

ECOSYSTEM SERVICES AND DISSERVICES OF BIRDS ON FARMS

by

SOFIA VARRIANO

(Under the Direction of William E. Snyder)

ABSTRACT

Integrated crop-livestock systems can restore ecosystem services like biological control and nutrient cycling to agroecosystems. However, the joint production of livestock and crops can pose food safety risks to consumers. Wild birds in particular have been identified as vectors of foodborne bacteria like *Salmonella* and *Campylobacter* to produce from livestock, while chickens are a large reservoir of bacteria in the US Southeast. Here, we consider the food safety risks of both wild birds and outdoor-access chickens on farms, while also describing the biological control services chickens can provide growers. We used a combination of bacterial cultures and PCRs to characterize bacterial prevalence in wild bird and chicken feces; this data was then used in several different statistical models to connect food safety risks to livestock presence, farm management, and wider landscape and weather variables. We used a DNA metabarcoding approach to characterize outdoor-access chicken diet and evaluate biocontrol potential of chickens. We found that *Salmonella* prevalence in wild birds was positively associated with livestock presence on-farm, although livestock were not the source of bacteria. In chicken feces, *Campylobacter* prevalence was positively associated with higher temperatures and the number of families of flies and plant phylogenetic diversity in chicken diet. This indicates that flies may be an important on-farm bacterial vector, and that chicken foraging behavior may

increase the risk of encountering environmental bacteria. We found that chickens foraged very generally, eating a wide array of both arthropods and plants, but we were unable to definitely conclude whether chickens had a net positive, negative, or neutral impact on insect pests and weeds. Growers may be able to better manage food safety risks while still gaining the benefits of livestock ecosystem services by managing bacterial vectors like wild birds and flies. In a brief literature review of management options for growers, we found that physical deterrents and barriers were more effective than scaring deterrents for managing wild birds; likewise, physically preventing flies and other insects from entering livestock areas has been shown to effectively reduce food safety risks.

INDEX WORDS: Ecosystem services, food safety, biological control, wild birds, pastured chickens, agroecology

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CHAPTER 1

INTRODUCTION

The need to produce food for a growing human population has caused significant shifts in land use in the US; in 2017, total US cropland acreage reached 390 million acres, or roughly 1/5 of total US land area (USDA 2025). With intensifying agricultural activity comes a need to balance food production with maintaining vital ecosystem services like nutrient cycling in the soil, carbon sequestration, and water filtration. Integrated crop-livestock systems, or farms in which crops and livestock are produced together, have been proposed as a solution for this problem (Hilimire 2011a). Livestock activity can benefit crops by providing nutrients in the form of fecal deposition and biological control services, while the production of crops and livestock together can help growers diversify production and use land more efficiently (Rocchi et al. 2019).

However, integrated crop-livestock production can also increase food safety risks to consumers (Hilimire 2011a). Foodborne bacteria like *Salmonella* and *Campylobacter* that are found in animal feces can be transmitted to both produce and animal products. Wild animals like birds that are associated with feedlots and livestock production may encounter bacteria and then transmit it to nearby crops (Langholz & Jay-Russell 2013). Several instances of foodborne illness caused by bacteria or bacterial transmission between livestock have been linked to wild birds (Gardner et al. 2011, Cernicchiaro et al. 2012). For these reasons, food safety risks have been thought to run counter to ecosystem services in integrated crop-livestock systems and on farms in general.

The purpose of this thesis is to investigate whether food safety risks on farms in the US Southeast can be better understood and managed to allow growers to take advantage of the ecosystem services wild animals and livestock can provide. We focus here on wild birds and chickens. The first two chapters of this thesis outline unique food safety threats that wild birds may pose in the Southeast and management strategies that growers may consider to ameliorate them. The final three chapters outline the benefits chickens can provide to growers on integrated crop-livestock farms and consider the food safety risks of such integration.

CHAPTER 2

WILD BIRDS POSE UNIQUE FOOD SAFETY THREATS IN THE US SOUTHEAST¹

¹ Varriano, S, JC Smith, OM Smith, PAP Rodrigues, Z Snipes, K Roach, JL Dawson, J Shealy, LL Dunn, NW Shariat, & WE Snyder.
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Abstract

Natural areas near farmland can provide refuge for birds that contribute to natural pest control. However, birds can endanger food safety by defecating on or near produce. Extensive work in the western US suggests that *Campylobacter* spp. are the potential foodborne pathogens most commonly associated with wild birds and that pathogen prevalence is higher in landscapes dominated by animal agriculture. However, relatively little is known about other fresh-market-produce growing regions. Working on produce farms in Florida, Georgia, South Carolina, and Tennessee, USA, we characterized bird communities, tested bird feces deposited on crop foliage for *Campylobacter* and *Salmonella*, searched for landscape features associated with heightened bird-associated food safety risks, and surveyed growers on their bird management attitudes and strategies. We found that bird communities on farms were generally similar across the Appalachian Mountain, Piedmont, and Southeastern Coastal Plains ecoregions. Surprisingly, *Campylobacter* was never detected from bird feces deposited on crop foliage, but *Salmonella* was detected in 8.6% of fecal samples. *Salmonella* prevalence in crop-surface-collected bird feces was highest when farms also produced livestock and when wetland cover was prevalent in the landscape. Farmer questionnaire surveys (n=49) indicated that growers with livestock on their farms were more likely to use bird deterrence measures, consistent with the positive association between *Salmonella* and livestock. Overall, our results suggest that on-farm livestock production may be an indicator of bird-associated food safety risks in the Southeast, as in the West. Yet, we most commonly detected *Salmonella* in bird feces, rather than *Campylobacter*, which was the most common pathogen in prior work in the western US. Further, we determined that wetland cover is strongly positively correlated with *Salmonella* prevalence. We suggest

there may be some similarities, but important differences, in food safety risks posed by birds in different US produce growing regions.

Introduction

A growing human population presents ever-greater challenges in conserving biodiversity while also maintaining robust food production (Tsiafouli et al. 2014, Outhwaite et al. 2022). Incorporation of natural areas into farmlands can help mitigate this conflict, as uncultivated areas can provide refuge for pollinators, predators, and decomposers that benefit crop production (Rusch et al. 2010, Anderson et al. 2012, Cole et al. 2017, Olimpi et al. 2022). For example, birds in farming landscapes can move from natural habitats into fields to consume crop pests, strengthening natural pest control (Kross et al. 2016). For many years, food safety was thought to run counter to these broader trends, with natural areas attracting birds and other wildlife that might defecate on nearby crops, risking contamination with *Salmonella*, *Campylobacter*, or other bacteria that cause foodborne illness in humans (Langholz & Jay-Russell 2013). These concerns led to pressure on fresh-market-produce growers to remove natural habitats from farms to deter wildlife and lessen food safety risks, despite the likely costs to other beneficial ecosystem services (NATTWG 2018).

More recently, extensive work, largely conducted on produce farms in the western US, has provided clear evidence that natural habitats can act to reduce, rather than enhance, food safety risks (Karp et al. 2015, Olimpi et al. 2020). For example, Smith et al. (2020a) found that foodborne pathogen prevalence in produce was reduced on farms embedded in more natural landscapes. In contrast, farming in landscapes with more dense cattle (*Bos taurus*) production and more actively grazed lands are correlated with increased food safety risks (Smith et al.

2020a, Olimpi et al. 2024). This may be because farming landscapes with greater natural habitat support bird species that are less likely to interact with domesticated livestock and therefore reduce the opportunities to encounter bacterial foodborne pathogens (Smith et al. 2020b, Olimpi et al. 2024). However, it remains unclear whether the drivers of bird-associated food safety risks seen in the western US are the same as those found in other produce-growing regions (Smith et al. 2020c, Smith et al. 2022). Thus, we are unsure whether we can draw general recommendations for all growers from the lessons learned in the western US, or if, instead, it will be necessary to develop region-specific recommendations for managing on-farm food safety risks posed by birds (Devarajan et al. 2023).

The southeastern US houses a growing fresh-market produce industry, with fields embedded in ecoregions that are distinctly different from the western US and often interspersed among wetlands and other natural habitats (USDA 2024). Surveys of potential foodborne pathogens associated with birds in this region have included wading birds, songbirds, and others, usually in non-agricultural habitats (Hernandez et al. 2012, Hernandez et al. 2016, Hudson et al. 2000). Bird communities found in or near produce fields, and their associated potential foodborne pathogens, have been relatively unexplored in the southeast (Smith et al. 2022). Here, we seek to fill this knowledge gap through three complementary objectives. First, working on the farms of cooperating produce growers, we conducted surveys of bird species associated with crop fields, to describe which species were present and whether bird assemblages differed among ecoregions, landscapes, and farm production types. Second, we searched fields for bird feces on crop plants, which were collected to determine *Salmonella* and *Campylobacter* prevalence. We then modeled landscape and local attributes (e.g., percent of wetlands and other natural cover types, presence of cattle or other livestock on the farm) that might be associated with a higher

risk of bird feces being contaminated with foodborne bacteria. Third, we surveyed grower attitudes and practices related to wild bird management to assess whether the intensity of grower concern about food safety risks posed aligned with the risk of bird-associated pathogen contamination problems on their farms. Our ultimate goal was to allow a comparison between the ecology of bird-associated foodborne pathogen transmission in the Southeast with what is known from the far-better-studied western US, with the goal of developing widely applicable plans to mitigate food safety risks posed by birds.

Methods

Data collection included (1) point count surveys of birds in or adjacent to produce fields, (2) local- and landscape-scale data that were used to examine correlates of *Salmonella* prevalence (*Campylobacter* was never detected, see below, and thus was not modeled) in crop-surface-collected bird feces, and (3) surveys administered to growers about their attitudes towards wild birds and their bird management practices. Characterization of *Salmonella* collected as part of the field work reported here was reported in a companion study, Smith et al. (2023). Here, we expand upon Smith et al. (2023) by examining (1) how bird communities in or near produce fields vary with ecoregion, landscape, and farm management; (2) how *Salmonella* prevalence in wild bird feces correlates local- and landscape-attributes; and (3) how grower characteristics and attitudes affect bird management practices.

Study Sites

Across 2 years, we surveyed bird communities and collected bird feces from crop foliage on 43 farms in north Florida (n=3), Georgia (n=26), South Carolina (n=10), and eastern Tennessee (n = 4), USA. We visited each farm 1-5 times across the 2-year study, between May-August 2021 and 2022 (total visits = 85; mean/farm = 2) (Figure 2.1; Smith et al. 2023). These

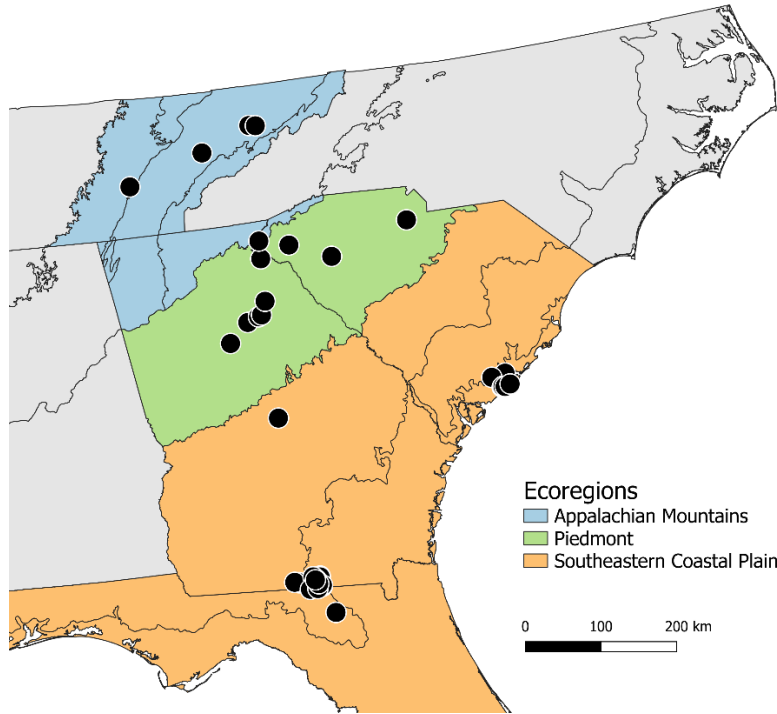


Figure 2.1. Map of farms included in our study ($n = 43$) from which we collected fecal samples. Color corresponds to ecoregion (blue = Appalachian mountains, green = Piedmont, and orange = Southeastern coastal plains). Farms included in this study are only those surveyed from May-August ($n = 43$), as opposed to those in Smith et al. (2023) ($n = 45$).

farms spanned a key produce-growing region of the southeastern US, an industry now worth ca. \$19.5 billion per year that delivers fresh-market produce to much of the eastern US (USDA 2024). Regional fruit and vegetable production spans at least three distinct ecoregions—Appalachian Mountains, Piedmont, and Coastal Plains (Figure 2.1)—which might house distinct wild bird communities (Bird Studies Canada & NABCI 2009). Farming landscapes in our study region are often diverse, with production fields interspersed with pine plantations, wetlands, and other less-intensively-managed habitats (Supplementary Table 2.1). This mosaic landscape

provides ample opportunity for birds to regularly forage in, or travel above, produce fields, and for farm-bird communities to be influenced by surrounding natural habitats (e.g., Zellweger-Fischer et al. 2018). Farms ranged from large monoculture fields (n=26) to smaller, highly diversified operations (n=17) that produced many non-vegetable crops [e.g., ornamentals, apples (*Malus domestica*), and pecans (*Carya illinoensis*)] alongside various vegetables [e.g., onions (*Allium cepa*), beans (*Phaseolus vulgaris*), and squash (*Cucurbita pepo*)]. The average farm size in this study was 22.1 ha $\pm$ 7.5 (SE; range 0.61–94.3 ha) (Table 2.1). Organic-only practices accounted for 32.6% (14/43) of farms, while the remaining farms used either conventional practices or a combination of both organic and conventional. Additionally, livestock was produced on 12 (27.9%) of these farms. Livestock produced on-farm included chickens (*Gallus gallus*; 8 farms), cattle (4), horses (*Equus caballus*; 3), goats (*Capra hircus*; 2), pigs (*Sus domesticus*; 1), donkeys (*Equus asinus*; 1), and/or ducks (*Anatidae* spp.; 1; Table 1).

Bird Fecal Sample Collection

We collected bird feces from crops that produce fruit or vegetables above ground (e.g., on stakes or trellises) to avoid collecting fecal samples from non-bird animals and limit contamination from splash-back or ground contact. Additionally, we selected crops that are commonly eaten uncooked, as these represent the largest food safety risk to consumers. Our selected crops included primarily tomatoes (*Solanum lycopersicum*), cucumbers (*Cucumis sativus*), bell peppers (*Capsicum annuum*), eggplants (*Solanum melongena*), and grapes, both table and wine (*Vitis* spp.). Fecal samples were collected from selected produce fields on each farm between sunrise and 11 a.m. as described in Smith et al. (2023). Briefly, the perimeter of

Table 2.1. Farm characteristics by state (TN = Tennessee, GA = Georgia, SC = South Carolina, FL = Florida). “Size” refers to farm size. Livestock were counted as present if they were within 250 m of the farm during at least one survey period. “Other” includes all other livestock species, i.e., horse, goat, llama, pig, donkey, and duck.

	TN	GA	SC	FL	Total
# Farms	4	26	10	3	43
0-4 ha	0	6	2	0	8
4.1-20 ha	1	12	4	1	18
20.1-40 ha	0	7	2	1	10
40+ ha	3	1	2	1	7
Cattle	3	7	0	1	11
Chicken	2	10	3	0	15
Other	1	3	3	0	7
Monoculture	3	19	2	2	26
Mixed crops	1	7	8	1	17

each field was surveyed for bird feces deposited on the leaves of plants; when field size allowed (20 ha or less), the interior was also sampled by walking in a step-wise pattern among the rows. Fecal samples were scored as either “dry” or “moist” based on visual appearance as an approximate measure of whether the sample was relatively freshly deposited or old. We found that this moist/dry designation was a strong predictor of whether *Salmonella* could be detected in a fecal sample, indicating that drier samples had likely been sitting for enough time that DNA had degraded or the pathogens had become nonviable (Smith et al. 2023). Feces were collected by clipping leaves into a resealable plastic bag filled with 2 mL buffered peptone water (BPW) recovery media. Plastic bags were placed on ice after collection until processing in the lab, which occurred within 24 hours (Smith et al. 2023). We finished collection at each farm after either

inspecting every plant or searching for 5 hours (until 11:00 a.m.), whichever occurred first. The number of fecal samples collected during a visit ranged from 0 to 30.

Objective 1: Characterizing Bird Communities

On-farm Point-Counts

Bird communities on each farm were surveyed via standardized point-counts (e.g., Smith et al. 2020b). One point-count was done for every 10 ha of sampled field when field conditions and harvesting schedules allowed (total point count locations = 106, mean/farm = 2.7). Point-counts were conducted on still, clear mornings between 6 and 10 am, all by the same observer. Points were positioned near the edges of fields to overlap with fecal sampling areas while still capturing birds moving in and out of produce fields. Points on the same farm were at least 200-m apart. All birds seen and heard within a 100-m radius during a 10-minute period were recorded, along with the habitats they were observed in. Birds flying overhead were excluded unless they were a species that forages aerially (e.g., Barn Swallows, *Hirundo rustica*), in which case a note was made that they were “aerial foraging”.

Landscape-Livestock Variables

We used land cover data from the National Land Cover Database (Dewitz 2021) to test for associations between land cover and bird communities. Land cover was categorized as “open water” (NLCD code 11), “barren” (NLCD code 31), “natural habitat” (NLCD codes 41-43, 51-52, 71-74, 90, 95), “developed” (NLCD codes 21-24), and “agricultural” (NLCD codes 81-82). We also tested “wetlands” (NLCD codes 90, 95) separately from other natural habitat due to the number of wetland-associated bird species that had *Salmonella* detected in their feces in prior work in the system (Smith et al. 2023).

We determined a biologically relevant landscape scale by weighting the home range of each bird species with known sizes, gathered from Birds of the World Online (BOW 2022), by the relative abundance of recorded individuals in our point-count surveys (e.g., Smith et al. 2020a). This resulted in a 4.5 km radius, which was subsequently used to generate land cover data from the center of each farm. Farm size was calculated by tracing around the edge of each farm in QGIS v3.28.0 (QGIS) and measuring the area of the subsequent polygon.

Additionally, for each farm, we calculated a series of values representing both natural habitat configurational and compositional heterogeneity in FRAGSTATS 4.2 (McGarigal et al. 2023; Supplementary Table 2.1) following Smith et al. (2020a). Landscape heterogeneity variables were highly correlated (Supplementary Figure 2.1), so we used only interspersions and juxtaposition index of natural cover types in our models. Livestock were recorded as “on-farm” (1) if they were present on-farm the day of sampling; “nearby” (2) if they were present within 250 m of the farm; or “absent” (0) if they were neither on-farm nor within 250 m of the farm the day of sampling.

Bird Community Analysis

A non-metric multidimensional scaling (NMDS) plot with a Bray-Curtis dissimilarity matrix was used to examine how bird communities varied across farms. Analyses were conducted in the R package *vegan* (v2.6.4, Oksanen et al. 2022). Species abundances were averaged across visits and point counts for each farm. We tested for the relationships between proportion of land cover values listed above and species abundances in the community (Bray-Curtis distances) with a series of Mantel tests, using livestock presence [“on-farm” (1) and “nearby” (2) as described above] and farm size as strata for permutations. Associations were tested for using Spearman’s correlation coefficients. We also tested whether bird communities

varied significantly with ecoregion, accounting for farm size and livestock presence, using a series of ANOSIM tests ($\alpha = 0.05$, permutations = 999) from the R package *vegan*. Indicator species were identified for each ecoregion using the function *multipatt* from the R package *indicspecies* ($\alpha = 0.05$; De Cáceres and Legendre 2009).

Objective 2: Linking *Salmonella* Prevalence to Local and Landscape Factors

Detection of Salmonella and Campylobacter Bacteria

We tested all foliage-collected bird fecal samples for the presence of *Salmonella* and *Campylobacter* by both culture and PCR screening. *Salmonella* testing procedures are described in detail by Smith et al. (2023). Briefly, samples and recovery media were homogenized prior to processing. For *Salmonella*, 750 μ L of sample and media homogenate were added into 9.25mL of BPW (Hardy Diagnostics, Ohio, USA). Following pre-incubation at 42°C for 24 hours, 1mL and 0.1mL of culture were sub-cultured in parallel into 9 mL Tetrathionate (TT, Neogen Diagnostics, Michigan, USA) and 9.9 mL Rapport-Vassiliadis (RV, Hardy Diagnostics, Ohio, USA) selective enrichment broths, respectively. Cultures were incubated for an additional 24 hours at 37°C before being streaked onto Xylose Lysine Tergitol-4 agar plates (XLT-4, Hardy Diagnostics, Ohio, USA). Plates were incubated at 37°C for 24-48 hours before being inspected for black colonies indicating the presence of *Salmonella*. For *Campylobacter*, 750 μ L of the sample and media homogenate were added into 8.5 mL of Bolton's broth (BB, Hardy Diagnostics, Ohio, USA) before placing samples in a sealed bag filled with blood-gas atmosphere and mixing gently. Samples were incubated at 42°C for 48 hours before being streaked onto Cefex agar plates (Hardy Diagnostics, Ohio, USA). Plates were placed in a bag filled with blood gas atmosphere and incubated at 42°C for another 48 hours. Plates were then visually inspected for *Campylobacter* colonies.

For PCR screening for both *Campylobacter* and *Salmonella*, total genomic DNA was extracted from 500 μ L of the remaining unincubated sample homogenate using the Genome Wizard kit (Promega, Wisconsin, USA). Extracted DNA was aliquoted into multiple tubes to limit freeze-thaw degradation, and these were stored at -20°C until PCRs were performed. DNA was tested for the presence of PCR inhibitors using an internal amplification control (IAC) PCR (Rosenstrauss et al., 1998). For *Salmonella* screening, we used an *invA* PCR (Rahn et al. 1992) as described in Smith et al. (2023). For *Campylobacter* screening, we first ran a general 16S PCR (Rinttilä et al. 2004). Each 16S reaction contained 3 μ L 10x reaction buffer, 100mM dNTPs, 0.3 μ M F primer, 0.3 μ M R primer, 1 U Taq, and 2 μ L DNA. Sterile water was added until the final reaction volume was 30 μ L. Amplification occurred with the following cycle: denaturation at 95°C for 2 minutes; 24 cycles of amplification (95°C for 30 sec, 51°C for 30 sec, 68°C for 30 sec); and a final extension at 68°C for 2 minutes. PCR products were visualized on a 1.5% agarose gel. *C. jejuni*, *C. coli*, and *C. lari* strains were included as a positive control.

Salmonella Prevalence Models

We focused on *Salmonella* prevalence in our models examining how local livestock and landscape factors impact wild bird-mediated food safety risks because we did not detect *Campylobacter* in any of the fecal samples. We considered a sample positive for *Salmonella* if either culture or PCR returned a positive result. *Salmonella* prevalence was significantly higher in moist [15.8% (45/285)] than dry samples [14.5%, (60/415)] ($\chi^2 = 30.44$, $p < 0.01$). Because our ability to detect *Salmonella* was higher when samples were moist (Smith et al. 2023), only moist samples (n=285) were considered in statistical models.

We used a series of generalized linear mixed effects models (GLMMs) fit in the R package *glmmTMB* (Brooks et al. 2017) to test the relationship between *Salmonella* prevalence

and (1) proportion developed, natural, agricultural, open water, and wetland land cover within 4.5 km of farms; (2) natural habitat heterogeneity; and (3) cattle, chicken, or any (cattle, chicken, or other) livestock presence on farms. Because ecoregion was not significantly associated with differences between bird communities, we did not include ecoregion in these models. Further, we counted livestock in these models as either “on-farm” (1) or “absent from farms” (0,2).

We considered both additive and interactive fixed effects between individual landscape variables and local livestock variables that we hypothesized would impact *Salmonella* prevalence (Supplementary Table 2.2). Farm visit was treated as a random effect nested within farm for all models, and year was included as a fixed effect in all models. Continuous variables were z-score transformed prior to analysis. Multicollinearity was assessed with the *performance* package in R (Lüdtke et al. 2021); any models with covariates that had a variance inflation factor (VIF) > 5 were not considered. We considered models well-supported based on the criteria of $\Delta AICc \leq 2$ from the most well-supported model (Burnham and Anderson 2002). Model predictions were generated for each model, weighted by the relativized AICc model weight, and then averaged to generate an overall *Salmonella* prevalence prediction. Weighted variance was calculated using the *wtd.var* function from the R package *Hmisc* (Harrell 2025).

Objective 3: Grower Survey

To gauge growers' attitudes towards birds and assess common bird deterrence methods, we constructed a 14-question anonymous survey in Qualtrics by referencing Smith et al. (2021). We distributed our survey through grower association mailing lists, social media (e.g., Instagram), and personal email contacts beginning in January 2022 and ending October 2022 (Appendix 1). We targeted respondents in our Southeast study region (Tennessee, Florida, Georgia, South Carolina) but also included respondents from North Carolina to increase the

number of responses. To further increase response rate, we distributed and collected printed versions of this survey in person at local “farm days” and at farms participating in our study; we also gathered responses from growers over the phone. We offered a chance for respondents to win a US\$50 gift card to incentivize responses. Altogether, we received 49 unique responses from 49 growers managing farms (Qualtrics n = 31; other n = 18).

The survey first asked a series of closed-ended questions about farm size, diversity of crops and livestock, and management style. The next section included closed-ended questions to establish what kinds of birds growers commonly observed and open-ended questions on any birds they considered beneficial to production. We also used a 5-point Likert scale to assess growers' attitudes towards bird management (1 = “encourage birds strongly,” 2 = “encourage birds a little,” 3 = “neither encourage nor discourage,” 4 = “discourage birds a little,” 5 = “discourage birds strongly”) and food safety concerns (1 = “not at all concerned,” 2 = “a little concerned,” 3 = “moderately concerned,” 4 = “very concerned,” 5 = “extremely concerned”). The final section asked growers about what kinds of preventative measures they used and asked them to rate how effective they thought each method used was on a 5-point Likert scale (1 = “not at all effective,” 2 = “slightly effective,” 3 = “moderately effective,” 4 = “very effective,” 5 = “extremely effective”). We also asked an open-ended question about what kinds of birds they wanted to discourage with the deterrents they used and a closed-ended question about how much money they spent on preventative measures annually.

Open-ended responses were coded taxonomically to identify the most common groups of birds that growers either observed or discouraged. Responses to open-ended questions were coded to the level of species (e.g., Redwing Blackbird (*Agelaius phoeniceus*)), family (e.g., flycatchers (Family Tyrannidae)), and order (e.g., songbirds (Order: Passeriformes, Suborder:

Passeri)) to the finest resolution possible. Using these recoded categories, we identified the most common responses among growers and binned all answers into these commonly mentioned groups (i.e., geese, pigeons, raptors, crows, and songbirds). We separated crows (*Corvus* spp.) from other songbirds in our figures and results to better reflect grower responses and explanations. To assess how grower concern about food safety was influenced by both farm characteristics and birds commonly observed by growers, we ran a series of ordinal logistic regressions using the *polr* function in the R package *MASS* (Venables & Ripley, 2002). Farm characteristics considered in these models included farm size; organic, conventional, or mixed management; number of types of crops grown (i.e., crop richness); number of types of livestock produced (i.e., livestock richness); and number of types and abundance of mammalian livestock produced (i.e., mammalian livestock diversity). Abundance of mammalian livestock was reported as a value range for each type of livestock (e.g., “1-25 individual cows”), coded as an integer, and then summed to get a measure of mammalian livestock density. Because only one grower indicated they were “extremely concerned” about birds as food safety hazards (response code 5), we binned response code 4 (“very concerned”) and 5 (“extremely concerned”) for analysis. Model assumptions (i.e., proportional odds and multicollinearity) were assessed using the *poTest* and *vif* functions in the R package *car* (Fox and Weisburg 2019), respectively. Models that did not meet model assumptions were excluded from further consideration. Models were ranked using AICc, and we considered models well-supported based on criteria of $\Delta AICc \leq 2$ from the most well-supported model (Burnham and Anderson 2002). All statistical analysis was performed in R (v. 4.3.2, 4.4.2) (R Core Team 2023).

