FINAL PERFORMANCE REPORT

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Foraging and Summer Roost Characterization of Tricolored Bats (*Perimyotis subflavus*) on the Deep Fork National Wildlife Refuge in Oklahoma

Oklahoma Department of Wildlife Conservation

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Abstract:

Rogers State University contracted Environmental Solutions & Innovations, Inc. (ESI) to complete a foraging study on the proposed for federal listing tricolored bat (*Perimyotis subflavus*; PESU) at the Deep Fork National Wildlife Refuge (NWR) in Okmulgee County, Oklahoma (Project; Figure 1). Information on home range size and core use areas of PESU is lacking in Oklahoma, thus study objectives include capturing and tracking PESU, collecting high-resolution location data, and analyzing cohorts and individuals to identify:

1. home range,
2. core use area (core-foraging range),
3. maximum distance traveled to foraging area, and
4. mean distance traveled to foraging area.

This report provides methods and results of mist netting and subsequent radio telemetry of PESU at the Deep Fork NWR in June 2024. Measurements provided throughout are included to the highest accuracy available.

Need:

The tricolored bat (Perimyotis subflavus, TCB), is a wide-ranging, insectivorous bat that occurs throughout eastern North America. TCBs typically roost in the foliage of trees during the summer and hibernate in caves, mines, and occasionally anthropogenic structures during the winter (e.g., bridges, roadway culverts, etc.) (USFWS 2021). Tricolored bats have experienced widespread population declines from White-Nose Syndrome, a disease that is caused by an invasive fungal pathogen. Following the conclusion of a Species Status Assessment, the TCB was proposed as endangered by the U.S. Fish and Wildlife Service in September 2022 (87 FR 56381). Therefore, it is imperative for natural resource agencies to understand information gaps related to habitat selection and life history for the TCB throughout its range.

Objectives:

1) Provide an estimated size for home range and core foraging areas for individual tricolored bats
2) Characterize summer roosting locations, both at the roost tree and forest stand level, for individual tricolored bats, especially reproductive females.

Summary of Progress:

Life History

Following USFWS guidance (USFWS 2024b), the active season for PESU includes spring staging, summer (including pup season), and fall swarming seasons. Spring staging occurs 15 April through 14 May, the summer season is 15 April through 30 September, the pup season is 1 June through 15 August, and fall swarming is 16 August to 31 October. The inactive season for PESU (time of year for PESU hibernation) is defined by the USFWS as 1 November to 14 April (USFWS 2024b). PESU is considered tree-dependent during the active season (e.g., roosting in forests, woodlands, and savannahs) and hibernaculum-dependent during the inactive season (caves, culverts, mines). Summer and winter ranges are not markedly different for the species due to their pattern of relatively short migrations with the maximum distance traveled between summer and winter habitat by a banded PESU recorded at approximately 136.79 kilometers (85 mi) (Griffin 1940).

Bats participate in a reproductive behavior known as fall swarming prior to entering hibernation. During this time (August to October) hundreds of bats fly in, out, and around cave and mine entrances (Humphrey and Cope 1976, Cope and Humphrey 1977). Once PESU leave hibernaculum, females may swarm in open areas of buildings before transitioning to smaller groupings to form maternity colonies in places such as leaf clusters (Whitaker et al. 2014). Males typically stay in the hibernaculum throughout summer (Whitaker and Rissler 1992) or roost in trees, live foliage, and clusters of dead trees like females (O'Keefe et al. 2009). PESU maternity colonies are most likely found in umbrella-shaped clusters of dead leaves; however, they also can be found in live foliage, patches of pine needles caught in tree limbs, lichens, buildings, caves, and rock crevices (Humphrey 1975, Veilleux et al. 2003, Veilleux and Veilleux 2004b; a, Veilleux et al. 2004, Perry and Thill 2007). Gestation for PESU is generally 44 days (Wimsatt 1945) and females typically produce twin pups approximately 44 to 54 percent of the size of the mother (Kurta and Kunz 1987). Young become volant at three weeks (Hoying and Kunz 1998).

Habitat Use

The species occupy relatively small home ranges based on the few telemetry studies of PESU foraging behaviors conducted. Reproductive females in Indiana traveled a maximum distance between foraging and roosting areas of 4.3 kilometers (2.7 mi) (Veilleux et al. 2003), while males traveled a maximum of 24.4 kilometers (15.2 mi) in Tennessee (Thames 2020). At the developing edge of the Indianapolis metropolitan area, Helms (2010) reported TCB travel approximately 1.6 kilometers (1 mi) on average with a maximum of 3.1 kilometers (1.9 mi) and occupying a home range averaging 323 hectares (798 ac) with a range of 67 to 613 hectares (116 to 1,515 ac). In Tennessee, male TCBs traveled a mean maximum distance of 11.4 kilometers while foraging each night and selected areas with more open water and wetlands than available (Thames 2020). In Nova Scotia, Quinn and Broders (2007) used acoustic sampling methods to identify key foraging sites and recorded 94 percent of TCB calls over rivers and lakes where insect biomass was highest.

PESU forage on a diet of Homoptera (leafhoppers, planthoppers, and tree hoppers), Hemiptera (true bugs), Diptera (true flies), and Lepidoptera (moths) (Brack and Whitaker 2004, Whitaker 2004, Caylor 2011) and generally prefer wooded habitats near water (Whitaker and Mumford 2009). PESU are also found foraging in old fields, grasslands, and agricultural habitats.

During the active season, PESU, unlike other tree-roosting bats, use highly-ephemeral roosts such as clusters of dead leaves, bony beard lichen, Spanish moss, squirrel nests, and piles of pine needles accumulated in the splits of trees (Davis and Mumford 1962, Veilleux et al. 2003, Perry and Thill 2007, Poissant et al. 2010). During the inactive season, PESU are obligatory hibernators. Typically, in the northeastern states, PESU hibernate in caves and abandoned mines while in the southern U.S. storm sewers (Goehring 1954), box culverts (Sandel et al. 2001), and surge tunnels at quarries (Slider and Kurta 2011) represent known PESU hibernacula. Use of culverts is potentially attributed to lack of karst landscapes (Leivers et al. 2019, Lutsch 2019, Meierhofer et al. 2019). More recent evidence indicates PESU also hibernate in rock faces in other areas of the country (White et al. 2016) and the species' winter range is wider than previously suspected. Hibernating PESU typically roost singly but form small clusters and often select a roost on the walls as opposed to the ceiling of the hibernaculum (Brack 1979, Kurta 2008).

Methods:

Mist Netting

Mist net sites were set in lowland forest surrounding the Deep Fork of the Canadian River adjacent ephemeral streams (Figure 2). Because PESU is a high-flyer, areas with tight flyways over water were prioritized for mist netting efforts additional to a known mine entrance (hereafter, the "cave"; Figure 2). Three to four mist net setups were deployed each night. Standardized bat capture data sheets were used to record morphometric data and are provided in Appendix A.

Protocol for Addressing White-nose Syndrome

All current federal and state guidelines for WNS decontamination, containment, and avoidance were implemented, and biologists were apprised of all current WNS regulations. Because the study is focused on foraging behaviors, bats were not assessed for WNS and non-target species were released immediately following morphometric processing. PESU were quickly processed, radio-tagged, and released.

Protocol for Addressing Covid-19

Bat handling follows guidance provided in the USFWS memorandum FWS/D/072688 dated 12 June 2020 (USFWS 2020) and protocol described in Oklahoma-issued Scientific Collectors Permits. Additionally, ESI biologists employ Center for Disease Control Guidelines, including N95 or equivalent, non-vented facemasks and single-use nitrile gloves (discarded after each bat is handled). Nets and clothing were decontaminated using WNS protocols for disinfecting, such as Covid-killing disinfectants and heating porous equipment at 55° Celsius (131° F) for at least 20 minutes.

Transmitter Attachment

Transmitters were activated and tested before attachment to individuals. A small sub- interscapular area was trimmed of fur and the transmitter attached to this area with non-toxic surgical adhesive (Perma-type Surgical Glue). The adhesive degrades over time (typically 1 to 4 weeks) and the transmitter is shed. Bats were released unharmed near the point of capture. Radio-tagging from capture to release was typically less than ten and no more than 15 minutes.

Lotek PicoPip Ag190 (0.21 grams [0.007 oz]) transmitters with frequencies ranging from 170.000-172.999 MHz were used for radio-tagging. Batteries typically last for four days. To meet federal permit requirements, transmitters did not comprise more than five percent of a bat's total weight.

Ground-based Foraging Telemetry

Azimuths of radio-tagged bats were obtained from at least three stationary locations per night for up to five hours, depending on weather conditions. Azimuths were gathered using Lotek Biotracker or Advanced Telemetry Systems R4500 scanning-receivers attached to five-element yagi antennas tuned to 170.000-172.999 MHz.

Synchronized searches on specific frequencies were conducted every three minutes from each telemetry station. After two minutes, telemetry stations were changed to the next active frequency. An azimuth was taken in the direction of the strongest audible signal or numeric reading on the receiver when a frequency was detected. Time, frequency, and azimuth from each station detecting the signal were recorded on standardized data sheets. Azimuths contain a sub-meter location of origin. Telemetry station designations corresponded to the individual taking the bearing as opposed to the location. When bats were not detected, locations were repositioned to facilitate detection. Telemetry stations were selected for higher vantage points or for assumed proximity to locations previously frequented by radio-tagged bats (Figure 3).

Home Range and Core-foraging Range

Location estimates were acquired using triangulation and biangulation from ground-based telemetry. Azimuths were compiled for individual bats, adjusted for declination (+2.7), and entered into the Location of a Signal (LOAS) program. LOAS uses several parameters to output location estimates and error polygons based on gathered azimuths. Data were classified by frequency, date, and time from all triangulation stations. All available azimuths for a particular time interval on a given frequency were analyzed to identify azimuths crossing on the landscape to estimate locations.

