Foraging ecology of wild turkey broods in Kansas

by

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B.S., The Ohio State University, 2024

A THESIS

submitted in partial fulfillment of the requirements for the degree

MASTER OF SCIENCE

Division of Biology
College of Arts and Sciences

KANSAS STATE UNIVERSITY
Manhattan, Kansas

2026

Approved by:

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Abstract

Complex landscape-specific interactions among predation, starvation, and hunting pressure influence game bird populations. The wild turkey (*Meleagris gallopavo*) is an economically important gamebird in Kansas, yet their reproductive success has declined, reflecting regional population trends. Poult survival is a key driver of recruitment, as wild turkey poults experience a survival bottleneck during the first 2 weeks of life, when they are flightless, and have high protein demands to sustain growth and development. To meet protein demands, poults rely heavily on arthropods that can vary in abundance due to landscape characteristics. Thus, selecting foraging habitats that provide sufficient food resources is important for poult survival, which exerts momentous influence on wild turkey population dynamics.

Despite this understanding, there is a lack of information regarding diet and foraging habitat selection during this critical life stage in Kansas. Past studies of wild turkey diets have used traditional methods (crop dissection, fecal dissection, and observation), which are invasive, fail to detect soft-bodied prey items, and limited in taxonomic resolution. DNA metabarcoding is a molecular approach that addresses these limitations. Therefore, my objectives were to characterize diets of wild turkey broods using DNA metabarcoding, and evaluate how habitat characteristics, plant nutrient availability, and arthropod communities influence brood foraging site selection.

I captured, marked with transmitters, and monitored wild turkey brood-rearing females in Kansas during 2024–2025 (n = 400). During weekly brood survival surveys, I collected fecal samples (n = 299) from brood-rearing females, associated poults, and opportunistic samples. I examined diets of wild turkey adults and poults during this critical brood rearing period using DNA metabarcoding and related prey consumption to the habitat where fecal samples were

collected. I used location data to compare habitat characteristics, plant nutrient availability and arthropod communities among used (n = 150) and available (n = 282) foraging sites. I hypothesized a bottom-up conceptual relationship that I fit into a piecewise structural equation model to investigate drivers of brood foraging site selection incorporating habitat characteristics, arthropod metrics, and plant nutrient availability.

Overall, the dominant orders detected in wild turkey diets, based on frequency of occurrence (n = 299), were Hemiptera (70%), Orthoptera (60%), Coleoptera (58%), Lepidoptera (57%), and Diptera (45%). At the species level, DNA metabarcoding revealed *Cicadettana calliope* (Southern grass cicada) and *Neotibicen pruinosus* (Scissor grinder cicada) were the most frequently consumed species for all age groups. Plant material consumed matched what was available across the landscape. Among study regions, arthropod species composition in diets varied for brood-rearing females and opportunistic samples, whereas brood-rearing females and poults shared similar diets. Woody cover correlated with the consumption of cicada (Hemiptera) and moth (Lepidoptera) species, whereas grass cover correlated with the consumption of grasshopper (Orthoptera) and spider (Araneae) species within habitats where fecal samples were collected.

Foraging habitats were characterized by greater forb cover, plant nutrient quality, horizontal visual obstruction (0.00–0.50 m) and arthropod morphospecies richness. Plant nutrient quality, particularly phosphorus and crude protein, combined with arthropod morphospecies richness directly influenced brood foraging site selection. Vegetation composition and structure did not directly influence selection at a fine scale (10 m); instead, their effect was mediated through arthropod morphospecies richness and plant nutrient availability. These findings indicate

resource-mediated selection, where wild turkey broods respond more strongly to the availability of food resources at fine spatial scales than to vegetation structure or composition alone.

In summary, this was the first known wild turkey diet study to use DNA metabarcoding, uncovering prey items that have not been previously described. At a fine-scale, foraging habitat selection was influenced by resource availability more than the compositional and structural components. Conservation that creates early successional habitats will be the most beneficial in supporting a wild turkey broods life cycle. In my study system, early successional habitats were defined by greater forb cover, intermediate herbaceous cover, and greater arthropod richness, ultimately driven by disturbance. Landowners and managers could utilize disturbance regimes (grazing, fire) that create beneficial foraging habitats, while accommodating for nesting and roosting habitats needed during the reproductive period.

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Acknowledgments

The research presented in this thesis is the result of a highly collaborative effort. Numerous individuals, organizations, and funding sources played integral roles in the execution and completion of this work. Thus, there are many to acknowledge and thank.

First and foremost, I would like to thank Dr. Daniel Sullins for his excellent mentorship throughout the duration of this project. His dedication to students and peers, research, education, conservation, and science provide a model that aspiring scientists should strive to emulate. Outside of research, I had the opportunity to hunt deer, turkey, waterfowl, and upland game birds alongside Dan. Even in those settings, he continued to cultivate learning opportunities and share wisdom that I will carry with me moving forward. I would also like to thank Dr. David Haukos for his exemplary leadership, guidance, support, and service on my committee. I greatly appreciate his openness to discuss any topic and the collaborative environment he fostered during weekly lab meetings. His mentorship ensures that the next generation of scientists is well equipped to navigate diverse and complex landscapes. Additionally, I would like to thank my remaining committee members, Dr. Tania Kim and Dr. Adam Ahlers, for their wisdom, guidance, and willingness to provide assistance whenever it was needed.

I am very fortunate to have had the opportunity to be part of a large collaborative project with other graduate students. Mary Ware, Caroline Skidmore, Grace Alford, and Sara Hansen, thank you for your hard work, and support over the past years. Caroline Skidmore was the glue of this project; she rarely took time away from the field, always picked up the phone when an issue arose, and was wholeheartedly dedicated to everyone around her, including myself. Her character inspired motivation in other grad students, as well as technicians in the field. The habitat data collected in Chapter 2 were based on protocols developed by Caroline, and I am

honored to have worked with her. Additionally, thanks to my fellow Michigander, Mary Ware for her friendship. Mary was someone who I could console about anything, and her steady support and humor made this experience fun.

Thanks to my colleague, officemate, field technician, and friend, Randall Wilson. Randy was the lead field technician for the West study region and was the first person I worked with upon arriving in Kansas. He never shied away from a long day and made the toughest days of the project fun. I also had the opportunity to share an office space with Randy and appreciate his willingness to listen to anything I had to say, whether it was something random, feedback on presentation slides, or just chatting.

This research could not have been conducted without the assistance of all private landowners that allowed access to their properties throughout the project. Several of these landowners were exemplary stewards of the land and wildlife centric.

I would like to thank Jonah Ventures for conducting DNA metabarcoding on fecal samples, results that are presented in chapter 1. Additionally, I would like to thank the Oklahoma State University Soil Testing Lab for conducting nutrient analyses on forage clippings presented in Chapter 2.

I thank all of the sponsors that provided financial and logistic support, including the Kansas Department of Wildlife and Parks, and the National Wild Turkey Federation. Thanks for support from: Jeff Rue, Steve Adams, Vickie Cikanek, Joe Daniels, Caleb Durbin, Kent Fricke, Cale Hedges, Kent Hensley, Lucas Kramer, Brent Konen, Keaton McGuire, Andy Nelson, Jeff Prendergast, James Svaty, and Brian Serpan. Specifically, I would like to thank Scott Tommason for his support of research conducted around Wilson Lake. He was quick to assist with coordinating landowner contacts and securing access to properties, eager to receive project

updates, and allowed us to host a project update for KDWP and local landowners at Wilson Lake. I would additionally like to thank Chris Rhodes, President of the Kansas Chapter of the National Wild Turkey Federation. Chris is a true wild turkey connoisseur who consistently showed interest in our project. He joined us during unsuccessful trapping efforts, provided valuable insight on wild turkey movements in Hays, Kansas, shared stories over dinner, and attended research updates. His enthusiasm and support for our work were a constant reminder of why we do this research.

Most importantly, I would like to thank my partner, Kelsey Wolf. She supported me throughout this project every single day. She was enthusiastic about the research, often joining me for fieldwork and trapping events. She helped me study for exams and listened to countless practice presentations, day after day. Honestly, she probably knows the project just as much as I do. I will forever appreciate her support and enthusiasm during this time.

I would like to thank my family, friends, and mentors back east of the Mississippi for their continued support throughout this process. I am especially grateful to my parents, Paul and Stephanie Marchese, for raising me to value determination, dedication, perseverance, and education. To my brother, Alec Marchese, thank you for your support and for the many wild turkey hunts we have shared. I also thank my grandparents, Ron and Vicki Marchese, for their encouragement and interest in this project. I am grateful to my grandfather for introducing me to wild turkeys at a young age, where we spent countless days chasing birds around a small property in Hillsdale County, Michigan. These experiences ultimately led me here. I would also like to thank my close friend, Kendall Byrd, whose motivation and dedication to science and research inspired me to pursue a graduate degree. He consistently took the time to listen to project updates, review presentations, and provide thoughtful feedback. Furthermore, I am

grateful to Dr. Bob Gates, Joseph Lauthenbach, Mark Wiley, and Nathan Stricker for the opportunities that preceded this work, which allowed me to contribute to a wild turkey project in Ohio, conduct extensive fieldwork, and develop the skills necessary to complete this project. Additionally, I thank Dr. Alexis Londo for her continued support following my undergraduate studies and her interest in my work.

Lastly, I would like to acknowledge the many field technicians who were instrumental in collecting the data that made this project possible. Long days in the field were often required to meet demanding expectations, and their efforts were critical to the success of this work. Many thanks to Randal Wilson, Corbin Kissinger, Susie Cantonwine, Sarah Shaffer, Luke Bays, Malia Agee, Ximena Larrieu, Lauren Bonavia, Tiffany Hough, Jay Mason, Paige Wimberly, John Ohlwein, Shelby Muntz, Audra Weber, Breck Aguinaga, Hunter Nipp, Paige Mongon, Cooper Williams, Devenny Widmer, Ella Cremer, and Sara Lukavsky. Specifically, I would like to thank Holly Henderson for her hard work and dedication as the lead field technician in the West study region during 2025. She demonstrated exceptional ability in working with landowners that led to securing access to several new properties and allowed for expanded data collection. She was also eager to assist other study regions, often driving several hours early in the morning to help with trapping efforts. Her work ethic ultimately led her to pursue her own graduate research project, and I look forward to her continued success. Additionally, I thank Jamie Trout, Kiersten Glass, Taylor Rodriguez-Bash, Arson Harris, Hannah Huyett, and Halle Barker for their work in the "Bug Lab." They were responsible for preparing approximately 500 forage samples for analysis and sorting over 8,000 insects to taxonomic order. Their efforts were foundational to the arthropod-related metrics presented in Chapter 2.

Throughout this thesis, I use “I” to describe tasks completed. However, as reflected in the acknowledgments above, this work was highly collaborative, and I have simply synthesized those collective efforts into written form.

Dedication

This thesis is dedicated to my grandfather, Ronald J. Marchese, who instilled in me a passion for the outdoors and wildlife that ultimately led me here. He was with me when I completed my hunter safety course, harvested my first wild turkey, and took my first white-tailed deer. He dedicated many hours to teaching me the skills needed not only to be a hunter, but to succeed in life. His unwavering support and the wisdom he passed down have shaped the man I am today.

Chapter 1 - Characterizing the Diets of Wild Turkey Broods in Kansas During a Survival Bottleneck

Introduction

Knowledge of wildlife diets is fundamental for understanding habitat associations (Gooch et al. 2015, Merems et al. 2020, Kovinka et al. 2023). Examining diets during critical life stages (e.g., brood rearing) may provide additional ecological insight into populations dynamics. For example, synchronization of peak food availability near hatch dates for several avian species highlights the potential importance of nutrition during this period (Davies & Deviche 2014). In mammals, nutritional conditions during gestation and lactation can influence offspring growth trajectories (McDonald & Fuller 2005, Monteith et al. 2009). In rodents, periods of population abundance can peak with food abundance following bumper mast events (Ostfeld et al. 1996). Outside of these examples, knowledge of dietary composition and nutritional dynamics during critical life stages remains limited for many species (Birnie-Gauvin et al. 2017, Sullins et al. 2018, Jarman et al. 2024). Diets are especially important during critical life stages such as the reproductive period in precocial birds, when females require substantial nutrients to produce eggs (Williams 2005) and newly hatched young must independently obtain high-quality foods to sustain growth (Starck & Ricklefs 1998). Inadequate nutrient intake during offspring rearing can reduce survival and reproductive output (Drut et al. 1994, Allen & Ullrey 2004). Gallinaceous young, including wild turkey (*Meleagris gallopavo*) poults, spend much of their time foraging (Chamberlain et al. 2020, Healy 1992). Their survival is closely linked to the habitat associations formed during foraging activities (Chamberlain et al. 2020). A greater understanding of selected foraging habitats, diet composition, and food availability may help explain regional patterns in wild turkey productivity.

Wild turkey declines have been observed throughout much of the North American where estimated abundances have fallen 3%, spring harvest 12%, and fall harvest 31% between 2014 – 2019 (Chamberlain et al. 2022). In Kansas, harvest, poults per hen, and population indices have declined over the past decade (Prendergast 2013, Prendergast 2025). Understanding factors that influence wild turkey population dynamics are critical for effective management and conservation. Nest success, hen survival, and poult survival are the most influential factors determining the overall demographic performance of populations (Vangilder and Kurzejeski 1995, Roberts and Porter 1995, Londe et al. 2023). Among these factors, poult survival plays a vital role in generating adequate recruitment. A regional 3:1 poult-to-hen ratio is thought necessary to sustain or grow a population (Hillestad and Speake 1970, Everett et al. 1980, Palmer et al. 1993, Rolley et al. 1998, Spears et al. 2007).

Wild turkey poults are precocial; they hatch with open eyes, are feathered, mobile, and consume food without facilitation from a brood-rearing female (Healy 1992). During the first three days, poults are thought to rely on yolk sac reserves, but for approximately two weeks, they require invertebrates to meet their high dietary protein demand where they need to consume 28% of their body mass in protein to sustain growth and development of flight feathers (Hurst 1992). This critical stage of life may be deemed a survival bottleneck; without their flight feathers, they are unable to effectively avoid predation. Previous studies have shown poult survival increases dramatically after the first two weeks of life when flight feathers are developed (Healy 1992, Spears at al. 2007, Chamberlain et al. 2020). The general diet and development of poults during this brooding stage have been described (Healy 1985, Hurst 1992, Rumble & Anderson 1996); however, fine-scale information on the specific food resources used and selected by wild turkey poults remains limited (Korschgen 1967). Most studies on poult diets have been limited by low

sample sizes of wild individuals ($n < 10$) or have studied poults imprinted on domestic chickens or turkeys (Hurst 1992, Tebo et al. 2022).

Wild turkey diet studies have primarily relied on traditional techniques such as crop dissection, fecal dissection, and observations (Tebo et al. 2022, Healy 1985, Rumble & Anderson 1996). For example, Tebo et al. (2022) dissected crops and gizzards of human-imprinted poults following euthanasia and documented a strong selection for the orders of Coleoptera, Hymenoptera, and Isopoda, while avoiding orders Araneae, Diptera, Hemiptera, Lepidoptera, and Orthoptera in grassland sections of reclaimed mine sites in Illinois. On the contrary, Healy (1985) observed the most consumed arthropod orders for human-imprinted poults were Diptera, Hemiptera, and Aranea. Microscopic fecal analyses were used by Rumble & Anderson (1996) to examine the diet compositions of poults and brood-rearing females. Coleopterans, Orthopterans, and Dipterans were among the most frequent arthropod orders consumed (Rumble and Anderson 1996). Stable isotope analysis ($\delta^{13}C$ and $\delta^{15}N$) has been used to document diets and foraging habitat of past and present wild turkey populations (McCaffery et al. 2014, Otieno & Frenette 2017) and involves measuring the ratios of isotopes derived from tissues that reflect food and water consumed.

Though traditional techniques provide knowledge of wild turkey diets, they are limited in detecting soft-bodied prey items, and fail to identify species level taxonomic resolution, relying on broad generalizations that arise from Order level identifications. Stable isotope analyses can provide insights into trophic relationships, but interpretations may be influenced by variability in diet–tissue fractionation factors, temporal variation in prey isotope signatures, and incomplete sampling of potential dietary sources, often resulting in broad trophic classifications rather than

identification of specific taxa (Crawford et al. 2008). Consequently, a more precise approach is needed to provide a deeper understanding of turkey diets.

DNA metabarcoding is a molecular approach that works rapidly in identifying organisms in environmental contents at fine-scale taxonomic resolution. It is particularly effective for detecting soft-bodied prey items that are often underrepresented in traditional methods such as visual gut or fecal analysis (Zeale et al 2011, Pompanon et al. 2012, Sullins et al. 2018). Early molecular diet analyses emerged in the early 2000s, with PCR-based techniques proving highly effective and versatile for detecting prey DNA (Symondson 2002). Deagle et al. (2009) demonstrated that sequencing DNA from seal (*Arctocephalus pusillus doriferus*) feces revealed geographic variation in diet, highlighting utility of the method. Sequencing DNA of fecal samples can also detect greater species diversity relative to morphological dietary techniques (Deagle et al. 2009). The continued advancement of molecular technologies led to the development of DNA metabarcoding, which further improved the speed and accuracy of eDNA identification. For example, Zeale et al. (2011) found that DNA-based methods provided greater taxonomic resolution than morphological analyses in bat (*Chiroptera*) species where direct observation was limited.

As with any method, there are limitations and challenges to using the DNA metabarcoding approach. Challenges include optimizing collection and extraction methods, minimizing contamination and primer bias, developing comprehensive reference databases, standardizing classification and bioinformatics workflows, and accounting for DNA degradation that can misrepresent true species presence (Ruppert et al. 2019). Methods that can address these challenges are currently being advanced and DNA metabarcoding provides an opportunity to fill knowledge gaps regarding wild turkey diets during a critically important life stage.

Despite methodological advancements, there is limited information on wild turkey diets during brood rearing with species level inference and limited dietary information from the Great Plains region. For example, it is unknown whether poults and brood-rearing females share similar diets. Moreover, there remains an important gap in species-level inference as most wild turkey diet studies have identified prey only to the order level (Healy 1985, Hurst 1992, Rumble & Anderson 1996, Tebo et al. 2022). These broad taxonomic generalizations limit ability by managers to link consumption patterns with specific habitat associations in the Great Plains. Therefore, I used DNA metabarcoding to address these knowledge gaps and build upon historical understandings of wild turkey diets during brood rearing.

My objectives were to: (1) identify the most frequent arthropod and plant taxa consumed by wild turkey poults and brood-rearing females; (2) assess age-related shifts in arthropod richness among poults; (3) investigate age-related and temporal variation in diets; and (4) evaluate the influence of foraging habitat composition on the presence of top arthropod taxa in fecal samples. I hypothesized that wild turkey diets will vary among age classes (poult vs. adult) and landscapes. Specifically, I predicted that poults will consume more soft-bodied prey items, including species from the order Lepidoptera, whereas adults will consume more hard-bodied prey items (e.g., Coleoptera). I further hypothesized that arthropod richness in poult diets will increase with age and body size, providing poults with a greater capacity to consume larger prey items as they age. Lastly, I predicted that foraging habitat composition will influence the occurrence of specific arthropod species, depending on the habitat associations of those food types.

Methods

Study Area

My study area encompassed three study regions in Kansas 39° to 38°N latitude and -100° to -97°W longitude (Figure 1.1). The study area included grassland and cropland with sparse forest cover that increases with annual average precipitation from west-to-east gradient (63.4 cm – 90.8 cm in 2024; 60.05 cm – 89.23 cm in 2025; NOAA National Centers for Environmental information, 2026). The study area was divided into West, Central, and East study regions. Within study regions, wild turkeys largely occupied landscape mosaics of wooded edges, cropland, and grasslands. Grasslands span the mixed-grass to tallgrass prairie ecoregions and included big bluestem (*Andropogon gerardii*), sideoats gramma (*Bouteloua curtipendula*) and switchgrass (*Panicum virgatum*). Most grassland in the study were managed for cattle production or enrolled in the U.S. Department of Agriculture Conservation Reserve Program. Croplands were predominantly planted to corn (*Zea mays*), soybeans (*Glycine max*), sorghum (*Sorghum bicolor*), wheat (*Triticum aestivum*), and alfalfa (*Medicago sativa*). Forest cover primarily included gallery cottonwoods (*Populus deltoides*), eastern redcedar (*Juniperus virginiana*), sumac (*Rhus* spp.), and common hackberry (*Celtis occidentalis*).

In 2024, the average temperature across study regions was 14.1 °C, with average daily minimum and maximum temperatures of 7.3 °C and 20.4 °C, respectively. During the 2024 brood rearing period Kansas experienced moderate drought; the statewide Palmer Drought Severity Indices (PDSI) were -2.50 in May, -2.40 in June, and -2.44 in July, and -2.19 in August but varied regionally (NOAA National Centers for Environmental Information 2026). In 2025, the yearly temperature among study regions was 13.47 °C. During the brood-rearing period in 2025, Kansas experienced mid-range drought conditions with the state-wide PDSI at -1.58 in

May, -0.99 in June, 1.0 in July, and 1.13 in August, highlighting a wetter year compared to 2024 (NOAA National Centers for Environmental Information 2026).

Mean elevation among study sites ranged between 300 and 700 m asl with variable topography that included riparian draws, valleys, and bluffs interspersed among rolling grassland uplands. These study regions and their respective study sites captured an ecological gradient in Kansas, reflecting variations in vegetation communities, soil composition, and land use, ultimately driven by an east-to-west precipitation gradient.

East Region- The East study region is comprised of nine study sites represented by capture locations, defined using non-overlapping minimum convex polygons (MCPs) from GPS-marked female wild turkeys occupying the Flint Hills and Osage Cuestas ecoregions of Kansas. Study sites included both private and public lands in Riley, Morris, Osage, Chase, Greenwood, Butler, and Coffey counties. Public lands included Fort Riley, and Tuttle Creek, Council Grove, Melvern, and Fall River Wildlife Areas. East study sites had a mean landcover composition of 68% grassland, 11% cropland, and 16% woodland (Table 1.1). Soybeans were the most dominant crop type averaging 6.8% of total land cover among regional study sites (Table 1.1). Dominant soil texture consisted of silt loams and silty clay loams (USDA Natural Resources Conservation Service 2025). Among study sites during the brood-rearing period in 2024 (May-August), the average temperature was 23.8 °C and the average precipitation was 11.0 cm. Long-term (1991–2020) average annual temperature and precipitation in the eastern study region were 12.9 °C and 101.5 cm, respectively (NOAA National Centers for Environmental Information 2026). Palmer Drought Severity Indices (PDSI) values were: -0.35 for May, -0.29 for June, -0.34 for July, and -0.18 for August. During the same period in 2025, the average temperature was 22.7 °C and the average precipitation was 14.2 cm (NOAA National Centers for Environmental

information 2026). Palmer Drought Severity Indices (PDSI) values were: -0.31 for May, 0.51 for June, 0.66 for July, and 0.73 for August.

Central Region- The Central study region consisted of two study sites within the Smoky Hills ecoregion of Kansas on public and private lands in Ellsworth, Mcpherson, Saline, and Marion counties. Public lands included McPherson and Kannapolis Wildlife Areas. Central region study sites averaged 65% grassland, 24% cropland, and 6.7% woodland (Table 1.1). The dominant crop type was winter wheat averaging 9.5% of total coverage among sites (Table 1.1). Dominant soil textures included loams and silty clay loams (USDA Natural Resources Conservation Service 2025). During the brood-rearing period in 2024, the average temperature was 24.1 °C while the average precipitation was 11.4 cm during the brood rearing period. Long-term trends (1991–2020) in the central study region indicate an average annual temperature of 12.7 °C and annual precipitation of 75.2 cm (NOAA National Centers for Environmental Information 2026). Palmer Drought Severity Indices (PDSI) values were: -2.97 for May, -2.85 for June, -3.04 for July, and -2.51 for August. In 2025, the average temperature was 22.7 °C and the average precipitation was 15.0 cm (NOAA National Centers for Environmental information 2026). Palmer Drought Severity Indices (PDSI) values were: -0.90 for May, -0.80 for June, -0.29 for July, and 0.96 for August.

West Region- The West study region encompassed four study sites within the Rolling Plains and Breaks Ecoregion of Kansas, which typically receives less precipitation and forest cover is sparse. West study sites were on private and public lands in Trego, Ellis, and Russell counties. Public lands included the Kansas State University agricultural research center, Wilson Wildlife Area, and federal lands surrounding Cedar Bluff reservoir. West region study sites averaged 61% grassland, 30% cropland, and 2.9% woodland (Table 1.1). The dominant crop types were winter

wheat and sorghum, both occupying ~9.7% of total coverage among sites (Table 1.1). Dominant soil textures included silt loams (USDA Natural Resources Conservation Service 2025). During the brood rearing period in 2024, the average temperature was 23.8 °C while the average precipitation was 9.0 cm. Long-term trends (1991–2020) in the western study region indicate an average annual temperature of 13.1 °C and annual precipitation of 63.1 cm (NOAA National Centers for Environmental Information 2026). Palmer Drought Severity Indices (PDSI) values were: -3.15 for May, -3.45 for June, -3.63 for July, and -2.71 for August. In 2025, the average temperature was 22.3 °C and the average precipitation was 7.3 cm (NOAA National Centers for Environmental information 2026). Palmer Drought Severity Indices (PDSI) values were: -1.90 for May, -2.02 for June, -2.15 for July, and -1.73 in August.

Capture and Handling

I captured wild turkey at all study sites during the winter months of 2024 and 2025 using walk-in funnel traps, drop nets, and rocket nets (Austin et al. 1973, Davis 1994). Wild turkeys were sexed based on the coloration of their breast feathers (Schroeder & Robb 2005). I aged individuals as either Adult or Juvenile depending on the color patterns, shape, and wear of the outermost primary feather (Schroeder & Robb 2005). I applied a uniquely numbered 7/8” (22.23 mm) riveted leg band (National Band & Tag Company, Newport, Kentucky, USA) to the right leg of each captured turkey (Diefenbach et al. 2009). Measurements taken included: mass (g), flattened wing chord (mm), exposed culmen (mm), tarsus, beard, and spur lengths (mm). Captured hens that met mass requirements (<4% of body mass; Ausprey 2023) were fitted with backpack harnesses (Guthrie et al. 2011) securing satellite GPS transmitters (G5-T2A Iridium GPS, Advanced Telemetry Systems, Isanti, MN; 152 g). Capture and handling were approved by

state capture permits and protocols by Kansas State University Animal Use and Care Committee (IACUC protocol 4906).

Fecal Collection

I tracked females to locate nests following determination of nest fate and females with broods were tracked for a four-week period. I collected fecal samples from brood-rearing females and their poults (separate vials for each) during weekly brood surveys occurring within an hour of sunrise (2-35 days old). Additionally, wild turkey fecal samples were collected opportunistically, and consisted of all samples found within the study sites that were not directly associated with a marked female. Fecal samples were collected using single-use small plastic sampling spoons and placed into 20-ml vials to minimize DNA contamination. I classified fecal samples as adult or poult samples based on relative size differences. I stored vials labeled with the date, unique adult female band ID, fecal moisture, and coordinates of the collection location in a freezer at field sites and Kansas State University before being shipped frozen overnight to Jonah Ventures (Boulder, CO).

Sequencing

Jonah Ventures (Boulder, CO) extracted genomic DNA from fecal samples using the Omega Biotek Mag-Bind® Universal Pathogen Core Kit (Omega Biotek, Norcross, GA). For arthropods, a portion of the mitochondrial cytochrome c oxidase subunit I (COI) gene was PCR amplified using specific arthropod primers- ZBJ-ArtF1c (5’ AGATATTGGAACWTTATATTTTATTTTTGG 3’) and ArtR2c (5’ WACTAATCAATTWCCAAATCCTCC 3’; Zeale et al. 2011). To determine the consumption of plant material, a portion of the chloroplast trnL intron was PCR amplified from each genomic DNA sample using c (5’ CGAAATCGGTAGACGCTACG 3’) and h (5’

CCATTGAGTCTCTGCACCTATC 3') primers (Taberlet et al. 2007). Each 25 µL reaction was mixed according to the Promega PCR Master Mix specifications (Promega Corporation; Madison, WI), with 3 µL of genomic DNA template. For COI, the PCR conditions included an initial denaturation at 94 °C for 5 minutes, followed by 45 cycles of 30 seconds at 94 °C, 45 seconds at 45 °C, and 45 seconds at 72 °C, with a final extension at 72°C for 10 minutes. For tnrL, PCR conditions included an initial denaturation at 94 °C for 3 minutes, followed by 40 cycles of 30 seconds at 94 °C, 30 seconds at 55 °C, and 1 minute at 72 °C, with a final extension at 72 °C for 10 minutes. Amplicons were then cleaned by incubating them with Exo1/SAP for 30 minutes at 37 °C followed by inactivation at 95 °C for 5 minutes and stored at -20 °C. A second PCR was conducted to finalize library construction by appending Illumina sequencing adapters and incorporating dual index sequences (2 x 10bp) unique to each sample. Final indexed amplicons were cleaned and normalized using Mag-Bind® normalization and sequenced on an Illumina MiSeq (San Diego, Ca) using the v2 500-cycle kit.