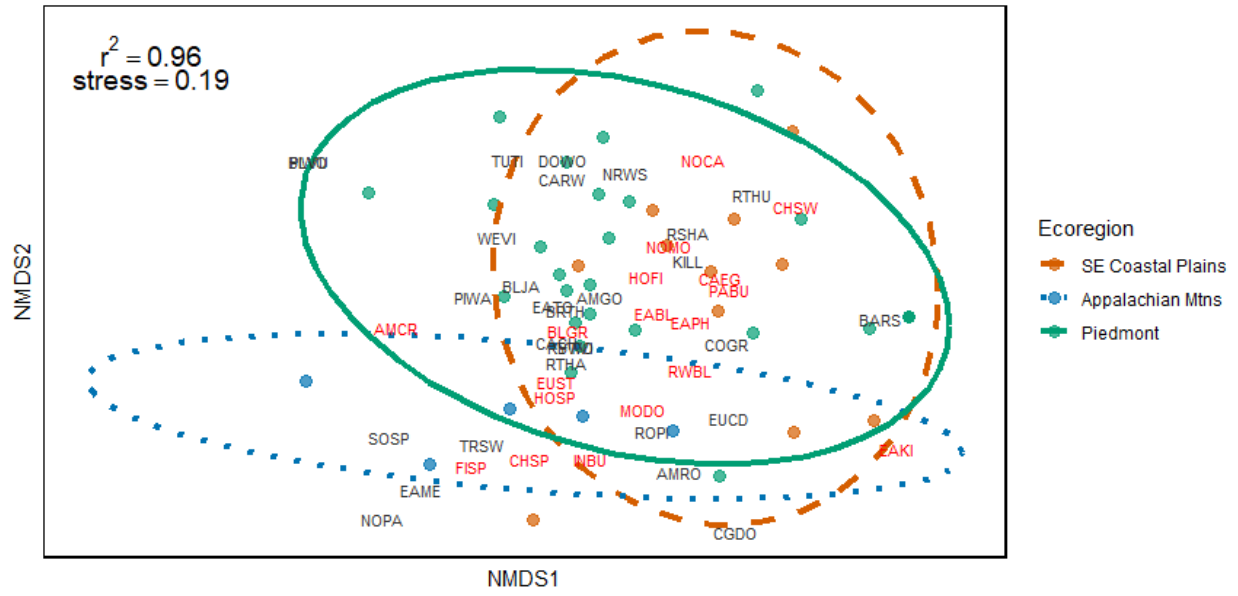


Figure 2.2. Bird species, given by four-letter alpha codes (text), were not noticeably clustered by ecoregion. Points indicate farms. Point color and ellipses indicate ecoregion of farm: SE Coastal Plains (orange, dashed), Appalachian Mountains (blue, dotted), and Piedmont (green, solid). Species indicated in red were the sources of crop-collected fecal samples, as determined from DNA barcoding (see Smith et al. 2023 for details).

Results

Objective 1: Bird Community Analysis

We identified 859 birds from 47 different species during point counts (Supplementary Table 2.3). The most abundant species detected included the Mourning Dove (*Zenaida macroura*), Rock Pigeon (*Columba livia*), Barn Swallow, and House Finch (*Haemorrhous mexicanus*). Five of the detected species—Eurasian Collared-Dove (*Streptopelia decaocto*),

European Starling (*Sturnus vulgaris*), House Finch, House Sparrow (*Passer domesticus*), and Rock Pigeon—were not native to the study area.

The bird community NMDS had a two-axis solution (stress = 0.19, $r^2 = 0.96$). The Appalachian Mountain and Coastal Plains regions clustered furthest away from each other, with the Piedmont region overlapping both. This corresponds to the latitudinal gradient of the area, although bird species were not noticeably clustered in any particular way between ecoregions (Figure 2.2), and bird community structure was not significantly associated with ecoregion ($p > 0.05$; Supplementary Table 2.4). Furthermore, Mantel tests indicated that community structure was not associated with proportion developed, natural, agricultural, open water, or wetland land cover ($p > 0.05$; Supplementary Table 2.5).

Using an indicator species analysis, we identified species that were significantly associated with certain ecoregions. The Cattle Egret (*Bubulcus ibis*) was associated with the Coastal Plains ecoregion ($p = 0.05$), and the Eastern Phoebe (*Sayornis phoebe*; $p = 0.02$), Eastern Towhee (*Pipilo erythrophthalmus*; $p = 0.02$), Indigo Bunting (*Passerina cyanea*; $p = 0.001$), Mourning Dove ($p = 0.04$), Song Sparrow (*Melospiza melodia*; $p = 0.001$), and Red-shouldered Hawk (*Buteo lineatus*; $p = 0.03$) were associated with the Appalachian Mountain ecoregion.

Objective 2: Variables Associated with *Salmonella* Prevalence

Salmonella was detected by culture or PCR in 8.6% (60/700) of total foliage-collected bird samples. We detected *Salmonella* in 1.6% (11/700) samples by culture and 7% (49/700) additional samples were identified by PCR. We had five well-supported models linking livestock and landscape variables to *Salmonella* prevalence (Supplementary Table 2.6). The interaction between on-farm cattle and wetlands was in three of the five models, while the interaction

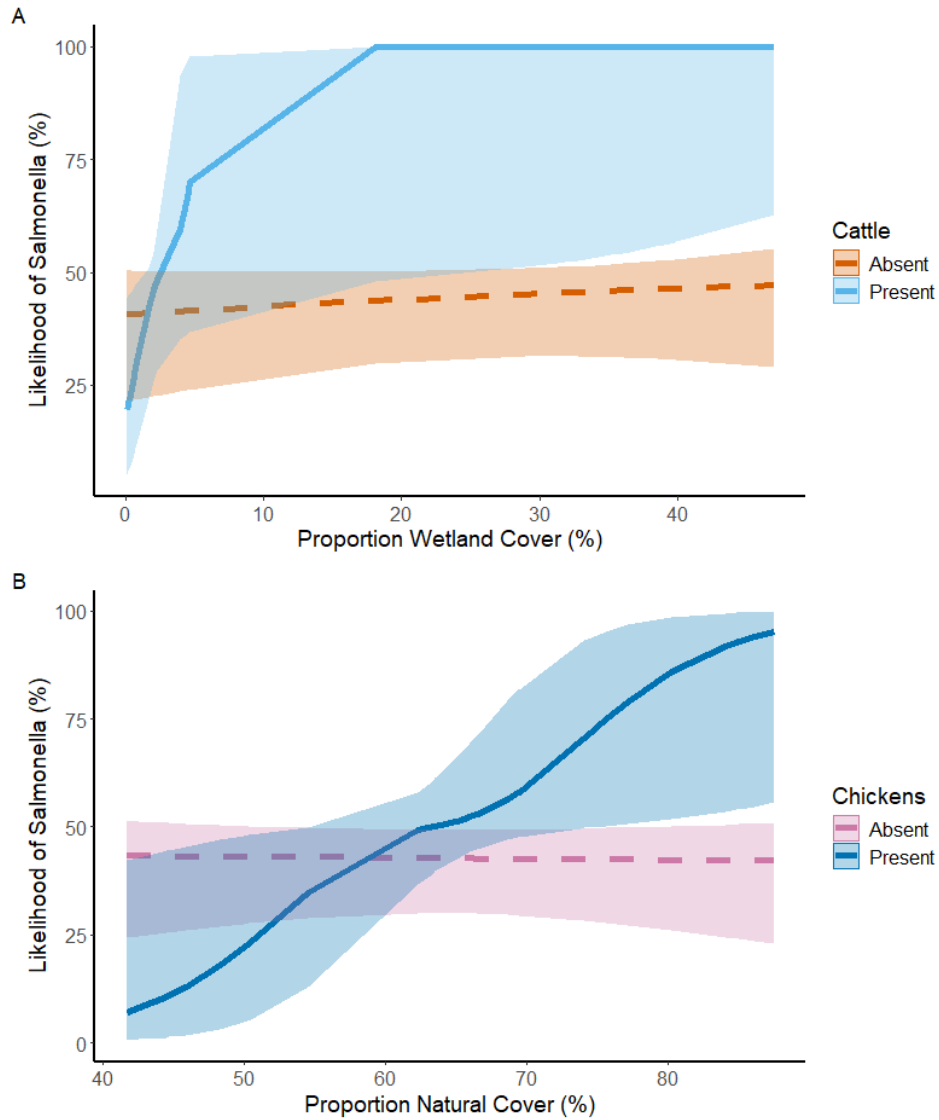


Figure 2.3. *Salmonella* prevalence was best predicted by the interaction between (A) on-farm cattle presence and a high proportion of wetland cover and (B) on-farm chicken presence and a high proportion of natural cover. Slopes come from top models as determined by AICc $\pm$ 95% CI. Color and line-type indicates (A) presence (blue, solid) or absence (red, dashed) of on-farm cattle and (B) presence (dark blue, solid) or absence (pink, dashed) of on-farm chickens.

between on-farm chickens and natural land cover was in two of the five. Other livestock, i.e., the presence of livestock on-farm that were not chickens or cattle, was in two of the five models.

As the proportion of wetland cover increased around farms, the presence of cattle on-farm was positively correlated with *Salmonella* prevalence in bird feces (Figure 2.3). The predicted likelihood of detecting *Salmonella* in bird feces increased from 25% to 99% when cattle were present on-farm at a proportion of wetland cover of 18%. Farms embedded in landscapes with a lower proportion of natural cover were more likely to have *Salmonella* detected in bird feces if they lacked chickens on-farm; however, at higher proportions of natural landscape cover, *Salmonella* was more likely to be detected in feces from farms that had chickens. The predicted likelihood of detecting *Salmonella* in bird feces increased from 23% to 43% when chickens were present on-farm at a proportion of natural land cover of 66%.

Objective 3: Grower Survey

A majority of growers (28/48 [58.3%]) expressed some or high concern (response codes 2-5) about birds as a food safety hazard to produce, although only a small minority (5/48 [10.4%]) expressed anything more than moderate concern (response codes 4-5; Appendix 2). We did not find any associations between grower concern and any of the variables examined, including the number of grower-observed bird groups, farm size, use of organic practices, crop richness, livestock richness, or mammalian livestock diversity (Supplementary Table 2.7).

Growers managing organic-only farms were more likely to respond that they encouraged birds compared to growers managing conventional-only farms. Of all 16 organic-only growers, none indicated they discouraged birds, and nearly half (7/16 [43.8%]) indicated they encouraged birds strongly. Conventional-only farms were also much less likely to have livestock on their farms. Only 10% of farms with livestock were conventional-only (2/21), while 37% of non-

livestock farms were conventional-only (10/27; Figure 2.4). Growers' concern about birds as food safety hazards seemed to strongly influence their bird management attitudes. Of all five growers who indicated they were more than moderately concerned about birds as food safety hazards (response level “4” or “5”), four (80%) discouraged birds.

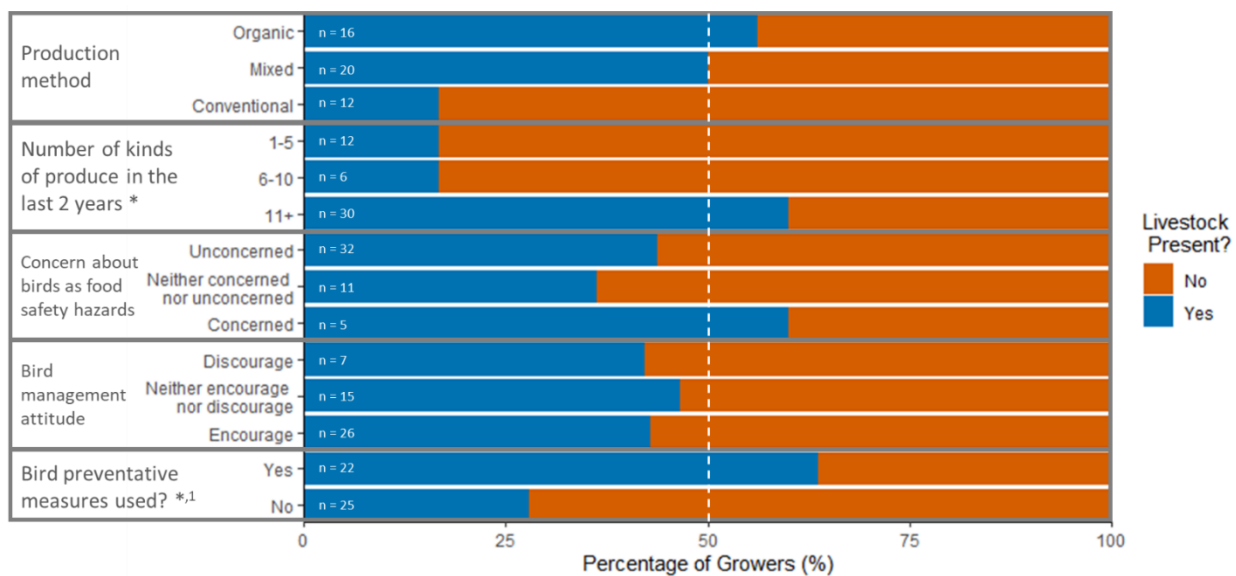


Figure 2.4. The percentage of surveyed growers producing a variety of crops and using bird preventative measures significantly differed between those with (blue, n=21) and without (orange, n=27) livestock on-farm. Questions in panels on the left come from our grower survey. Asterisks indicate questions in which the responses between growers with and without on-farm livestock significantly differed ($p < 0.05$).

¹One respondent did not indicate whether they used preventative measures or not, so the total of growers without livestock is n = 26 for the last question only.

Nearly half (22/48 [45.8%]) of surveyed growers indicated that they used some kind of preventative measure to discourage birds. A quarter (4/16) of organic-only growers used preventative measures, while more than half (18/33 [54.5%]) of conventional-only and mixed production farms used preventative measures. The majority of growers with cattle on their farms indicated that they used preventative measures (4/5 [80%]). The most common type of preventative measure was reflective surfaces or mirrors (10/22 [45.5%]), followed by netting (7/22 [31.8%]) and decoy birds or predators (6/22 [27.3%]; Figure 2.5). Growers indicated in open-ended responses that non-crow songbirds were the most common type of bird targeted by preventive measures (8/19 [42.1%]), followed by crows (5/19 [26.3%]), and hawks and eagles (Family: Accipitridae; 4/19 [21.1%]; Figure 5). Songbird species targeted were all either frugivorous or granivorous species (e.g., Cedar Waxwing, *Bombycilla cedrorum*; Northern Cardinal, *Cardinalis cardinalis*) or colonial roosting species known to colonize farm buildings (e.g., European Starlings, Barn Swallows). Hawks and eagles were only targeted by growers with poultry on their farms, while growers with no livestock more frequently identified raptors as beneficial (Appendix 2).

Some growers reported that their preventative measures were not at all or not very effective at discouraging birds (6/22 [27.3%]), even when they indicated they were spending in excess of US\$ 100 trying to discourage birds (Appendix 2). More than half (13/22 [59.1%]) of growers who used preventive measures spent more than US\$ 100 annually; three growers, ranging in size from 20 ha to over 120 ha, reported spending more than US\$ 1000 annually.

Discussion

The Appalachian Mountain, Piedmont, and Coastal Plains ecoregions differ broadly in climate, topography, soil types, human land use, and plant communities, and correspond to three distinct Bird Conservation Regions (Bird Studies Canada & NABCI 2009). Thus, it is perhaps surprising that we failed to find significant differences in the bird communities detected in produce fields in these different ecoregions (Figure 2.2). One possible explanation is that farming landscapes, regardless of the ecoregion they are embedded in, primarily attract and harbor the same synanthropic bird species tolerant of disturbance and/or that benefit from the open habitats that farming provides (Sambell et al. 2019). Overall, a fifth of the farms we surveyed were over 40 ha. (Table 1). Large, monoculture farms tend to have the same widely distributed, generalist species, even in different regions and landscapes (Flohre et al. 2011). Consistent with this possible explanation, many of the most common bird species observed in our Southeastern produce fields are the same as those observed in better studied western US produce farming systems. Song Sparrows (*Melospiza melodia*), Barn Swallows, and House Finches were all among the most commonly recorded species in our and similar west coast studies (Gonthier et al. 2019, Smith et al. 2020a, Olimpi et al. 2024). Likewise, in a survey of north-central Florida farms, Jones et al. (2005) recorded the Northern Cardinal and Northern Mockingbird (*Mimus polyglottos*)—the two species we also observed at the most farms—twice as frequently as the next most common species, and found that these two birds were associated with monoculture farms.

We found that *Salmonella* prevalence in foliage-collected bird feces was best predicted by two different interactions: it was higher when (1) cattle were observed on the farm and farms

were surrounded by wetlands, and (2) chickens were observed on the farm and farms were surrounded by natural habitat (Figure 3). Both wetlands and livestock are known to be reservoirs for *Salmonella* (Wells et al. 2001, Skov et al. 2008, Bolton et al. 2011, Levantesi et al. 2012). Smith et al. (2023) used whole-genome sequencing to characterize 19 *Salmonella* isolates from the same bird fecal samples analyzed in our study, and searched for genetic similarities to *Salmonella* isolates previously linked to various environmental (e.g., rivers and ponds) and agricultural (e.g., cattle or poultry production facilities) bacterial reservoirs. Interestingly, Smith et al. (2023) found that four out of the 19 avian-derived *Salmonella* isolates were most closely related to isolates previously collected from surface water, consistent with the positive correlation we found between wetland prevalence in the landscape and *Salmonella* prevalence in surface-collected bird feces (Figure 2.3). Several foodborne *Salmonella* outbreaks that impacted human health have been linked to contamination of nearby water sources (Greene et al. 2007, Kovačić et al. 2017), including a significant outbreak in cucumbers in 2024 (FDA 2024). We identified several *Salmonella*-positive samples from our plant-surface collections as having been deposited by the wetland-associated Cattle Egret and Fish Crow (*Corvus ossifragus*) (Smith et al. 2023). In a similar whole genome sequencing study, Fu et al. (2022) found that *Salmonella* lineages collected from wading birds were most genetically similar to isolates from water sources. Additionally, Gorski et al. (2011) linked *Salmonella* isolates found in surface water to those recovered from several species of wild birds, including crows.

Despite our finding that on-farm cattle and chickens were predictors of *Salmonella* prevalence (Figure 2.3), Smith et al. (2023) found that none of the 19 sequenced *Salmonella* isolates were closely related to *Salmonella* isolated from cattle. Three isolates were somewhat similar to isolates from chickens, but the chicken isolates were from geographically distant

states. This puzzling result, and previous work elsewhere that has linked *Salmonella* from livestock to that found in wild birds (e.g., Navarro-Gonzalez et al. 2020), could have several non-mutually exclusive explanations. Livestock and their associated habitat may draw in competent *Salmonella* reservoirs like Cattle Egrets, heightening food safety risks in nearby areas (Callaway et al. 2014), even if the livestock themselves are not the source of the pathogens. In that case, there would be an apparent correlation between livestock and heightened food safety risks, but the livestock would only be causing an aggregation of hosts. For example, Pao et al. (2014) recovered the same *Campylobacter* strain from different species of wild birds trapped at different ruminant pastures, but found that there was no transmission of bacteria between birds and ruminants. Phalen et al. (2010) found that Cattle Egrets and horses (*Equus caballus*) had the same *Salmonella* serovars, but that these bacteria came from a common source and were likely not transmitted between species. Another possible explanation is that the livestock near our produce fields were grazing in open pasture or coops at relatively low densities. Conversely, most databank sequences (which were used in the Smith et al. (2023) study) originate from regulatory samples collected from slaughterhouses or from animals grown in high-density feedlots, dairies, and broiler houses (Roy et al. 2002, Callaway et al. 2005, Gaukler et al. 2009, Carlson et al. 2010, Carlson et al. 2011, Carlson et al. 2015). That is, the prior analysis on isolates from farms in this study may have missed a link between low-density, pastured livestock and *Salmonella* found in bird feces because the databank isolates they made comparisons to are biased towards sequences from high-density processing facilities. Clearly, more work is needed to detail where specifically wild birds are acquiring the potential foodborne pathogens that they later might spread to fresh produce fields, beyond the broad habitat associations reported here and elsewhere (e.g., Zellweger-Fischer et al. 2018, Smith et al. 2020a, Olimpi et al. 2024).

The ecology of foodborne pathogen dissemination by wild birds has been most intensively studied in the western US (Smith et al. 2020a, Olimpi et al. 2020, Navarro-Gonzalez et al. 2020, Smith et al. 2022, Spence et al. 2025). In several respects, we found patterns in our southeastern produce fields that broadly mirror previous results. In the west, as in our study region, livestock production, and particularly cattle production, was correlated with increased prevalence of potential foodborne pathogens in bird feces deposited on crops (Smith et al. 2020a, Olimpi et al. 2024). This suggests that produce growers in both regions that also raise livestock or are surrounded by livestock production should consider utilizing mitigation efforts to decrease bird-associated food safety risks (Rivadeneira et al. 2016), which aligns with grower-reported behavior in this study.

We also found several key differences from what has been reported for the western US. Most dramatically, whereas in the western fields *Campylobacter* spp. were by far the most common detected foodborne bacteria in bird feces, detected in ca. 3-13% of bird fecal samples (Smith et al. 2020a, Olimpi et al. 2022, Olimpi et al. 2024), we never detected any *Campylobacter* from the feces collected in the Southeast. In stark contrast, we detected *Salmonella* in 1.6% of the bird fecal samples by culture from southeastern produce fields, whereas these bacteria were only found in $\leq 0.5\%$ of western bird feces (Gorski et al. 2011, Fonseca et al. 2020, Navarro-Gonzalez et al. 2020, Smith et al. 2020a, Olimpi et al. 2022, Olimpi et al. 2024). It is unclear if this difference between regions reflects true differences in prevalence of the pathogen taxa (*Campylobacter* versus *Salmonella*), differences in the importance or abundance of surrounding wetlands, or some other factor such as regional differences in presence of competent avian hosts. The geographically closest equivalent studies we could find come from southeast Texas, where Grigar et al. (2017) reported *Salmonella* rates of 0.5% in waterfowl taken

from the Gulf Coast, while Brobey et al. (2017) found *Salmonella* rates of 17% in wild birds trapped from suburban and urban sites. In Florida, Hernandez et al. (2016) reported a *Salmonella* prevalence of 13% from White Ibis (*Eudocimus albus*). It is also important to note that some of our comparisons of bacterial prevalence to studies in the western US are limited due to differences in how fecal samples were collected and stored, which could have differently affected *Campylobacter* and *Salmonella* survival and detection. Overall, our findings suggest the need for more comparative studies in the ecology of bird-associated food safety risks between regions, using identical methods, to determine what specific regional and environmental differences best explain pathogen prevalence in agroecosystems.

The survey responses from growers suggest that consideration of food safety risks may play a part in grower deployment of bird deterrence measures, although, based on grower responses to open-ended questions, growers' primary concern seemed to be avoiding crop damage (Figure 2.5). Although food safety concern was similar between growers with and without livestock, growers with livestock were much more likely to use bird prevention methods (Figure 2.4). One reason could be that growers with chickens were managing for raptors, which could injure or kill their flocks. Some bird species, like European Starlings and Rock Pigeons, may also roost in barns and become a nuisance. Interestingly, although organic-only farms were more likely to house livestock than others, organic-only growers were far less likely to use preventative measures than conventional-only and mixed-production growers. Organic-only growers indicated they encouraged birds more strongly than other growers, similar to previous studies (Silva-Andrade et al. 2016, Kross et al. 2017), which could have influenced this decision. No growers mentioned attempting to deter wetland-associated birds like shorebirds and herons that this and previous studies have indicated may pose the biggest food safety risk (Waldenström

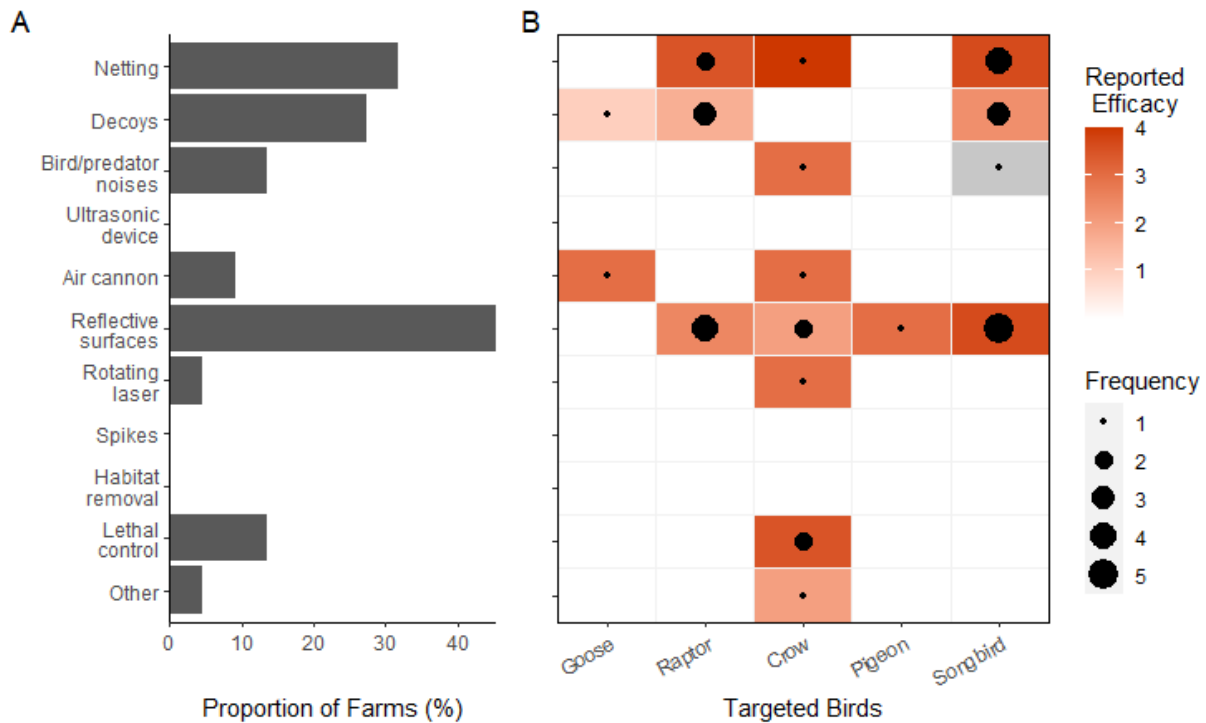


Figure 2.5. (A) A bar graph depicting the total percentage of farms using each measure out of all farms that reported using any measure (n=22). (B) A heatmap depicting the frequency (dots) of each measure used to target a specific group of birds. Color represents the average reported efficacy of each bird-measure combination (1 = “not at all effective”, 2 = “a little effective”, 3 = “moderately effective”, 4 = “very effective”, 5 = “extremely effective”); gray represents no efficacy rating given. The group 'raptor' includes both hawks and eagles, and the group 'songbird' includes birds from 6 different families: Bombycillidae, Cardinalidae, Hirundinidae, Mimidae, Sturnidae, and Turdidae.

et al. 2002, Minias 2020), despite many observations of species like Killdeer (*Charadrius vociferus*) and Cattle Egrets in fields and pastures (Supplementary Table 2.3, Figure 2.5). Our results indicate that growers may not be fully aware of which bird species pose the greatest food safety risk to produce, similar to growers in western regions (Smith et al. 2021), but, because growers with livestock are more likely to use bird preventative measures, growers may still be reducing food safety risk, albeit incidentally. Overall, growers did not rate their chosen strategies as very effective at deterring wild birds, as in other studies (Anderson et al. 2013). Empirical research also suggests conventional “scaring” strategies like cannons and mirrors do not significantly reduce crop damage nor food safety risks. For example, Gonthier et al. (2019) reported that deterrents, including sound cannons and other deterrents reported here, were positively correlated with strawberry damage, although Olimpi et al. (2020) found that farms that used a number of various deterrence practices had less strawberry damage. Growers might reduce food safety risks more effectively by preventing birds from interacting with crops or entering livestock facilities by using physical barriers like netting. For example, Carlson et al. (2011) found that removal of starlings prevented *Salmonella* prevalence from increasing in cattle, compared to a control facility where starling presence was associated with increasing *Salmonella* prevalence.