Estimated parameters were based on a Maximum Likelihood Estimate (MLE) of available data using 60 iterative scenarios of crossing azimuths. If MLE failed to produce an acceptable estimate, the best biangulation method was used (two-azimuth crossings). Not all azimuths taken resulted in a location. Triangulations require four azimuths, and biangulations require two to three azimuths.

Home range was defined as an area polygon where an individual spends 95 percent of its time, within a discreet time-period (e.g., summer foraging). Core-foraging range was defined as an area where an individual spends 50 percent of its time within the above-mentioned, discrete time-period. The core-foraging range is usually the most concentrated cluster of points and potentially includes a combination of roosting, foraging, and commuting areas. Roost fidelity can lead activity-bias toward the roost area in core-foraging analysis (multiple points are gathered commuting to or from a roost).

Estimation of home range requires time-independent locations to prevent autocorrelation and subsequent underestimates of range size (Rooney et al. 1998). The time interval necessary to consider two locations as time-independent accounts for location error, travel speed, and travel distance. Enough time was allowed to pass between locations to conclude a bat is either traveling or foraging in a relatively small area. Five-minute intervals were considered suitable for PESU.

Some studies recommended 30 or more locations to reach optimal smoothing parameters for uniform distribution (Seaman et al. 1999). Others call for at least 10 locations to show a normal (or uniform) distribution (Swihart and Slade 1985). Moore et al. (2017) achieved satisfactory results with a minimum of 15 time-independent locations. Using more locations produces a more accurate, uniform kernel analysis. Upon establishing 15 locations for a single PESU, the bat was deprioritized to record additional locations for other radio-tagged bats. Locations derived from ground-based telemetry azimuths were compiled and analyzed in Program Biotas (Ecological Software Solutions, LLC). The fixed-kernel (FK) density estimation method (uniform distribution) was used with least-squares cross validation for all group-level and individual-level home range (95% of locations) and core-foraging range (50% of locations) analyses.

Diurnal Telemetry

To locate roosting bats, ESI biologists tracked radio-telemetry signals using a Lotek Biotracker scanning-receiver with five-element folding Yagi directional antennas manufactured by either Wildlife Materials®, Inc. or Titley Electronics, PTY LTD®.

Beginning the day after bat capture and transmitter attachment, telemetry was used to locate each bat's diurnal roost. Roosting area was prioritized instead of the exact tree, given difficulties involved in identifying exact location. Typical vegetation plot metrics were recorded for analysis. The roost tree was identified to species and diameter at breast height (dbh) was measured using a dbh tape or Biltmore stick. The approximate height at which the bat was roosting and general condition of the roost tree (dead, live, dying, % bark cover, etc.) were noted. A description of habitat near the roost tree was recorded. Bats were tracked for a maximum of four hours per day or until the bat was found, for up to five days after the date of capture or until the transmitter was shed or fails. No emergence counts were conducted. If a roost tree occured in an area where biologists were not permitted access, triangulation was used to estimate its location.

Foraging Analysis

Landscape data used to run the foraging analysis were derived from multiple sources. A digital elevation model (DEM) tile with 1/3rd arc-second resolution (approximately 10- m [32.8-ft] grid cells) for Oklahoma was acquired through the U.S. Geologic Survey National Map service (available at: https://www.usgs.gov/programs/national- geospatial-program/national-map; data accessed October 2024). Although the DEM can be used to generate additional topographic layers (e.g., aspect, slope, and solar radiation), predictors are not appropriate for the study described herein given topographic homogeneity of the study area. A 4.8-kilometer (3.00-mi) radius circle was drawn around the study area, using the mean center of all PESU locations identified in the study. The circle acted as a boundary for the analysis and extended beyond the traditionally recognized flight distance of PESU, estimated at 1.9 kilometers (1.2 mi) for typical foraging activities with a maximal flight distance of 3.1 kilometers (1.9 mi; Helms 2010). Use of a 4.8-kilometer (3.0-mi) boundary is also consistent with USFWS guidance for foraging PESU (USFWS 2024a).

Land cover layers consisted of the 2021 National Land Cover Database (NLCD) and the U.S. Forest Service 2021 Tree Canopy Cover Dataset (Canopy) acquired through the Multi-resolution Land Characteristics Consortium (available at: https://www.mrlc.gov/).

NLCD is a 30-meter (98.4-ft) resolution layer derived from remote sensing to classify the landscape into one of 16 classes. The Canopy dataset is a Landsat-based, 30-meter (98.4-ft) resolution layer providing percentage canopy cover. The two datasets were resampled to the same resolution as the DEM described above using a nearest neighbor sampling technique in ArcPro (vers. 3.3.0).

Layers for wetlands and surface waters were sourced from the National Wetlands Inventory (available at: https://www.fws.gov/wetlands/data/mapper.html; data accessed October 2024) and clipped to include the study area described above. Euclidean distance was calculated from each wetland and water surface to allow assessment of individual proximity to water features ("WetDist").

Distance to roads ("RoadDist"), recreational trails ("TrailDist"), the cave ("CaveDist"), and roost trees identified in the study ("RoostDist") allowed for evaluation of landscape features and their relative importance associated with PESU foraging. Roads and recreational trails within the study area were acquired from the USGS National Transportation Dataset using The National Map service described above (data accessed October 2024).

Presence/Absence Data

To assess relative foraging use of the landscape, locations ascertained through telemetry (Section 3.2) were used as presence points and absence points (10 times the number of presence points) and were randomly generated within the 4.8-kilometer (3.0- mi) study area (Figure 2). The full dataset of presence and absence points was filtered to ensure only a single point falls within individual cells to avoid spatial autocorrelation. Fifteen percent of the dataset was withheld for testing predictive power of the final model (the "testing" dataset) while 85 percent of the dataset was used for model development (the "training" dataset).

Variable Reduction

Generalized linear models (GLMs) are generally robust to deviations from normality; however, collinear predictor variables can result in unstable parameter estimation, inflated estimate standard error, and biased inferential statistics bias (Dormann et al. 2013). Before conducting statistical analysis, predictors were evaluated for collinearity among one another. Pairwise correlation coefficients and variance inflation factor (VIF) (Naimi and Araújo 2016) were used to evaluate collinearity among predictors and determined if predictors should be excluded from the analysis. Variables with a correlation coefficient greater than 0.6 or VIF greater than 10 were excluded from analysis.

Statistical Model

Binomial GLMs were used to assess the role of landscape features (including DEM; percent canopy cover; distance to water, road, trail, cave, and roost tree features; and NLCD landcover types) in describing probability of species presence. Landscape features were regressed on the presence (equal to 1 or 100% probability) or absence (equal to zero or 0% probability) of individuals within the models to evaluate the relative importance of each environmental/topographic layer and provide a model of foraging preference. Interactions (e.g., an interaction between percent canopy cover and elevation) and non-linear terms (e.g., WetDist^2) were also investigated for each landscape feature.

Models (types) were built separately to evaluate inclusion of simple linear terms ("base"), non-linear terms (up to cubic terms; "non-linear" = base terms + non-linear terms), interactions among variables (only including two-way interactions; "interaction" = base terms + interaction terms), and combinations of the three ("combination" = base terms + non-linear terms + interaction terms). Integration of variables from more simplistic (e.g., base) to more complex (e.g., combination) affords assessment of how landscape features interact with one another (e.g., distance to water features within certain landcover types), and if there may be optima among variables (e.g., greater presence probability at intermediate values of landscape variables rather than at extremes).

Step-wise model reduction was used to identify the "best fit" of each model type (i.e., the best-fit base model, the best-fit interaction model, etc.). To illustrate, the initial ("Full") base model includes DEM, Canopy, NLCD, WetDist, RoadDist, TrailDist. CaveDist, and RoostDist. The model summary suggests removal of Canopy was appropriate. Upon removing Canopy from the model (the "Full – Canopy" model), comparison with Full indicated deviation does not significantly increase ($\chi^2 = 0.131$, $p = 0.717$) and instead the model was improved, resulting in a more parsimonious (i.e., simpler) model. Next, the summary of the Full – Canopy model was investigated to identify which terms could be removed and removal of the term suggested was investigated, like with Canopy, to identify if removal of the suggested term significantly increased model deviance. If removal of the predictor did not make the model worse, then the predictor was kept out and the model further investigated for terms that could be removed. This process was repeated until only predictors whose removal made the model significantly worse (i.e., significantly increases deviance) remained, producing the best-fit model.

Step-wise model reduction allows identification of the most parsimonious but also informative model of landscape usage for foraging. The reduced, best-fit models were compared to one another using (1) likelihood ratio tests (LRT; values closer to zero are better), (2) Akaike Information Criteria (AIC; smaller numbers are better) (Akaike 1974), and variation explained (D^2; an analog of r^2 reflecting the percent of variation explained – larger numbers mean more variation explained) (Guisan and Zimmermann 2000). Unconfounded variation of each individual model parameter was also evaluated by calculating the change in D^2 when the model parameter was removed.

Foraging Probability Prediction

Following identification of variables important to describing presence/absence within the study area, a ‘final’ binomial linear model consisting of variables identified during model selection was used to generate predictions. Predictions were overlain across the landscape to provide a spatial context of where PESU are most likely found foraging in the summer.

Accuracy of presence probability was tested using the training and test datasets described in Section 3.3.2: 85 percent of PESU locations were used for model training and 15 percent were used for model testing. Data withheld for testing prior to model development were used to generate model predictions (namely, landscape attributes at each test location were used to generate predictions of whether PESU was present or not). Predictions were then compared to the known value at each testing location and results compared using a confusion matrix, an approach affording calculation of model sensitivity and specificity. Highly sensitive models are good at predicting true positives or accurately predicting where individuals are present, while high specificity models are good at predicting true negatives, or accurately predicting where individuals are not present.

