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RESEARCH ARTICLE

Integrating fecal DNA and telemetry to estimate wildlife densities in anthropogenic landscapes

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Abstract

Density estimation is central to wildlife management efforts but can be challenging in anthropogenically-dominated landscapes due to small parcel sizes, access restrictions, and limited green space. Reliable density estimates are especially important for managing white-tailed deer (*Odocoileus virginianus*), whose high abundance in urbanized areas increases the need for accurate population assessments to guide management and reduce negative human–wildlife interactions. Herein, we evaluated (a) the use of a plot-based spatial capture-recapture sampling design to estimate deer density in developed landscapes and (b) if integrating telemetry data improved the precision or biological inferences of density estimates. We conducted fecal sampling at 2 study areas reflecting different characteristics of the urbanization gradient in Durham and eastern Orange counties, North Carolina: (1) rural (i.e., forested, large parcels) and (2) suburban (i.e., small parcels, limited continuous access, diversity of landscape features). We collected 223 fecal samples during a 3-week sampling period in July and September 2022, resulting in 157 individual deer detected (112 F:45 M). Rural densities were estimated at 54 deer/km^2 (95% CI = 35–84) and suburban densities at 75 deer/km^2 (95% CI = 48–117). Integrating telemetry data allowed estimation of sex-specific space use and densities,

which were not possible from fecal data alone; however, precision of total density estimates was similar across integrated and fecal-only analyses. Overall, our results highlighted key trade-offs inherent to plot-based spatial capture-recapture in suburban landscapes, most notably low recapture rates, accessibility challenges to maintain optimal trap spacing, and the importance of considering auxiliary data streams as part of the study design.

KEYWORDS

anthropogenic landscapes, density estimation, fecal DNA, North Carolina, *Odocoileus virginianus*, telemetry, white-tailed deer

Population density estimation is central to wildlife management efforts as population numbers are a baseline parameter for understanding how human activities and management strategies impact a focal species (Witmer 2005, Schaus et al. 2020). In anthropogenic landscapes, however, the ability to estimate density in using methods such as transect sampling or physical capture-recapture is increasingly difficult due to reduced green spaces, parcelization, and challenges of accessing private property (Fusaro et al. 2017, van Heezik and Seddon 2017, Young et al. 2019). As urbanization continues to increase across the globe, sampling methods need to be evaluated to provide researchers and managers with ecological, social, and logistically-feasible options when working in anthropogenic landscapes.

Non-invasive genetic sampling is an increasingly popular method for estimating wildlife population parameters (Waits and Paetkau 2005, Ferreira et al. 2018) and may help overcome challenges in anthropogenic landscapes. Non-invasive genetic sampling relies on extracting DNA from shed materials such as feces, hair, or feathers to produce genotypic data that can be used to identify individual animals across space and time (Gardner et al. 2009). Shed materials, and by extension individual animals, can be collected in high numbers without physical restraint or stress and provide data suitable to estimate density via standard capture-recapture or spatially explicit capture-recapture (SCR) frameworks (Williams et al. 2002, Royle et al. 2013). Genetic material can be collected at points (e.g., hair snare), small plots (e.g., searches for fecal material), or along transects, which creates flexibility for sampling in a variety of landscapes (Poutanen et al. 2019, Gurney et al. 2020, Rounsville et al. 2022).

Spatial capture-recapture frameworks using fecal DNA (fDNA) data provide flexible approaches to link individual-level data to population-level processes such as abundance, density, and demographic rates (Donihue and Lambert 2015, Royle et al. 2018, Miles et al. 2021, Theng et al. 2022). Spatial capture-recapture data collection can accommodate various sampling designs (e.g., point, plot, transect) and integrate auxiliary information (e.g., telemetry data), providing flexibility to design studies that reflect their objectives and study-specific logistical constraints (Royle et al. 2013). Obtaining adequate recaptures often remains a key challenge in SCR studies as low recapture rates can lead to low precision of density estimates (Greenspan et al. 2020, Schmidt et al. 2022). To overcome challenges of low recapture rates, integrating auxiliary data streams like trail cameras (Gopalaswamy et al. 2012, Brommer et al. 2021) and telemetry data (Furnas et al. 2018, Curtis 2020, Ruprecht et al. 2021) is increasingly used in SCR, with improvements to precision and biological inferences (Whittington et al. 2017).