Jona Ventures conducted demultiplexing using Pheniqs v2.1.0 with strict barcode matching (Galanti et al. 2021). Primer sequences were removed using Cutadapt v3.4, discarding read pairs lacking primers at the expected 5' position (error rate <0.15) (Martin 2011). Read pairs were merged using VSEARCH v2.15.2, and sequences were filtered by length and error rate: 300–450 bp for COI and ≥100 bp for trnL, both with a max expected error rate ≤0.5 (Torbjørn et al. 2016).

Jonah Ventures inferred exact sequence variants (ESVs) using UNOISE3 (alpha = 5), with sequences occurring fewer than eight times discarded (Edgar 2016). Chimeric sequences were removed with UCHIME3 implemented in VSEARCH (Edgar & Flyvbjerg 2015). Taxonomic assignments for each ESV were made using a custom best-hits algorithm against

GenBank (Benson et al. 2005) and Jonah Ventures voucher databases. A consensus taxonomy was accepted when >90% of top hits agreed at a given taxonomic level.

Characterizing Diets

I analyzed eDNA from fecal samples to identify patterns in arthropod and plant taxa representation, starting at the order level, and evaluating species-level identification when sufficient data were available. I determined the top five arthropod and plant orders within fecal samples by calculating the frequency of occurrence (% of samples) based on a presence/absence framework. These steps were repeated to determine the top-ranked arthropod and plant taxa by study region, age class (Adult, Poult, Unknown), and the combined factors of study region and age class.

Dietary Variations

To evaluate differences in diet composition among demographic groups, I conducted ordinations using non-metric multidimensional scaling (NMDS) using Jaccard dissimilarity based on presence–absence data generated from DNA metabarcoding. I performed analyses at the species level. Species occurring in fewer than 5 samples were removed prior to analysis to reduce the influence of rare taxa. Two separate comparisons were conducted: (1) brood-rearing females (tagged adult hens) versus poults and (2) brood-rearing females versus non-tagged adults. Year (2024–2025) and study region (East, Central, West) were retained as factors in all ordinations and permutational multivariate analysis of variance (PERMANOVA) models to account for temporal and spatial structure in the data. For each comparison, NMDS was fitted on the filtered species-by-sample matrix, and differences in multivariate composition were tested using PERMANOVA with 999 permutations, implemented with the adonis2() function in the vegan package in R. Multivariate dispersion was assessed with betadisper() function in the vegan

package to evaluate heterogeneity of dispersion among groups. All analyses were completed in R (R Core Team 2025).

Arthropod Diversity in Poult Diets

Arthropod dietary diversity in poults was analyzed using Generalized Linear Models (GLMs) with a negative binomial distribution to account for overdispersion. The response variable was ESV richness detected in poult samples (n = 88). Exact sequence variants represent unique sequence-level taxonomic units derived from metabarcoding and provide a standardized and reproducible measure of diversity (Porter & Hajibabaei 2020). Because ESVs resolve sequence variation at single-nucleotide resolution, ESV richness may exceed true species richness by capturing intraspecific haplotypes (Olds et al. 2016). Predictor variables included poult age (days since hatch), region, and Julian date, as well as read depth to account for variation in sequencing effort among samples (Kleine Bardenhorst et al. 2022). The model suite included additive and interaction terms among predictors, as well as single-variable models, each fitted with and without the read-depth covariate. A null (intercept-only) model was also fitted. Models were compared using the Akaike Information Criterion corrected for small sample sizes (AICc) to assess relative support for age, region, day, or the null model. I considered models ecologically relevant models if ranked higher than both the null and the read depth–only models based on AICc. Predicted values and confidence intervals were generated from the best-supported model and visualized across the range of days since hatch.

Habitat Influences on Arthropod Consumption

I used distance-based redundancy analysis (dbRDA) with Jaccard dissimilarity to evaluate relationships between the most consumed arthropod taxa at species level and habitat characteristics, specifically percent grassland, woody cover, cropland, and crop types. The

response data were structured in a presence/absence framework for the top arthropod taxa detected in fecal samples. Cover type percentages were extracted from 95% minimum convex polygon (MCP) 48-hour home ranges (n = 155) developed for each GPS-tagged female wild turkey from which fecal samples were collected. A 48-hour home range was selected because it reflected the spatiotemporal foraging extent incorporated into the fecal samples (Sullins et al. 2018). For opportunistic fecal samples with no tag association, a standardized buffer (Area = 95,000 m^2) was applied. This buffer size was derived by averaging the area of 48-hour home ranges created for tagged females during the brood-rearing period. Cover type percentages were then extracted from these standardized buffers to evaluate habitat influence on diets (Boyce 2006). Both 48-hour home ranges and standardized buffers were created in ArcGIS Pro. I used the Kansas Ecological Systems Map (Kansas Applied Remote Sensing Program 2022), projected in WGS_1984_Albers (units: meters), as the landcover layer, and aggregated its 33 ecological classes into three cover classes- grassland, woody, and cropland, to classify home ranges and buffers. The dbRDA was conducted using the vegan package in R. Results were interpreted using ordination plots to visualize relationships between arthropod consumption and habitat composition (Schwab et al. 2006).

Results

Arthropods

The DNA metabarcoding approach identified a total of 5,885 arthropod ESVs using COI DNA sequences from wild turkey fecal samples (*n* = 299; Table 1.2). Results included 5 classes encompassing Insecta, Arachnida, Collembola, Diplopoda and Malacostraca. Among these 5 classes, 27 Orders, 195 Families, and 528 species were identified. Dominant orders detected in wild turkey diets, based on frequency of occurrence (*n* = 299), were Hemiptera (70%),

Orthoptera (60%), Coleoptera (58%), Lepidoptera (57%), and Diptera (45%; Figure 1.2), which were consistently represented across study regions (Figure 1.3), years (Figure 1.4), and age groups (Figure 1.5).

Of the 195 families identified in fecal samples, Acrididae (55%; Orthoptera), Cicadidae (47%; Hemiptera), and Curculionidae (26%; Coleoptera) were dominant, with similar representation across study regions and age groups (Table 1.3). Family level richness was greatest within Diptera, Lepidoptera, Coleoptera, and Hemiptera.

Species-level summaries were restricted to samples with ≥1 species-level identification (*n* = 258; Table 1.4). I identified 528 arthropod species among all fecal samples. Notably, two species from the Cicadidae family (Hemiptera) were the top species identified in fecal samples that achieved species level taxonomic resolution; *Cicadettana calliope* (26%) and *Neotibicen pruinosus* (18%) were representative across study regions and age classes. Other dominant species detected were *Epicaerus imbricatus* (Coleoptera), *Conocephalus strictus* (Orthoptera), and *Argiope trifasciata* (Araneae; Table 1.5).

Plants

Plant DNA was successfully recovered from 235 fecal samples collected in 2024. A total of 37,165 ESVs were identified, representing three classes, 40 orders, 74 families, and 89 species. Grasses (Poales) and asters (Asterales) were present in 82% and 80% samples, respectively (Figure 1.6). The most frequently detected species were *Bromus inermis* (smooth brome), and *Digitaria sanguinalis* (large crabgrass; Table 1.6).

Dietary Variations

The NMDS ordination (stress = 0.118; Figure 1.7) based on arthropod species consumed by brood-rearing females and poults indicated differences in prey composition among study

regions (PERMANOVA: $R^2 = 0.063$, $F_{2,119} = 4.24$, $p = 0.001$) and years (PERMANOVA: $R^2 = 0.038$, $F_{1,119} = 5.04$, $p = 0.001$). No significant variation was detected between brood-rearing female and poult diets (PERMANOVA: $R^2 = 0.009$, $F_{1,119} = 1.18$, $p = 0.253$). Dispersion tests revealed homogeneity of variance within groups for Age (ANOVA: $F_{1,} = 1.080$, $p = 0.299$) and Year (ANOVA: $F_{1,} = 0.792$, $p = 0.374$), and slight heterogeneity for Region (ANOVA: $F_{2,} = 2.44$, $p = 0.089$), indicating observed differences in multivariate composition reflect true group differences rather than differences in within-group dispersion. Together, study region and year explained approximately 10.1% of the variation in prey consumption, indicating moderate structuring that may reflect landscape composition across the precipitation gradient as well as interannual variation.

The NMDS ordination (stress = 0.108, Figure 1.8) based on variation in diets between brooding females and non-tagged adults revealed marginal differences in arthropod dietary composition (PERMANOVA: $R^2 = 0.0116$, $F_{1,119} = 1.55$, $p = 0.077$). Differences in prey composition were found among study regions (PERMANOVA: $R^2 = 0.0569$, $F_{2,119} = 3.80$, $p = 0.001$) and between years (PERMANOVA: $R^2 = 0.0353$, $F_{1,119} = 4.72$, $p = 0.001$). Dispersion tests indicated homogeneity of variance for Year (ANOVA: $F_{1,122} = 0.03$, $p = 0.873$) and Adult Group (ANOVA: $F_{1,122} = 0.43$, $p = 0.511$), with only slight heterogeneity among regions (ANOVA: $F_{2,121} = 2.74$, $p = 0.069$), suggesting that observed differences in multivariate composition reflected true group differences rather than differences in within-group dispersion.

Arthropod Diversity in Poult Diets

Including read depth as a covariate indicated that variation in richness was biologically meaningful beyond biases in sequencing depth, as all models containing biological predictors ranked higher than both the null and read-depth–only models (Table 1.7). The most

parsimonious model describing changes in poult arthropod ESV richness included Year and accounted for 39% of the AICc weight (Table 1.7). The Year + read-depth model supported lower richness in 2025 relative to 2024 (Figure 1.9; 2025 $\beta = -0.712 \pm 0.224$). The multiplicative effect of the 2025 coefficient was 0.49, corresponding to a 51% decline in predicted richness from 2024 to 2025 (mean richness = 24.5 in 2024 vs. 11.9 in 2025). Two additional competitive models also included days-since-hatch; however, in both models, the 95% confidence intervals for days-since-hatch overlapped zero, indicating a lack of support for an age-related effect on richness.

Habitat Influences on Arthropod Consumption

Distance-based Redundancy Analysis (dbRDA) using Jaccard dissimilarity (presence–absence) revealed significant variation in arthropod prey occurrence driven by environmental and regional predictors. The full dbRDA model included percent grass, percent woody, and percent crop cover as continuous predictors, and study region as a categorical factor (East, Central, West) and identified arthropod prey species as the dependent variable. Multicollinearity assessment indicated high collinearity among predictors (VIF range = 2 – 18). Therefore, crop cover was removed from the model to reduce collinearity, resulting in a reduced model with acceptable VIFs (VIF range = 1.91-2.68; Table 1.8) that included woody cover, grass cover, and region as a factor.

The reduced dbRDA model explained 4.8% of the total variation in arthropod community composition in diets (constrained inertia = 7.148 of 148.829 total; pseudo-$F = 2.40$, $p = 0.001$). Although the proportion of explained variation was modest, permutation test (999) revealed the first two constrained axes (CAP1 and CAP2) were significant and explained 46.73% and 31.05% of the constrained variation, respectively. Woody cover was the strongest driver of variation

(pseudo-F = 2.76, p = 0.001; Table 1.9), whereas grass cover was also significant (pseudo-F = 1.71, p = 0.023; Table 1.9). The woody vector was oriented negatively along CAP1 and CAP 2 (-0.674, -0.739) while the grass vector was oriented positively along CAP1 and CAP2 (0.937, 0.350). Regional variation was significant (Region, pseudo-F = 2.56, p = 0.001) where the Central and East study regions were oriented negatively on CAP1 and CAP2 (-0.704, -0.480; -1.16, -0.182) while the West study region was oriented positively (0.786, 0.214; Figure 1.10).

Species-level responses to spatial and compositional environmental gradients reflected differences in habitat associations among the most frequently identified arthropods in diets. Most species were clustered along the main environmental gradients of grass and woody cover. Grass cover was associated with species from the order Orthoptera, including *Conocephalus strictus* (Tettigoniidae), *Boopedon gracile* (Acrididae), and *Melanoplus packardii* (Acrididae). In contrast, woody cover was associated with cicada species (*Cicadettana calliope* and *Neotibicen pruinosus*; Hemiptera: Cicadidae; Figure 1.10).

Separation of regional centroids was indicative of landscape differences within Kansas. The East and Central study regions were strongly aligned with woody cover and cicada species (Cicadidae), whereas the West region was associated with grass cover and Orthopteran species (Figure 1.10).

Discussion

My study represents the first known application of DNA metabarcoding to characterize diets of wild turkey resulting in one of the most comprehensive evaluation of foods consumed, advancing past coarse morphological classification or order-level generalizations with increased taxonomic resolution. The DNA metabarcoding approach proved to be successful, revealing female wild turkeys and poults consumed a diverse array of arthropod species. Beyond

descriptions of diet, several additional findings provided insight into the foraging ecology of wild turkey during brood-rearing, including the prevalence of cicadas, interannual and age-related variation in diets, and habitat influences on arthropod consumption.

Overall, wild turkeys in Kansas consumed a variety of arthropods from the orders Hemiptera, Orthoptera, Lepidoptera, and Coleoptera. Plant material consumed was highly representative of dominant grasses and forbs across the landscape. As predicted, poults consumed Lepidopterans at a higher frequency and Coleopterans at a lower frequency, compared to adults. Lepidopterans in their soft-bodied caterpillar form may be easily digestible by poults during early stages of development. These findings were emphasized in our 2025 data where 95% of poult samples contained Lepidopteran DNA compared to 80% of adult samples, reinforcing the role of soft-bodied prey in early poult diets.

These findings on arthropod orders consumed by wild turkey corroborate those of past studies (Healy 1985, Hurst 1992, Rumble & Anderson 1996), which documented the orders Hemiptera, Orthoptera, Coleoptera, and Diptera in wild turkey diets. In contrast, Tebo et al. (2022) noted wild turkey poults exhibited a strong selection for the orders Hymenoptera (ants) and Isopoda in a grassland system, and though present in our fecal samples, they were not dominant. Collectively order-level similarities among studies likely reflect consistent prey selection for abundant, protein-rich arthropods during the brood-rearing period. Differences among studies, such as the prominence of Hymenoptera and Isopoda in Tebo et al. (2022), may be driven by landscape scale variations altering arthropod availability rather than prey preferences. Plant quality (Welti et al. 2019, 2020, 2022; Lu et al. 2020), disturbance regimes (Debinski 2023), precipitation and temperature (Debinski 2023) influence arthropod community composition, potentially altering the prey available to foraging poults.

Unlike the previous research, use of DNA metabarcoding provided an approach to achieve fine-scale taxonomic identification of food sources. Beyond order-level patterns, the species-level resolution achieved through DNA metabarcoding revealed several prey taxa not previously documented in wild turkey diets. For example, the frequent detection of *Cicadettana calliope* (Hemiptera), *Neotibicen pruinosus* (Hemiptera) and *Epicaerus imbricatus* (Coleoptera) provided an advantage of revealing species-level habitat associations of food prey as compared to order-level generalizations. *Cicadettana calliope* is a grassland-associated cicada, with a positive association between its consumption and grassland cover. In contrast, *Neotibicen pruinosus* is a cicada species whose consumption was positively associated with woody cover. These results demonstrate how DNA metabarcoding can reveal intra-family habitat associations that may have gone undetected using traditional dietary analysis methods. Similarly, *Epicaerus imbricatus*, a broad-nosed weevil commonly associated with woody vegetation, was more frequently consumed in woodland-dominated sites within the Central and East study regions.

While these findings provide insight into fine-scale wild turkey diet structure, they also reveal broader ecological inference for gallinaceous productivity. Like wild turkey, prairie-chickens (*Tympanuchus* spp.), northern bobwhite (*Colinus virginianus*), and ring-necked pheasants (*Phasianus colchicus*) produce precocial young that require a high protein demand to sustain growth and development. Sullins et al. (2018) similarly reported strong reliance on Lepidopterans in lesser prairie-chicken (*T. pallidicinctus*) chick diets, suggesting comparable forage use among gallinaceous species.

Cicadas in Wild Turkey Diets

The predominate consumption of Hemipteran food sources during the brood-rearing period was no surprise; however, due to the advances in DNA metabarcoding, I uncovered the

dominance of Cicadas in adult and poult diets. Greater than ~1/2 of poult and ~ 1/3 of adult fecal samples contained Cicada DNA. Ultimately, DNA metabarcoding revealed the presence of 8 Cicada species. Among the most dominant were *Cicadettana calliope* and *Neotibicen pruinosus* across age groups and study regions. Cicadas as a prominent food source for wild turkey may have been limited in past research by the ability to detect prey items at fine scale resolution. To my knowledge, there has been one peer reviewed article mentioning cicada presence in wild turkey diets. Wallace et al. (2010) found that cicadas accounted for 7.5% of the aggregate volume of all food items analyzed from 115 wild turkey crops, primarily from adult wild turkey, while species were not identified.

No study mentions Cicadas as a major food source for poults. However, recent observations in Ohio have linked increases in wild turkey productivity to periodical cicada (Magicicada) emergences. Wiley et al. (unpubl. data) reported that during emergence years, poult recruitment, harvest numbers, and population indices all rose substantially, suggesting that cicadas are an important food source for wild turkey, and when abundant during hatches, periodical cicadas can greatly increase recruitment. Cicadas are an important dietary component for various avian species, occurring in 38–80% of riparian bird diets (Rosenburg et al.1982) and representing a primary food source for Mississippi Kites (*Ictinia mississippiensis)* (Chiavacci et al. 2014). Beyond direct nutritional benefits, large-scale emergences can create cascading ecological effects by altering predator-prey dynamics. For example, Periodical cicadas provide an abundant, temporary prey source for mammals such as Raccoons (*Procyon lotor*), Virginia opossums (*Didelphis virginiana*), and coyotes (*Canis latrans*) (Proudman et al. 2024, Tomita 2025), which may, in turn, reduce predation pressure on wild turkey or other ground-nesting

birds. However, during our study period there were no periodical cicada emergences and only annual cicada species were detected.

Annual cicadas are less abundant than periodical cicadas and begin to emerge from the ground when the soil temperatures reach 18 °C (Sato & Sato 2015). Males begin singing to attract females to mate shortly after emerging (Walgenbach & Schoof 2015). Each female can lay 300 or more eggs in groups of 10-16, typically in slits of trees or shrubs or grass twigs, and eggs can hatch over 100 days after being laid (Moulds 2009). The first instar nymphs fall to the ground and begin feeding on root sap within the soil (Moulds 2009). The time annual cicadas reside underground in their nymphal stages is lacking; however, the minimum appears to be 4 years (Walker & Moore 2005).

Emergence patterns of annual cicadas at the Konza Biological Research Station located in the tallgrass prairie of Kansas were studied by Callaham (2000). It was documented that *Cicadetta calliope* was the first to emerge on June 23, followed by *Neotibicen pruinoses* on July 18, and *Megatibicen auifera* and *Megatibicen dorsata* on August 2. In contrast to the findings of Callaham (2000), the first detection of *Cicadettana calliope* in wild turkey fecal samples was May 24 in 2024 and June 3 in 2025. Further, the earliest detection of *Neotibicen pruinoses* in fecal samples was May 24 in 2024 and July 7 in 2025. This later emergence trend in my 2025 data was consistent across most cicada species detected in fecal samples and aligns closely with findings by Callaham (2000). Early detection of cicadas in fecal samples, and thus earlier emergence, may be indicative of interannual variation, which is strongly influenced spatially by soil temperature and precipitation (Sato & Sato 2015, Tsujimoto et al. 2024, Tomita 2025).

Soil temperatures must reach approximately 18 °C to initiate cicada emergence (Sato and Sato 2015). Across Kansas, averaged 10-cm soil temperatures reached this threshold on 11 May

2024 and 10 May 2025 (Kansas Mesonet, 2026), indicating similar statewide emergence timing between years. However, site-specific patterns differed. At Konza Prairie Biological Station located within my East study region, soil temperatures reached 18 °C on 4 April 2024, compared to 9 May 2025. In more southern study sites near McPherson located within the Central study region, the threshold was reached on 14 April 2024 and 15 April 2025 (Kansas Mesonet 2026). These weather patterns suggest that cicada emergence timing likely varies both spatially and temporally across Kansas, reflecting regional differences in soil warming dynamics, and thus, possible variation in timing cicadas are available for consumption by wild turkey.

Cicada emergence phenology may also be disturbance driven (Callaham et al. 2002, Smith et al. 2006). Grassland systems rely on periodic disturbance for their sustainability and maintenance, including fire and grazing (Vinton & Collins 1997, Ratajczak et al. 2014, Wilcox et al. 2022); however, knowledge of how disturbance influences cicada emergence is limited (Callaham et al. 2002). Callaham et al (2002) studied cicada emergence patterns in relation to long-term fire, mowing, and fertilization within experimental plots at the Konza Prairie Biological Research Station in the tallgrass prairie of Kansas. The focal species were C*icadetta calliope* and *Megatibicen aurifera*. The results demonstrated interspecific variation, whereas *Cicadetta calliope* was almost exclusively collected from burned plots and demonstrated positive interactions with mowing and fertilization. Conversely, *Megatibicen aurifera* was collected primarily from unburned plots with minimal influence of burning and mowing on their emergence densities. For both species, females collected in fertilized treatments were larger in size (Callaham et al. 2002). A similar study was conducted in riparian areas of central New Mexico and found that *Neoibicen dealbatus* emergence densities did not vary among burned and unburned sites; however, emergence was earlier within the burned sites (Smith et al. 2006).

These findings indicate spatial and temporal resource partitioning, and differential responses to disturbance, among species, ultimately influencing the temporal and spatial availability of these important food sources (Callaham et al. 2002, Smith et al. 2006).

Cicadas are a highly nutritious and calorie-dense food source, providing approximately 6.82 kJ of energy per adult (Rosenberg et al. 1982). They are particularly rich in protein, with analyses of Asian cicada species showing adult composition of ~56% protein and ~13% fat on a dry-weight basis (Li et al. 2024). Considering the dietary needs of wild turkey poults (requiring daily protein intake equivalent to ~28% of body mass; Healy 1992), cicadas represent a valuable and efficient source of protein. For example, even under conservative assumptions, if 1.2-g cicadas (wet weight, Hastings et al. 2010) supplied half of a 70-g poult's daily protein requirement, the poult would need to consume roughly 50 adult cicadas per day, demonstrating that cicadas could meet a substantial portion of poult protein demand.

Variations in Wild Turkey Diets

The similarity between brood-rearing hen and poult diets at the arthropod species level was not expected; however, given they forage within the same areas and are presented with similar prey communities, this pattern is not surprising. In contrast, differences observed between brood-rearing hens and opportunistic samples may reflect foraging behavior tradeoffs associated with brood rearing. Additionally, interannual variation in all diets were evident across age groups, including shifts in ESV richness within poult samples, indicating that temporal dynamics can shape dietary composition.

Interannual dietary variations are likely representative of changes in arthropod community composition across the landscape. Certain arthropods are directly sensitive to rainfall, which alters their activity, emergence patterns, and overall abundance, and also

indirectly influenced by precipitation through its effects on plant cover (Barnett & Facey 2016, Stack Whitney et al. 2016, Fischer et al. 2022). For example, cicadas show a lagged response to rainfall, with the strongest activity occurring 12–19 days after precipitation events and are also indirectly influenced by rainfall through its positive effects on plant cover (Fischer et al. 2022). Although there were not substantial interannual differences in monthly average precipitation across study sites during the brood-rearing period (May-August; 2024: 10.69 cm; 2025: 12.62 cm), fine-scale rainfall patterns not captured by monthly precipitation totals may explain variations in arthropod communities. Similarly, temperature is a primary driver of arthropod phenology and developmental rates (Forrest 2016; Bale et al. 2002). The average temperature among study sites during May was approximately 2.2 °C cooler in 2025 (16.7 °C) compared to 2024 (18.9 °C), which may have contributed to interannual variation in arthropod availability and consumption.

While interannual differences in wild turkey diets likely reflect temporal variation in arthropod availability likely driven by weather, regional differences in diet were also evident across the study area, suggesting that landscape composition further influenced which arthropod taxa were available to wild turkey. For example, I observed more frequent occurrence of grasshoppers across the landscape in the West study region as compared to the East and Central study regions. Grasshopper (Acrididae) DNA was present in 66% of fecal samples collected from the West study region compared to only in 43% of samples collected from the East study region. These variations in consumed arthropods become more pronounced at the species level.

It was unexpected that brood-rearing females and poults did not differ in diet composition at the species level. At the order level, I hypothesized that poults would consume more soft bodied prey items (e.g., Lepidoptera), whereas adults would consume more hard-bodied prey

items (e.g., Coleoptera), but, at the species level, brood-rearing females and poult diets did not differ. Significant variation in diets between brood-rearing females and opportunistic samples were detected and may be indicative of a change in foraging behavior by brood-rearing females to guide their poults to sufficient protein intake. Poults are precocial upon hatching, they are mobile and responsible for feeding themselves with no assistance from their brood-rearing female (Hurst 1992). Poults can initiate foraging bouts by first separating from the brood-rearing female to begin foraging activity, then the female will stand and follow (Healy 1992). It appears while brood-rearing, the female sacrifices her typical foraging behavior and possible nutrient intake, to accommodate the foraging behavior of her poults. Possibly explaining the difference in diets between brood-rearing females and non-tagged adults that I detected.

Habitat Influences on Arthropod Consumption

I correctly predicted that cover-type composition (e.g., grass and woody cover) of a wild turkey's foraging habitat will influence the consumption of arthropod species, generally aligning with past findings. For example, Healy et al. (1985) found broods foraging in hardwood-dominated sites consumed more Dipterans, whereas when foraging in opening and clearing, consumed more Hemipterans. Similarly, Rumble & Anderson (1996) documented differences in arthropod abundances by cover type. Species-level associations between arthropod prey and habitat characteristics in this study indicated that variation in cover-type composition within brood-foraging habitats influenced which arthropod taxa were consumed. Additionally, there was clear regional separation driving consumption of frequently consumed arthropod species, indicating spatial variation in prey availability.

The strong grass:woody cover gradient observed across study regions influenced arthropod prey available to broods. Grass-dominated foraging sites, primarily in the West study

region, were associated with orthopteran taxa, consistent with the expectation that open grassland systems support grass-specialist arthropods (Rumble & Anderson 1996, Nelson et al. 2022). In contrast, woody cover in the East and Central study regions aligned with Coleopteran, Lepidopteran, and cicada taxa. Specifically, *Caenurgina erechtea* (forage looper moth, Lepidoptera) was associated with woody cover; however, this species is commonly reported in grasslands, meadows, old fields, and roadside habitats. This apparent difference in habitat associations may reflect habitat heterogeneity, where broods forage within open patches embedded within landscapes that contain greater woody cover at broader spatial scales. Additionally, *Neotibicen pruinosus* (Scissor-grinder cicada, Hemiptera) was among the most frequently consumed species by wild turkeys and strongly associated with woody cover. My findings of land cover use by this species aligns with its documented association with riparian woodlands (Callaham et al. 2000) and suggests a shared habitat relationship between this prey species and wild turkeys.

Invertebrates (arthropods) are often neglected in conservation, which may be attributed to a need for improvement of sampling (Cardoso et al. 2011). DNA metabarcoding using eDNA derived from fecal samples, or other biological mechanisms, provides an efficient method for detecting taxa and inferring habitat-level associations. Moreover, application of metabarcoding could potentially serve as a valuable tool for arthropod community research more broadly.