Results:

Mist Netting

Mist netting was completed on 18 through 20, 23 and 24, and 26 and 27 June 2024 totaling 23 net nights worth of effort. In total, 27 bats representing four species were captured including 14 eastern red (*Lasiurus borealis*), 9 PESU, 3 evening (*Nycticeius humeralis*), and 1 big brown bat (*Eptesicus fuscus*) (Table 1).

Table 1. Total bat captures on the PESU Foraging Study on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

Adult	Adult Female[1]		Juvenile				
Species	**Male**	**L**	**PL**	**Male**	**Female**	**Total**	**Percent**
Big brown bat	0	0	0	1	0	**1**	4
Eastern red bat	0	6	1	4	3	**14**	52
Evening bat	0	0	0	3	0	**3**	11
Tricolored bat	7	0	0	2	0	**9**	33
Total	**7**	**6**	**1**	**10**	**3**	**27**	100

[1] Reproductive condition of adult female bats: L = Lactating; PL = Post Lactating

Ground-based Foraging Telemetry

Ground-based foraging telemetry was conducted for eight nights (21, 22, 24, 26 – 30 June 2024) on six PESU captured on the Deep Fork NWR (Table 2). A four-person team gathered azimuths from 10 telemetry stations. An estimated 40 hours of foraging telemetry was completed (160 biologist-hours), resulting in the identification of 92 time-independent locations (Figure 4). An adequate number of locations (≥ 15) for completing individual home range and core-foraging area calculations was obtained for two of six PESU.

Uniform distribution FK home ranges (95%) for PESU varied from 340.5 to 810.2 hectares (841.4 to 2,002.1 ac), and core-foraging areas (50%) ranged from 50 to 149.7 hectares (123.6 to 369.9 ac).

Species-level home range and core-use area for all points (*n* = 92) totaled 365.9 hectares (904.2 ac) and 52.5 hectares (129.7 ac), respectively (Figure 5).

Mean and Maximum Distance

The maximum distance traveled from the cave to foraging area by an individual PESU (Bat 172.123) in this study was 7,612.31 meters (4.73 mi). The minimum distance traveled by an individual PESU was Bat 172.606 and traveled 80.21 meters (0.05 mi). The mean distance traveled by all bats in this study was 593.26 ± 151.44 meters (0.37 ± 0.09 mi). The mean and maximum distance traveled by bats is represented in Table 2.

Tracking

Six bats were captured and tracked during the Project; however, only two individuals exceeded the threshold of locations adequate to further delineate individual home ranges and core-foraging ranges. PESU tracking activities associated with the foraging study are detailed below and in Table 2.

Table 2. Bat Capture, Distances Traveled, and Home and Core-foraging Range Sizes for the PESU Foraging Study on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

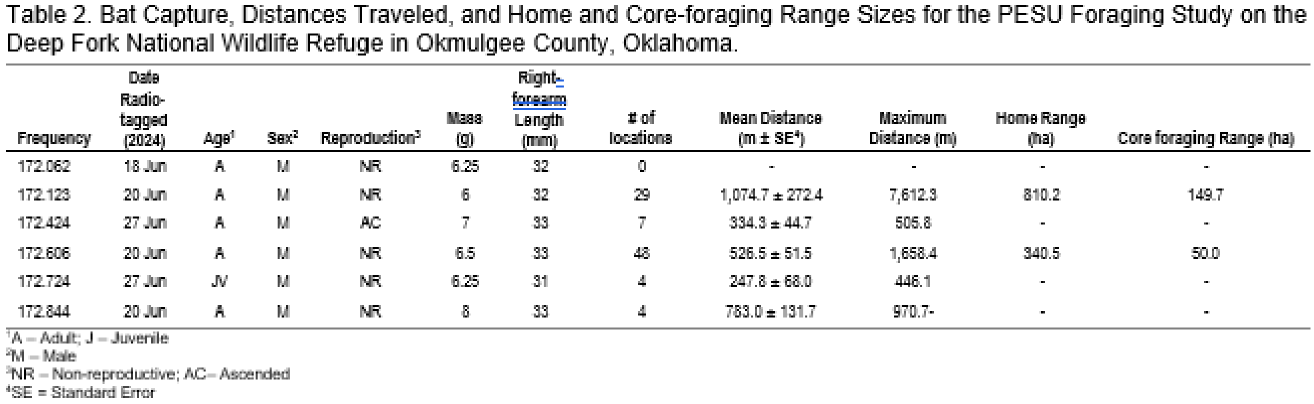

Table 2. Bat Capture, Distances Traveled, and Home and Core-foraging Range Sizes for the PESU Foraging Study on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

Frequency	Date Radio-tagged (2024)	Age[1]	Sex[2]	Reproduction[3]	Mass (g)	Right-forearm Length (mm)	# of locations	Mean Distance (m ± SE[4])	Maximum Distance (m)	Home Range (ha)	Core foraging Range (ha)
172.062	18 Jun	A	M	NR	6.25	32	0	-	-	-	-
172.123	20 Jun	A	M	NR	6	32	29	1,074.7 ± 272.4	7,612.3	810.2	149.7
172.424	27 Jun	A	M	AC	7	33	7	334.3 ± 44.7	505.8	-	-
172.606	20 Jun	A	M	NR	6.5	33	48	526.5 ± 51.5	1,658.4	340.5	50.0
172.724	27 Jun	JV	M	NR	6.25	31	4	247.8 ± 68.0	446.1	-	-
172.844	20 Jun	A	M	NR	8	33	4	783.0 ± 131.7	970.7-	-	-

[1] A – Adult; J – Juvenile
[2] M – Male
[3] NR – Non-reproductive; AC– Ascended
[4] SE = Standard Error

Bat 172.062

Bat 172.062 was an adult male captured 18 June 2024. During tracking activities, zero time-independent locations were gathered, thus Bat 172.062 did not meet threshold criteria for individual analysis and contributed zero locations for species-level home range and core foraging nor the mean and maximum distance traveled analyses.

Bat 172.123

Bat 172.123 an adult male captured 20 June 2024. During tracking activities, 29 time-independent locations were gathered, providing information for individual analysis of home range and core-foraging range (Table 2; Figure 5). The home range of Bat 172.123 was 8,170.2 hectares (20,189.0 ac) and the core-foraging range was 149.7 hectares (370.10 acres). On average, Bat 172.123 was approximately 1,074.73 ± 272.40 meters (0.66 ± 0.16 mi) from the cave and the maximum distance detected was 7,612.31 meters (4.73 mi; Table 2).

Bat 172.424

Bat 172.424 was an adult male captured 27 July 2024. During tracking activities, seven time-independent locations were gathered, thus Bat 172.424 did not meet the threshold criteria for individual analysis. However, it did contribute to the species-level home range and core foraging analyses. On average, Bat

172.424 was approximately 334.25 ± 44.72 meters (0.21 ± 0.03 mi) from the cave and the maximum distance detected was 505.79 meters (0.31 mi; Table 2, Figure 5).

Bat 172.606

Bat 172.606 was an adult male captured 20 June 2024. During tracking activities, 48 time-independent locations were gathered, providing information for individual analysis of home range and core-foraging range (Table 2). Bat 172.606 home range was 3,404.5 hectares (8,412.8 ac), and core-foraging range was 50.0 hectares (123.6 ac). On average, Bat 172.606 was approximately 526.50 ± 51.51 meters (0.32 ± 0.03 mi) from the cave and the maximum distance detected was 1,658.36 meters (1.03 mi; Table 2; Figure 5).

Bat 172.724

Bat 172.724 was a juvenile male captured 27 June 2024. During tracking activities, four time-independent locations were gathered, thus Bat 172.606 did not meet the threshold criteria for individual analysis. However, it did contribute to the species-level home range and core foraging analyses (Table 2). On average, Bat 172.724 was approximately 247.83 ± 68.03 meters (0.15 ± 0.04 mi) from the cave and maximum distance detected was 446.11 meters (0.28 mi; Table 2).

Bat 172.844

Bat 172.844 was an adult male captured 20 June 2024. During tracking activities, four time-independent locations were gathered, thus Bat 172.844 did not meet the threshold criteria for individual analyses. However, Bat 172.844 did contribute to the species-level home range and core foraging analyses. On average, Bat 172.844 was approximately 783 ± 131.66 meters (0.48 ± 0.08 mi) from the cave and maximum distance detected was 970.66 meters (0.60 mi, Table 2).

Diurnal Tracking

Diurnal tracking on the Project yielded two PESU roosting locations with a third location triangulated outside of the Deep Fork NWR property boundary. On 21 June 2024, Bat 172.606 was tracked to a cluster of dead leaves on a broken branch hanging in an eastern sycamore tree (*Platanus occidentalis)* approximately 1.8 meters (6.0 ft) above ground level. Surrounding habitat consisted of mature lowland forest floodplain bordering the Deep Fork of the Canadian River. Dominant canopy species were identified as eastern sycamore, sugar maple (*Acer saccharum*), and American elm (*Ulmus americana*) with a moderately closed canopy. On 21 June 2024, Bat 172.844 was tracked to a dead leaf cluster in a live pignut hickory (*Carya glabra*; 18 centimeters [7.1 in] dbh) approximately 5 meters (16.4 ft) above ground level. Surrounding habitat consisted of mature lowland forest and tributaries bordering the Deep Fork of the Canadian River. Dominant canopy species included pignut hickory, pecan (*Carya illinoinensis*), and white oak (*Quercus alba*) with a moderately closed canopy.

Foraging Analysis

Variable Reduction

CaveDist, RoostDist, and TrailDist were all highly correlated with one another (Pearson $r > 0.7$, d.f. = 848, $p < 2.2e^{-16}$), thus selection of an individual variable to carry forward through modeling was necessary. Separate full models with all variables described above and only one of three correlated variables (CaveDist, RoostDist, or TrailDist) were generated to determine which of the three correlated variables reduced variation the most. The model with CaveDist (log-likelihood$_{\text{Cave model}}$ [$LL_{\text{Cave model}}$] = -88.9) was significantly better than either the RoostDist model ($LL_{\text{Roost model}} = -110.9$; $X^2 = 44.1$, $p < 2.2e^{-16}$) or the TrailDist model ($LL_{\text{Trail model}} = -139.4$; $X^2 = 101.1$, $p < 2.2e^{-16}$), therefore CaveDist was used in subsequent models and RoostDist and TrailDist were omitted. VIF and correlation analysis on remaining continuous variables (i.e., excepting NLCD) suggested collinearity was not present among other variables used for modeling ($VIF \leq 1.5$; $r < 0.6$).