Overall, the results presented here suggest several next steps for better understanding how natural habitats on or near farms interact with regional bird communities to determine birds’ threat to food safety. First, it appears that there may be some similarities, but many key differences, between US regions in landscape drivers of bird-associated food safety risks and in the pathogen taxa most likely to be transmitted. This primarily suggests the need for more widespread studies into the ecology of birds and food safety in other important produce growing

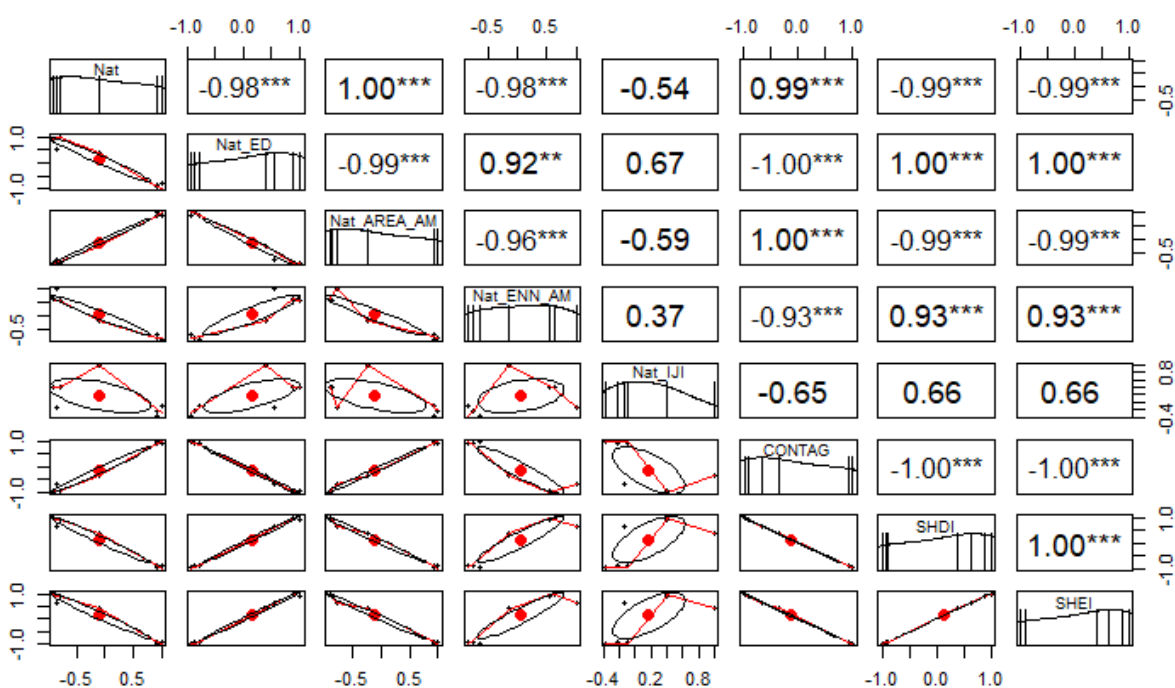
regions in North America and elsewhere. Additionally, complementary genetic inference of pathogen sources in Smith et al. (2023) match the landscape correlates we found in terms of wetlands appearing as both a risk factor associated with *Salmonella* detection in bird feces and as the likely environmental source of these bacteria. Yet, while livestock appeared as clear correlates of pathogen detection in bird feces here and in the west (Smith et al. 2020a, Olimpi et al. 2024), genetic tracking did not detect *Salmonella* isolates typically found in cattle nor chickens (Smith et al. 2023). This suggests the need for more work directly linking habitats to potential foodborne pathogens that birds may be exposed to, in many different produce growing regions. Further, we suggest a clear need to identify specific links between a given level of pathogen prevalence in bird feces and the later risk to human consumers. It is likely that temperature, humidity, irrigation practices, etc., all impact pathogen persistence after fecal deposition, although these effects are relatively understudied (but see Jeamsripong et al. 2019, Fonseca et al. 2020, and Spence et al. 2025). Finally, we know that birds can contribute to natural control of insect and rodent pests of agriculture (Díaz-Sieffer et al. 2022), and also weed control (Navntoft et al. 2009), but relatively few studies simultaneously look at both ecosystem services and disservices provided by birds in the same cropping fields (but see Garcia et al. 2020, Olimpi et al. 2020, and Olimpi et al. 2022). Ultimately, it is the balance of these beneficial and harmful impacts of birds that will determine whether productive farming and bird conservation can be compatible goals.

Supplementary Material

Supplementary Table 2.1. Landscape and livestock factors examined in relation to *Salmonella* prevalence. Values are mean and (min-max values). We selected which natural cover configurational and compositional heterogeneity variables to include in models based on their Pearson's correlation coefficients (Supplementary Figure 2.1). Landscape metrics use a 4.5 km radius.

Category	Metric Type	Class	Used in analysis	Definition
% Open Water	landscape composition	percentage mean: 2.98 (0.1-19.52)	yes	Proportion of open water
% Developed	landscape composition	percentage mean: 11.21 (2.22-42.04)	yes	Proportion of developed habitat (NLCD codes 21-24)
% Barren	landscape composition	percentage mean: 0.19 (0-1.02)	no	Proportion barren habitat (NLCD code 31)
% Agricultural	landscape composition	percentage mean: 18.12 (2.65-47.06)	yes	Proportion of agricultural habitat (NLCD codes 81-82)
% Natural	landscape composition	percentage mean: 67.40 (41.71-92.49)	yes	Proportion of natural habitat (NLCD codes 41-743, 51-52, 71-74, 90, 95)
% Wetland	landscape composition	percentage mean: 24.28 (0.13-54.23)	yes	Proportion of wetland (NLCD codes 90, 95)
Nat_ED	configurational	numeric mean: 45.08 (18.89-74.00)	no	Edge Density of natural habitat
Nat_AREA_AM	configurational	numeric mean: 3352.34 (252.64-5883.01)	no	Area weighted mean patch area
Nat_ENN_AM	configurational	numeric mean: 59.93 (59.33-61.63)	no	Euclidean Nearest Neighbor Distance
Nat_IJI	configurational	numeric mean: 62.05 (50.92-84.50)	yes	Interspersion and Juxtaposition Index
CONTAG	configurational	numeric mean: 62.31 (41.74-85.39)	no	Contagion Index across all land cover types

SHDI	compositional	numeric mean: 0.82 (0.32-1.23)	no	Shannon's Habitat Diversity Index
SHEI	compositional	numeric mean: 0.51 (0.20-0.77)	no	Shannon's Habitat Evenness Index
Chicken	on-farm livestock	presence/absence	yes	Chickens within 250 m
Cow	on-farm livestock	presence/absence	yes	Cows within 250 m
Other	on-farm livestock	presence/absence	yes	Other livestock within 250 m
Livestock	on-farm livestock	presence/absence	yes	Any livestock within 250 m



Supplementary Figure 2.1. Pearson correlation values for proportion natural (NLCD) and calculated natural configurational and compositional heterogeneity in a 4.5 km radius around farms. Abbreviations used are defined in Supplementary Table 2.3. Bolded values indicate correlations significant at $p < 0.05$; asterisks indicate correlations significant at $p < 0.01$.

Supplementary Table 2.2. List of generalized linear mixed effects models used to test associations between landscape and on-farm livestock variables as predictors of *Salmonella* prevalence in foliage-collected bird feces. Refer to Supplementary Table 2.1 for explanations of fixed effects. Year was included in all models as a fixed effect. (1|Farm/Visit) represents the random effect, wherein visit is nested within farm.

#	Model Structure
Null	Year + (1 Farm/Visit)
1	% Open Water + Year + (1 Farm/Visit)
2	% Developed + Year + (1 Farm/Visit)
3	% Agricultural + Year + (1 Farm/Visit)
4	% Natural + Year + (1 Farm/Visit)
5	% Wetland + Year + (1 Farm/Visit)
6	Nat_IJI + Year + (1 Farm/Visit)
7	Chicken + Year + (1 Farm/Visit)
8	Cow + Year + (1 Farm/Visit)
9	Other + Year + (1 Farm/Visit)
10	Livestock + Year + (1 Farm/Visit)
11	% Open Water + Chicken + Year + (1 Farm/Visit)
12	% Developed + Chicken + Year + (1 Farm/Visit)
13	% Agricultural + Chicken + Year + (1 Farm/Visit)
14	% Natural + Chicken + Year + (1 Farm/Visit)
15	% Wetland + Chicken + Year + (1 Farm/Visit)
16	Nat_IJI + Chicken + Year + (1 Farm/Visit)
17	% Open Water * Chicken + Year + (1 Farm/Visit)
18	% Developed * Chicken + Year + (1 Farm/Visit)
19	% Agricultural * Chicken + Year + (1 Farm/Visit)
20	% Natural * Chicken + Year + (1 Farm/Visit)
21	% Wetland * Chicken + Year + (1 Farm/Visit)
22	Nat_IJI * Chicken + Year + (1 Farm/Visit)
23	% Open Water + Cow + Year + (1 Farm/Visit)
24	% Developed + Cow + Year + (1 Farm/Visit)
25	% Agricultural + Cow + Year + (1 Farm/Visit)
26	% Natural + Cow + Year + (1 Farm/Visit)
27	% Wetland + Cow + Year + (1 Farm/Visit)
28	Nat_IJI + Cow + Year + (1 Farm/Visit)
29	% Open Water * Cow + Year + (1 Farm/Visit)
30	% Developed * Cow + Year + (1 Farm/Visit)
31	% Agricultural * Cow + Year + (1 Farm/Visit)
32	% Natural * Cow + Year + (1 Farm/Visit)

33	% Wetland * Cow + Year + (1 Farm/Visit)
34	Nat_IJI * Cow + Year + (1 Farm/Visit)
35	% Open Water + Other + Year + (1 Farm/Visit)
36	% Developed + Other + Year + (1 Farm/Visit)
37	% Agricultural + Other + Year + (1 Farm/Visit)
38	% Natural + Other + Year + (1 Farm/Visit)
39	% Wetland + Other + Year + (1 Farm/Visit)
40	Nat_IJI + Other + Year + (1 Farm/Visit)
41	% Open Water * Other + Year + (1 Farm/Visit)
42	% Developed * Other + Year + (1 Farm/Visit)
43	% Agricultural * Other + Year + (1 Farm/Visit)
44	% Natural * Other + Year + (1 Farm/Visit)
45	% Wetland * Other + Year + (1 Farm/Visit)
46	Nat_IJI * Other + Year + (1 Farm/Visit)
47	% Open Water + Livestock + Year + (1 Farm/Visit)
48	% Developed + Livestock + Year + (1 Farm/Visit)
49	% Agricultural + Livestock + Year + (1 Farm/Visit)
50	% Natural + Livestock + Year + (1 Farm/Visit)
51	% Wetland + Livestock + Year + (1 Farm/Visit)
52	Nat_IJI + Livestock + Year + (1 Farm/Visit)
53	% Open Water * Livestock + Year + (1 Farm/Visit)
54	% Developed * Livestock + Year + (1 Farm/Visit)
55	% Agricultural * Livestock + Year + (1 Farm/Visit)
56	% Natural * Livestock + Year + (1 Farm/Visit)
57	% Wetland * Livestock + Year + (1 Farm/Visit)
58	Nat_IJI * Livestock + Year + (1 Farm/Visit)
59	Chicken + Cow + Year + (1 Farm/Visit)
60	Chicken + Other + Year + (1 Farm/Visit)
61	Cow + Other + Year + (1 Farm/Visit)
62	Chicken * Cow + Year + (1 Farm/Visit)
63	Chicken * Other + Year + (1 Farm/Visit)
64	Cow * Other + Year + (1 Farm/Visit)
65	% Open Water * Chicken + Cow + Year + (1 Farm/Visit)
66	% Developed * Chicken + Cow + Year + (1 Farm/Visit)
67	% Agricultural * Chicken + Cow + Year + (1 Farm/Visit)
68	% Natural * Chicken + Cow + Year + (1 Farm/Visit)
69	% Wetland * Chicken + Cow + Year + (1 Farm/Visit)
70	Nat_IJI * Chicken + Year + Cow + Year + (1 Farm/Visit)
71	% Open Water * Cow + Chicken + Year + (1 Farm/Visit)
72	% Developed * Cow + Chicken + Year + (1 Farm/Visit)
73	% Agricultural * Cow + Chicken + Year + (1 Farm/Visit)
74	% Natural * Cow + Chicken + Year + (1 Farm/Visit)
75	% Wetland * Cow + Chicken + Year + (1 Farm/Visit)

76	Nat_IJI * Cow + Chicken + Year + (1 Farm/Visit)
77	% Open Water + Cow * Chicken + Year + (1 Farm/Visit)
78	% Developed + Cow * Chicken + Year + (1 Farm/Visit)
79	% Agricultural + Cow * Chicken + Year + (1 Farm/Visit)
80	% Natural + Cow * Chicken + Year + (1 Farm/Visit)
81	% Wetland + Cow * Chicken + Year + (1 Farm/Visit)
82	Nat_IJI + Cow * Chicken + Year + (1 Farm/Visit)
83	% Open Water * Chicken + Other + Year + (1 Farm/Visit)
84	% Developed * Chicken + Other + Year + (1 Farm/Visit)
85	% Agricultural * Chicken + Other + Year + (1 Farm/Visit)
86	% Natural * Chicken + Other + Year + (1 Farm/Visit)
87	% Wetland * Chicken + Other + Year + (1 Farm/Visit)
88	Nat_IJI * Chicken + Other + Year + (1 Farm/Visit)
89	% Open Water * Other + Chicken + Year + (1 Farm/Visit)
90	% Developed * Other + Chicken + Year + (1 Farm/Visit)
91	% Agricultural * Other + Chicken + Year + (1 Farm/Visit)
92	% Natural * Other + Chicken + Year + (1 Farm/Visit)
93	% Wetland * Other + Chicken + Year + (1 Farm/Visit)
94	Nat_IJI * Other + Chicken + Year + (1 Farm/Visit)
95	% Open Water + Other * Chicken + Year + (1 Farm/Visit)
96	% Developed + Other * Chicken + Year + (1 Farm/Visit)
97	% Agricultural + Other * Chicken + Year + (1 Farm/Visit)
98	% Natural + Other * Chicken + Year + (1 Farm/Visit)
99	% Wetland + Other * Chicken + Year + (1 Farm/Visit)
100	Nat_IJI + Other * Chicken + Year + (1 Farm/Visit)
101	% Open Water * Cow + Other + Year + (1 Farm/Visit)
102	% Developed * Cow + Other + Year + (1 Farm/Visit)
103	% Agricultural * Cow + Other + Year + (1 Farm/Visit)
104	% Natural * Cow + Other + Year + (1 Farm/Visit)
105	% Wetland * Cow + Other + Year + (1 Farm/Visit)
106	Nat_IJI * Cow + Other + Year + (1 Farm/Visit)
107	% Open Water * Other + Cow + Year + (1 Farm/Visit)
108	% Developed * Other + Cow + Year + (1 Farm/Visit)
109	% Agricultural * Other + Cow + Year + (1 Farm/Visit))
110	% Natural * Other + Cow + Year + (1 Farm/Visit)
111	% Wetland * Other + Cow + Year + (1 Farm/Visit))
112	Nat_IJI * Other + Cow + Year + (1 Farm/Visit)
113	% Open Water + Other * Cow + Year + (1 Farm/Visit)
114	% Developed + Other * Cow + Year + (1 Farm/Visit)
115	% Agricultural + Other * Cow + Year + (1 Farm/Visit)
116	% Natural + Other * Cow + Year + (1 Farm/Visit)
117	% Wetland + Other * Cow + Year + (1 Farm/Visit)
118	Nat_IJI + Other * Cow + Year + (1 Farm/Visit)

Supplementary Table 2.3. Total number of individuals of each bird species recorded during point count surveys. Total N = total observed across all surveys, Native = native to region pre-European colonization. Asterisks next to scientific names indicate species which were observed interacting with crops (e.g., perched on trellises, entering grow tunnels); for total number of contacts per species see Smith et al. (2023).

Scientific Name	Common Name	Total N	Native	IUCN Red List Status
<i>Buteo jamaicensis</i>	Red-tailed Hawk	1	native	least concern
<i>Buteo lineatus</i>	Red-shouldered Hawk	6	native	least concern
<i>Chaetura pelagica</i>	Chimney Swift	7	native	vulnerable
<i>Archilochus colubris</i> *	Ruby-throated Hummingbird	1	native	least concern
<i>Coragyps atratus</i>	Black Vulture	9	native	least concern
<i>Charadrius vociferous</i> *	Killdeer	8	native	least concern
<i>Columba livia</i> *	Rock Pigeon	107	non-native	least concern
<i>Columbina passerina</i> *	Common Ground Dove	4	native	least concern
<i>Streptopelia decaocto</i> *	Eurasian Collared-Dove	6	non-native	least concern
<i>Zenaidura macroura</i> *	Mourning Dove	108	native	least concern
<i>Cardinalis cardinalis</i> *	Northern Cardinal	51	native	least concern
<i>Passerina caerulea</i> *	Blue Grosbeak	8	native	least concern
<i>Passerina ciris</i>	Painted Bunting	2	native	least concern
<i>Passerina cyanea</i> *	Indigo Bunting	4	native	least concern
<i>Corvus brachyrhynchos</i> *	American Crow	26	native	least concern
<i>Cyanocitta cristata</i> *	Blue Jay	14	native	least concern
<i>Haemorhous mexicanus</i> *	House Finch	61	non-native	least concern
<i>Spinus tristis</i> *	American Goldfinch	7	native	least concern
<i>Hirundo rustica</i> *	Barn Swallow	67	native	least concern
<i>Stelgidopteryx serripennis</i>	Northern Rough-winged Swallow	4	native	least concern
<i>Tachycineta bicolor</i>	Tree Swallow	1	native	least concern
<i>Agelaius phoeniceus</i> *	Red-winged Blackbird	12	native	least concern
<i>Quiscalus quiscula</i>	Common Grackle	3	native	near threatened
<i>Sturnella magna</i> *	Eastern Meadowlark	4	native	near threatened
<i>Mimus polyglottos</i> *	Northern Mockingbird	49	native	least concern
<i>Toxostoma rufum</i> *	Brown Thrasher	4	native	least concern
<i>Baeolophus bicolor</i> *	Tufted Titmouse	8	native	least concern
<i>Poecile carolinensis</i>	Carolina Chickadee	11	native	least concern

<i>Setophaga americana</i>	Northern Parula	1	native	least concern
<i>Setophaga pinus</i>	Pine Warbler	1	native	least concern
<i>Melospiza melodia</i> *	Song Sparrow	30	native	least concern
<i>Pipilo erythrophthalmus</i>	Eastern Towhee	12	native	least concern
<i>Spizella passerine</i> *	Chipping Sparrow	41	native	least concern
<i>Spizella pusilla</i> *	Field Sparrow	9	native	least concern
<i>Passer domesticus</i>	House Sparrow	1	non-native	least concern
<i>Sturnus vulgaris</i> *	European Starling	16	non-native	least concern
<i>Thryothorus ludovicianus</i> *	Carolina Wren	38	native	least concern
<i>Sialia sialis</i> *	Eastern Bluebird	33	native	least concern
<i>Turdus migratorius</i>	American Robin	5	native	least concern
<i>Sayornis phoebe</i> *	Eastern Phoebe	28	native	least concern
<i>Tyrannus tyrannus</i> *	Eastern Kingbird	4	native	least concern
<i>Vireo flavifrons</i>	Yellow-throated Vireo	2	native	least concern
<i>Vireo griseus</i> *	White-eyed Vireo	11	native	least concern
<i>Bubulcus ibis</i> *	Cattle Egret	18	native	least concern
<i>Dryobates pubescens</i> *	Downy Woodpecker	5	native	least concern
<i>Dryocopus pileatus</i>	Pileated Woodpecker	1	native	least concern
<i>Melanerpes carolinus</i>	Red-bellied Woodpecker	5	native	least concern

Supplementary Table 2.4. R statistics and *p* values for bird community ANOSIM tests. The “strata” column defines the strata used in the function *anosim* from the *vegan* R package. “Livestock presence” refers to whether any livestock were present on-farm. Each row refers to a separate test, with permutations within each strata, which were tested separately due to the low number of farms at some values.

Model	Strata	R	p
Ecoregion	field size	0.05	0.24
Ecoregion	livestock presence	0.05	0.25

Supplementary Table 2.5. R statistics and *p* values for bird community Mantel tests that examined relationships between land cover variables and Bray-Curtis dissimilarity matrices. The “strata” column defines the strata used in the function *mantel* from the *vegan* R package. “Livestock presence” refers to whether any livestock were present on-farm. Each row refers to a separate test, with permutations within each strata, which were tested separately due to the low number of farms at some values.

Model	Strata	R	p
Proportion Developed Land	field size	-0.07	0.81
Proportion Developed Land	livestock presence	-0.07	0.90
Proportion Natural Land	field size	-0.04	0.75
Proportion Natural Land	livestock presence	-0.04	0.71
Proportion Agricultural Land	field size	0.06	0.14
Proportion Agricultural Land	livestock presence	0.06	0.19
Proportion Wetlands	field size	0.02	0.31
Proportion Wetlands	livestock presence	0.02	0.09

Supplementary Table 5.6. Models estimates with values $\pm$ 95% confidence intervals (CIs) in columns. Only those with $> 5\%$ of AIC_c model weight are shown. “Wet” and “Nat” refer to proportion of wetlands and natural habitat, respectively, in a 4.5 km radius around a farm. “Cattle”, “Chick”, and “Other” refer to whether cattle, chickens, or other livestock, respectively, were present on-farm. Bolded values indicate values where 95% CIs do not overlap 0.

Model	Wet	Cattle	Wet:Cow	Nat	Chick	Nat:Chick	Other	Year	ΔAIC_c	AIC_c Weight
Wet * Cattle + Year	0.16 $\pm$ 4.66	4.35 $\pm$ 4.43	11.38 $\pm$ 10.83					-1.07 $\pm$ 1.02	0.00	0.22
Wet * Cattle + Chick + Year	0.22 $\pm$ 0.50	4.16 $\pm$ 4.47	11.01 $\pm$ 10.89		0.65 $\pm$ 1.09			-1.10 $\pm$ 1.10	0.71	0.15
Nat * Chick + Other + Year				-0.03 $\pm$ 0.56	0.35 $\pm$ 1.07	2.52 $\pm$ 1.77	-0.90 $\pm$ 1.23	-1.03 $\pm$ 0.93	1.89	0.08
Nat * Chick + Year				-0.12 $\pm$ 0.58	0.18 $\pm$ 1.11	2.31 $\pm$ 1.68		-1.28 $\pm$ 0.96	1.90	0.08
Wet * Cattle + Other + Year	0.14 $\pm$ 0.48	4.40 $\pm$ 4.45	11.44 $\pm$ 10.87				-0.17 $\pm$ 1.24	-1.05 $\pm$ 1.01	2.05	0.08

Supplementary Table 5.7. AIC_c table for ordinal regressions measuring grower concern about birds as food safety hazards. Columns 2-4 represent coefficient values $\pm$ 95% confidence intervals. Only models with $\Delta\text{AIC}_c \leq 2$ are shown.

Model	# Grower Bird Groups Observed	On-farm Livestock Richness	On-farm Produce Richness	Mammalian Livestock Diversity	ΔAIC_c	AIC _c Weight
Null Model					0.00	0.17
# Grower Bird Groups Observed	-0.18 $\pm$ 0.26				0.07	0.16
On-farm Livestock Richness		0.14 $\pm$ 0.50			1.79	0.07
On-farm Produce Richness			-0.02 $\pm$ 0.09		1.80	0.07
Mammalian Livestock Diversity				0.08 $\pm$ 0.34	1.89	0.07

CHAPTER 3

DETECTING WILD BIRDS DURING FRUIT AND VEGETABLE PRODUCTION²

² Varriano, S, WE Snyder, JC Smith, NW Shariat, & LL Dunn. 2024. *Food Protection Trends*. 45(1): 27-35.

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Abstract

Wild birds can be serious pests on farms by damaging produce and introducing food safety hazards to production fields and packinghouses. The most serious crop damage is usually caused by fruit- or seed-eating species like blackbirds, cardinals, robins, or crows, while other species like sparrows, finches, and starlings can take up residence in farm buildings and quickly become a nuisance. Creating an effective management plan to deter wild birds from fields and buildings begins with correctly identifying bird species and the damage they are likely to cause. Just as different kinds of pest insects target different plants at different times of year, not all birds feed in the same way, nor at the same time. Targeting deterrence strategies towards specific species is more cost-effective than a “catch-all” approach and reduces the likelihood that non-target species are affected. The most effective management plan will be targeted towards specific problem species at specific times of year and may involve mixing and matching different deterrence strategies.

Introduction

Wild birds can cause significant damage to fresh produce, and the extent of damage can vary greatly depending on geographic location and commodity type (Elser et al. 2019; Wang et al. 2020). Estimates of damage based on grower surveys from five states ranged from \$42/acre for Oregon tart cherry growers to \$2,941/acre for growers of Honeycrisp apples in Washington State (Anderson et al. 2013). Beyond product consumed by birds, losses occur from pecking damage, produce knocked off the plant, and increased susceptibility to plant disease due to bird-inflicted damage. American robins and cedar waxwings have been identified as significant fruit consumers across multiple regions (Hannay et al. 2019). Losses because of food safety concerns

include unharvestable produce due to fecal deposition as bird feces can contain bacterial pathogens such as *Salmonella enterica* and *Campylobacter jejuni* (Keller et al. 2011; Smith et al. 2020). European starlings have been identified as vectors of bacterial pathogens of concern for public health from livestock operations (Steensma et al. 2016).

Growers have options regarding mitigation strategies to reduce bird damage, although a survey by Keller et al. (2011) indicated that most growers employ management tools only when bird damage results in significant economic loss. Some deterrents have been reported by growers or researchers to be more effective than others (Steensma et al. 2016). However, labor, expense, overall efficacy, geospatial and temporal factors, target bird species (Figure 3.1), crop characteristics, and consumer perceptions should all be considerations for growers selecting deterrents intended to protect produce crops.

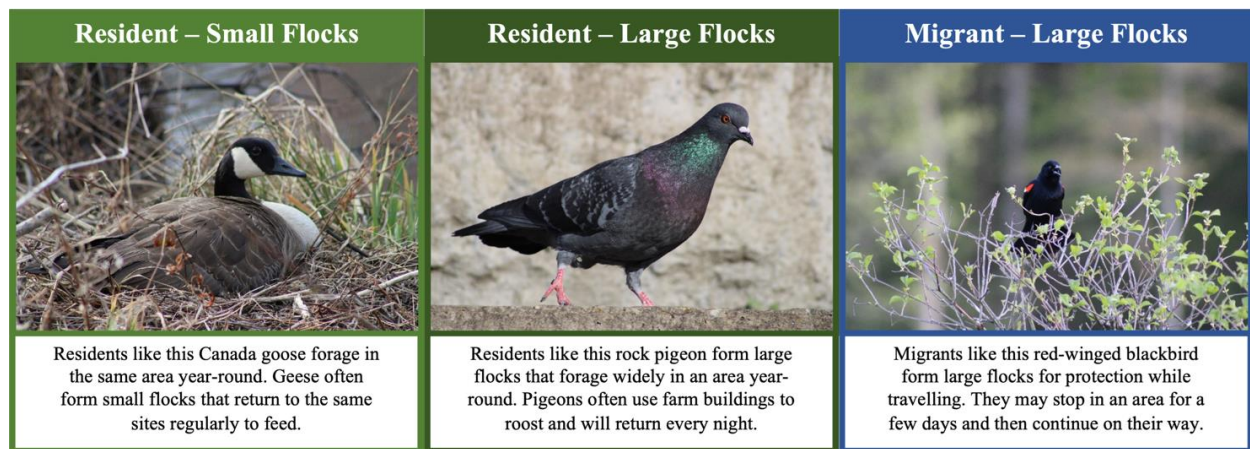


Figure 3.1. Examples of different foraging and residency behaviors: 1) resident and small flocks; 2) resident and large flocks, and 3) migrant and large flocks. These three types of birds may require different management strategies. *Photo Credit: Julia Berliner.*

This review provides an overview of deterrents commonly used in fruit and vegetable production areas, as well as advantages and disadvantages to their implementation in a production environment. It is not intended to serve as an endorsement for any strategy or technology, and growers are advised to conduct their own assessments to determine if methods are appropriate for their own operations.

Site Cleanliness

Managing waste and leftover produce should be the first priority for any operation as they look to manage their pest populations, including wild birds. In a packing facility, especially one that is open to the environment, emptying cull bins frequently, keeping material swept off of floors and surfaces, and ensuring food waste does not accumulate within the facility will reduce the likelihood of birds entering in search of food. Likewise, dumpsters and other trash collection areas likely to attract birds should be closed off, when possible, emptied regularly, and managed to reduce bird access. Reducing access to readily available food sources will greatly increase the effectiveness of other implemented deterrent or control measures.

Scaring Deterrents

The most common types of bird deterrents use “scaring” strategies that startle and drive birds away from fields. Tools like scarecrows, predator decoys, and loud noises can be effective in the short term, but over time and with repeated exposure, birds will become accustomed to and learn to ignore most of these devices. Pairing visual stimuli like decoys with auditory cues like predator noises or distress calls can increase the effectiveness of scaring deterrents (Tracey et al. 2007). Changing the types and locations of stimuli can also prevent birds from becoming habituated to any one technique.

It should be noted that using scaring techniques may increase crop damage, especially if they are used after birds have already formed the habit of foraging at a particular location. Birds may be temporarily startled but then return, resuming feeding activities in a different part of the field and spreading damage across a wider area. Species that pluck fruit like crows and starlings may be startled into dropping already picked fruit, but then return once the stimuli is gone to pluck more. Therefore, it is important to think carefully about the intended effect and timing when using scaring deterrents.

Timing of Scaring Deterrents

The effectiveness of scaring deterrents largely depends on the kind of bird being targeted and when scaring deterrents are deployed. Scaring techniques are most effective when birds encounter them before they have formed a habit of visiting a field to forage, usually before crops have reached peak ripeness. However, because birds may habituate to scaring techniques over time, these tools should not be deployed too early or they will be ineffective when it matters. Waiting until just before crops ripen or as soon as birds begin to show interest in a field can help ensure scaring techniques work as intended. Regularly scouting fields for signs of birds or bird intrusion will help determine when deterrents need to be implemented.