Limitations of DNA Metabarcoding

This study demonstrates that DNA metabarcoding can be used to advance understanding of wildlife diets. However, there are still limitations that should be considered. First, DNA degradation in fecal samples limits the length of fragments that can be successfully amplified by PCR (Pompanon et al. 2012). This was evident in this study as 31 of the 345 fecal samples

collected yielded no readable DNA. Additionally, DNA metabarcoding uses primers with broad taxonomic coverage and can detect non-target taxa (Pompanon et al. 2012). To combat this limitation, I restricted ESV data to only include reads from arthropods and plants known to reside in Kansas. *Tanacetum cinerariifolium* was detected as a dominant plant species in fecal samples, despite its distribution not including Kansas. *Tanacetum cinerariifolium* is the active ingredient in the pesticide Permethrin. Permethrin was commonly used throughout the study area on field clothes to treat against ticks, the presence of this plant may be due to cross contamination. In Kansas, Permethrin is also used as a pesticide on crops such as alfalfa, soybeans, corn, wheat, and sorghum, prior to harvest (Zuckoff et al. 2026a,b,c,d,e). Thus, detection of this plant may also reflect indirect ingestion through permethrin-treated forage.

Additionally, DNA metabarcoding does not have the ability to assess population structure, size, and sex and age ratios (Ruppert et al. 2019). In my study, a presence-absence data frame was used for all analyses conducted. I was unable to infer biomass and abundance from fecal samples based on current methodological biases (Olds et al. 2016). However, validation studies have demonstrated DNA metabarcoding can move beyond simple species occurrence in individuals (Serrana et al. 2019, Verkuil et al. 2022). For instance, Verkuil et al. (2022) used camera-recorded provisioning of pied flycatcher (*Ficedula hypoleuca*) nestlings to validate fecal metabarcoding results and showed strong correlations between COI read abundance and the size-adjusted relative biomass of prey taxa. Similarly, Serrana et al. (2019) compared morphological identification and DNA metabarcoding of stream macroinvertebrate communities and reported a significant positive correlation between high-throughput sequencing (HTS) read depth and morphologically assessed abundance. Collectively, these studies highlight the continued advancement of DNA metabarcoding as a tool not only for characterizing species occurrence in

diets, but also for approximating relative biomass and abundance in systems, which could be used to deepen our understanding of wild turkey nutritional requirements and foraging ecology.

Management Implications

Wild turkey broods relied on a diverse array of arthropods, with several frequently consumed species exhibiting clear habitat associations with grass- and woody-dominated landscapes, indicating heterogenous landscapes may provide access to a diverse arthropod community. Grass-dominated landscapes supported grasshoppers (Orthoptera), katydids (Orthoptera), and spiders (Araneae), while woody-dominated landscapes supported weevils (Coleoptera) and moths (Lepidoptera). Management that promotes structural heterogeneity, such as prescribed fire and grazing, may increase arthropod diversity and forage opportunities. Because arthropods are a critical component of poult diets, maintaining habitat that support abundant and diverse arthropod communities may benefit wild turkey productivity.

Annual cicadas were a dominant component of wild turkey diets. Additional information regarding annual cicada ecology in Kansas is needed. Land managers may consider implementing monitoring programs to assess interannual variation in cicada emergence phenology and abundance. Linking cicada availability with annual wild turkey productivity indices collected by state agencies could provide insight into potential relationships between cicada emergence and wild turkey productivity.

Conclusion

Use of DNA metabarcoding proved to be an informative tool for identifying dietary components of wild turkeys and for assessing age, spatial, and temporal-related shifts in foraging patterns. In this study, DNA metabarcoding revealed a high presence of cicadas in diets among regions, age classes, and years, at levels that to my knowledge, have not previously been

reported in the literature for wild turkeys. Additionally, a grass:woody cover gradient was associated with frequently consumed arthropod taxa using fecal DNA metabarcoding, allowing prey-level habitat associations to be identified at the species level. These patterns suggest that spatial heterogeneity is important in maintaining diverse prey opportunities for wild turkey broods. DNA metabarcoding may be a useful tool for all avian species or other species that exhibit cryptic foraging behavior. As this approach continues to advance, it will likely become a hallmark in wildlife foraging ecology.

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Table 1.1 Proportion of major cover types and crop categories for study sites across the three study regions in Kansas. Values represent percent area within each site based on minimum convex polygons from Figure 1.1. Study sites containing multiple capture locations are denoted by the number in parentheses. Cover type classifications were derived from the Kansas Ecological Systems Map produced by the Kansas Applied Remote Sensing (KARS) Program (Kansas Applied Remote Sensing Program 2022). Crop-specific categories were extracted from the 2024 USDA Cropland Data Layer (USDA National Agricultural Statistics Service 2024). All spatial analyses were conducted using layers projected in WGS 1984 Albers (units: meters

Region	Study Site(s)	Area (km²)	Grass (%)	Woody (%)	Crop (%)	Other (%)	Winter Wheat (%)	Sorghum (%)	Soybeans (%)	Corn (%)	Fallow (%)	Alfalfa (%)
East	Eureka	37.8	85.0	10.6	2.9	1.5	0.0	0.0	0.5	0.2	0.0	0.0
	Fall River (2)	83.7	67.8	21.1	9.3	1.8	0.0	0.2	9.0	0.6	0.0	0.0
	Cottonwood Falls	189.2	81.1	6.6	10.3	2.1	1.2	0.0	5.4	1.8	0.0	0.1
	Lebo	94.1	53.3	14.4	28.7	3.6	0.6	0.3	19.1	4.5	0.0	0.0
	Reading (2)	137.8	58.2	15.7	21.1	5.0	0.3	0.2	11.6	6.4	0.2	0.3
	Council Grove	188.8	70.2	10.0	10.8	8.9	1.1	1.1	5.6	2.5	0.0	0.1
	Weller	37.7	61.0	27.5	2.1	9.4	0.0	0.9	0.8	0.4	0.0	0.0
	Riley Co. (3)	176.5	71.1	20.8	5.5	2.6	0.3	0.3	2.7	2.4	0.0	0.2
Central	Kanopolis (2)	494.2	72.1	6.7	16.4	4.8	6.4	3.4	1.9	1.5	0.8	0.6
	Durham (3)	564.7	59.5	6.8	32.5	1.2	12.6	3.6	5.9	4.7	0.0	1.0
West	Cedar Bluff	703.0	67.2	0.4	26.4	6.0	8.5	8.7	0.0	2.1	8.1	0.32
	Hays	27.7	46.1	4.7	45.9	3.4	12.8	13.7	0.0	6.3	10.3	1.0
	Ellis	100.6	56.4	2.2	36.5	4.9	13.3	12.6	0.0	2.1	6.6	1.7
	Wilson	300.3	75.2	4.4	13.4	7.0	4.5	3.6	1.1	1.6	1.8	0.1

Table 1.2 Number of fecal samples from wild turkeys (*Meleagris gallopavo*) in Kansas that yielded detectable arthropod and plant DNA, summarized by year, age class, and study region. In 2024, 246 fecal samples were collected and analyzed for both arthropod and plant DNA; of these, 204 contained detectable arthropod DNA and 235 (3 samples excluded from the table due to lost meta data) contained plant DNA. In 2025, 99 fecal samples were collected, and 94 yielded detectable arthropod DNA. Values in the table represent only samples with successful sequence reads.

		DNA Type					
		Arthropod			Plant		
Year	Region	Adult	Poult	Unknown	Adult	Poult	Unknown
2024	East	16	16	24	20	19	25
	Central	18	9	6	23	11	7
	West	65	39	11	74	42	11
2025	East	32	3	4			
	Central	14	9	0			
	West	19	12	0			

Table 1.3 Top arthropod families detected in wild turkey fecal samples by age class and region during the brood-rearing period (May–August), Kansas, 2024–2025. Values represent the percentage of samples containing ≥1 detection of each family; *n* represents total samples per study region.

Age class	Region	Family	Detections	*n*	Percentage (%)
Adult	Central	Acrididae	13	30	43.3
		Curculionidae	13	30	43.3
		Cicadidae	12	30	40.0
		Noctuidae	10	30	33.3
		Erebidae	9	30	30.0
	East	Curculionidae	28	48	58.3
		Chrysomelidae	25	48	52.1
		Noctuidae	22	48	45.8
		Erebidae	18	48	37.5
		Acrididae	17	48	35.4
	West	Acrididae	57	84	67.9
		Cicadidae	41	84	48.8
		Pentatomidae	26	84	31.0
		Curculionidae	24	84	28.6
		Erebidae	22	84	26.2
Poult	Central	Acrididae	11	18	61.1
		Chrysomelidae	9	18	50.0
		Noctuidae	9	18	50.0
		Curculionidae	7	18	38.9
		Gryllidae	7	18	38.9
	East	Acrididae	11	19	57.9
		Cicadidae	9	19	47.4
		Erebidae	8	19	42.1
		Carabidae	5	19	26.3
		Gryllidae	5	19	26.3
	West	Acrididae	34	50	68.0
		Cicadidae	31	50	62.0
		Curculionidae	20	50	40.0
		Araneidae	18	50	36.0
		Noctuidae	18	50	36.0

Table 1.4 Top arthropod species detected in wild turkey fecal samples during the brood-rearing period (May–August), Kansas, 2024–2025. Detections are based only on samples that yielded species-level DNA reads.

Species	Family	Detections	*n*	Percentage (%)
Cicadettana calliope	Cicadidae	68	258	26.4
Neotibicen pruinosus	Cicadidae	46	258	17.8
Epicaerus imbricatus	Coleoptera	43	258	16.7
Conocephalus strictus	Orthoptera	36	258	14.0
Argiope trifasciata	Araneae	34	258	13.2
Spodoptera ornithogalli	Lepidoptera	31	258	12.0
Tibellus chamberlini	Araneae	30	258	11.6
Caenurgina erechtea	Lepidoptera	29	258	11.2
Melanoplus packardii	Orthoptera	25	258	9.7
Boopedon gracile	Orthoptera	24	258	9.3

Table 1.5 Top arthropod species detected in wild turkey fecal samples by age class and region during the brood-rearing period (May–August), Kansas, 2024–2025. Detections are based only on samples yielding species-level DNA assignments. Taxa were restricted to those within the known Kansas range when possible and include species-level identifications, Barcode Index Number (BIN) assignments, and provisional identifications (e.g., "nr." taxa).

Age class	Region	Species	Detections	*n*	Percentage (%)
Adult	Central	*Melanoplus confusus*	8	26	30.8
		Neotibicen pruinosus	7	26	26.9
		Cicadettana calliope	6	26	23.1
		Epicaerus imbricatus	5	26	19.2
		Tibellus chamberlini	5	26	19.2
		Caenurgina erechtea	4	26	15.4
		Chloealtis abdominalis	4	26	15.4
		Acrolophus plumifrontella	3	26	11.5
		Chelymorpha phytophagica	3	26	11.5
		Hemaris diffinis	3	26	11.5
	East	*Epicaerus imbricatus*	16	45	35.6
		Cicadettana calliope	10	45	22.2
		Iridopsis humaria	9	45	20.0
		Spodoptera ornithogalli	8	45	17.8
		Caenurgina erechtea	7	45	15.6
		Calomycterus setarius	7	45	15.6
		Neotibicen pruinosus	6	45	13.3
		Rabidosa rabida	6	45	13.3
		Tibellus chamberlini	6	45	13.3
		Argiope trifasciata	5	45	11.1
	West	*Cicadettana calliope*	22	75	29.3
		Conocephalus strictus	16	75	21.3
		Melanoplus packardii	14	75	18.7
		Argiope trifasciata	12	75	16.0
		Epicaerus imbricatus	11	75	14.7
		Aeoloplides turnbulli	10	75	13.3
		Leptinotarsa decemlineata	10	75	13.3
		Boopedon gracile	9	75	12.0
		Eleodes tricostata	9	75	12.0
		Neotibicen pruinosus	9	75	12.0
Poult	Central	*Gryllus sp. BOLD:ABX6481*	6	13	46.2
		Cicadettana calliope	4	13	30.8
		Melanoplus confusus	4	13	30.8
		Parcoblatta sp. BOLD:AAG9937	4	13	30.8

Table 1.5 Cont.

Age class	Region	Species	Detections	*n*	Percentage (%)
Poult	Central	*Rabidosa rabida*	4	13	30.8
		Chloealtis abdominalis	3	13	23.1
		Chloealtis conspersa	3	13	23.1
		Hemaris diffinis	3	13	23.1
		Neotibicen nr. canicularis DCM-2015	3	13	23.1
		Peridroma saucia	3	13	23.1
	East	*Neotibicen pruinosus*	6	17	35.3
		Caenurgina erechtea	5	17	29.4
		Chloealtis conspersa	4	17	23.5
		Cicadettana calliope	4	17	23.5
		Neotibicen nr. canicularis DCM-2015	4	17	23.5
		Calomycterus setarius	3	17	17.6
		Gryllus sp. BOLD:ABX6481	3	17	17.6
		Hypena scabra	3	17	17.6
		Neotibicen lyricen	3	17	17.6
		Anaxipha sp. BOLD:AAN8461	2	17	11.8
	West	*Cicadettana calliope*	15	46	32.6
		Argiope trifasciata	13	46	28.3
		Conocephalus strictus	11	46	23.9
		Galanga labeculata[1]	11	46	23.9
		Melanoplus packardii	9	46	19.6
		Spodoptera ornithogalli	9	46	19.6
		Tibellus chamberlini	8	46	17.4
		Boopedon gracile	7	46	15.2
		Lepyronia gibbosa	7	46	15.2
		Neotibicen pruinosus	7	46	15.2

[1]*Galanga labeculata* is not currently documented within Kansas; this assignment may represent a closely related regional species or reflect limitations in metabarcoding reference databases.

Table 1.6 Most frequent plant species detected in wild turkey fecal samples during the brood-rearing period (May–August), Kansas, 2024. Detections are based only on samples yielding species-level DNA assignments (*n* = 172).

Species	Detections	Percentage (%)
Bromus inermis	36	20.93
Tanacetum cinerariifolium[1]	25	14.53
Digitaria sanguinalis	23	13.37
Arenaria serpyllifolia	22	12.79
Lactuca saligna	20	11.63
Glycine max	13	7.56
Grindelia squarrosa	13	7.56
Bouteloua dactyloides	12	6.98
Cannabis sativa	12	6.98

[1] *Tanacetum cinerariifolium* distribution does not include Kansas and is the active ingredient in the pesticide Permethrin.

Table 1.7 Model AICc, number of parameters, delta AICc, and model weight of beta regression models explaining drivers of exact sequence variant (ESV) richness in poult diets in Kansas 2024-2025. The term "days" implies days since hatch of wild turkey broods.

Model	*K*	AICc	ΔAICc	*w*	Deviance
year+depth	4	449	0	0.39	-220.04
days*year+depth	6	449	0.27	0.34	-217.72
days+year+depth	5	450	0.97	0.24	-219.32
depth	3	455	6.50	0.02	-224.45
days+depth	4	457	8.34	0.01	-224.21
juliandate+depth	4	458	8.82	0	-224.45
quaddays+depth	5	459	10.55	0	-224.11
days+juliandate+depth	5	460	10.74	0	-224.21
quadjuliandate+depth	5	460	10.83	0	-224.25
days*juliandate+depth	6	460	11.05	0	-223.11
days*juliandate	5	511	61.71	0	-249.69
days	3	512	63.52	0	-252.96
quaddays	4	513	64.21	0	-252.15
days+year	4	513	64.56	0	-252.32
days*year	5	514	65.24	0	-251.46
days+juliandate	4	514	65.60	0	-252.84
year	3	517	67.75	0	-255.07
Null	2	519	69.74	0	-257.19
juliandate	3	520	71.50	0	-256.95
quadjuliandate	4	523	73.78	0	-256.93

Table 1.8 Variance inflation factors (VIFs) for predictors included in the full and reduced distance-based redundancy analysis (dbRDA) models examining habitat influences on arthropod occurrence in wild turkey diets in Kansas (2024 – 2025). High collinearity among percent grass, woody, and crop cover in the full model (VIF = 10–18) resulted in the removal of crop cover, producing acceptable VIF values (< 3) for the reduced model.

Model	Variable	VIF
Full	grass_pct	18.21
	woody_pct	12.56
	crop_pct	10.37
	RegionEast	2.42
	RegionWest	2.70
Reduced	grass_pct	1.92
	woody_pct	2.23
	RegionEast	2.27
	RegionWest	2.68

Table 1.9 Marginal F-tests from the distance-based redundancy analysis (dbRDA) examining relationships between habitat characteristics and arthropod prey composition detected in fecal samples. Percent woody cover, percent grass cover, and Region were significant predictors ($p < 0.05$) based on 999 permutations.

	Df	F	p-value
grass_pct	1	1.71	*0.023*
woody_pct	1	2.76	*0.001*
Region	2	2.56	*0.001*

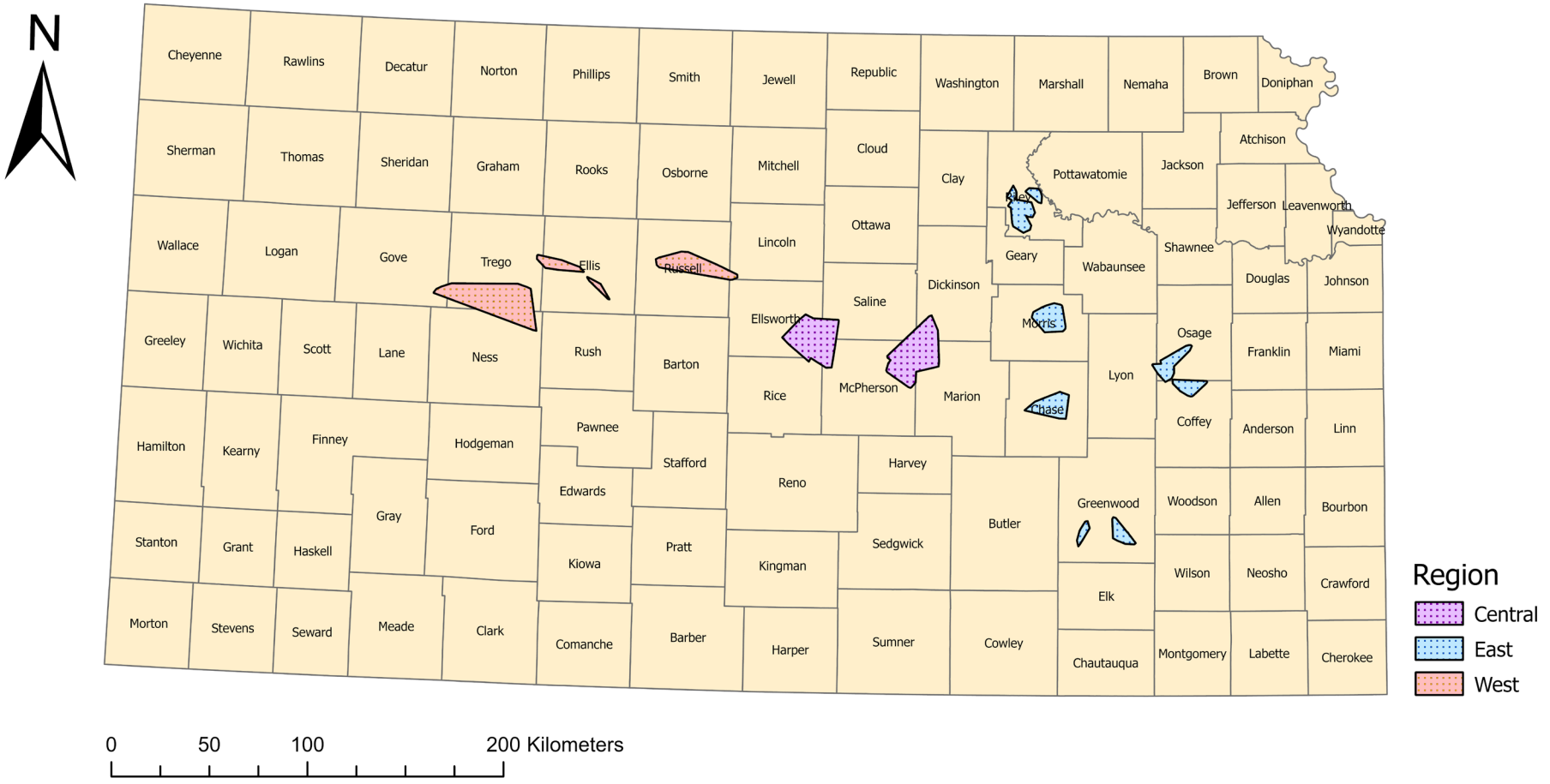

Figure 1.1 Ninety-five percent minimum convex polygons (MCPs) generated from GPS-marked female wild turkeys during the brood-rearing period (May–August 2024–2025) in Kansas, USA. Polygons represent spatial extents of capture locations used to delineate non-overlapping study sites and are grouped by study region (West, Central, East), indicated by color.

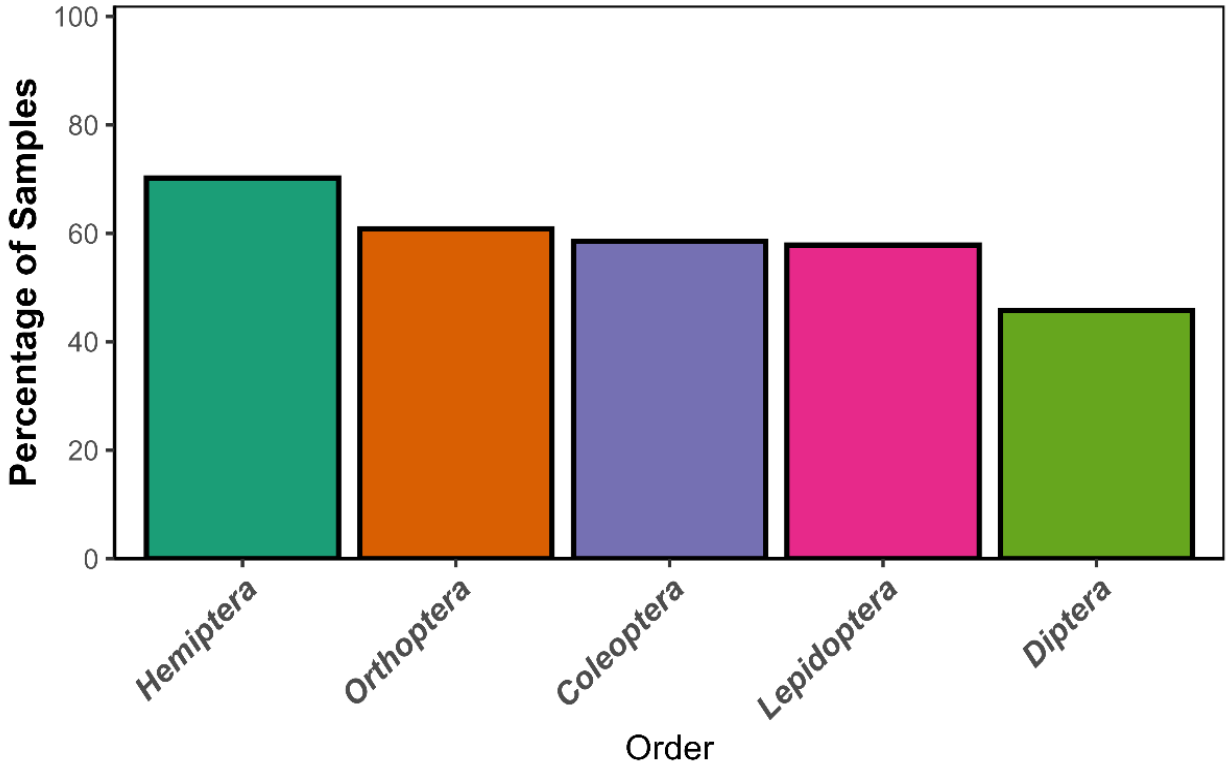

Figure 1.2 Top arthropod orders detected in fecal samples (*n* = 299) from brood-rearing females, poults, and opportunistic adult samples of unknown sex collected during the brood-rearing period (May–August) in Kansas (2024–2025).

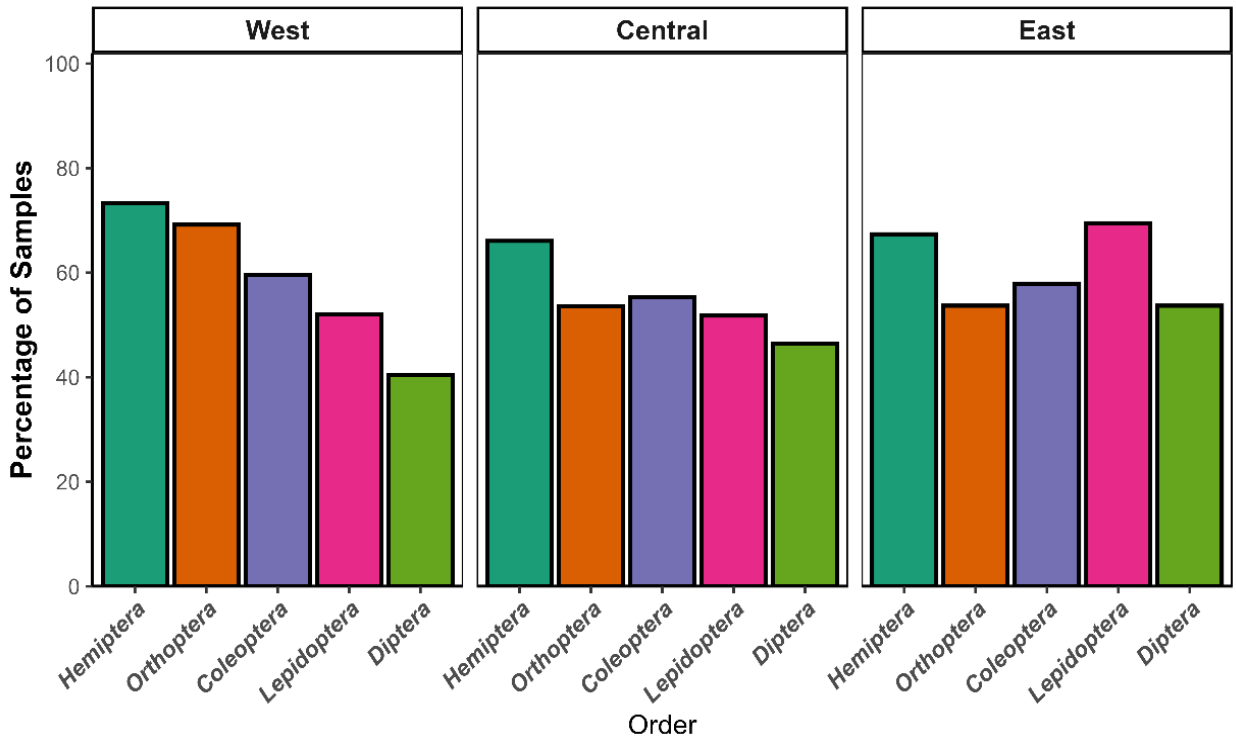

Figure 1.3 Top arthropod orders detected in fecal samples (*n* = 299) from brood-rearing females, poults, and opportunistic adult samples of unknown sex, separated by study region (West: *n* = 146; Central: *n* = 56; East: *n* = 95), during the brood-rearing period (May–August) in Kansas (2024–2025).

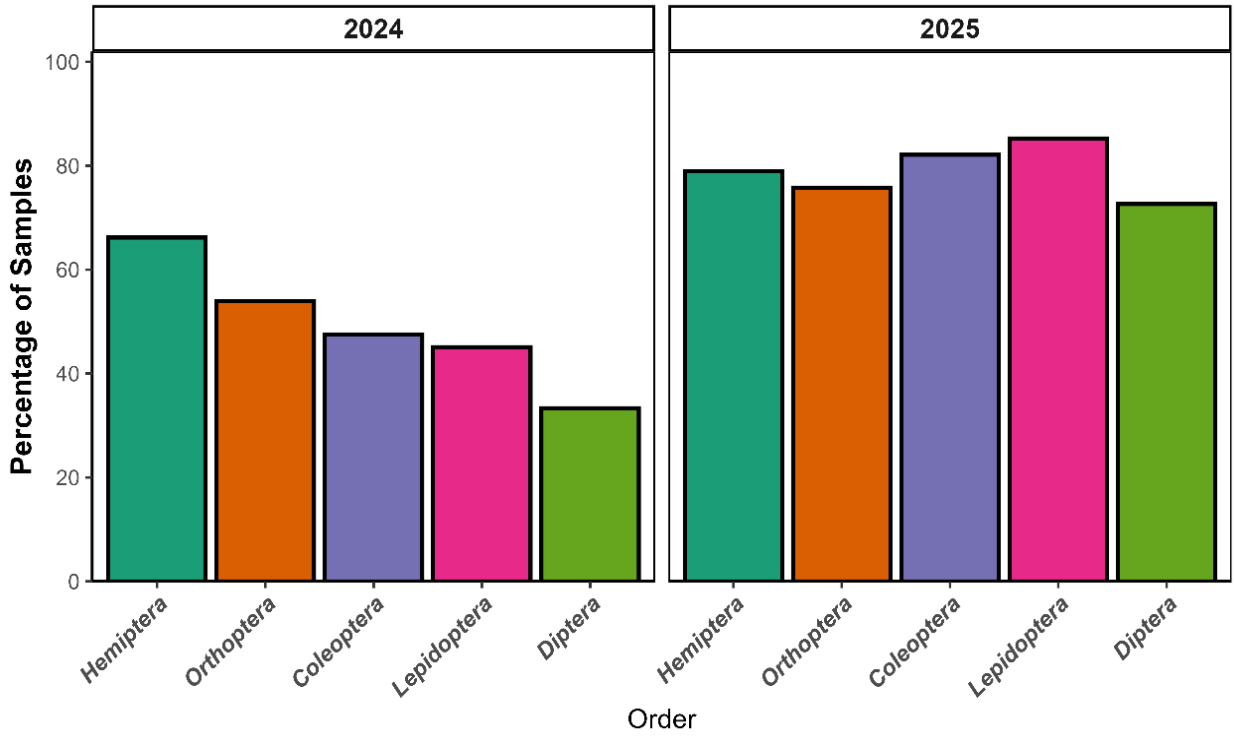

Figure 1.4 Yearly comparison of the top arthropod orders detected in fecal samples (*n* = 299) from brood-rearing females, poults, and opportunistic adult samples of unknown sex collected during the brood-rearing period (May–August) in Kansas (2024: *n* = 204; 2025: *n* = 95).