Statistical Model

The original full model comprised Canopy, CaveDist, DEM, NLCD, RoadDist, and WetDist and explained significantly more variation in foraging use than random ($X^2 = 2,105$, d.f. = 16, $p < 2.2e^{-16}$; $LL_{\text{Full model}} = -106.4$; $LL_{\text{Null}} = -1,159$). The full model also showed no signs of under-/overdispersion (i.e., variance of the response[presence/absence] is less/greater than what the model assumes; dispersion = 0.942, p = 0.696). All reduced, best-fit models performed significantly better than random ($X^2 \geq 342.5$; $p < 2.2e^{-16}$; Table 4) and the Combination model was the best model of foraging for bats associated with the current study, performing significantly better than either the Non-linear model ($X^2 = 10.3$, d.f. = 0, $p < 2.2e^{-16}$) or the Interaction model ($X^2 = 5.0$, d.f. = 1, $p = 2.6e^{-2}$; Table 3). The Combination model also did not show signs of under-/overdispersion (dispersion = 0.95, p = 0.672) and explained nearly 70 percent of variation ($D^2 = 69.7$).

Table 3. Comparison of fully reduced model types to predict PESU foraging on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

Likelihood Ratio Testing[2, 3]

Model type	Model terms[1]	AIC	Log-likelihood	X^2	d.f.	p-value
Null	1	523.2	-260.6	363.2	1	$< 2.2e^{-16}$
Full	Canopy + CaveDist + DEM + NLCD + RoadDist + WetDist	213.7	-88.88	19.74	18	$1.96e^{-2}$
Base	CaveDist + NLCD	206.6	-89.30	20.59	14	$0.966e^{-4}$
Non-linear	Canopy + Canopy^2 + Canopy^3 + CaveDist + CaveDist^2 + WetDist + WetDist^2 + WetDist^3	186.3	-84.15	10.29	9	$< 2.2e^{-16}$
Interaction	Canopy + CaveDist + DEM + RoadDist + *Canopy x CaveDist* + *Canopy x RoadDist* + *DEM x RoadDist*	179.0	-81.50	4.98	8	$2.56e^{-2}$
Combination	Canopy + CaveDist + CaveDist^2 + RoadDist + WetDist + WetDist^2 + WetDist^3 *Canopy x RoadDist*	176.0	-79.00	-	9	-

[1] Terms in italics are associated with interactions.

[2] All models are significantly better than the null model ($X^2 \geq 342.5$, $p < 2.2e^{-16}$).

[3] Model types compared to the Combination model.

The best-fit model for foraging PESU investigated in the current study was a combination of non-linear and interaction terms incorporating canopy cover, elevation, and distance to the cave, roads, and water features. Direction (positive or negative) and magnitude of parameter estimates provide a general sense of the influence of each predictor on presence/absence of individuals (Table 4). Negative parameter estimates indicate increasing values of the parameter (e.g., increasing distance from the cave) result in lower likelihood of presence while positive parameter estimates indicate smaller values (e.g., close to water features) have higher likelihood of presence. Partial predictive plots are a method of showing how predictions change relative to specific landscape predictors while holding other predictors at their mean values (Figure 6). Doing so allows for assessment of how individual landscape features potentially influence presence or absence of individual PESU, and thus likelihood of use during foraging.

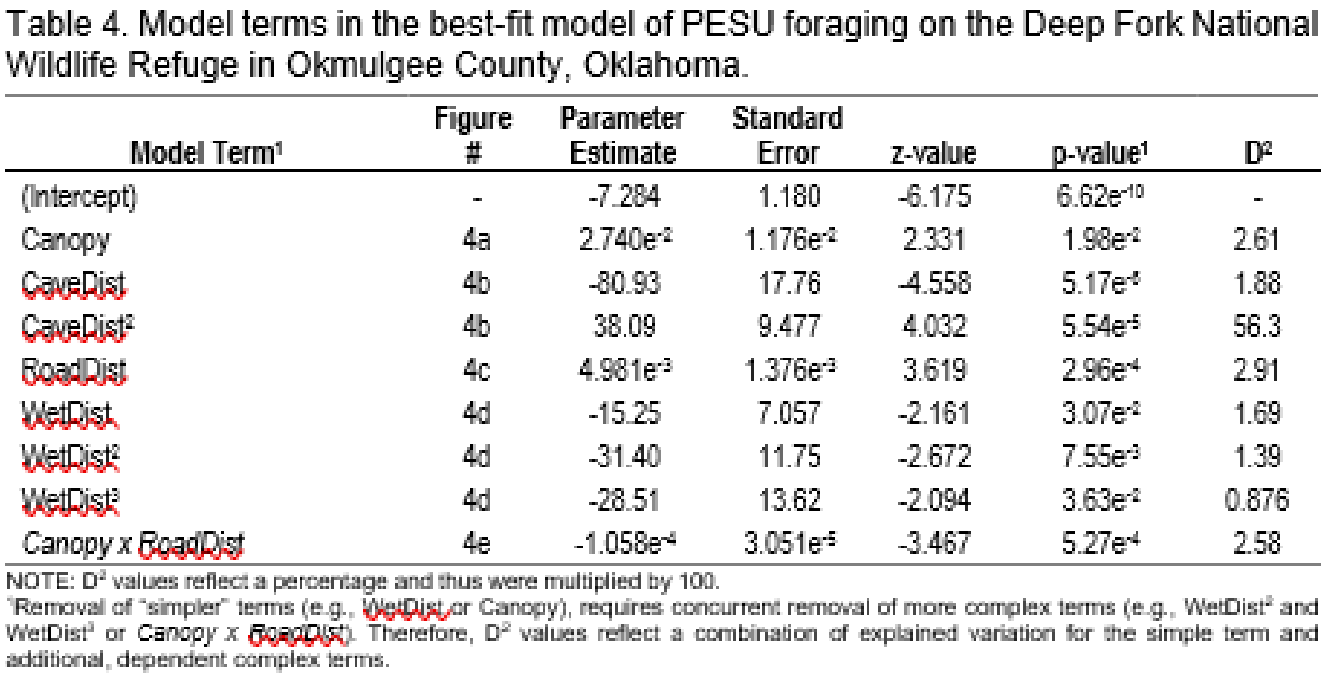

Table 4. Model terms in the best-fit model of PESU foraging on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

Model Term[1]	Figure #	Parameter Estimate	Standard Error	z-value	p-value[1]	D^2
(Intercept)	-	-7.284	1.180	-6.175	$6.62e^{-10}$	-
Canopy	4a	$2.740e^{-2}$	$1.176e^{-2}$	2.331	$1.98e^{-2}$	2.61
CaveDist	4b	-80.93	17.76	-4.558	$5.17e^{-6}$	1.88
$CaveDist^2$	4b	38.09	9.477	4.032	$5.54e^{-5}$	56.3
RoadDist	4c	$4.981e^{-3}$	$1.376e^{-3}$	3.619	$2.96e^{-4}$	2.91
WetDist	4d	-15.25	7.057	-2.161	$3.07e^{-2}$	1.69
$WetDist^2$	4d	-31.40	11.75	-2.672	$7.55e^{-3}$	1.39
$WetDist^3$	4d	-28.51	13.62	-2.094	$3.63e^{-2}$	0.876
Canopy x RoadDist	4e	$-1.058e^{-4}$	$3.051e^{-5}$	-3.467	$5.27e^{-4}$	2.58

NOTE: D^2 values reflect a percentage and thus were multiplied by 100.

[1] Removal of "simpler" terms (e.g., WetDist or Canopy), requires concurrent removal of more complex terms (e.g., $WetDist^2$ and $WetDist^3$ or *Canopy x RoadDist*). Therefore, D^2 values reflect a combination of explained variation for the simple term and additional, dependent complex terms.

Foraging probability showed a small but generally monotonic decrease with increasing canopy cover (Figure 6a; however, note the predictive plot does not account for the interaction between canopy cover and distance to roads). Combined with the interaction between canopy cover and distance to roads, canopy cover explained approximately 3 percent of variation in foraging probability ($D^2 = 2.61$; Table 4). Presence probability was extremely high proximate the cave and gradually decreased to zero as distance approached 2 kilometers (1.2 mi; Figure 6b). Distance from the cave explained over 56 percent of variation in foraging probability ($D^2 = 1.88$ for the linear term and $D^2 = 56.3$ for the quadratic term; Table 4), far more than any other predictor. Foraging probability generally increased farther from roads; however, the increase was slight (Figure 6c). Combined with the interaction between canopy cover and road distance, road distance explained nearly 3 percent of variation in foraging probability ($D^2 = 2.91$; Table 4). Distance to water showed a cubic relationship with foraging probability such that probability was elevated proximate water bodies, even higher at approximately 200 meters (656.2 ft), and nearly absent as distance approached 400 meters (1,312.3 ft; Figure 6d). Distance to water explained nearly 2 percent of variation in foraging probability ($D^2 = 1.69$ for the linear term, $D^2 = 1.39$ for the quadratic term, and $D^2 = 0.876$ for the cubic term; Table 4). The interaction between road distance and canopy cover suggested at far distances from roads (>1,000 meters [>3,280.8 ft] where canopy cover is low (<25%), foraging probability is high compared to nearer roads or at higher percentages of canopy cover (>25%; Figure 6e).

