During the spring and fall wild turkey hunting seasons, an online website and phone line were made available for hunters to report marked birds that were harvested. All wild turkeys harvested by hunters must be reported to a registration station within 18 hours, where band information is also recorded if a hunter declines to contact us directly. For each bird harvested, we obtained identification codes from all tags that remained on the bird, the date and time of harvest, the town in which the bird was harvested, and whether the bird was seen with any other turkeys.

Nest Monitoring

We monitored tagged hens for suspected nesting behavior from April 15 to July 30. Locations of VHF-marked individuals were collected at least twice a week via short-distance triangulation. If a hen was found alive in the same location during two successive visits, she was assumed to be on a nest. After 2 weeks, we approached the hen's location and flushed her to confirm nesting and locate the nest. We then floated 3-4 eggs to determine incubation stage, estimate the initiation date of the nest (Westerskov 1950), and to predict a hatch date. We continued to monitor the nest at least once a week, with a goal of 3 visits per week when possible. We increased visits around suspected hatch date to better determine actual hatch date. Once a hen was suspected to have left the nest, we approached the nest to assess its fate, hatched or failed. If a nest failed, we assessed whether it was abandoned, depredated, or if the hen was killed by a predator.

Location data from GPS-marked hens was downloaded weekly and point locations were reviewed in Google Earth. If we observed that a hen was making repeated visits to a single location around the same time of day, or had settled in a location she had previously visited

regularly, we assumed she was nesting. Once the hen began regular movements or discontinued regular daily visits in the case of failure during the laying phase, we visited the suspected nest site to verify the nest and its fate. We did not disturb GPS hens while on nests so that we could assess the effect of nest monitoring, which was based on comparison between nests of VHF-marked hens (flushed, regularly visited) and GPS-marked hens (never disturbed while nesting).

Land Cover Types

We estimated the percentage of land cover type used at the flock level. We applied a dynamic Brownian Bridge Movement Model to GPS data collected from a single bird in each flock between January 1 and March 15 to determine winter home range size. Then, we created a buffer around each flock home range with an area 1.25x larger than the mean home range size of all sampled individuals to account for variation in movement of individuals. We overlaid these data with land cover data from the National Land Cover Database to estimate the percent of agriculture, developed, and forested land cover within each buffer.

Molecular Detection of LPDV and REV

We extracted DNA from cloacal swabs, bone marrow, and blood using the Qiagen DNeasy Blood and Tissue Kit (Qiagen, Valencia, CA). Cloacal swabs were allowed to thaw prior to using the TissueLyser LT (Qiagen, Valencia, CA) to dislodge material for DNA extraction. A negative control was included in each extraction batch. We measured the DNA concentration of each extraction using a Nanodrop Spectrophotometer or Qubit Fluorometric Quantitation (Thermo Fisher Scientific, Waltham, MA).

For detection of LPDV, a 413 base pair region of the retroviral *gag* gene was amplified through PCR using the following primer sequences: LPDV-F 5'-ATGAGGACTTGTTAGATTGGTTAC-3', and LPDV-R 5-TGATGGCGTCAG GGCTATTTG-3 (Allison et al. 2014). PCR reactions were a total volume of 25uL, using the following reagent concentrations: 0.558 ng to 1,268 ng DNA extract (from blood, bone marrow, or cloacal swabs), 0.2 μM primers (Integrated DNA Technologies, Coralville, IA), 1.5 mM $MgCl_2$ (7.5mM; Promega, Madison, WI), 0.2mM dNTPS (New England Biolabs, Ipswich, MA), and 0.625 units of GoTaq¨ Flexi DNA Polymerase and buffer (Promega, Madison, WI). The PCR cycling conditions involved an initial denaturation at 95^0C for 3 minutes, followed by 34 cycles of 95^0C for 30 seconds, 54^0C for 30 seconds, and 68^0C for 1 minute, and ended with a final elongation step for 5 minutes at 68^0C. For cloacal swab samples, we used a multi-tube approach with three total PCR replicates per sample, and increased the cycles to 40. For bone marrow, PCR cycling conditions involved an initial denaturation at 94°C for 2 minutes, followed by 44 cycles of 94°C for 45 seconds, 50°C for 1 minute, and 72°C for 1 minute, and ended with a final elongation step for 2 minutes at 72°C.

For detection of REV, a 580 base pair region of the retroviral *pol* gene was amplified through PCR using the following primer sequences: REV-F 5'-TGCCACCCGAGACTTACTCA-3', and REV-R 5- CTGCCCGAAGGTAAGTTTAGAG-3 (Bohls et al. 2006). The PCR protocol for REV was performed using the following previously described methods by Bohls et al. (2006): PCR reactions were a total volume of 50uL, using the following reagent concentrations: 0.558 ng to 231 ng DNA extract (from blood), 0.2 μM primers (Integrated DNA Technologies, Coralville, IA), 1.2 mM $MgCl_2$ (7.5mM; Promega, Madison, WI), 0.2mM dNTPS Promega, Madison, WI), and 1.25 units of GoTaq¨ Flexi DNA Polymerase

and buffer (Promega, Madison, WI). The PCR cycling protocol involved an initial denaturation step at 95℃ for 5 minutes, followed by 40 cycles at 95℃ for 30 seconds, 55℃ for 30 seconds and 72℃ for 2 minutes, and a final incubation step at 72℃ for 7 minutes before storing at 4℃.

We confirmed amplification of the proviral DNA target region for both LPDV and REV by electrophoresis, using a 1% agarose gel, and visualized with an Azure c150 Imaging System (Azure Biosystems, Dublin, CA). Both extraction and PCR negative controls were used. In addition, a positive PCR control was included from either a previously identified LPDV- or REV-positive wild turkey in Maine, courtesy of Dr. Pete Milligan (University of Maine-Augusta). Exonuclese 1 and Shrimp Alkaline Phosphatase (ExoSAP-IT; Applied Biosystems, Foster, CA) were used to clean-up PCR products prior to sequencing. All positive PCR products were sent to the UMaine Sequencing Facility for genetic sequencing in both forward and reverse directions using the same primers listed above. During future analyses we will use the LPDV sequence data for genetic characterization of the virus and to examine LPDV transmission dynamics and strain diversity.

Serum Diagnostics for Detection of Mycoplasma and Salmonella Exposure

We performed a plate agglutination test to detect the presence of host *Mycoplasma* and *Salmonella* antibodies. The plate agglutination protocol involved combining 20µl turkey blood serum with one drop of either *Mycoplasma* antigen (A5969 strain, Charles River Laboratories, Wilmington, MA) or *Salmonella* antigen (Charles River Laboratories, Wilmington, MA) on a glass plate, and mixing to homogenize. A positive (Charles River Laboratories, Wilmington, MA) and negative (saline) control were included each processing batch. Pathogen exposure was determined by coagulation in less than two minutes upon continuous gentle mixing. A positive serum test indicates previous exposure to the pathogen, not an active infection.

Analytical Methods

Population Estimation

To estimate population size of adult and juvenile male wild turkeys prior to the spring hunting season, we created an integrated population model (IPM) that combines band recovery, harvest reporting, and telemetry data. WMD-specific estimates of harvest rates (*h)* were produced using a band recovery model that most closely resembles a Brownie parameterization (Brownie et al. 1985). To control for mortalities that occurred between banding and the hunting season, we linked survival in the band recovery model to a weekly survival rate estimated using a daily nest survival framework (Dinsmore et al. 2002; described further in concept below). Within this component of the model, we estimated annual survival rates (*S*) for juvenile and adult male wild turkey by exponentiating weekly survival rate (*s*) by the number of weeks in a year (*m = 52*) such that $S = s^m$. We incorporated a Spatial Predictive Process (Viana et al. 2013) into the band recovery model to control for spatial variation in *h* between capture sites and to allow for estimation of *h* in WMDs where we did not band turkeys. Final estimates of population size were calculated using a Lincoln estimator (Lincoln 1930, Alisauskas et al. 2013), where WMD-specific estimates of *h* were divided by the total number of harvests within each WMD reported to MDIFW during each spring bearded turkey hunting season ($N = \frac{H}{h}$). We used a Bayesian approach in which we estimated posterior distributions of parameters of interest using Markov chain Monte Carlo methods. We used JAGS (Plummer 2003) in the R programming environment (R Core Team 2020) to fit models of harvest rate and abundance of wild turkeys. We ran the model for 40,000 iterations, discarding the first 20,000 to allow for convergence. We assessed convergence within the model by reviewing scale reduction factors ($\hat{R}$) for each parameter as described by Gelmin and Rubin (1992). We produced estimates of abundance (*N*), by WMD, for

2019, but did not derive estimates for 2020 at the time of this report because of changes in harvest reporting procedures associated with the COVID-19 pandemic. Variable size of WMDs may make comparison of turkey populations between WMDs difficult. To control for variable WMD size, we also produced estimates of density calculated as abundance divided by total area within a WMD.

Weekly Survival Rate

We compiled weekly live/dead status for each VHF- and GPS-marked wild turkey to create an encounter history which indicated the week the turkey was captured (First Found), the last week it was found alive (Last Alive), the last week it was checked (Last Checked), and its final status at the end of the monitoring period for this report (Fate). Turkeys that died within 14 days post capture were censored from this analysis. Following the two-week post-capture period, any deaths were attributed to normal causes and assumed to not be capture-related. When a radio-marked turkey was reported harvested, we set "Last Alive" to the week previous to harvest and left the subsequent entries as no data. We modeled weekly survival probability for females using the nest survival model in the RMark package (Laake 2013) in program R (R Core Team 2020). We chose this approach because it allowed for irregular monitoring of individuals, which best fit our study design where we were not always able to locate turkeys following extended or irregular movements. We compared univariate weekly survival probability models based on age and sex of the turkey, month, year, study area, WMD, MDIFW management region, transmitter type (backpack or necklace), and pathogen infection status (LPDV, *Mycoplasma*, and REV).

Post-release Mortality

Wild turkeys are often found to experience elevated mortality following capture and release (Nicholson et al 2000). To assess the potential for mortalities related to capture and

handling in the 30 days post capture, we modeled daily survival rate (DSR) with a log-log link function using the RMark package (Laake 2013) in program R (R Core Team 2020). All models included a covariate based on the natural log of the number of days since the capture event, which allows the model to reflect an increase in daily survival probability out to a potential threshold, presumably reflecting the point at which capture-related mortality no longer persists (Blomberg et al. 2018). One additional covariate related to the trapping event or the individual turkeys was added for each model as an interaction with the ln (days post-capture) term, which allowed us to test whether these factors contributed to post-release mortality. These covariates included age and sex of the turkey, transmitter harness type (backpack vs necklace mounted), study area, trapping location, date of capture, pathogen infection status (LPDV, REV, *Mycoplasma*), whether a hematoma occurred during blood collection, and handling time. Mean temperature and daily precipitation covariates related to the trapping event and the following week were compiled using the prism package in program R (Edmund et al 2018). To further define a cut off for trapping mortality, we compared a series of models in which a threshold point was set that allowed daily survival to differ between days before and after the threshold but did not differ within the respective intervals (Blomberg et al 2018). This allowed us to observe shifts in daily survival, define a threshold date for post-release mortality, and evaluate an appropriate censoring period for other survival analyses.

Daily Nest Survival Rate

We modeled nest daily survival rate (DSR) using the RMark package (Laake 2013) in program R (R Core Team 2020). To produce a probability of nest success, we exponentiated the DSR by the average nest exposure period (average length of laying and incubation periods observed during this study; 38 days). We compared models of nest survival to identify important

predictors of nest success. Models were based on day of the year, age of the nest in days, nest initiation year, age of the turkey, study area, transmitter type (VHF vs GPS), and pathogen infection status (LPDV, REV, *Mycoplasma*). We compared model sets individually for DSR and parameter coefficients using the same criteria described for our survival analysis above.

Nesting Behavior and Hunter Effort

We compared the timing of nesting activity (nest initiation and onset of incubation) relative to both the timing of the spring hunting season and variation in relative hunter effort throughout the season. For the latter, we quantified the number of male turkeys harvested on each day of the season based on harvest reporting data during the 2018 and 2019 spring bearded turkey hunting seasons. We assumed that the distribution of harvest timing was correlated with relative hunter effort (e.g. number of persons hunting) throughout the season, and provided a reasonable proxy for potential disturbance of nesting females, removal of their potential mates, and likelihood of illegal killing of females. We used nest initiation (defined as the date a female laid her first egg for a given nesting attempt), onset of incubation, and termination dates recorded for VHF- and GPS-marked females as previously described. We then reconstructed the frequency distribution of the proportion of females actively incubating nests on each day of the nesting season. We compared the distribution of nest initiation dates and female incubation with hunting season timing and harvest distributions for each study year using a series of visual plots. We included both first attempts and re-nesting attempts in our descriptive assessment of nesting activity.

We used linear regression to identify sources of variation in nest initiation date related to spatial covariates and individual female characteristics. For our regression analysis, we only used initiation dates from first nesting attempt within a year because the timing of initiation for

replacement nests is inherently confounded with date of failure of the earlier attempt. We hypothesized that initiation date would differ according to land cover class, longitude, latitude, age, pathogen infection status (*Mycoplasma*, REV, and LPDV), body condition, year, the distance between the capture site and the nesting location and elevation. To delineate the pre-nesting period, we examined turkey movement patterns from capture through the first nest attempt, and identified the period of predictable decrease in distance moved between GPS fixes following spring seasonal movements between winter and nesting home ranges, but before hens were known to initiate egg-laying.

We considered that variation in nest initiation among years may alter the rate at which the nesting season progresses, which may not be fully captured by simple summary metrics such as the mean or median nest initiation date. For example, if the onset of nesting is delayed due to prolonged winter conditions (Vangilder et al. 1987), more females may initiate nests relatively early in the nesting season, producing a shift in the overall distribution of nest initiation dates among years. To explore this possibility, we used a chi-square contingency analysis to test the null hypothesis that there was no difference in the distribution of nest initiation dates between year 1 and year 2. Within each year, we standardized nest initiation dates so the first nest was the first day of the nesting season, and then grouped nest initiations into 1 week (i.e. 7 day) periods. Expected values for the chi-square were based on the proportion of total nests initiated during each 1-week interval in year 1, where rejection of the null hypothesis would reflect a difference in the distribution of nest initiation timing after accounting for the difference in the onset of the nesting season in year 2. Because of lower number of nest initiations in later weeks, we grouped the final two weeks within each year to avoid issues with expected values of 0 for a given week.

Clutch Size

We used linear regression to identify sources of variation in clutch size between nests. Covariates of interest included date of initiation, turkey age, year, study area, disease status, and whether the nest was a first nest or renest.

Seasonal Home Range and Movements

We fit dynamic Brownian Bridge Movement Models (dBBMM) to the movement track of each GPS-marked hen using the move package (Kranstauber and Smolla 2013) in program R (R Core Team 2020). We *a priori* described expected categories of seasonal movement behavior, which included winter, winter to pre-nesting movement, pre-nesting, and summer. Brownian motion variance (σ_m^2) is a measure of how irregular the path of an animal is between successive locations (Byrne et al 2014) by accounting for changes in movement distance and direction. We delineated seasonal changes in movement behavior by quantifying changes in daily σ_m^2 over time (Kranstauber et al 2012), averaged across all marked hens. Based on patterns of individual changes in σ_m^2, we subset movement tracks into seasonal categories of movement and created individual utilization distributions (UDs) for each category of movement for each hen. If a hen did not survive from capture to August 1, it was censored from estimation of average total home range size. 95% UD were estimated for each bird's seasonal home range. Seasonal movements between winter and nesting home ranges were quantified as the distance between the centroids of the winter range and the nesting range. We separately compared regressions of winter home range size, prenesting home range size, and distance traveled between winter and prenesting ranges. Covariates compared included study area, turkey age, and disease status.

Pathogen Coinfection

All pathogen data were analyzed in RStudio (Version 1.3.1093) using Program R (R Core Team 2019; version 3.6.2). We evaluated whether infection with LPDV, REV, or *Mycoplasma*

was independent of additional pathogen infection using a Pearson's chi-squared test with Yates' continuity correction on contingency tables. For this analysis, $p>0.05$ indicates independence of the variables, while $p<0.05$ signifies a correlation between variables. If two pathogens were correlated, we ran a generalized linear model with a binomial distribution to determine if there was a negative or positive relationship.

Risk Factors for Pathogen Infection

We used generalized linear models assuming a binomial distribution with a logit link function to test the effect of the predictor variables (age, sex, year of collection, WMD of collection, region of collection, land cover type usage, density and, when applicable, LPDV infection status and REV infection status) on the probability of pathogen (LPDV, REV, or *Mycoplasma*) infection. Akaike Information Criteria (AIC) model selection was used to determine the top model by including all variables that performed better than the null. We then assessed the summary statistics on those models to determine which variables were significant ($p<0.05$) and which were not significant (but their inclusion in the final model was still supported because they performed better than the null model). We considered WMD and region of collection as accounting for the same source of spatial variation, and, thus, if both were initially included in the final model, we used AIC to determine which one was a better model fit by comparing the version of the final model with WMD to the version of the final model with region. Additionally, we tested for correlation between numeric variables in the final model using Pearson's product-moment correlation and removed any with a test statistic greater than 0.70. We also tested for multicollinearity among all variables using the R package regclass (Petrie 2020) and removed any variable with a variance inflation factor greater than 4, indicating strong correlation. Lastly, we used a likelihood ratio test to assess the model fit of our final

model (R package lmtest: Zeileis and Hothorn 2002). Odds ratios were estimated using the R package questionr (Barnier et al. 2018) for GLM output. We obtained contrasts between each level of multilevel variables included in the final model using the R package emmeans (Lenth 2020) and calculated odds ratios by exponentiating the coefficients and confidence intervals. For instance, if we found in the GLM output that the interaction of age and agriculture was significant, we then used the R package emmeans to quantify this difference in the effect of agriculture on LPDV infection in adults and also in juveniles. We estimated prevalence and 95% confidence intervals using the Wilson method within binom R package (Dorai-Raj 2014).

Cloacal Swabs as an LPDV Detection Method

We assessed the diagnostic sensitivity and specificity of cloacal swab samples for LPDV detection, compared with paired blood or bone marrow samples, which are considered to be the standard sample types for LPDV detection antemortem and postmortem, respectively. Cloacal swab samples were considered to be LPDV-positive if at least one of the three PCR replicates was positive, and considered to be negative if all three replicates were negative. The LPDV PCR results from blood or bone marrow (i.e., hereafter standard sample types) were considered to be the measure of true infection status. Therefore, a swab sample PCR was considered a true positive or negative result if it matched that of the paired standard sample type. Likewise, a false result occurred when the PCR outcomes using the paired swab and standard sample types did not match. We quantified both the sensitivity (proportion of true positives) and specificity (proportion of true negatives) of using cloacal swabs as a sampling method for LPDV detection in both live-captured and hunter-harvested birds. Furthermore, we calculated true prevalence (calculated using the standard sample type) and apparent prevalence (calculated using cloacal swab samples) for each collection method.

We used the R package epiR (Stevenson et al. 2019) to estimate Cohen's Kappa (Kappa; Cohen 1960, McHugh 2012), which identifies the level of agreement beyond chance between two sets of binary variables on a spectrum of 0–1, with 0 indicating agreement is equivalent to chance, and 1 indicating perfect agreement (beyond chance alone; Cohen 1960, McHugh 2012). We employed a Z-test on this Kappa statistic to determine the level of significance of the test statistic. We also used a Z-test to identify if there was a difference in sensitivity and specificity of cloacal swabs compared with the paired standard sample type between the two different collection methods (hunter-harvested and live-captured; i.e., did the sensitivity of cloacal swabs in detecting LPDV differ between hunter-harvested and live-captured individuals). We used a McNemar test to identify if there was a difference between the prevalence calculated from the cloacal swab sample (apparent prevalence) and the prevalence calculated from the standard sample types (true prevalence). We also used a generalized linear model with a logit link function with time (mins) between harvest and sample collection as the independent variable and the ability to detect a positive as the dependent variable to assess if a time delay between harvesting and sampling might decrease the ability to detect a positive.

Results

Capture and Sampling

Over the course of the three years of data collection, we captured and banded 890 unique wild turkeys across the state. During Year 1, we captured and banded 124 unique wild turkeys between our four primary study areas. During Year 2, we captured and banded 395 unique wild turkeys, 140 of which were in our primary study areas. During Year 3, we captured and banded

371 unique wild turkeys, 98 of which were in our primary study areas. We captured 187 adult males, 219 juvenile males, 324 adult females, and 160 juvenile females. Of turkeys caught outside of the primary study areas, 38 were captured in WMD 12, 105 were captured in WMD 17, 146 were captured in WMD 18, 167 were captured in WMD 23, 152 were captured in WMD 26, 24 were captured in WMD 6, 20 were captured in WMD 27, and 59 was captured in WMD 28 (Table 1). Of turkeys caught in the primary study areas during the entire duration of the study, 108 turkeys were captured at NW, 122 were captured at NC, 58 were captured at NE, and 76 were captured at S. We fitted 121 females with VHF backpack transmitters (96 on adults and 25on juveniles), 30 females with VHF necklace transmitters (18 on adults and 12 on juveniles), and 59 females with GPS transmitters (41 on adults and 18 on juveniles). We fitted 57 males with VHF necklace transmitters, 32 on adults and 25 on juveniles (Table 2). We also fitted 2 adult males with used GPS transmitters which operated from March 14, 2019 to May 3, 2019 and from January 31, 2020 to April 28, 2020, (Figure 2).

We collected blood samples (370 whole blood, 256 buffy coat, and 235 serum) from 626 unique live-captured turkeys and bone marrow from a single turkey postmortem two weeks after capture (89 from 2018, 280 from 2019, 258 from 2020; 243 adult female, 131 adult male, 108 juvenile female, and 145 juvenile males). The 627 birds sampled for pathogen diagnostic purposes spanned 41 towns within 11 WMDs. Finally, we collected cloacal swabs from 85 live-Table 1.

Table 1. Unique wild turkey captures, by year, sex, and age in Maine, USA during January through March f 2018 through 2020. Birds were captured in the areas of Exeter/Corinth (NW), Orono/Bangor (NC), Stud Mill Rd./Greenfield (NE), Gorham/Gray (S), and WMDs 6, 12, 17, 18, 23, 26, 27, and 28.

	2018				2019				2020				
	Female		Male		Female		Male		Female		Male		
	Adult	Juv	Adult	Juv	Adult	Juv	Adult	Juv	Adult	Juv	Adult	Juv	**Total**
NC	-	-	-	4	34	17	8	12	21	3	12	11	**122**
NE	12	-	7	1	11	5	-	-	15	1	5	1	**58**
NW	34	20	18	-	9	8	5	4	-	3	-	7	**108**
S	17	2	1	8	8	5	4	12	2	-	12	5	**76**
WMD 6	-	-	-	-	6	2	8	8	-	-	-	-	**24**
WMD 12	-	-	-	-	5	5	8	15	-	-	3	2	**38**
WMD 13	-	-	-	-	-	-	-	-	23	3	1	5	**32**
WMD 14	-	-	-	-	-	-	-	-	19	17	17	18	**71**
WMD 18	-	-	-	-	13	3	9	7	17	10	5	4	**68**
WMD 23	-	-	-	-	24	10	34	46	9	9	18	17	**167**
WMD 26	-	-	-	-	12	8	5	4	5	1	6	6	**47**
WMD 27	-	-	-	-	5	9	-	6	-	-	-	-	**20**
WMD 28	-	-	-	-	-	-	1	-	23	19	-	16	**59**
Total	**63**	**22**	**26**	**13**	**127**	**72**	**82**	**114**	**134**	**66**	**79**	**92**	**890**

captured turkeys (that also had paired blood samples) during the 2018 trapping season and 54 hunter-harvested wild turkeys (that also had paired bone marrow samples) during the 2017 and 2018 turkey hunting seasons.

Harvest Reporting

Five of 39 males banded during 2018 were harvested and reported during the 2018 spring turkey hunting season, while 2 of the 85 females we banded during 2018 were reported during the 2018 fall either sex hunting season. In this later case, one radio-marked hen was shot, recovered, and reported, while a banded-only female was shot and not initially recovered but was found later and reported. Forty one banded males were harvested during the 2019 spring turkey hunting season, 4 of which were banded in Year1 and 37 that were banded in Year2. Five of the 41 were radio-marked in Year 2. Two banded hens and 4 banded males were harvested during the 2019 fall either sex hunting season. One of those banded males was radio-marked. Fifty-four banded males were harvested during the 2020 spring turkey hunting season, 5 of which were banded in Year-1, 21 in Year-2, and 28 in Year-3. Three of the 54 were radio-marked in Year-2 and 5 in Year-3. Six banded hens and 7 banded males were harvested during the 2020 fall either sex hunting season. Two of those banded males were radio-marked and one hen was GPS-marked.

For the three options available for reporting the harvest of a banded turkey, 13 (10.8%) were reported only to the check station, 31 (25.8%) were reported only to the website, 33 (27.5%) were reported only by phone, and 39 (32.5%) were reported to more than one of the three options. Four banded turkey harvests were reported outside of these three options (Table 3).