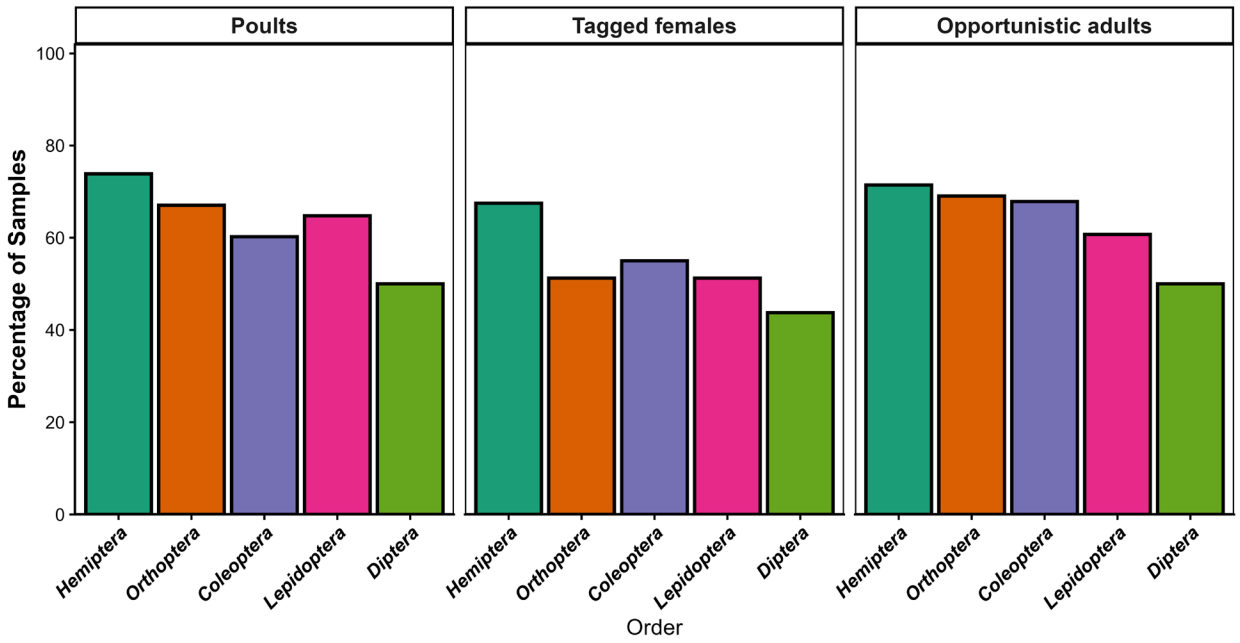

Figure 1.5 Top arthropod orders detected in fecal samples from brood-rearing females (*n* = 80), poults (*n* = 88), and opportunistic adult samples of unknown sex (*n* = 84), shown separately by age class, during the brood-rearing period (May–August) in Kansas (2024–2025).

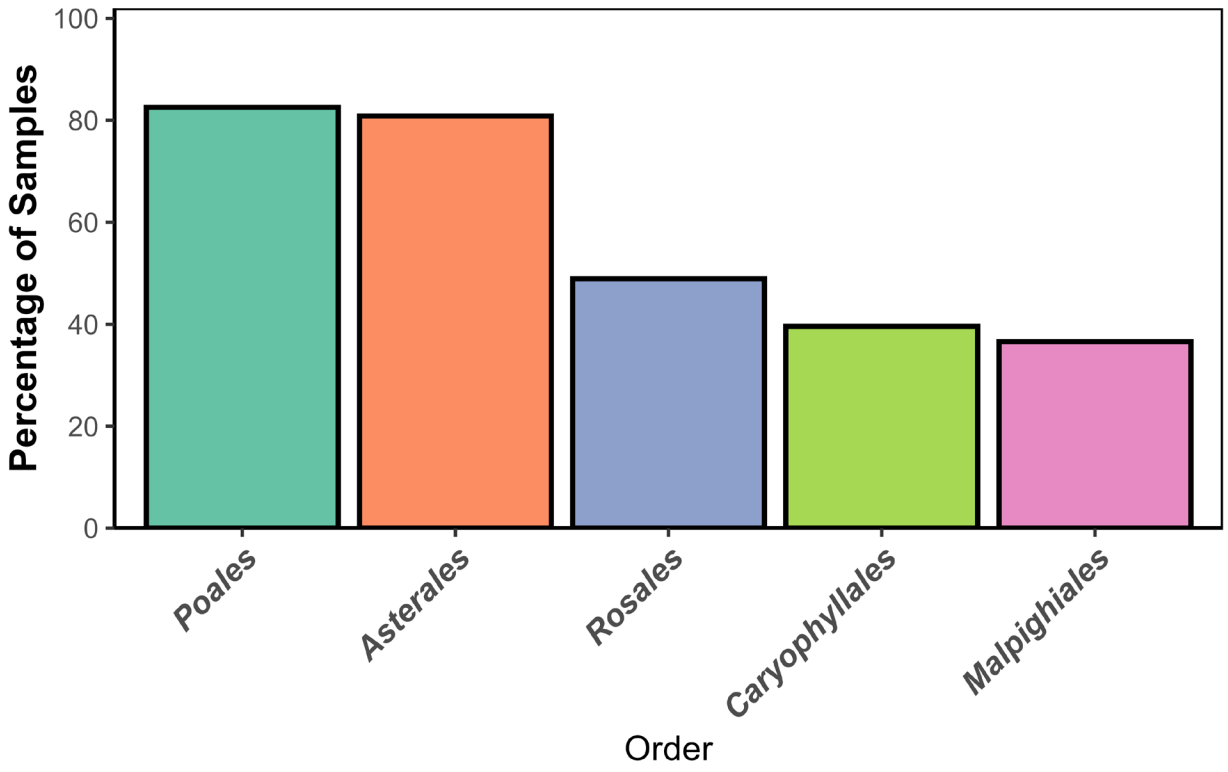

Figure 1.6 Top plant orders detected in fecal samples (*n* = 235) from brood-rearing females, poults, and opportunistic adult samples of unknown sex, during the brood-rearing period (May–August) in Kansas (2024).

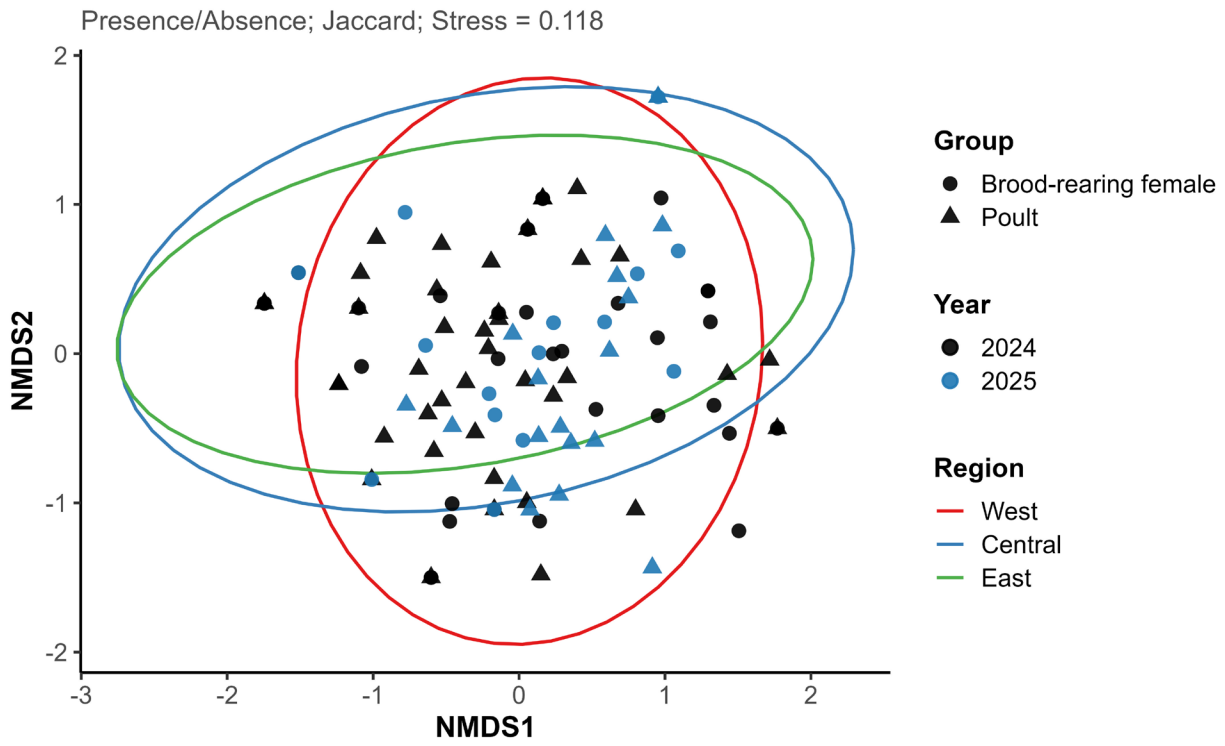

Figure 1.7 Non-metric multidimensional scaling (NMDS) ordination of species-level diet composition for brood-rearing female wild turkeys and poults based on presence–absence data (Jaccard distance), Kansas, 2024–2025. Ellipses represent 95% confidence regions for study areas (East, Central, West), and points show individual fecal samples.

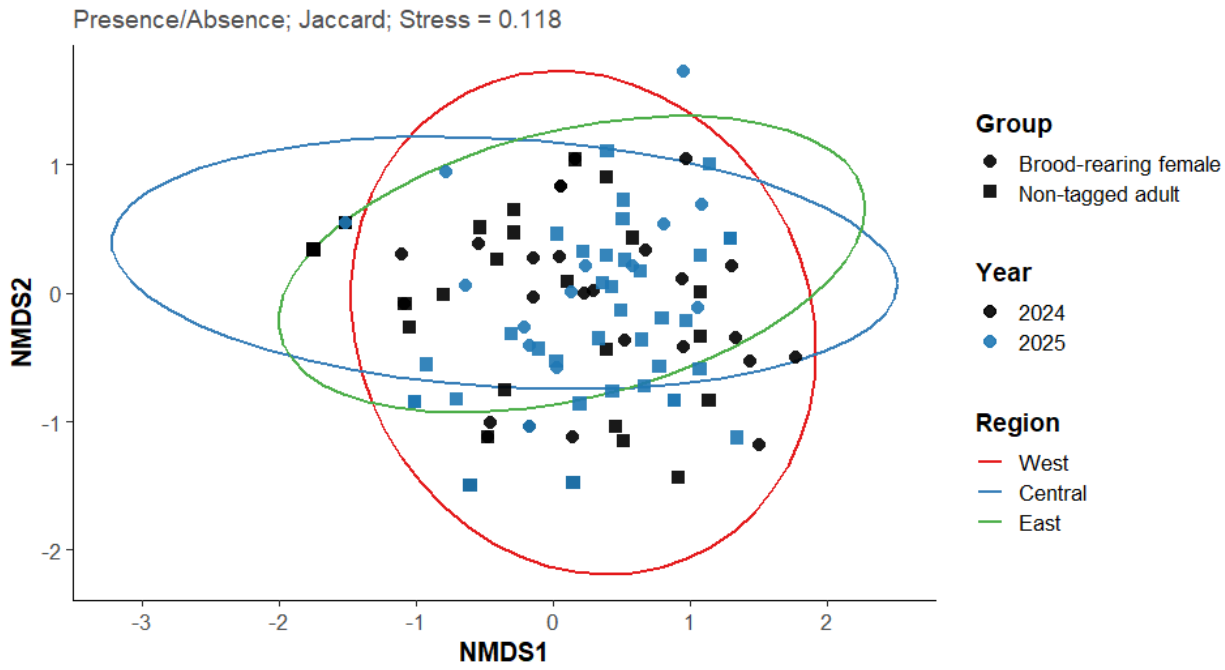

Figure 1.8 Non-metric multidimensional scaling (NMDS) ordination of species-level diet composition for brood-rearing female wild turkeys and non-tagged adults based on presence–absence data (Jaccard distance), Kansas, 2024–2025. Ellipses represent 95% confidence regions for study areas (East, Central, West), and points show individual fecal samples.

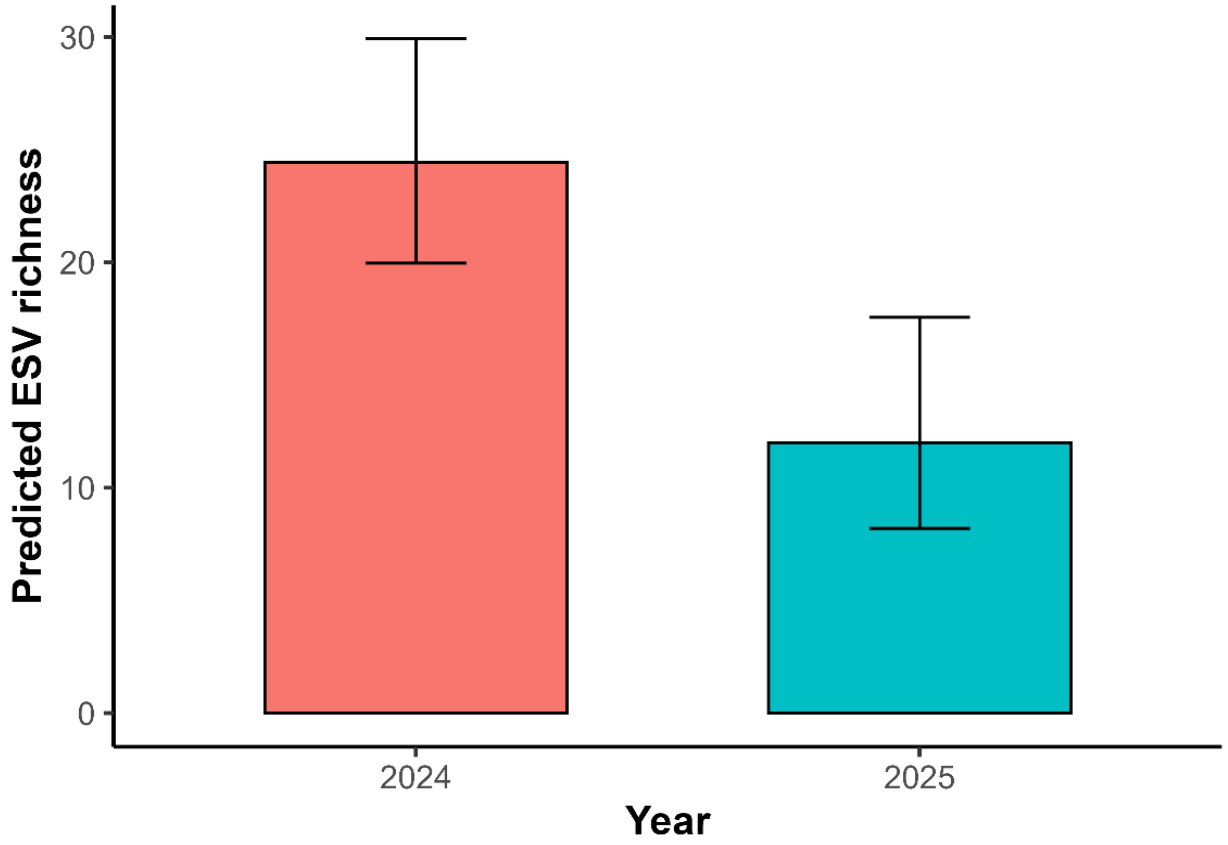

Figure 1.9 Predicted arthropod exact sequence variant (ESV) richness of wild turkey poults in 2024 and 2025 from the most supported negative binomial model including year and read depth as predictors. Predictions were generated while holding read depth at its mean value. Error bars represent 95% confidence intervals.

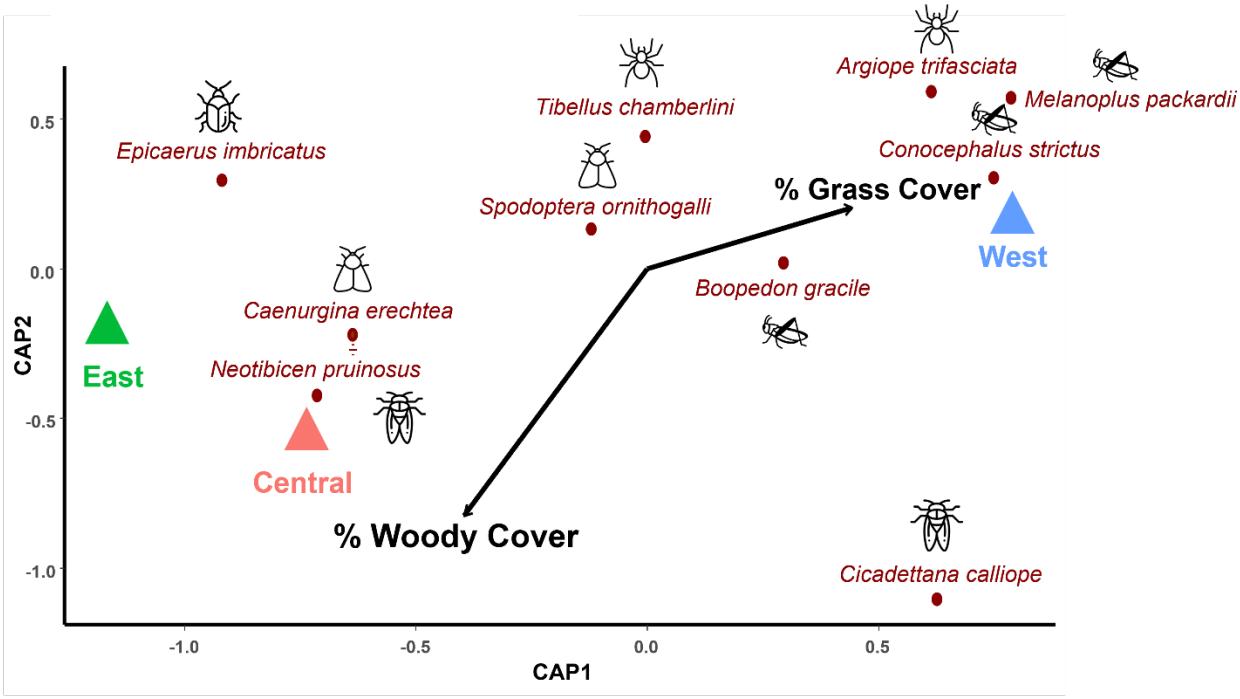

Figure 1.10 Distance-based redundancy analysis (dbRDA; Jaccard distance, reduced model) showing relationships between arthropod prey composition and habitat characteristics. Percent grass cover and percent woody cover were significant predictors structuring arthropod community composition, and samples clustered broadly by region (East, Central, West). Species centroids and environmental vectors (arrows) indicate the direction and strength of associations between arthropod taxa and habitat gradients.

Chapter 2 - Bottom – Up Drivers Influencing Wild Turkey Brood Foraging Site Selection

Introduction

Persistence of populations ultimately depends on the availability and distribution of limiting resources that influence survival and reproduction (Morrison 2001). Producers, carnivores, and decomposers are limited by resource availability more so than being limited by predators (Hairston et al. 1960). More specifically, food resources are known to directly influence survival across many taxa (Oro & Furness 2002, White 2008). The availability of important food resources can be mediated by habitat structure and composition (Pinotti et al. 2012). Thus, organisms are expected to select habitats that provide adequate food resources that promote survival (Fretwell & Lucas 1970).

The relationship between a selected foraging habitat and available food resources is particularly important during offspring-rearing periods, when nutritional demands are high and offspring development and survival is dependent on access to high-quality food resources (Schwagmeyer & Mock 2008, Scornavacca et al. 2016). For example, supplementing arthropods to diets of northern wheatears (*Oenanthe oenanthe*) in their breeding grounds can increase juvenile survival 1.56-fold as compared to control treatments (Seward et al. 2013). Similarly in ungulates, survival in nutrient-limited pastures can be 50% lower than in areas with greater nutrient availability (Scornavacca et al. 2016). Access to high-quality food resources is especially important for ground-nesting avian species that rear precocial young (Healy 1992, Reeves 2018, Sullins et al. 2018,). Wild turkey (*Meleagris gallopavo*) poults are precocial and because of this, experience a survival bottleneck during the first two weeks of life when high

protein intake is required to support body growth and development of flight feathers necessary for predator avoidance (Hurst 1992, Healy 1992, Spears et al. 2007, Chamberlain et al. 2020).

To meet high nutritional demands that enhance survival, brood foraging site selection must balance areas that provide sufficient food sources and provide concealment from predation (Healy 1992, Rumble & Anderson 1996, Spears 2007, McCord et al. 2014). What has previously been defined as "ideal brood-rearing habitat" can vary throughout the range of the wild turkey. For instance, broods selected mature bottom-land hardwoods with sparse understory and moderate herbaceous cover, while avoiding pine stands with a dense ground layer of woody vegetation in central Missouri (Phalen et al. 1986). In the Black Hills of South Dakota, broods selected meadow edges that were in proximity to forest edge, most likely to facilitate predator avoidance (Rumble & Anderson 1996). In the southeastern United States, open areas were generally selected; however, there was an increase in selection of hardwoods as the broods aged (Chamberlain et al. 2020). Broods in the Pacific Northwest occupied a variety of habitat types, but used meadows, mixed hardwood/conifer forest, and savannahs more than expected (Keegan & Crawford 1997). Although these examples highlight regional variation in brood habitat use, a general pattern emerges with broods selecting relatively open areas having adequate herbaceous cover and nearby concealment, which is characteristic of early successional cover types (Sisson et al. 1991, Chamberlain et al. 2020).

The early successional cover types selected by broods are commonly maintained through periodic disturbance, which not only influences vegetation structure but also governs availability of key foraging resources (Sission et al 1991, Chamberlain et al. 2020). Disturbance essentially resets succession to promote ground cover of forbs and grasses, where the resulting vegetation growth is tall enough to conceal poults from predators but not restricting their movement

(Sission et al. 1991). The diverse influx of forbs and grasses in early successional cover types provide a broad array of foraging opportunities for wild turkey and other Galliformes (Chamberlian et al. 2020). A critical resource offered by these early successional cover types is arthropod availability (Chamberlain et al. 2020, Nelson et al. 2022).

Arthropods serve as a nutritious food resource for wild turkey during the breeding period. Wild turkey poults especially rely on arthropods to meet a high protein demand (28%) required to sustain growth and development of flight feathers (Healy 1992, Hurst 1992,). Arthropods consumed by wild turkey poults have been well documented at the order level of taxonomy but vary spatially across their range and foraging habitat type associations (Healy 1985, 1992; Rumble & Anderson 1996; Wallace et al. 2010; Tebo et al 2022). Wild turkey brood-rearing hens share similar dietary preferences, consuming species from the orders Orthoptera, Hemiptera, and Lepidoptera. More specifically, *Cicadettana calliope* (Hemiptera) and *Neotibicen pruinosus* (Hemiptera) were frequently detected in diets, representing the first species-level documentation of annual cicadas as a dietary component in Kansas (Chapter 1). Additionally, there was evidence of habitat associations, where cicada consumption was positively influenced by woody cover and orthopteran consumption was related to grass cover (Chapter 1). Thus, arthropod availability is likely influenced by landscape composition and configuration and needs further evaluation to improve survival of wild turkeys broods during a survival bottleneck.

Arthropod richness, abundance, and biomass tend to increase with increasing plant diversity (Srivastava and Lawton 1998, Crutsinger et al. 2006, Welti et al. 2017, Minor et al. 2021), while plant functional group composition can independently influence what type of arthropods are available (Healy 1985, Symstad et al. 2000, Laird-Hopkins 2017). For example,

Coleopteran and Homopteran (now Hemiptera) species richness may increase with forb coverage, while Hemipteran and Hymenopteran richness can decrease with warm-season grass coverage (Symstad et al. 2000). Furthermore, arthropod abundance may respond positively with grass and forb cover, while having a negative relationship with dense woody understory (Nelson et al. 2022). A study on poult feeding activity in West Virginia found that Hemipterans were consumed more often in clearings, whereas Dipterans and Lepidopteran larvae were consumed more in forested areas (Healy 1985), Ground litter coverage and type can also alter arthropod communities present (Laird-Hopkins 2017). Though arthropod availability is partly driven by the structure of the landscape, plant nutrient composition also influences their availability (Lu et al. 2020, Welti et al. 2020).

Plant tissue nutrient concentrations can positively influence arthropod communities (Welti et al. 2019, 2020; Lu et al. 2020; Prather et al. 2021) and indigestible compounds such as acid-detergent lignin (ADL) may decrease arthropod richness and density (Zhender et al. 2009, Lu et al. 2020). Specifically, Orthopterans respond positively with increased plant nutrient quality in grassland systems (Welti et al. 2019). Dipterans and Coleopterans require nutrient-rich plant communities for egg development, larval growth, and oviposition, whereas plant communities with elevated ADL concentrations may deter these taxa (Lu et al. 2020). However, these relationships are not uniform across feeding guilds. In experimental plots manipulating nitrogen, phosphorus, and sodium availability, all herbivores increased under nitrogen–phosphorus enrichment treatments, whereas only chewing herbivores responded positively to sodium fertilization, and parasitoids and predator numbers responded more strongly to plant biomass (Prather et al. 2021). Similarly, potassium and sodium additions in Kansas grasslands increased arthropod herbivore abundances (Welti et al. 2020). These findings demonstrate that

plant nutrient concentrations can restructure arthropod communities through bottom-up processes.

Variation in plant-nutrient concentrations occurs both among and within plant functional groups (Lee 2018). Thus, sites dominated by one or the other (i.e. forb dominated vs grass dominated) will be expected to vary in quantities of nutrients available in their tissues and subsequently delivered to consumers such as arthropods. Forbs tend to have greater crude protein and phosphorus concentrations compared to grasses (Belesky et al. 2020), whereas woody vegetation typically contains larger concentrations of ADL, which reduces digestibility (Lee 2018). In the Great Plains, cool-season grasses trend higher in crude protein and phosphorus concentration than warm-season grasses, though both groups show declines with maturity and vary throughout the year (Williams 1953). Within forbs, legumes tend to have greater protein concentrations as compared to non-legume forbs (Lee 2018). These nutrient-mediated effects associated with vegetation composition may influence the presence and abundance of primary consumers (arthropods) and, subsequently, secondary consumers such as wild turkeys.

Conceptually, relationships among arthropod communities, nutrient availability, and vegetation structure and composition, indicate wild turkey brood foraging site selection may be driven through cascading and bottom-up effects. Vegetation composition may influence nutrient availability, nutrient availability may influence arthropod communities, and wild turkey poults rely heavily on arthropods as a key dietary component, indicating a likely influence on their foraging site selection. Brood foraging site selection has been studied throughout the wild turkey range; however, previous studies primarily draw conclusions from direct vegetation composition and structural characteristics while failing to evaluate indirect and interacting effects that may be mediated through nutrients and arthropods. Therefore, pathways linking habitat composition to

brood foraging site selection remain unclear. I evaluated whether bottom-up drivers influence brood foraging site selection in Kansas and the relative roles of indirect effects.