Foraging Probability Prediction

Across the study area, foraging predictions suggest the highest likelihood of PESU presence proximate the cave (Figure 7). Faint traces of higher suitability habitat follow along the Deep Fork of the Canadian River riparian corridor, but highest suitability foraging habitat is proximate the cave with limited effects from land cover type and landscape features present. Accuracy of the probability predictions was 91.39 percent, indicating the majority of test dataset samples were correctly classified. Sensitivity of the model was also very high, at 97.00 percent, indicating the model is very good at predicting where individuals are present; however, specificity was substantially lower, at 69.23 percent, indicating the model is worse at handling true negatives, or identifying where individuals are not present.

Discussion and Conclusions:
Location information from ground-based telemetry was used to develop individual and species-level polygons for the PESU foraging study at the Deep Fork NWR in Okmulgee County, Oklahoma in June 2024. Species-level polygons represent PESU landscape use.

Two of six radio-tagged male PESU had sufficient time-independent points to analyze home range and core foraging areas. The uniform distribution FK home ranges (95%) varied from 340.5 to 810.2 hectares (841.4 to 2,002.1 ac), and core foraging areas (50%) ranged from 50 to 149.7 hectares (123.6 to 369.9 ac). The species-level home range and core-use area totaled 365.9 hectares (904.2 ac) and 52.5 hectares (129.7 ac). The maximum distance traveled from the cave by an individual PESU was 7,612.31 meters (4.73 mi). The minimum distance traveled by an individual PESU was 80.21 meters (0.05 mi). The mean distance traveled by all bats in this study was 593.26 ± 151.44 meters (0.37 ± 0.09 mi). Variation in home range, core-foraging areas, and maximum distance traveled is possibly because all bats radio-tagged in the current study were males. Unlike females, at this time of year males are not a part of a maternity colony, indicating males have more options for roosting and foraging locations.

Dirunal tracking yielded two roost locations. Bats 172.606 and 172.844 were both tracked to dead leaf clusters in live trees. Bat 172.606 was found roosting in a dead leaf cluster in a live eastern sycamore and bat 172.844. was found in a live pignut hickory. Finding PESU in substrate of trees (such as Spanish moss, pine needles, and leaf clusters) is not uncommon and findings coincide with other studies (Davis and Mumford 1962, Veilleux et al. 2003, Perry and Thill 2007).

Cave distance, roost distance, and trail distance all highly correlated to each other regarding foraging probability, but selection of an individual variable to carry through modeling was necessary. The model with cave distance was significantly better than models with roost and trail distance. Thus, distance to cave represented the highest foraging probability factor. Other factors showing a positive foraging probability included canopy cover, distance to road, and water. Foraging probability showed a small but monotonic decrease with increasing canopy cover and distance to roads. Also, foraging probability slightly increased farther from roads. Proximity to water bodies elevated foraging probability as well. Importantly, the foraging probability model is accurate at predicting where individuals are present but is not as good at predicting where individuals are not, meaning the model potentially has a high number of false positives and could be overrepresenting where individuals are foraging.

From a management perspective, maintaining the integrity of entrance to the cave (mine) is important to ensure PESU continue its use as a roosting location. Past forest management practices used at the Deep Fork NWR appear effective as PESU are present at the location. However, males represented the only PESU sex captured during the current study indicating maternity colonies are not likely present or at least not in high numbers in the area. Managing forests specific to maternity colonies is potentially advantageous in increasing the PESU population around the cave. Because proximity to water was another positive foraging probability factor, maintaining riparian areas adjacent the cave also offers positive implications for PESU foraging.

Significant Deviations:
None.

Equipment:
No equipment purchased for this grant.

Prepared by: Dr. Mark Peaden, Professor, Rogers State University

Date: March 8, 2025

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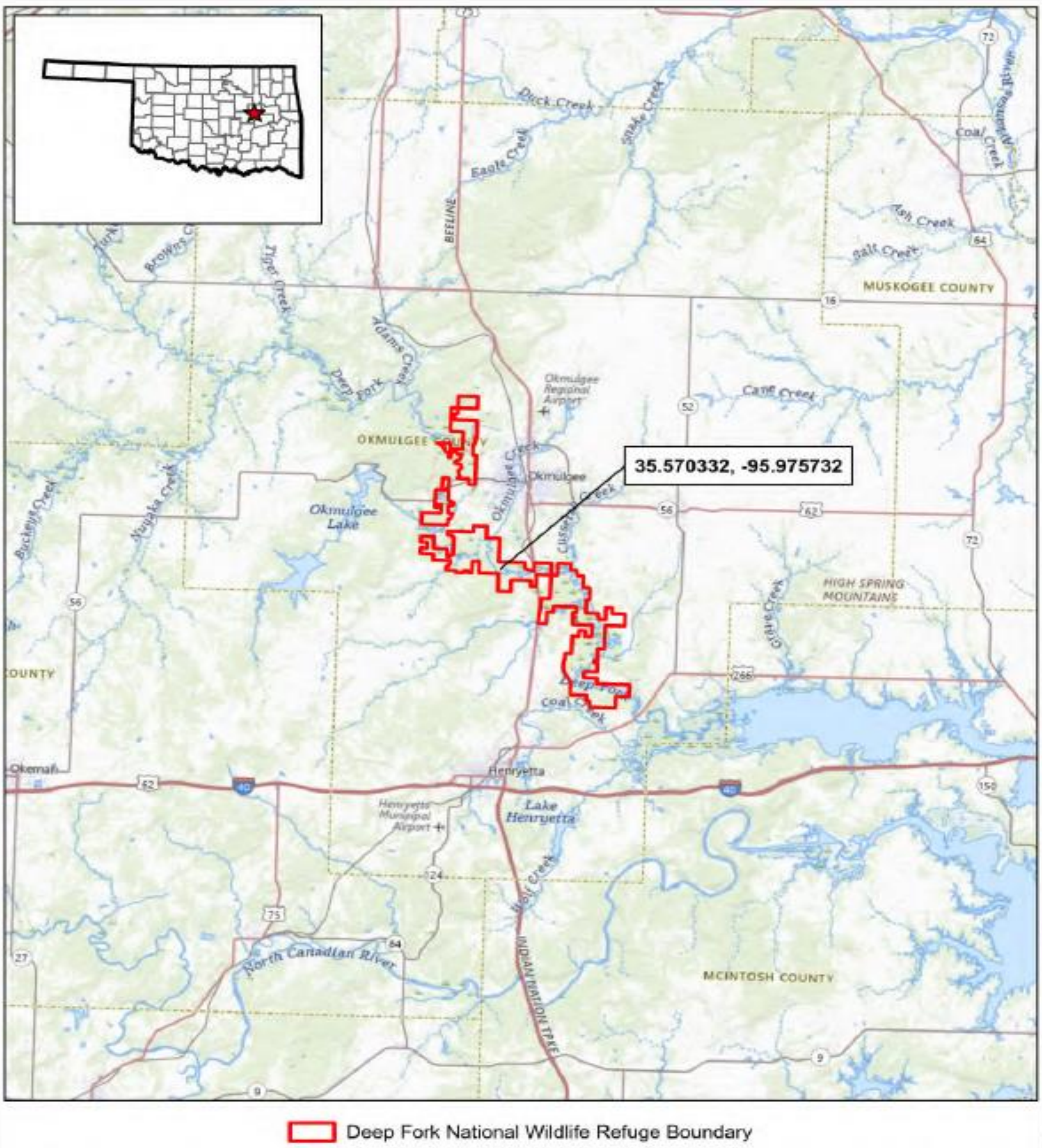

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Figure 1. Location of the PESU foraging study on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

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2329

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Base Map: USGS Topographic Map

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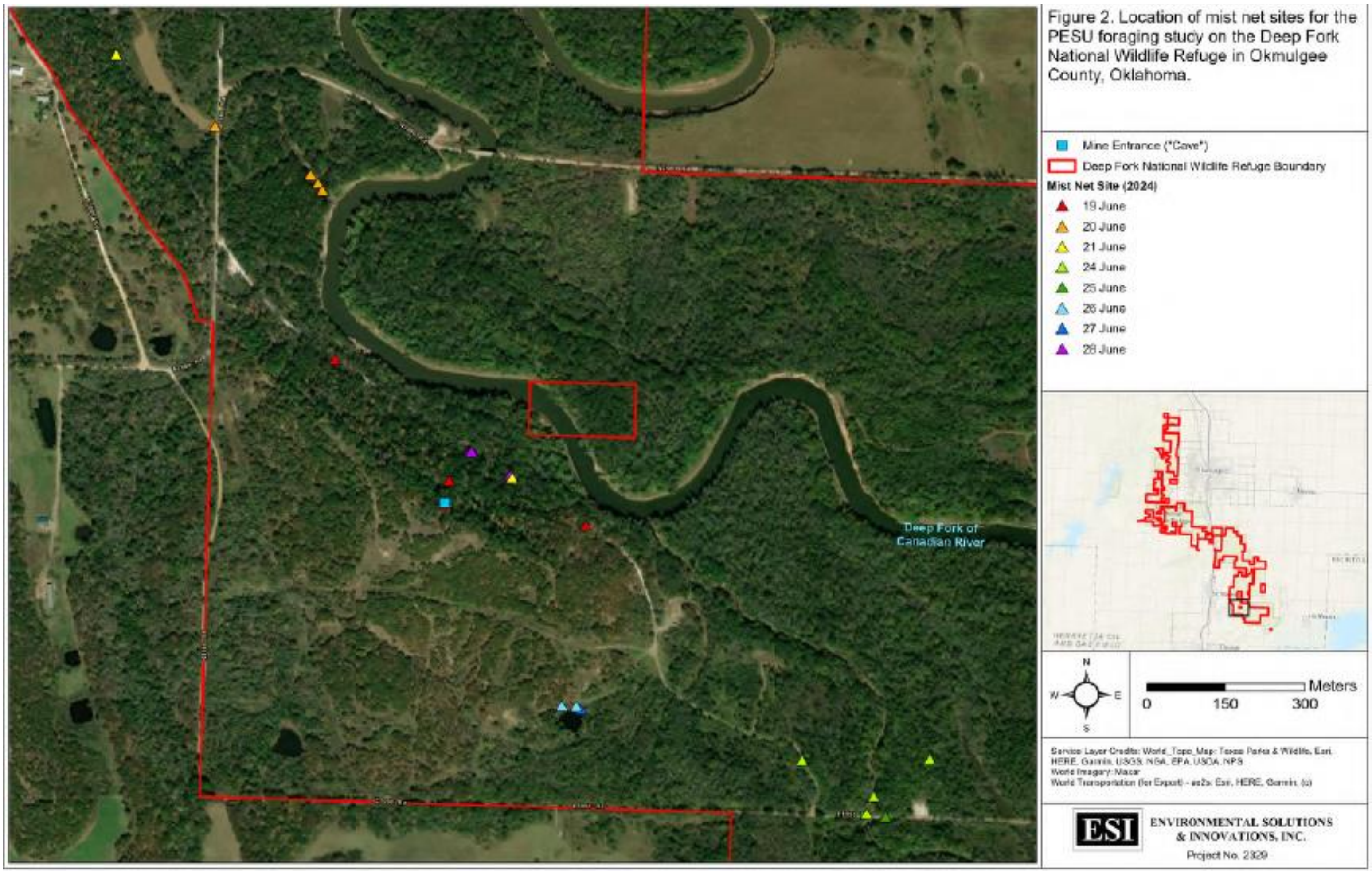