Integrate Population Model Estimates

Due to a lower sample size of banded individuals in 2018, we only present estimates for *h* for 2019 and 2020. In 2019, we found that adult male turkeys had a greater harvest rate (*h*= 0.261; 0.168–0.371 95% CI) during the spring hunting season than juvenile male turkeys (*h*= 0.107; 0.058–0.169 95% CI). Similarly, in 2020, adult male turkeys had a greater harvest (*h*= 0.244; 0.165–0.345 95% CI) during the spring hunting season compared to juvenile male turkeys *(h*= 0.099; 0.052–0.164 95% CI). We produced WMD-specific estimates of *h* by incorporating a SPP into our model that accounted for spatial variation across the state (Figure 3, Table 4). In 2019, we observed estimated harvest for adult males ranged from *h*=0.250 (*h*= 0.151–0.365 95% CI; WMD 10) at its lowest to *h*=0.277 (0.167–0.425 95% CI; WMD 13) at its greatest. For juvenile males, we observed estimates of harvest ranging from *h*=0.102 (0.051–0.166 95% CI; WMD 10) at its lowest to *h*=0.116 (0.058–0.201 95% CI; WMD 13) at its greatest. In 2020, we observed estimated harvest for adult males ranging from *h*= 0.233 (0.149–0.342 95% CI; WMD 10) at its lowest to *h*= 0.259 (0.164–0.388 95% CI; WMD 13) at its greatest. For juvenile males, we observed estimated harvest ranging from *h*= 0.095 (0.047–0.161 95% CI; WMD 10) at its lowest to *h*= 0.108 (0.053–0.188 95% CI; WMD 113) at its greatest.

Table 2. Summary of transmitter deployments in Maine, USA during January through March of 2018 through 2020. Transmitters were deployed in the areas of Exeter/Corinth (NW), Orono/Bangor (NC), Stud Mill Rd./Greenfield (NE), and Gorham/Gray (S).

	Female		Male		
	Adult	Juv	Adult	Juv	**Total**
GPS Backpack	41	18	2	-	**61**
VHF Backpack	96	25	-	-	**121**
VHF Necklace	18	12	32	25	**87**
Band Only	169	105	153	194	**621**
Total	**324**	**160**	**187**	**219**	**890**

Table 3. Summary of methods for reporting of harvested banded turkeys during Maine's spring or fall wild turkey hunting seasons in 2018 through 2020.

Check Station	Online	Phone	Total	%
Y	-	-	13	0.108
-	Y	-	31	0.258
-	-	Y	33	0.275
Y	Y	-	8	0.067
Y	-	Y	14	0.117
-	Y	Y	12	0.100
Y	Y	Y	5	0.042
-	-	-	4	0.033

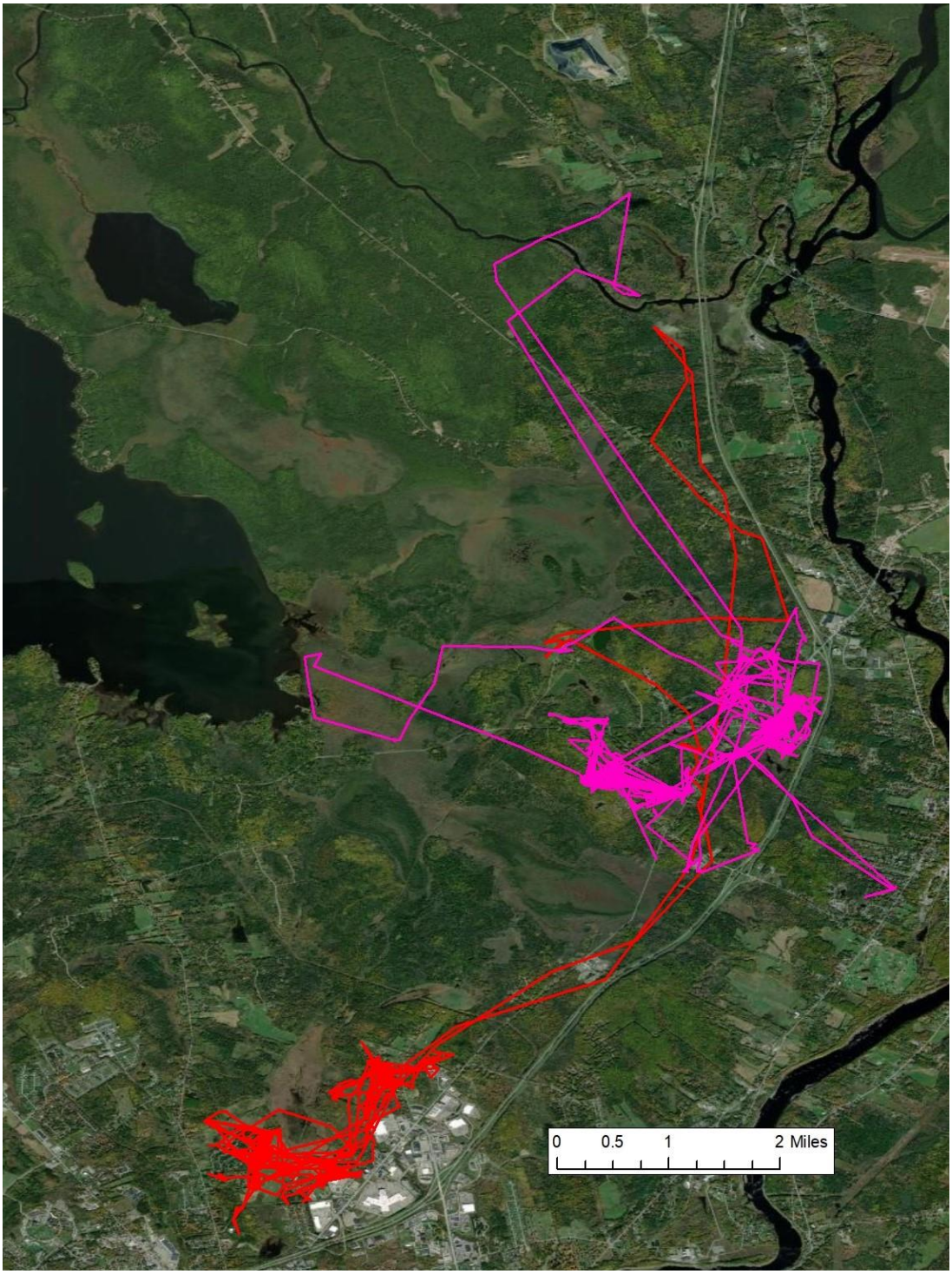


Figure 2. Aerial photograph of Bangor, Maine, USA, with GPS tracks of the two adult male wild turkeys fit with GPS transmitters which operated from between March 14, 2019 through May 3, 2019 (red) and from January 31, 2020 through April 28, 2020 (pink).

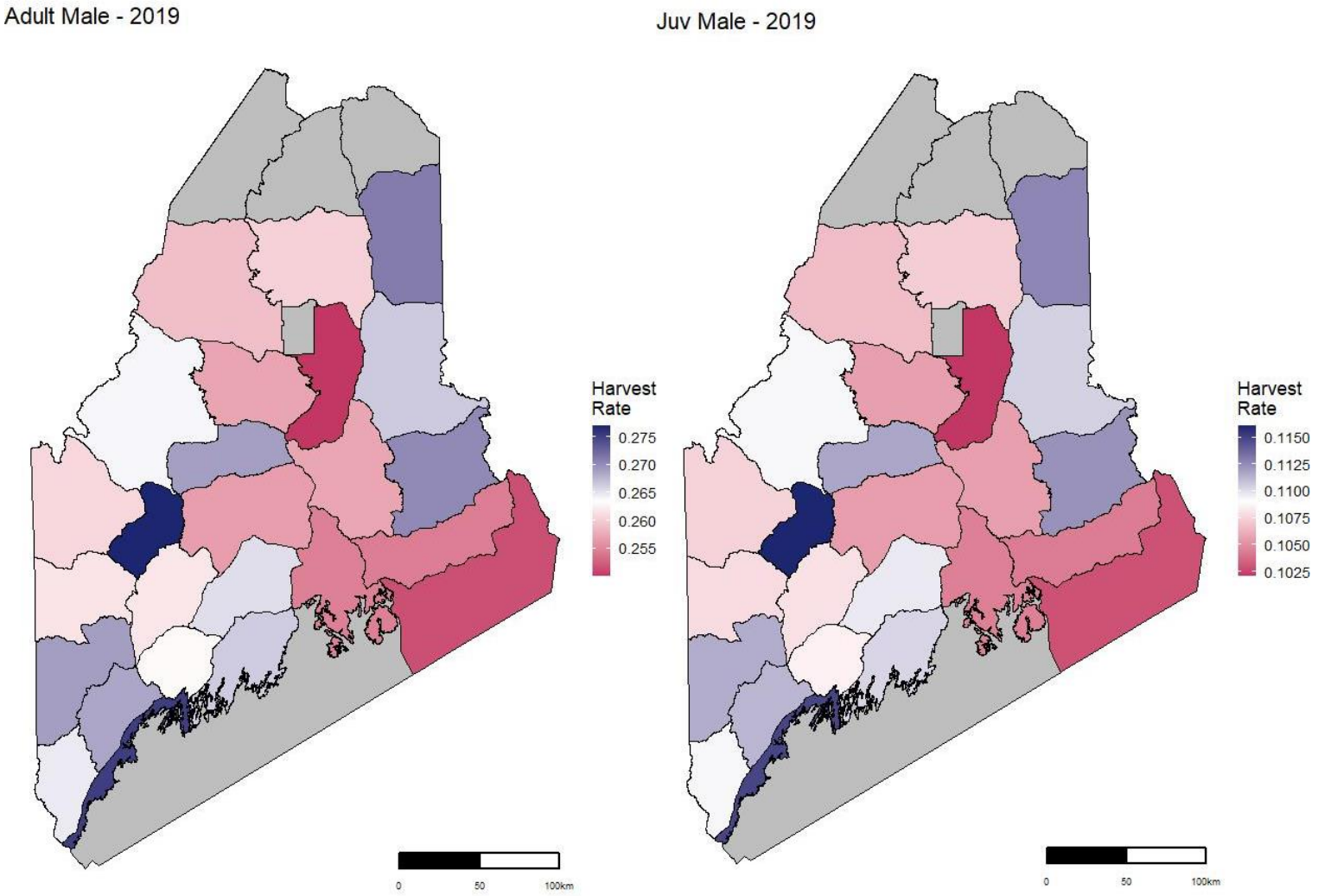


Figure 3. Map of Maine, USA, showing outlines of Maine Department of Inland Fisheries and Wildlife management districts. Where estimates were possible, polygon color depict harvest rate estimates for adult (left) and juvenile (right) male turkeys during the 2019 spring hunting season.

Table 4. WMD specific estimates of male wild turkey harvest rates for the 2019 and 2020 spring bearded turkey hunting season.

	Adult						Juvenile					
	2019			2020			2019			2020		
WMD	Estimate	LCL	UCL	Estimate	LCL	UCL	Estimate	LCL	UCL	Estimate	LCL	UCL
4	0.259	0.159	0.382	0.242	0.157	0.357	0.107	0.056	0.175	0.099	0.049	0.167
5	0.260	0.163	0.386	0.243	0.159	0.356	0.107	0.055	0.177	0.099	0.050	0.167
6	0.271	0.165	0.405	0.254	0.159	0.380	0.113	0.058	0.190	0.105	0.051	0.180
7	0.261	0.163	0.378	0.244	0.160	0.349	0.107	0.056	0.174	0.100	0.051	0.167
8	0.264	0.161	0.394	0.247	0.160	0.359	0.109	0.056	0.181	0.101	0.051	0.172
9	0.257	0.161	0.371	0.240	0.160	0.341	0.106	0.055	0.170	0.098	0.051	0.164
10	0.250	0.151	0.365	0.233	0.149	0.342	0.102	0.051	0.166	0.095	0.047	0.161
11	0.267	0.169	0.382	0.249	0.166	0.355	0.110	0.059	0.177	0.102	0.053	0.170
12	0.262	0.166	0.380	0.245	0.161	0.352	0.108	0.057	0.175	0.100	0.052	0.167
13	0.277	0.167	0.425	0.259	0.164	0.388	0.116	0.058	0.201	0.108	0.053	0.188
14	0.269	0.163	0.392	0.251	0.164	0.359	0.112	0.057	0.183	0.103	0.052	0.173
15	0.269	0.170	0.388	0.252	0.165	0.365	0.111	0.059	0.180	0.104	0.053	0.173
16	0.262	0.164	0.373	0.245	0.162	0.347	0.108	0.057	0.175	0.100	0.052	0.167
17	0.257	0.163	0.369	0.240	0.155	0.351	0.106	0.055	0.172	0.098	0.049	0.167
18	0.257	0.163	0.372	0.240	0.160	0.347	0.106	0.056	0.170	0.098	0.050	0.164
19	0.270	0.167	0.409	0.253	0.162	0.375	0.112	0.058	0.190	0.104	0.052	0.176
20	0.265	0.165	0.387	0.248	0.158	0.365	0.109	0.057	0.178	0.102	0.051	0.174
21	0.269	0.169	0.388	0.251	0.165	0.363	0.111	0.059	0.179	0.103	0.053	0.173
22	0.263	0.163	0.380	0.246	0.158	0.355	0.109	0.056	0.176	0.101	0.051	0.170
23	0.265	0.171	0.378	0.248	0.164	0.358	0.110	0.058	0.176	0.102	0.052	0.173
24	0.275	0.162	0.412	0.258	0.159	0.381	0.115	0.058	0.191	0.107	0.052	0.184
25	0.266	0.170	0.383	0.249	0.164	0.356	0.110	0.058	0.179	0.102	0.052	0.171
26	0.255	0.158	0.372	0.238	0.150	0.354	0.104	0.054	0.171	0.097	0.048	0.169
27	0.251	0.159	0.367	0.235	0.155	0.341	0.103	0.055	0.168	0.095	0.049	0.160
28	0.254	0.161	0.368	0.238	0.158	0.342	0.104	0.055	0.169	0.097	0.050	0.162

We estimated the risk of non-harvest related mortality for adult and juvenile male turkeys (Table 5). We estimated a mean annual survival of 0.716 (0.341 – 0.927, 95% CI) for adult males and 0.721 (0.346 – 0.932, 95% CI) for juvenile males. Adult male survival ranged from 0.432 (0.0 – 1.0, 95% CI) in WMD 16 to 0.985 (0.807 – 0.1.0, 95% CI) in WMD 27. Juvenile male survival ranged from 0.435 (0.0 – 1.0, 95% CI) in WMD 6 to 0.986 (0.812 – 1.0, 95% CI) in WMD 27.

WMD-specific estimates of turkey abundance were generated for 2019 (Figure 4, Table 6). The greatest estimates of abundance of turkeys within a WMD were *N*=2,495 (1,663–3,737 95% CI; WMD 25) for adults and *N*=2,031 (1,146–3,599 95% CI; WMD 20) for juveniles. Density of adult male turkeys was greatest at 1.242 individuals per km^2 (0.821–1.910 95% CI) in WMD 22 and least at 0.0 per km^2 (0.0–0.0 95% CI) in WMD 4 (Figure 4). Density of juvenile male turkeys was greatest at 1.181 individuals per km^2 (0.666–2.092 95% CI) in WMD 20 and least at 0.0 per km^2 (0.0–0.0 95% CI) in WMD 9 (Figure 4).

In the 2018 spring turkey harvest, 4,733 adult males and 1,454 juvenile males were reported, which corresponds to an estimate of *N*=18,110 (12,752–28,207 95% CI) adults males and *N*=13,567 (8,579–25,140 95% CI) juvenile males, using the estimate of *h* from 2019 for both groups. During spring 2019, 5,283 adult males and 1,318 juvenile males were reported, which corresponds to an estimate of *N*=20,214 (14,234–31,485 95% CI) adults males and *N*=12,298 (7,776–22,789 95% CI) juvenile males. Due to COVID-19 related restrictions, we do not have the exact number of the reported harvest in 2020. MDIFW performed a hunter survey following the 2020 spring turkey hunting season and estimated that 6,216 (5,861–6,572 95% CI) total turkeys of either age class were harvested, but these survey-based results lack age-class specific estimates of harvest. Assuming that a similar ratio of adults to juveniles were harvested in 2020

Table 5. WMD-specific estimates of male wild turkey survival (non-harvest mortality) for adults and juveniles. Estimates are presented with lower (LCL) and upper (UCL) 95% confidence limits.

	Adult			Juvenile		
WMD	Mean	LCL	UCL	Mean	LCL	UCL
6	0.432	0.000	1.000	0.435	0.000	1.000
12	0.719	0.103	1.000	0.724	0.109	1.000
13	0.943	0.297	1.000	0.945	0.322	1.000
14	0.761	0.439	0.969	0.765	0.427	0.971
15	0.567	0.153	0.930	0.573	0.157	0.934
17	0.668	0.476	0.828	0.675	0.482	0.833
18	0.775	0.627	0.885	0.779	0.620	0.898
21	0.618	0.425	0.786	0.625	0.431	0.802
23	0.662	0.348	0.966	0.671	0.360	0.965
26	0.596	0.408	0.764	0.603	0.410	0.781
27	0.985	0.807	1.000	0.986	0.812	1.000
28	0.872	0.016	1.000	0.875	0.021	1.000

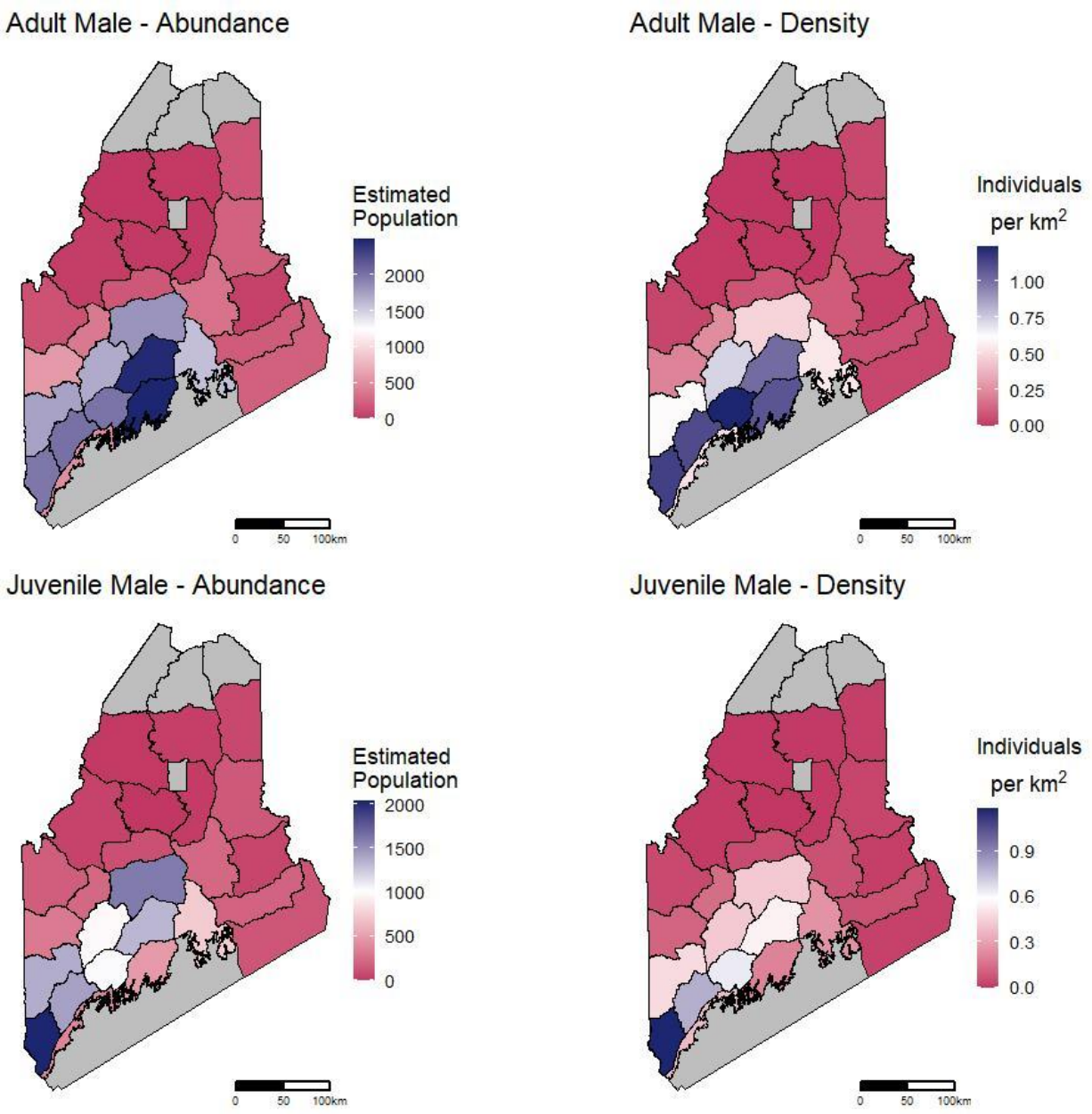


Figure 4. Map of Maine, USA, showing outlines of Maine Department of Inland Fisheries and Wildlife management districts. Where estimates were possible, polygon color depict harvest rate (left) and density (right) estimates for adult (top) and juvenile (bottom) male turkeys during the 2019 spring hunting season.

Table 6. WMD-specific estimates of male wild turkey abundance at the start of the 2019 bearded turkey hunting season.

	Adult			Juvenile		
WMD	Estimate	LCL	UCL	Estimate	LCL	UCL
4	0	0	0	10	6	18
5	12	8	18	30	17	54
6	159	101	248	68	37	121
7	141	92	215	172	98	301
8	36	23	56	50	28	89
9	16	11	25	0	0	0
10	8	5	13	21	12	39
11	235	157	355	147	85	255
12	579	382	871	312	177	544
13	378	233	593	219	115	399
14	172	112	270	108	60	192
15	1740	1155	2630	1369	781	2373
16	1694	1139	2596	983	560	1721
17	1816	1208	2742	1597	903	2812
18	333	220	502	226	129	390
19	55	34	84	58	32	103
20	1984	1295	3039	2031	1146	3599
21	2019	1337	3078	1421	815	2461
22	2002	1323	3078	1032	584	1839
23	2469	1663	3673	1329	766	2308
24	511	322	821	373	204	676
25	2495	1663	3737	481	274	839
26	1581	1032	2436	741	414	1314
27	229	150	345	137	77	238
28	197	130	299	198	112	347

as in 2018 and 2019, we estimate 4,865 (4,587–5,144 95% CI) adult males and 1,351 (1,274–1,428 95% CI) juvenile males were harvested. Using estimates of *h* from 2020, this corresponds to an estimate of *N*=19,913 (13,311–31,140 95% CI) adults males and *N*=13,587 (7,752–27,586 95% CI) juvenile males.

Weekly Adult Survival Rate

Of 270 turkeys fitted with a transmitter, 51 were censored due to death within the first two weeks after release from capture. The majority of censored turkeys appeared to be killed by predators around capture areas, however we cannot rule out death due to other causes (e.g. capture myopathy) followed by scavenging. Of those birds not censored, 106 transmitters were active as of August 1, 2020 (not been confirmed dead), when we cut off data collection for our analysis. Weekly survival rates were compared only for female wild turkeys (n = 166). For male survival, see previous section "Integrated Population Model Estimates."

Our top model of weekly survival probability was based on Month of the year (ΔAIC = 0.0; Table 7). The lowest weekly survival probability occurred during the month of May (0.948; 0.927 – 0.963, 95% CI) and the highest was in January (.996; 0.975-1.000, 95% CI). September and November had an estimated survival rate of 1.0, this was likely due to lower telemetry check frequency at the end of the field season. Weekly survival rate was variable throughout the length of the project (Figure 5). The second best supported model was based on REV infection status (ΔAIC = 15.327; Table 7). Turkeys infected with REV had a lower weekly survival probability (β = -0.685; -1.152 – -0.219, 95% CI) compared to uninfected turkeys. The weekly survival probability was 0.983 (0.979–0.987, 95% CI) for uninfected turkeys and 0.967 (0.936–0.983, 95% CI) for REV-infected turkeys. When exponentiated across one year (52 weeks), this difference in weekly survival rate translates to a cumulative probability of survival of 0.413

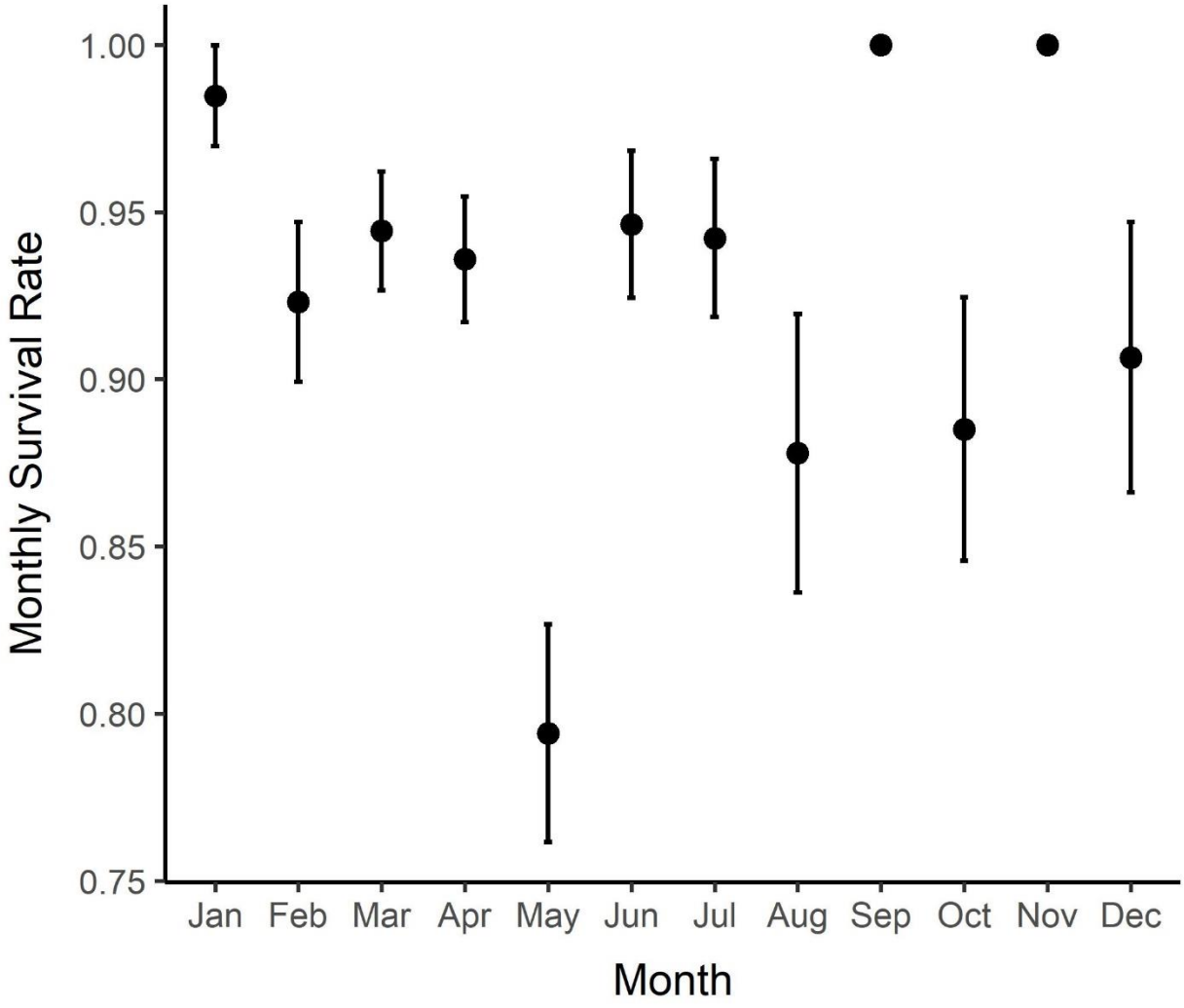


Figure 5. Weekly survival rates, by month, for wild turkeys in Maine, USA, from January 30, 2018 to August 1, 2020. Estimates were derived from the best performing weekly survival model according to AIC. Estimates are presented with error bars representing 95% confidence intervals.