The migratory and foraging behavior of the targeted species can also greatly affect the effectiveness of scaring deterrents. Birds can be divided into two main categories: resident species that live in a region or specific location year-round, and migratory species that are only in a specific region or location for part of the year (Table 3.1). Many resident species have small territories which they actively defend, so only one or a few individuals occupy the space at a time. However, some residents like starlings are more nomadic, forming large flocks that move among different feeding locations across a wider landscape. Some migratory species hold small

territories for part of the year, while others may forage in large flocks at a specific location for a few days or weeks. Scaring techniques are more likely to be effective when used against nomadic residents that forage at different sites, or migrants that are passing through an unfamiliar area. Many resident species that hold territories have nowhere else to go once they are established at a specific location and are thus less likely to be scared off entirely. Identifying when migratory or nomadic species are likely to threaten crops can ensure scaring devices are in place in time to deter birds. Several types of scaring deterrents are described below, and a list of advantages, disadvantages, and cost estimates for the described methods is provided in Table 3.2.

Types of Scaring Deterrents

Reflective surfaces like mirrors, reflective tape, or CDs can be used directly in crop fields as well as in raptor and martin nest boxes to keep out unwanted species. Tape can be tied directly to trellises, stakes, or trees to protect crops by flapping and reflecting light, although care should be taken that trailing tape does not interfere with farm equipment or harvesting procedures. The density at which tape is positioned in the field is important; if gaps are left between taped areas, birds may simply reposition from taped rows or trees to non-taped ones (Conover & Dolbeer 1989, Gorenzel & Salmon 1992). While tape has been used to deter geese, doves, crows, blackbirds, and black-capped chickadees (Censky & Ficken 1982, Firake et al. 2016), not all birds are repelled by tape (Dolbeer et al. 1986) and those that are may quickly habituate (Summers and Hillman 1990). Likewise, while mirrors in nest boxes may deter some species, they are ineffective at keeping out others like starlings (Seamans et al. 2001). In fact, some birds, particularly those that are highly territorial, may confuse reflections of themselves with competitors and become aggressive towards mirrors instead of being repelled.

Table 3.1. Common problematic species and their residency status and foraging and nesting behavior.

Species	Residency	Dates in GA	Foraging Behavior	Nesting Behavior*
Canada goose	resident	year-round	Pairs or small flocks	
rock pigeon	resident	year-round	Large flocks	colonial cavity nester
American crow	resident	year-round	Small, nomadic flocks	
barn swallow	summer migrant	March to September	Large flocks	colonial cavity nester
European starling	resident	year-round	Large, nomadic flocks	colonial cavity nester
brown thrasher	resident	year-round	Individually or in pairs within territory	
northern mockingbird	resident	year-round	Individually or in pairs within territory	
American robin	resident	year-round; large flocks October and March	Small flocks year-round, but large, nomadic flocks often pass through areas in mid fall and early spring as individuals migrate to and from more northern states	
cedar waxwing	fall migrant	September to May	Large, nomadic flocks	
house sparrow	resident	year-round	Small or large flocks	cavity nester
house finch	resident	year-round	Small or large flocks	occasional cavity nester
red-winged blackbird	resident			
common grackle	resident	year-round; large flocks	Small flocks during spring and summer; large, nomadic flocks during fall and winter as individuals from more northern states take up winter residence	
brown-headed cowbird	resident	September to May		nest parasite
northern cardinal	resident	year-round	Individually or in pairs within territory	

*Nesting behavior can guide management plans—for example, cavity nesters can be dissuaded from nesting in buildings by physical barriers. This is not intended as an endorsement of any

manufacturer or product type, and effectiveness may vary based on geographic location, climate, weather, crop type, production practices, and other factors.

Decoys include tools like predator statues, scarecrows, hawk and falcon kites, and scare-eye balloons. Similar to reflective surfaces, decoys may be useful at repelling some species but not others. Predator decoys, for example, may actually attract blackbirds and crows as these species frequently engage in “mobbing” behavior towards hawks. Predator models can be placed on top of buildings or mounted to posts in fields. Some models are available that can move in the wind, which might be more effective than stationary models (Conover 1985). While scarecrows and predator decoys have been found to repel birds in the short-term, birds typically habituate after a few days (Conover 1979), so these must be moved regularly to remain effective. Hawk and falcon kites are kites printed or colored to look like predatory birds. They can either be tethered directly to a stake on a long line or flown underneath a helium balloon. Kites tethered beneath balloons may be more effective than those tethered to the ground; balloon-tethered kites were successful in reducing crop damage in both grapes and corn (Hothem and DeHaven 1982, Conover 1984). Scare-eye balloons, or more generally, scare-eye spots, mimic the reflective eyes of owls or other predators to deter birds. Balloons, similar to reflective tape, can be hung directly in crops and moved around as needed. Scare-eye balloons are only effective at short distances of 15-20 m (Fukuda et al. 2008), and birds may habituate after 1-2 weeks (Hickling 1995). The most effective decoys are those that are lifelike, involve movement (e.g., flapping, flying), change locations frequently, are paired with auditory cues, and are installed before birds have habituated to agricultural fields (Tracey et al. 2007).

Lasers include light-emitting devices like pointers and guns that can be flashed in fields or fired at perched or roosting birds. Lasers are most effective at dusk and dawn when ambient

light levels are low. Repeated targeting of roosting cormorants and crows by lasers has been reported to successfully clear roosts and buildings for a few hours or days (Bishop et al. 2003). Some species appear to be more sensitive to laser light than others; in one study, lasers were used to drive off geese, herons, cormorants, pelicans, and diving ducks, but were ineffective when fired at gulls, shorebirds, grebes, coots, or dabbling ducks (Gorenzel et al. 2010). Stationary devices that emit moving lasers in fields can drive birds away from fields, especially if alternative food sources are nearby (Brown and Brown 2021). While stationary devices may be more time- and cost-effective than using guns or pointers which often require user training, indiscriminate laser use can also drive away non-target birds.

Predator sounds like hawk screams and distress sounds of target birds can be used alone or in conjunction with visual scaring deterrents to increase their effectiveness (Berge et al. 2007). Bird vocalizations, just like human language, vary by situation and region. Birds have a wide range of sounds and calls they use to defend territory, communicate their location, warn of predators, and attract mates. Many devices preloaded with predator and distress noises are available and can be connected to speaker systems or mounted in-field and set to play at random intervals. Other recordings, including CDs and digital audio files, can also be used.

Alarm calls are used by birds to warn of nearby danger and are usually species-specific. Species that are gregarious and forage together, like blackbirds and grackles or titmice and chickadees may respond to each other's alarm calls. Using alarm calls of a specific targeted species might be more effective than distress or alarm calls of unrelated species as some birds ignore the vocalizations of others, especially if they are not known to forage or interact with each other regularly. Distress sounds are made by caught birds and are used to startle predators to try and escape rather than to warn of danger. Rather than being repelled by distress sounds, some

birds are attracted by distress noises to try and gather information about what types of danger are in the area (Conover 1994). Using alarm calls or distress sounds alone may not be very effective, as behavioral trials indicate birds may need to both hear an auditory cue and observe a threat visually to be deterred from a particular location (Griffin et al. 2010).

Predatory birds such as hawks and eagles also vocalize for much the same reasons other birds do. Predators do not tend to vocalize while hunting, so using predator sounds alone, may not be very effective at repelling birds as the sound alone may not indicate an immediate threat. Like predator decoys, birds more quickly to habituate to predator and distress noises if they are repetitive and sound frequently from the same location. Prior to implementing bird vocalizations as a deterrent strategy, growers should consider the bird species they need to target, the quality of the sound recording they are using, and the placement and orientation of broadcasting equipment. Additionally, pairing visual deterrents such as predator decoys with audio deterrents may increase efficacy of both deterrents.

Ultrasonic devices and sonic nets both use non-biological noise to deter birds. Ultrasonic devices use sounds at high frequencies to drive birds away, although there is limited evidence that ultrasonic devices work as intended. Although bird calls are often high-pitched, birds cannot actually hear at the ultrasonic range (>20 kHz; Beason 2004). Sonic net devices emit white noise, which makes it harder for birds to hear each other and disrupts communication. Because birds are unable to communicate, they may feel that they are in more danger from predation and leave the area. Sonic nets have been used to successfully deter starlings and blackbirds from fields (Mahjoub et al. 2015, Werrell et al. 2021) and grain storage (Woods et al. 2022), although some of these effects diminished after a few days. Both sonic net and ultrasonic devices can be mounted in-field on posts; commercially available devices are usually solar panel compatible.

Drones, either remote-controlled boats or unmanned aerial vehicles (UAVs), can be used to harass and drive off birds from fields, buildings, or bodies of water. Drones, especially when paired with auditory cues like predator noises or distress calls, can present a more realistic threat to birds than other scaring devices, but, as with other kinds of predator decoys, they may be more effective at deterring some bird species than others. Crows or birds of prey may attack UAVs that they perceive as threats or prey. RC boats were used in combination with dogs to successfully remove geese from waterways, although geese often returned when boats and dogs were no longer present (Holevinski et al. 2007). UAVs were successfully used to clear rock pigeons from buildings for short periods of time (Schiano et al. 2021) and reduced damage in vineyards from crows when paired with sounds and a crow effigy (Wang et al. 2020). Most drones require user training before use, although some systems have been designed with set flight paths in order to reduce the amount of user training required (Grimm et al. 2012).

Nest boxes can be placed in fields to attract local falcons and other raptors whose presence will deter smaller birds from fields. Kestrels, which breed in Georgia and readily take up take up residence in cavities, are common nest box species. Nest boxes are available commercially and can be mounted in fields on tall posts. The presence of falcons using nest boxes greatly reduced crop damage in vineyards and crop damage and fecal droppings in cherry orchards (Kross et al. 2011, Shave et al. 2018), although, depending on the season, falcon impact on other bird species may vary. In studies evaluating the use of falcon nest boxes in agricultural fields, kestrel presence in nest boxes successfully reduced crop damage in sweet cherry orchards but not in blueberries (Olivia Smith, *pers. comm.*). This may be because during the study, sweet cherries, but not blueberries, were ripening during the kestrel fledgling period (Figure 3.2). During this time, adult birds have to feed both themselves and their growing offspring and may

therefore be more actively hunting in the immediate vicinity. Therefore, the timing of crops and falcon fledgling period should be considered before relying entirely on nest boxes to manage birds. Nest boxes may be more effective for summer or year-round crops than those grown in other seasons. Nest boxes require at least annual cleaning and some year-round maintenance to keep out unwanted species like starlings and squirrels.

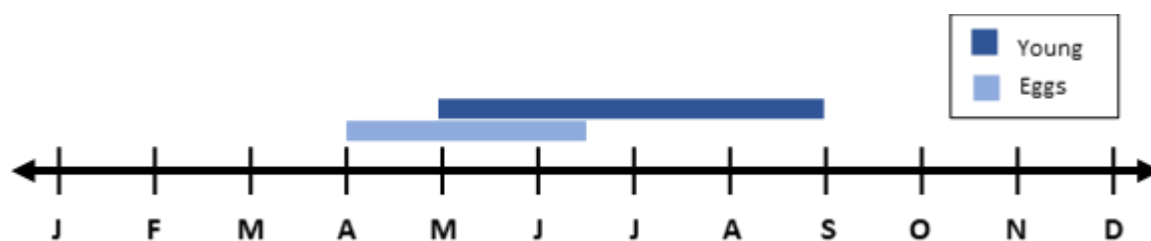


Figure 3.2. Egg-laying and fledgling period for kestrels (Birds of the World Online).

Trained falcons can be deployed periodically to chase and scare birds away from fields. Falconry as a deterrence method involves an expert handler letting a trained bird fly or hunt in a specific area. Falconry has been used to successfully deter birds from agricultural fields for several days during and after treatment (Navarro-Gonzalez & Jay-Russell 2016). While effective, this method is expensive and may be less practical for regular use in an agricultural environment.

Alternative Resources and Sacrificial/Lure Crops

Alternative resources for birds, such as nearby fields, bird feeders, or buildings can reduce the efficacy of scaring deterrents as birds may simply move to a nearby location and then return when they perceive the threat has passed. If the goal of deterrence is short-term

management of a particular field or building, alternative resources may not be a concern, but if long-term or farm-wide management is desired, identification and management of alternative resources should be considered. Early ripening crops, for example, may attract birds to an area before other crops start to produce. Delaying planting or harvesting early may help deter crop damage from birds.

Using lure or sacrificial crops, on the other hand, can enhance the effect of scaring deterrents as birds will move from the “scary” field to the safer and less threatening one (Knittle and Porter 1988). Lure and sacrificial crops may be costly and labor-intensive to use but can potentially save money in the long-term (Klosterman et al. 2013). Lure crops can be made more appealing to birds by reducing disturbances, selecting areas closer to roosts, and choosing crops that ripen slightly before or at the same time as non-lure produce (Owen 1977).

Physical Deterrents

Physical deterrents include tools like nets and spikes that prevent birds from roosting or foraging effectively. In most studies that compared the efficacy of various scaring deterrents with physical deterrents, physical deterrents were as good or better than scaring deterrents in preventing crop damage (Wang et al. 2020). The main considerations when using physical deterrents like netting and spikes are the price, installation time, and risk of physical contamination. Installing netting to protect grapes may be possible for a small vineyard, for example, but might become prohibitively expensive or time-consuming for larger fields. Physical contamination is also a serious concern, particularly if devices are installed in packinghouses or above produce processing or packing areas. Regular inspection and maintenance are important to ensure both continued effectiveness of and reduce the risk of contamination of produce or

equipment from physical deterrence devices. Additional information regarding advantages, disadvantages, and cost estimates for physical deterrents is provided in Table 3.2

Physical Deterrents in Agricultural Structures and Packinghouses

Many of the bird species that frequently forage in agricultural fields commonly or exclusively roost in buildings. Starlings, rock pigeons, house sparrows, and house finches often take up residence in rafters, ledges, or lofts of farm buildings and forage in nearby fields. Preventing birds from roosting or nesting in buildings can reduce damage to adjacent crops (Khidr & Yacoub 2021). Birds nesting in buildings can also be problematic because of food safety and property damage concerns. Birds perching or roosting in packinghouses or above food processing areas represent a significant food safety concern as feces and detritus from nests can drop down onto produce processing surfaces, equipment, and produce. Bird feces can contain harmful bacteria like *Salmonella* and *Campylobacter* that can contaminate produce and potentially cause illness in workers and consumers (Tizard 2004, Keller et al. 2011).

Types of Physical Deterrents

Netting can be placed around and over bushes, trees, trellises, and stakes to prevent birds from damaging crops. Netting or screens can also be installed in rafters and over grates and openings to prevent birds from roosting in or entering buildings and other farm structures. Netting is generally very effective at reducing crop damage by birds in fields (Bruggers & Ruelle 1982, Wang et al. 2020) and bales (McNamara et al. 2002). Birds will take advantage of any tears or rips that develop in netting during storms or strong winds, so frequent inspection and maintenance is required. Netting in fields also has the potential to interfere with farm equipment and may be cumbersome to remove before harvest. Netting is also useful for keeping birds like starlings from roosting in rafters (Medhanie et al. 2015), although sometimes birds will tear and

remove netting or screens, so regular inspection and maintenance is also required for netting used in buildings. Netting with larger holes is ineffective at deterring smaller species, so carefully consider bird size before purchasing. Materials like chicken wire or plastic might be appropriate for buildings, but may damage plants or fall apart due to exposure when used in the field.

Spikes and wires can be installed on or near ledges or rafters to keep birds from perching. Blunt metal or plastic spikes are available in different sizes and configurations and can be installed directly onto ledges. Larger sized spikes are ineffective at keeping smaller birds from roosting, so consider bird size when purchasing. Thin wires can also be installed parallel to ledges or beams to keep birds from perching, although, again, smaller birds may be able to perch between wires if they are spaced too far apart. Birds can sometimes pry off or break spikes, so regular inspection and maintenance is required, particularly if spikes are installed in packinghouses or above food processing areas.

Habitat modification or habitat removal can deprive birds of resources and make an area more inhospitable. Some birds like geese and starlings prefer to forage in short grass, so allowing grass to grow longer may deter them from foraging near crops (Brough & Bridgman 1980, Marateo et al. 2015). Birds are more likely to forage on the edges of fields than the center, so reconfiguring fields to increase the area to perimeter ratio could help reduce crop damage. Removing natural habitat around fields can actually increase crop damage and food safety concerns (Smith et al. 2020, Olimpi et al. 2022), as birds have less access to alternative food sources, perches, and roosts. Therefore, large-scale habitat modification or habitat removal is not generally a recommended bird management strategy in agroecosystems.

Table 3.2. Common scaring and physical deterrents and their price (\$USD), advantages, and disadvantages.

Deterrent	Price (\$USD)	Advantages	Disadvantages
<i>Scaring Deterrents</i>			
Reflective surfaces (e.g., mirrors, tape)	5-30	• Relatively inexpensive • Easy to install	• Not effective for some species • Potential to be caught in farm equipment
Decoys (e.g., hawk kites, statues)	10-200	• Relatively inexpensive • Easy to install	• Effects may be short-term • Only effective at short distances
Lasers	200-400	• Can be targeted towards specific species or individuals	• Expensive • May require user training • Effects may be short-term • Light nuisance
Predator/distress sounds	10-20 CDs 150-300 machine	• Can be targeted towards specific species • Can be broadcast over large areas	• Effects may be short-term • Noise nuisance
Ultrasonic devices	250-650	• Little maintenance	• Expensive • Limited evidence these work
Sonic nets	2500	• Little maintenance	• Expensive
Drones	500-5000	• Can be targeted towards specific species or individuals	• Expensive • Requires user training • Effects may be short-term
Nest boxes	50-100	• Little maintenance • Support bird conservation	• Effectiveness may vary with time of year
Trained falcons	1000-6000	• Very effective • Can be targeted towards specific species	• Expensive • Requires trained handler to supervise
<i>Physical Deterrents</i>			
Netting	50-500/ft	• Very effective	• Can be expensive and timely to install • Can interfere with farm operations
Spikes/wires	20-30/10 ft	• Prevents roosting and perching	• Risk of physical contamination • Can be expensive and timely to install • Risk of physical contamination

Conclusion

Managing wild birds on produce can be difficult and expensive, but by focusing management on particular pest species, growers can reduce the financial and labor costs. Management plans should be informed by the species and its timing and behavior. Growers may have to spend time initially monitoring their fields and making observations. When the time comes to use deterrence, growers may have to test several different strategies to find what works best for them. In the long term, however, this informed, species-specific approach will save growers time and money.

CHAPTER FOUR

OUTDOOR-ACCESS CHICKEN DIET VARIES WITH SEASON³

³ Varriano, S, K Solis, A Ryan, & WE Snyder. To be submitted to a peer-reviewed journal.

Abstract

Integrated crop-livestock systems have the potential to sequester biological control services into agroecosystems. Pastured chickens are known to eat pest insects and weeds, but, as generalists, they also consume beneficial natural predators, making their contributions to biological control unclear. We used a metabarcoding approach to characterize the arthropod and plant diet of pastured chickens during spring and fall from feces collected from 8 different farms. We identified 96 arthropod species and 157 plant species, including many common agricultural pests and natural enemies. Chicken arthropod diet was significantly affected by season, while plant diet was not significantly different between spring and fall. While taxonomic composition of diet varied across season, the functional composition—relative proportion of arthropod and plant pests and natural enemies—was consistent. Chicken diet diversity for both arthropods and plants was not significantly affected by season. Growers may be able to prescriptively pasture chickens in order to target specific agricultural pests at certain times of year.

Introduction

The push for more sustainable food production has led to a renewed interest in integrated crop-livestock production among growers and consumers. Integrating livestock with crops can reintroduce ecosystem services to agroecosystems, including increased soil fertility, nutrient cycling, and biological control (Xu et al. 2014, Soares et al. 2022). These services can subsequently reduce the amount of inputs like fertilizers and pesticides, providing financial as well as environmental gains to farms (Rocchi et al. 2019, Zhang et al. 2020).

Chickens are a popular choice for integration for several reasons, including egg production and smaller space requirements as compared to mammalian livestock (Hilimire 2011b). Pastured

chickens also consume many insect pests and weed seeds, providing important biological control, especially on organic farms (Glatz et al. 2005, Xu et al. 2014). For example, in grassland plots grazed by chickens, grasshopper populations were suppressed for the following five years (Sun et al. 2014). In dissections of chicken crop from individuals pastured in a potato-apple system, Clark & Gage (1996) found many insect pests and weed seeds, including Japanese beetles (*Popillia japonica*), flea beetles (Family:Chrysomelidae), and shield-backed bugs (Family:Scutelleridae).

However, chickens have also been observed eating beneficial arthropods, including many natural enemies like ground beetles (Family:Carabidae) and wolf spiders (Family:Lycosidae; Clark & Gage 1996). Some of these ground beetles, in addition to eating insect pests, may also be important predators of weed seeds (Bohan et al. 2011). This intraguild predation may ultimately outweigh the benefits of chicken grazing, causing an increase in the relative abundance of insect pests and weeds. For example, the introduction of a generalist, intraguild predator in a controlled agroecosystem disrupted herbivore control and led to an increase in herbivore populations (Snyder & Ives 2001). In a recent pastured chicken study, plots with chickens had a higher abundance of both natural enemies and known crop pests (Garcia et al. 2023). Therefore, it is unclear whether the sum impact of chicken grazing is beneficial to growers or not.

Here, we characterized pastured chicken diet across two different seasons by sequencing arthropod and plant DNA from chicken feces. We quantified the relative contributions of ecological guilds, including pests and predators, to chicken diet in order to assess the potential of pastured chickens to contribute to biological control.

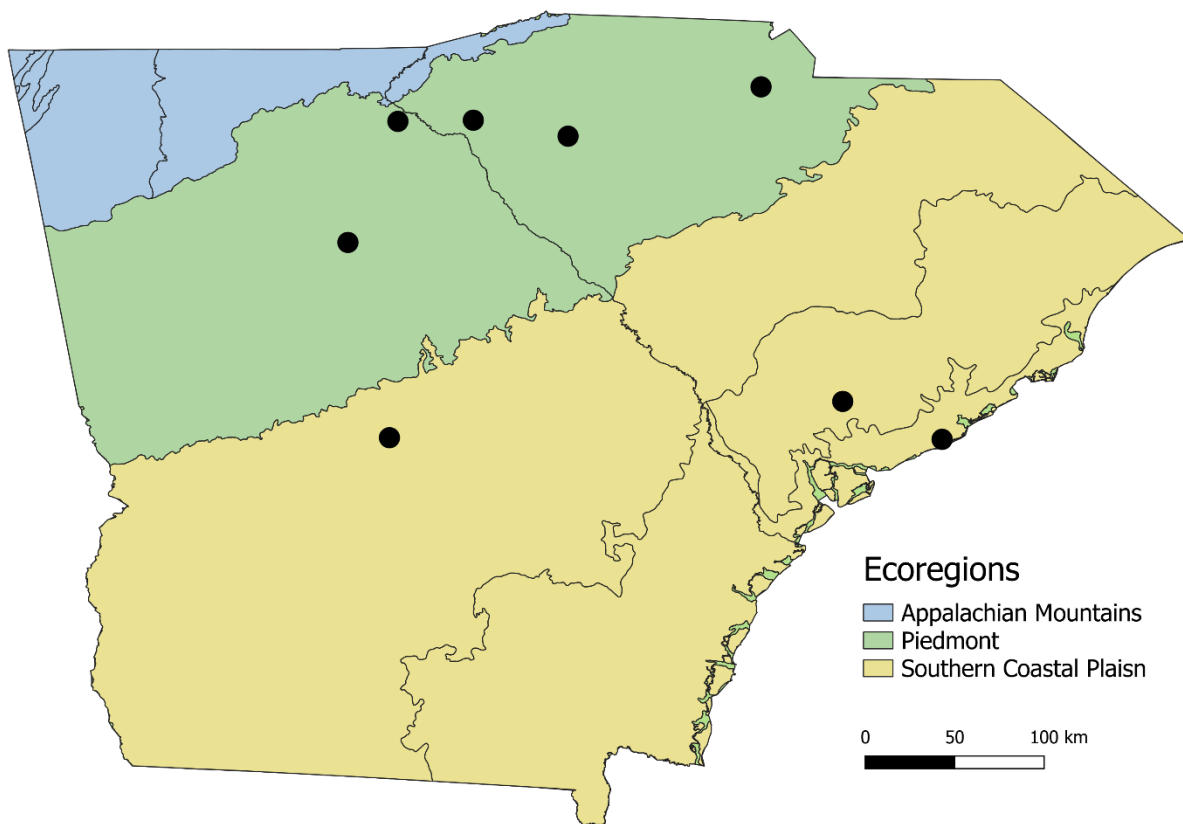


Figure 4.1. Map of eight sampled farms. Ecoregion is indicated by color (blue = Appalachian Mountains, green = Piedmont, yellow = Southern Coastal Plains).

Methods

Sample Collection

Fecal samples were collected from pastured chicken flocks from eight different organic, crop-livestock integrated farms across Georgia and South Carolina (Figure 4.1). All chickens had access to the outdoors for the majority of the day most days, but specific management styles varied. Four farms rotated chickens around pasture in tractor houses or moveable fences; three

farms housed chickens in stationary coops with outdoor runs; and one farms allowed chickens to roam freely around the farm area. Flock size, rotation frequency, and feed were recorded at each visit. Flock size (i.e., the number of chickens housed together at the time of collection) ranged from 2 to 300 chickens, with some farms having several smaller flocks of chickens of different breeds or ages (mean flock size = 62.8). Breed of chicken included Ameraucana, Australorp, Brahma, Dominique, Marans, Orpington and Rhode Island Red.

Samples were collected fall (October) and spring (March-April) from fall 2020 to spring 2022 for a total of four collection periods. A total of 10 fecal samples that appeared to be relatively freshly deposited, and that were widely dispersed in an attempt to reduce chances that multiple feces came from the same chicken, were collected at each farm between 7 and 11 am (total sample n = 450). Samples were preserved in 100% ethanol and immediately placed on ice for transport.

DNA Extraction, Amplification, and Sequencing

DNA extraction was performed following Zeale et al. (2010) with a bead-beating step added to aid lysis (Appendix 3). Four negative controls were extracted with the same reagents and protocol, but without any DNA added. Of the 320 samples collected, 83 (18.4%) were selected for diet analysis on the basis on DNA concentration, along with the four controls (total sample n = 87). All farms were represented in these 87 samples (Supplementary Table 4.1). DNA concentration was standardized to between 7-30 ng/μL, and 40 μL were sent to Novogene for amplification and sequencing. Two primer pairs, ZBJ-ArtF1c and ZBJ-ArtR2c (Zeale et al. 2010), and UniPlantF and UniPlantR (Moorhouse-Gann et al. 2018), were used to amplify arthropod and plant DNA, respectively, in each sample (Supplementary Table 4.2). DNA was sequenced by Novogene using Illumina NovaSeq Pe250 at 0.1 M raw reads per sample. Four

samples did not yield any arthropod DNA and were discarded from further arthropod analysis (Supplementary Table 4.1).

Sequence Processing and Taxonomic Assignment

Raw sequences were processed via the DADA2 pipeline. Arthropod sequences were first classified against a custom cytochrome c oxidase subunit 1 (CO1) database of sequences from the Barcode of Life Database (BOLD) library filtered to include only arthropod sequences and trimmed to the ZBJ product (O'Rourke et al. 2020, Robeson II et al. 2021) using the default cutoff of similarity > 0.7. Arthropod sequences were also compared against the BLAST nucleotide database and the sequence with the lowest e-score was selected. These two “most similar” IDs were compared against each other, and the lowest common taxonomy was selected. CO1 sequences associated with “non-diet” taxa were removed prior to analysis. Non-diet taxa included chickens (*Gallus gallus*), one species of flatworm common in soil (*Platydemus manokwari*), and several different soil bacteria. Plant sequences were assigned using a curated BLAST database, PlanITS (Banchi et al. 2020). Plant taxonomic ranks were then assigned based on % identity: 98% for species and genus, 96.5% for family, and 95% for order, following Alberdi et al. (2018), Azipurua et al. (2018), and Jarrett et al. (2020). All classification was performed in QIIME v2021.1.