Study objectives were to: (1) identify relationships among arthropod communities, plant nutrient composition, habitat characteristics, and brood foraging site selection; (2) assess differences in arthropod communities and plant-nutrient concentrations between used and available foraging sites; and (3) evaluate bottom-up drivers influencing brood foraging site selection. I hypothesized that broods will select sites with greater arthropod richness and greater plant nutrient availability. Arthropod availability is expected to be positively associated with crude protein and phosphorus concentrations and negatively associated with acid detergent lignin (ADL). Sites characterized by greater forb cover are predicted to positively influence arthropod richness and nutrient concentrations. Lastly, I hypothesize that habitat structural and compositional characteristics will not have a direct effect on brood foraging site selection, and their influence will be mediated through plant nutrient composition and arthropod availability.

Methods

Study Area

My study area encompassed three study regions (East, Central, and West) in Kansas 39° to 38°N latitude and -100° to -97°W longitude (Figure 1.1). The East study region consisted of tallgrass prairie, whereas the Central and West study regions were characterized by mixed-grass prairie ecotypes. For a detailed description of the study area, please refer to Chapter 1.

Capture and Handling

I captured wild turkey at all study sites during the winter months of 2024 and 2025 using walk-in funnel traps, drop nets, and rocket nets (Austin et al. 1973, Davis 1994). Wild turkeys were sexed based on the coloration of their breast feathers (Schroeder & Robb 2005). Individuals

were aged as either Adult or Juvenile depending on the color patterns, shape, and wear of the outermost primary feather (Schroeder & Robb 2005). I applied a uniquely numbered 7/8" (22.23 mm) riveted leg band (National Band & Tag Company, Newport, Kentucky, USA) to the right leg of each captured turkey (Diefenbach et al. 2009). Measurements taken included: mass (g), flattened wing chord (mm), exposed culmen (mm), tarsus, beard, and spur lengths (mm). Captured hens that met mass requirements (<4% of body mass; Ausprey 2023) were fitted with backpack harnesses (Guthrie et al. 2011) securing satellite GPS transmitters (G5-T2A Iridium GPS, Advanced Telemetry Systems, Isanti, MN; 152 g). Capture and handling were approved by state capture permits and protocols by Kansas State University Animal Use and Care Committee (IACUC protocol 4906).

Arthropod Sampling

Sample Design- I collected arthropods at brood foraging locations during May to August, 2024 and 2025. These locations were identified by randomly selecting from a pool of locations grouped by the 1000- and 1400-time stamps received via GPS transmitters during which I assumed wild turkeys were foraging. These times were considered representative of brood foraging locations as broods forage most of their time during the day (Healy 1992, Chamberlain et al. 2020). For each tagged hen with a brood, I selected three locations during the early (0–14 days) and late (15–28 days) brood-rearing periods, resulting in three used forage locations per period. I sampled two paired random locations per foraging location to compare use and availability. I generated paired random locations relative to a used forage location using a random number generator to select an azimuth (0°-360°) and distance (100-360 m). Up to 6 used and 12 available locations per tagged brood-rearing hen were sampled, dependent on brood survival.

Arthropod Collection- I sampled arthropods using suction sampling with a modified leaf-blower vacuum (Husqvarna 125BVx 28-cc, Charlotte, NC, USA; Zou et al. 2016), following the protocol used by Nelson et al. (2022). Traditional methods such as sweep netting and ground traps (pitfall and sticky traps) bias results toward middle vegetation-dwelling and ground-dwelling arthropods, respectively. In contrast, suction sampling captures arthropods across all vegetation levels (Zou et al. 2012, 2016). I suctioned arthropods from within a cylindrical quadrat receptacle (e.g., a 66 × 55-cm trash can, 156.7 L) designed to encompass ground to mid-level vegetation.

This receptacle was fitted with an open bottom for direct ground contact and a nylon-screened top with an opening for hose insertion. At the brood foraging location, I rapidly placed the receptacle at the central point to reduce bias in underestimating easily disturbed arthropods. After placing the receptacle, I inserted the vacuum hose through the nylon screening, suctioning for 55 seconds, starting from the top and moving downward in a spiraling motion. I repeated this process 10 m north and south of the central location, totaling three suctioning events at each brood foraging used and paired random locations.

I deposited collected arthropods into a plastic bag immediately following each suctioning event. I labeled bags with a unique point ID, hen band number, and GPS coordinates. I stored samples in a freezer at field sites and Kansas State University prior to sorting.

Arthropod Sorting- I sorted arthropods to Order, except for those in the Order Orthoptera, which I sorted to family because they serve as valuable forage for wild turkeys and other upland game birds (Hurst 1992). Additionally, I sorted the family Cicadidae (Hemiptera) into species in 2025 because they were found to be a valuable food source during 2024 (Chapter 1). I grouped

individuals within each Order by size class (0–2 mm, 2.1–5 mm, 5.1–10 mm, 10.1–15 mm, >15.1 mm) and counted individual specimens.

I estimated arthropod diversity by identifying apparent morphospecies within each order based on external morphological characteristics, following methods modified from Oliver & Beattie (1993,1996a,b). Within each Order, I distinguished morphospecies using obvious morphological traits such as body shape, coloration, patterning, and appendage structure. Minor size differences alone were not used as criteria for defining separate morphospecies. I assigned a unique morphospecies identifier (e.g., M.1, M.2) for specimens within each Order, with identifiers reset for each Order present in samples. I treated occurrences of a unique M.ID (e.g., M.1, M.2) within the same Order but across multiple size classes as single morphospecies for richness estimates.

I conservatively grouped immature spiders (spiderlings) and ant larvae into distinct "immature morphospecies" only if clear morphological differences were visible beyond life stage alone. Otherwise, I grouped spiderlings and ant larvae into a single M.ID within their respective Order (Oliver and Beattie 1996b). I assigned damaged or indistinct specimens to an "Unknown Morphospecies" within the appropriate Order and were excluded from richness estimates.

Arthropod sorters independently re-estimated morphospecies richness for a pool of randomly selected samples from each year. I quantified discrepancy among sorters as proportional difference between the initial and correspondence counts, expressed as a percentage, and averaged by year to assess correspondence trends. Percent discrepancy was calculated as:

$$\frac{Initial\ Count - Correspondence\ Count}{Initial\ Count}\ x\ 100$$

I calculated sample-level morphospecies richness as the total number of unique morphospecies per Order and summed across all Orders within a sample to represent alpha-diversity. After estimating morphospecies richness, I grouped size classes within the same Order were weighed (g) and summed across Orders to obtain a combined biomass of all specimens within the sample. Due to instrumental detection limits, some groups yielded a mass of 0.000. These groups were scaled up to the minimum detectable non-zero mass (0.001g). I placed specimens in their respective Orders within individual bags, then placed bags of each Order into their original sample bags and stored them in a freezer for preservation.

Forage Collection

I collected forage clippings in conjunction with arthropod sampling at brood foraging locations, totaling 3 sampled locations per survey area. Immediately after I sampled arthropods, I placed a 0.1-m^2 clipping frame on the ground and clipped all herbaceous vegetation 2 cm above ground to avoid soil contamination.

I placed vegetation material in paper bags immediately after collection (Lashley et al. 2014) and labeled the bag with a unique sample ID, hen tag, and GPS coordinates (latitude and longitude). I transported samples to Kansas State University, where they began air drying prior to nutrient analyses. Proper drying and storage techniques were used as they are critical to prevent sample degradation and maintain nutrient integrity, ensuring accurate nutritional assays (Lashley et al. 2014).

Habitat Sampling

I collected and recorded habitat-related data immediately after collecting and properly storing arthropods. I visually measured vegetation functional groups within a modified

Daubenmire frame (1 x 1 m; Daubenmire 1959) as % grass cover, % forb, % woody, % litter, and % bare ground at the central point and four radial points 10 m from the central point in each cardinal direction (5 estimates/point). I identified flora species composition within the Daubenmire frame at the central point. I recorded visual obstruction readings using a modified coverboard (0.5 m x 2 m; Nudds 1997) for the 0.0 m – 0.25 m and 0.25 m – 0.50 m strata at the central point and four radial points (8 readings/point). In addition, I classified the dominant cover type (e.g., cropland, woodland, grassland, shrubland) at a 10-m radius surrounding the sample point. I averaged measurements of functional groups and visual obstruction to obtain site means. I quantified flora species composition at the central point to obtain a measurement of alpha-diversity.

Plant Nutrient Analyses

I submitted collected forage clippings to Oklahoma State University Soil, Water and Forage Analytical Laboratory (Stillwater, OK) for nutrient and mineral analyses (Oklahoma State University Extension, n.d.). The lab followed standardized forage-testing procedures for assessment of forage nutritional quality. Nutrients quantified included crude protein, fiber fractions, and mineral concentrations, which were used to evaluate variations in forage quality across brood foraging used and available locations.

Crude Protein- Crude protein was estimated using dry combustion on a LECO carbon/nitrogen analyzer (LECO Corporation, St. Joseph, Michigan, USA) to measure percent nitrogen; percent nitrogen was then multiplied by 6.25 to estimate crude protein. This conversion factor is standard for forage samples and assumes that plant protein contains approximately 16–17.5% nitrogen and non-protein nitrogen is negligible (National Forage Testing Association 1993).

Fiber Fractions- Fiber fractions represent chemically defined components of plant structural material and include neutral detergent fiber (NDF; hemicellulose, cellulose, lignin), acid detergent fiber (ADF; cellulose and lignin), and acid detergent lignin (ADL; lignin). The lab used

detergent solutions to dissolve soluble cell components and minerals, with fiber fractions quantified gravimetrically as the remaining residues. The lab determined ADL by further digesting ADF residues using 72% sulfuric acid and the remaining residue was quantified gravimetrically (Mertens 1998; National Forage Testing Association 1993; ANKOM Technology 2002, 2017).

Mineral composition-Minerals quantified included phosphorus (P %), calcium (Ca %), potassium (K %), magnesium (Mg %), sulfur (reported as sulfate–sulfur, SO_4–S %), sodium (Na %), copper (Cu ppm), iron (Fe ppm), and zinc (Zn ppm). The lab determined concentrations using nitric acid digestion and inductively coupled plasma (ICP) spectrometry, with concentrations reported on a dry-matter basis (Soil Science Society of America 1990; Western States Laboratory Proficiency Testing Program 1997).

Differences in Arthropod Metrics among Used and Available Sites

I summarized arthropod community metrics, including morphospecies richness, abundance, and biomass, to describe differences between used and available brood foraging locations. I calculated arthropod metrics independently for each sampling location and then averaged values across all used sites and all available sites separately. I used standard deviations to assess variation within each group.

I evaluated differences in arthropod community metrics between used and available brood-foraging sites using multivariate analysis of variance (MANOVA) followed by univariate one-way analyses of variance (ANOVA) for each arthropod metric conditional on significant results from MANOVA ($P < 0.05$). I excluded extreme outliers from morphospecies richness estimates because richness values were derived from morphospecies classifications and therefore, represented estimates rather than exact counts. Outliers were identified using an

interquartile range (IQR) method (k = 3), where values exceeding the upper quartile plus three times the IQR were removed (Tukey 1997). I applied a log(x + 1) transformation to metrics exhibiting strong right skew prior to analysis to improve normality (West 2022).

Differences in Plant Nutrients Among Used and Available Sites

I summarized plant-nutrient concentrations including crude protein (%), acid detergent lignin (ADL %), phosphorus (P %), calcium (Ca %), potassium (K %), magnesium (Mg %), sulfur (reported as sulfate–sulfur, SO_4–S %), sodium (Na %), copper (Cu ppm), iron (Fe ppm), and zinc (Zn ppm), to describe differences between used and available brood foraging locations. I calculated nutrient composition from forage clippings collected at brood foraging used and available sites and then averaged separately for used and available sites. I used standard deviations to assess variation within each group.

I evaluated differences in forage nutrient concentrations between used and available brood foraging sites using MANOVA followed by ANOVA for each nutrient concentration conditional on significant results from MANOVA ($P < 0.05$). Sodium (Na) was excluded from these analyses because measurements were incomplete for many samples. To ensure comparability across multivariate tests, analyses were conducted using a complete-case dataset in which samples missing any nutrient measurements were removed. I applied a log (x + 1) transformation to metrics exhibiting a strong right skew prior to analysis to improve normality (West 2022).

Data Preparation for Regression Analyses

For subsequent regression analyses, I screened predictor and response variables for data quality and model assumptions. Extreme high-end outliers of arthropod morphospecies richness were excluded when richness was included as either a response or predictor variable in statistical

models to reduce undue influence on parameter estimation (Tukey 1977). Outliers were identified using an interquartile range (IQR) criterion (Q3 + 3×IQR), while zero values were retained. I evaluated predictor distributions using histograms, boxplots, and skewness metrics. I applied a log-transformation using log (x + 1) when necessary to reduce strong right skewness and improve linearity between predictors and the response (West 2022). I standardized continuous predictors to *z*-scores (mean = 0, SD = 1) to facilitate comparison of effect sizes among metrics. I assessed collinearity among predictor variables using variance inflation factors (VIFs) derived from global models and excluded variables with VIF > 5 (Kim 2019).

I used complete case data for all analyses; thus, sample sizes varied among models depending on the response and predictor variables included. I evaluated model parsimony using Akaike's Information Criterion corrected for small sample sizes (AICc), considered models within $\Delta AICc \leq 2$ as competitive (Burnham & Anderson 2002), and summarized uncertainty around parameter estimates using 85% confidence intervals (Arnold 2010).

Arthropod Community Influence on Brood Foraging Site Selection

I evaluated the influence of arthropod metrics on brood foraging site selection at used and paired random brood foraging sites using a Resource Selection Function (RSF) implemented as a logistic regression model (Boyce et al. 2002). I implemented a used-available design, where brood foraging sites were coded as 1 (used) and paired random sites as 0 (available). I conducted analyses at the sample level where each arthropod suction sample (bag) represented an independent observational unit. Predictor variables consisted of arthropod morphospecies richness, arthropod abundance, arthropod biomass, and grasshopper abundance summarized for each location. I constructed a candidate model set including a null model, single-predictor

models for each arthropod metric, and a global model incorporating arthropod richness, biomass, and grasshopper abundance. Arthropod abundance was excluded from the global model due to collinearity with other arthropod metrics (VIF > 5; Kim 2019). The arthropod metric from the most parsimonious model was carried forward for subsequent habitat-based analyses.

Plant Nutrient Influence on Brood Foraging Site Selection

I evaluated the influence of plant nutrient composition on brood foraging site selection at used and paired random brood foraging locations using a RSF implemented as a logistic regression model. The response variable was used (1) vs. available sites (0). I included nutrient compositions derived from forage clippings at used and available brood foraging locations as predictors - crude protein (%), acid detergent lignin (ADL %), phosphorus (P %), calcium (Ca %), potassium (K %), magnesium (Mg %), sulfur (reported as sulfate–sulfur, SO_4–S %), sodium (Na %), copper (Cu ppm), iron (Fe ppm), and zinc (Zn ppm). I constructed a candidate model set that included a null model, single-predictor models for each plant nutrient, and a global model.

Habitat Influences on Arthropod Richness

I evaluated the influence of habitat characteristics on arthropod morphospecies richness because arthropod morphospeices richness was the most parsimonious predictor of brood foraging-site selection (based on RSF above). I modeled relationships between habitat variables and arthropod richness using a generalized linear model (GLM), with a negative binomial error distribution to account for over-dispersed count data (Ford 2024). Predictor variables consisted of habitat characteristics measured at used and available brood foraging sites, including site-level mean percent cover of functional groups (grass, woody vegetation, forbs, bare ground, and litter), site-level mean vertical obstruction readings (VOR; 0.00–0.25 m and 0.25–0.50 m), dominant

cover type within a 10-m radius (categorical; grassland, woodland, cropland, shrubland), and floral species richness. I constructed a candidate model set including a null model, single-predictor models for each habitat characteristic, and a global model incorporating all predictors described above.

Plant Nutrients Influencing Arthropod Morphospecies Richness

I evaluated the influence plant nutrient concentrations have on arthropod richness because arthropod richness was the most parsimonious predictor of brood foraging site selection (based on RSF above). I used a GLM with a negative binomial error distribution to account for over-dispersed count data. Predictor variables included crude protein (%), acid detergent lignin (ADL %), phosphorus (P %), calcium (Ca %), potassium (K %), magnesium (Mg %), sulfur (reported as sulfate–sulfur, SO_4–S %), sodium (Na %), copper (Cu ppm), iron (Fe ppm), and zinc (Zn ppm). I constructed a candidate model set that included a null model, single-predictor models for each plant nutrient, and a global model.

Habitat Influences on Phosphorus Concentrations

I evaluated the influence of habitat characteristics phosphorus concentrations in forage clippings by fitting beta regression models with a logit link to account for response values bounded between 0 and 1 (Ferrari & Cribari-Neto 2004). Models were implemented using the **betareg** package in R (Cribari-Neto & Zeileis 2010). Phosphorus concentration analyzed from forage clippings at used and available brood foraging sites was the response variable. I included habitat measurements obtained from used and available brood foraging sites as predictor variables consisting of site mean % functional groups (grass, woody, forb), site mean VOR (0.00 m – 0.25 m ,0.25 m – 0.50 m), dominant cover type at 10 m (categorical), and flora species

richness. I constructed a candidate model set that included a null model, single-predictor models for each habitat characteristic and a global model.

Bottom – Up Drivers Influencing Brood Foraging Site Selection

I investigated bottom-up drivers influencing brood foraging site selection using a piecewise structural equation model (piecewise SEM; Lefcheck 2016). Piecewise SEM, implemented as confirmatory path analysis, estimates a hypothesized causal network by fitting each directed relationship as a separate regression model. Piecewise SEM allows for variables to serve as predictors and responses within a causal network accounting for direct and indirect effects. I developed a conceptual *a priori* hypothesized model following causal modeling principles described by Grace and Irvine (2020) and Grace et al. (2012). I conducted statistical evaluation using the piecewiseSEM framework (Lefcheck 2016).

I hypothesized multiple bottom-up pathways in which habitat structure and composition would exert on brood foraging site selection indirectly (Figure 2.1). I expected habitat composition and structure to have direct effects on flora richness, forage quality, and arthropod morphospecies richness. I predicted flora species richness would influence forage quality and arthropod richness, while arthropod richness would influence brood use, representing food resource driven selection.

I included percent cover of functional vegetation groups (grass, forb, woody), ground-layer components (bare ground, litter), visual obstruction (0.00–0.25 m; 0.25–0.50 m), flora species richness, plant nutrient composition derived from clippings (protein, P, Ca, K), arthropod morphospecies richness, and brood foraging site use (1 = used; 0 = available). I screened continuous habitat and nutrient indicators for right skewness and applied a log(x+1) transformation to strongly right skewed predictors when necessary (West 2021).

I reduced collinearity among correlated predictors using principal component analysis (PCA)–based composite indices to represent habitat composition (percent grass, forb, woody), habitat structure (visual obstruction strata plus bare ground and litter), and plant nutrient composition (protein, P, Ca, K) as PC1 scores (Welti et al. 2019). I fit component models using their appropriate error distributions and further assessed collinearity using variance inflation factors of each component models (Kim 2019). I assembled component models into a candidate piecewise structural equation model using the R package piecewiseSEM (Lefcheck 2016). I evaluated model structure using tests of directed separation (d-sep), with global goodness-of-fit assessed using Fisher's C statistic, which follows a χ^2 distribution (Lefcheck 2016). I locally estimated causal path uncertainty using 95% confidence intervals (Lefcheck 2016).

Results

Arthropod Sorting

I sampled arthropods at used (n = 200) and available (n = 362) brood foraging locations during May-August 2024 and 2025 across 3 study regions in Kansas (Table 2.1). A total of 8,016 arthropods representing 27 Orders were collected (Table 2.2).

The Central study region had the highest average abundance (16.17 ± 15.47) and morphospecies richness (9.2 ± 6.11) per sample, compared to the East and West study regions (Table 2.3). Hemiptera was the most dominant Order collected in all study regions in terms of abundance and presence (Table 2.2, 2.4).

Correspondence checks on arthropod morphospecies estimations indicated high consistency among sorters. In 2024, discrepancies in morphospecies richness estimates occurred in 4.9% of samples, whereas discrepancies occurred in 9.03% of 2025 samples. Overall, morphospecies richness estimates were highly uniform among sorters.

Plant Nutrient Analyses

I collected forage clippings and measured their nutrient concentrations at used (n = 191) and available (n = 358) brood foraging locations during May-August 2024 and 2025 among 3 study regions in Kansas (Table 2.5). Due to limitations, not all nutrient concentrations were measured for each sample (Table 2.6).

Differences in Arthropod Metrics and Plant Nutrients Among Used and Available Sites

Arthropod Metrics - Mean arthropod metrics (abundance, biomass (g), and morphospecies richness were similar among used (n = 183) and available (n = 327) brood foraging sites (Table 2.8). Average nutrient concentrations can be referenced in Table 2.7. Overall arthropod metrics did not differ between used and available brood-foraging sites (*MANOVA:* $F_{4,554}$ = 1.46, P = 0.21).

Plant Nutrient Composition- Mean nutrient concentration from forage clippings collected at used (n = 191) and available (n = 355) brood foraging sites differed among sites (Table 2.9, Figure 2.2). Multivariate analysis of variance indicated that overall nutrient composition differed between used and available brood-foraging sites (*MANOVA:* $F_{10,442}$ = 2.37, P = 0.010). Follow-up one-way ANOVAs indicated larger concentrations of phosphorus, calcium, potassium, sulfur, zinc, and protein at used relative to available brood-foraging sites (Table 2.9). No differences were detected for ADL, magnesium, copper, or iron.

Relationships Among Arthropod Metrics, Plant Nutrient Composition, Habitat characteristics, and Brood Foraging Site Selection

Arthropod community influence on brood foraging site selection- I collected arthropods at used (n = 183) and available (n = 327) brood foraging sites. At a foraging site scale, arthropod

morphospecies richness received the greatest model support (w_i = 0.42), compared to abundance (ΔAICc = 2.70, w_i = 0.11), biomass (ΔAICc = 3.14, w_i = 0.09), and grasshopper abundance (ΔAICc = 3.27, w_i = 0.08, Table 2.10). Arthropod morphospecies richness showed a positive association with probability of use (β = 0.17 ± 0.01, P < 0.1, Figure 2.3) and did not overlap zero at the 85% confidence interval.

However, the null model (ΔAICc = 1.35; w_i = 0.21) was competitive with the top-ranked model indicating modest support for the model. Because arthropod richness outperformed other arthropod metrics, it was retained as the focal arthropod variable in subsequent analyses and incorporated as an observed variable in the piecewise structural equation model.

Plant nutrients influence on brood foraging site selection- Among used (n = 161) and available (n = 292) brood foraging sites, phosphorus (% P) was the most parsimonious model predicting brood-foraging site selection (w_i = 0.73) relative to other nutrients (Table 2.11). Phosphorus exhibited a positive association with probability of use (β = 0.36 ± 0.09, P < 0.05, Figure 2.4), corresponding to a predicted use 1.89 times greater at sites with phosphorus concentrations one standard deviation above the mean compared to one standard deviation below the mean.

Several other nutrients exhibited positive associations with probability of use but received less support than the top-ranked model. Zinc (Zn), potassium (K), crude protein, calcium (Ca), and sulfur (S) exhibited positive effects on brood foraging site selection, with standardized coefficients ranging from β = 0.23 to 0.32 (SE = 0.09–0.10, Table 2.11). Based on their effect sizes, I retained potassium (K), crude protein, and calcium (Ca) as observed variables for the structural equation model. Phosphorus, which received the strongest model support, was

retained as the focal forage response variable in subsequent analyses evaluating habitat-related influences on nutrient availability.

Habitat influences on arthropod richness- Bare-ground quadratic was the most parsimonious model predicting arthropod morphospecies richness among combined used and available brood foraging sites (n = 430; w_i = 0.66), compared to other habitat predictor models (Table 2.12). Bare ground exhibited a quadratic negative association with predicted arthropod morphospecies richness (β = 0.05 ± 0.02, $P < 0.05$, Figure 2.5) and did not overlap zero at the 85% confidence interval. Among models exhibiting positive relationships with arthropod morphospecies richness, visual obstruction (0.00-0.25) was the highest-ranked model (β = 0.12 ± 0.03 SE; ΔAICc = 4.29, w_i = 0.08) and did not overlap zero at the 85% confidence interval, though did not receive adequate model support.

The cover type model was not competitive in predicting arthropod morphospecies richness (ΔAICc = 13.80, w_i = 0.00). However, descriptive summaries indicated substantial variability in arthropod morphospecies richness among dominant cover types within a 10-m radius of sample sites (Table 2.13). Mean richness was similar among cropland, forest, grassland, and shrubland dominated sites.

Plant nutrients influencing arthropod richness- I collected plant nutrient concentrations and arthropod species richness at 358 brood foraging sites (used and available combined). I retained the following nutrients for analyses; % Protein, % Phosphorus, % Magnesium, % Sulfur, % Calcium, % Potassium, Iron (ppm), Zinc (ppm), Copper (ppm), and % Acid Detergent Lignin.

The most parsimonious model predicting arthropod morphospecies richness was Phosphorus (w_i = 0.79), relative to other single variable nutrient models (Table 2.14). Phosphorus showed a positive association with predicted arthropod morphospecies richness (β =

0.11 ± 0.03, $P < 0.05$, Figure 2.6), and the 85% confidence interval excluded zero. The predicted arthropod morphospecies richness 1.26 times greater at sites with phosphorus concentrations one standard deviation above the mean compared to one standard deviation below the mean.

Habitat influences phosphorus concentrations-The most parsimonious model predicting phosphorus concentrations was the categorical cover type model ($w_i = 0.99$, Table 2.15) including dominant cover types identified within a 10-m radius at a samples site. Phosphorus concentrations contrasted among cover types (Figure 2.7). Grassland and shrubland sites exhibited lower phosphorus concentrations than cropland (grassland: $\beta = -0.51$, $P < 0.005$; shrubland: $\beta = -0.52$, $P < 0.005$), whereas forest sites did not differ from cropland ($\beta \approx 0$, $P = 0.98$).

Notably, the flora richness models (Flora Richness, Grass Richness, and Forb Richness) had unexpected negative associations with Phosphorus concentrations (Table 2.15). Whereas forb cover had a positive association ($\beta = 0.12 \pm 0.03$, $P < 0.05$; Table 2.15).

Bottom–Up Drivers Influencing Brood Foraging Site Selection

I retained habitat characteristics, plant nutrient concentrations, and arthropod morphospecies richness, measured at 150 used and 282 available brood foraging sites during May – August 2024 and 2025 to assess bottom-up drivers influencing brood-site section. A total of 47 unique wild turkey broods were sampled, with a mean of 9.68 ± 5.30 points per brood. I developed an *a priori* hypothesized structural equation model to guide subsequent analyses (Figure 2.1). I employed principal components analysis (PCA) to reduce multivariate data to three composite indices representing habitat structure, habitat composition, and forage quality.

PCA Weighted Indices

Habitat Composition- I derived the habitat composition composite using percent forb, percent grass, and percent woody cover. Principal components analysis (PCA) indicated that PC1 explained 50.6% of the total variance (Figure 2.8). Percent grass (loading = −0.73) and percent forb (loading = 0.68) were the primary contributors to PC1. Percent grass loaded negatively on PC1, whereas percent forb loaded positively. Percent woody cover aligned more strongly with PC2 (loading = 0.90) and contributed minimally to PC1 (loading = 0.11). Thus, sites with greater forb cover and lower grass cover received positive index scores (PC1 > 0), whereas grass-dominated sites were characterized by negative index values.

Habitat Structure- I derived the habitat structure composite using percent litter, percent bare ground, and visual obstruction readings (VOR 0.00 – 0.25; VOR 0.25 – 0.50). The first principal component explained 50.3% of the total variance (Figure 2.9). The strongest positive contributors to PC1 were VOR 0.00–0.25 m (loading = 0.64) and VOR 0.25–0.50 m (loading = 0.58) In contrast, percent bare ground (loading = −0.42) and percent litter (loading = −0.29) loaded negatively on PC1. Thus, sites with greater visual obstruction (3-dimensional assessment of vegetation density) from 0-0.5-m tall received positive index scores (PC1 > 0), whereas sites characterized by greater bare ground and litter were associated with negative index values.