Figure 2. Location of mist net sites for the PESU foraging study on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

Service Layer Credits: World_Topo_Map: Texas Parks & Wildlife, Esri, HERE, Garmin, USGS, NGA, EPA, USDA, NPS
World Imagery: Maxar
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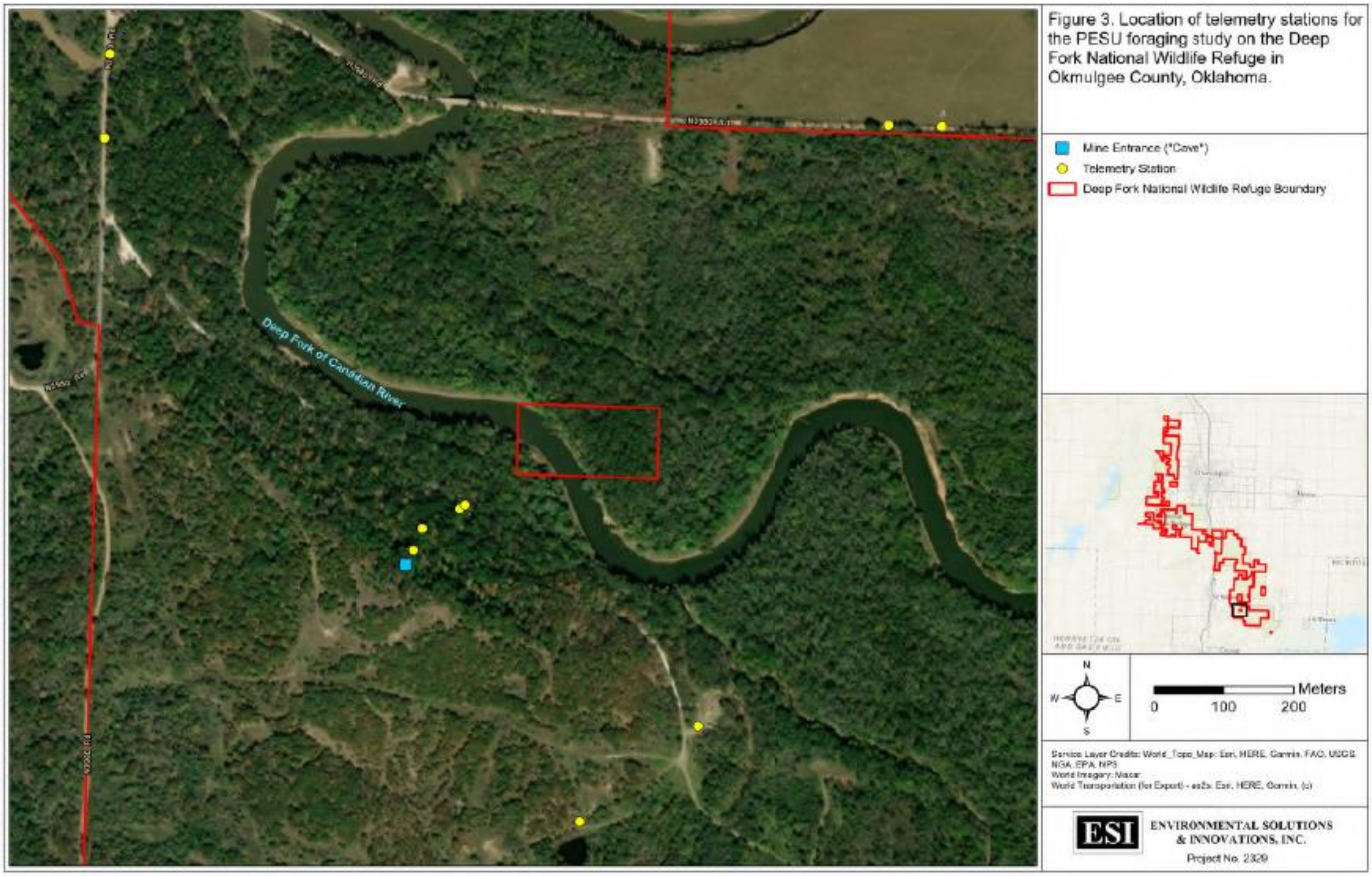

Figure 3. Location of telemetry stations for the PESU foraging study on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

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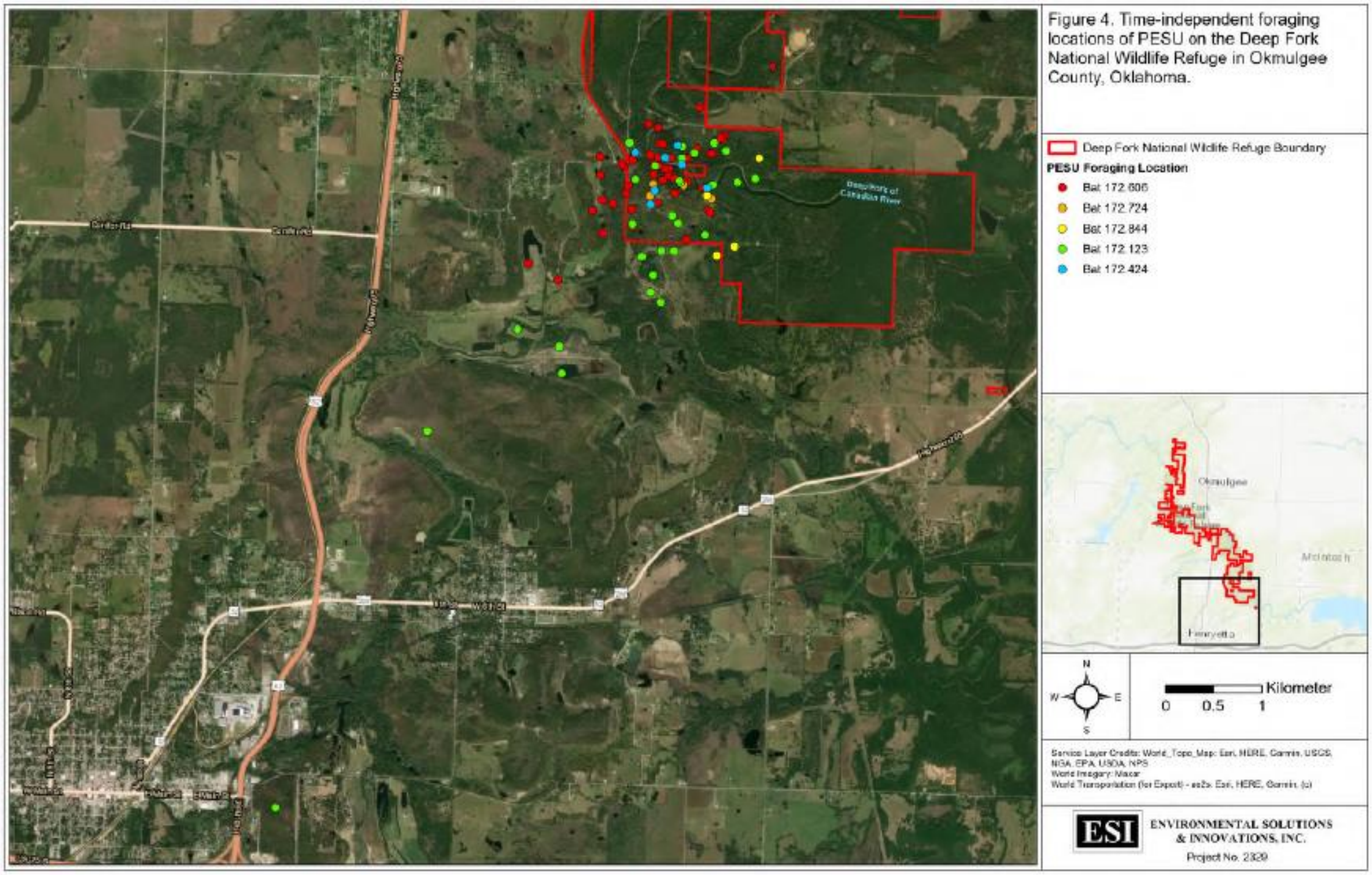

Figure 4. Time-independent foraging locations of PESU on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