White-tailed deer (*Odocoileus virginianus*; hereafter deer) are a generalist species that can occur at high densities across developed landscapes, driving the need for accurate abundance and density estimates to guide management and reduce negative human–deer interactions (Decker and Richmond 1995, Urbanek and

Nielsen 2013, Potratz et al. 2019, Curtis 2020). Density estimation of cervids using SCR often relies on transect-based sampling, where sign or genetic samples are collected along long (>500 m), continuous trails, roads, or similar features (e.g., Brinkman et al. 2011, Brazeal et al. 2017, Ebert et al. 2021, Braunstein et al. 2025). Multiple studies have now demonstrated that plot-based SCR sampling designs can also yield reliable estimates of ungulate abundance, including deer (e.g., Goode et al. 2014, Poutanen et al. 2019) and elk (*Cervus canadensis roosevelti;* Henk et al. 2022). Plot-based SCR designs involve repeated area-searches of spatially discrete plots that are distributed across a landscape according to a defined sampling scheme (e.g., random, stratified). Because plots can be small (e.g., <0.1 ha) and can be disjunct in space, these designs can alleviate logistical constraints common in developed areas where parcelization, heterogeneous land ownership, and limited access complicate long transect surveys. As such, plot-based SCR approaches using fDNA offer a flexible method for estimating abundance and density across urbanization gradients. However, tradeoffs in access, sampling effort, recapture rates, and the potential value of auxiliary data (e.g., telemetry) should be evaluated relative to the study system and species of interest.

Herein, we (1) evaluated the effectiveness of a plot-based fDNA SCR design for estimating deer density across an urbanization gradient and (2) tested whether integrating telemetry data into the fDNA SCR analysis improved the precision or biological interpretation of density estimates. While telemetry data alone cannot reliably estimate density/abundance, Ruprecht et al. (2021) found telemetry data improved fDNA estimates and precision when recaptures were low across multiple species. We applied these methods at 2 study areas representing different points along an urbanization gradient: one rural study area characterized by large, forested parcels, and one suburban area with smaller parcels, limited continuous access, and a mix of developed and undeveloped land. We predicted that (1) deer density would be higher in the suburban area, (2) plot-based fDNA sampling would provide broad access to the full mosaic of suburban landscape features (e.g., parks, greenways, parcels of varying sizes), and (3) low recapture rates would necessitate auxiliary telemetry data to improve precision and enable sex-specific density estimation. Together, we demonstrated an approach highlighting and overcoming key challenges and considerations for designing SCR studies in developed landscapes, including access constraints, trap spacing, recapture rates, and the potential benefits of integrating auxiliary data streams.

STUDY AREA

Our study was in Durham and eastern Orange counties, North Carolina (NC), in the Piedmont ecoregion (Figure 1). We had 2 study areas (~8.9 km^2 each): Eno River State Park (ER) and Umstead Road (UR). Eno River State Park was 1,748 ha and was primarily a forested property representing characteristics of a rural landscape (i.e., a single parcel of undeveloped land). The park had ~48 km of trails and several campgrounds with an average elevation of 167 m. In contrast, UR was a suburban study area (24 houses/km^2) with a mix of private and public lands and an average elevation of 117 m. Average annual precipitation in the region was 119 cm. Both areas contained mixed pine-hardwood forests with dense tree cover and sparse understory. Canopy trees included white oak (*Quercus alba*), hickory (*Carya* spp.), American sweetgum (*Liquidambar styraciflua*) and red maple (*Acer rubrum*). Midstory vegetation included flowering dogwood (*Cornus florida*), American holly (*Ilex opaca*) and sugar maple (*Acer saccharum*).