Table 7. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect weekly survival probability (S) of wild turkey hens in the Exeter/Corinth, Stud Mill Rd./Greenfield, and Gorham/Gray study areas in Maine, USA. We modeled S as a function of Region of capture, WMD of capture, transmitter type, age, sex, study area, disease infection status (LPDV, MD, REV), and Month of the year using a daily survival rate approach (Laake 2013). All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
~Month	899.032	0.000	0.999	12	874.972
~REV	914.359	15.327	0.000	2	910.357
~IFWReg	918.644	19.612	0.000	4	910.636
~LPDV	919.149	20.117	0.000	2	915.147
~1	919.725	20.693	0.000	1	917.724
~WMD	921.109	22.077	0.000	7	907.087
~Adult	921.235	22.203	0.000	2	917.232
~*Mycoplasma*	921.512	22.480	0.000	2	917.510
~Trans.Type	921.711	22.679	0.000	2	917.709
~Year	923.537	24.505	0.000	3	917.532
~Study.Area	965.705	66.673	0.000	7	951.683

[a]LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; *Mycoplasma*: Infected, Uninfected, Unkown; Month: January-December; Adult: 1, 0; Study.Area: NC, NW, S, NE, WMD; IFWReg: A, B, F; Sex: Male, Female; WMD: 17, 18, 21, 23, 26; Trans.Type: Back, Neck; Year: 2018, 2019, 2020

[b]Difference in AIC compared with the lowest AIC model score

[c]AIC model weight

[d]Number of model parameters

[e]Model Deviance

(0.330–0.495 95% CI) for uninfected turkeys compared to 0.176 (0.033–0.417 95% CI) for infected turkeys. Although neither model performed as well as the above models, models based on the MDIFW region where turkeys were captured and LPDV-infection status performed better than the null model (Table 7). Of the four Regions turkeys were captured in, survival was highest in Region E (0.986; 0.948–0.997 95% CI) and lowest in Region B 0.975 (0.967–0.981 95% CI), although there was overlap with survival estimates in Region A and F. The weekly survival probability of LPDV-infected turkeys was 0.979 (0.952–0.991, 95% CI) and 0.985 (0.978–0.990, 95% CI) for uninfected turkeys. We did not find strong support for differences in weekly survival rates between year of the study, *Mycoplasma* infection status, WMD or study area of capture, age classes, sex, or transmitter type (Table 7).

Post-release Mortality

Our initial model comparisons showed that a relationship between survival and the natural log of days post capture best described the overall trend in daily survival rates. To compare covariates of interest, each model included a covariate for natural log of days post capture ("LN") and an interaction term. Our best performing model from this comparison was based on the total amount of time the bird was held from the trap being triggered to the bird's final release ("HandTime"; ΔAIC = 0.0; Table 8). As handling time increased, there was an observed increase in survival rate in the days following capture (Figure 7). A bird held for the average amount of time for this study (109 minutes) had an initial daily survival rate of 0.980 (0.958–0.990 95% CI). The second ranked model was based on transmitter type (ΔAIC = 5.415; Table 8), where we compared survival of birds fit with backpack- or necklace-style transmitters. Our model showed that birds with backpack transmitters had a survival rate of 0.962 (0.929–0.979 95% CI) on the day post capture compared to a survival rate of 0.997 (0.963–1.000 95% CI) for birds with necklace

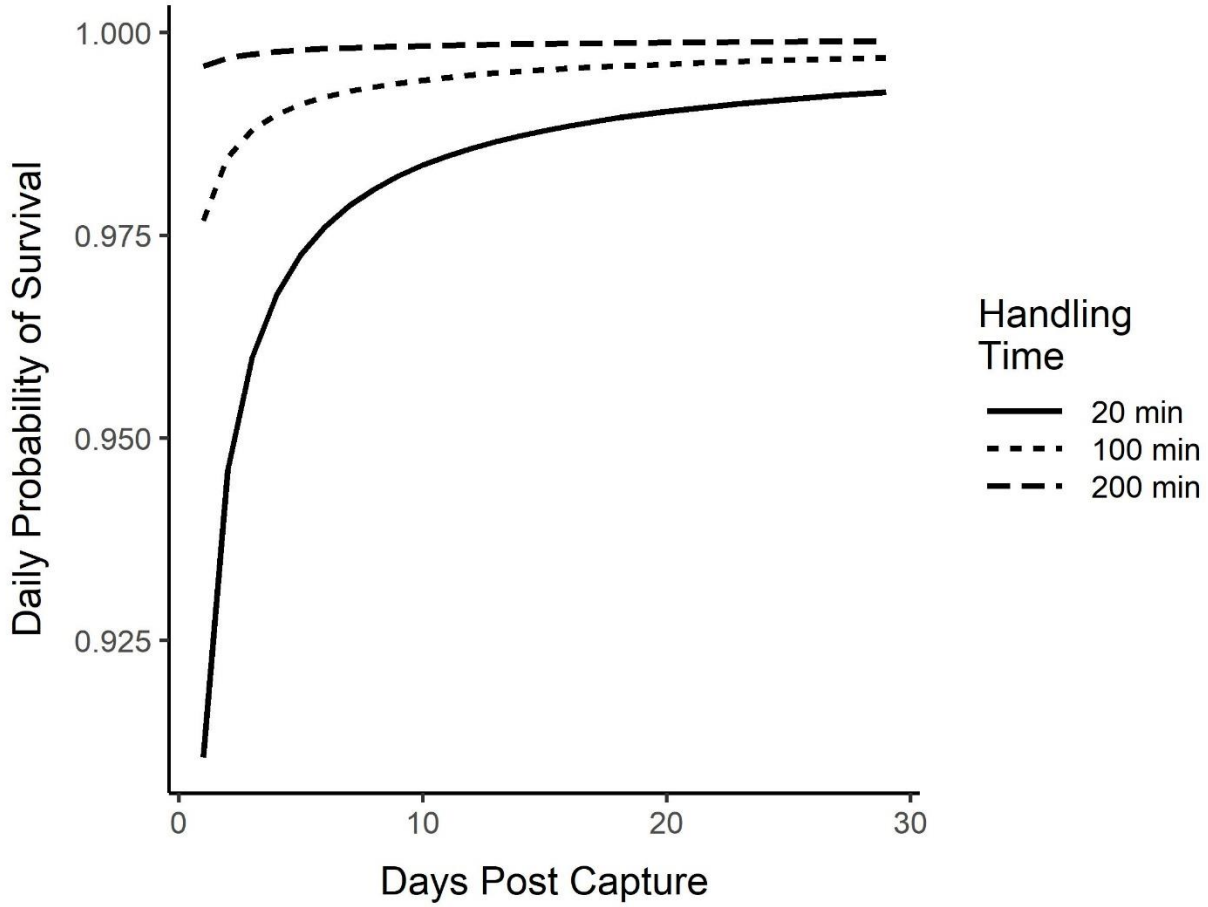


Figure 7. Daily survival probability, by handling time, for wild turkeys in Maine, USA, for 30 days post capture. Estimates for handling times of 20 minutes (solid), 100 minutes (short dashes), and 200 minutes (long dashes) represent approximate minimum, mean, and maximum values for the project.

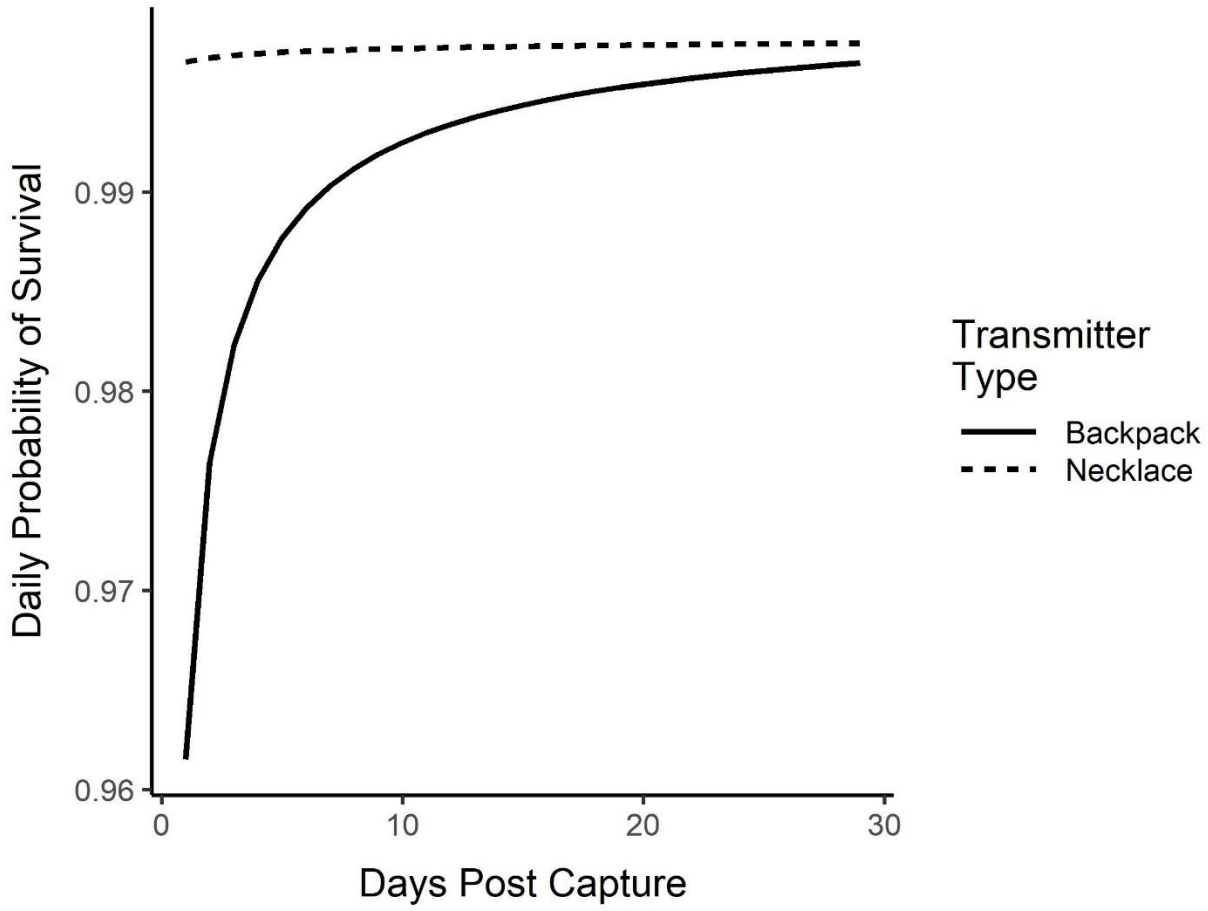


Figure 8. Daily survival probability, by transmitter style, for wild turkeys in Maine, USA, for 30 days post capture. Estimates were derived from the top performing daily survival model according to AIC, where days post-capture (natural log transformation) was allowed to interact with transmitter type.

Table 8. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect post capture survival probability (S) of radio-marked wild turkeys in Maine, USA. All models include natural log of days post capture (LN) and interaction term. We modeled S as a function of transmitter type, age, sex, study area, disease infection status (LPDV, MD, REV), time of the year, precipitation the day of capture (pcpCDy) and through the week (avgpcpWk), minimum temperature the day of capture (mtCDy) and through the week (avgmtWk), and trap site location using a daily survival rate approach (Laake 2013). All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
~HandTime * LN	371.963	0.000	0.895	4	363.957
~Trans.Type * LN	377.378	5.415	0.060	4	369.372
~TurkAge * LN	379.437	7.474	0.021	4	371.431
~mtCDy * LN	382.590	10.627	0.004	4	374.584
~REV * LN	382.966	11.003	0.004	4	374.960
~avgmtWk * LN	383.526	11.563	0.003	4	375.520
~LN	383.696	11.732	0.003	2	379.694
~*Mycoplasma* * LN	383.984	12.020	0.002	4	375.977
~Sex * LN	384.010	12.046	0.002	4	376.003
~Time	384.960	12.997	0.001	2	380.959
~avgpcpWk * LN	385.185	13.221	0.001	4	377.179
~Time + I(Time^2)	385.265	13.301	0.001	3	379.261
~Hematoma * LN	386.389	14.425	0.001	4	378.382
~LPDV * LN	386.834	14.871	0.001	4	378.828
~pcpCDy * LN	386.994	15.030	0.000	4	378.987
~YearDay * LN	387.285	15.322	0.000	4	379.279
~Study.Area * LN	395.033	23.070	0.000	14	366.968
~1	397.506	25.542	0.000	1	395.505
~Location * LN	431.070	59.106	0.000	66	297.674
~HandTime * LN	371.963	0.000	0.895	4	363.957

[a]LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; *Mycoplasma*: Infected, Uninfected, Unkown; Trans.Type: Back, Neck; HandTime: time in minutes; TurkAge: Adult, Juvenile; LN: natural log of day post capture; Time: day post capture; pcpCDy: precipitation day of capture; mtCDy: minimum temperature day of capture; Sex: Male, Female; Hematoma: 1, 0; YearDay: Julian day of the year for capture; avgmtWk: average minimum temperature for week post capture; Pat.Tag: 1, 0; avgpcpWk: average precipitation for week post capture; Study.Area: NC, NW, NE, S, WMD; Location: categorical for trapping location.
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameter
[e]Model Deviance

transmitters (Figure 8). For turkeys fit with a backpack-style transmitter, the cumulative survival rate 10 days post-capture was 0.858 (0.788–0.905 95% CI), 0.836 (0.758–0.890 95% CI) to 14 days, and 0.783 (0.678–0.856 95% CI) to 29 days. For turkeys fit with a necklace style transmitter, cumulative survival rate was 0.970 (0.883–0.991 95% CI) to 10 days post capture, 0.960 (0.862–0.986 95% CI) to 14 days, and 0.922 (0.770–0.972 95% CI) to 29 days.

We observed a difference in adult versus juvenile survival rates post capture (ΔAIC = 7.474; Table 8), where adult initial survival rate was 0.984 (0.959–0.993 95% CI) compared to 0.949 (0.889–0.977 95% CI) for juveniles (Figure 9). Models based on the mean temperature on the day of capture ("mtCDy"; ΔAIC = 10.627; Table 8) and averaged across the week following capture ("avgmtWk"; ΔAIC = 11.563; Table 8) both performed better than the null. In both cases, we observed a relationship where turkeys that experienced colder temperatures had a lower cumulative probability of survival to 30 days post capture (Figure 10). We observed a difference in post capture survival according to REV infection status (ΔAIC = 11.003; Table 8), where birds that tested positive for REV infection had a lower initial survival probability than those that tested negative but maintained a higher survival probability on average over 30 days post capture which results in a higher cumulative survival for REV-infected individuals (Figure 11). We did not find strong support for an effect of sex, precipitation, LPDV or *Mycoplasma* infection status, or location on post-release survival probability (Table 8). Our AIC comparison for threshold day at which to stop censoring birds for post-release mortality showed that 4 days post capture performed best (ΔAIC = 0.0; Table 9), with days 2-10 falling with 2.0 ΔAIC of the best model. After day 10, there was a gradual decline in model deviance until around day 17, where values began to level off (Figure 12).

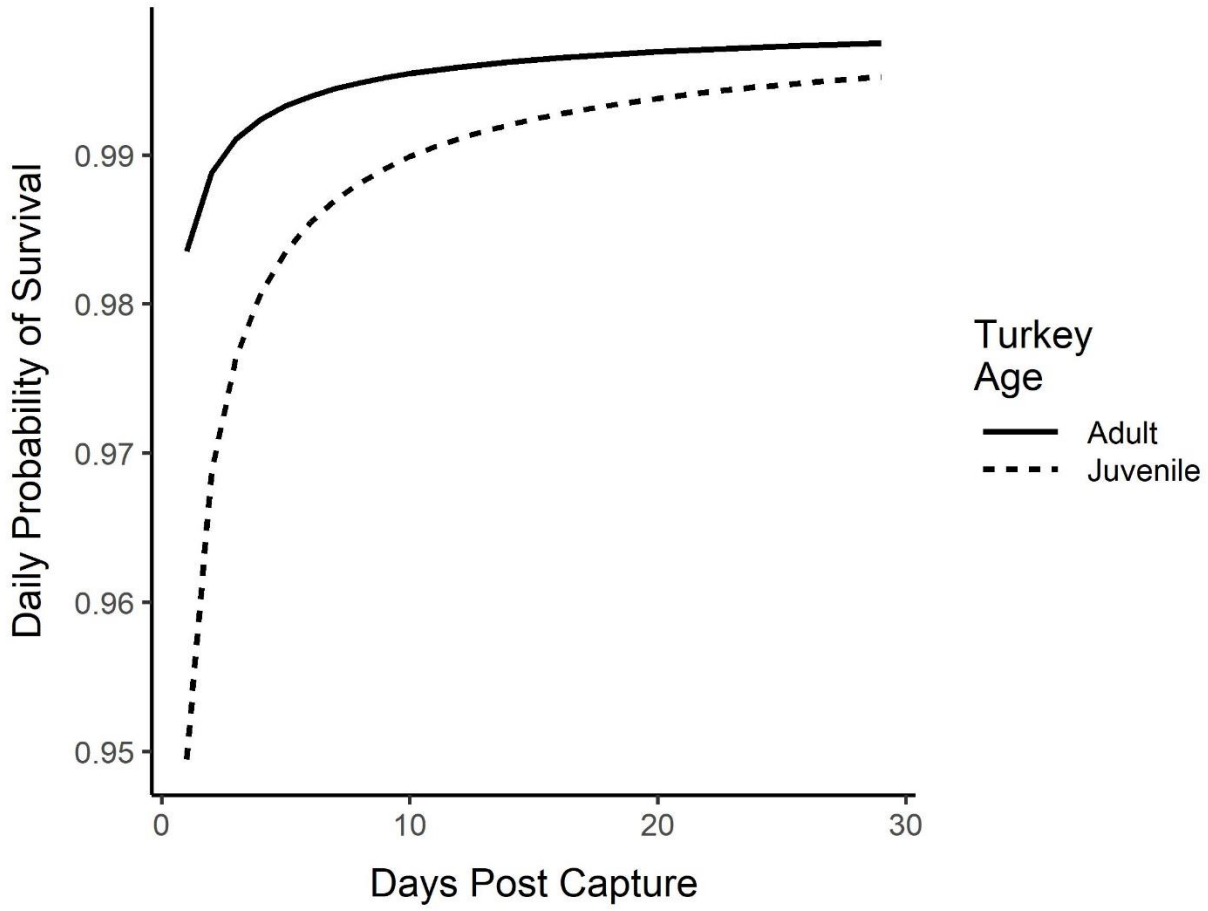


Figure 9. Daily survival probability, by turkey age at capture, for wild turkeys in Maine, USA, for 30 days post capture. Graph compares post capture survival for adults (solid) and juveniles (dashed).

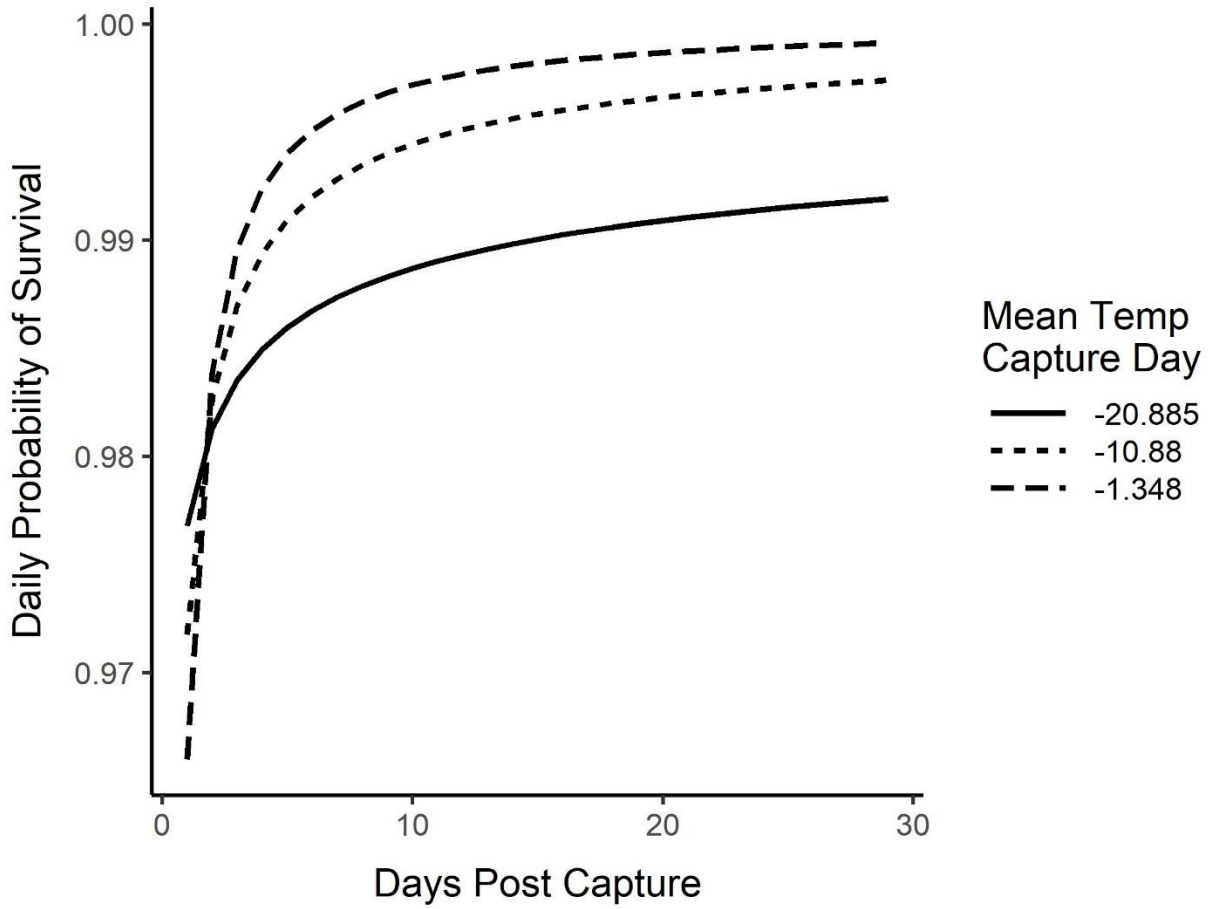


Figure 10. Daily survival probability, by mean temperature on day of capture, for wild turkeys in Maine, USA, for 30 days post capture. Graph compares post capture survival for the minimum (-20.885; solid), mean (-10.88; short dashed), and max (-1.348; long dashed) temperatures observed.