▭ Deep Fork National Wildlife Refuge Boundary

PESU Foraging Location

- ● Bat 172.606
- ● Bat 172.724
- ● Bat 172.844
- ● Bat 172.123
- ● Bat 172.424

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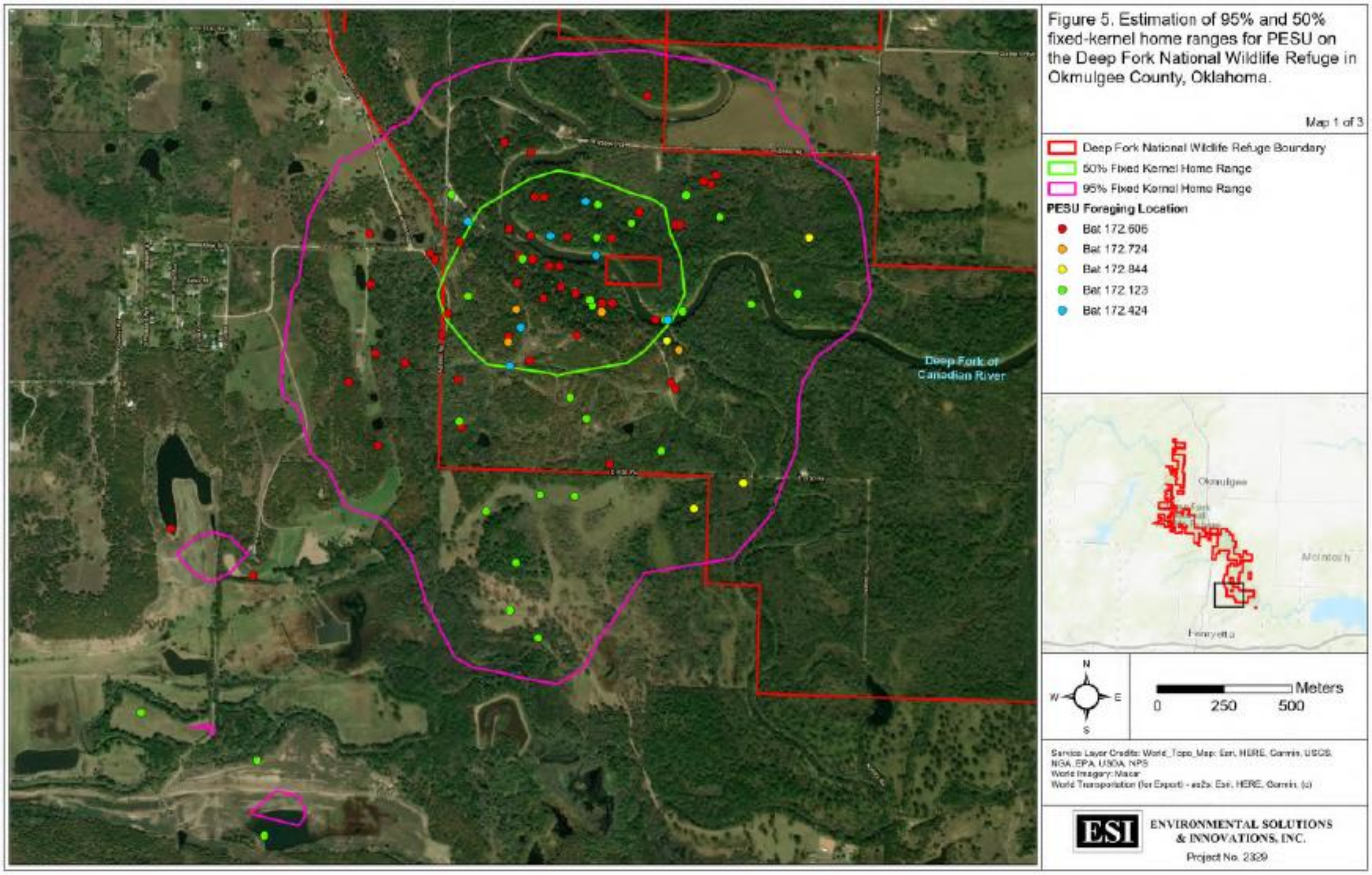

Figure 5. Estimation of 95% and 50% fixed-kernel home ranges for PESU on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

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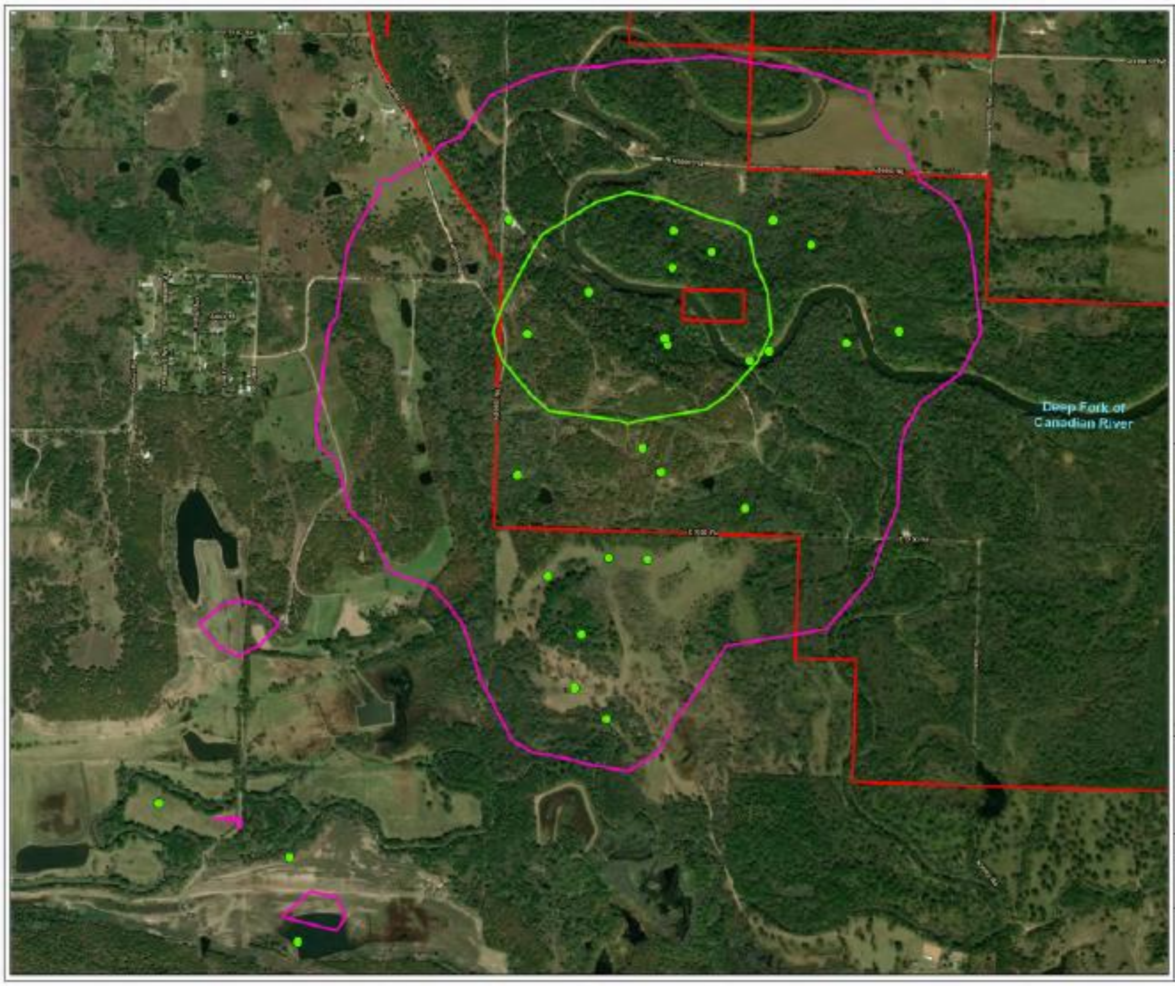
Figure 5. Estimation of 95% and 50% fixed-kernel home ranges for PESU on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

Map 2 of 3



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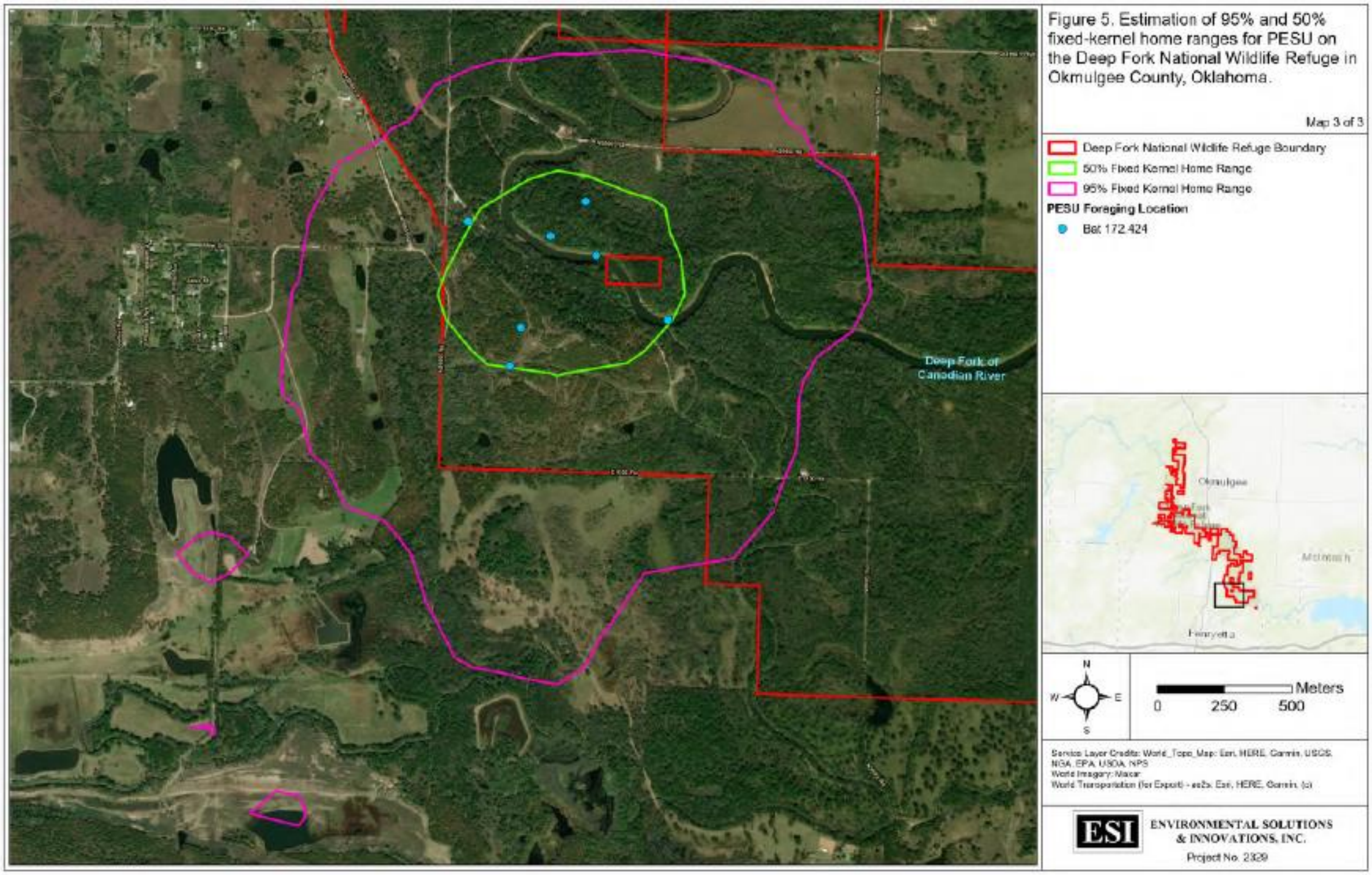