Of the four negative controls, two did not yield any DNA; the other two were used to filter out potential contamination using the *decontam* package in R (Davis et al. 2017). Sequences with fewer than five reads across all samples were discarded in an attempt to account for secondary consumption. Residency of both plant and arthropod species was verified against previous records of that species in the study area (GBIF; BugGuide.net); if no records existed, the next highest taxonomy was assigned. All arthropod taxa were assigned a feeding guild:

predator, which encompassed both carnivorous arthropods and parasitoids; agricultural pests, which encompassed both herbivorous pests of crops and human and livestock pests; decomposers; and grain pests. When adult and larval diets differed, guild was assigned based on which life stage was most likely consumed, e.g., butterflies and moths (Order:Lepidoptera) were assigned as herbivores instead of nectar-feeders. Plants classified to species were likewise assigned as weeds, feed, i.e., plants present in chicken feed, grown in pasture, or provided by the grower as food scraps, or other, which encompassed native plants, trees, and ornamentals.

Statistical Analysis

Because arthropod and plant communities are large and contain many rare taxa, and because recovery of DNA from feces is often difficult due to partial digestion (Deagle et al. 2018), we calculated two different metrics based on sample prevalence to quantify chicken diet following Xiong et al. (2017). Percent frequency of occurrence in samples (%FC) was calculated as:

$$\%FC_i = \left(\frac{N_i}{N} \right) * 100$$

where N_i is the number of samples containing that food item and N was the total number of samples. Proportion of occurrence of a particular food item (%TX) was calculated as:

$$\%TX_i = \left(\frac{N_i}{\sum N_i} \right) * 100$$

Sequences were rarefied without replacement in QIIME. 70 of 79 arthropod samples and 77 of 83 plant samples were retained after rarefaction (Supplementary Table 4.1). An unweighted UniFrac distance matrix was generated from rarefied ASVs. We plotted a two-axis NMDS for both arthropod ($r^2 = 0.948$, stress = 0.22) and plant ($r^2 = 0.963$, stress = 0.19) samples. We used a PERMANOVA from the *adonis2* function in the R package *vegan* (permutations = 999, $\alpha = 0.05$; Oksanen et al. 2022) to examine the significance of season to variation in the distance matrix. Farm was used as the strata. To determine whether differences between seasons were due to dispersion within seasons or spatial separation between seasons, we also calculated the distance between samples to the spatial mean for each farm using the *betadisper* function from *vegan*. Finally, we calculated the phylogenetic diversity of each sample using the *pd* function from the R package *picante* (Kembel et al. 2010). All analysis was performed in R v4.4.3.

Results

We recovered 4,034 unique arthropod ASVs, which represented 88 species of insects, 4 species of spiders, and 4 of other arthropods (orders Trombidiformes, Diplopoda, Isopoda; Appendix 4). Millipedes (Order:Polydesmida), beetles (Order:Coleoptera), flies (Order:Diptera), moths and butterflies (Order:Lepidoptera), and isopods (Order:Isopoda) were identified in all 79 samples (Supplementary Figure 4.1). Chicken consumption of plants was likewise highly diversified. We recovered 35,310 unique plant ASVs, which represented 157 species of plants across 34 orders and 76 families (Appendix 5). Daisies (Family:Asteraceae), legumes (Family:Fabaceae), and grasses (Family:Poaceae) were identified in all 83 samples (Supplementary Figure 4.1).

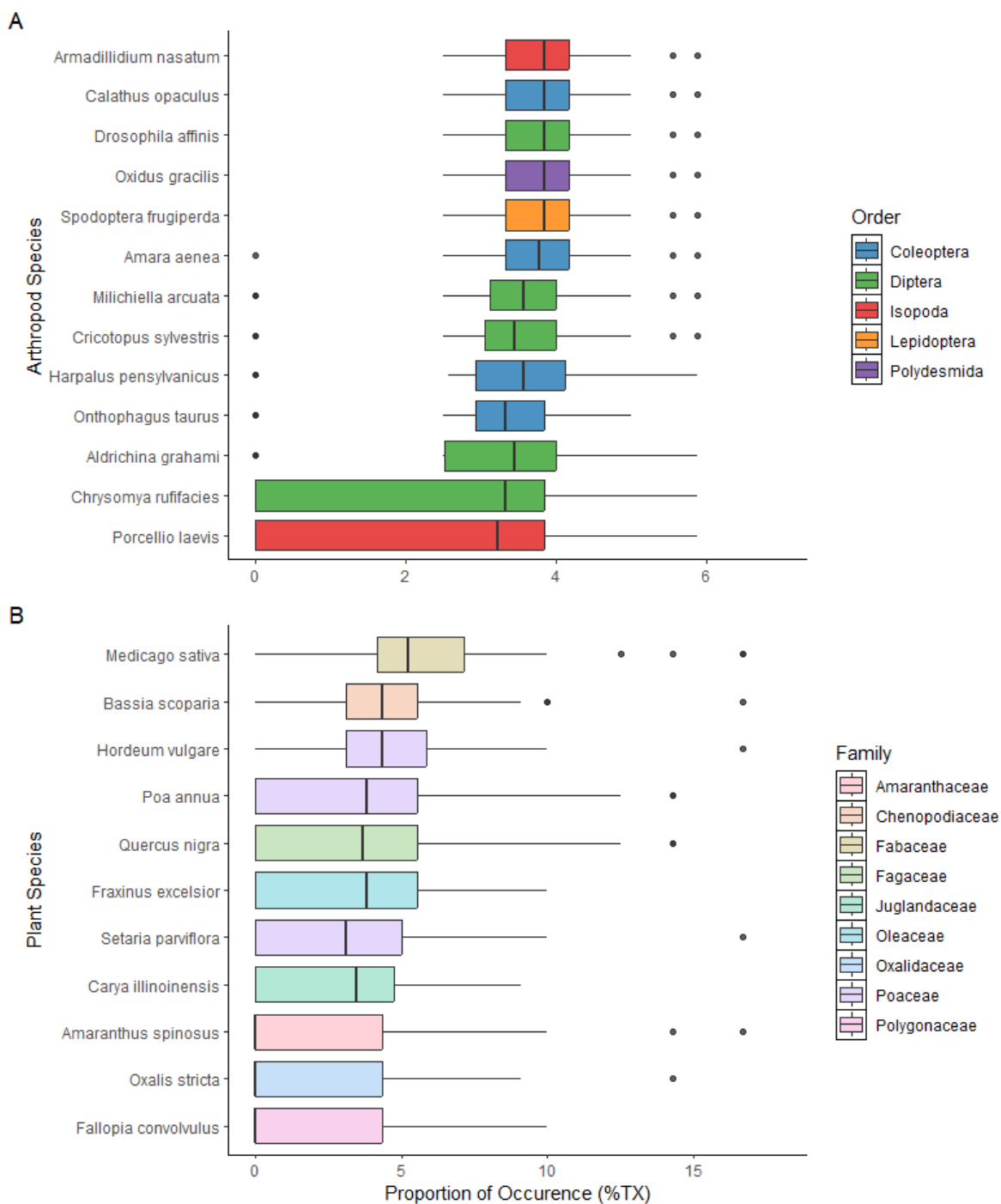


Figure 4.2. Proportion of occurrence (%TX) of (A) arthropod and (B) plant species in chicken diets. Boxes are colored by (A) order or (B) family. Only arthropod species with a %TX > 2.5% and plant species with %TX > 2% are shown.

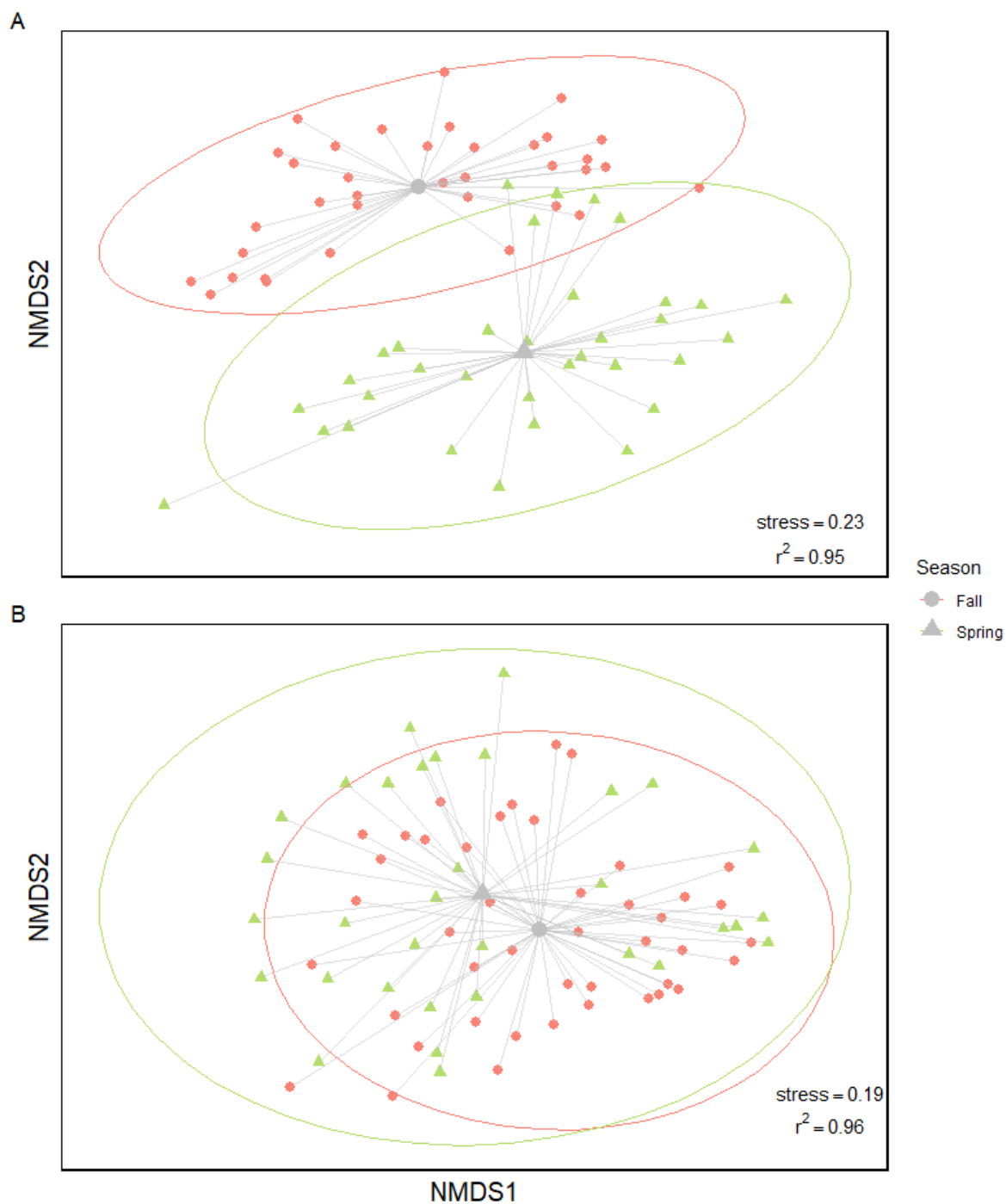


Figure 4.3. NMDS plot for (A) arthropods and (B) plants. Points represent samples. Orange circles are samples collected in fall, and green triangles are samples collected in spring. Gray shapes represent the centroids of each season.

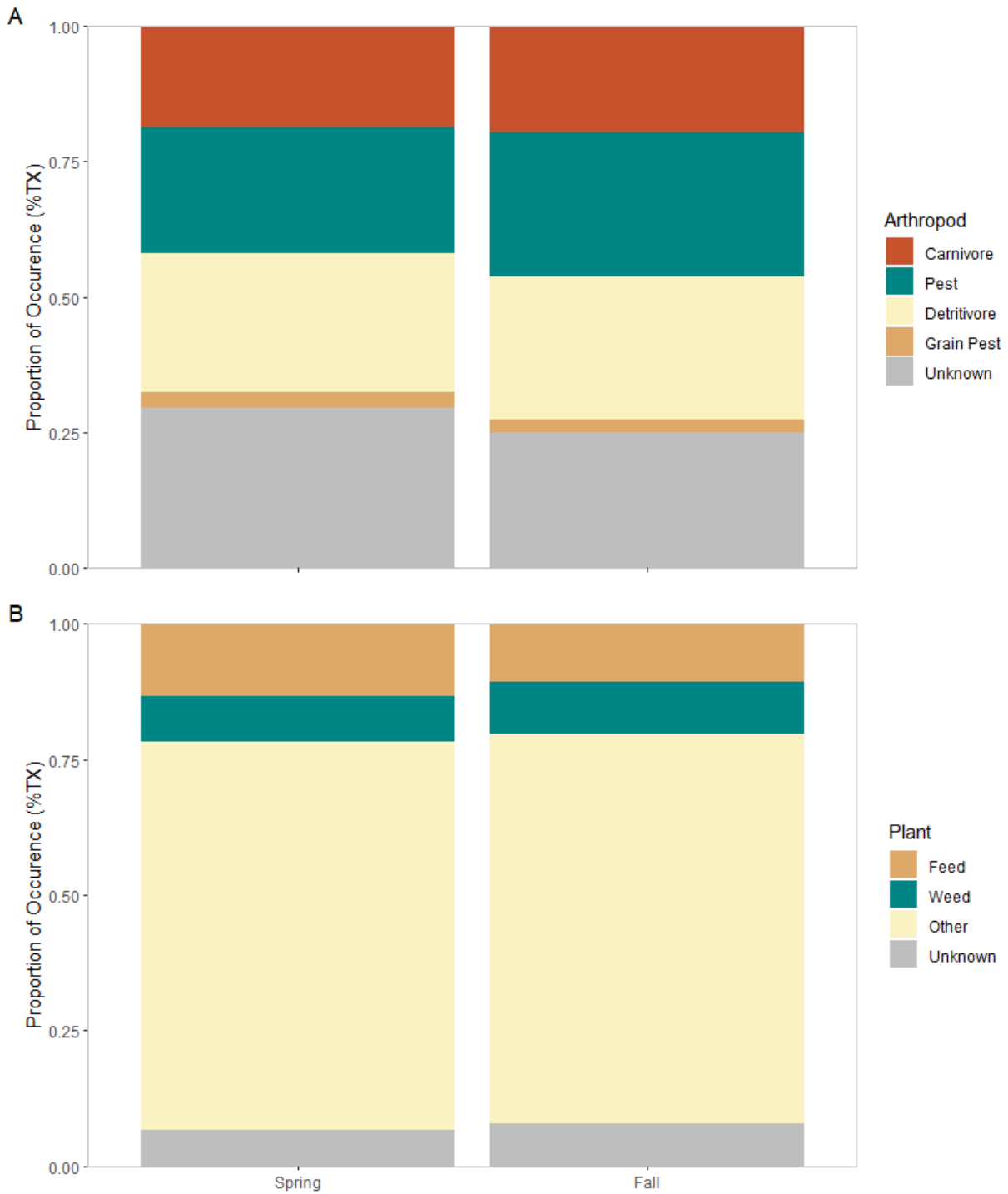


Figure 4.4. Proportion of occurrence (%TX) for (A) arthropod feeding guild and (B) plant ecological guild.

We found that chickens were heavily feeding on both agricultural pests and natural enemies. For example, the most abundant arthropods identified in chicken diets included fall armyworm (*Spodoptera frugiperda*), two different species of carnivorous ground beetle (*Calathus opaculus* and *Amara aenea*), and several agricultural weeds (*Bassia scoparia* and *Poa annua*; Figure 4.2). Importantly, many of the ground beetles upon which chickens were feeding, including *Amara aenea* and *Harpalus pensylvanicus*, are also known to be seed predators that can help control weeds. Individual chickens were also eating a wide variety of species; the average number of arthropod species we were able to identify in one sample was 27.2 (min = 17, max = 40), while the average number of detected plant species was 19 (min = 6, max = 36).

Chicken arthropod diet varied significantly between spring and fall ($p = 0.002$; Figure 4.3). The mean phylogenetic diversity of chicken arthropod diet was not significantly different between spring and fall ($p = 0.41$; Supplementary Figure 4.2). The mean distance between arthropod samples and the spatial mean of each farm was also not significantly different between spring and fall ($p = 0.29$; Supplementary Figure 4.3). This indicates that, while phylogenetic and taxonomic diversity did not differ in terms of chicken arthropod diet between seasons, chickens were eating different taxa in spring than fall. In terms of chicken plant diet, there was not significant difference between samples collected in spring and fall ($p = 1.04$).

The relative proportion of arthropod feeding guilds in chicken diet was consistent across season (Figure 4.4). Decomposers made up roughly 25% of chicken diet, followed by herbivores (24.5%), predators (19%) and grain pests (2.6%). Likewise, the relative proportion of plant guilds did not change with season: plants classified as “other” made up the vast majority of diet (71%), followed by weeds (11.5%) and feed (9%).

Discussion

Here we present the first molecular diet analysis of pastured chickens. We found a surprising diversity of both arthropods and plants in chicken diet, although some taxa were eaten by almost every individual, including beetles, flies, grasses, and legumes (Supplementary Figure 4.1). Comparing our results to the only other comprehensive diet analysis of pastured chickens (Clark & Gage 1996), we found a much higher frequency of moths and butterflies, millipedes, and isopods in chicken diet. Weeds were also identified at a much higher rate. In a similar metabarcoding study of wild farmland bird diet in Spain, Cabodevilla et al. (2021) found very different relative contributions of arthropod orders to game bird diet: proturans and springtails (Class:Ellipura) were found at a much higher frequency, and moths and caterpillars were almost entirely absent. These birds were presumably foraging in cereal, rather than vegetable, crops, and so may not have had access to the same types of arthropods that the chickens in this study did. Regardless, previous work may have underestimated the contributions to biological control that pastured chickens provide.

We found that season significantly affected chicken arthropod diet but not plant diet. Chicken arthropod diet diversity, both phylogenetically and taxonomically, was not significantly affected by season. That is, chickens were not eating a significantly wider variety of arthropods individually, or significantly more different arthropods from each other, in one season compared to the other. Rather, chicken arthropod diet in the spring simply consisted of different taxa than chicken arthropod diet in the fall. This difference may reflect the availability of prey between seasons. In similar metabarcoding studies, season was found to significantly impact diet in both gamebirds (Cabodevilla et al. 2021) and geese (*Anseranas semipalmata*; Corriveau et al. 2022), although neither of these studies compared diversity indices or diet breadth between seasons.

Despite this difference between chicken arthropod diet in spring and fall, we found that ecological guilds of both arthropods and plants contributed to chicken diet relatively consistently. That is, chickens consistently ate the same proportion of predator, pest, and decomposer arthropods, and weeds, feed, and other kinds of plants. This result is in contrast to Clark & Gage (1996), who found that chickens in a potato-apple system ate fewer carnivores and more herbivores in July compared to June. However, these results were confounded by the grazing of geese prior to chicken grazing, which greatly reduced weed density and subsequently suitable habitat for carnivores like ground beetles. The results from our study suggest that chickens, because they are such wide generalists, and because they are exponentially bigger than the arthropods and seeds upon which they feed, have a consistent impact on weed and arthropod communities despite changes in the potential availability of diet items.

The relative contribution of feed to chicken diet—around 9%—was very surprising to us and deserves some explanation. We assigned ecological guild to taxa only when we could be sure of the niche it occupied. There were many grasses (Family:Poaceae), legumes (Family:Fabaceae), and other families of plants that we were not able to confidently assign to a guild, even though many of these sequences could and probably did correspond to feed plants. Nevertheless, the wide diversity of weeds and other plants we were able to identify suggest that chickens forage more widely than previously thought.

Previous studies have found that chickens can suppress pest insects like grasshoppers in pasture and grassland systems (Sun et al. 2014, Xu et al. 2014), although their ability to control other arthropods and weeds in agroecosystems is more variable (Clark & Gage 1996, Pederson et al. 2004, Bosshardt et al. 2024). This first assessment of chicken potential as biological control on mixed-crop vegetable farms indicates chickens may be useful biocontrol agents, particularly

for organic growers, based on the diversity and abundance of pest arthropods and weeds we identified. It is important to note that in this study we only considered the arthropods and plants upon which chickens were feeding. Other chicken activity like scratching, defecation, and plant removal that have been recorded in other studies (Fukumoto & Replotle 1999, Gait et al. 2021) can also have a significant impact on pests and natural enemies. For example, Garcia et al. (2023) found that pastured chickens significantly reduced cover crop biomass, leading to a significant reduction in plant-dwelling arthropods but an increase in ground-dwelling arthropods. These indirect effects of chicken activity on arthropod and plant communities could have large implications for biological control potential outside of direct feeding on pests and natural enemies.

Previous ecosystem service assessments of integrated crop-chicken systems have focused on benefits like soil fertility, nutrient cycling, and carbon sequestration (Sanderson et al. 2013, Lemiare et al. 2014). However, we propose that biocontrol services provided by chickens could significantly influence agroecosystems, particularly for small and organic farmers. Most other studies evaluating chicken biological control potential have considered either grassland or agroforestry systems (Pederson et al. 2004, Glatz et al. 2005, Sun et al. 2014, Xu et al. 2014, but see Garcia et al. 2023). Further studies should consider the impact of chickens on pest arthropods and weeds on row crop and vegetable farms.

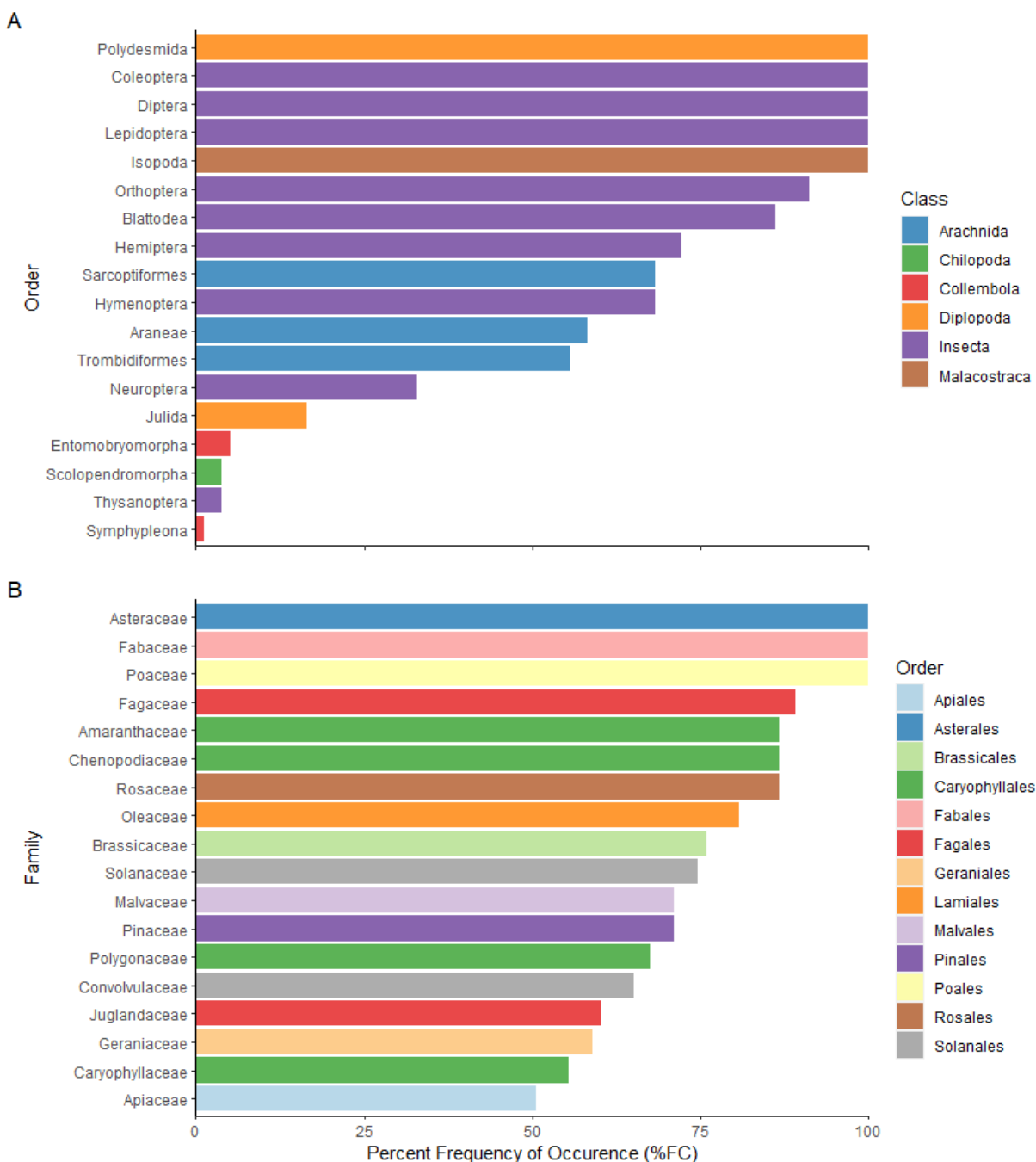
Supplementary Material

Supplementary Table 4.1. Sample metadata for chicken feces.

Sample Category	# Total Samples	# Arthropod Samples	# Plant Rarefied Samples	# Arthropod Rarefied Samples
Season – Fall	47	45	44	46
Season – Spring	36	34	33	34
Farm – Farm 1	14	14	14	14
Farm – Farm 2	9	8	9	8
Farm – Farm 3	8	6	7	6
Farm – Farm 4	16	15	15	11
Farm – Farm 5	14	14	12	13
Farm – Farm 6	5	5	3	2
Farm – Farm 7	10	10	10	10
Farm – Farm 8	7	7	7	6
Total	83	79	77	70

Supplementary Table 4.2. Primer sequences used to amplify arthropod (ZBJ) and plant (UniPlant) DNA.

Primer	Sequence	Reference
ZBJ-ArtF1c	AGATATTGGAACWTTATATTTTATTTTGG	Zeale et al. 2010
ZBJ-ArtR2c	WACTAATCAATTWCCAAATCCTCC	Zeale et al. 2010
UniPlantF	TGTGAATTGCARRATYCMG	Moorhouse-Gann et al. 2018
UniPlantR	CCCGHYTGAYYTGRGGTDCD	Moorhouse-Gann et al. 2018



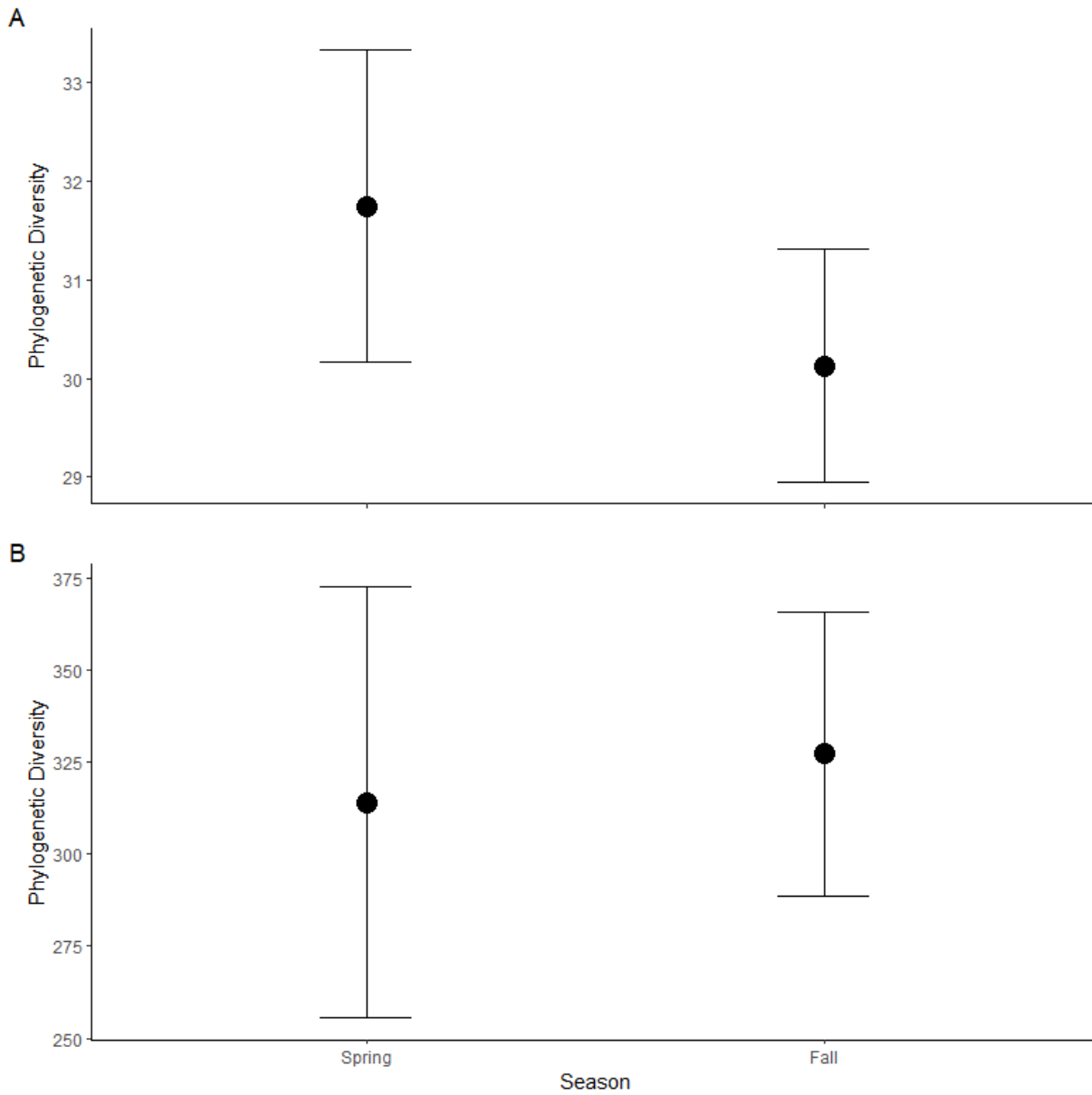
Supplementary Figure 4.1. Percent frequency (%FC) of occurrence of arthropod orders (A) and plant families (B). Bar color corresponds to arthropod class and plant order. Only plant families present in more than 50% of samples are shown.