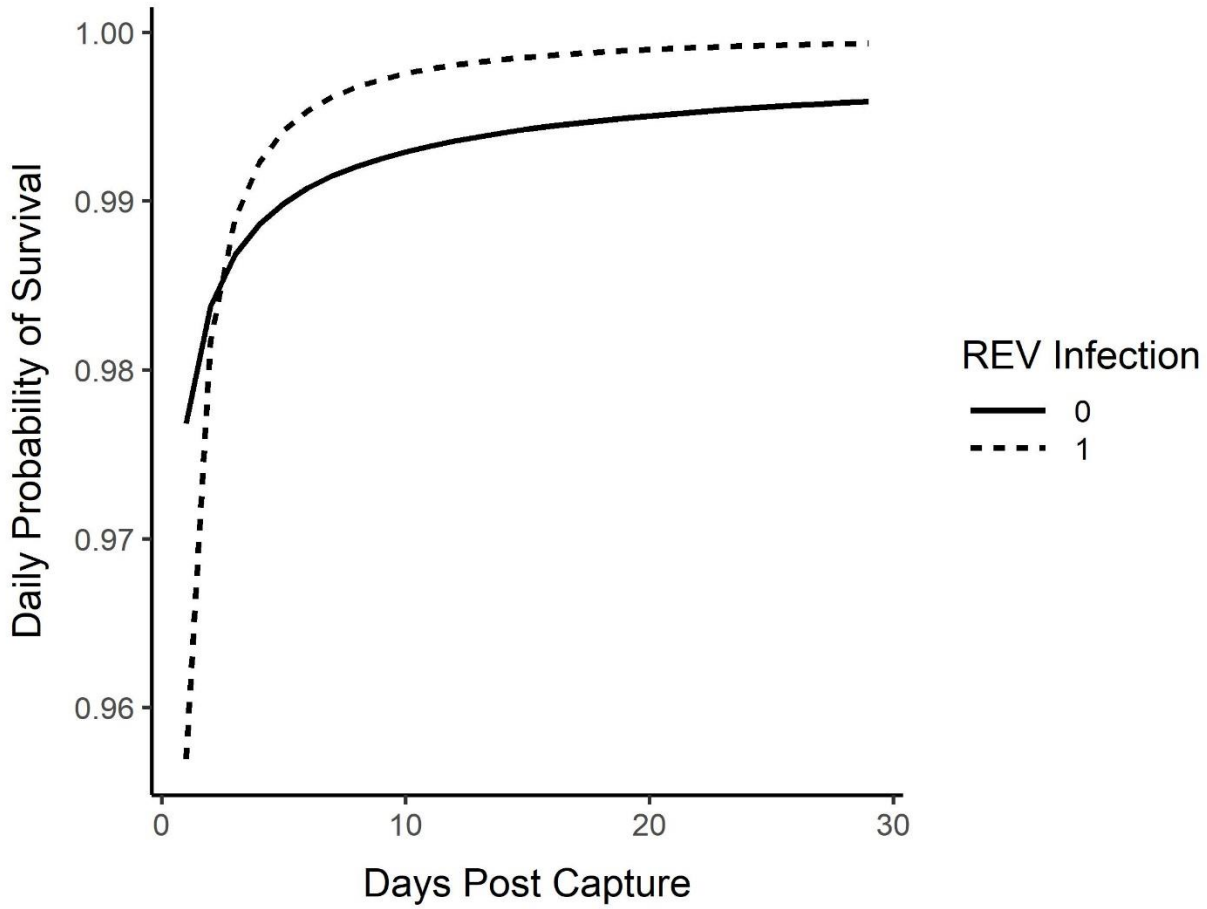


Figure 11. Daily survival probability, by REV infection status, for wild turkeys in Maine, USA, for 30 days post capture. Graph compares post capture survival for REV negative (solid) and REV positive

(dashed) individuals.

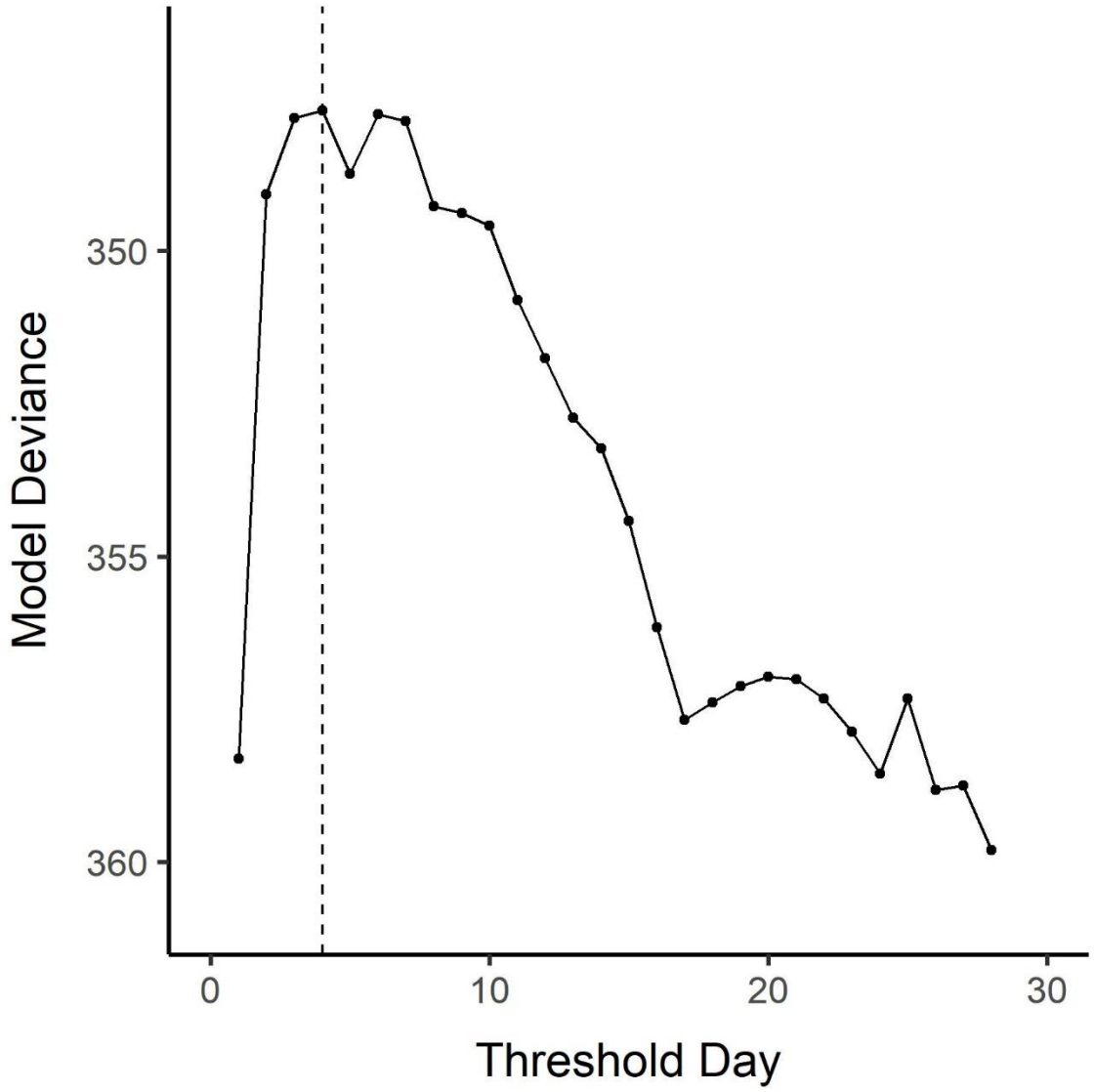


Figure 12. Model deviance among all potential daily thresholds for post-release mortality of wild turkeys captured in Maine, USA, from January through March 2018 and 2019. The y-axis is inverted, and smaller deviance values indicate better fit, where the best-fit model is indicated by the dashed vertical line. All models were run as nest survival analyses, implemented in Program MARK (White and Burnham 1999) using the R package RMark (Laake 2016).

Table 9. Model selection results for daily survival rate analyses that describe post capture survival probability of Wild Turkey for 30 days following release and radiomarking. Models were implemented in Program MARK using the R package RMark (Laake 2016). Models represent discrete threshold points of postrelease mortality.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
~Days4 + Trans.Type + TurkAge + HandTime	357.716	0.000	0.146	5	347.707
~Days6 + Trans.Type + TurkAge + HandTime	357.771	0.054	0.142	5	347.761
~Days3 + Trans.Type + TurkAge + HandTime	357.835	0.118	0.138	5	347.825
~Days7 + Trans.Type + TurkAge + HandTime	357.884	0.168	0.134	5	347.875
~Days5 + Trans.Type + TurkAge + HandTime	358.748	1.031	0.087	5	348.738
~Days2 + Trans.Type + TurkAge + HandTime	359.080	1.364	0.074	5	349.071
~Days8 + Trans.Type + TurkAge + HandTime	359.279	1.563	0.067	5	349.269
~Days9 + Trans.Type + TurkAge + HandTime	359.389	1.673	0.063	5	349.380
~Days10 + Trans.Type + TurkAge + HandTime	359.598	1.882	0.057	5	349.589
~Days11 + Trans.Type + TurkAge + HandTime	360.813	3.097	0.031	5	350.804
~Days12 + Trans.Type + TurkAge + HandTime	361.769	4.053	0.019	5	351.760
~Days13 + Trans.Type + TurkAge + HandTime	362.740	5.023	0.012	5	352.730
~Days14 + Trans.Type + TurkAge + HandTime	363.237	5.521	0.009	5	353.228
~Days15 + Trans.Type + TurkAge + HandTime	364.431	6.714	0.005	5	354.421
~Days16 + Trans.Type + TurkAge + HandTime	366.168	8.452	0.002	5	356.159
~Days20 + Trans.Type + TurkAge + HandTime	366.974	9.258	0.001	5	356.965
~Days21 + Trans.Type + TurkAge + HandTime	367.022	9.305	0.001	5	357.012
~Days19 + Trans.Type + TurkAge + HandTime	367.132	9.416	0.001	5	357.123
~Days22 + Trans.Type + TurkAge + HandTime	367.336	9.620	0.001	5	357.327
~Days25 + Trans.Type + TurkAge + HandTime	367.337	9.621	0.001	5	357.328
~Days18 + Trans.Type + TurkAge + HandTime	367.397	9.680	0.001	5	357.387
~Days17 + Trans.Type + TurkAge + HandTime	367.687	9.971	0.001	5	357.678
~Days23 + Trans.Type + TurkAge + HandTime	367.878	10.162	0.001	5	357.869
~Days1 + Trans.Type + TurkAge + HandTime	368.320	10.603	0.001	5	358.310
~Days24 + Trans.Type + TurkAge + HandTime	368.564	10.848	0.001	5	358.555
~Days27 + Trans.Type + TurkAge + HandTime	368.765	11.048	0.001	5	358.755
~Days26 + Trans.Type + TurkAge + HandTime	368.835	11.119	0.001	5	358.826
~Days28 + Trans.Type + TurkAge + HandTime	369.816	12.100	0.000	5	359.807

[a]Trans.Type: Back, Neck; TurkAge: Adult, Juvenile; HandTime: time in minutes; Day#: Threshold Day
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

Daily Nest Survival Rate

During Spring 2018 through 2020, we located 123 wild turkey nests, 120 belonging to marked hens and 3 belonging to unmarked hens. Of the 120 nests of marked hens, 101 were the first discovered attempt for the female, 18 were known second attempts, and 1 was a known third attempt. Thirty three of 101 first attempted nests hatched, seven of 18 second nests hatched, and the single third attempt nest hatched.

The top model for predicting nest DSR was based on a linear relationship with age of the nest (ΔAIC = 0.0; Table 10). As nest age increased in days, the probability of daily survival decreased (β = -0.050; -0.075 – -0.024, 85% CI). Nest DSR was 0.989 (0.980-0.994, 95% CI) on Day 1 compared with 0.936 (0.904-0.958 95% CI) on Day 38, the approximate hatch date for a bird with the average clutch size of 11 (Figure 13). The probability a nest survived a 38-day exposure period was 0.310 (0.192–0.432, 95% CI; Figure 14). We did not find strong support for differences in nest DSR when comparing nest initiation date, disease status, transmitter type, study area, or year (Table 10).

Nesting Behavior and Hunter Effort

Of hens marked with transmitters in 2018, 41 were known alive one week prior to the earliest known nest initiation date in 2018 (April 17). Of hens marked with a transmitter in 2018 or 2019, 72 were known alive one week prior to the earliest known nest initiation date in 2019 (April 24). Of hens marked with a transmitter in 2018 through 2020, 73 were known alive one week prior to the earliest known nest initiation date in 2020 (April 10). The median date of initiation for first nests was April 27 in 2018, May 5 in 2019, and April 27 in 2020 (Figure 15). The median date of initiation for second nests was June 3 in 2018, June 3 in 2019, and May 29 in

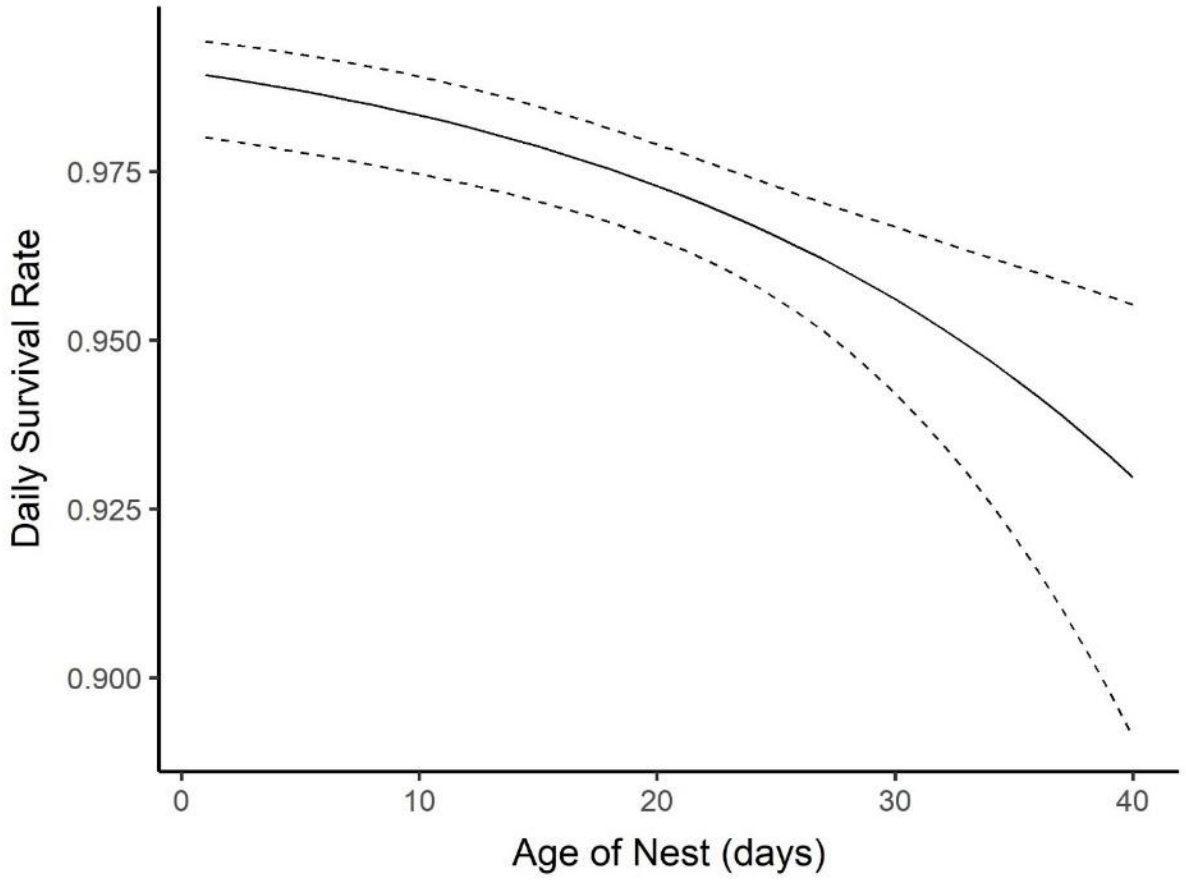


Figure 13. Daily survival rates, by age of nest, for wild turkey nests in Maine, USA, from April to July 2018 through 2020. Estimates were derived from the top performing daily survival rate model according to AIC. Estimates are presented with upper and lower 95% confidence intervals (dotted lines).

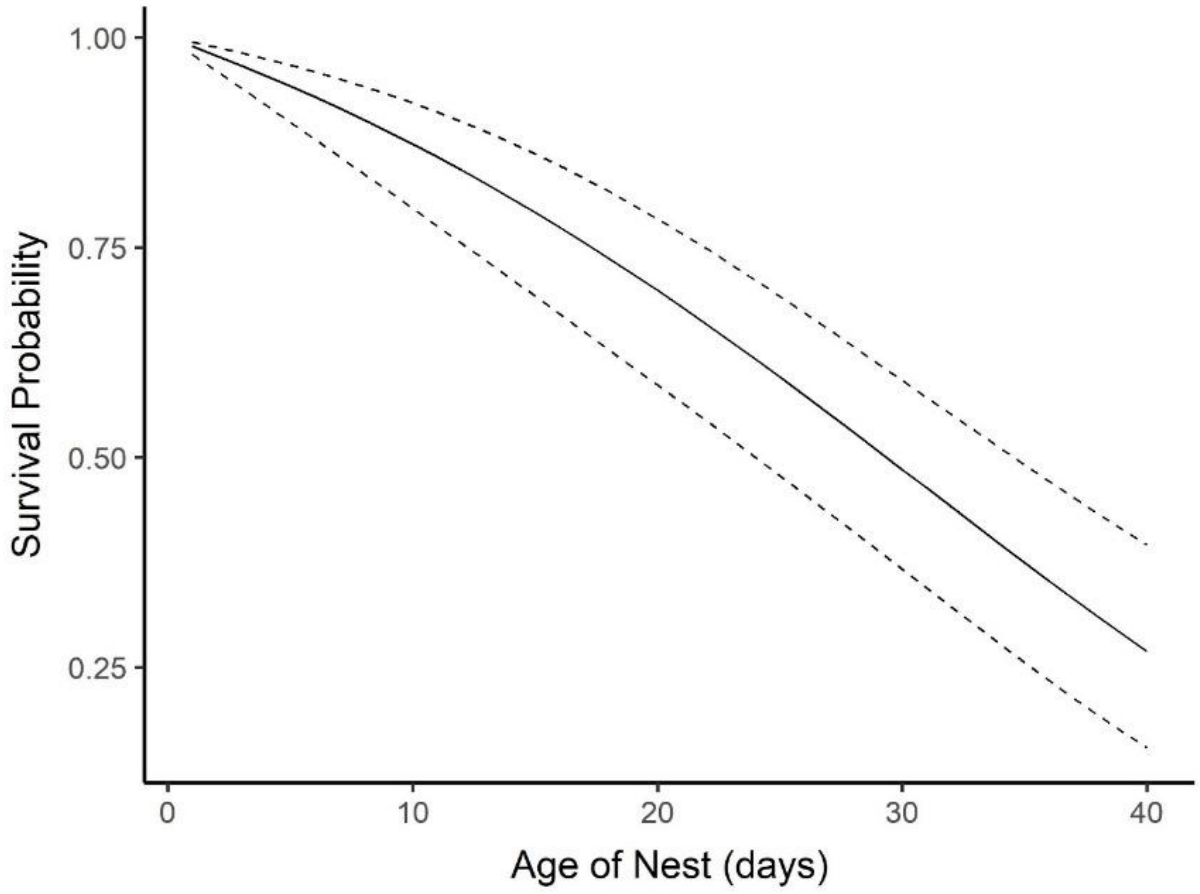


Figure 14. Cumulative probability of nest survival throughout a 40-day exposure period for wild turkey nests in Maine, USA, from April to July 2018 through 2020. Estimates were derived from the top performing daily survival rate model according to AIC. Estimates are presented with upper and lower 95% confidence intervals (dotted lines).

Table 10. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect daily survival rate (S) of wild turkey nests in the Exeter/Corinth, Stud Mill Rd./Greenfield, and Gorham/Gray study areas in Maine, USA. We modeled S as a function of day of the year, age of the nest, initiation date, age of the turkey, study area, transmitter type, and disease infection status (LPDV, REV, and *Mycoplasma*) using a daily survival rate approach (Laake 2013). All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	Dev[e]
~NestAge	510.395	0.000	0.993	2	506.390
~1	523.762	13.366	0.001	1	521.760
~Time	524.175	13.779	0.001	2	520.169
~Turk.Age	524.241	13.845	0.001	2	520.235
~Study.Area	524.381	13.985	0.001	7	510.330
~*Mycoplasma*	524.881	14.486	0.001	2	520.876
~Nest.Attempt	524.976	14.581	0.001	3	518.966
~LPDV	525.381	14.985	0.001	2	521.375
~REV	525.461	15.066	0.001	2	521.456
~NestYear	527.563	17.168	0.000	3	521.552
~Trans.Type	527.642	17.247	0.000	3	521.632

[a]NestAge: number of days since nest established; Nest.Init: Date nest established; LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; *Mycoplasma*: Infected, Uninfected, Unkown; Turk.Age: Adult, Juvenile; Trans.Type: Neck, Back; Study.Area: NW, S, NE, time: days since first nest found

[b]Difference in AIC compared with the lowest AIC model score

[c]AIC model weight

[d]Number of model parameters

[e]Model Deviance

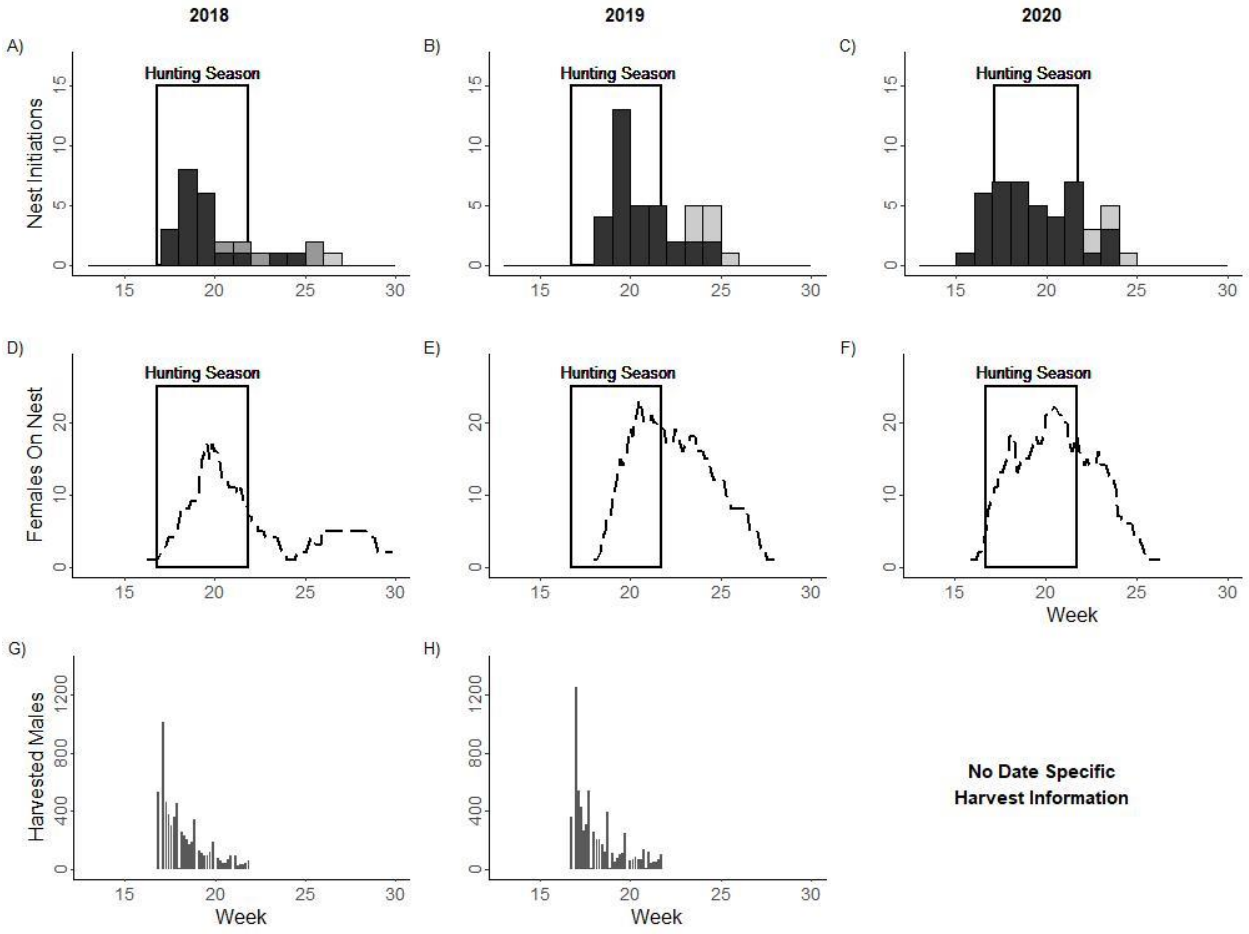


Figure 15. (A, B, C) Total counts of nests initiation by week for monitored wild turkeys, grouped according to nest attempt: first attempt (dark grey) and renest (light grey). (D, E, F) Total count of females incubating on a given day over time. (G, H) Total number of male wild turkeys harvested and reported to MDIFW by day of the year.

2020. The single third nest attempt was initiated on June 23, 2018. The number of incubating hens peaked at 66.6% of all available nests on May 17 in 2018, 52.5% on May 23 in 2019, and 47.8% on May 22 and 23 in 2020 (Figure 15). The Maine spring bearded turkey hunting season took place from April 30 through June 2 in 2018, April 29 through June 1 in 2019, and May 4 through June 6 in 2020. A youth spring hunting day took place on April 28, 2018, April 27, 2019, and May 2, 2020, prior to the general opening of the turkey hunting season. Due to COVID-19 restrictions on wild turkey tagging, we are limited to 2018 and 2019 for date-specific harvest information. The peak in number of turkeys harvested and reported occurred on the first day of the general hunting season for both years (Figure 15). In 2018, 32.0% of harvests occurred before the median date of nest initiation compared to 65.7% of harvests in 2019. In general, peak hunter effort occurred immediately following (2018) or concurrent with (2019) the peak of nest initiation (Figure 15). The peak of hunter harvest occurred prior to the onset of the majority of the incubation period during both years, with 83.3% (2018) and 89.6% (2019) of harvests occurring before the peak in female incubation (Figure 15).

Variation in nest initiation date was best described by a model based on the percentage of developed and agricultural land cover surrounding the nest as well as a year effect ($\Delta AIC = 0$, Table 11). According to our top performing model, for every 1 standard deviation (14.5%) increase in developed land cover, nest initiation dates shifted 3.274 (SE = 1.713) days earlier. For every 1 standard deviation (13.2%) increase in agricultural land cover, nest initiation dates shifted 2.928 (SE = 1.559) days later. According to our top model, nests were initiated 10.035 (SE = 4.110) days earlier on average in 2018 compared with 2019 and there was no significant difference in nest initiation dates for first nests between 2018 and 2020. Parameters for both the latitude of the nest and *Mycoplasma* infection status were included in models performing within

Table 11 Model selection results based on Akaike's Information Criterion (AIC) for models of wild turkey nest initiation date (first attempts) based on spatial and individual female covariates during the spring 2018 and 2019 nesting seasons in Maine, USA. All models with ΔAIC < 2 are shown, as well as null (intercept only) and global (all parameters) models for contrast. K is the number of parameters estimated and *w* is model weight.