METHODS

We defined a plot as a 0.1-ha area, which was the approximate average size of a single parcel yard in the suburban study area. Within each study area, we arranged plots in a 2×2 formation (i.e., a cluster of 4 plots, hereafter cluster; Poutanen et al. 2019). Centroids for each cluster were randomly selected from a fishnet of 0.1-ha plots using ArcGIS Pro (version 2.9; Esri, Redlands, CA, USA) with a restriction of being at least 400 m apart. Plots within a cluster were then placed 60 m apart. Plot and cluster spacing addressed the competing needs of adequate spatial

FIGURE 1 Locations of the study areas in A) Eno River State Park in Orange County, North Carolina, USA, where the 54 sampling plots (black squares) generally consisted of a 2×2 formation and B) Umstead Road in Durham County, North Carolina, which consisted of 52 plots on 35 parcels (blue), where larger parcels incorporated multiple plots (black squares), but smaller parcels counted as a singular plot. Inset panels show each study area's location in North Carolina.

coverage across the study area (400 m cluster spacing) and the need to obtain spatial recaptures by placing multiple plots within an average home range size (60-m plot spacing; Sollmann et al. 2012). Prior analyses of telemetry data indicated the average 3-week female range distribution was ~1 km^2, thus 60-m plot spacing provided opportunities for spatial recaptures within a cluster, while 400-m spacing between clusters improved spatial coverage but resulted in a lower likelihood of recaptures across clusters.

The rural study area (ER) was an 8.9-km^2 area within park boundaries (Figure 1). We selected 15 clusters (54 plots) that were scouted prior to field collection to ensure accessibility. While we attempted to maintain a 2×2 formation, one exception occurred due to mowing under a powerline. Vegetation around this powerline was high and inaccessible, so we placed plots along the cleared powerline.

For the suburban study area (UR), we used a similar sampling strategy as described above, but maintaining the 2×2-plot spacing was more difficult due to landowner access. Once cluster centroids were randomly selected, we identified parcels of land via Durham County Parcel Layer (North Carolina OneMap 2022) and conducted community outreach (e.g., door knocking and fliers) to gain access. If plots in a potential cluster spanned multiple parcels, all associated landowners were contacted for access (up to 8 landowners as plots could encompass multiple parcels). At some clusters, >4 landowners granted access, and we increased the number of plots to a maximum of 6 to offset other clusters with <4 plots (Figure 1). Denial of access was not biased towards any discernable landscape features (e.g., parcel size), thus minimizing potential sampling bias from accessibility.

Fecal collection occurred in July (UR) and September (ER) of 2022. Sampling in both study areas occurred once per week during a 3-week period (i.e., 3 sampling occasions per site). We conducted area searches in each 0.1-ha plot with 1 to 5 technicians. Effort was consistent with each plot being surveyed for 20 person-minutes (i.e., person-specific survey time decreased with each technician in the plot). All fecal samples were collected in week 1, but only fresh samples (e.g., mucus coating, green tint, soft to the touch) were collected in the subsequent weeks due to low amplification in older samples. We collected 3 to 4 pellets from each pile and placed them in a 15 mL conical tube containing 100% molecular grade ethanol. All sized pellets were collected as fawns and adults were difficult to distinguish during our sampling period. Tubes were labeled with the cluster number, plot number, and occasion (1–3); each fecal pile within a plot was given an additional identifier (A-Z). We stored samples at 2°C until DNA extraction.