Supplementary Table 4.3. Adonis table for arthropod samples.

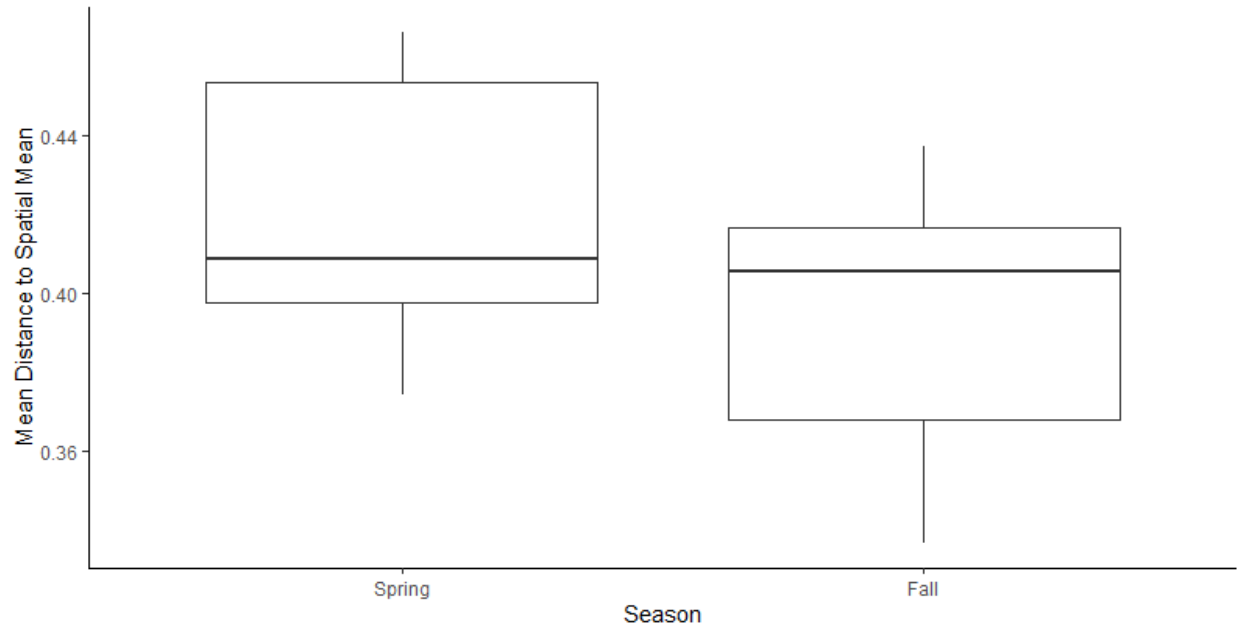
	df	Sum of Squares	r ²	F	p
Season	1	1.51	0.10	7.37	0.001
Residual	68	13.97	0.90		
Total	69	15.49	1		

Supplementary Table 4.4. Adonis table for plant samples.

	df	Sum of Squares	r ²	F	p
Season	1	0.67	0.02	1.66	0.104
Residual	75	30.10	0.98		
Total	76	30.77	1		



Supplementary Figure 4.2. Mean phylogenetic diversity for each sample $\pm$ SE for spring (left) and fall (right) for (A) arthropods and (B) plants.



Supplementary Figure 4.3. The mean distance from each sample to the spatial mean of the farm from which it came, averaged for spring (left) and fall (right).

CHAPTER FIVE

FLIES COULD INCREASE FOOD SAFETY RISKS OF OUTDOOR-ACCESS CHICKENS
ON FARMS⁴

⁴ Varriano, S, K Solis, PAP Rodrigues, NW Shariat, & WE Snyder.
To be submitted to a peer-reviewed journal.

Abstract

Integrated crop-livestock farms have the potential to restore ecosystem services to agroecosystems, but may also harbor unique food safety risks. Pastured chickens may be exposed to a greater diversity and prevalence of food-borne bacteria like *Campylobacter* in the environment, and these bacteria may be transmitted from chickens to on-farm crops. We assessed the prevalence of *Campylobacter* and *Salmonella* in chicken feces collected from eight crop-livestock farms across spring, summer, and fall for two years. *Campylobacter* was detected in 37.1% of samples, and *Salmonella* was detected in 5.8% of samples. Season did not have a significant effect on bacterial prevalence, but increased temperature and humidity were associated with a higher *Campylobacter* prevalence. We also found a positive correlation between plant diet breadth and the richness of fly species and *Campylobacter* prevalence. Overall, chickens in our study had a relatively low prevalence of *Campylobacter* and *Salmonella* in their feces, but their ability to forage freely may increase their risk of encountering foodborne bacteria. Growers on integrated crop-livestock farms could potentially manage bacterial vectors, rather than change chicken management, to reduce food safety risks.

Introduction

Integrated crop-livestock farms have the potential to restore ecosystem services like nutrient cycling, biological control, and carbon sequestration to agroecosystems (Hilimire 2011a, Tully & Ryals 2017). However, producing crops and livestock jointly or within the same farm can also increase food safety risks (Wadamori et al. 2017). Foodborne bacteria like *Campylobacter* and *E. coli* can persist in manure or soil and be transmitted to produce (Loncarevic et al. 2005, Jäderlund et al. 2011). Further, vectors like houseflies can potentially

transmit bacteria from livestock to crops (Salaheen et al. 2015, Nayduch et al. 2023). For example, Talley et al. (2009) detected *E. coli* in 61% of filth flies (Muscidae and Calliphoridae) caught in produce fields adjacent to pasture.

Potential insect vectors have been particularly studied in relation to chicken production. Hald et al. (2004) detected *Campylobacter* in 70.2% of flies caught entering and leaving broiler houses. Buyukyavuz et al. (2024) found that flies carried *Salmonella* from chicken houses up to 100 m away. Insects may also serve as sources of bacterial contamination of poultry. For example, Bates et al. (2004) found that darkling beetles (*Alphitobius diaperinus*) and chickens shared the same *Campylobacter* subtypes, indicating transmission between species.

Chickens that have access to the outdoors may also encounter bacteria from other environmental reservoirs, including contaminated water and soil (Rivoal et al. 2005). Further, weather effects like high winds and temperatures can increase survival and transmission of bacteria in outdoor flocks (Hwang et al. 2020, Smith et al. 2023). Multiple studies have found higher rates of *Campylobacter* in chickens in organic and alternative production systems as compared to those in conventional systems, citing the increased risk of bacterial contamination of outdoor-access chickens as a cause (Avrain et al. 2003, Overbeke et al. 2006, Heuer et al. 2008).

In this study, we collected chicken feces across three different seasons from eight different crop-livestock integrated farms to evaluate the prevalence of *Salmonella* and *Campylobacter*. Further, we tested for associations between *Campylobacter* prevalence in feces and weather effects and flock size of chickens. Finally, we connected bacterial prevalence data with chicken diet data detailed in Varriano et al. (2025) to evaluate whether chicken foraging behavior and abundance of flies and other decomposers increased food safety risks.

Methods

Sample Collection and DNA Extraction

Sample collection and extraction methods are detailed in Varriano et al. (2025). Briefly, 10 fecal samples were collected from each of eight organic, crop-livestock integrated farms across Georgia and South Carolina every summer (August), fall (October), and spring (March-April) from summer 2020 to spring 2022, for a total of 450 samples. Average flock size on these farms was 66 (minimum = 2, maximum = 300). DNA extraction was performed following the protocol of Zeale et al. (2010).

Bacterial PCRs

We tested for the presence of the 23S gene in *Campylobacter* spp., the *hipO* gene from *C. jejuni*, and the *glyA* gene from *C. coli* using a multiplex PCR reaction (Wang et al. 2002). Each reaction contained 2.5 μ L 10x reaction buffer, 200 μ M dNTPs, 2 mM $MgCl_2$, 2 μ M 23S primers, 2.5 μ M *C. jejuni* primers, 5 μ M *C. coli* primers, 1.25 U *Taq* polymerase, and 1 μ L DNA. Sterile water was added until the final reaction volume was 25 μ L. Amplification occurred with the following cycle: denaturation at 95°C for 6 minutes; 40 cycles of amplification (95°C for 30 sec, 56°C for 30 sec, 72°C 30 sec); and a final extension at 72°C for 7 minutes. Products were visualized on a 2% agarose gel.

Prior to *Salmonella* screening, we tested for the presence of PCR inhibitors using an internal amplification control (IAC; Rosenstraus et al. 1998). The IAC sequence was (5'-AGTTGCAGTGTAACCGTCATGTACCAGTAATCTGCGTCGCACGTGTGCACCTAGTCTAATCACTTATGACTCAGATAACTTAACAGCAGAGTCTCGTCGA-3'). Each reaction contained 4 μ L 10x reaction buffer, 12.5 μ M dNTPs, 1.25 μ M IAC, 5 μ M IAC primers, 1 U *Taq* polymerase, and 2 μ L DNA. Sterile water was added until the final reaction volume was 40 μ L.

The cycle conditions were: denaturation at 95°C for 2 minutes; 20 cycles of amplification (94°C for 30 sec, 66°C for 30 sec, 72°C for 30 sec); extension at 94°C for 30 seconds and then 56°C for 30 seconds. There was some evidence of inhibition, so a 1:100 dilution of DNA to sterile water was used for subsequent *Salmonella* PCRs.

We tested for the presence of the *invA* gene from *Salmonella* (Rahn et al. 1992). Each reaction contained 2.5 µL 10x reaction buffer, 30 µM dNTPs, 1 µg/µL bovine serum albumin (BSA), 8 µM *invA* primers, 0.06 U *Taq* polymerase, and 3 µL DNA. Sterile water was added until the final reaction volume was 25 µL. The cycle conditions were: denaturation at 95°C for 3 minutes; 40 cycles of amplification (95°C for 30 secs, 64°C for 30 secs, 72°C for 30 secs); extension at 72°C for 2 minutes. Products were visualized on a 1.5% agarose gel.

DNA Sequencing, Processing, and Taxonomic Assignment

Sequencing, processing, and taxonomic assignment are detailed in Varriano et al. (2025). We selected 85 samples from spring and fall on the basis of DNA concentration to undergo sequencing; all farms were represented in these 85 samples. Arthropod DNA was amplified with the primer pair ZBJ-ArtF1c and ZBJ-ArtR2c (Zeale et al. 2010) while plant DNA was amplified using UniPlantF and UniPlantR (Moorhouse-Gann et al. 2018). PCR products were sequenced by Novogene using Illumina NovaSeq Pe250 at 0.1 M raw reads per sample. Raw sequences were processed via the DADA2 pipeline.

Arthropod sequences were assigned taxonomy in QIIME v2021.1 using the BLAST database and a custom CO1 database from the BOLD library (O'Rourke et al. 2020, Robeson II et al. 2021) using the default cutoff of similarity > 0.7. Plant sequences were assigned using the curated BLAST database PlanITS (Banchi et al. 2020) with taxonomic ranks assigned using %

identity cut-offs (Alberdi et al. 2018, Azipurua et al. 2018, Jarrett et al. 2020). All arthropods classified to species were assigned a feeding guild: predator, pest, grain pest, and decomposer.

Weather and Management Effects on Bacterial Prevalence

Mean temperature, precipitation, wind speed, and humidity were collected from the nearest weather station for each collection date and the preceding six (7 days total; Weather Underground). We chose these variables based on similar past studies that have found correlations between these variables and bacterial prevalence in pastured poultry (Hwang et al. 2020, Smith et al. 2023). We tested the association between these weather variables, flock size, and *Campylobacter* prevalence in a series of binomial generalized linear mixed models (GLMMs) using the R package *glmmTMB* (Brooks et al. 2017). All single, additive, and interactive models were tested using the function *dredge* from the package *MuMIn* (v1.47.5, Bartón 2023). Because the number of samples testing positive for *Salmonella* was so low, we only included total *Campylobacter* prevalence in our analysis. Farm visit was included as a random effect nested within farm in all models; year was included as a fixed effect in all models. Continuous variables were standardized prior to analysis using a z-transformation. We assessed multicollinearity using the *performance* package (Lüdtke et al. 2021). Models were compared using AIC_c; top-performing models were considered as those with $\Delta AIC_c \leq 2$ (Burnham & Anderson 2002). Top models were averaged with zero-biasing using the *model.avg* function from the package *MuMIn*.

Diet Effects on Bacterial Prevalence

For the subset of fecal samples which we sequenced for diet items (n = 85), we ran a series of binomial GLMMs evaluating the effects of the weather and flock size appearing in our top models above and four different diet diversity and composition factors that might have

affected bacterial transmission—the phylogenetic diversity of arthropods and plants; the relative proportion of abundance of decomposers; and the family richness of flies (Order:Diptera; Supplementary Table 5.1). Before calculating diversity indices, sequences were rarefied without replacement in QIIME, resulting in 67 samples retained after rarefaction that included both arthropod and plant diet indices.

We tested all single, additive, and interactive models using the same *dredge* function from *MuMIn*. We used the same random effect (farm visit nested within farm) and in all models, with year included as a fixed effect in all models and continuous variables standardized using the same z-transformation. We assessed multicollinearity using the *performance* package (Lüdtke et al. 2021); models not meeting assumptions were excluded from further analysis. Models were compared using AIC_c; top-performing models were considered as those with $\Delta\text{AIC}_c \leq 2$ and $\Delta\text{AIC}_c >$ the null model (Burnham & Anderson 2002). Top models were averaged with zero-biasing using the *model.avg* function from the package *MuMIn*.

Results

Bacterial Prevalence

Total *Campylobacter* prevalence across all samples was 37.1% (167/450). Mean prevalence within a collection period was consistently lower in the spring (23.57% in 2021 and 25.71% in 2022) than in summer or fall, although there was not a significant difference in *Campylobacter* prevalence across season ($p = 0.09$; Figure 5.1). *C. coli* and *C. jejuni* prevalence was 18.2% (82/450) and 12% (54/450) across all samples, respectively. Total *Salmonella* prevalence across all samples was 5.8% (26/450).

Weather and Flock Size Effects on Bacterial Prevalence

There were four top models that associated *Campylobacter* prevalence with weather

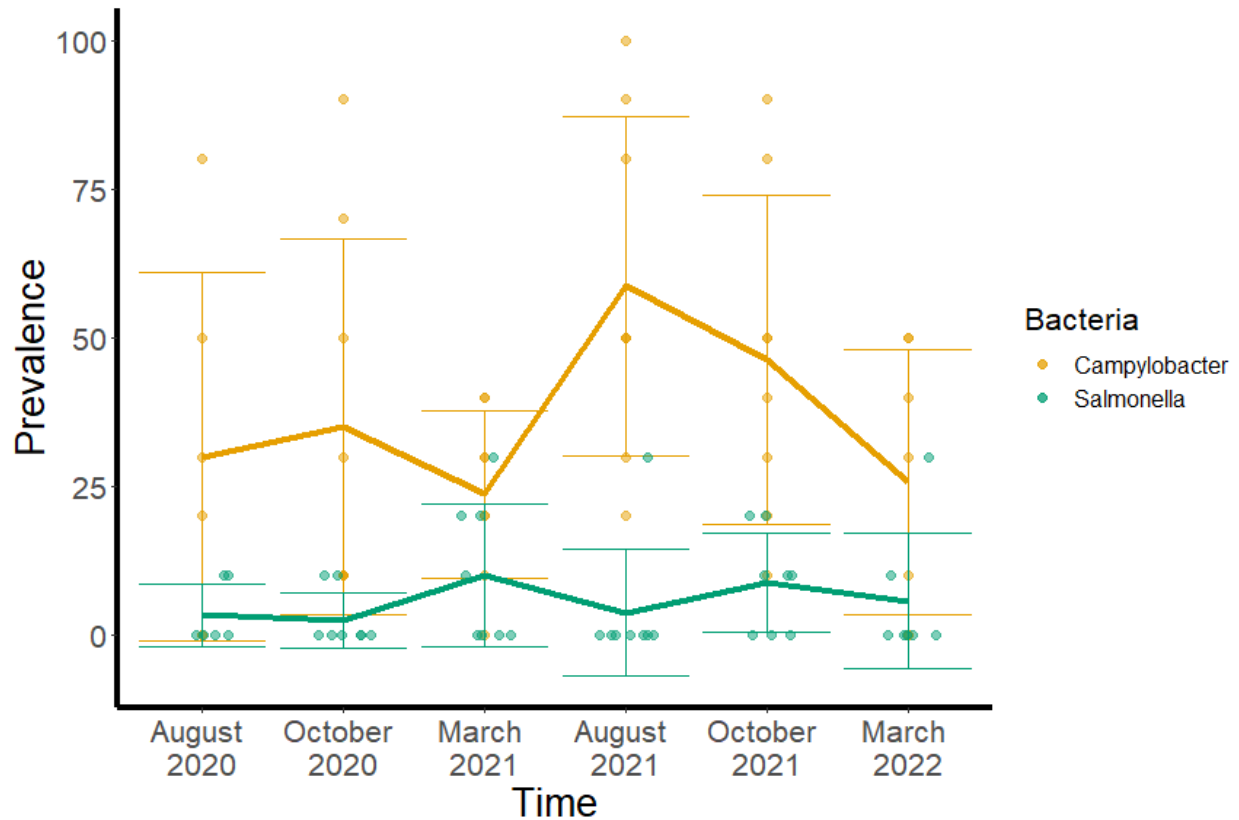


Figure 5.1. Prevalence of total *Campylobacter* (gold) and *Salmonella* (green) for each collection period from August 2020 to March 2022. Bold lines indicate the mean prevalence values for each collection period; thin lines represent standard deviation.

effects and flock size. Temperature was a factor in 3/4 (75%) models, and humidity was a factor in 2/4 (50%) models. As temperature ($\beta = 0.24 \pm 0.53$) and humidity ($\beta = 0.22 \pm 0.51$) increased, so did the prevalence of total *Campylobacter* (Figure 5.2). The number of individuals in a flock was negatively associated with *Campylobacter* prevalence (Supplementary Table 5.3). We did not find a relationship between wind speed or precipitation and *Campylobacter* prevalence.

Diet Effects on Bacterial Prevalence

There were four top models that associated *Campylobacter* prevalence with diet and other effects. Temperature was present in all four models, while the phylogenetic diversity of chicken plant diet and the number of dipteran families were present in two of these models. As the phylogenetic diversity of plants ($\beta = 0.24 \pm 0.35$) and number of dipteran families ($\beta = 0.30 \pm 37$) increased, so did the prevalence of total *Campylobacter* (Figure 5.3). Likewise, as temperature increased ($\beta = 1.33 \pm 0.69$), so did *Campylobacter* prevalence.

Discussion

We found an overall prevalence of 37.1% of *Campylobacter* in our study. These rates are comparable to previous studies evaluating *Campylobacter* prevalence in outdoor-access flocks: Smith et al. (2023) recorded a *Campylobacter* prevalence of 26% from pastured chicken feces in the western US; Robino et al. (2013) a rate of 18.3% from rural farms in Italy, Carrique-Mas et al. (2013) a rate of 31.9% from backyard chickens in Vietnam, and Xu et al. (2021) a rate of 61.1% from pastured chicken feces in the southeastern US. We found that *C. coli* was more prevalent in our samples than *C. jejuni*. Rossler et al. (2019) found that hens were more likely overall to carry *C. jejuni* than *C. coli*, although several experimental studies of chickens in pastured or free-range systems have reported higher rates of *C. coli* than *C. jejuni* (Colles et al. 2008, Esteban et al. 2008). We found that 5.8% of our samples contained *Salmonella*. This is comparable to other studies, although *Salmonella* rates in chickens raised in organic or alternative systems seem to vary widely, even in the same Southeast region. For example, Alali et al. (2010) reported a *Salmonella* prevalence of 5.6% from chicken feces in North Carolina,

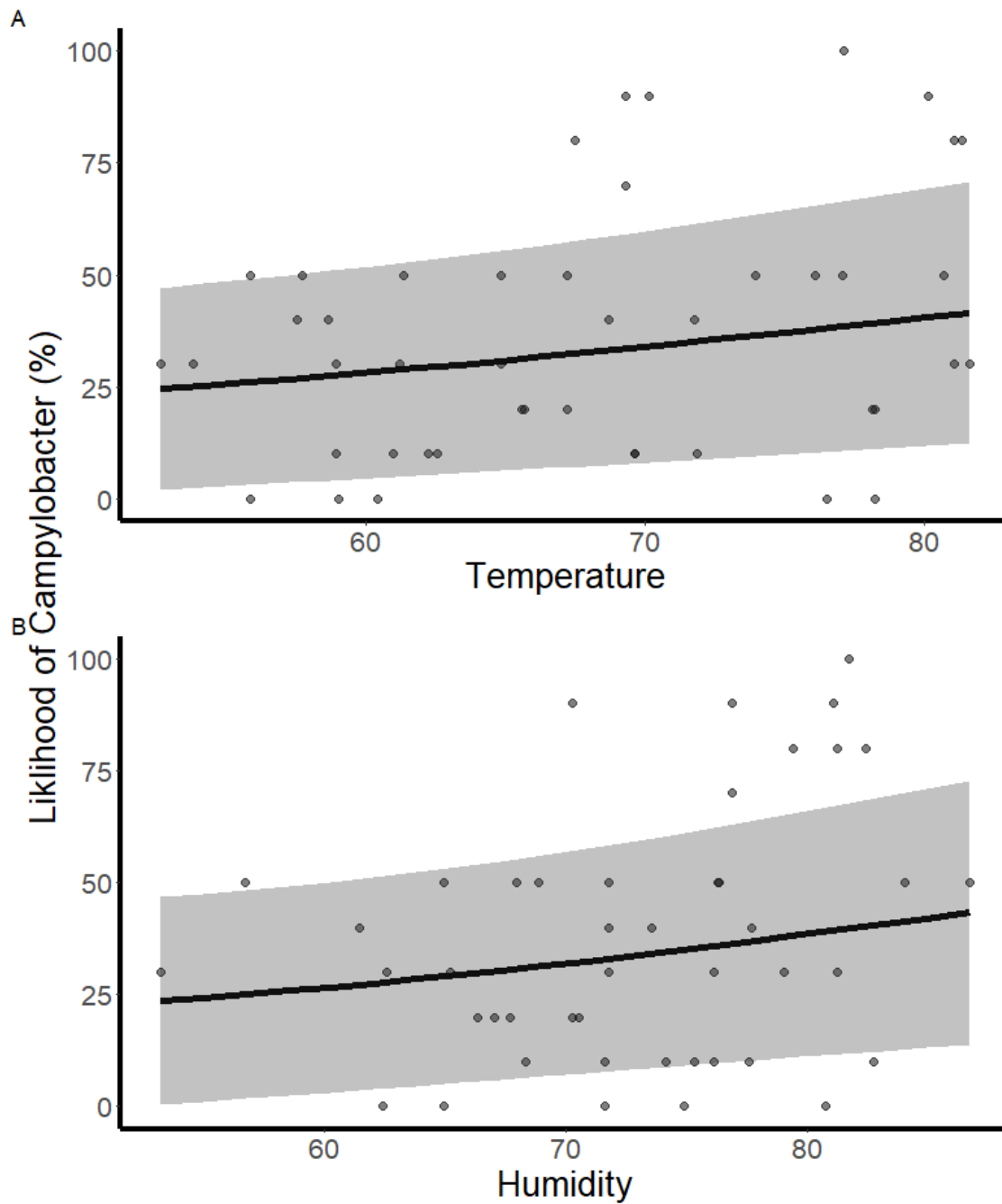


Figure 5.2. The relationship between the likelihood of *Campylobacter* in a sample, humidity (A) and temperature (B). Lines represent values averaged from top models with zero-biasing. Ribbons represent 95% confidence intervals. Dots represent prevalence of *Campylobacter* per farm per visit. (Supplementary Table 5.3).

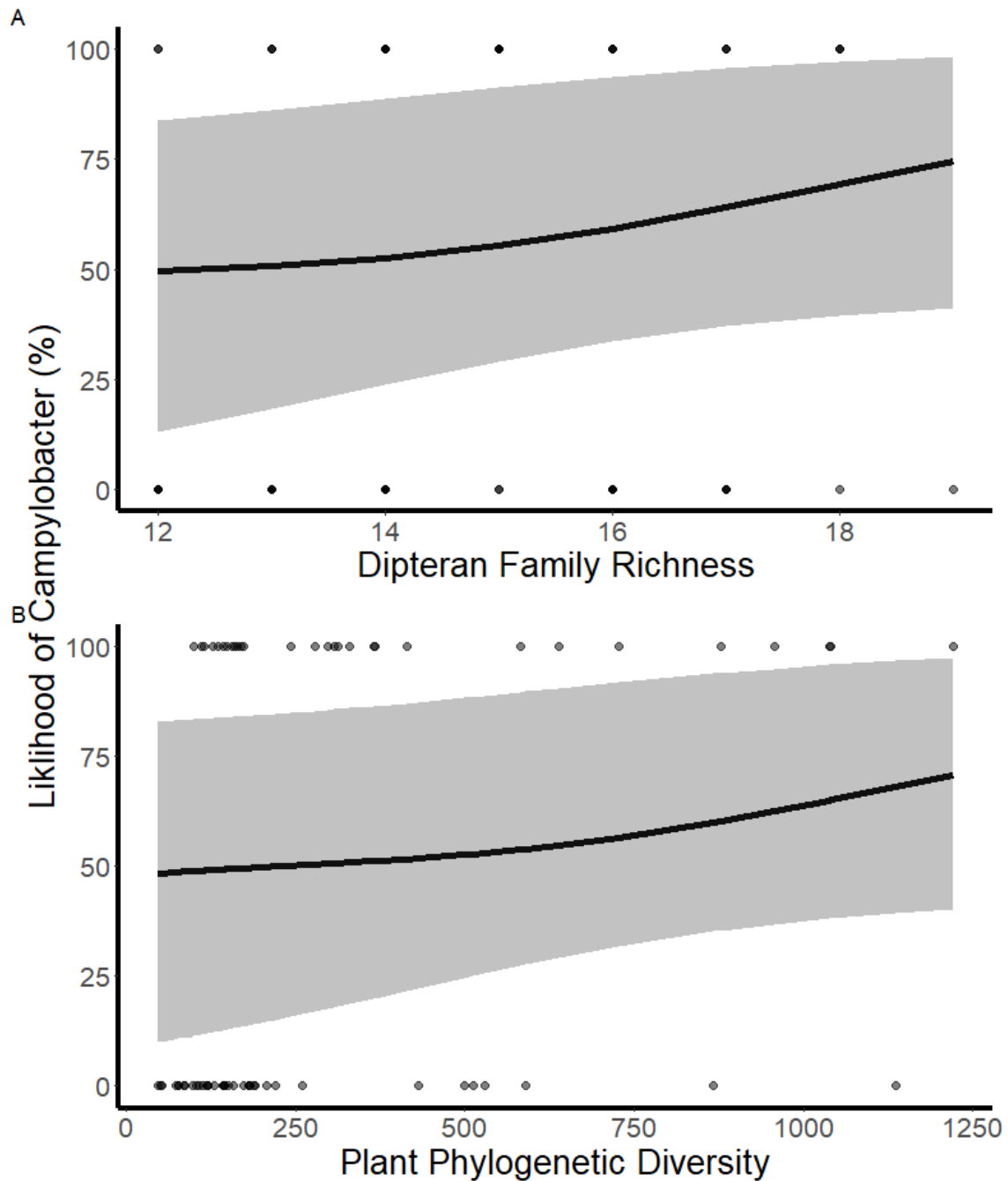


Figure 5.3. The relationship between the likelihood of *Campylobacter* in a sample, dipteran family richness (A), and plant phylogenetic diversity (B). Lines represent the prediction generated from top model containing that coefficient. Ribbons represent 95% confidence intervals. (Supplementary Table 5.5).

while Siemon et al. (2007) Hwang et al. (2020) reported rates of 14% and 16%, respectively, of *Salmonella* in feces.