Model[a]	K	AICc	ΔAICc	*w*
~Developed + Ag + Year	6	590.795	0.000	0.197
~Ag	3	591.707	0.912	0.125
~Developed + *Mycoplasma* + Ag + Year	7	591.929	1.134	0.112
~Developed + Ag + TurkAge + Year	7	592.104	1.309	0.102
~Developed + Year	5	592.111	1.316	0.102
~Ag + Year	5	592.238	1.443	0.096
~*Mycoplasma* + Ag	4	592.596	1.801	0.080
~Developed + *Mycoplasma* +Year	6	592.705	1.910	0.076
~Developed + Latitude + Ag + Year	7	592.778	1.983	0.073
~Null Model	2	594.095	3.299	0.038
~Global Model	22	628.254	37.459	0.000

[a] Developed: percent areas within 1002m of nest location comprised of all land cover associated with human development; Ag: percent areas within 1002m of nest location comprised of land cover associated with agriculture, grasslands, and barrens; Deciduous: percent areas within 1002m of nest location comprised of deciduous forest; Year: year of nest initiation; *Mycoplasma*: *Mycoplasma gallisepticum* infection status at capture. Other variables that were considered in an all-combinations approach, but that were not supported, include: percent areas within 1002m of nest location comprised of land cover associated forested landcover, latitude of nest site, REV and LPDV infection status at capture, and distance traveled by hen between trap and nest locations

ΔAIC < 2. In all cases, they were considered uninformative parameters as these models did not perform better than models without the addition of the parameter (Burnham and Anderson 2002). We did not find evidence to support an effect of latitude, age of turkey, LPDV infection status, REV infection status, study area, distance traveled between wintering and nesting location, or body condition on the timing of nest initiation.

We found that the distribution of nest initiation dates in 2018 and 2019 did differ from the distribution observed in 2020 (Table 12). The calculated chi-square statistic was 29.049 compared to a critical value of 26.296 (df = 16, $\alpha = 0.05$), indicating that we can reject the null hypothesis that there was no difference in the distribution of nest initiations between the years of our study. The distribution of nest initiations in 2020 was flatter and more prolonged than in 2018 or 2019, suggesting some amount of adjustment by hens laying in 2020.

Clutch Size

Average clutch size of VHF marked hens across both years of the study was 11.38, with the largest clutch size being 20 and the smallest being 6. The best model according to AIC was based on a quadratic relationship with nest initiation date (ΔAIC = 0.0; Table 13). Mean clutch size was greater earlier in the year, 14.91 (13.80-16.02 95% CI) on ordinal day 101, compared with later in the year, 8.64 (6.82-10.46 95% CI; Figure 16) on ordinal day 174. Models for a linear relationship with nest initiation (ΔAIC = 1.30; Table 13) and whether a nest was a renest (ΔAIC = 47.30; Table 13) were both supported over the null model. We found support for a model including LPDV infection status at capture (ΔAIC = 54.07; Table 13). Hens that had a positive LPDV status at capture had an average clutch size of 11.08 (10.53-11.62 95% CI) eggs compared to 12.27 (11.41-13.14 95% CI) for those with a negative LPDV status (Figure 17). We

Table 12. Chi-square table comparing the difference in distribution of nest initiations over time (grouped by week) during the spring 2018 and 2019 nesting seasons in Maine, USA.

		Week								
		1	2	3	4	5	6	7	8	9
2018	Observed	5	7	5	1	1	0	2	0	0
	Expected	3	4	2.5	2.5	3.5	2	2	1	0.5
2019	Observed	7	13	6	2	2	1	2	0	0
	Expected	4.7	6.3	3.9	3.9	5.5	3.1	3.1	1.6	0.8
2020	Observed	6	8	5	5	7	4	4	2	1

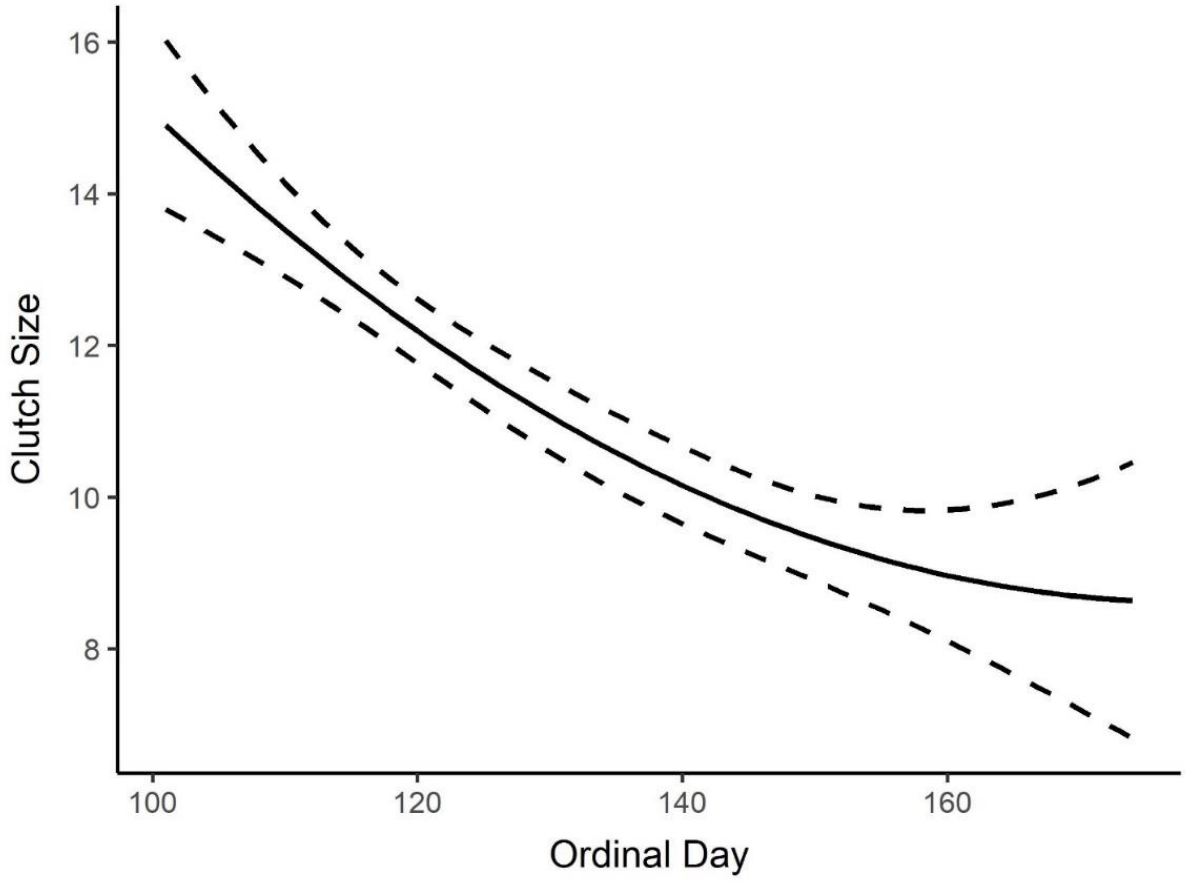


Figure 16. Clutch sizes of wild turkey hens in Maine, USA, from April through July 2018 through 2020. Clutch size is plotted according to ordinal day of the year of laying initiation.

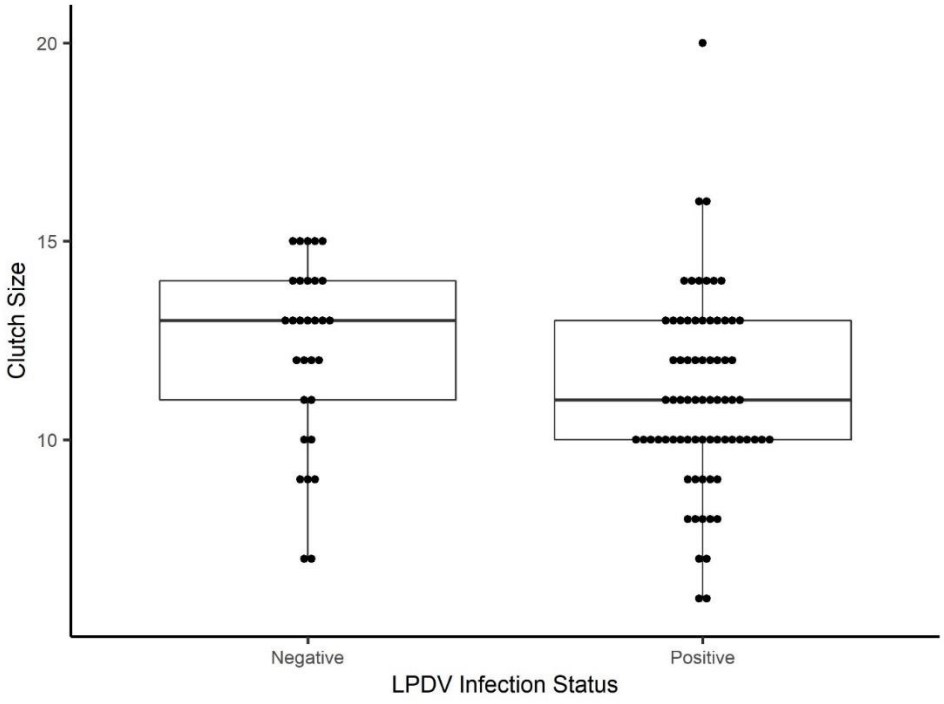


Figure 17. Clutch sizes of wild turkey hens in Maine, USA, from April through July 2018 through 2020. Nests are grouped according to hen LPDV infection status at capture.

Table 13. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect clutch size (CS) of wild turkey nests in the Exeter/Corinth, Stud Mill Rd./Greenfield, and Gorham/Gray study areas in Maine, USA. We modeled CS as a function of initiation date, age of the turkey, study area, year, whether the nest was a renest, and disease infection status (LPDV, REV, and *Mycoplasma*) using linear regression. All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]
~Init2	424.148	0.000	0.713	3
~Init	425.970	1.822	0.287	2
~Renest	472.268	48.120	0.000	2
~Weight	477.709	53.561	0.000	2
~LPDV	478.098	53.950	0.000	2
~1	481.629	57.480	0.000	1
~TurkAge	481.726	57.578	0.000	2
~Study.Area	483.262	59.113	0.000	7
~REV	483.617	59.469	0.000	2
~*Mycoplasma*	483.745	59.596	0.000	2

[a]; LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; *Mycoplasma*: Infected, Uninfected, Unkown; Init: Julian day of nest initiation; Init2: quadratic term for julian day of nest initiation; Renest: 1, 0; TurkAge: Adult, Juvenile; Year: 2018, 2019; StudyArea: NC, NE, NW, S, WMD

[b]Difference in AIC compared with the lowest AIC model score

[c]AIC model weight

[d]Number of model parameters

[e]Model Deviance

also found support for a model based on age of the turkey at capture (ΔAIC = 57.22; Table 13), where adult hens laid 1.37 (±0.94) more eggs than juvenile hens.

Seasonal Home Range and Movements

Of the 59 hens fitted with GPS transmitters, 13 died within the first two weeks post-capture and were censored from analysis. Additionally, a subset of females have been categorized as missing despite extensive searches with hand held, truck mounted, and aerial telemetry. In most cases it is assumed that these missing birds are a result of transmitter malfunction or battery depletion. Data for these females were included in the analysis until their disappearance. For hens that did not survive the entire year, we included their data in the analysis up until their deaths. For hens that survived from capture to the next year, we included data from the later year as a separate track in the analysis of home ranges.

Over the three years of data collection, average area of use (95% UD) for GPS-marked females that survived from capture until August 1 was 6.81 km^2 (1.61 km^2 – 21.42 km^2, Figure 18). The average area of use (95% UD) for GPS-marked females that survived from capture until August 1 was 6.940 km^2 (2.836 km^2 – 21.421 km^2) in 2018, 6.093 km^2 (1.637 km^2 – 20.160 km^2) in 2019, and 7.975 km^2 (1.605 km^2 – 16.306 km^2; Table 14, Figure 18, 19, 20) in 2020. The average area of seasonal use (95% UD within each discrete season) for wintering home ranges was 1.286 km^2 (0.804 km^2 – 2.438 km^2) in 2018, 2.356 km^2 (0.171 km^2 – 11.575 km^2) in 2019, and 2.939 km^2 (0.375 km^2 – 8.865 km^2) in 2020. Average area of use for pre-nesting home ranges prior to the first attempt was 2.374 km^2 (1.433 km^2 – 3.260 km^2) for 2018, 2.115 km^2 (0.501 km^2 – 3.617 km^2) for 2019, and 3.431 km^2 (0.584 km^2 – 9.749 km^2) for 2020. Average area of use for summer home ranges following nesting was 7.354 km^2 (0.138 km^2 – 27.396 km^2) in 2018, 1.977 km^2 (0.332 km^2 – 5.406 km^2) in 2019, and 2.950 km^2 (0.984 km^2 – 4.435 km^2) in 2020. The average seasonal movement distance between wintering home range and nesting home

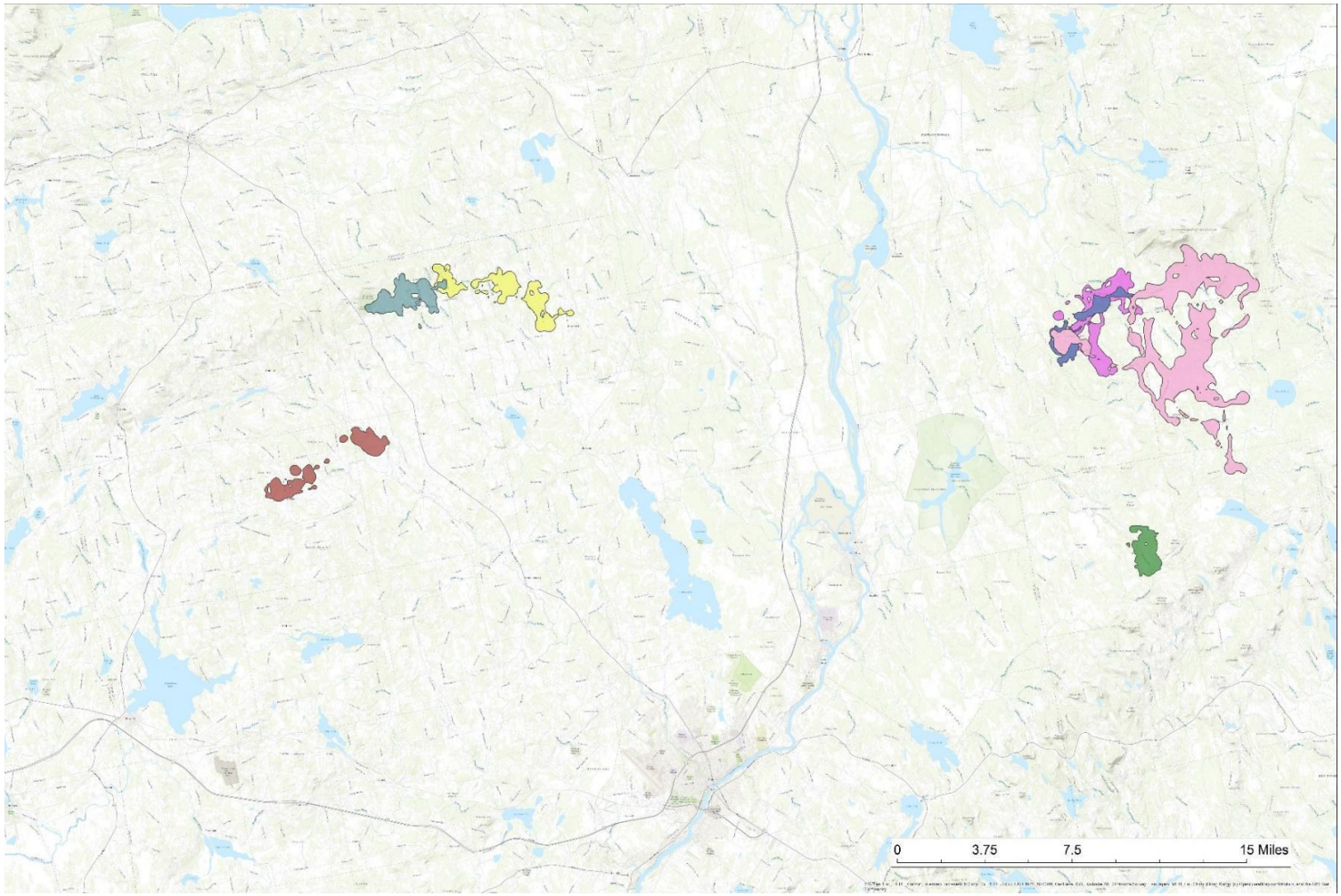


Figure 18. 99% Utilization Distributions (UD) depicting space use of individual wild turkey hens from capture through July 31, 2018 in central Maine, USA. UDs were derived using dynamic Brownian Bridge Movement Models. Individuals are represented by unique colors.

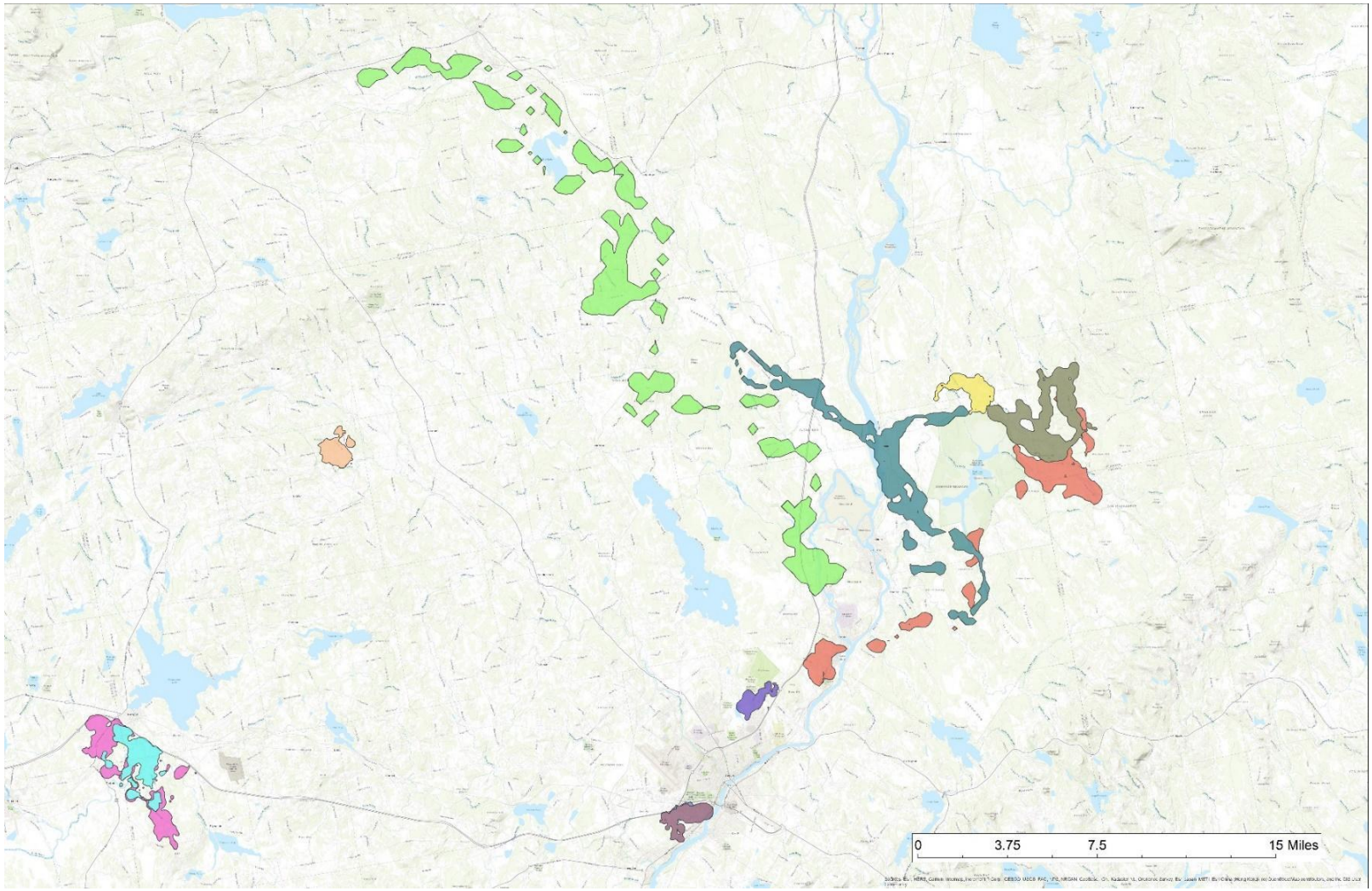


Figure 19. 99% Utilization Distributions (UD) depicting space use of individual wild turkey hens from capture through July 31, 2019 in central Maine, USA. UDs were derived using dynamic Brownian Bridge Movement Models. Individuals are represented by unique colors.

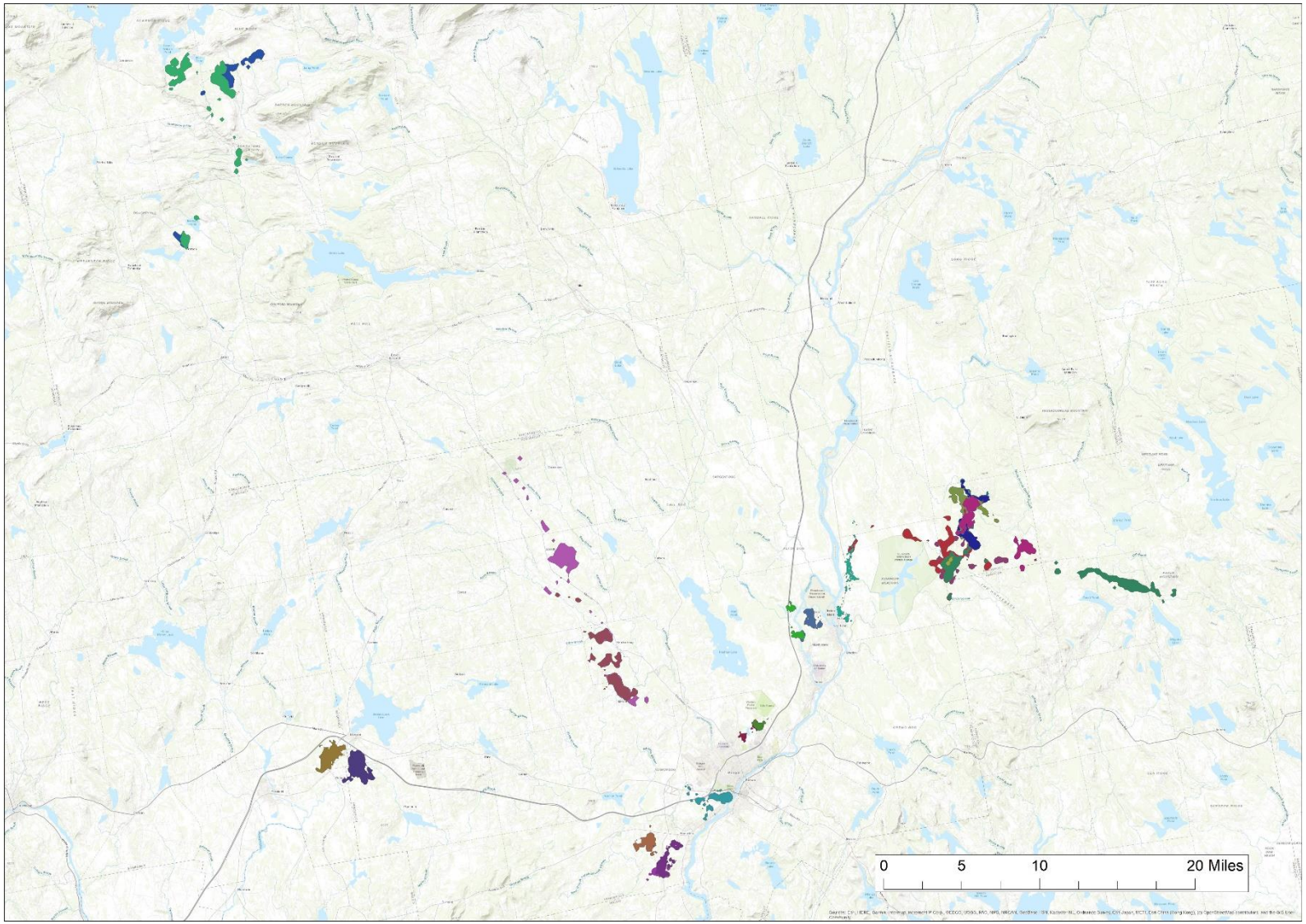


Figure 20. 99% Utilization Distributions (UD) depicting space use of individual wild turkey hens from capture through July 31, 2020 in central Maine, USA. UDs were derived using dynamic Brownian Bridge Movement Models. Individuals are represented by unique colors.