Fecal DNA extractions were completed using the NucleoSpin DNA Stool kits (Macherey-Nagel, Düren, Germany). We incubated 1 to 2 pellets at 70°C for 45 min to remove all ethanol. Pellets were placed into a 5-mL tube with 1 mL of ST1 lysis buffer (NucleoSpin), incubated at 70°C for 10 min, and vortexed for 10 min. We then followed the published protocol with a final elution volume of 50 µL. Microsatellite amplification occurred in 2 multiplexes. The first multiplex was developed for mule deer (*Odocoileus hemionus*; Lounsberry et al. 2015) and included 6 primers: SBT06, TGLA94, SBT05, ETH152, SBT07, and BM6506. The second multiplex containing a sex-determining marker, SRY, and 3 primers (Ohe256, OheC273, and OarFCB) was developed for white-tailed deer (Hamlin et al. 2021). All PCRs were carried out in 13 µL volumes containing 4 µL DNA, 6 µL of Qiagen Multiplex PCR Master Mix (Valencia, CA, USA), and 3 µL of each primer plex (each primer concentration = 0.25–0.6 µM; Table S1, available in Supporting Information). The touchdown PCR reaction conditions included an initial denaturation at 95°C for 5 min followed by 4 cycles of denaturation at 95°C for 45 sec. The first phase of the touchdown protocol is reduced by 2°C every successive cycle from 68°C to 60°C for 5 min, and extension at 75°C for 1 min. Next, a single touchdown cycle drop took place from 56°C to 54°C for 2 min, and an extension at 72°C for 1 min occurred before a set of 31 cycles of denaturation at 95°C for 45 sec, annealing 54°C for 2 min, and extension at 72°C for 1 min with a final extension of 72°C for 10 min. PCR products were analyzed on an Applied Biosystems Sequencer 3500 and sized via 600 LIZ size standard (Applied Biosystems Inc., Waltham, MA, USA). We called allele sizes in the program Geneious Prime (Kearse et al. 2012).

All samples were amplified in duplicate to ensure accurate calling, and any mismatches were amplified a third time. For quality control, we calculated genotyping error rates (i.e., allelic dropout and false alleles) for each locus. An allelic dropout occurred when 2 duplicates were mismatched, and the third amplification confirmed a

heterozygote whereas the opposite was defined as a false allele. We calculated Probability of Identity (P_{ID}) and Probability of Identify for siblings (P_{SIB}) via the program GenAlEx 6.2 (Peakall and Smouse 2012) to verify our microsatellite dataset contained sufficient power to discern individuals and siblings.

We obtained deer telemetry data from a concurrent collaring study in the Durham, North Carolina, area. Deer were captured and fitted with GPS collars (Model G5-2D; Advanced Telemetry Systems, Isanti, MN, USA) from January to May 2022. Locations were recorded every 2 hours by the GPS collars. For SCR analysis, we limited telemetry data to one random point per day to reduce possible autocorrelation in locations.

We fit SCR models using the package secr (Efford 2004) in R (version 4.2, R Core Team 2024). We created a detection history for each individual that included the plot, unique deer ID, occasion, and sex. Additionally, each study area had a file that notated spatial locations of each plot. We fit 2 SCR models: one using only fDNA and a second that integrated fDNA and telemetry data (hereafter, integrated; Sollmann et al. 2013). For both models, we used a hazard half-normal detection function with a proximity detector for detection probability (i.e., individuals could be detected at multiple plots during a single occasion; Efford 2004, 2011). Baseline detection probability (g_0) was held constant across sites, while space use (σ) varied by sex, and density (D) varied by sex and study area (rural and suburban). Plots were buffered by 3,000 m (>4σ), and we verified any further increase to the buffer did not change parameter estimates (Efford 2023). We report results as estimates with 95% confidence intervals and include coefficient of variation (CV; standard error/mean) for total density estimates.

RESULTS

In the rural study area, we sampled 54 plots. Plots were mostly in mixed-hardwood forested areas, but a subset was located within a mowed powerline without canopy cover. These plots reflected the homogeneous rural landscape (Figure 1). In the suburban study area (UR), we sampled 52 plots across 35 unique landowners. Plots were distributed across a range of landscape types and parcel sizes, from greenspaces to private yards, reflecting the heterogeneous suburban mosaic (Figure 1).

We collected 223 fecal pellets ($n_{ER} = 83$, $n_{UR} = 140$), but after quality control we retained 197 samples to calculate densities within ER and UR (Table 1). Genotyping errors had 0 false alleles and an allelic dropout of 0.02% across all loci with an amplification success of 88%. We verified the microsatellite dataset had high power to discern individuals (probability of 2 individuals sharing the same genotype by chance; $P_{ID} = 6.30 \times 10^{-13}$) and siblings (probability of 2 siblings sharing the same genotype by chance; $P_{Sib} = 7.70 \times 10^{-5}$). Genetic analyses resulted in 177 detections of 157 unique deer, with 64 individuals at ER (48 F:16 M) and 93 individuals at UR (64 F:29 M; Table 1). Of the 20 recaptures, 18 were females and 2 were males.