We found that higher temperatures and humidity was associated with *Campylobacter* prevalence. This probably represents a relationship between these factors and *Campylobacter* survival in feces. Higher temperatures, and especially humidity, are associated with higher survival rates of foodborne bacteria in wild bird feces (Fonseca et al. 2020, Smith et al. 2023, Spence et al. 2025). For example, Hwang et al. (2020) reported that temperature and humidity were two of the variables best associated with higher *Salmonella* prevalence in chicken feces. We did not find a relationship between wind speed and *Campylobacter* prevalence, in contrast to Smith et al. (2023). This could be due to a couple of differences. First, our Southeast study region had lower average wind speeds than the west coast studies. Wind may not be as significant a transmission factor of bacteria in the Southeast region, although Hwang et al. (2020) found that higher wind speed was positively associated with *Salmonella* prevalence in chicken feces. Secondly, Smith et al. (2023) used a culture-based detection method, while our study used a PCR method, which may have detected non-viable *Campylobacter* in addition to live bacteria (Smith et al. 2023). We also found a negative correlation between flock size and *Campylobacter* prevalence, again, in contrast to Smith et al. (2023) and other previous studies (Daily et al. 2017). This could be because, generally, the farms in our study that had larger flocks “turned over” their flocks every year, whereas farms with smaller flocks kept the same individuals from year to year, although we did not record exact flock age in our study. Generally, *Campylobacter* prevalence increases in flocks as chickens age (Evans & Sayers 2000, Herman et al. 2003, Overbeke et al. 2006).

We found that higher phylogenetic diversity of chicken plant diet was associated with higher *Campylobacter* prevalence. This might indicate that, as chickens forage more widely and encounter more varied diet items, their risk of exposure to environmental bacteria increases. In wild birds, for example, opportunistic feeders and species that consume more plants carry higher rates of *Campylobacter* (Waldenström et al. 2002, Smith et al. 2021). Colles et al. (2008) examined *Campylobacter* in broiler chickens and found no correlation between bacterial shedding and ranging behavior, although the chickens in that study were much younger, in much larger flocks, and made less use of outdoor space than the chickens in this study. We also found a positive association between the richness of flies and *Campylobacter* prevalence. Flies and other insects are significant vectors of foodborne bacteria on farms and between chickens (Nayduch et al. 2023). Several studies have reported recovering foodborne bacteria from flies in or near conventional chicken houses (Hald et al. 2004, Hald et al. 2008, Buyukyavuz et al. 2024), but our study is the first to indicate that flies may also be important bacterial vectors in outdoor chicken flocks. Insect bacterial vectors may be of particular risk on integrated crop-livestock farms, such as the ones in our study, because of the proximity of livestock to produce. Rates of *Campylobacter* and *Salmonella* recovered from flies on integrated crop-livestock farms producing cattle range from 2-60% (Talley et al. 2009, Hamilton et al. 2021), representing a potentially significant food safety risk.

Overall, our results suggest that outdoor-access chickens do not pose a higher food safety risk in terms of bacterial prevalence than chickens raised in conventional systems (Siemon et al. 2007, Hoogenboom et al. 2008), but the proximity of crops to livestock may provide more opportunities for vectors like flies to transmit bacteria to produce. This risk may be elevated in the spring and summer, when insects are at higher abundances and higher temperatures allow for

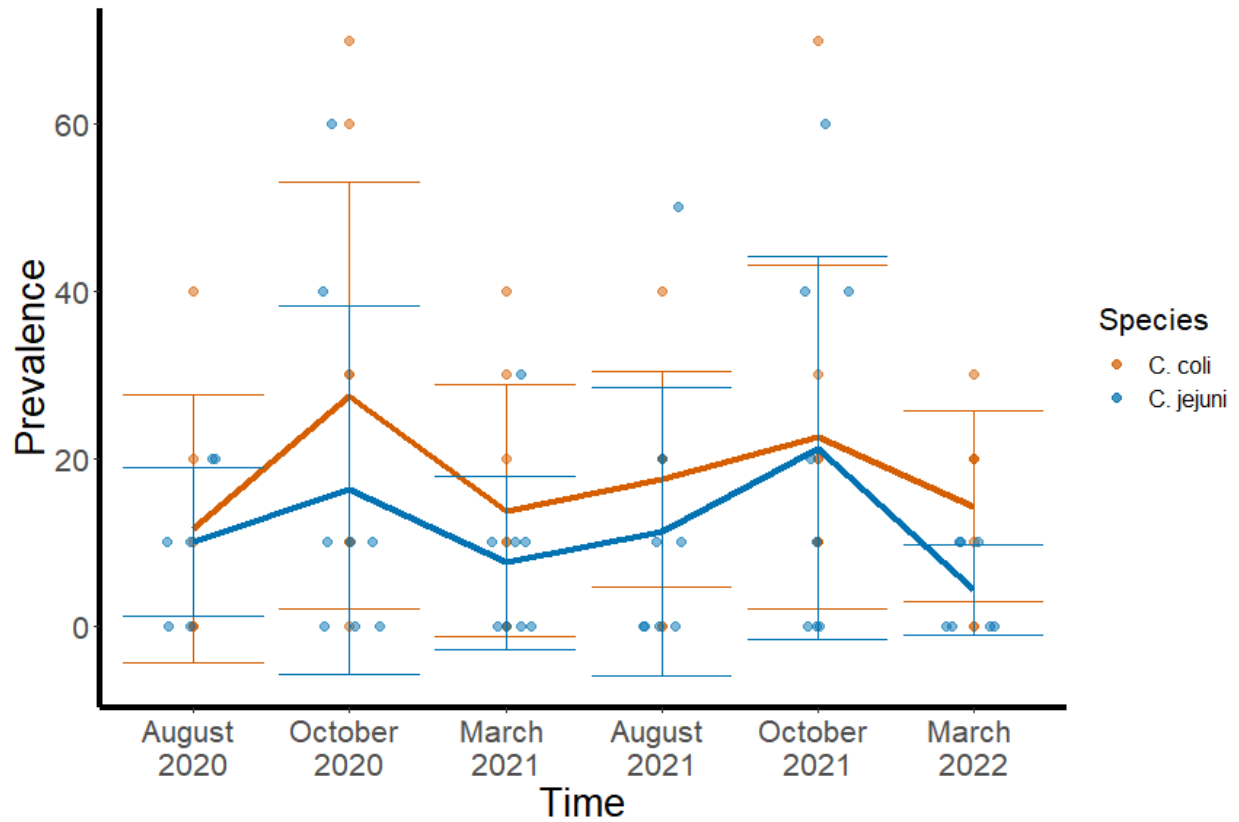
longer bacterial survival, although we did not find a significant relationship between season and *Campylobacter* or *Salmonella* prevalence in our study. However, Hwang et al. (2010) found that *Salmonella* prevalence in feces was highest in the spring compared to other seasons. Both Hald et al. (2008) and Hamilton et al. (2021) found that foodborne bacterial prevalence from flies peaked in late summer (July-Sept.). This discrepancy in peak bacterial prevalence dates indicates that simply screening for bacterial prevalence in chicken feces may underestimate or misunderstand the food safety risks on integrated crop-livestock farms. Further study is needed to understand the role insect vectors play in bacterial transmission, with special consideration given to testing of produce surfaces near livestock to assess bacterial transmission and survival.

Integrated crop-chicken farms can greatly benefit both growers and consumers economically and ecologically (Hilimire 2011a). However, food safety risks remain one of the largest barriers to integrated crop-livestock production (Hilimire 2011b). Our results suggest that growers looking to reduce food safety risks that come with co-managing livestock and produce may want to consider managing for insect vectors around their livestock. For example, Hald et al. (2007) found that chickens that had fly screens installed on their houses had *Campylobacter* rates of 15.4%, compared to 51.4% prevalence among unscreened chickens. Higher temperatures and humidity also represent heightened food safety risks—growers may want to pasture their chickens further away from crops when it is warmer and wetter outside. Considered management of food safety risks may allow growers to minimize harms while still reaping the benefits of integrated crop-livestock systems.

Supplementary Material

Supplementary Table 5.1. The four diet diversity and composition factors included in GLMMs.

Factor	Description	Explanation for how affects prevalence
Arthropod_PD	The phylogenetic diversity of arthropods in a sample	Higher diet breadth means chickens are foraging more widely—greater chance for bacterial contact
Plant_PD	The phylogenetic diversity of plants in a sample	Higher diet breadth means chickens are foraging more widely—greater chance for bacterial contact
Detritivore_PO	The relative proportion of occurrence of detritivores	Greater relative abundance of detritivores in environment may increase the chance for horizontal transmission Some detritivores help break down feces, which may reduce opportunities for horizontal transmission
Dipteran_FR	The family richness of flies (Order:Diptera)	Greater diversity and abundance of flies in the environment increases the chance for horizontal transmission



Supplementary Figure 5.1. Prevalence of *Campylobacter coli* (red) and *Campylobacter jejuni* (blue) for each collection period from August 2020 to March 2022. Bold lines indicate the mean prevalence for each collection period; thin lines represent standard deviation.

Supplementary Table 5.2. AIC_c values and model weights for total *Campylobacter* GLMMs. Values in columns 2-6 represent coefficient values [standard error]. Only models with AIC_c < 2 are shown.

Model	Humidity	Temperature	# Individuals	Year	ΔAIC_c	Weight
Humidity + Year	0.44 [0.21]			0.86 [0.41]	0	0.36
Temperature + Year		0.43 [0.22]		0.70 [0.42]	0.39	0.27
Temp + Humidity + Year	0.29 [0.25]	0.25 [0.26]		0.77 [0.42]	1.10	0.21
# Individuals + Temperature + Year		0.46 [0.22]	-0.16 [0.22]	0.72 [0.42]	1.93	0.14

Supplementary Table 5.3. Coefficient values and standard errors for model-averaged effects associated with total *Campylobacter* prevalence.

Coefficient	Value	Std Error	95% CI
Humidity	0.22	0.26	0.51
Temperature	0.24	0.27	0.53
# Individuals	-0.02	0.10	0.20
Year	0.78	0.42	0.82

Supplementary Table 5.4. AIC values for diet/weather *Campylobacter* models. Values in columns 2-7 represent coefficient values [standard error]. Only models with AIC_c > the null model (Model 3 in the list below) are shown.

Model	Dipteran_FR	Plant_PD	Year	ΔAIC_c	Weight
Dipteran_FR + Plant_PD + Year	0.53 [0.36]	0.61 [0.38]	1.00 [1.64]	0	0.10
Plant_PD + Year		0.58 [0.37]	0.71 [1.50]	0.02	0.10
Year			0.02 [1.52]	0.29	0.09

Supplementary Table 5.5. Coefficient values and standard errors for model-averaged diet/weather effects associated with total *Campylobacter* prevalence.

Coefficient	Value	Std Error	95% CI
Dipteran_FR	0.27	1.40	2.74
Plant_PD	0.6	0.39	0.76
Year	0.86	1.61	3.16

CONCLUSIONS

This dissertation considered the food safety risks and biological control of wild birds and outdoor-access chickens, with a focus on managing risks to consumers. We found that on-farm livestock presence was associated with higher *Salmonella* prevalence in wild bird feces, although livestock may not be the source of bacteria themselves. Instead, livestock may attract birds onto farms that are more likely to encounter and shed bacteria, although the risk of bacterial contamination of produce is low. We also found that flies may serve as important bacterial vectors on farms, particularly integrated crop-livestock farms where livestock and crop production are spatially close. The family richness of flies in outdoor-chicken diets was positively associated with higher *Campylobacter* prevalence in chicken feces. Thus, we identified two potential bacterial vectors on farms in the southeast US.

Both wild birds, from previous studies, and outdoor-access chickens, from this dissertation, may significantly contribute to biological control of pest arthropods and weeds. We found that outdoor-access chickens ate a wide variety of arthropods and plants, including many pests, although we were not able to definitely conclude whether chickens had a net positive, negative, or neutral impact on biological control services. Additionally, we found that outdoor-access chickens had relatively low rates of *Salmonella* and *Campylobacter* in their feces compared to raised in conventional systems. Growers may want to continue chicken production alongside crops while managing for potential vectors like wild birds and flies.

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APPENDIX A: GROWER SURVEY

Southeast US Bird-Grower Survey

This survey is intended to gauge both growers' attitudes towards birds and the bird prevention methods commonly used by growers in the southeast United States. Your answers to this survey are highly valued and will be used to develop educational materials for growers about birds and bird prevention strategies on farms. This survey should take no more than 15 minutes to complete.

1. How many total acres of farmland do you manage? _____
2. List all of the states in which your farmland is located. _____
3. What kind of production method do you use?

Organic

Conventional

Mix of organic and conventional

4. Select all of the crops you have produced on your farm in the last 2 years.

Fruit		Vegetable		Cucurbit		Greens		Other
☐	Apple	☐	Bean	☐	Cantaloupe	☐	Broccoli	☐ Grape/Muscadine
☐	Peach	☐	Corn	☐	Cucumber	☐	Cabbage	☐ Peanut
☐	Blueberry	☐	Eggplant	☐	Pumpkin	☐	Leafy greens	☐ Pecan
☐	Strawberry	☐	Okra	☐	Squash			☐ Soybean
☐	Blackberry	☐	Pepper	☐	Watermelon			
☐	Raspberry	☐	Tomato					
		☐	Zucchini					

Other: _____

5. List the kind and average number of individuals of any livestock herd you've kept on your farm in the past 2 years. If you've kept chickens, please indicate if they were indoor or outdoor.

Livestock	# Ind.	Livestock	# Ind.

6. What kind of birds do you observe most often on your farm?

- | | | |
|---|--|--|
| ☐ Raptors (e.g., hawks, vultures) | ☐ Doves/pigeons | ☐ Hummingbirds |
| ☐ Corvids (e.g., crows) | ☐ Woodpeckers | ☐ Waterfowl (e.g., ducks, geese) |
| ☐ Songbirds (e.g., bluebirds, cardinals) | ☐ Flycatchers | ☐ Shorebirds (e.g., egrets, killdeer) |

Other: _____

7. What is your relationship to bird management on your farm?

- | | | | | |
|-----------------------------|-----------------------------|-------------------------------------|------------------------------|------------------------------|
| Encourage birds
strongly | Encourage birds a
little | Neither encourage
nor discourage | Discourage birds a
little | Discourage birds
strongly |
|-----------------------------|-----------------------------|-------------------------------------|------------------------------|------------------------------|

8. Please list any birds you consider beneficial to production.

9. How concerned about you about birds as a food safety hazard to your produce?

- | | | | | |
|----------------------|--------------------|-------------------------|----------------|---------------------|
| Not at all concerned | A little concerned | Moderately
concerned | Very concerned | Extremely concerned |
|----------------------|--------------------|-------------------------|----------------|---------------------|

10. Select which season(s) you are most concerned about birds as a food safety hazard to produce.

- | | | | | |
|------|--------|--------|--------|----------------------------|
| Fall | Winter | Spring | Summer | No season in
particular |
|------|--------|--------|--------|----------------------------|

11. Select the preventative measures you take to discourage birds on your farm and rate how effective you think each method is.

- ☐ I don't use any preventative measures

Measure	Not at all effective	Slightly effective	Moderately effective	Very effective	Extremely effective
☐ Netting					
☐ Decoys					
☐ Natural birds/predator noises					
☐ Ultrasonic devices					
☐ Air cannons					
☐ Reflective tape/surface					
☐ Spikes					
☐ Remove habitat (hedge, water, etc.)					

☐ Lethal control (poison, shooting, etc.)					
☐					
☐					

12. Which birds in particular are you trying to discourage with these measures? *If you don't use any preventative measures, please leave blank.*

13. Estimate how much money, on average, you spend on bird prevention methods annually. *If you don't use any preventative measures, please leave blank.* _____

APPENDIX 2: GROWER SURVEY RESPONSE TABLE

Response table to grower survey. "ID" refers to the individual respondent.

ID	Size (acres)	State	Method	# Crops	Livestock	Attitude	Beneficial Birds	Concern	Concern Season	# Prev. Methods	Cost (US\$)
1	<10	SC	C	1	None	3		2	Summer	0	
2	<10	GA	O	18	Swine	3	Hummingbird	2	None	0	
3	<10	GA	O	19	None	1	Raptor	2	None	0	
4	<10	GA	O	13	None	1	Songbird, raptor	3	None	0	
5	51-100	GA	M	13	None	4	Raptor, hummingbird, other	1	Summer	3	100-500
6	<10	NC	M	1	None	1	All	1	None	0	
7	11-50	NC	C	2	Goat	3		3	None	1	<100
8	11-50	SC	M	19	Poultry, cow, goat	1		2	None	2	100-500
9	51-100	SC	C	2	None	4		4	Fall	1	<100
10	<10	SC	M	17	Poultry	3		3	Summer	2	<100
11	<10	SC	C	2	None	2		1	None	0	
12	51-100	SC	M	9	None	2	None	1	None	0	
13	<10	SC	O	13	Poultry	1	Songbird, raptor, hummingbird	1	None	0	
14	101-150	SC	O	14	Poultry, goat	1	All	1	None	0	
15	<10	GA	O	15	Poultry	1	Songbird	1	None	0	
16	<10	SC	O	10	None	3		2	None	0	
17	51-100	SC	M	11	None	2	Songbird, vulture	2	Spring, Summer	3	100-500

18	11-50	GA	O	18	Poultry, goat	1	Songbird	2	Spring	2	100-500
19	<10	SC	O	11	Poultry	3	Songbird	2	Spring, Summer	2	<100
20	51-100	SC	M	15	Poultry	4	None	4	Fall, Winter	1	100-500
21	<10	SC	O	11	Poultry, sheep	2	Songbird	4	Fall, Spring, Summer	0	
22	11-50	SC	O	14	Poultry	2		1	None	0	
23	<10	GA	O	11	Poultry	1		1	None	1	<100
24	151-200	GA	M	6	Poultry, cow, swine, donkey	2		2	None	0	
25	<10	GA	M	1	None	2		1	None	0	
26	<10	GA	M	0	Poultry, swine	1		NA		0	
27	51-100	SC	C	12	Cow	4		2	None	2	<100
28	>300	FL, SC, PA	M	8	None	4		3	None	1	<100
29	<10	SC	M	4	Poultry	3		3	Summer	2	100-500
30	101-150	SC	M	12	Poultry, cow, swine	3	Raptor	3	Spring	1	500-1000
31	<10	SC	M	7	None	1		1	None	0	
32	>300	SC	O	15	None	2	Songbird	1	None	0	
33	11-50	GA	M	18	Poultry	3	Songbird	1	None	3	100-500
34	11-50	GA	M	17	Poultry	2	Crow	1	Summer	1	100-500
35	11-50	GA	C	17	None	2	Raptor	3	Spring	1	<100
36	<10	SC	O	14	None	2	Not sure	2	None	0	

37	>300	GA	O	2	None	3	None	3	Summer	0	
38	<10	TN	C	17	None	1	Hummingbird	1		0	
39	251-300	GA	M	11	None	3	None	3	None	1	100-500
40	51-100	SC	C	16	Poultry	5		5	Fall, Spring	1	1000-2500
41	101-150	SC	M	1	None	5		4	Spring	2	1000-2500
42	>300	SC	M	1	None	3	Egret	1	Summer	1	1000-2500
43	11-50	SC	C	1	None	1	Songbird, hummingbird, woodpecker	1	Summer	0	
44	101-150	SC	C	16	None	3	Songbird	1	Spring	0	
45	11-50	SC	C	12	None	3	Songbird	3	All	0	
46	<10	SC	O	13	Poultry, cow	2	Cowbird, raptor	1	Spring	1	<100
47	<10	SC	M	3	None	2		2	Summer	0	
48	<10	SC	C	10	None	1	Songbird, raptor	3	Spring, Summer	0	
49	51-100	GA	M	16	None	3		1	Summer	0	

APPENDIX 3: DNA EXTRACTION PROTOCOL

Adapted from Zeale et al. (2010).

1. Add 200 mg (wet weight) of sample to bead tube (0.1 beads)
2. Add 1.2 mL ASL
3. Heat suspension for 10 min at 70°C and 1000 rpm in thermomixer
4. Beat samples for 60 sec at 4000 rpm in PowerLyzer bead beater
5. Centrifuge samples at 14000 rpm for 1 min
6. Pipet 1.2 mL of the supernatant into new 2 mL microcentrifuge tube
7. Add 800 µL InhibitEx and vortex for 10 sec to mix. Incubate for 1 min
8. Centrifuge at 14000 rpm for 1 min
9. Pipet all supernatant into new 2 mL microcentrifuge tube and centrifuge at 14000 rpm for 3 min
10. Pipet 20 µL Proteinase K into new 2 mL microcentrifuge tube, then add 600 µL of supernatant from step 9
11. Add 600 µL Buffer AL, vortex for 15 sec, and incubate at 70°C and 300 rpm overnight
12. Add 600 µL of 100% ethanol and mix by vortexing
13. Apply 600 µL of lysate to QIAamp spin column. Centrifuge at 14000 rpm for 1 min. Place spin column in new collection tube and discard the tube containing the filtrate.
14. Repeat step 13 twice to load second and third aliquot of the lysate to the spin column.
15. Add 500 µL Buffer AW1. Centrifuge at 14000 rpm for 1 min. Place spin column in new collection tube and discard the tube containing the filtrate.
16. Add 500 µL Buffer AW2. Centrifuge at 14000 rpm for 3 min. Place spin column in new collection tube and discard the tube containing the filtrate.
17. Place spin column in new collection tube. Centrifuge at 14000 rpm for 1 min. Discard tube containing the filtrate.
18. Transfer the spin column to a new 1.5 centrifuge tube and pipette 50 µL Buffer EB directly onto the spin column membrane. Incubate for 1 min at room temperature then centrifuge at 14000 rpm for 1 min to elute DNA.

APPENDIX 4: CHICKEN ARTHROPOD DIET LIST

Taxonomic classification of arthropod diet items identified from chicken feces by DNA analysis. “% Similarity” shows the percent similarity of closest match on the BOLD database. Blank cells indicate taxa that were assigned to a higher level because of discrepancies between databases or geography and so don’t have a similarity index for the taxonomic level shown.

Class	Order	Family	Genus	Species	Common Name	Feeding Guild	Season	% Similarity
Arachnida	Araneae	Corinnidae	<i>Castianeira</i>	<i>Castianeira variata</i>	variegated ant-mimic sac spider	Predator	Both	100.0
		Linyphiidae	<i>Ceratinopsis</i>	<i>Ceratinopsis laticeps</i>		Predator	Both	100.0
		Philodromidae	<i>Thanatus</i>	<i>Thanatus arcticus</i>		Predator	Fall	99.8
		Pisauridae	<i>Pisaurina</i>	<i>Pisaurina mira</i>	American nursery web spider	Predator	Spring	100.0
	Sarcoptiformes	Unknown	Unknown	Unknown sp.		Unknown	Both	99.9
	Trombidiformes	Eupodidae	Unknown	Unknown sp.		Unknown	Both	99.8
		Tarsonemidae	Unknown	Unknown sp.		Pest	Both	99.4
Chilopoda	Scolopendromorpha	Unknown	Unknown	Unknown sp.		Unknown	Both	99.2
Collembola	Entomobryomorpha	Unknown	Unknown	Unknown sp.		Unknown	Both	90.7
	Symphyleona	Unknown	Unknown	Unknown sp.		Unknown	Both	88.7
Diplopoda	Julida	Julidae	<i>Brachyiulus</i>	<i>Brachyiulus</i> sp.		Decomposer	Spring	100.0
	Polydesmida	Eurymerodesmidae	Unknown	Unknown sp.		Decomposer	Both	100.0
		Paradoxosomatidae	<i>Oxidus</i>	<i>Oxidus gracilis</i>	greenhouse millipede	Decomposer	Both	100.0
		Xystodesmidae	Unknown	Unknown sp.		Decomposer	Both	99.5
Insecta	Blattodea	Blaberidae	<i>Pycnoscelus</i>	<i>Pycnoscelus surinamensis</i>	Surinam cockroach	Decomposer	Both	100.0
		Ectobiidae	<i>Blattella</i>	<i>Blattella germanica</i>	German cockroach	Decomposer	Spring	100.0
				<i>Blattella</i> sp.		Decomposer	Both	100.0
			<i>Parcoblatta</i>	<i>Parcoblatta</i> sp.		Decomposer	Both	100.0

Coleoptera	Anthribidae	<i>Araecerus</i>	<i>Araecerus fasciculatus</i>	coffee bean weevil	Grain Pest	Both	100.0
	Carabidae	<i>Agonum</i>	<i>Agonum</i> sp.		Predator	Both	99.7
		<i>Amara</i>	<i>Amara aenea</i>	common sun beetle	Predator	Both	98.7
			<i>Amara</i> sp.		Predator	Both	97.8
		<i>Calathus</i>	<i>Calathus opaculus</i>		Predator	Both	100.0
			<i>Calathus</i> sp.		Predator	Both	98.9
		<i>Clivina</i>	<i>Clivina</i> sp.		Predator	Spring	100.0
		<i>Harpalus</i>	<i>Harpalus pensylvanicus</i>		Predator	Both	98.2
			<i>Harpalus</i> sp.		Predator	Fall	86.8
		<i>Pterostichus</i>	<i>Pterostichus</i> sp.		Predator	Both	100.0
		<i>Selenophorus</i>	<i>Selenophorus</i> sp.		Predator	Fall	100.0
		<i>Stenolophus</i>	<i>Stenolophus lineola</i>	seedcorn beetle	Predator	Both	99.9
		<i>Tetragonoderus</i>	<i>Tetragonoderus</i> sp.		Unknown	Both	
		<i>Trichotichnus</i>	<i>Trichotichnus fulgens</i>		Predator	Spring	99.7
	Chrysomelidae	<i>Paria</i>	<i>Paria fragariae</i>	strawberry rootworm	Pest	Fall	100.0
	Curculionidae	<i>Ceutorhynchus</i>	<i>Ceutorhynchus pallidactylus</i>	cabbage stem weevil	Pest	Spring	100.0
		<i>Hypera</i>	<i>Hypera postica</i>	alfalfa weevil	Pest	Both	99.5
		<i>Listroderes</i>	<i>Listroderes costirostris</i>	vegetable weevil	Pest	Spring	98.9
		<i>Sitona</i>	<i>Sitona hispidulus</i>	clover weevil	Pest	Spring	100.0
			<i>Sitona lineatus</i>	pea leaf weevil	Pest	Both	100.0
		<i>Sitophilus</i>	<i>Sitophilus oryzae</i>	rice weevil	Grain Pest	Both	100.0
			<i>Sitophilus zeamais</i>	maize weevil	Grain Pest	Both	100.0
	Histeridae	<i>Carcinops</i>	<i>Carcinops pumilio</i>		Predator	Spring	100.0
	Hydrophilidae	<i>Cercyon</i>	<i>Cercyon haemorrhoidalis</i>		Predator	Both	98.7
	Nitidulidae	<i>Carpophilus</i>	<i>Carpophilus dimidiatus</i>	cornsap beetle	Pest	Fall	100.0
	Phalacridae	<i>Stilbus</i>	<i>Stilbus</i> sp.		Decomposer	Spring	99.7

	Ptinidae	<i>Stegobium</i>	<i>Stegobium paniceum</i>	drugstore beetle	Grain Pest	Fall	100.0
	Scarabaeidae	<i>Cyclocephala</i>	<i>Cyclocephala lurida</i>	southern masked chafer	Pest	Fall	99.7
		<i>Onthophagus</i>	<i>Onthophagus hecate</i>	scooped scarab	Decomposer	Both	100.0
			<i>Onthophagus taurus</i>	bull-headed scarab	Decomposer	Both	100.0
		<i>Phanaeus</i>	<i>Phanaeus</i> sp.		Decomposer	Both	100.0
		<i>Phyllophaga</i>	<i>Phyllophaga hirticula</i>		Pest	Spring	99.9
			<i>Phyllophaga</i> sp.		Unknown	Spring	100.0
		<i>Popillia</i>	<i>Popillia japonica</i>	Japanese beetle	Pest	Fall	100.0
		<i>Serica</i>	<i>Serica</i> sp.		Pest	Spring	91.7
	Silvanidae	<i>Ahasverus</i>	<i>Ahasverus advena</i>	foreign grain beetle	Grain Pest	Fall	100.0
		<i>Oryzaephilus</i>	<i>Oryzaephilus surinamensis</i>	sawtoothed grain beetle	Grain Pest	Spring	100.0
		<i>Telephanus</i>	<i>Telephanus</i> sp.		Decomposer	Both	100.0
	Staphylinidae	Unknown	Unknown sp.		Unknown	Both	
	Tenebrionidae	<i>Tribolium</i>	<i>Tribolium confusum</i>	confused flour beetle	Grain Pest	Both	100.0
Diptera	Agromyzidae	<i>Phytomyza</i>	<i>Phytomyza</i> sp.		Pest	Spring	100.0
	Anthomyiidae	<i>Anthomyia</i>	<i>Anthomyia</i> sp.		Decomposer	Both	99.9
		<i>Botanophila</i>	<i>Botanophila</i> sp.		Unknown	Spring	98.0
		<i>Delia</i>	<i>Delia platura</i>	seedcorn maggot	Pest	Both	98.8
		<i>Pegomya</i>	<i>Pegomya winthemi</i>		Pest	Fall	77.8
	Anthomyzidae	<i>Mumetopia</i>	<i>Mumetopia occipitalis</i>		Pest	Spring	100.0
	Calliphoridae	<i>Aldrichina</i>	<i>Aldrichina grahami</i>		Decomposer	Both	100.0
		<i>Chrysomya</i>	<i>Chrysomya megacephala</i>	Oriental latrine fly	Decomposer	Spring	85.5
			<i>Chrysomya rufifacies</i>	hairy maggot blow fly	Decomposer	Both	100.0
			<i>Chrysomya</i> sp.		Unknown	Both	100.0
		<i>Lucilia</i>	<i>Lucilia cuprina</i>	Australian sheep blow fly	Decomposer	Fall	86.6
			<i>Lucilia</i> sp.		Unknown	Both	100.0