Plant quality- I derived the forage quality composite index using percent protein, percent phosphorus, percent calcium, and percent potassium. The first principal component explained 69.2% of the total variance (Figure 2.10). Potassium (loading = 0.52), protein (loading = 0.51), and phosphorus (loading = 0.51) contributed most strongly and positively to PC1. Calcium loaded moderately on PC1 (loading = 0.45) but aligned more strongly with PC2 (loading = −0.81). Thus, sites with greater concentrations of these nutrients received positive index scores (PC1 > 0), representing greater overall plant nutrient availability.

A priori hypothesized SEM model fit

The hypothesized model (Figure 2.1) consisted of four subcomponent models (Table 2.16) and lacked global fit, indicated through Chi-squared test ($\chi^2 = 12.496$, df = 4, $P = 0.014$) and Fisher's C test (Fisher's C = 18.529, df = 8, $P = 0.018$). Furthermore, tests of directed separation (dsep) identified a meaningful missing path: the direct effect of the forage quality composite index on brood foraging site selection (use ~ plant quality; $P = 0.005$; Table 2.17). I considered ecological importance of this path and fit it into a refined model.

Refined SEM Model Fit

The refined model (Figure 2.11), including the missing path identified by test of directed separation, demonstrated adequate model fit ($\chi^2 = 1.478$, df = 2, $P = 0.478$, Fisher's C = 3.322, df = 4, $P = 0.505$). Furthermore, tests of directed separation did not identify additional meaningful paths (Table 2.18). The brood-foraging site use sub-model explained 5% of the variation in site selection (Nagelkerke $R^2 = 0.05$).

There was no direct effect from the exogenous variables- habitat composition and structure, on brood site-use or flora richness (Table 2.19). Habitat composition did not directly influence arthropod richness ($P = 0.056$). Flora richness did not influence arthropod richness ($P = 0.61$). Forage quality had the strongest direct effect on brood site-use ($\beta = 0.19$, $P < 0.01$; Table 2.19, Figure 2.12) and arthropod richness also had a positive direct effect on use ($\beta = 0.11$, $P < 0.05$; Table 2.19, Figure 2.12). Habitat composition influenced brood site-use indirectly through its positive effect on forage quality ($\beta = 0.52$, $P < 0.001$; Table 2.19, Figure 2.12), which in turn positively influenced use. Habitat structure indirectly influenced use through its positive effect on arthropod richness ($\beta = 0.13$, $P < 0.001$; Table 2.19, Figure 2.12), and in turn positively

influenced use. Flora richness did not have a direct effect on use but had an unexpected negative effect on forage quality ($\beta = -0.17$, $P < 0.001$; Table 2.19, Figure 2.12).

Discussion

This study represents the most comprehensive understanding of wild turkey brood foraging-site selection in Kansas to date, going beyond linking selection to general habitat structural and compositional characteristics, and emphasizing the importance of resource availability. For instance, plant nutrient and arthropod availability had direct influences on selection, while their availability was largely shaped by habitat composition and structure. Beyond linking habitat features to selection, several additional findings provided insight into the foraging ecology of wild turkey during brood rearing, including greater plant nutrient quality at used locations, importance of phosphorus, and resource-mediated selection.

Previous studies have reported direct relationships between habitat composition and structure with brood site selection (Phalen et al. 1986, Keegan & Crawford 1997, Spears et al. 2007, Nelson et al. 2022). For example, Nelson et al. (2022) found that greater visual obstruction, greater grass and forb cover, and lower temperatures were positively associated with brood selection at a fine scale. Specific to Kansas, Spears et al. (2007) found that increased horizontal visual obstruction, particularly shrub density, was sought by broods for ground roosting and use throughout the day. Similarly, I found forb cover and visual obstruction were important components for selection. However, when habitat composition and structure were evaluated within a bottom-up framework, their effects on selection were not independent. Instead, habitat composition (ground cover) and structure (visual obstruction) influenced selection indirectly through plant nutrient availability and arthropod morphospecies richness. Where previous work has incorporated habitat compositional and structural variables as direct

predictors of brood-site selection, my study indicates that these variables exert influence through an underlying bottom-up process. Ultimately, this finding suggests that at a fine scale, broods respond to resource availability rather than composition and structure.

Overall, wild turkey broods in Kansas selected areas with greater plant nutrient availability, and arthropod richness, characterized by sites with greater forb cover and visual obstruction. Specifically, crude protein, phosphorus, calcium, potassium, copper, and zinc were selected more than was available. Plant nutrient availability varied by region, the West study region had less crude protein and phosphorus on average relative to the East and Central study region, highlighting landscape variation driven by a precipitation gradient, and subsequently land use change (Waterman et al. 2022). Arthropod community metrics (biomass [g], abundance, and morphospecies richness) revealed minute differences among used and available brood foraging sites, as well as between study regions, providing no evidence arthropod communities may be limited in Kansas landscapes.

Bottom – Up Drivers

Results from piecewise structural equation modeling suggest that structural and compositional characteristics of a foraging habitat are not as important as the resources they offer at a fine scale (10 m). As hypothesized, there was not a direct influence from habitat structure or composition on brood foraging site use, instead effects were mediated though forage quality and arthropod richness. Contrary to expectations, forage quality exhibited a direct positive effect on brood foraging site selection and was substantially shaped by habitat composition, particularly gradients in forb versus grass cover. Kansas exhibits significant landscape variations along precipitation (Tomlinson & Knapp 2012) and soil gradients (Perkins & Schrenk 1948). Thus, landscape variation across Kansas coupled with the generalist nature of wild turkey ecology

creates a challenge in identifying relationships between fine-scale foraging site selection and general habitat composition and structural characteristics (e.g., forb cover, visual obstruction). My study, however, emphasizes the importance of habitat composition and structural characteristics through the resources they provide to wild turkey broods via bottom-up cascading effects.

The direct effect of forage quality on brood foraging site selection may suggest that broods are responding more specifically to variations in plant nutrient quality itself, rather than to habitat structure or composition features at the fine scale. Wildlife species are known to respond to variation in nutrient availability when making foraging decisions (Beck et al. 2006). Though poults rely heavily on arthropods during the first weeks of life, they are known to ingest more plant materials as they age (Healy 1985, Hurst 1992, Rumble and Anderson 1996). Thus, forage quality not only shapes arthropod communities that are available for broods, but can directly supply nutrition to broods as a forage component itself, possibly explaining the direct nature of the effect.

Sites characterized by greater forage quality were associated with larger forb cover relative to grass cover. Forbs tend to contain greater concentrations of nutrients within their tissues relative to grass (Lee 2018, Belesky 2020), potentially enhancing both arthropod communities and direct plant-based forage resources available to broods. Previous research has documented positive associations between forb cover and brood use (Nelson et al. 2022). My findings corroborate those by linking forb-dominated sites indirectly to selection through nutrient mediated resource availability.

Phosphorus and Crude Protein

Phosphorus was a particularly important nutrient in structuring brood foraging site selection. In single-variable regressions, phosphorus exerted direct positive influences on both arthropod morphospecies richness and brood foraging site selection, relative to other nutrients. When nutrients were evaluated collectively within a plant quality index, phosphorus was a dominant component. Plant quality directly influenced arthropod morphospecies richness and selection whereas other vegetation composition and structural characteristics included in the model were not independently linked to selection.

Phosphorus is an essential part of terrestrial systems (Tiessen 2008, Khan et al. 2023). In plants, it is integral in supporting genetic, metabolic, structural and regulatory molecules, all of which sustain growth and fecundity (White & Hammond 2008). Moreover, plant phosphorus availability is known to influence arthropod communities (Joern et al. 2012, Lu et al. 2020). Interestingly, in poultry species, dietary phosphorus plays an important role in egg production and bone quality (Nie et al. 2018, Wei et al. 2022). Collectively, these findings suggest that phosphorus availability may structure brood foraging site selection by simultaneously enhancing plant quality, supporting arthropod communities, and meeting the nutritional demands of rapidly developing poults.

Though phosphorus was the strongest single plant nutrient predictor of arthropod richness and brood foraging site selection relative to other nutrients, in a single variable regression, crude protein also exhibited a substantial positive association with both response variables. Additionally, crude protein was included with phosphorus in the plant quality index developed using PCA, revealing phosphorus and crude protein had profound effects on the probability of

brood foraging site selection directly and indirectly through shaping arthropod morphospecies richness.

Crude protein measurements are derived from total plant tissue nitrogen (N × 6.25). Therefore, crude protein reflects variation in plant nitrogen availability across a landscape. Nitrogen is an essential element for biological systems and required for the synthesis of amino acids, proteins, nucleic acids, and metabolic compounds that sustain organismal growth and development (Ferousi et al. 2020, Mattoo et al. 2025). Moreover, nitrogen is essential in supporting growth of plants and subsequently, the herbivores that feed on them (Mason et al. 2022). In this study, variations in plant crude protein likely reflect differences in nitrogen driven forage quality that may influence arthropod communities and brood foraging site selection. Wild turkey poults have high protein demand early in life, for which they rely heavily on arthropods and take in more plant material as they age (Healy 1985). Thus, plant nitrogen availability may influence poults indirectly by promoting arthropod communities and directly by increasing the nutritional value of plant forage. Unfortunately, global declines in terrestrial nitrogen availability have been documented, and attributed to elevated atmospheric CO_2 levels, harvesting of biomass from ecosystems, and increased frequency of fire over decadal time scales (Mason et al. 2022).

Patterns of nutrient limitation in grasslands suggest nitrogen-only limitation and/or nitrogen–phosphorus colimitation (Craine et al. 2008, Craine & Jackson 2009). For example, Craine & Jackson (2009) added nitrogen, phosphorus, and nitrogen + phosphorus across 98 North American grassland soils and found that all three treatments increased plant biomass. However, high phosphorus systems were primarily limited by nitrogen, and low phosphorus systems were primarily limited by a nitrogen + phosphorus collimation. Nitrogen is required to produce phosphatases (enzymes) that are released by plants into the soil to enhance phosphorus

acquisition; thus, nitrogen limitation may indirectly restrict a plant's ability to access soil phosphorus (Craine & Jackson 2009). Because nitrogen is required for phosphorus acquisition, phosphorus limitations may depend on nitrogen availability, leading to growth responses from the additions of nitrogen, phosphorus, or both.

Interestingly, plant tissue phosphorus concentrations were greatest in cropland and forest dominated brood foraging sites, relative to grasslands and shrublands. One explanation of elevated phosphorus in cropland-dominated sites is fertilization. In Kansas, phosphorus fertilizers are commonly applied to crops such as corn, soybeans, winter wheat, and sorghum, at various rates (< 0.1 – 0.6 (g P m^{-2}); Cao et al. 2024). Timing of application varies and typically occurs at planting, during the fall (previous year), or spring (prior to planting; Cao et al. 2024). Although only 56 brood foraging sites were identified as being cropland dominant, it is plausible that forage clippings collected contributed substantially to overall phosphorus concentrations due to its application. Furthermore, brood foraging sites classified as forest dominated had similar phosphorus concentrations available in plant tissues. Considering the application of phosphorus before or at planting (Cao et al. 2024), and that forested areas frequently occur adjacent to croplands within the study system, it is possible that phosphorus is lost from agricultural fields and leaches into nearby forested areas, increasing its availability in surrounding vegetation.

Collectively, phosphorus and nitrogen structure plant and herbivore communities, while limitations of these nutrients can have cascading effects on trophic webs. In my study, the positive associations between these nutrients (N and P) and arthropod morphospecies richness, coupled with their elevated concentrations at used brood-foraging sites, and influence on selection directly, suggest that nitrogen and phosphorus availability plays a pivotal role in brood foraging site selection. While this study did not experimentally test nutrient limitation, the

observed patterns are consistent with the possibility that arthropod communities and brood foraging site selection respond to sites where both phosphorus and nitrogen concentrations are elevated. My research did not test the effect of the availability of these nutrients on survival and should be an aim of future research.

Acid Detergent Lignin

Contrary to my hypothesis, acid detergent lignin (ADL) did not meaningfully influence arthropod morphospecies richness or, subsequently, brood foraging site selection. One possible explanation is that arthropod groups differ in feeding strategies, such as chewing herbivores versus sapsuckers. Chewing herbivores are likely more constrained by higher ADL concentrations, whereas sucking insects may be less sensitive to certain measures of leaf mechanical resistance provided by lignin (Peeters et al. 2007). As a result, species richness may not fully capture the effects of ADL if lignin primarily deters certain taxa, such as coleopterans and hemipterans, rather than the arthropod community as a whole (Lu et al. 2020).

Arthropods

Arthropod richness showed the strongest effect on brood foraging site selection compared to abundance and biomass; however, its standalone effect was modest, as the null model was competitive in regression analyses. This pattern suggests that arthropod richness alone does not strongly drive brood foraging site selection independently but instead operates within a broader influence. For instance, when arthropod morphospecies richness was incorporated into the piecewise SEM framework, it had a direct effect on selection, while it was strongly influenced by plant quality. Thus, arthropod richness appears to influence brood-site selection more meaningfully when accounting for plant quality within a structured bottom-up pathway rather than by itself.

Few studies have explicitly evaluated brood response to arthropod richness. Yet, it is clear that poults rely heavily on arthropods during the first weeks of life (Healy 1985, 1992; Hurst 1992). Arthropods vary in nutrient quality. For example, spiders (Araneae) and grasshoppers (Orthoptera) have lower exoskeleton content and greater protein content compared to Hymenopterans and Coleopterans (Reeves 2020). Thus, arthropod diversity among landscapes may provide a broad array of nutrients and prey types, potentially increasing forage efficiency and nutrient intake for poults.

Brood Foraging Habitat

Broods selected sites characterized by increased forb cover, elevated plant nutrient concentrations, and increased arthropod richness. These characteristics are commonly associated with vaguely defined early successional cover types (Harper 2007, Chamberlain et al. 2020). Though early successional cover types are typically measured at the patch scale, or gap scale in forested ecosystems (Shrue et al. 2006), my study emphasizes that early successional conditions may influence brood foraging at finer scales in grasslands than previously documented.

Early successional cover type typically result from a disturbance mechanism (Harper 2007, White et al. 2011). For example, grazing can create early successional cover types at a fine scale by removing herbaceous materials that allow for new herbaceous growth, while reducing grass dominance by releasing light and space, ultimately allowing forb establishment (Hayes and Holl 2003, Segre et al. 2016). Grazing is a common land-use practice in Kansas; cattle presence was documented at 48% of used brood foraging sites. This pattern suggests that disturbance-maintained heterogeneity by grazing may play a pivotal role in creating fine-scale resource conditions necessary to support brood foraging while also maintaining nearby cover for nesting.

Another disturbance maintaining early successional cover types across Kansas is fire. Fire (prescribed or wildfire), like grazing, removes mature growth from the ground allowing for new growth and resulting in early successional cover types (Harper 2007, White et al. 2011). Burning is known to be a useful tool in managing for wild turkey brood foraging habitat (Hurst 1972, Hon et al. 1978, Little et al. 2016). Though burning was not directly linked in my study, it is a common practice in the Flint Hills ecoregion of Kansas, which contains all of the East study region sites (Figure 1.1). In 2024, 365,073 acres were burned (prescribed or wildfire) between February 14 and April 29 in 6 counties that contained study sites (Riley, Morris, Chase, Osage, Coffey, Greenwood; Kansas Department of Health and Environment 2024). In the same counties in 2025, 762,334 acres were burned between March 5 and May 4 (Kansas Department of Health and Environment 2025). Future research in Kansas should focus on linking burning to wild turkey brood success, where burning may create early-successional cover types with greater plant nutrient availability.

Collectively, these results suggest that wild turkey brood foraging habitat should be considered at a finer scale, in which structural and compositional components are functionally important through the resources that they provide. The forb-dominated, resource-rich conditions identified in this study are characteristic of early successional cover types, suggesting that even at a fine scale, they provide the resources necessary for brood foraging.

Caveats

This study presented a simplified version of a complex process in a complex system. My piecewise SEM only included a small number of the variables that influence wild turkey brood foraging site selection. For instance, soils, weather and predator occupancy are influential to all wild turkey behavior (Nelson et al. 2022, Londe et al. 2023); thus, they too are important to

consider when investigating selection. However, perhaps an abstraction of this complex reality is needed to understand the most important factors. Moreover, exclusion of these important variables could explain the low explanatory power from the subcomponent model predicting brood use (5%), even though low explanatory power is common with logistic regression models (Boyce et al. 2002). Future work could attempt to use a more robust response variable such as linking survival or mass (g) of poults to habitat selection or overall habitat quality.

My measure of arthropod morphospecies richness was the most efficient way in obtaining a proxy to richness. A limitation to this method is it is not exact and could be an over/under estimation of the actual arthropod species richness. Correspondence checks on arthropod richness sorted indicated consistency among sorters, however, there were no exact estimates done by trained taxonomist to cross reference and obtain an error rate to be applied to statistical analyses.

I recommend future studies build off this framework to understand the "why" of wild turkey response to management. Wild turkey are complex species that require complex solutions and require a large number of habitats to fulfill their lifecycles. Specific to brood foraging habitat, management should focus on creating large numbers of micro early successional habitats where wild turkey occupy. For instance, burning or grazing within proximity of a forest edge (< 300 m; C. Skidmore, unpublished data) would not only be efficient, but would provide adequate forage habitat needed with nearby concealment opportunities and roosting habitats.

Management Implications

Management of wild turkey brood-rearing habitat is central to sustaining wild turkey productivity during a critical life stage and should prioritize a balance between foraging and concealment opportunities. In my study system, wild turkey brood rarely foraged at sites >300 m

from riparian corridors or forested edge. Thus, management efforts ought to focus on these "core" areas to be most effective and efficient.

Brood habitat can best be managed by disturbance, which creates early successional patches that promote quality forbs, arthropod richness, and herbaceous cover. A variety of tools can be used to create disturbance, including burning and grazing. Burning is a widely used management tool used to promote general wild turkey habitat, and more specifically, foraging opportunities. It is recommended that burning is conducted during the late dormant season (March) or late growing season (July – October) to ensure wild turkey nesting is not disturbed. Burning during the late dormant season reduces cool-season grasses that have begun to germinate and stimulates germination of forbs (Harper 2019). Arthropod communities present will be directly affected: however, charred arthropods can become quality source of calcium for soon to be nesting hens, while allowing the arthropod community to reset before the brood rearing period. Likewise, burning during the late growing season will stimulate forb and herbaceous cover for the following brood-rearing season, while reducing woody encroachment. Burning patches within the buffer zone previously described will offer foraging opportunities, improve edge, and keep concealment opportunities in proximity. Grazing is a common practice throughout Kansas and should continue to be used to create early successional habitats (10 m^2; Spender et al. 2024). Mowing is not an advisable method to manage for wild turkey brood foraging habitat as it has many implications on wild turkey and other wildlife species such as white-tail deer (*Odocoileus virginianus*), and ground nesting passerines.

Cool-season food plots (e.g., clover or alfalfa) should be strategically placed within areas occupied by wild turkeys. Species such as alfalfa provide high nutritional value and can promote arthropod diversity, creating favorable foraging opportunities for broods. Food plots should be

managed to allow early successional plants such as ragweed and goldenrod to persist, which can provide additional concealment for poults. For example, at Wilson Lake Wildlife Management Area off Anspaugh Road, a ~4-acre irregularly shaped alfalfa plot bordering a riparian area was repeatedly used by multiple successful broods during the brood-rearing period.

Conclusion

Including resource availability into a bottom-up framework assessing factors influencing brood foraging site selection provided a new perspective on fine-scale foraging behavior. For instance, I did not detect a direct effect of habitat composition or structure variables on the probability of use. Instead, their effects were mediated through plant quality and arthropod richness. These findings indicate resource-mediated selection at the fine-scale (10 m), where resource availability drives fine-scale selection. This is not to say the compositional and structural components are not important; they are important *because* of the resources they provide to wild turkey broods. Additionally, Phosphorus (%) concentration of plant tissues played a pivotal role in shaping arthropod community richness and brood foraging sites selection, directly. Future research could adapt upon this framework further to deepen our understanding of wild turkey brood rearing behavior by including landscape scale variables, predator occupancy, weather patterns, and disturbance regimes

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Table 2.1 Number of arthropod samples collected at wild turkey brood foraging used and available sites in Kansas during May-August 2024–2025, separated by study region.

Study Region	*n*	Used	Available
West	214	75	139
Central	176	64	112
East	172	61	111
Total	562	200	362

Table 2.2 Abundance of arthropod orders sampled from wild turkey brood foraging used and available sites in Kansas during May–August, 2024–2025, separated by study region.

Arthropod Order	Central	East	West	Order Totals
Hemiptera	924	720	1212	2856
Hymenoptera	337	367	423	1127
Orthoptera	250	234	612	1096
Coleoptera	667	159	231	1057
Araneae	248	311	206	765
Diptera	269	209	145	623
Lepidoptera	39	45	65	149
Acari	26	24	29	79
Isopoda	6	5	57	68
Thysanoptera	59	2	5	66
Phasmatodea	0	2	36	38
Mallophaga	0	21	0	21
Neuroptera	7	4	10	21
Blattodea	6	1	3	10
Odonata	0	10	0	10
Amphipoda	0	0	4	4
Mantodea	1	2	1	4
Spirobolida	4	0	0	4
Opiliones	1	2	0	3
Zygentoma	0	1	2	3
Ephemeroptera	0	0	2	2
Ixodida	0	0	2	2
Julida	1	0	1	2
Pseudoscorpiones	0	0	2	2
Stylomatophora	0	2	0	2
Lithobiomorpha	1	0	0	1
Plecoptera	0	0	1	1
Region Totals	2846	2121	3049	
Study Wide Total				8016

Table 2.3 Mean (± SD) arthropod abundance, biomass, and richness (morphospecies richness) at combined wild turkey brood foraging used and available sites in Kansas during May–August in 2024 and 2025, separated by study region (East, Central, West). Arthropods were collected from a receptacle (156.7 L) using a modified leaf blower vacuum. Reported metrics represent 3 suctioning events per site, averaged across study region.

Region	*n*	Abundance	Biomass (g)	Richness
Central	176	16.17 ± 15.47	0.35 ± 0.65	9.20 ± 6.11
East	172	12.33 ± 11.02	0.40 ± 0.80	8.33 ± 5.74
West	214	14.25 ± 21.78	0.55 ± 0.79	7.92 ± 6.20
Total	562	14.26 ± 17.15	0.44 ± 0.76	8.45 ± 6.05

Table 2.4 Occurrence (number and percentage of samples) of arthropod orders collected at combined wild turkey brood foraging used and available sites in Kansas during May–August in 2024 and 2025, separated by study region (East, Central, West).

Order	Total	Central	East	West
Hemiptera	421 (74.9%)	131 (74.4%)	141 (82.0%)	149 (69.6%)
Araneae	350 (62.3%)	109 (61.9%)	118 (68.6%)	123 (57.5%)
Orthoptera	348 (61.9%)	97 (55.1%)	85 (49.4%)	166 (77.6%)
Hymenoptera	302 (53.7%)	99 (56.2%)	95 (55.2%)	108 (50.5%)
Coleoptera	277 (49.3%)	104 (59.1%)	79 (45.9%)	94 (43.9%)
Diptera	201 (35.8%)	82 (46.6%)	62 (36.0%)	57 (26.6%)
Lepidoptera	118 (21.0%)	33 (18.8%)	38 (22.1%)	47 (22.0%)
Acari	45 (8.0%)	19 (10.8%)	12 (7.0%)	14 (6.5%)
Isopoda	30 (5.3%)	5 (2.8%)	5 (2.9%)	20 (9.3%)
Neuroptera	17 (3.0%)	6 (3.4%)	4 (2.3%)	7 (3.3%)
Phasmatodea	15 (2.7%)	0 (0%)	2 (1.2%)	13 (6.1%)
Thysanoptera	11 (2.0%)	4 (2.3%)	2 (1.2%)	5 (2.3%)
Odonata	8 (1.4%)	0 (0%)	8 (4.7%)	0 (0%)
Blattodea	7 (1.2%)	4 (2.3%)	1 (0.6%)	2 (0.9%)
No Arthropods	7 (1.2%)	2 (1.1%)	2 (1.2%)	3 (1.4%)
Mantodea	4 (0.7%)	1 (0.6%)	2 (1.2%)	1 (0.5%)
Opiliones	3 (0.5%)	1 (0.6%)	2 (1.2%)	0 (0%)
Julida	2 (0.4%)	1 (0.6%)	0 (0%)	1 (0.5%)
Zygentoma	2 (0.4%)	0 (0%)	1 (0.6%)	1 (0.5%)
Amphipoda	2 (0.4%)	0 (0%)	0 (0%)	2 (0.9%)
Ixodida	2 (0.4%)	0 (0%)	0 (0%)	2 (0.9%)
Pseudoscorpiones	2 (0.4%)	0 (0%)	0 (0%)	2 (0.9%)
Lithobiomorpha	1 (0.2%)	1 (0.6%)	0 (0%)	0 (0%)
Spirobolida	1 (0.2%)	1 (0.6%)	0 (0%)	0 (0%)
Mallophaga	1 (0.2%)	0 (0%)	1 (0.6%)	0 (0%)
Stylomatophora	1 (0.2%)	0 (0%)	1 (0.6%)	0 (0%)
Ephemeroptera	1 (0.2%)	0 (0%)	0 (0%)	1 (0.5%)
Plecoptera	1 (0.2%)	0 (0%)	0 (0%)	1 (0.5%)

Table 2.5 Number of forage clippings collected for nutrient analyses at wild turkey brood foraging used and available sites in Kansas during May-August in 2024 and 2025, separated by study region (East, Central, West).

Region	*n*	Used	Available
Central	167	62	105
East	194	65	129
West	188	64	124
Totals	549	191	358

Table 2.6 Sample sizes for individual plant nutrient concentrations measured at wild turkey brood foraging used and available sites in Kansas during May–August in 2024 and 2025. Sample sizes varied for nutrient analyses due to desired limits.

Nutrient	*n*	Used	Available
Protein	546	190	356
Ca	546	190	356
K	546	190	356
Fe	546	190	356
Zn	546	190	356
P	545	189	356
Mg	545	189	356
S	545	189	356
Cu	525	184	341
ADL	475	167	308
Na	158	56	102

Table 2.7 Mean (± SD) plant nutrient concentrations at wild turkey brood foraging used and available sites in Kansas during May–August 2024–2025, separated by study region(East, Central, West).

	Protein (%)		Phosphorus (%)		Calcium (%)		Potassium (%)		Magnesium (%)	
Region	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Central	10.73	4.97	0.24	0.10	0.84	0.55	1.90	0.79	0.23	0.12
East	10.21	4.39	0.23	0.13	1.16	0.55	2.01	0.93	0.28	0.19
West	9.35	3.66	0.17	0.07	1.11	0.56	2.02	1.18	0.19	0.10
Total	10.07	4.38	0.21	0.11	1.04	0.57	1.98	0.99	0.23	0.14

Table 2.7 Cont.

	Sulfur (%)		Sodium (%)		Copper (ppm)		Iron (ppm)		Zinc (ppm)		Acid Detergent Lignin (%)	
Region	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Central	0.18	0.08	0.02	0.03	12.63	29.66	506.37	1165.29	29.44	12.00	8.65	2.98
East	0.19	0.11	0.02	0.04	20.82	59.19	618.40	1219.56	31.68	12.46	8.48	2.75
West	0.19	0.08	0.02	0.06	20.60	63.98	269.94	203.88	31.47	9.99	6.97	1.69
Total	0.18	0.09	0.02	0.04	18.34	54.30	464.15	984.01	30.92	11.54	8.08	2.66

Table 2.8 Raw-scale mean (± SD) arthropod metrics collected at wild turkey brood foraging used and available sites combined in Kansas during May–August in 2024 and 2025. Differences between site types were evaluated using one-way analysis of variance conducted on log(x + 1)-transformed abundance and biomass.

	Used		Available		ANOVA	
Metric	Mean	SD	Mean	SD	F_{1,df_2}	P
Morphospecies Richness	8.55	5.81	7.63	5.12	3.41	0.065
Abundance	12.79	11.17	11.82	10.43	0.67	0.415
Biomass (g)	0.31	0.42	0.29	0.43	0.23	0.633

Table 2.9 Raw mean (± SD) plant nutrient concentrations at wild turkey brood foraging used and available sites combined in Kansas during May–August in 2024 and 2025, separated by study region. Differences between site types were evaluated using one-way analysis of variance conducted on log (x + 1) transformed crude protein, K, Mg, S, Cu, and Fe.