Due to the low number of male recaptures ($n = 2$), the sex-specific SCR model using only fDNA had difficultly converging, produced unrealistic density estimates (>200 deer/km^2), and remained sensitive to the size of the state space.

TABLE 1 Number of white-tailed deer fecal samples collected (samples), genotypes at ≥8 loci (genotypes), spatial detections used for spatially explicit capture-recapture inputs (detections), and individuals identified (individuals), along with total number of females (F) and males (M), and the number of total recaptures (recaptures) and sex-specific recaptures (F/M) from each sampling site in Durham and Orange counties, North Carolina, USA, summer 2022.

Sampling site	Samples	Genotypes	Detections	Individuals	F	M	Recaptures (F/M)
Eno River	83	67	66	64	48	16	2 (2/0)
Umstead Road	140	130	111	93	64	29	18 (16/2)
Total	223	197	177	157	112	45	20 (18/2)

As such, we fit a reduced fDNA-only model that excluded sex-specific estimates. Under this reduced fDNA-only model, estimated density was 54 deer/km^2 in ER (95% CI = 34–88; CV = 0.25) and 79 deer/km^2 in UR (95% CI = 50–124; CV = 0.24; Table 2, Figure 2). Space use (σ) was 189 m (95% CI = 151–236), and baseline detection (g_0) was 0.04 (95% CI = 0.02–0.06; Table 2).

Integrating telemetry data with the fDNA model, we estimated deer densities were 54 deer/km^2 at ER (95% CI = 35–84; CV = 0.23) and 75 deer/km^2 at UR (95% CI = 48–117; CV = 0.23), providing similar estimates to the fDNA-only model and modest reductions in CVs (0.25 to 0.23; Table 2, Figure 2). However, sex-specific parameters remained estimable in the integrated model, particularly due to telemetry data informing the male space use parameter (σ). At both sites, female densities were significantly greater than male densities (Table 2, Figure 2). Specifically, female densities at ER and UR were 48 females/km^2 (95% CI = 30–76) and 64 females/km^2 (95% CI = 40–101), respectively. Conversely, estimated male densities at ER and UR were 6 males/km^2 (95% CI = 4–11) and 11 males/km^2 (95% CI = 6–18), respectively (Table 2, Figure 2). Finally, estimated female space use (σ; 193 m; 95% CI = 184–202) was significantly smaller than male space use (330 m; 95% CI = 316–345), which was only identifiable in the integrated model.

DISCUSSION

Our study demonstrated that the plot-based fDNA SCR sampling design successfully estimated deer density in rural and suburban landscapes but also revealed important design considerations and limitations that arise in areas with fragmented access and small parcel sizes. Plot-based SCR approaches using fDNA have gained attention as a flexible alternative to traditional transect-based SCR to sample cervid populations, particularly where access constraints, parcelization, and heterogeneous land uses limit linear sampling designs (e.g., Goode et al. 2014, Poutanen et al. 2019, Henk et al. 2022). Consistent with this prior work, our study demonstrates that plot-based

TABLE 2 Parameter estimates from white-tailed deer density analysis using fecal DNA (fDNA) only or integrating fecal DNA and telemetry data (Integrated) at Eno River (ER) and Umstead Road (UR), Durham and Orange counties, North Carolina, USA, during the summer of 2022. Fecal DNA estimates are based on the model (D~ study area, $g_0 \sim 1$, $\sigma \sim 1$), whereas integrated estimates are based on (D~ study area, $g_0 \sim 1$, σ~ sex). Included parameters are density (D) in km^2, space use (σ) in meters, baseline detection probability (g_0), and female sex ratio (π). All parameters are reported with their 95% confidence intervals; total density estimates also include coefficients of variation (CV).