Figure 5. Estimation of 95% and 50% fixed-kernel home ranges for PESU on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.

Service Layer Credits: World_Topo_Map: Esri, HERE, Garmin, USGS, NGA, EPA, USDA, NPS
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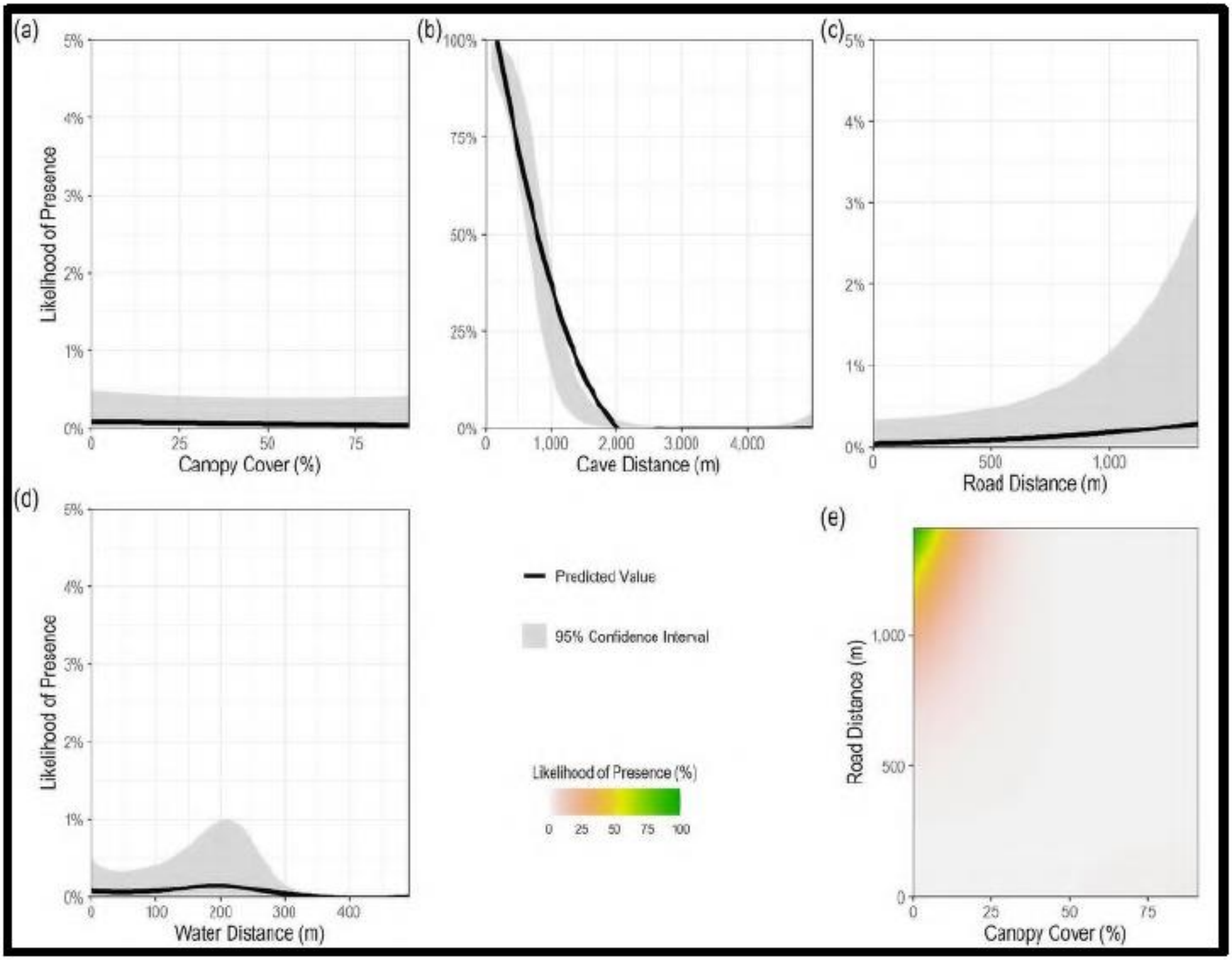
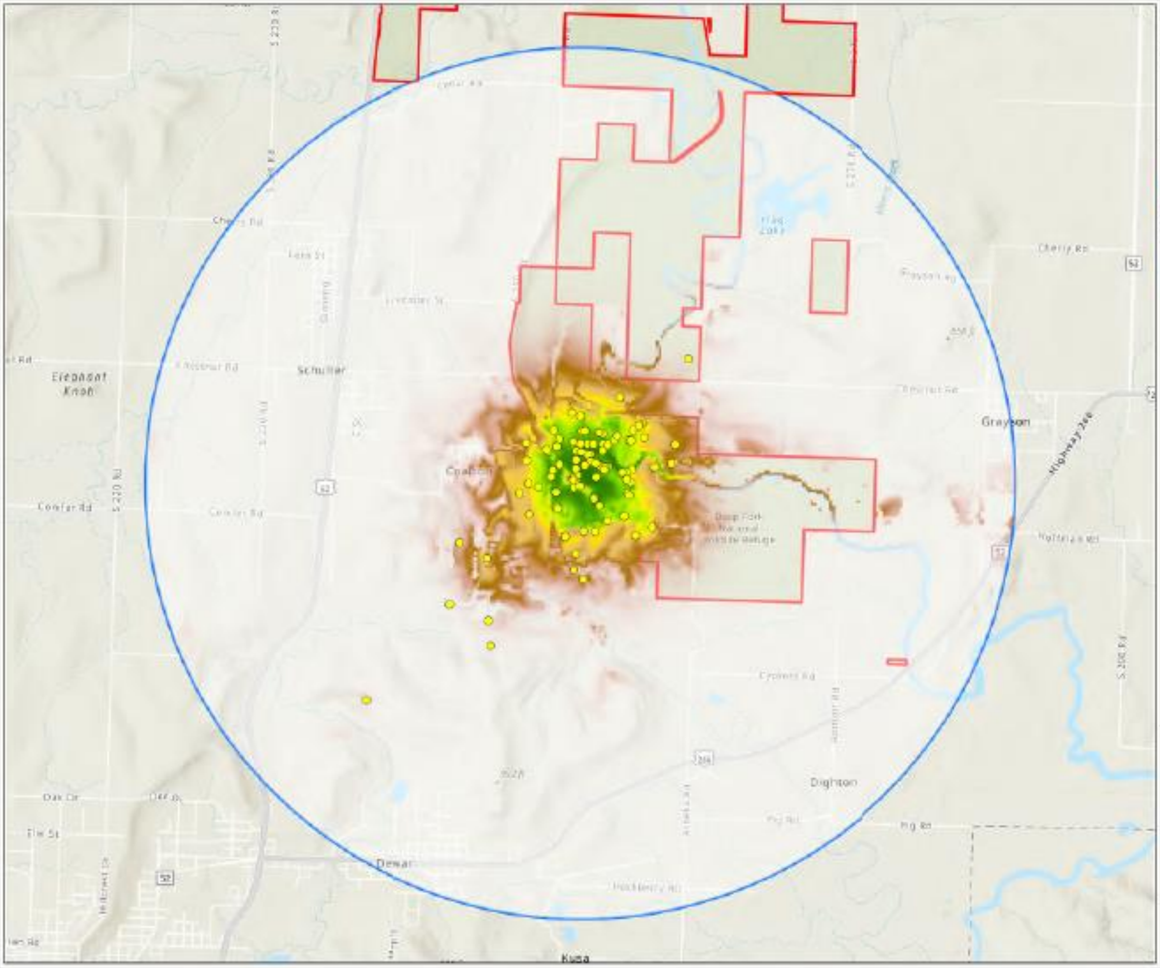
Figure 6: Marginal predictive plots of variables used to describe PESU foraging on the Deep Fork National Wildlife Refuge in Okmulgee County, OK



NOTE: Extents of y-axes vary among continuous variable plots. Likewise, linear predicitive plots for canopy cover (a) and distance to roads (c) do not capture the interaction between these two variables and so should be interpreted with caution.

Figure 7. Presence probability of PESU on the Deep Fork National Wildlife Refuge in Okmulgee County, Oklahoma.



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