Table 14. Average area estimates for 95% Utilization Distributions (UD) by season for wild turkey hens at NW, NC, NE study areas, Maine, USA, from January through July 2018 through 2020. Estimates are presented in mi^2 and were derived using dynamic Brownian Bridge Movement Models. Estimates are presented with the number of individuals sampled (n), the maximum value recorded during a given season (Max.), the minimum value recorded during a given season (Min.).

	n	Average	Max.	Min.
Capture-to-August 1				
2018	7	6.940	21.421	2.836
2019	11	6.093	20.160	1.637
2020	6	7.975	16.306	1.606
Winter				
2018	10	1.286	2.438	0.804
2019	21	2.356	11.575	0.171
2020	23	2.939	8.865	0.375
Winter-to-Nest				
2018	8	4.255	9.067	1.655
2019	12	5.479	23.216	0.402
2020	19	4.974	18.137	0.238
Nesting (1st Attempt)				
2018	8	2.314	3.260	1.433
2019	12	2.115	3.617	0.501
2020	19	3.431	9.749	0.584
Nesting (2ndAttempt)				
2018	3	1.315	1.815	0.791
2019	2	1.574	1.791	1.356
2020	1	0.981	0.981	0.981
Nesting (3rd Attempt)				
2018	1	0.379	0.379	0.379
2019	-	-	-	-
2020	-	-	-	-
Summer				
2018	6	7.354	27.396	0.138
2019	11	1.977	5.406	0.332
2020	6	2.950	4.435	0.984

range was 4.255 km in 2018, 5.479 km in 2019, and 4.974 km in 2020. Individual female movements between winter and nesting home ranges varied from 0.238 km to 23.216 km. Qualitative observations of hen movement indicated that individual females employed a variety of movement strategies, including among females from within the same study area or winter flock (Figure 21, 22). Strategies included overlapping winter and prenesting home ranges, short and long range travel between wintering and prenesting ranges, and long range dispersal followed by a partial return towards the wintering range.

Across the 3 analyses, we observed a variety of factors that affected wild turkey hen seasonal movements. No models describing variation in winter home range size performed better than the null model (Table 15). A model based on LPDV infection status had the closest AIC score (ΔAIC = 0.866; Table 15) and showed that individuals with a positive LPDV status had a winter home range size 0.829 km^2 (±0.715 km^2, p = 0.251) greater than those with a negative status. Variation in pre-nesting home range size was best explained by *Mycoplasma* infection status (ΔAIC = 0.0; Table 16). Individuals with a positive *Mycoplasma* status had a pre-nesting home range size 1.740 km^2 (±0.565 km^2, p = 0.004) less than those with a negative status. A model based on year of observation (ΔAIC = 2.959; Table 16) showed that pre-nesting home ranges for birds observed in 2020 were 1.478 km^2 (±0.595 km^2, p = 0.017) larger than in 2018. There was no significant difference in pre-nesting home range size between 2018 and 2019. Variation in distance traveled between winter and pre-nesting home ranges was best explained by study area (ΔAIC = 0.0; Table 17). This relationship appears to be largely driven by the two hens captured in WMD 14 that both moved over 13 km from winter to pre-nesting home range. A model based on REV infection status (ΔAIC =

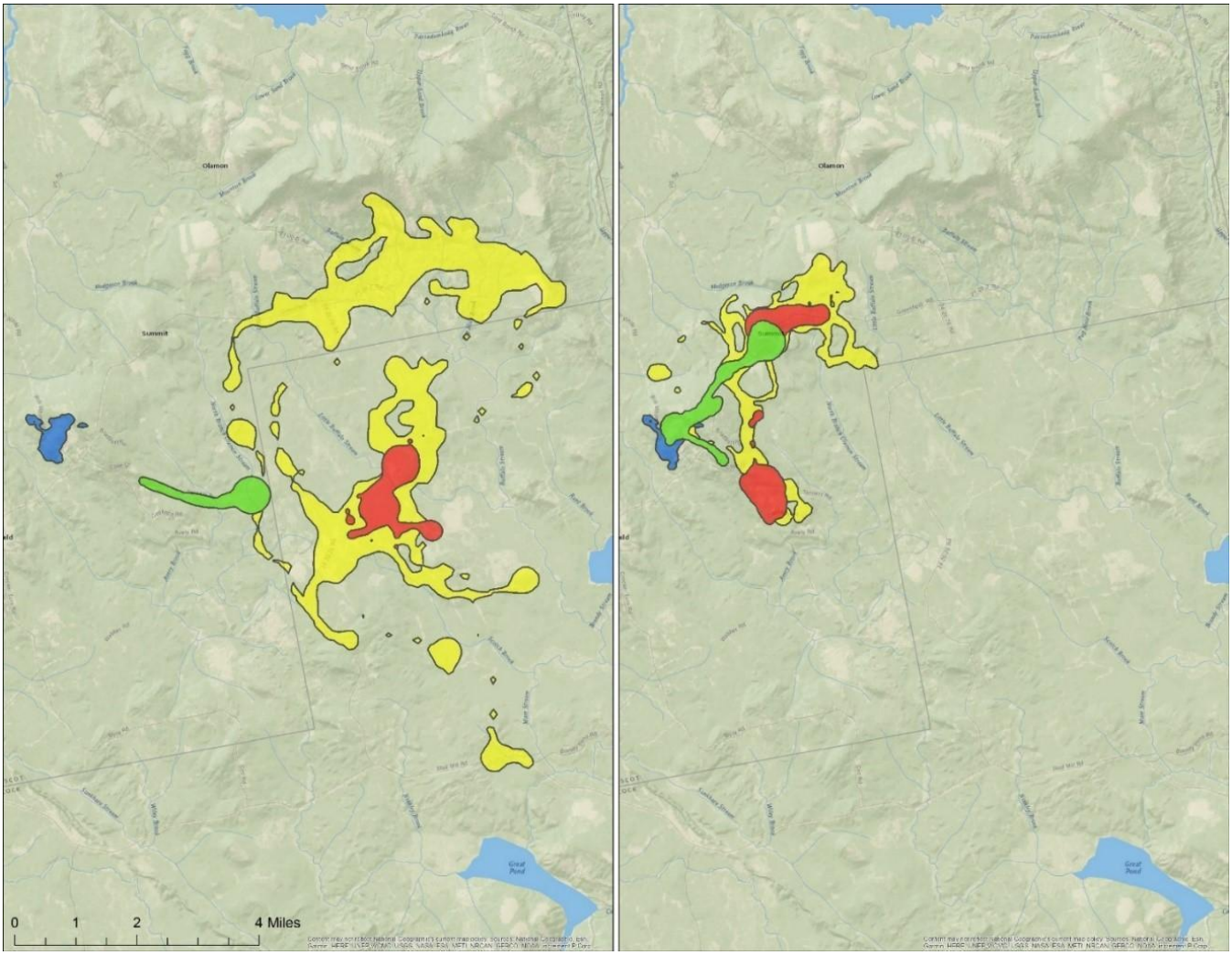


Figure 21. Example of 95% Utilization Distributions for seasonal home ranges of two wild turkey hens (ID 251, left panel, and 361, right panel) from the same flock in the NE study area, Maine, USA. This figure illustrates the potential variation in seasonal movements and home range sizes for female wild turkeys inhabiting the same area. Seasonal ranges were derived using dynamic Brownian Bridge Movement Models. Seasons are Winter (Blue), Winter to Nest Movement (Green), Nesting (Red), and Summer (Yellow). All maps displayed using the same scale and cover the same area.

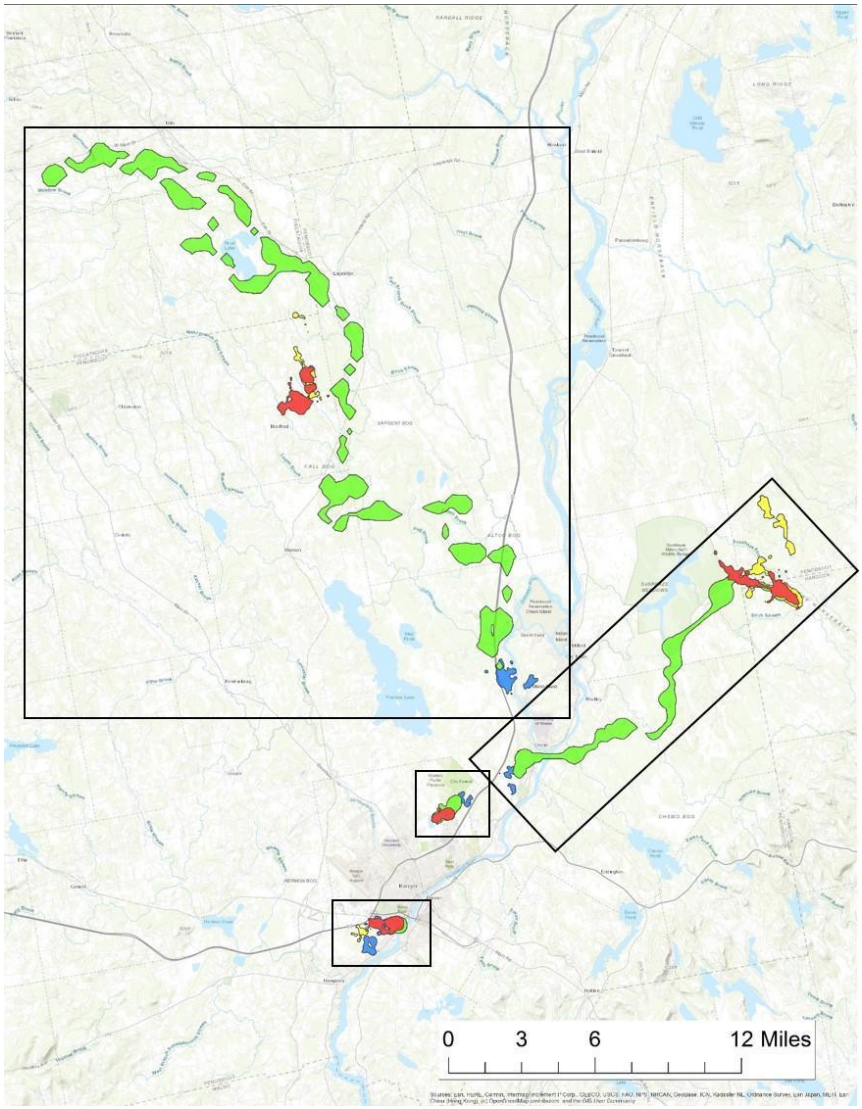


Figure 22. Example of 95% Utilization Distributions for seasonal home ranges of four wild turkey hens capture in the NC study area, Maine, USA. This figure illustrates the potential variation in seasonal movements and home range sizes for female wild turkeys inhabiting the same area. Black boxes individuate individual hen UDs. Seasonal ranges were derived using dynamic Brownian Bridge Movement Models. Seasons are Winter (Blue), Winter to Nest Movement (Green), Nesting (Red), and Summer (Yellow). All maps displayed using the same scale and cover the same area.

Table 15. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect winter home range size (WHR) of GPS-marked wild turkey hens in Maine, USA. We modeled WHR as a function of age of the turkey, study area, and disease infection status (LPDV, REV, and *Mycoplasma*) using linear regression. All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]
~1	249.218	0.000	0.284	1
~LPDV	250.083	0.866	0.185	2
~StudyArea	250.554	1.336	0.146	4
~TurkAge	250.719	1.501	0.134	2
~REV	251.438	2.220	0.094	2
~*Mycoplasma*	251.462	2.244	0.093	2
~Year	252.187	2.969	0.064	4

[a]LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; *Mycoplasma*: Infected, Uninfected, Unkown; Turk.Age: Adult, Juvenile; Study.Area: NW, S, NE, NC, WMD.
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

Table 16. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect pre-nesting home range size (PNHR) of GPS-marked wild turkey hens in Maine, USA. We modeled PNHR as a function of age of the turkey, study area, and disease infection status (LPDV, REV, and *Mycoplasma*) using linear regression. All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]
~*Mycoplasma*	173.762	0.000	0.720	2
~Year	176.720	2.959	0.164	3
~StudyArea	179.199	5.437	0.048	4
~1	180.438	6.676	0.026	1
~TurkAge	181.055	7.293	0.019	2
~LPDV	181.586	7.824	0.014	2
~REV	182.496	8.735	0.009	2

[a]LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; *Mycoplasma*: Infected, Uninfected, Unkown; Turk.Age: Adult, Juvenile; Study.Area: NW, S, NE, NC, WMD.
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

Table 17. Model selection results based on Akaike's Information Criterion (AIC) to determine which group covariates affect distance between winter and pre-nesting home ranges (SD) of GPS-marked wild turkey hens in Maine, USA. We modeled SD as a function of age of the turkey, study area, and disease infection status (LPDV, REV, and *Mycoplasma*) using linear regression. All models compared are shown.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]
~StudyArea	255.409	0.000	0.386	4
~REV	256.806	1.397	0.192	2
~1	257.429	2.020	0.141	1
~LPDV	257.747	2.338	0.120	2
~*Mycoplasma*	258.699	3.291	0.074	2
~TurkAge	258.728	3.319	0.073	2

[a]LPDV: Infected, Uninfected, Unkown; REV: Infected, Uninfected, Unkown; *Mycoplasma*: Infected, Uninfected, Unkown; Turk.Age: Adult, Juvenile; Study.Area: NW, S, NE, NC, WMD.
[b]Difference in AIC compared with the lowest AIC model score
[c]AIC model weight
[d]Number of model parameters
[e]Model Deviance

2.959; Table 17) showed that individuals with a positive REV status traveled 4.384 km (±2.560 km, p = 0.095) less than those with a negative status.

Brownian motion variance (σ_m^2) appeared to correspond with changes in seasonal movement behavior throughout the year (Figure 23). Using the average daily σ_m^2 calculated from full dBBMM assessment of home ranges for January through July, we identified 4 periods of distinct movement that appeared differed among years. The winter period was characterized by steady, low values for σ_m^2 as females made regular movements throughout relatively consistent winter home ranges. Females initiated movements from winter to nesting ranges in early April, when σ_m^2 values gradually increased for a relatively short period (~3 weeks). Females entered nesting home ranges during the last week of April, which was characterized by the greatest daily average σ_m^2 values as females established nest sites and began laying eggs. Average motion variance then gradually decreased as birds began incubation. In 2018, we observed an increase in σ_m^2 (the second peak in Figure 23) that was not observed in 2019. This second peak in 2018 may be associated with renesting attempts when nests hatched and females moved into their summer brood ranges, or as nests failed and females attempted a second nest. 2018 had a higher proportion of identified renesting attempts by GPS marked hens compared to 2019, which may explain the lack of a pronounced peak in σ_m^2 during the second year. We observed an early, small peak σ_m^2 in late March 2020 that preceded a larger peak more indicative of seasonal movements. This could indicate an early phase of movements by individuals related to milder winter conditions during 2020. During July, the beginning of the summer brood rearing season, σ_m^2 values began to level off at values slightly higher than winter but lower than peak movement times during pre-nesting.

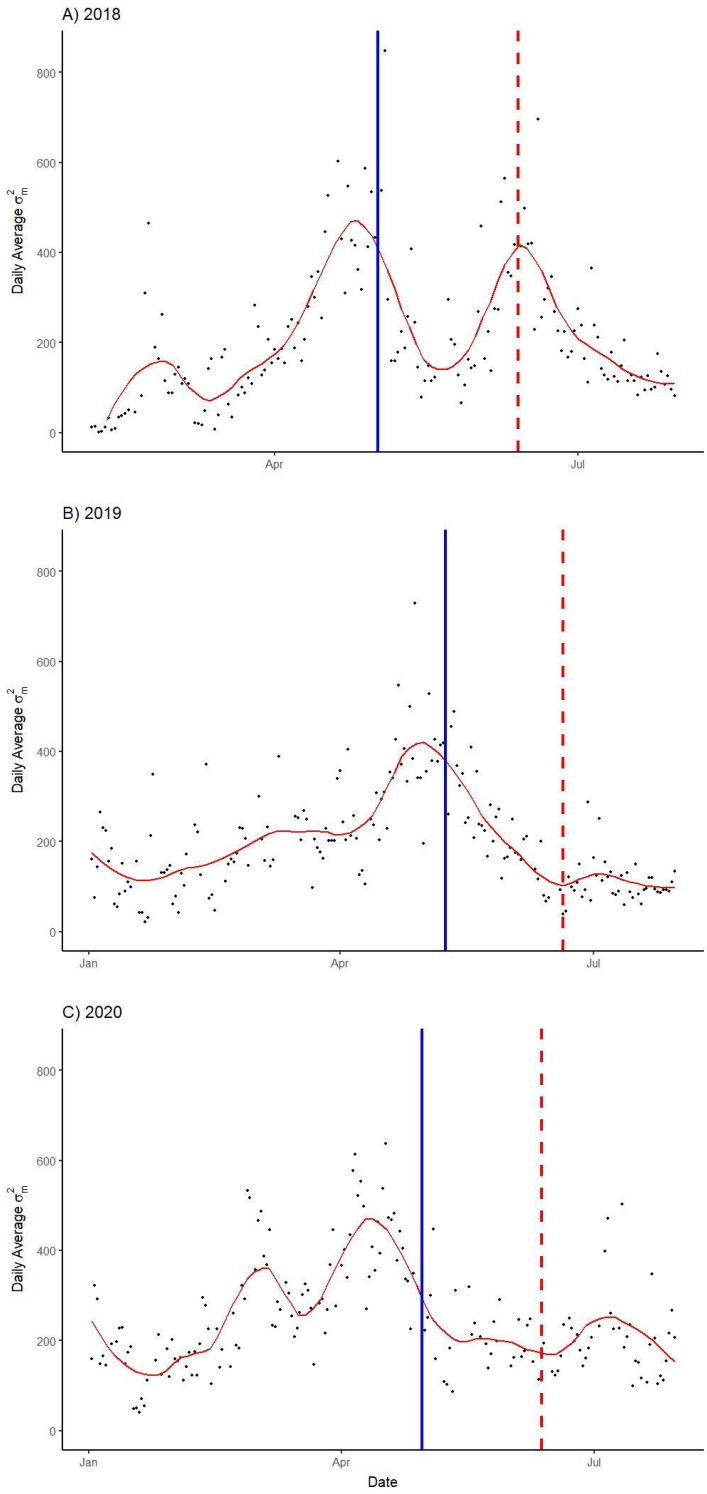


Figure 23. Daily average Brownian Motion Variance (σ_m^2), by date, for wild turkey hens in Maine, USA, from January 1 through July 31 in 2018 through 2020. σ_m^2 was derived using dynamic Brownian Bridge Movement Models. σ_m^2 are presented with a spline trend line, and vertical lines indicate mean nest initiation (blue solid) and mean estimated hatch (red dashed) dates.

Pathogen Infection and Coinfection Prevalence

We found an overall prevalence of 56.5% (354/627) for LPDV infection, 17.2% (108/627) for REV infection, 74.5% (175/235) for *Mycoplasma* exposure, and 3.4% (8/235) for *Salmonella* exposure. Pearson's chi-squared test was used to analyze whether the rate of infection with any two pathogens was correlated but we not find any evidence to support this for LPDV and REV infection ($\chi^2_1 = 1.94$, $n = 627$, $p = 0.164$), with 10.8% (68/627) coinfected with both, or for LPDV infection and *Mycoplasma* exposure ($\chi^2_1 = 0.34$, $n = 235$, $p = 0.558$), with 51.1% (120/235) coinfected with both (Table 18). However, infection with REV was correlated with exposure to *Mycoplasma* ($\chi^2_1 = 5.585$, $n = 235$, $p = 0.018$), with 16.2% (38/235) infected with both pathogens (Table 18). Exploration of this relationship via logistic regression revealed that exposure to *Mycoplasma* was negatively correlated with REV ($\beta = -0.81 \pm 0.32$, $p = 0.012$; Figure 24). Twenty-five turkeys (10.6%, $n = 235$) were infected with all three pathogens (LPDV, REV, *Mycoplasma*). We could not include *Salmonella* in this analysis due to the small sample size of positive individuals. Descriptively however, of the eight individuals infected with *Salmonella*, one was solely infected with *Salmonella*, two were coinfected with LPDV, one was coinfected with only *Mycoplasma*, and four were infected with both LPDV and *Mycoplasma*. Therefore, of the those infected with *Salmonella*, 87.5% (7/8) were coinfected with at least one other pathogen (Table 18). No individual exposed to *Salmonella* was infected with REV (Table 18), and, subsequently, no turkey was infected with all four pathogens (LPDV, REV, *Mycoplasma*, *Salmonella*). Prevalence of *Salmonella* was too low to include in statistical analysis, but, descriptively, prevalence was greater in adults (7/159, 4.4%) than juveniles (1/76, 1.3%) and greater in females (8/150, 5.3%) than males (0/85, 0%). Adult females comprised 87.5% (7/8) of those infected while juvenile females

comprised 12.5% (1/8) of those infected. Prevalence decreased by year from 5.9% (5/85) in 2018 to 3.3% (3/91) in 2019 to 0% (0/59) in 2018.

Risk Factors of Pathogen Infection

LPDV: We found that age, sex, year, and region were significant factors in predicting LPDV infection (Tables 19 and 20; Figures 25–28). Adults were 4.7x (95% CI: 3.2–6.9) more likely to be infected with LPDV than juveniles, with adults experiencing a higher prevalence (71.1% vs. 34.8%; Tables 20 and 21, Figure 25). Females were 1.5x (95% CI: 1.1–2.2) more likely to be infected with LPDV than males, with females experiencing a higher prevalence (64.1% vs. 46.7%; Tables 20 and 21, Figure 26). An individual captured in 2018 was 4.2x (95% CI: 1.8–9.9), and an individual captured in 2019 was 2.1x (95% CI: 1.3–3.6) more likely to be infected with LPDV than an individual captured in 2020 (Table 20). Prevalence of LPDV decreased from 77.5% (95% CI: 67.8–85.0%) in 2018 to 54.3% (95% CI: 48.4–60.0%) in 2019 to 51.6% (95% CI: 45.5–57.6%) in 2020 (Table 21, Figure 27). Lastly, an individual captured in region C was 4.9x (95% CI: 1.1–22.1) more likely to be infected with LPDV than an individual captured in region D, with a prevalence of 68.4% (95% CI: 52.5–80.9%) in region C versus 47.2% (95% CI: 34.4–60.3%) in region D (Tables 20 and 21; Figure 28). Though not significant, there was model support for infection with REV, percent agriculture cover, and percent forested cover for inclusion in the final model (Table 19). Though the previous chi-squared analysis did not show any correlation between LPDV and REV when assessed independently, this particular analysis also takes into account the effect of all other variables included in the model. There was no model support for percent developed cover. WMD and density were removed due to correlation and multicollinearity, respectively. The likelihood ratio test supported model fit of the final model ($\chi^2_{13} = 139.3$, $p < 0.001$).

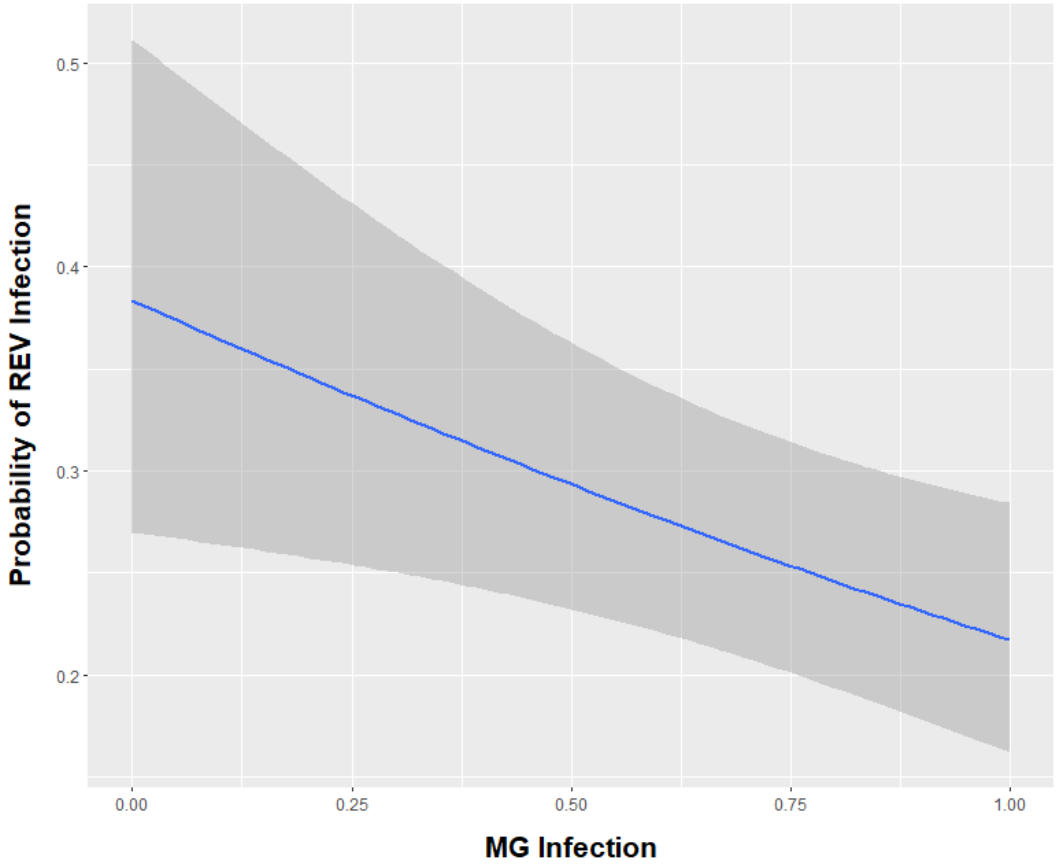


Figure 24. Effect of *Mycoplasma* exposure on infection with REV in turkeys sampled from 2018 to 2020 in Maine.

Table 18. Coinfection prevalence of live-captured turkeys sampled from 2018 to 2020 in Maine of lymphoproliferative disease virus (LPDV), reticuloendotheliosis virus (REV), *Mycoplasma gallisepticum* (*Mycoplasma*), and *Salmonella pullorum* (*Salmonella*). Coinfection prevalence with 3 pathogens was 10.6% (25/235) and coinfection prevalence with all 4 pathogens was 0%.