Parameters	fDNA (95% CI)	Integrated (95% CI)
D (ER)	54 (34–88; 0.25)	54 (35–84; 0.23)
D (ER - males)	—	6 (4–11)
D (ER - females)	—	48 (30–76)
D (UR)	79 (50–124; 0.24)	75 (48–117; 0.23)
D (UR - males)	—	11 (6–18)
D (UR - females)	—	64 (40–101)
σ (male)	—	330 (316–345)
σ (female)	—	193 (184–202)
σ (combined)	189 (151–236)	—
g_0	0.04 (0.02–0.06)	0.03 (0.02–0.05)
π (female)	—	0.83 (0.23–0.78)

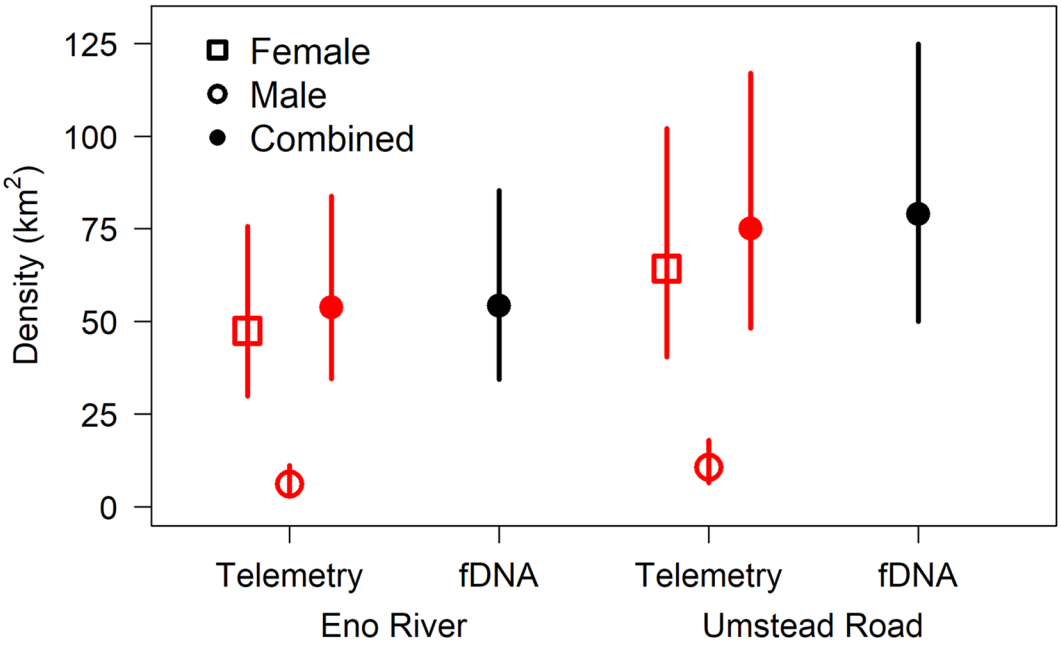

FIGURE 2 White-tailed deer density estimates from spatial capture-recapture (SCR) models that used only fecal DNA (fDNA; black) or integrated fDNA and telemetry data (Telemetry; red). Data were from Eno River State Park (Eno River) and Umstead Road, Durham and Orange Counties, North Carolina, USA, during the summer of 2022. Spatial capture-recapture models that integrated telemetry data provided sex-specific density estimates, while the fDNA only SCR model only estimated total density.

fDNA sampling can successfully generate individual encounter histories across a spectrum of landscapes, including suburban mosaics where access to continuous transects is often infeasible. Across both study areas, we obtained high-quality genetic data with low genotyping error rates and high amplification success; however, recaptures remained sparse, especially for males, demonstrating a key challenge in fDNA-based SCR studies where high abundance, demographic structure, sex-biased space use, and patchy sampling can influence encounter rates. Integration of telemetry data helped overcome the challenge of low sex-specific recaptures but did little to improve precision of density estimates. Overall, our results highlighted key trade-offs inherent to plot-based SCR in suburban landscapes, most notably low recapture rates, accessibility challenges to maintain optimal trap spacing, and the importance of considering auxiliary data streams as part of the study design.