	Used		Available		ANOVA	
Nutrient	Mean	SD	Mean	SD	F_1, df_2	P
ADL (%)	8.16	2.20	8.03	2.89	0.27	0.606
Ca (%)	1.11	0.62	1.01	0.54	0.54	0.033
K (%)	2.11	1.05	1.91	0.94	0.94	0.014
Mg (%)	0.24	0.14	0.23	0.15	0.15	0.144
P (%)	0.24	0.12	0.20	0.10	0.10	< 0.001
Protein (%)	10.44	4.32	9.87	4.40	4.40	0.058
S (%)	0.20	0.11	0.18	0.08	0.08	0.037
Zn (ppm)	32.51	12.04	30.07	11.18	11.18	0.018
Cu (ppm)	14.44	35.07	20.46	62.27	62.27	0.573
Fe (ppm)	420.34	534.48	487.72	1155.76	1155.76	0.376

Table 2.10 Model selection results for logistic regression models predicting wild turkey brood foraging site use as a function of arthropod metrics collected at brood foraging used and available sites in Kansas May-August, 2024-2025. Beta coefficients were z standardized.

Model name	K	AICc	ΔAICc	*w*	Deviance	*β*	SE	*p*
Richness	2	666.45	0	0.42	662.43	0.17	0.09	0.06
Null	1	667.80	1.35	0.21	665.79	-	-	-
Abundance	2	669.14	2.69	0.10	665.12	0.08	0.09	0.41
Biomass	2	669.58	3.13	0.08	665.57	0.04	0.09	0.63
Global	4	669.68	3.23	0.08	661.61	-	-	-

Table 2.11 Model selection results for logistic regression models predicting wild turkey brood foraging site use as a function of plant nutrient concentrations from forage clippings collected at brood foraging used and available sites in Kansas May-August, 2024-2025.

Model Names	K	AICc	ΔAICc	*w*	Deviance	*β*	SE	*p*
P	2	579.99	0.00	0.74	575.97	0.36	0.10	0.000
Zn	2	583.83	3.83	0.11	579.80	0.32	0.10	0.002
K	2	584.06	4.07	0.10	580.03	0.31	0.10	0.002
Protein	2	587.03	7.04	0.02	583.00	0.25	0.10	0.011
Ca	2	587.82	7.83	0.01	583.79	0.23	0.09	0.017
S	2	588.02	8.03	0.01	584.00	0.23	0.10	0.020
Mg	2	591.52	11.53	0.00	587.50	0.13	0.09	0.149
Null	1	591.57	11.58	0.00	589.56	-	-	-
Global	7	591.60	11.60	0.00	577.34	-	-	-
Fe	2	592.76	12.77	0.00	588.74	0.09	0.10	0.362
Cu	2	592.85	12.86	0.00	588.82	0.09	0.10	0.388
ADL	2	593.56	13.57	0.00	589.54	0.02	0.10	0.873

Table 2.12 Model selection results for negative binomial generalized linear models predicting arthropod morphospecies richness as a function of habitat characteristics measured at wild turkey brood foraging used and available sites in Kansas, May–August 2024–2025.

Model Names	K	AICc	ΔAICc	*w*	Deviance	*β*	SE	*p*
Bare Ground[q][1]	4	2654.81	0.00	0.66	2646.72	-0.05	0.02	0.033
Bare Ground	3	2657.12	2.31	0.21	2651.07	-0.12	0.03	0.000
VO 0.00-0.25	3	2659.10	4.29	0.08	2653.05	0.107	0.03	0.002
Global	9	2661.34	6.53	0.03	2642.91	-	-	-
Litter	3	2663.57	8.76	0.01	2657.51	-0.07	0.03	0.025
VO 0.25-0.50	3	2665.50	10.69	0.00	2659.45	0.05	0.03	0.094
Grass Cover	3	2666.14	11.33	0.00	2660.09	0.05	0.03	0.147
Null	2	2666.25	11.44	0.00	2662.22	-	-	-
Woody Cover	3	2666.70	11.89	0.00	2660.64	0.039	0.03	0.220
Forb Cover	3	2667.25	12.43	0.00	2661.19	0.034	0.03	0.298
Forb Cover[q]	4	2667.42	12.61	0.00	2659.32	-0.03	0.02	0.176
Woody Cover[q]	4	2667.44	12.63	0.00	2659.34	0.03	0.02	0.264
Grass Cover[q]	4	2667.69	12.88	0.00	2659.60	0.02	0.03	0.474
Forb Richness	3	2667.86	13.04	0.00	2661.80	0.02	0.03	0.515
Grass Richness	3	2668.07	13.26	0.00	2662.01	-0.01	0.03	0.647
Cover type	5	2668.61	13.80	0.00	2658.47	-	-	-

[1] *β_1 (Bare ground) = −0.051; β_2 (Bare ground²) = −0.051*

Table 2.13 Mean (± SD) arthropod morphospecies richness and plant nutrient concentrations collected at wild turkey brood foraging used and available sites in Kansas, May–August 2024–2025, separated by dominant cover type within a 10-m radius.

	Arthropod Richness		Phosphorus (%)		Protein (%)		Calcium (%)		Potassium (%)	
Cover type	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Cropland	9.96	8.12	0.28	0.14	14.06	7.96	1.25	0.83	2.28	1.37
Forest	9.92	5.99	0.26	0.09	11.70	3.23	1.19	0.59	2.36	0.85
Grassland	8.85	5.56	0.17	0.07	8.57	2.63	0.94	0.51	1.78	0.94
Shrubland	8.26	6.94	0.17	0.08	9.32	2.99	0.96	0.39	1.87	0.93

Table 2.14 Model selection results for negative binomial generalized linear models predicting arthropod morphospecies richness as a function of plant nutrient concentrations from forage clippings collected at wild turkey brood foraging used and available sites in Kansas, May–August in 2024 and 2025.

Model Names	K	AICc	ΔAICc	*w*	*Deviance*	*β*	SE	*p*
P	3	2216.38	0.00	0.80	2210.31	0.11	0.03	0.001
Protein	3	2221.01	4.64	0.08	2214.95	0.08	0.03	0.017
K	3	2222.37	5.99	0.04	2216.30	0.07	0.03	0.041
S	3	2223.09	6.71	0.03	2217.02	0.07	0.03	0.053
Null	2	2224.22	7.84	0.02	2220.18	-	-	-
Ca	3	2225.56	9.18	0.01	2219.49	0.03	0.04	0.412
ADL	3	2225.92	9.55	0.01	2219.86	0.02	0.04	0.551
Fe	3	2225.97	9.59	0.01	2219.90	0.02	0.04	0.584
Cu	3	2226.02	9.65	0.01	2219.96	0.02	0.04	0.486
Mg	3	2226.12	9.74	0.01	2220.05	-0.10	0.04	0.694
Zn	3	2226.20	9.83	0.01	2220.14	-0.10	0.04	0.821
Global	9	2230.10	13.73	0.00	2211.59	-	-	-

Table 2.15 Model selection results for beta regression models predicting plant tissue phosphorus concentration as a function of habitat characteristics collected at wild turkey brood foraging used and available sites in Kansas, May–August in 2024 and 2025.

Model Names	K	AICc	ΔAICc	*w*	Deviance	*β*	SE	*p*
Cover type	5	-966.17	0.00	1.00	-976.30	-	-	-
Global	9	-954.53	11.64	0.00	-972.94	-	-	-
Grass Cover	3	-928.02	38.15	0.00	-934.08	-0.19	0.02	<0.001
Grass Richness	3	-921.94	44.23	0.00	-927.99	-0.18	0.03	<0.001
Forb Cover	3	-902.78	63.39	0.00	-908.84	0.13	0.02	<0.001
Flora Richness	3	-898.82	67.35	0.00	-904.87	-0.12	0.03	<0.001
Forb Richness	3	-889.78	76.39	0.00	-895.84	-0.09	0.03	0.001
Woody	3	-884.93	81.24	0.00	-890.99	0.07	0.03	0.008
VO 0.25-0.50	3	-882.89	83.28	0.00	-888.94	0.06	0.03	0.029
VO 0.00-0.25	3	-882.06	84.11	0.00	-888.11	-0.05	0.03	0.045
Null	2	-880.30	85.87	0.00	-884.32	-	-	-

Table 2.16 Subcomponent generalized linear models included in the piecewise structural equation model evaluating bottom-up drivers of wild turkey brood foraging site selection. For each response variable, the associated predictor variables, error distribution (family), and link function are provided. Models were structured to reflect hypothesized causal pathways linking habitat composition and structure to flora richness, plant quality, arthropod richness, and brood foraging use.

Response	Predictor(s)	family	link
Flora richness	Habitat composition, Habitat structure	negative Binomial	log
Plant quality	Habitat composition, Habitat structure, flora richness	gaussian	identity
Arthropod richness	Habitat composition, Habitat structure, flora richness, plant quality	negative Binomial	log
Brood foraging use	Arthropod richness, plant quality[1]	binomial	logit

[1]A direct path form plant quality was included in the refined model following tests of directed separation which indicated the path was meaningful.

Table 2.17 Tests of directed separation (independence claims) for excluded paths in the piecewise structural equation model evaluating brood foraging site selection. Each row represents a conditional independence test between wild turkey brood foraging use and not directly linked in the hypothesized model. Test type (Wald coefficient test), degrees of freedom (df), test statistic (Crit. Value), and associated *p*-values are reported. Non-significant results ($P > 0.05$) indicate that excluded pathways were consistent with the proposed causal structure.

Independ.Claim	Test.Type	DF	Crit.Value	P.Value	
use ~ Habitat composition	coef	429	1.852867	0.063901	
use ~ Habitat structure	coef	429	0.815356	0.414868	
use ~ Flora richness	coef	427	-0.34022	0.733691	
use ~ Plant quality	coef	426	2.815497	0.00487	**

Table 2.18 Tests of directed separation (independence claims) for excluded paths in the piecewise structural equation model evaluating wild turkey brood foraging site selection in Kansas, May–August in 2024 and 2025. Each row represents a conditional independence test between brood foraging use and not directly linked in the refined model. Test type (Wald coefficient test), degrees of freedom (df), test statistic (Crit. Value), and associated *p*-values are reported. Non-significant results ($P > 0.05$) indicate that excluded pathways were consistent with the proposed causal structure.

Independency Claim	Test.Type	df	Crit.Value	*p*
use ~ Habitat composition	coef	428	0.074557	0.940567
use ~ Habitat Structure	coef	428	1.1819	0.237245
use ~ Flora Richness	coef	426	0.254201	0.79934

Table 2.19 Standardized and unstandardized path coefficients from the hypothesized piecewise structural equation model evaluating relationships among habitat composition, habitat structure, plant nutrient quality, plant richness, arthropod richness, and brood-site use at wild turkey brood foraging sites in Kansas, May–August in 2024 and 2025. Habitat composition was a composite derived from forb, woody, and grass cover. Habitat structure was a composite derived from visual obstruction (VO) 0.00-0.25, VO 0.25-0.50, bare ground cover (%), and litter cover (%). Plant quality was a composite derived from percent concentrations of K, Ca, crude protein, and P.

Response	Predictor	Std Error	*df*	Crit.Value	*p*	β	
Flora richness	Habitat composition	0.03	429	-1.37	0.17	-0.06	
Flora richness	Habitat structure	0.03	429	1.08	0.28	0.05	
Plant quality	Habitat composition	0.05	428	12.80	<0.01	0.51	***
Plant quality	Habitat structure	0.05	428	-1.23	0.22	-0.05	
Plant quality	Flora richness	0.02	428	-4.35	<0.01	-0.17	***
Arthropod richness	Habitat composition	0.03	427	-1.91	0.06	-0.09	
Arthropod richness	Habitat structure	0.02	427	3.39	<0.01	0.13	***
Arthropod richness	Flora richness	0.01	427	0.51	0.61	0.02	
Arthropod richness	Plant quality	0.02	427	3.02	<0.01	0.14	**
Brood foraging use	Arthropod richness	0.02	428	2.08	0.04	0.11	*
Brood foraging use	Plant quality	0.07	428	2.73	0.01	0.18	**
~Habitat composition	~Habitat structure	-	430	-1.09	0.28	-0.05	

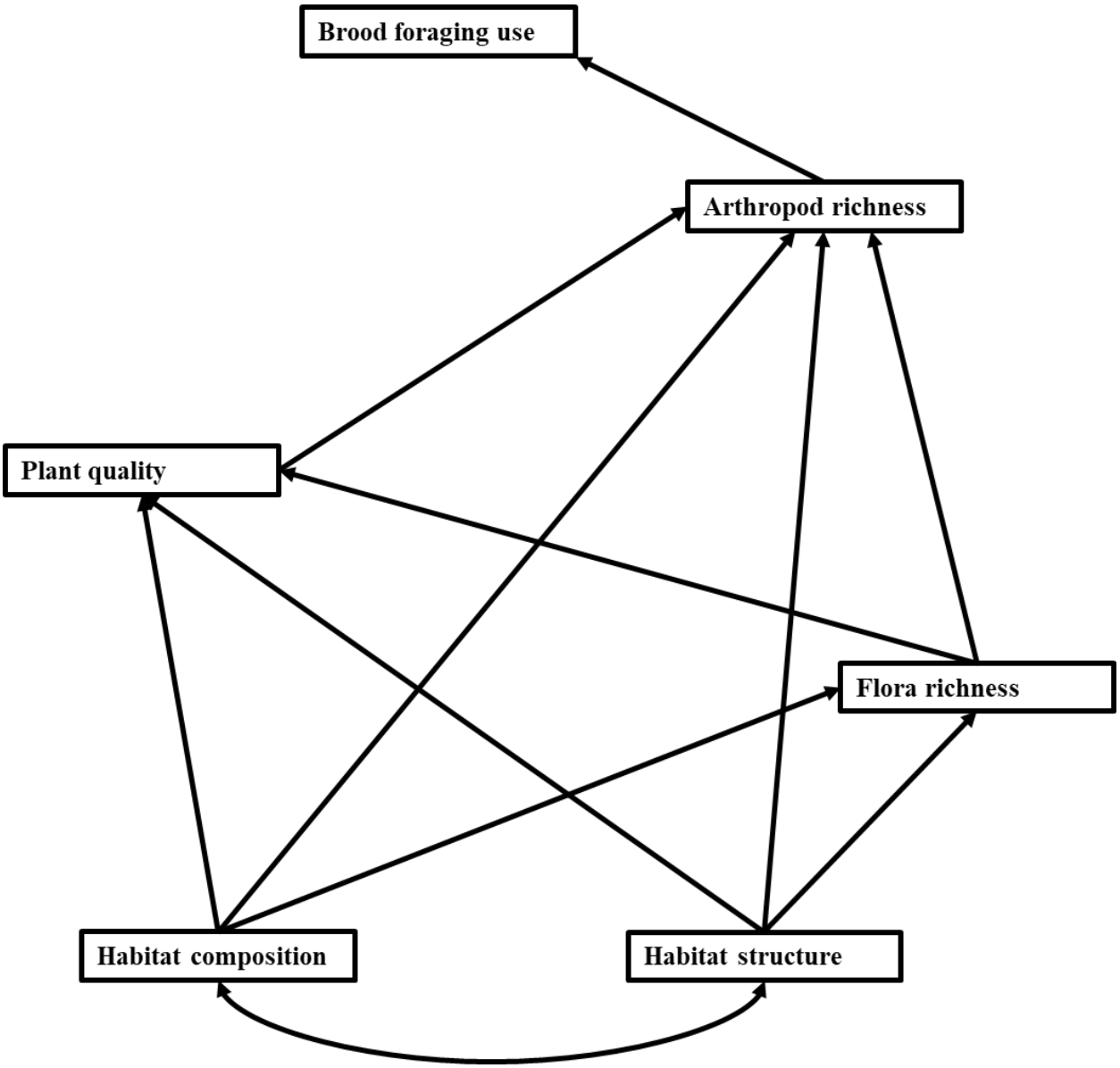

Figure 2.1 Conceptual diagram of the hypothesized structural equation model evaluating bottom-up relationships among habitat composition, habitat structure, plant nutrient composition, plant richness, arthropod richness, and brood-site use at brood foraging sites in Kansas, May–August in 2024 and 2025. Habitat composition is the first principal components axis (PCA) axis of functional group cover and includes grass (%), woody (%) and forb (%). Habitat structure is the first PCA axis including bare ground, litter, visual obstruction (VO) 0.00-0.25, and VO 0.25-0.50. Plant quality is the first PCA axis of plant nutrient concentrations and includes crude protein, potassium, phosphorus, and calcium. The model included a direct pathway from plant nutrient composition to brood-site use. Arrows represent hypothesized relationships.

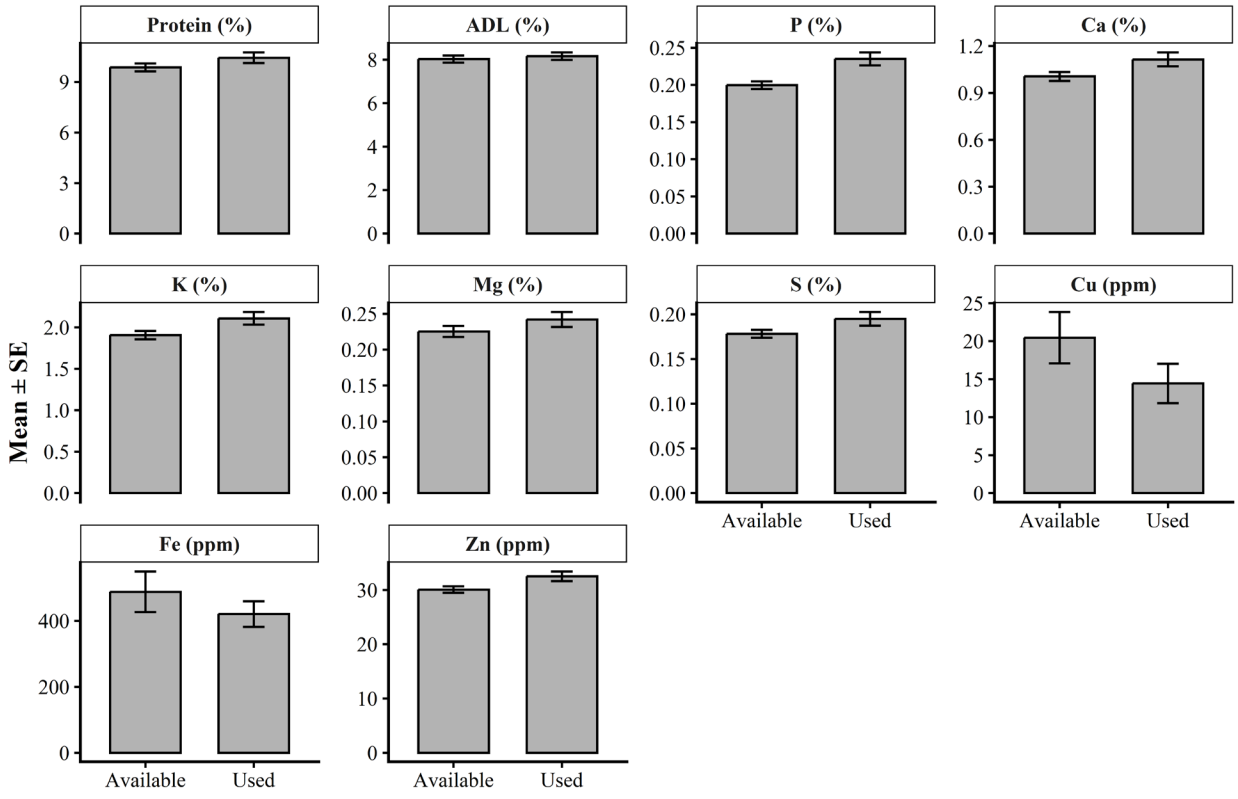

Figure 2.2 Mean (± SE) plant nutrient concentrations at brood foraging used and available sites in Kansas, May–August during 2024–2025. Nutrients evaluated include crude protein, acid detergent lignin (ADL), phosphorus (P), calcium (Ca), potassium (K), magnesium (Mg), sulfur (S), copper (Cu), iron (Fe), and zinc (Zn). Bars represent means and error bars represent standard errors.

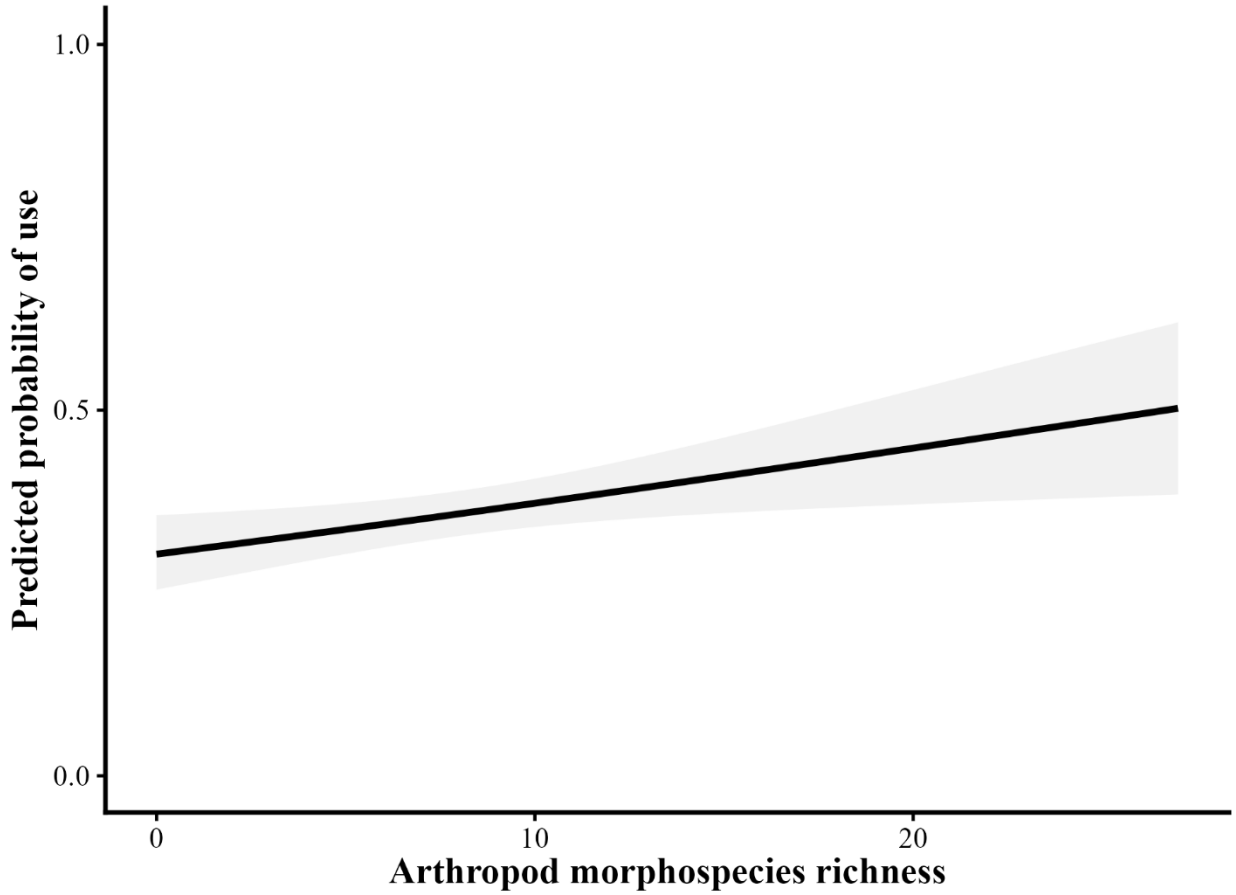

Figure 2.3 Predicted probability of brood foraging site use as a function of arthropod morphospecies richness at brood foraging sites in Kansas, May–August in 2024 and 2025. The solid line represents the fitted logistic regression relationship, and the shaded region represents 85% confidence intervals.

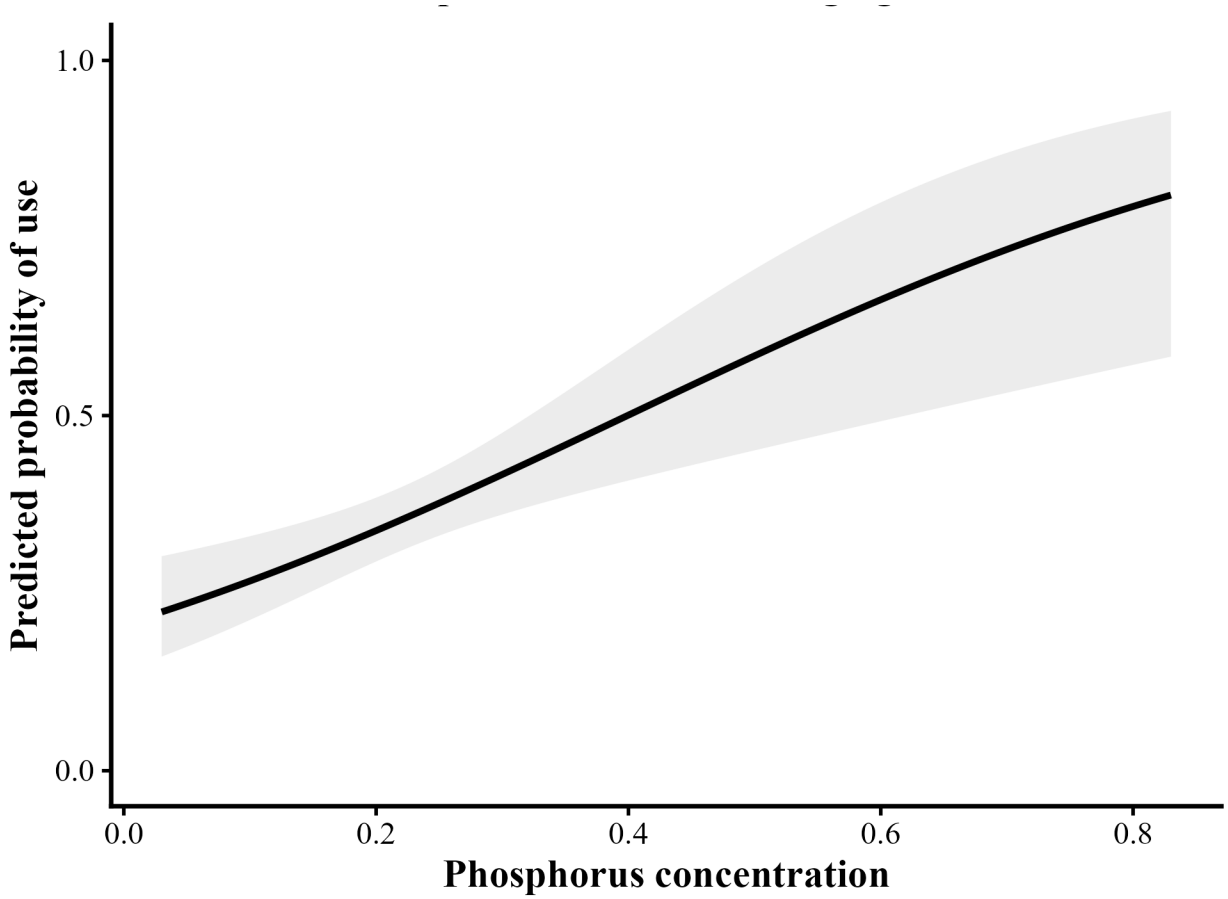

Figure 2.4 Predicted probability of brood foraging site use as a function of plant tissue phosphorus concentration at brood foraging sites in Kansas, May–August in 2024 and 2025. The solid line represents predicted probabilities from the logistic regression model. The shaded region represents 85% confidence intervals.