Pathogen 1	**Pathogen 2**	**# Coinfected**	**Total**	**Coinfection Prevalence**
LPDV	REV	68	627	10.8%
LPDV	*Mycoplasma*	120	235	51.1%
LPDV	*Salmonella*	6	235	2.6%
REV	*Mycoplasma*	38	235	16.2%
REV	*Salmonella*	0	235	0.0%
Mycoplasma	*Salmonella*	5	235	62.5%

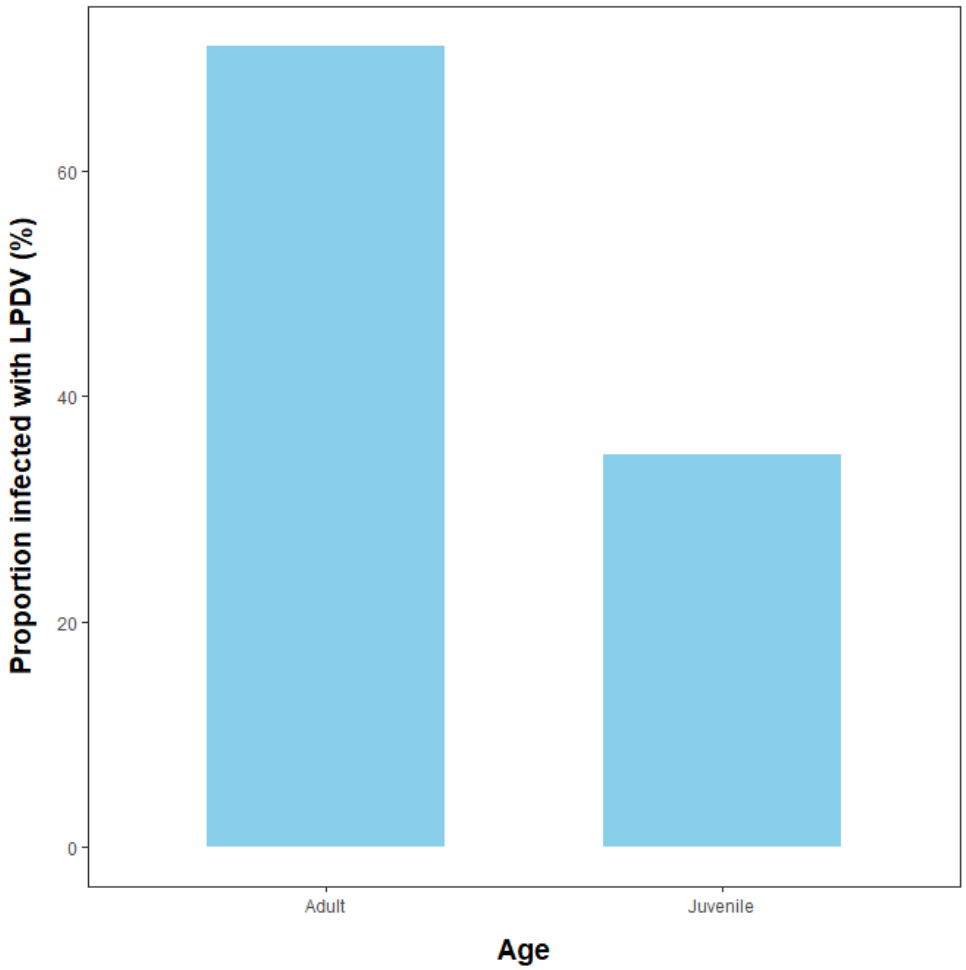


Figure 25. Prevalence of LPDV by age in turkeys sampled from 2018 to 2020 in Maine.

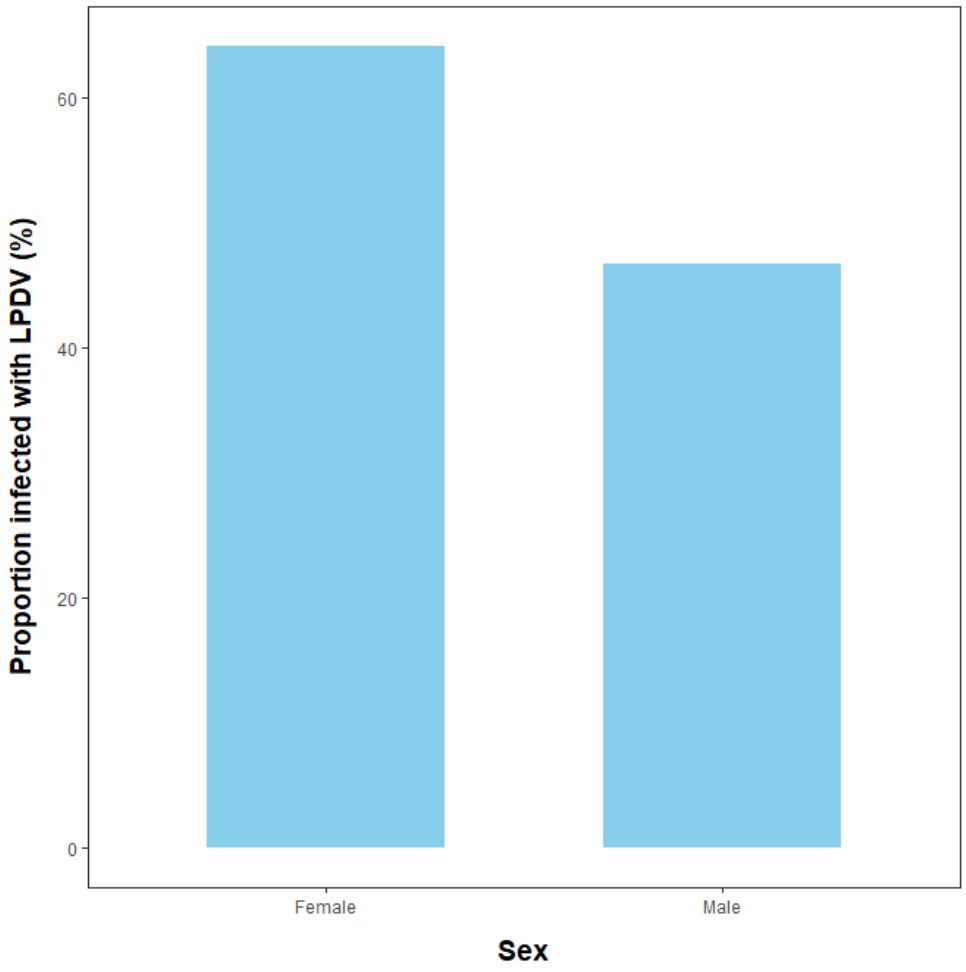


Figure 26. Prevalence of LPDV by sex of turkeys sampled from 2018 to 2020 in Maine.

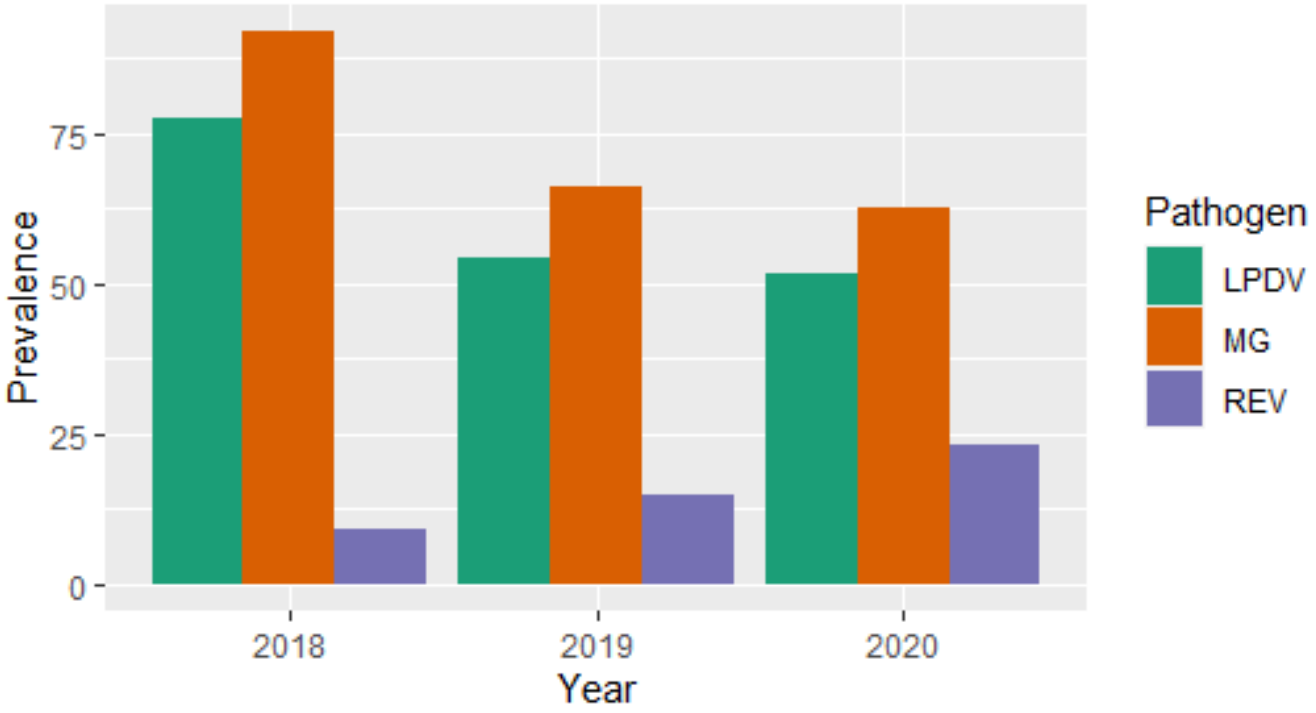
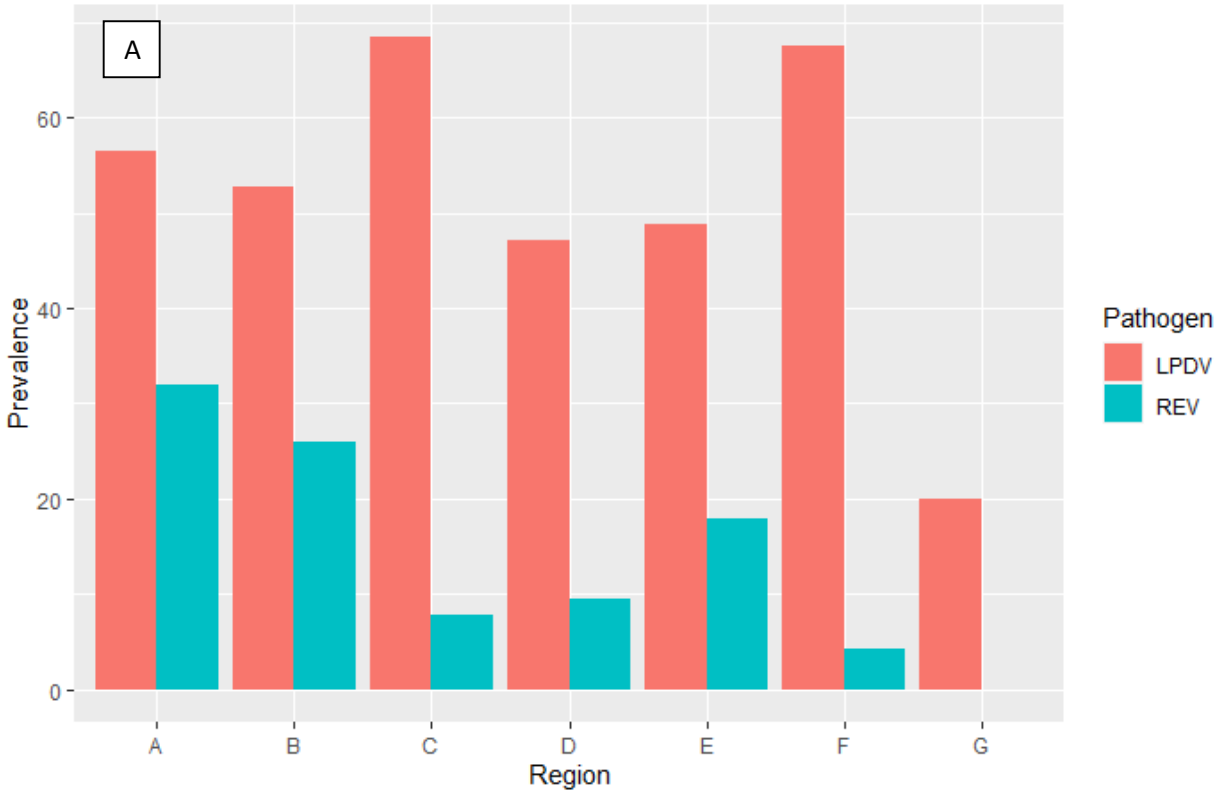


Figure 27. Prevalence of LPDV, REV, and *Mycoplasma* by year in turkeys sampled from 2018 to 2020 in Maine.



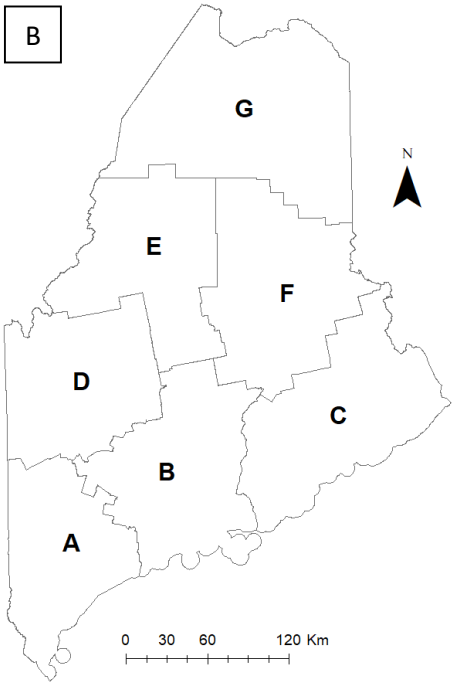


Figure 28. (A) Prevalence of LPDV and REV by region of collection in turkeys sampled from 2018 to 2020 in Maine. (B) Geographic location of each region in Maine.

Table 19. Model selection results based on Akaike's Information Criterion (AIC) to determine which risk factors are predictors of lymphoproliferative disease virus (LPDV) infection in turkeys sampled from 2018 to 2020 in Maine.

Model[a]	**AICc**	**AICc**	**ΔAICc**[b]	***w***[c]	**K**[d]
~Age	780.524	0.000	1	2	-388.252
~WMD	841.235	60.711	6.56E-14	11	-409.403
~Sex	843.745	63.221	1.87E-14	2	-419.863
~Year	844.398	63.874	1.35E-14	3	-419.18
~Agriculture	847.188	66.664	3.34E-15	2	-421.584
~Forested	849.368	68.844	1.12E-15	2	-422.675
~Region	849.567	69.043	1.02E-15	7	-417.693
~Density	858.948	78.424	9.34E-18	2	-427.464
~REV	860.461	79.937	4.38E-18	2	-428.221
~Null	860.720	80.196	3.85E-18	1	-429.357
~Developed	862.702	82.178	1.43E-18	2	-429.341

[a]Age: Adult, Juvenile; Sex: Male, Female; WMD: Wildlife Management District of collection; Region: region of collection; Year: Year of collection; Agriculture: percent Agriculture cover based on capture site location; Forested: percent forested cover based on capture site location; Developed: percent developed cover based on capture site location; Density: Density at the WMD scale; REV: reticuloendotheliosis virus infection status.
[b]Difference in AIC compared with the lowest AIC model score.
[c]AIC model weight.
[d]Number of model parameters.
[e]Model log likelihood.

Table 20. Variables included in top model as risk factors for lymphoproliferative disease virus infection in turkeys sampled from 2018 to 2020 in Maine based on Akaike's Information Criterion (AIC).

Variable	Level	Beta ± SE	Odds Ratio (95% CI)	Z value or ratio	P value
Age	Adult	1.5521 ± 0.193	4.717 (3.245–6.920)	8.04	<0.001[b]
Agriculture	NA	-0.0204 ±0.012	0.980 (0.958–1.002)	-1.777	0.076
Forested	NA	0.009 ± 0.007	1.009 (0.996–1.022)	1.372	0.17
Region[a]	C-D	1.586 ± 0.512	4.885 (1.078–22.131)	3.095	0.032[b]
REV	NA	0.355 ± 0.258	1.426 (0.864– 2.376)	1.378	0.168
Sex	Male	-0.425 ± 0.189	0.654 (0.451–0.948)	-2.247	0.025[b]
Year[a]	2020-2018	1.429 ± 0.365	4.175 (1.774–9.875)	3.913	<0.001[b]
	2020-2019	0.753 ± 0.224	2.123 (1.255–3.597)	3.356	0.002[b]

[a]Significant (p<0.05) contrasts of multi-level variables using R package emmeans (Lenth 2020).
[b]Indicates significance (p<0.05).

Table 21. Lymphoproliferative disease virus (LPDV) prevalence for significant contrasts from top model for risk factors predicting LPDV infection in turkeys sampled from 2018 to 2020 in Maine based on Akaike's Information Criterion (AIC). Prevalence and 95% Confidence Intervals calculated using the Wilson method within the R package binom (Dorai-Raj 2014).

Variable	Class	Positive	Sample Size	Prevalence	95% CI
Overall	NA	354	627	56.50%	52.6–60.3%
Age	Adult	88	374	71.10%	66.3–75.5%
	Juvenile	266	253	34.80%	29.2–40.8%
Region	C	26	38	68.40%	52.5–80.9%
	D	25	53	47.20%	34.4–60.3%
Sex	Female	225	351	64.10%	56.0–68.9%
	Male	129	276	46.70%	40.9–52.6%
Year	2018	69	89	77.50%	67.8–85.0%
	2019	152	280	54.30%	48.4–60.0%
	2020	133	258	51.60%	45.5–57.6%

REV: We identified that infection with LPDV, region of collection and year of collection are significant risk factors predicting REV infection (Tables 22 and 23, Figures 27–29). Individuals infected with LPDV were 1.7x (95% CI: 1.0–2.8) more likely to be infected with REV than those not infected with LPDV (Tables 23, Figure 29). Individuals infected with LPDV (n = 354) had an REV prevalence of 19.2% (95% CI: 15.4–23.6%), while individuals not infected with LPDV (n = 273) had an REV prevalence of 14.7% (95% CI: 11.0–19.3%; Table 24). Turkeys sampled in region A were 5.4–15.7x more likely to be infected than those sampled in regions C, D, E, and F, and turkeys sampled in region B were 6.8x (95% CI: 1.0–45.6) and 7.7x (95% CI: 2.2–27.1) more likely to be infected than regions C and F, respectively (Tables 23 and 24, Figure 28). Turkeys captured and sampled in 2020 were 4.5x (95% CI:1.4–14.7) and 2.7x (95% CI:1.4–5.1) as likely to be infected with LPDV than those captured in 2018 and 2019, respectively (Tables 23 and 24, Figure 27). Variation in prevalence across the three years ranged from 9.0 to 22.9% and variation in prevalence by region ranged from 4.2 to 31.9% (Table 24, Figures 27 and 28, respectively). There was model support for age and percent developed cover, but these variables were not significant (Table 22). No variables were correlated, but density was removed due to multicollinearity. The likelihood ratio test supported model fit of the final model (χ^2_{11} = 84.9, $p < 0.001$).

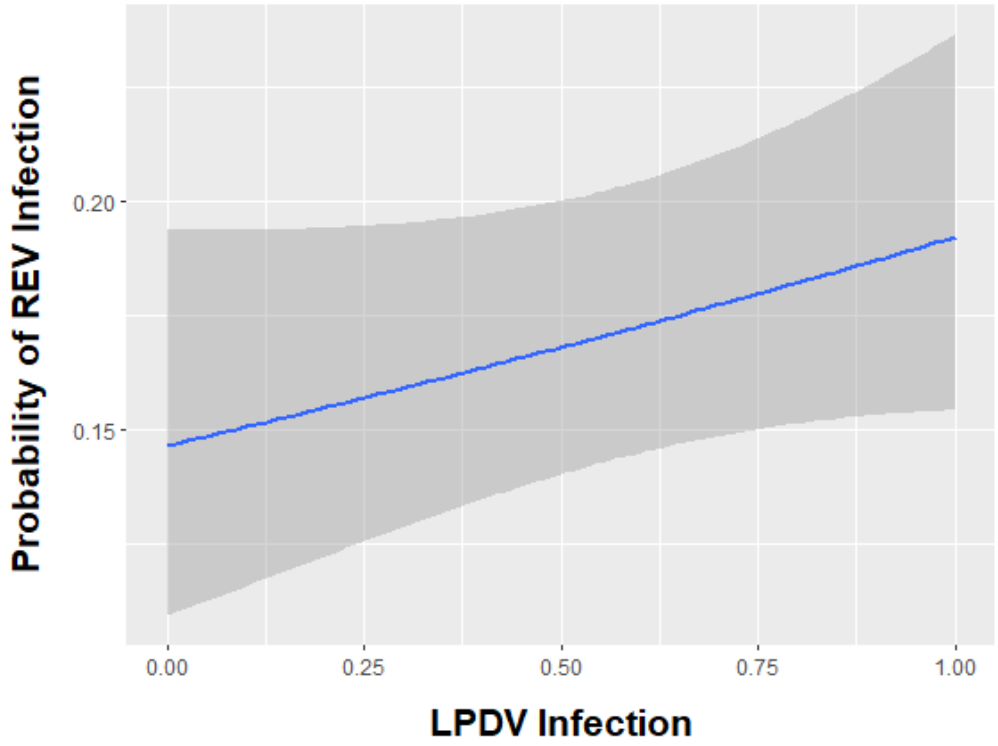


Figure 29. Effect of LPDV infection on infection with REV in turkeys sampled from 2018 to 2020 in Maine.

Table 22. Model selection results based on Akaike's Information Criterion (AIC) to determine which risk factors are predictors of reticuloendotheliosis virus (REV) infection in turkeys sampled from 2018 to 2020 in Maine.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	LL[e]
~WMD	527.443	0.000	0.908859	11	-252.507
~Region	532.042	4.600	0.091141	7	-258.931
~Density	562.097	34.654	2.71E-08	2	-279.039
~Year	570.506	43.063	4.05E-10	3	-282.234
~Developed	574.268	46.825	6.17E-11	2	-285.124
~Age	577.431	49.988	1.27E-11	2	-286.706
~LPDV	577.878	50.436	1.02E-11	2	-286.93
~Null	578.137	50.694	8.92E-12	1	-288.065
~Agriculture	578.521	51.078	7.36E-12	2	-287.251
~Sex	580.042	52.599	3.44E-12	2	-288.011
~Forested	580.130	52.688	3.29E-12	2	-288.055

[a]Age: Adult, Juvenile; Sex: Male, Female; WMD: Wildlife Management District of collection; Region: region of collection; Year: Year of collection; Agriculture: percent Agriculture cover based on capture site location; Forested: percent forested cover based on capture site location; Developed: percent developed cover based on capture site location; Density: Density at the WMD scale; LPDV: lymphoproliferative disease virus infection status.
[b]Difference in AIC compared with the lowest AIC model score.
[c]AIC model weight.
[d]Number of model parameters.
[e]Model log likelihood.

Table 23. Variables included in top model as risk factors for reticuloendotheliosis virus infection in turkeys sampled from 2018 to 2020 in Maine based on Akaike's Information Criterion (AIC).

Variable	Level	Beta ± SE	Odds Ratio (95% CI)	Z value or ratio	P value
Age	Male	0.306 ± 0.258	1.358 (0.822–2.263)	1.186	0.236
Developed	NA	0.008 ± 0.008	1.008 (0.992–1.024)	1.073	0.283
LPDV	Positive	0.503 ± 0.257	1.654 (1.005–2.754)	1.961	0.0499[b]
Region[a]	A–C	2.633 ± 0.714	13.915 (1.696–114.43)	3.688	0.004[b]
	A–D	1.929 ± 0.582	6.883 (1.238–38.475)	3.314	0.016[b]
	A–E	1.694 ± 0.555	5.441 (1.006–27.938)	3.053	0.037[b]
	A–F	2.751 ± 0.491	15.658 (3.670–66.686)	5.605	<0.001[b]
	B–C	1.917 ± 0.645	6.801 (1.016–45.604)	2.973	0.047[b]
	B–F	2.035 ± 0.429	7.652 (2.158–27.113)	4.471	<0.001[b]
Year[a]	2018–2020	-1.495 ± 0.508	0.224 (0.068–0.738)	-2.941	0.009[b]
	2019–2020	-0.993 ± 0.266	0.370 (0.198–0.690)	-3.74	0.001[b]

[a]Significant (p<0.05) contrasts of multi-level variables using R package emmeans (Lenth 2020).
[b]Indicates significance (p<0.05).

Table 24. Prevalence of reticuloendotheliosis virus (REV) for significant contrasts from top model for risk factors predicting REV infection in turkeys sampled from 2018 to 2020 in Maine based on Akaike's Information Criterion (AIC). Prevalence and 95% Confidence Intervals calculated using the Wilson method within the R package binom (Dorai-Raj 2014).

Variable	Class	Positive	Sample Size	Prevalence	95% CI
Overall	NA	108	627	17.20%	14.5–20.3%
LPDV	Positive	68	354	19.20%	15.4–23.6%
	Negative	40	273	14.70%	11.0–19.3%
Region	A	22	69	31.90%	22.1–43.6%
	B	64	247	25.90%	20.8–31.7%
	C	3	38	7.90%	2.7–20.8%
	D	5	53	9.40%	4.1–20.3%
	E	7	39	17.90%	9.0–32.7%
	F	7	166	4.20%	2.1–8.4%
Year	2018	8	89	9.00%	4.6–16.7%
	2019	41	280	14.60%	11.0–19.3%

Mycoplasma: Year of collection was the only factor considered a significant predictor of *Mycoplasma* infection and the only factor that received model support (Tables 25 and 26). A turkey captured and sampled in 2018 was 5.7x (95% CI: 2.5–15.0) and 6.6x (95% CI: 2.7–18.2) more likely to be infected than a turkey sampled in 2019 and 2020, respectively (Table 26). Prevalence of *Mycoplasma* decreased from 87.6% (95% CI: 79.2–93.0%) in 2018 to 21.4% (95% CI: 17.0–26.6%) in 2019 to 14.3% (95% CI: 10.6–19.1%) in 2020 (Table 27, Figure 27). There was model support for infection with REV and percent forested cover along with year of collection, but year of collection performed better on its own then with REV and percent forested cover. The likelihood ratio test supported model fit of the final model ($\chi^2_2 = 24.0$, $p < 0.001$).