Density estimates in both study sites were higher than regional deer estimates based on harvest but may reflect suburban densities when high numbers of fawns are present (Urbanek and Nielsen 2013, Williams et al. 2013, North Carolina Wildlife Resources Commission 2020). Hunter harvest is a common method to estimate relative deer abundance; however, low hunting pressure in suburban areas and the spatial scale of harvest reporting (often at the county level) limits the comparison to more urbanized areas. In 2020, post-harvest density estimates for Orange and Durham counties were 15–19 deer/km^2 and >19 deer/km^2, respectively (North Carolina Wildlife Resources Commission 2020). Our analysis occurred pre-hunt when fawns may comprise 40%-50% of the population (Poutanen et al. 2019). The high number of fawns and subsequent mortality for all age-classes (e.g., predation, vehicle collisions, harvest) may explain some of the differences in pre-hunt versus post-hunt densities (i.e., those based on harvest data). Additionally, our fecal sampling occurred at a finer spatial scale and showed different densities between the rural and suburban areas, information that is lost when scaled up to a county. Therefore, if managers or researchers are interested in comparing densities between landscape types or areas within a county or

management unit, especially at a fine spatial scale, harvest data may not be a reliable estimate based on the differing spatial scales of interest.

Integrating telemetry data improved model performance by stabilizing sex-specific parameter estimates, particularly male space use, despite only modest improvements in precision overall. Male space use was substantially larger than female space use, which may reflect sex differences in home-range size, dispersal tendency, and exploratory movements (Diefenbach et al. 2008) and drive lower male recapture rates. Conversely, females with offspring in early fall may use smaller areas, especially in suburban environments with high resource availability (Gaughan and DeStefano 2005). Regardless of the mechanisms, low male capture rates prevented sex-specific density estimation from fDNA alone, which was addressed by integrating telemetry data. These results reinforce the conclusion that telemetry data can be particularly beneficial when recapture rates are low, space-use parameters differ among demographic classes, or management decisions require class-specific estimates or detailed habitat relationships (e.g., Sollmann et al. 2013, Linden et al. 2018). For many applications, especially in suburban deer management where female abundance is key to population growth, the ability to estimate sex-specific abundance may represent a meaningful advantage despite minor gains in overall precision.

Plot-based sampling provided access to heterogeneous suburban landscapes; however, access constraints were pervasive in the suburban area, creating challenges in achieving the sampling effort required to obtain adequate recaptures. Despite sampling 52 plots at UR and 54 plots at ER, recaptures were restricted almost entirely to plots within clusters spaced ~60 m apart, with no individuals detected across clusters (>400 m), indicating that within-cluster spacing strongly governs the likelihood of obtaining the spatial recaptures needed for SCR analyses. This finding is consistent with known deer movement ecology, particularly for females with small home ranges, and supports prior recommendations for close trap spacing or clustered sampling designs in SCR studies (Goode et al. 2014, Clark 2019, Poutanen et al. 2019). Further methods to improve recapture probability include an increase in sampling plots on the landscape, the number of sampling occasions, or both (Pfeiler et al. 2020, Brommer et al. 2021). Similar to other studies employing plot-based SCR designs (Goode et al. 2014, Poutanen et al. 2019), our approach enabled sampling across the full suite of landscape features in suburban areas, a key requirement for density estimation. Overall, combining plot-based SCR methods with non-invasive fDNA can fill critical gaps for areas where agencies lack population data by increasing access and reducing the need to handle animals with inexpensive laboratory costs (~$8–10/fecal pellet; Curtis 2020).

MANAGEMENT IMPLICATIONS

Plot-based SCR sampling using non-invasive fDNA provides a framework to estimate deer density in suburban landscapes. Small plots allow coverage across diverse land uses and parcel types that may be inaccessible by continuous transects, thus reducing logistical barriers while still capturing landscape heterogeneity. Plot spacing that prioritizes recaptures while also sampling the diversity of landscapes remains a requirement for unbiased and precise estimates of density, where clustered sampling designs may improve efficiency. Alternative data streams (e.g., telemetry) may be needed when insufficient recaptures prevent or produce imprecise density estimates; however, study-specific objectives and logistics will drive the selection of cost-efficient methods (e.g., cost and effort of supplemental data versus costs of increased fDNA sampling).

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

ETHICS STATEMENT

Capture and handling protocols were approved by the Institutional Animal Care and Use Committee at North Carolina State University (IACUC Protocol No. 21-370).

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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