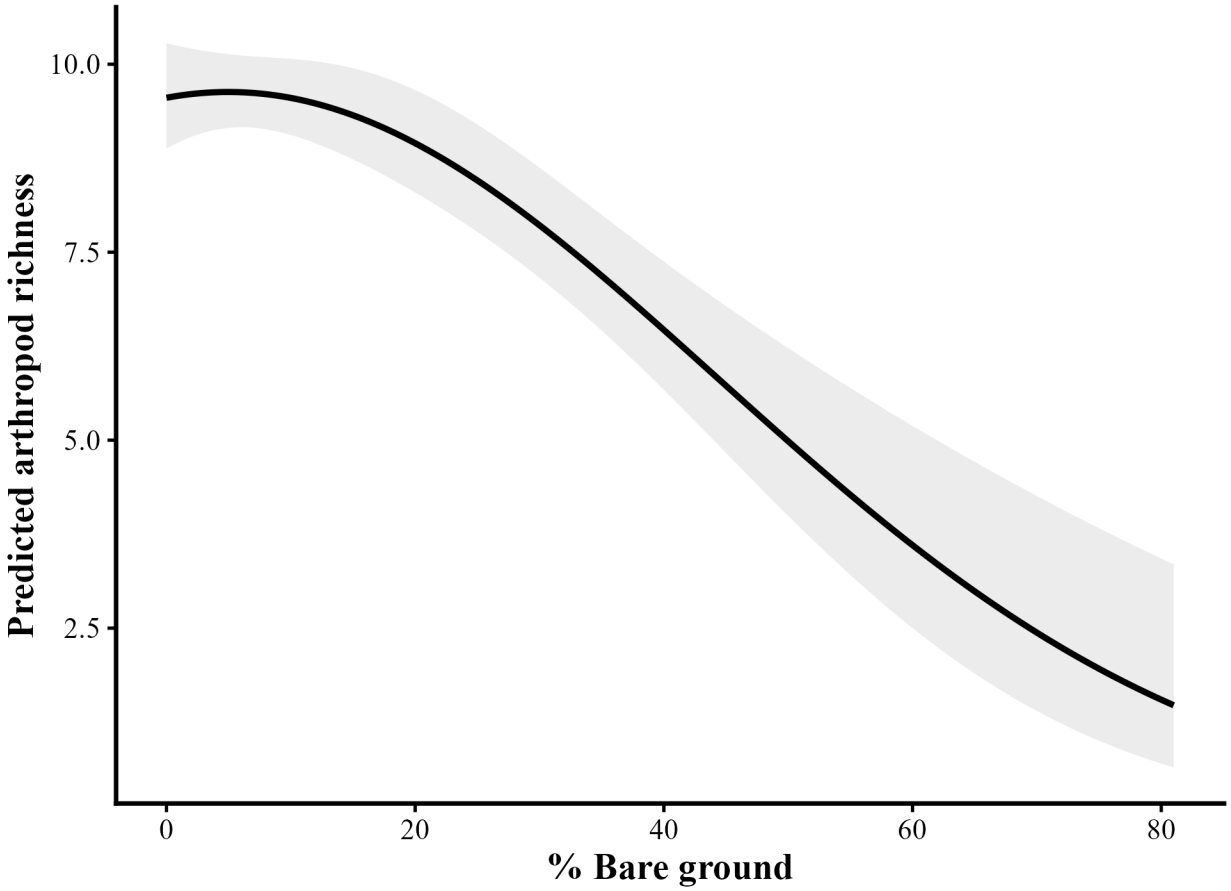

Figure 2.5 Predicted arthropod morphospecies richness as a function of percent bare ground at brood foraging sites in Kansas, May–August in 2024 and 2025. The solid line represents predictions from the most supported negative binomial generalized linear model including a quadratic term for bare ground, and the shaded region represents 85% confidence intervals.

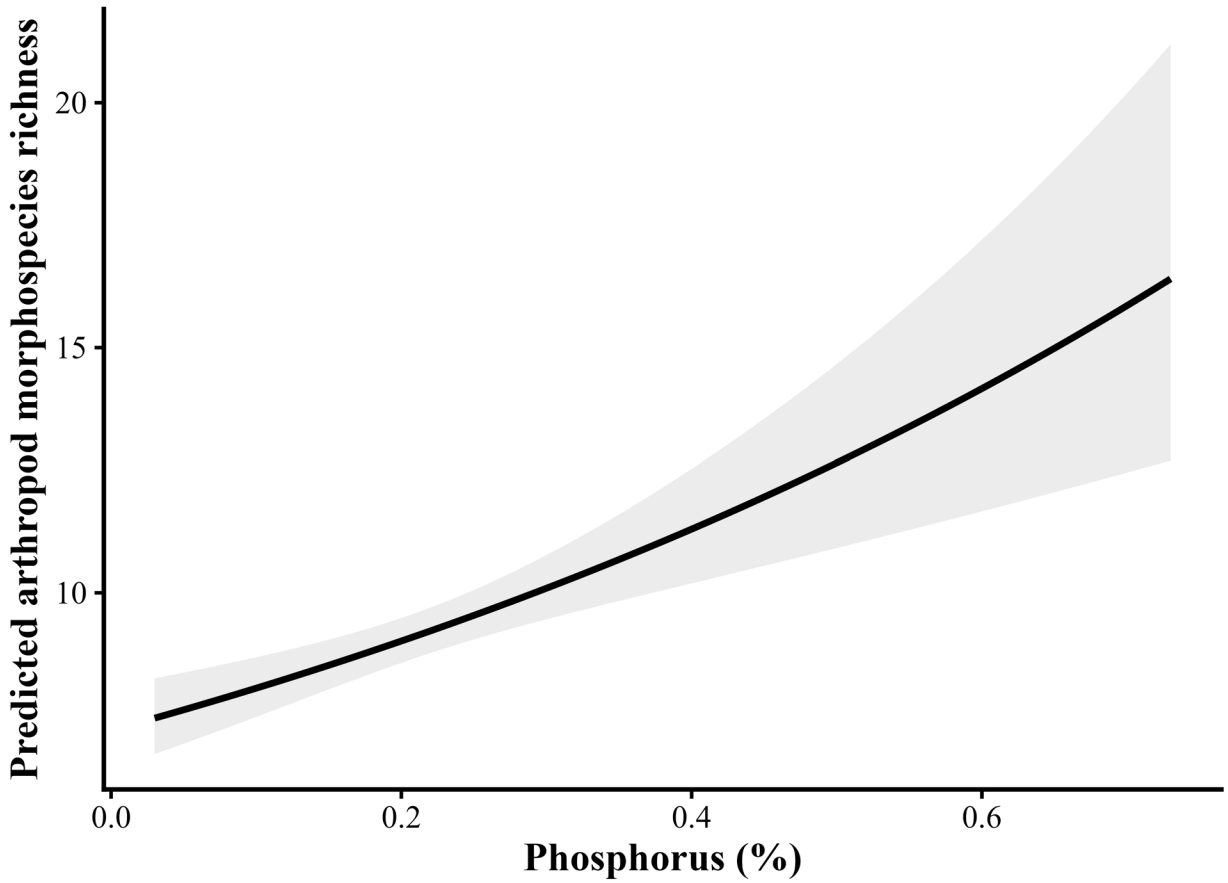

Figure 2.6 Predicted arthropod morphospecies richness as a function of plant tissue phosphorus concentration at brood foraging sites in Kansas, May–August in 2024 and2025. The solid line represents predictions from the most supported negative binomial generalized linear model, and the shaded region represents 85% confidence intervals.

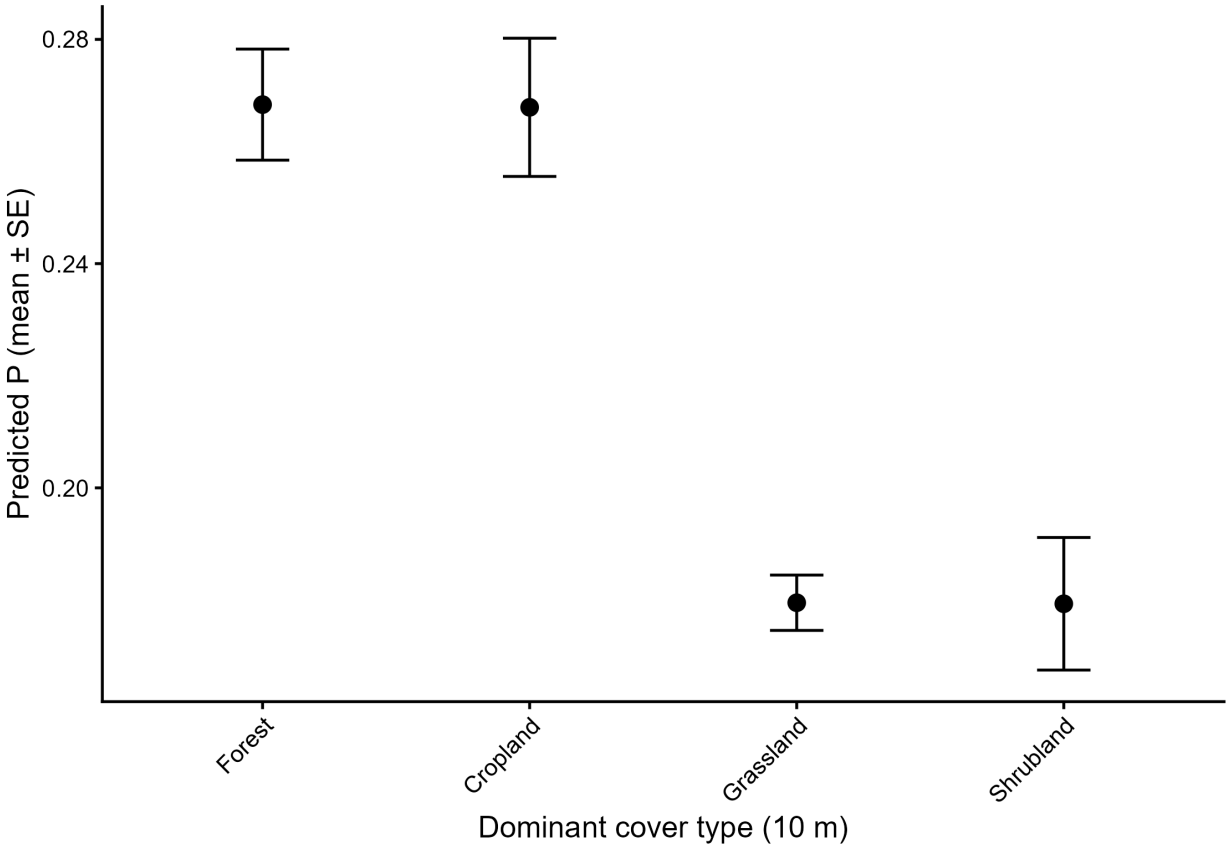

Figure 2.7 Model-predicted plant tissue phosphorus concentration (%) by dominant cover type within a 10-m radius at brood foraging sites in Kansas, May–August in 2024 and2025. Points represent predicted means from the beta regression model, and error bars represent ± SE.

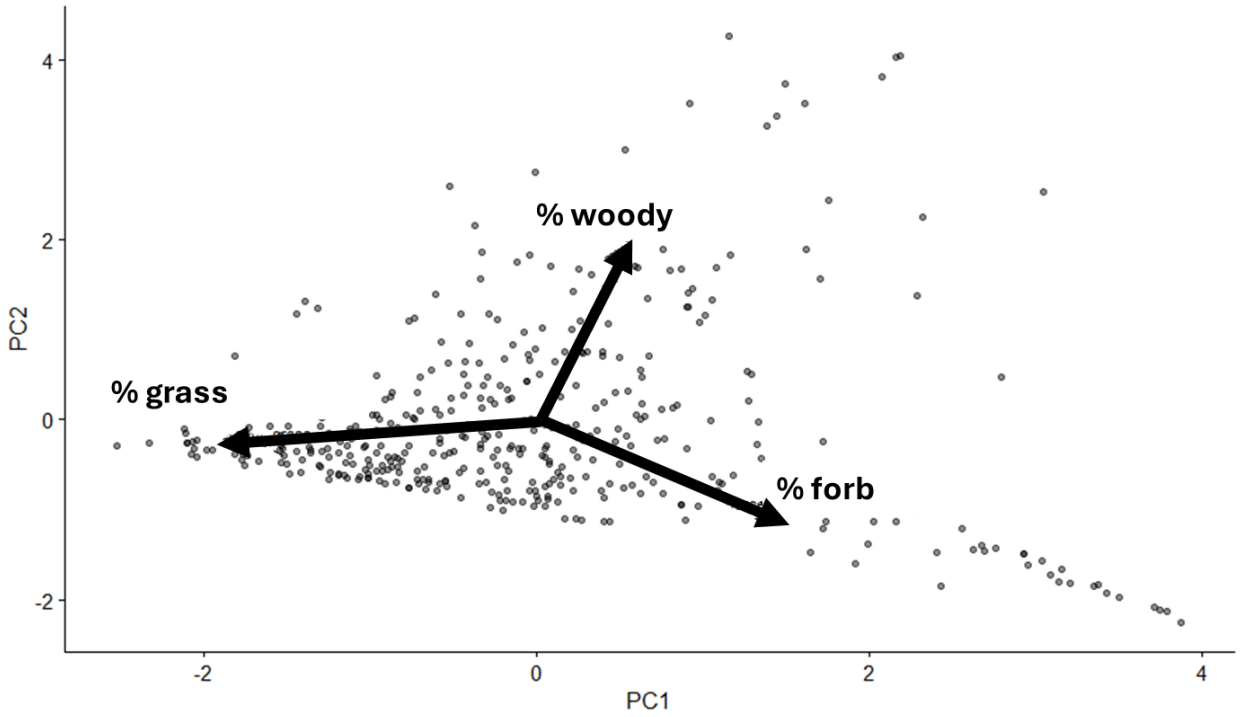

Figure 2.8 Principal components analysis (PCA) ordination of habitat composition variables (% grass, % forb, and % woody cover) measured within a 10-m radius at brood foraging sites in Kansas, May–August in 2024 and2025. Points represent individual sampling locations, and arrows represent variable loadings on the first two principal components. PC1 was retained as a composite habitat composition index for use in the structural equation model.

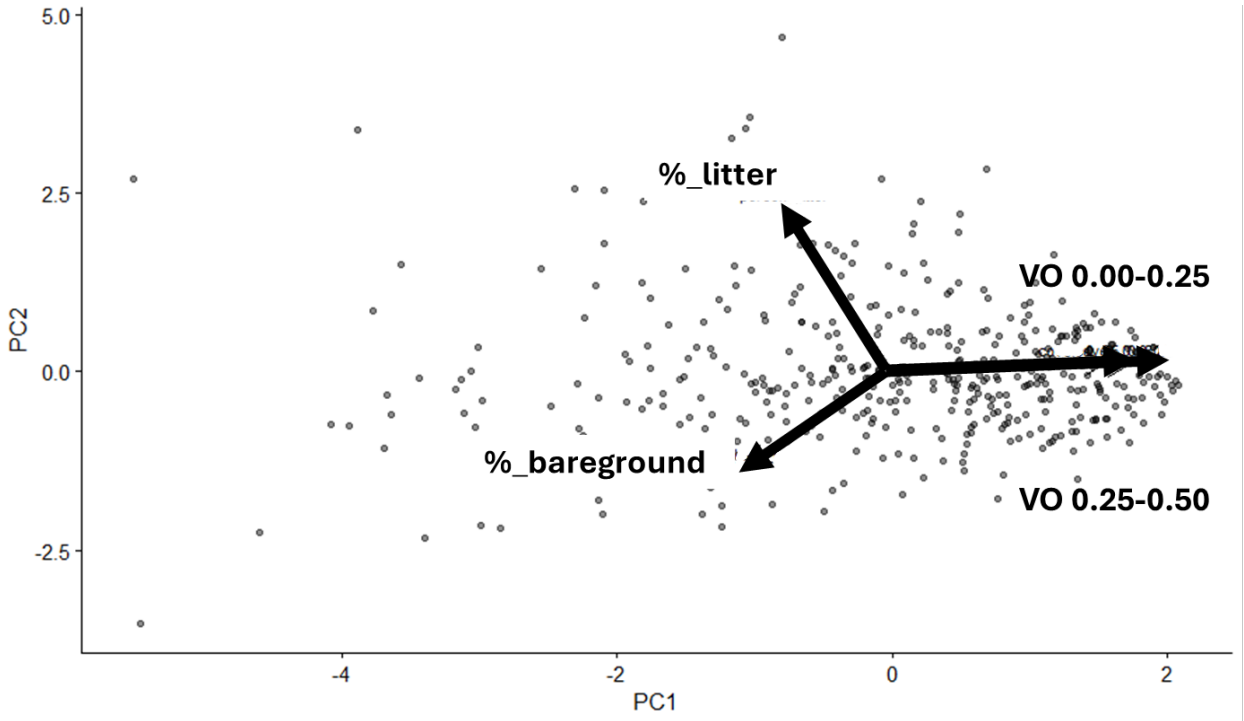

Figure 2.9 Principal components analysis (PCA) ordination of habitat structural variables (% litter, % bare ground, VOR 0.00-0.25, VOR 0.25-0.50) measured within a 10-m radius at brood foraging sites in Kansas, May–August in 2024 and 2025. Points represent individual sampling locations, and arrows represent variable loadings on the first two principal components. PC1 was retained as a composite habitat composition index for use in the structural equation model.

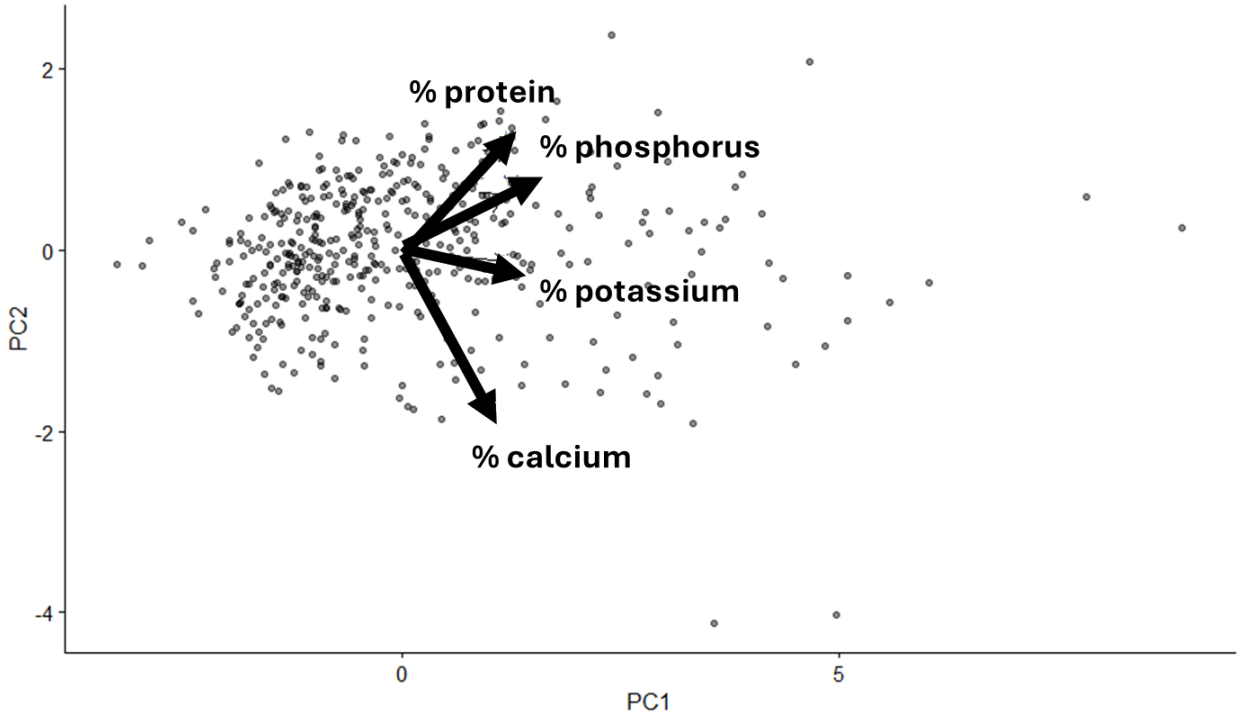

Figure 2.10 Principal components analysis (PCA) ordination of plant nutrient quality (% protein, % phosphorus, % potassium, and % calcium) measured from forage clippings collected within a 10-m radius at brood foraging sites in Kansas, May–August in 2024 and 2025 Points represent individual sampling locations, and arrows represent variable loadings on the first two principal components. PC1 was retained as a composite habitat composition index for use in the structural equation model.

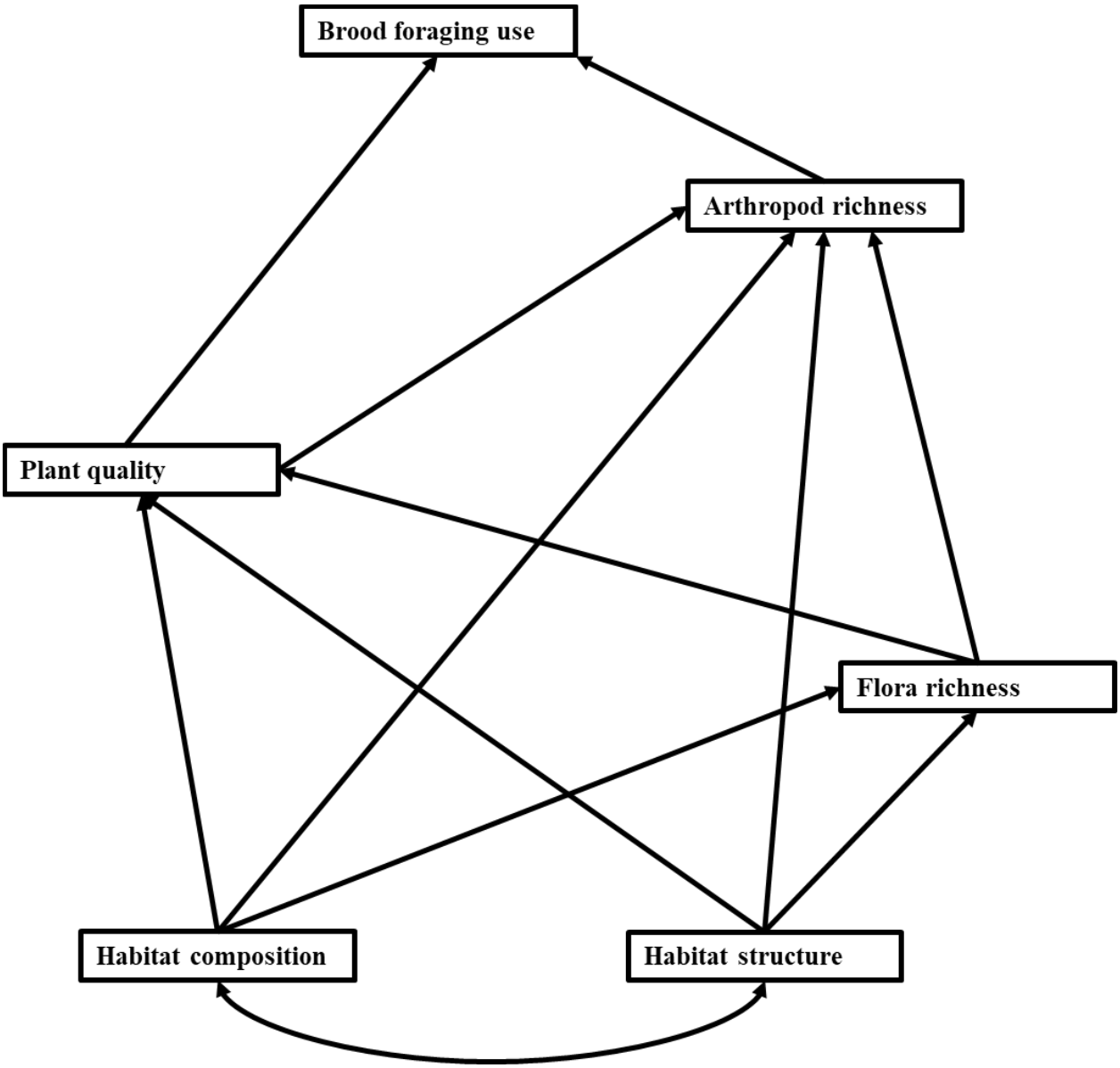

Figure 2.11 Refined structural equation model evaluating bottom-up relationships among habitat composition, habitat structure, plant nutrient composition, plant richness, arthropod richness, and brood-site use at brood foraging sites in Kansas, May–August in 2024 and 2025. Test of directed separation indicated a plant quality ~ Use was a missing meaningful path, thus was included in the refined model. Habitat composition is the first PCA axis of functional group cover and includes grass (%), woody (%), and forb (%). Habitat structure is the first PCA axis including bare ground, litter, visual obstruction (VO) 0.00-0.25, and VO 0.25-0.50. Plant quality is the first PCA axis of plant nutrient concentrations and includes crude protein, potassium, phosphorus, and calcium. The model includes a direct pathway from plant nutrient composition to brood-site use. Arrows represent hypothesized relationships.

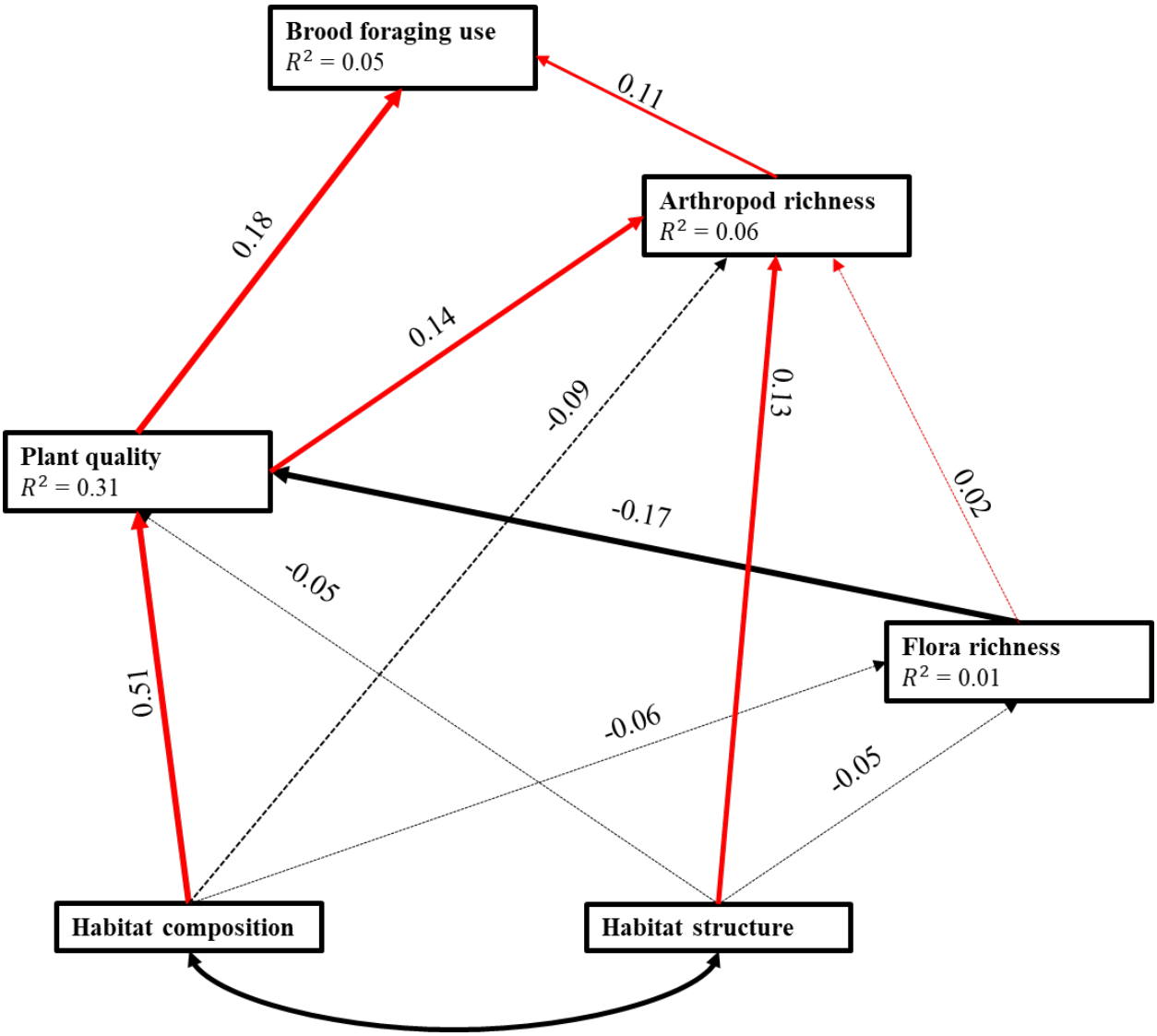

Figure 2.12 Refined piecewise structural equation model describing relationships among habitat composition, habitat structure, plant nutrient quality, plant richness, arthropod morphospecies richness, and brood-site use at brood foraging sites in Kansas, May–Augustin 2024 and 2025. Habitat composition is the first PCA axis of functional group cover and includes grass (%), woody (%), and forb (%). Habitat structure is the first PCA axis including bare ground, litter, visual obstruction (VO) 0.00-0.25, and VO 0.25-0.50. Plant quality is the first PCA axis of plant nutrient concentrations and includes crude protein, potassium, phosphorus, and calcium. Red arrows indicate positive and black arrows indicate negative relationships. Solid lines indicate significant relationships, whereas dashed lines indicate non-significant relationships. Line thickness indicates size of path estimates. The proportion of variance in each predicted variable is given as the R^2 value and standardized path estimates are provided next to each path.