Flock Size: While there was support for including flock size in models predicting both LPDV and REV infection, for both models it was not significant and did not perform better than the null model in predicting *Mycoplasma* exposure (Tables 28–30). Therefore, we cannot conclude that local density, as indexed by flock size, resulted in greater risk of pathogen infection.

Cloacal Swabs as an LPDV Detection Method

Cloacal swab samples collected from live-captured (n=85) turkeys had a sensitivity of 88% and specificity of 75% compared with blood, while swab samples collected from hunter-harvested turkeys (n=54) had a sensitivity of 31% and specificity of 80% compared with bone marrow (Table 31). When we compared swab samples collected during live-capture with coupled blood samples, we found a moderate level of agreement (k = 0.60, 0.38–0.81 95% CI) beyond agreement due to chance. A significant Z-test revealed that this kappa statistic is different from zero (Z = 5.52, $p < 0.001$). Additionally, there was no significant difference

Table 25. Model selection results based on Akaike's Information Criterion (AIC) to determine which risk factors are predictors of *Mycoplasma gallisepticum* infection in turkeys sampled from 2018 to 2020 in Maine.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	LL[e]
~Year	249.149	0.000	0.999215	3	-121.522
~REV	264.958	15.809	0.000369	2	-130.453
~Forested	266.084	16.935	0.00021	2	-131.016
~Null	269.026	19.877	4.82E-05	1	-133.504
~Agriculture	270.374	21.225	2.46E-05	2	-133.161
~Developed	270.416	21.267	2.41E-05	2	-133.182
~Region	270.433	21.284	2.39E-05	3	-132.164
~LPDV	270.511	21.362	2.30E-05	2	-133.229
~Sex	270.553	21.404	2.25E-05	2	-133.251
~Age	270.802	21.654	1.98E-05	2	-133.375
~Density	270.919	21.770	1.87E-05	2	-133.433
~WMD	276.663	27.514	1.06E-06	5	-133.2

[a]Age: Adult, Juvenile; Sex: Male, Female; WMD: Wildlife Management District of collection; Region: region of collection; Year: Year of collection; Agriculture: percent Agriculture cover based on capture site location; Forested: percent forested cover based on capture site location; Developed: percent developed cover based on capture site location; Density: Density at the WMD scale; REV: reticuloendotheliosis virus infection status; LPDV: lymphoproliferative disease virus infection status.
[b]Difference in AIC compared with the lowest AIC model score.
[c]AIC model weight.
[d]Number of model parameters.
[e]Model log likelihood.

Table 26. Variables included in top model as risk factors for *Mycoplasma gallisepticum* infection in turkeys sampled from 2018 to 2020 in Maine based on Akaike's Information Criterion (AIC).

Variable	Level	Beta ± SE	Odds Ratio (95% CI)	Z value or ratio	P value
Year[a]	2019-2018	-1.750 ± 0.452	0.174 (0.067–0.401)	-3.87	<0.001[b]
	2020-2018	-1.891 ± 0.478	0.151 (0.055–0.369)	-3.959	0.002[b]

[a]Full model did not perform better than year alone.
[b]Indicates significance (p<0.05).

Table 27. *Mycoplasma gallisepticum* (*Mycoplasma*) prevalence for significant contrasts from top model for risk factors predicting *Mycoplasma* infection in turkeys sampled from 2018 to 2020 in Maine based on Akaike's Information Criterion (AIC). Prevalence and 95% Confidence Intervals calculated using the Wilson method within the R package binom (Dorai-Raj 2014).

Variable	Class	Positive	Sample Size	Prevalence	95% CI
Overall	NA	175	235	74.5%	68.5–79.6%
Year	2018	78	89	87.6%	79.2–93.0%
	2019	60	280	21.4%	17.0–26.6%
	2020	37	258	14.3%	10.6–19.1%

Table 28. Model selection results based on Akaike's Information Criterion (AIC) to determine if flock size is a predictor of lymphoproliferative disease infection in a subset of turkeys containing flock size data sampled from 2018 to 2020 in Maine.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	LL[e]
~Age	652.590	0.000	1	2	-324.28
~Agriculture	688.882	36.292	1.32E-08	2	-342.43
~Sex	695.380	42.791	5.11E-10	2	-345.68
~WMD	696.834	44.244	2.47E-10	11	-337.15
~Forested	704.086	51.496	6.57E-12	2	-350.03
~Region	704.376	51.786	5.69E-12	7	-345.08
~REV	706.325	53.735	2.15E-12	2	-351.15
~Density	707.493	54.904	1.20E-12	2	-351.73
~Flock Size	707.589	54.999	1.14E-12	2	-351.78
~Null	707.723	55.133	1.07E-12	1	-352.86
~Year	709.034	56.444	5.54E-13	2	-352.51
~Developed	709.580	56.990	4.21E-13	2	-352.78

[a]Age: Adult, Juvenile; Sex: Male, Female; WMD: Wildlife Management District of collection; Region: region of collection; Year: Year of collection; Agriculture: percent Agriculture cover based on capture site location; Forested: percent forested cover based on capture site location; Developed: percent developed cover based on capture site location; Density: Density at the WMD scale; REV: reticuloendotheliosis virus infection status.
[b]Difference in AIC compared with the lowest AIC model score.
[c]AIC model weight.
[d]Number of model parameters.
[e]Model log likelihood.

Table 29. Model selection results based on Akaike's Information Criterion (AIC) to determine if flock size is a predictor of reticuloendotheliosis virus infection in a subset of turkeys containing flock size data sampled from 2018 to 2020 in Maine.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	LL[e]
~WMD	433.743	-	0.999956	11	-205.607
~Region	453.800	20.057	4.41E-05	7	-219.789
~Density	474.101	40.358	1.72E-09	2	-235.039
~Year	487.819	54.076	1.81E-12	2	-241.898
~Age	488.108	54.365	1.57E-12	2	-242.042
~Flock Size	490.890	57.147	3.90E-13	2	-243.433
~Developed	491.196	57.453	3.34E-13	2	-243.586
~LPDV	491.413	57.669	3.00E-13	2	-243.695
~Null	492.811	59.067	1.49E-13	1	-245.401
~Agriculture	493.466	59.722	1.08E-13	2	-244.721
~Forested	493.809	60.066	9.05E-14	2	-244.893
~Sex	494.613	60.870	6.06E-14	2	-245.295

[a]Age: Adult, Juvenile; Sex: Male, Female; WMD: Wildlife Management District of collection; Region: region of collection; Year: Year of collection; Agriculture: percent Agriculture cover based on capture site location; Forested: percent forested cover based on capture site location; Developed: percent developed cover based on capture site location; Density: Density at the WMD scale; LPDV: lymphoproliferative disease virus infection status.
[b]Difference in AIC compared with the lowest AIC model score.
[c]AIC model weight.
[d]Number of model parameters.
[e]Model log likelihood.

Table 30. Model selection results based on Akaike's Information Criterion (AIC) to determine if flock size is a predictor of *Mycoplasma gallisepticum* infection in a subset of turkeys containing flock size data sampled from 2018 to 2020 in Maine.

Model[a]	AICc	ΔAICc[b]	*w*[c]	K[d]	LL[e]
~Sex	196.334	0.000	0.161	2	-96.126
~REV	196.621	0.288	0.140	2	-96.270
~Null	196.873	0.539	0.123	1	-97.423
~Flock Size	197.117	0.783	0.109	2	-96.518
~Agriculture	197.304	0.971	0.099	2	-96.611
~Developed	198.037	1.704	0.069	2	-96.978
~Forested	198.638	2.304	0.051	2	-97.278
~Region	198.708	2.374	0.049	3	-96.272
~Year	198.765	2.432	0.048	2	-97.342
~Density	198.885	2.552	0.045	2	-97.402
~Age	198.887	2.554	0.045	2	-97.403
~LPDV	198.896	2.562	0.045	2	-97.407
~WMD	201.013	4.679	0.016	5	-95.298

[a]Age: Adult, Juvenile; Sex: Male, Female; WMD: Wildlife Management District of collection; Region: region of collection; Year: Year of collection; Agriculture: percent Agriculture cover based on capture site location; Forested: percent forested cover based on capture site location; Developed: percent developed cover based on capture site location; Density: Density at the WMD scale; REV: reticuloendotheliosis virus infection status; LPDV: lymphoproliferative disease virus infection status.
[b]Difference in AIC compared with the lowest AIC model score.
[c]AIC model weight.
[d]Number of model parameters.
[e]Model log likelihood.

(McNemar = 0.69, $p = 0.41$) between prevalence based on cloacal swab samples (apparent prevalence; 73%) and prevalence based on blood (true prevalence; 76%; Table 31). However, paired samples between cloacal swabs and bone marrow collected from hunter-harvested individuals paint a different picture. There was no agreement beyond that due to chance (k = 0.07, −0.11–0.25 95% CI), between the two sample types in hunter-harvested individuals, and the kappa statistic was not significantly different than zero ($Z = 0.79$, $p = 0.21$). Furthermore, the McNemar test (McNemar = 19.20, $p < 0.001$) indicated there was a significant difference in the apparent prevalence (28%) estimated using cloacal swab assay results and the true prevalence (72%) estimated using bone marrow assay results (Table 31). Overall, cloacal swab samples from live-captured individuals had a significantly greater sensitivity to blood (88%) than swab samples from hunter-harvested did when compared with bone marrow (31%; $\chi_1^2 = 32.87$, n = 139, $p < 0.001$; Table 31). Alternatively, the specificities between live-capture and hunter-harvested collection methods did not differ ($\chi_1^2 < 0.001$, $n = 139$, $p = 1.00$; Table 31). Lastly, time between harvest and sampling did not affect the ability to detect a positive result using cloacal swab samples (β = −0.01, −0.04 – −0.00 95% CI, $n = 39$, $p = 0.12$).

Table 31. Metrics evaluating the detection of lymphoproliferative disease virus in Maine during 2017 and 2018 using cloacal swabs samples, compared with blood and bone marrow from live-captured or hunter-harvested wild turkey collection methods, respectively.

Metrics	**Live-captured**	**Hunter-harvested**
Sample size	85	54
Sensitivity	88%	31%
Specificity	75%	80%
Apparent prevalence	73%	28%
True prevalence	76%	72%

Conclusions and Future Directions

Band recovery and harvest

Thanks to increased trapping efforts supported by MDIFW regional offices, our final total of captured turkeys reached 890 unique individuals distributed throughout the state. This has also led to an increase in reported harvests of banded individuals, which will improve the precision of harvest rate and population size estimates. In 2018, we were unable to generate harvest estimates for all WMDs due to lack of captures in some WMDs, and low capture success and/or harvest in certain areas. With the increase in sample size and expanded trapping efforts into additional areas throughout Maine, combined with an improved statistical approach, wewere able to generate estimates of harvest rate and abundance for 2019 and 2020 in all but 5 northern WMDs with generally low turkey density.

From the 406 male turkeys we banded and released, we estimated age- and WMD-specific harvest rates that ranged from 0.065 to 0.277 during the 2018 through 2020 spring bearded turkey hunting seasons. Harvest rates tended to be higher in the southwest and decreased in more northern WMDs, although considerable variation was observed especially at the eastern state line. This may be attributed to a relatively smaller sample size in these WMDs compared to the southwestern WMDs. These recovery rate estimates account for mortality that occurs between banding and the hunting season by incorporating weekly survival rates estimated from telemetry data. While the assumption that negligible mortality occurs between banding and harvest has been found by some researchers to be generally valid (Diefenbach et al. 2012), we observed relatively large changes in estimates compared to our initial approach that did not account for such mortality. Estimates of harvest rate increased as we accounted for the loss of banded birds available that died prior to beginning of the hunting season, and were not available

to be harvested. When integrating this joint band recovery and telemetry model with a Lincoln Estimator, as expected the corrected harvest rate estimates translated to lower estimates of population size. We used our estimates of adult and juvenile harvest rates in combination with the number of harvested and reported turkeys provided by MDIFW to estimate statewide population size. We estimated Maine's total male turkey population as 31,677 in 2018, 32,512 in 2019, and 33,500 in 2020. Compared to estimates of statewide male turkey populations produced in 2019 that did not account for mortality between banding and harvest, we estimated 1,097 fewer individuals using these updated methods. Additionally, by accounting for spatial variation of harvest, we were better able to estimate harvest rates by WMD, especially where we had few or no banded individuals, which in turn allowed us to derive more precise WMD-specific estimates of abundance and density. Moving forward, these models can be incorporated into a more sophisticated adaptive harvest management tool that is tailored to deal with the localized management needs across Maine.

Survival

We found multiple factors had apparent influences on post-release mortality of wild turkeys following capture. The most significant difference in post-release survival was related to handling time, where turkeys that experienced longer handling times had lower post-release mortality rates. A previous study of wild turkeys in Oklahoma (Nicholson et al 2000) found an opposite relationship, where decreased handling time lead to lower post-release mortality. While we both followed similar methods for trapping and handling, the differences in climate between Oklahoma and Maine in the winter may have led to differing results. We also found that style of transmitter impacted post-release survival, with backpack transmitters showing lower survival than necklaces. Transmitter effects on avian species have been well documented (Barron et al

2010, Bernardo et al 2011), although how and to what degree an animal is affected can be variable depending on transmitter type and species' characteristics. Although turkeys primarily walk on the ground, their ability to quickly escape predators and roost at night are reliant on their ability to fly. If there is a period following capture during which flight abilities are compromised, turkeys may be more susceptible to predation as they acclimate to their transmitters. Comparatively, necklace style transmitters are much smaller and less obtrusive to turkeys, which may explain the lower mortalities rates post-release. We also identified an effect of temperature on post-release mortality, although the relationship was not clear. Individuals experiencing higher temperatures on the day of capture had lower initial survival rates but a higher overall survival rate. Nicholson et al (2000) identified humidity and ambient temperature as having an effect on mortality, possibly suggesting that birds are more affected by higher temperatures and humidity rather than lower. We found that adult post-release mortality was lower than that of juveniles, which has been observed in multiple studies of wild turkeys (Nicholson et al 2000, Spraker et al 1987).

We found evidence for variable survival rates throughout the year, with the greatest apparent decrease in survival occurring in May, which corresponded with peak nesting activity for hens based on our Brownian Motion Variance analysis. This decline in survival during the spring nesting season has been observed in other studies of wild turkeys (Kurzejeski et al 1987, Hubbard et al 1999) and likely is caused by increased vulnerability to predation of hens while nesting (Speake 1980). A recent study of ruffed grouse in Maine also found that female survival was substantially reduced during nesting (Mangelinckx et al. 2020), and it is likely that ground nesting birds are particularly vulnerable to predation, in general, during this period.

Pathogen dynamics

In addition, we found evidence that variation in survival rates can in part be explained by REV infection status. Reticuloendotheliosis virus is a geographically widespread avian retrovirus that has a broad host range including poultry and wild avian species (Brash et al. 2013). It generally occurs at a low prevalence in wild turkey populations, but prevalence varies across studies and geographic regions. Even on a localized scale within Maine, region of collection is a significant predictor of REV infection (Tables 21–23. Figure 28). Peterson et al. (2002) identified REV proviral DNA in two out of 70 (2.9%) apparently healthy turkeys in Texas, though there was a significant difference in body mass between infected and uninfected individuals. Alternatively, serology tests indicated 63% (15/24) of apparently healthy wild turkeys had been exposed to REV in southern Georgia (Ingram et al. 2015).

Reticuloendotheliosis virus can either be asymptomatic or can manifest in non-specific disease syndromes such as anemia, runting, neoplasia, and immunosuppression (Payne and Venugopal 2000). Oncogenic symptoms have been shown to increase in chickens upon additional pathogenic infections. For instance, secondary pathogen infection of REV-infected chickens can exacerbate the rate of tumor formation (Mays et al. 2012). Furthermore, secondary infection with REV has been shown to increase immunosuppressive effects of another avian retrovirus, avian leukoisis virus (ALV; Guo et al. 2010). Though ALV mostly infects chickens, it is closely related to LPDV since they share the same genus, *Alpharetrovirus*, and we found that infection with LPDV was identified as a significant predictor of REV infection (Tables 21–23, Figure 29). In other studies, REV was detected in 46% (19/41) of clinically ill, LPDV-infected wild turkeys submitted to veterinary diagnostic labs throughout 18 eastern states (Allison et al. 2014). Additionally, MacDonald et al. (2019*a*) found REV in 4% (5/119) of apparently healthy

LPDV-infected wild turkeys in Ontario, Canada. In comparison, we found that 19.2% of LPDV-infected turkeys and 14.7% of LPDV-uninfected turkeys were infected with REV. Therefore, it warrants investigation to determine if additive effects of coinfection occur in wild turkeys. To our knowledge, our findings are the first to conclude the negative effects of REV infection on survival of wild turkeys, though it has been shown to reduce reproductive output in experimentally infected Japanese quail (Barbosa et al. 2006). Reticuloendotheliosis virus infection also varied significantly by year in our study (Tables 21–23, Figure 27), suggesting that other factors that vary annually, such as weather, could impact infection probability.

Niemanis and Leighton (2004) deemed REV of little economic or ecological importance when assessing the health risk of translocating wild turkeys into Nova Scotia, Canada. However, it appears as though the effects of REV on wild turkeys may be more cryptic and complex than once thought, given the previous findings of immunosuppressive effects in chickens (Mays et al. 2012; Guo et al. 2010), negative reproductive effects in Japanese quail (Barbosa et al. 2006), and newfound survival effects in wild turkeys along with variability in infection rates across years. Additionally, wild turkeys can act as a reservoir for REV transmission to nearby poultry or captive breeding locations of other gamebirds or endangered species. Recently, wild turkeys were implicated as a reservoir host responsible for transmitting REV to a captive breeding facility for the endangered Attwater's Prairie Chickens, which was the cause of death in nearly 50% of the adult individuals (Stewart et al. 2019). Beyond the concern of REV infection in wild turkeys (especially regarding translocation campaigns), there is a risk of spillover to and negative impacts on other bird species, specifically poultry and other upland gamebirds.

LPDV is a neoplastic avian oncogenic retrovirus that was known to infect domestic turkeys in Europe and Israel before it was first identified in a wild turkey in Arkansas in 2009. A

subsequent survey of hunter-harvested wild turkeys from 17 states revealed an overall prevalence of 47%, with variation by state ranging 26–83% (Thomas et al. 2015). It was later found in Ontario with 65% prevalence (MacDonald et al. 2019*a*) and subsequently in Manitoba and Quebec with 35% prevalence (MacDonald et al. 2019*b*). While the majority of infected birds appear asymptomatic (Thomas et al. 2015), infection can cause skin lesions and lymphoid tumors in multiple organs (Biggs et al. 1978). Chickens have proven to be susceptible to LPDV in an experimental setting and LPDV has been linked with mortality of wild turkeys (Allison et al. 2014) and domestic turkeys (Biggs 1997), raising justifiable concern for spillover potential to backyard poultry farms and suggesting the disease could have negative effects on domestic and wild turkey population viability. The observed decrease in clutch size of infected individuals and the negative effect of LPDV infection on weekly survival combined with the large proportion of individuals infected (56.5%), supports previous claims that LPDV may influence wild turkey population dynamics. Additionally, LPDV prevalence was found to increase with turkey age and was found to be higher in females, which may impact population demographic structure and have a weighted negative effect at the population level since adults may contribute more to population growth via increased nesting rates, larger clutch sizes, and increased nest success rates (Paisley et al 1998, Norman et al 2001, Thogmartin and Johnson 1999), and females carry the majority of the burden associated with reproductive output. The increase in LPDV infection with age has been documented previously (Alger et al. 2017) and may indicate that turkeys are able to survive and harbor chronic pathogen infections, increasing the potential of exposure to others. The significant effects of region and year on LPDV infection indicate other factors may be at play including spatial variables such as land cover type (for which there was model support, but it was not found to be significant) and annual variation in weather. We plan to assess genetic

sequence data from LPDV-infected birds that will enable us to distinguish between LPDV strains and examine spatial clustering, data which may be used to describe potential transmission pathways.

Mycoplasma gallisepticum is a geographically widespread bacterial pathogen with a prevalence that varies across studies and geographic regions. The bacterium is mostly known to infect chickens and turkeys but has occurred in other species such as partridge, pheasants, quail, ducks, geese, and pigeons (Brash et al. 2013). It is considered to be one of the most costly diseases in the commercial poultry industry (Ley and Yoder 1997). It was first described in wild turkeys in 1982 as the cause of infectious sinusitis (Davidson et al. 1982), which affects the respiratory system and is easily spread through infectious aerosols and environmental contamination (Brash et al. 2013). *Mycoplasma* prevalence was 28% (200/724) in visibly healthy wild turkeys from 6 western states (Fritz et al. 1992), and seroprevalence was 80% (56/70) in wild turkeys in Texas (Peterson et al. 2002); whereas, 0% (0/44) of wild turkeys trapped in Arkansas for relocation were sero-negative (Hopkins et al. 1990). We found that exposure to MG best explains variation in pre-nesting home range size, where individuals with a positive MG status had a smaller pre-nesting home range size. Recently, the pathogen has been identified in house finches where it manifests as conjunctivitis and can cause mortality (Ley et al. 1996; Brash et al. 2013). Infected house finches were found to be less mobile and were more likely to be feeding alone than their uninfected counterparts (Dhondt et al. 2005; Hotchkiss et al. 2005). This may explain the negative relationship between MG exposure and REV infection, in that infection with MG reduces host movement and, subsequently, exposure probability to other pathogens. This is a two-way street because host behaviors such as movement and social interaction can

drive disease establishment, persistence, and spread, while disease itself can dictate host movement and social interaction.

We found a low overall prevalence of *Salmonella* exposure (3.4%) in our wild turkeys, which decreased by year from 5.9% (5/85) in 2018 to 3.3% (3/91) in 2019 to 0% (0/59) in 2018. *Salmonella pullorum* is a bacterial pathogen with a small host range, rarely causing disease in species besides chickens and turkeys (Shivaprasad 1997), though other species are susceptible (Niemanis and Leighton 2004). Peterson et al. (2002) reported 0% exposure to *Salmonella* in 70 live-captured wild turkeys in Texas, and Hopkins et al. (1990) found 0% (0/44) exposure in live-captured individuals trapped in Arkansas for relocation purposes. However, six of 249 (2.4%), one of 24 (4.2%), one of 47 (2.1%), eight of 292 (2.7%) and 19 of 524 (3.6%) turkeys were seropositive for *Salmonella* in Texas (Hensley and Cain 1979), Georgia and Florida (Ingram et al. 2015), Kansas (Crupper and Applegate 2002), South Dakota, and California, respectively (Charlton 2000). The health risk of *Salmonella* to wild turkeys remains low due to low prevalence, but continued surveillance is warranted because prevalence appears to vary by year. Furthermore, risk of transmission from wild turkeys to poultry is a concern because outbreaks of *Salmonella* are economically devastating to poultry industries (commercial or backyard; Niemanis and Leighton 2004). However, wild turkeys had lower *Salmonella* exposure than backyard turkeys in California (Charlton 2000), justifying concern for risk of transmission from poultry to wild turkeys.

We found that pathogen prevalence (or sero-prevalence) varied by year, warranting continued surveillance to track annual changes. Pathogen data will be valuable for predicting disease outbreaks and for satisfying MDIFW's objective to explore turkey population models that include the effects of disease on vital rates. It is additionally critical to monitor for these four

pathogens because they are generally outwardly asymptomatic, allowing them to go undetected. In sum, we recommend continued pathogen monitoring for the following purposes: (1) during health assessments for translocation campaigns, (2) to assess risk of and identify hotspots for spillover to or from poultry operations and captive breeding facilities, (3) in other wild species to track the host range for each pathogen, and (4) to determine risk to humans as human-wildlife interactions continue to increase.

We assessed whether cloacal swabs could be used as an alternate sample type than either blood or bone marrow to detect LPDV in live-captured or hunter-harvested turkeys, respectively, to reduce personnel and time requirements of LPDV surveillance. Ultimately, based on specificity and sensitivity, cloacal swabs can be used as an efficient and low-cost sample type for live-captured individuals, but not for hunter-harvested individuals. We did not find a decrease in detection probability as time increased between harvest and sampling for hunter-harvested individuals. While it may be an artifact of sample size, the mechanism driving this difference remains unknown.

Movements and space use

Using GPS transmitters, we collected data on wild turkey hen locations which showed apparent variability in movement patterns among seasons and individuals. Moving forward, we plan to use this information in two capacities. First, we will incorporate landcover characteristics to identify potential sources of variation in movement throughout the year. We will identify sources of variation in probability of use within each season as well as seasonal movements across the landscape. Second, we will use individual variation in movement behavior to account for individual heterogeneity in nest survival. We will quantify movement variables including

seasonal movement distance, pre-nesting home range size, laying movements, movement phenology, and nesting home range fidelity to identify variation in individual hen nest success.

Our three years of data collection has afforded us insight into turkey population ecology through the integration of demographic, spatial ecology, harvest, landscape ecology, and disease ecology data to inform Maine Department of Inland Fisheries and Wildlife's goal to "maintain a healthy turkey population below biological carrying capacity while providing hunting and viewing opportunity." Now that we have completed data collection, translating what we have observed into applicable information on turkey ecology will enable us to better address MDIFW management goals.

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