	Cecidomyiidae	Unknown	Unknown sp.	Unknown	Both	99.1
	Ceratopogonidae	<i>Forcipomyia</i>	<i>Forcipomyia</i> sp.	Decomposer	Both	98.7
	Chironomidae	<i>Cricotopus</i>	<i>Cricotopus annulator</i>	Pest	Fall	100.0
			<i>Cricotopus sylvestris</i>	Pest	Both	94.9
		<i>Procladius</i>	<i>Procladius</i> sp.	Predator	Spring	98.5
	Chloropidae	<i>Apallates</i>	<i>Apallates</i> sp.	Pest	Both	99.7
	Chyromyidae	Unknown	Unknown sp.	Decomposer	Spring	78.1
	Culicidae	<i>Culex</i>	<i>Culex</i> sp.	Pest	Both	100.0
	Dolichopodidae	<i>Hercostomus</i>	<i>Hercostomus</i> sp.	Unknown	Both	99.1
		<i>Pelastoneurus</i>	<i>Pelastoneurus vagans</i>	Predator	Both	100.0
	Drosophilidae	<i>Chymomyza</i>	<i>Chymomyza amoena</i>	Decomposer	Both	99.8
			<i>Chymomyza</i> sp.	Decomposer	Spring	80.7
		<i>Drosophila</i>	<i>Drosophila affinis</i>	Decomposer	Both	99.9
			<i>Drosophila immigrans</i>	Decomposer	Both	100.0
			<i>Drosophila simulans</i>	Decomposer	Fall	100.0
			<i>Drosophila suzukii</i>	Decomposer	Both	100.0
			<i>Drosophila</i> sp.	spotted-wing drosophila		
				Unknown	Spring	80.2
	Empididae	<i>Rhamphomyia</i>	<i>Rhamphomyia</i> sp.	Predator	Spring	73.8
	Heleomyzidae	<i>Suillia</i>	<i>Suillia</i> sp.	Unknown	Fall	
	Limoniidae	<i>Rhipidia</i>	<i>Rhipidia</i> sp.	Unknown	Spring	87.0
	Milichiidae	<i>Milichiella</i>	<i>Milichiella arcuata</i>	Decomposer	Both	100.0
	Muscidae	<i>Dasyphora</i>	<i>Dasyphora</i> sp.	Unknown	Both	99.7
		<i>Helina</i>	<i>Helina</i> sp.	Unknown	Both	99.9
		<i>Phaonia</i>	<i>Phaonia</i> sp.	Unknown	Both	
		<i>Stomoxys</i>	<i>Stomoxys calcitrans</i>	Decomposer	Fall	84.7
			<i>Thricops</i>			
		<i>Thricops</i>	<i>Thricops</i> sp.	Unknown	Fall	
	Phoridae	<i>Megaselia</i>	<i>Megaselia scalaris</i>	Decomposer	Both	99.9
	Pipunculidae	<i>Tomosvaryella</i>	<i>Tomosvaryella</i> sp.	Predator	Spring	99.6
	Psychodidae	<i>Psychoda</i>	<i>Psychoda alternata</i>	Decomposer	Spring	100.0

			<i>Psychoda</i> sp.		Decomposer	Both	97.0
	Sarcophagidae	<i>Oxysarcodexia</i>	<i>Oxysarcodexia</i> sp.		Unknown	Both	99.4
		<i>Ravinia</i>	<i>Ravinia stimulans</i>		Decomposer	Both	100.0
	Scatopsidae	<i>Scatopse</i>	<i>Scatopse</i> sp.		Decomposer	Spring	97.4
	Sciaridae	<i>Sciara</i>	<i>Sciara humeralis</i>		Decomposer	Spring	99.6
	Sepsidae	<i>Sepsis</i>	<i>Sepsis punctum</i>		Decomposer	Both	99.9
	Simuliidae	<i>Simulium</i>	<i>Simulium</i> sp.		Unknown	Spring	
	Sphaeroceridae	<i>Leptocera</i>	<i>Leptocera erythrocer</i>		Decomposer	Spring	99.7
	Stratiomyidae	<i>Allognosta</i>	<i>Allognosta fuscitarsis</i>		Decomposer	Both	100.0
		<i>Hermetia</i>	<i>Hermetia illucens</i>	black soldier fly	Decomposer	Both	99.7
		<i>Microchrysa</i>	<i>Microchrysa flaviventris</i>		Decomposer	Both	100.0
		<i>Sargus</i>	<i>Sargus fasciatus</i>		Decomposer	Spring	100.0
	Syrphidae	<i>Allograpta</i>	<i>Allograpta obliqua</i>	common oblique syrphid	Predator	Both	99.2
			<i>Allograpta</i> sp.		Predator	Both	99.3
		<i>Eristalis</i>	<i>Eristalis tenax</i>	drone fly	Decomposer	Both	99.9
		<i>Eupeodes</i>	<i>Eupeodes</i> sp.		Predator	Both	
		<i>Platycheirus</i>	<i>Platycheirus</i> sp.		Predator	Spring	94.1
		<i>Syrphus</i>	<i>Syrphus torvus</i>	hairy-eyed flower fly	Predator	Spring	99.4
		<i>Toxomerus</i>	<i>Toxomerus</i> sp.		Predator	Spring	100.0
	Tachinidae	Unknown	Unknown sp.		Predator	Both	
	Tephritidae	Unknown	Unknown sp.		Pest	Spring	
	Therevidae	Unknown	Unknown sp.		Predator	Spring	88.4
	Tipulidae	<i>Nephrotoma</i>	<i>Nephrotoma ferruginea</i>		Decomposer	Both	99.1
		<i>Tipula</i>	<i>Tipula</i> sp.		Decomposer	Spring	87.5
Hemiptera	Anthocoridae	<i>Orius</i>	<i>Orius insidiosus</i>	insidious flower bug	Predator	Both	100.0
	Aphididae	<i>Hysteroneura</i>	<i>Hysteroneura setariae</i>	rusty plum aphid	Pest	Both	100.0
	Cicadellidae	<i>Balclutha</i>	<i>Balclutha</i> sp.		Pest	Fall	
		<i>Homalodisca</i>	<i>Homalodisca insolita</i>		Pest	Spring	100.0
	Delphacidae	Unknown	Unknown sp.		Pest	Spring	
	Miridae	<i>Lygus</i>	<i>Lygus</i> sp.		Pest	Both	100.0

		<i>Trigonotylus</i>	<i>Trigonotylus</i> sp.		Pest	Fall	91.6
Hymenoptera	Braconidae	<i>Lysiphlebus</i>	<i>Lysiphlebus testaceipes</i>		Predator	Fall	100.0
	Ichneumonidae	<i>Cryptanura</i>	<i>Cryptanura</i> sp.		Predator	Both	
	Pergidae	<i>Acordulecera</i>	<i>Acordulecera dorsalis</i>		Pest	Spring	100.0
	Xyelidae	<i>Xyela</i>	<i>Xyela</i> sp.		Pest	Spring	100.0
Lepidoptera	Adelidae	Unknown	Unknown sp.		Pest	Both	88.4
	Cosmopterigidae	<i>Anatrachyntis</i>	<i>Anatrachyntis badia</i>	Florida pink scavenger	Pest	Both	99.9
	Crambidae	<i>Diatraea</i>	<i>Diatraea lisetta</i>		Pest	Fall	92.2
		<i>Ostrinia</i>	<i>Ostrinia penitalis</i>	American lotus borer	Pest	Spring	100.0
		<i>Samea</i>	<i>Samea baccatalis</i>		Pest	Spring	99.2
		<i>Spoladea</i>	<i>Spoladea recurvalis</i>	beet webworm moth	Pest	Fall	99.8
		<i>Udea</i>	<i>Udea rubigalis</i>	celery leaf-tier	Pest	Fall	84.2
	Erebidae	<i>Bleptina</i>	<i>Bleptina caradrinalis</i>	bent-winged owlet	Pest	Both	79.1
		<i>Cissusa</i>	<i>Cissusa spadix</i>	black-dotted brown moth	Pest	Spring	99.6
			<i>Cissusa</i> sp.		Pest	Both	100.0
		<i>Estigmene</i>	<i>Estigmene acrea</i>	salt marsh moth	Pest	Fall	100.0
		<i>Hypena</i>	<i>Hypena scabra</i>	green cloverworm	Pest	Spring	99.5
		<i>Mocis</i>	<i>Mocis marcida</i>	withered mocis	Pest	Both	86.2
	Geometridae	<i>Disclisioprocta</i>	<i>Disclisioprocta stellata</i>	somber carpet	Pest	Both	90.1
		<i>Eois</i>	<i>Eois</i> sp.		Pest	Spring	78.2
		<i>Eupithecia</i>	<i>Eupithecia swettii</i>		Pest	Spring	99.6
		<i>Hypagyrtis</i>	<i>Hypagyrtis</i> sp.		Pest	Both	99.6
		<i>Lambdina</i>	<i>Lambdina</i> sp.		Pest	Both	74.0
	Noctuidae	<i>Mythimna</i>	<i>Mythimna unipuncta</i>	armyworm moth	Pest	Spring	94.9
		<i>Peridroma</i>	<i>Peridroma saucia</i>	variegated cutworm	Pest	Fall	99.7
		<i>Spodoptera</i>	<i>Spodoptera frugiperda</i>	fall armyworm	Pest	Both	93.3
	Papilionidae	<i>Parnassius</i>	<i>Parnassius</i> sp.		Pest	Both	85.2

		Pieridae	<i>Colias</i>	<i>Colias</i> sp.		Pest	Both	100.0
		Pyralidae	<i>Plodia</i>	<i>Plodia interpunctella</i>	Indianmeal moth	Grain Pest	Both	99.6
		Sphingidae	<i>Lapara</i>	<i>Lapara</i> sp.		Pest	Both	89.7
		Tineidae	<i>Acrolophus</i>	<i>Acrolophus</i> sp.		Pest	Both	82.5
			<i>Xystrologa</i>	<i>Xystrologa</i> sp.		Pest	Spring	89.5
		Tortricidae	<i>Argyrotaenia</i>	<i>Argyrotaenia</i> sp.		Pest	Spring	98.3
			<i>Epiblema</i>	<i>Epiblema strenuana</i>	ragweed borer	Pest	Spring	100.0
Neuroptera		Chrysopidae	<i>Chrysoperla</i>	<i>Chrysoperla</i> sp.		Predator	Both	82.2
		Hemerobiidae	<i>Micromus</i>	<i>Micromus posticus</i>		Predator	Both	100.0
Orthoptera		Acrididae	<i>Dichromorpha</i>	<i>Dichromorpha viridis</i>	short-winged green grasshopper	Pest	Both	100.0
			<i>Melanoplus</i>	<i>Melanoplus packardii</i>	Packard's grasshopper	Pest	Fall	99.9
				<i>Melanoplus</i> sp.		Pest	Both	100.0
		Gryllidae	<i>Gryllus</i>	<i>Gryllus</i> sp.		Pest	Both	100.0
			<i>Miogryllus</i>	<i>Miogryllus saussurei</i>	eastern striped cricket	Pest	Both	100.0
		Trigonidiidae	<i>Allonemobius</i>	<i>Allonemobius fasciatus</i>	striped ground cricket	Pest	Fall	99.2
				<i>Allonemobius</i> sp.		Pest	Both	100.0
Thysanoptera		Thripidae	<i>Thrips</i>	<i>Thrips</i> sp.		Pest	Spring	98.0
Malacostraca	Isopoda	Armadillidiidae	<i>Armadillidium</i>	<i>Armadillidium nasatum</i>		Decomposer	Both	100.0
				<i>Armadillidium</i> sp.		Decomposer	Both	100.0
		Porcellionidae	<i>Porcellio</i>	<i>Porcellio laevis</i>	swift woodlouse	Decomposer	Both	100.0

APPENDIX 5: CHICKEN PLANT DIET LIST

Taxonomic classification of plant diet items identified from chicken feces by DNA analysis.

Order	Family	Genus	Species	Common Name	Ecological Guild	Season
Alismatales	Alismataceae	<i>Echinodorus</i>	<i>Echinodorus</i> sp.		Other	Spring
Apiales	Apiaceae	<i>Anthriscus</i>	<i>Anthriscus sylvestris</i>	wild chervil	Weed	Both
		<i>Chaerophyllum</i>	<i>Chaerophyllum tainturieri</i>	Southern chervil	Other	Spring
		<i>Coriandrum</i>	<i>Coriandrum sativum</i>	cilantro	Feed	Spring
		<i>Cuminum</i>	<i>Cuminum</i> sp.		Unknown	Both
		<i>Daucus</i>	<i>Daucus carota</i>	wild carrot	Other	Both
		<i>Smyrniun</i>	<i>Smyrniun olusatrum</i>	Alexanders	Other	Both
	Araliaceae	<i>Hedera</i>	<i>Hedera</i> sp.		Other	Spring
		<i>Hydrocotyle</i>	<i>Hydrocotyle umbellata</i>	manyflower marsh-pennywort	Other	Both
			<i>Hydrocotyle</i> sp.		Unknown	Both
		<i>Panax</i>	<i>Panax</i> sp.		Unknown	Both
Aquifoliales	Aquifoliaceae	<i>Ilex</i>	<i>Ilex cassine</i>	Dahoon holly	Other	Spring
Asparagales	Amaryllidaceae	<i>Allium</i>	<i>Allium vineale</i>	wild garlic	Unknown	Fall
	Orchidaceae	<i>Anoectochilus</i>	<i>Anoectochilus</i> sp.		Unknown	Both
Asterales	Asteraceae	<i>Ambrosia</i>	<i>Ambrosia trifida</i>	giant ragweed	Other	Both
			<i>Ambrosia</i> sp.		Unknown	Both
		<i>Anthemis</i>	<i>Anthemis arvensis</i>	mayweed	Other	Spring
		<i>Artemisia</i>	<i>Artemisia biennis</i>	biennial wormwood	Weed	Fall
			<i>Artemisia</i> sp.		Unknown	Both
		<i>Baccharis</i>	<i>Baccharis</i> sp.		Other	Spring
		<i>Bidens</i>	<i>Bidens alba</i>	common beggarticks	Other	Both
			<i>Bidens</i> sp.		Unknown	Spring
		<i>Chrysanthemum</i>	<i>Chrysanthemum</i> sp.		Unknown	Fall
		<i>Cichorium</i>	<i>Cichorium</i> sp.		Unknown	Spring
		<i>Coreopsis</i>	<i>Coreopsis tinctoria</i>	plains coreopsis	Other	Spring
		<i>Cosmos</i>	<i>Cosmos bipinnatus</i>	garden cosmos	Other	Both

		<i>Erechtites</i>	<i>Erechtites hieraciifolius</i>	American burnweed	Weed	Spring
		<i>Erigeron</i>	<i>Erigeron strigosus</i>	daisy fleabane	Other	Both
			<i>Erigeron</i> sp.		Unknown	Both
		<i>Eupatorium</i>	<i>Eupatorium</i> sp.		Unknown	Both
		<i>Facelis</i>	<i>Facelis retusa</i>	trampweed	Weed	Spring
		<i>Gamochaeta</i>	<i>Gamochaeta americana</i>	American everlasting	Other	Both
		<i>Helianthus</i>	<i>Helianthus</i> sp.		Unknown	Both
		<i>Hypochaeris</i>	<i>Hypochaeris radicata</i>	flatweed	Weed	Both
			<i>Hypochaeris</i> sp.		Unknown	Fall
			<i>Iva</i> sp.		Other	Fall
		<i>Krigia</i>	<i>Krigia cespitosa</i>	dwarf dandelion	Other	Both
		<i>Lactuca</i>	<i>Lactuca</i> sp.		Unknown	Both
			<i>Packera</i> sp.		Other	Spring
		<i>Petasites</i>	<i>Petasites hybridus</i>	butterbur	Other	Spring
		<i>Pyrrhopappus</i>	<i>Pyrrhopappus</i> sp.		Unknown	Both
		<i>Senecio</i>	<i>Senecio</i> sp.		Unknown	Spring
		<i>Soliva</i>	<i>Soliva sessilis</i>	field burweed	Weed	Both
			<i>Soliva</i> sp.		Unknown	Spring
		<i>Sonchus</i>	<i>Sonchus arvensis</i>	milk thistle	Weed	Both
			<i>Sonchus asper</i>	rough milk thistle	Weed	Both
			<i>Sonchus</i> sp.		Unknown	Both
		<i>Taraxacum</i>	<i>Taraxacum</i>	red-seeded dandelion	Weed	Spring
			<i>erythrospermum</i>			
			<i>Taraxacum kok-saghyz</i>	Kazakh dandelion	Weed	Both
			<i>Taraxacum</i> sp.		Unknown	Both
		<i>Verbasina</i>	<i>Verbesina</i> sp.		Other	Fall
		<i>Xanthium</i>	<i>Xanthium</i> sp.		Unknown	Spring
		<i>Zinnia</i>	<i>Zinnia elegans</i>		Other	Fall
	Campanulaceae	Unknown	Unknown sp.		Unknown	Both
Boraginales	Boraginaceae	<i>Myosotidium</i>	<i>Myosotidium hortensium</i>	Chatham Island forget-me-not	Other	Spring
			<i>Myosotis</i> sp.		Unknown	Fall
			<i>Pentaglottis</i> sp.		Unknown	Both
	Hydrophyllaceae	<i>Phacelia</i>	<i>Phacelia cicutaria</i>	caterpillar phacelia	Other	Spring
			<i>Phacelia</i> sp.		Unknown	Fall
Brassicales	Brassicaceae	<i>Alliaria</i>	<i>Alliaria petiolata</i>	garlic mustard	Weed	Spring
			<i>Brassica</i> sp.		Unknown	Both

			<i>Camelina</i> sp.		Unknown	Both
			<i>Capsella</i> sp.		Unknown	Both
		<i>Chorispora</i>	<i>Chorispora tenella</i>	purple mustard	Weed	Fall
		<i>Descurainia</i>	<i>Descurainia sophia</i>	flixweed	Weed	Both
			<i>Draba</i> sp.		Unknown	Spring
			<i>Eruca</i> sp.		Unknown	Fall
		<i>Erysimum</i>	<i>Erysimum repandum</i>	spreading wallflower	Weed	Fall
			<i>Raphanus</i> sp.		Unknown	Fall
	Moringaceae	<i>Moringa</i>	<i>Moringa</i> sp.		Other	Both
	Resedaceae	Unknown	Unknown sp.		Unknown	Fall
Caryophyllales	Amaranthaceae	<i>Amaranthus</i>	<i>Amaranthus hybridus</i>	smooth pigweed	Weed	Both
			<i>Amaranthus spinosus</i>	spiny pigweed	Weed	Both
			<i>Amaranthus</i> sp.		Unknown	Both
	Caryophyllaceae	<i>Cerastium</i>	<i>Cerastium</i> sp.		Unknown	Both
		<i>Minuartia</i>	<i>Minuartia</i> sp.		Unknown	Fall
		<i>Scleranthus</i>	<i>Scleranthus</i> sp.		Unknown	Spring
		<i>Silene</i>	<i>Silene latifolia</i>	white campion	Other	Spring
			<i>Silene</i> sp.		Unknown	Both
		<i>Spergula</i>	<i>Spergula arvensis</i>	corn spurry	Weed	Both
		<i>Stellaria</i>	<i>Stellaria media</i>	chickweed	Feed	Spring
			<i>Stellaria nemorum</i>	wood stichwort	Other	Spring
	Chenopodiaceae	<i>Atriplex</i>	<i>Atriplex</i> sp.		Unknown	Both
		<i>Bassia</i>	<i>Bassia scoparia</i>	ragweed	Other	Both
			<i>Bassia</i> sp.		Unknown	Both
		<i>Caroxylon</i>	<i>Caroxylon vermiculatum</i>	Mediterranean saltwort	Weed	Both
		<i>Chenopodium</i>	<i>Chenopodium</i> sp.		Unknown	Both
		<i>Haloxyton</i>	<i>Haloxyton</i> sp.		Unknown	Both
		<i>Oxybasis</i>	<i>Oxybasis glauca</i>	oak-leaved goosefoot	Weed	Both
		<i>Salsola</i>	<i>Salsola paulsenii</i>	barbwire Russian thistle	Weed	Both
		<i>Spinacia</i>	<i>Spinacia</i> sp.		Unknown	Both
	Nyctaginaceae	<i>Mirabilis</i>	<i>Mirabilis</i> sp.		Other	Spring
	Polygonaceae	<i>Fallopia</i>	<i>Fallopia convolvulus</i>	black bindweed	Weed	Both
		<i>Persicaria</i>	<i>Persicaria pensylvanica</i>	Pennsylvania smartweed	Other	Both
			<i>Persicaria</i> sp.		Unknown	Both
		<i>Polygonum</i>	<i>Polygonum pinicola</i>		Other	Spring
			<i>Polygonum</i> sp.		Unknown	Both
			<i>Rumex</i> sp.		Unknown	Fall

	Portulacaceae	<i>Portulaca</i>	<i>Portulaca oleracea</i>	common purslane	Other	Both
Cornales	Nyssaceae	<i>Nyssa</i>	<i>Nyssa sylvatica</i>	black tupelo	Other	Both
			<i>Nyssa</i> sp.		Unknown	Fall
Cucurbitales	Cucurbitaceae	<i>Cucumis</i>	<i>Cucumis sativus</i>	cucumber	Feed	Both
		<i>Cucurbita</i>	<i>Cucurbita</i> sp.		Unknown	Both
Cupressales	Cupressaceae	<i>Platycladus</i>	<i>Platycladus</i> sp.		Unknown	Both
Dipsacales	Adoxaceae	<i>Viburnum</i>	<i>Viburnum rigidum</i>	canary laurustinus	Other	Both
Ericales	Ebenaceae	<i>Diospyros</i>	<i>Diospyros virginiana</i>	common persimmon	Other	Fall
	Ericaceae	<i>Andromeda</i>	<i>Andromeda polifolia</i>	bog rosemary	Other	Both
		<i>Calluna</i>	<i>Calluna vulgaris</i>	common heather	Other	Both
		<i>Rhododendron</i>	<i>Rhododendron occidentale</i>	western azalea	Other	Both
			<i>Rhododendron</i> sp.		Unknown	Both
	Primulaceae	<i>Androsace</i>	<i>Androsace</i> sp.		Unknown	Spring
		<i>Maesa</i>	<i>Maesa</i> sp.		Unknown	Spring
	Theaceae	<i>Camellia</i>	<i>Camellia fluviatilis</i>		Other	Fall
			<i>Camellia reticulata</i>		Other	Both
			<i>Camellia</i> sp.		Unknown	Both
Fabales	Fabaceae	<i>Arachis</i>	<i>Arachis</i> sp.		Unknown	Fall
		<i>Dalbergia</i>	<i>Dalbergia</i> sp.		Unknown	Both
		<i>Desmodium</i>	<i>Desmodium</i> sp.		Unknown	Spring
		<i>Glycine</i>	<i>Glycine</i> sp.		Unknown	Fall
		<i>Kummerowia</i>	<i>Kummerowia striata</i>	Japanese clover	Weed	Both
		<i>Lespedeza</i>	<i>Lespedeza</i> sp.		Unknown	Both
		<i>Medicago</i>	<i>Medicago lupulina</i>	black medic	Feed	Both
			<i>Medicago sativa</i>	alfalfa	Feed	Both
			<i>Medicago</i> sp.		Unknown	Fall
		<i>Phaseolus</i>	<i>Phaseolus vulgaris</i>	common bean	Feed	Both
		<i>Pisum</i>	<i>Pisum</i> sp.		Feed	Fall
		<i>Robinia</i>	<i>Robinia</i> sp.		Other	Spring
		<i>Samanea</i>	<i>Samanea saman</i>	monkey pod tree	Other	Both
		<i>Senna</i>	<i>Senna obtusifolia</i>	sicklepod	Weed	Both
		<i>Sesbania</i>	<i>Sesbania vesicaria</i>	bladder pod	Other	Spring
		<i>Tamarindus</i>	<i>Tamarindus indica</i>	tamarind	Feed	Both
		<i>Trifolium</i>	<i>Trifolium micranthum</i>	slender trefoil	Other	Both
			<i>Trifolium</i> sp.		Unknown	Both
		<i>Vicia</i>	<i>Vicia faba</i>	fava bean	Feed	Both
			<i>Vicia sativa</i>	common vetch	Feed	Both

			<i>Vicia tetrasperma</i>	smooth vetch	Weed	Spring
		<i>Vigna</i>	<i>Vicia villosa</i>	hairy vetch	Weed	Both
			<i>Vigna radiata</i>	mung bean	Feed	Fall
			<i>Vigna unguiculata</i>	black-eyed pea	Feed	Both
			<i>Vigna</i> sp.		Unknown	Fall
	Polygalaceae		<i>Polygala</i>	<i>Polygala sibirica</i>	Siberian milkwort	Other
	Betulaceae	<i>Betula</i>	<i>Betula nigra</i>	river birch	Other	Both
			<i>Betula</i> sp.		Unknown	Spring
		<i>Carpinus</i>	<i>Carpinus caroliniana</i>	American hornbeam	Other	Spring
	Fagaceae	<i>Fagus</i>	<i>Fagus</i> sp.		Unknown	Both
		<i>Quercus</i>	<i>Quercus nigra</i>	water oak	Other	Both
			<i>Quercus stellata</i>	post oak	Other	Spring
			<i>Quercus</i> sp.		Unknown	Both
		Juglandaceae	<i>Carya</i>	<i>Carya illinoensis</i>	pecan	Feed
		<i>Juglans</i>	<i>Juglans</i> sp.		Unknown	Both
	Myricaceae	Unknown	Unknown sp.		Other	Both
Gentianales	Apocynaceae	<i>Apocynum</i>	<i>Apocynum</i> sp.		Other	Both
	Rubiaceae	<i>Sherardia</i>	<i>Sherardia arvensis</i>		Weed	Both
	Geraniaceae	<i>Erodium</i>	<i>Erodium</i> sp.		Unknown	Fall
		<i>Geranium</i>	<i>Geranium dissectum</i>	cutleaf geranium	Weed	Spring
			<i>Geranium molle</i>	dove's foot crane-bill	Other	Spring
			<i>Geranium</i> sp.		Unknown	Both
Isoetales	Isoetaceae	<i>Isoetes</i>	<i>Isoetes</i> sp.		Unknown	Fall
Lamiales	Lamiaceae	<i>Lamium</i>	<i>Lamium</i> sp.		Unknown	Spring
		<i>Ocimum</i>	<i>Ocimum basilicum</i>	basil	Feed	Spring
		<i>Salvia</i>	<i>Salvia reflexa</i>	mintweed	Other	Both
			<i>Salvia rosmarinus</i>	rosemary	Feed	Both
	Oleaceae	<i>Fraxinus</i>	<i>Fraxinus excelsior</i>	European ash	Other	Both
			<i>Fraxinus</i> sp.		Unknown	Both
		<i>Ligustrum</i>	<i>Ligustrum lucidum</i>	glossy privet	Other	Fall
			<i>Ligustrum</i> sp.		Unknown	Fall
			<i>Osmanthus</i>	<i>Osmanthus</i> sp.		Unknown
	Orobanchaceae	<i>Bellardia</i>	<i>Bellardia trixago</i>	Mediterranean lineseed	Weed	Spring
		<i>Rehmannia</i>	<i>Rehmannia glutinosa</i>		Other	Spring
	Pedaliaceae	<i>Sesamum</i>	<i>Sesamum indicum</i>	sesame	Feed	Spring
	Plantaginaceae	<i>Mecardonia</i>	<i>Mecardonia procumbens</i>	baby jump-up	Other	Spring
		<i>Penstemon</i>	<i>Penstemon</i> sp.		Unknown	Fall

		<i>Plantago</i>	<i>Plantago lanceolata</i>	ribwort plantain	Weed	Both
			<i>Plantago rugelii</i>	American plantain	Other	Both
			<i>Plantago</i> sp.		Unknown	Both
		<i>Veronica</i>	<i>Veronica arvensis</i>	corn speedwell	Weed	Both
			<i>Veronica persica</i>	Persian speedwell	Weed	Spring
			<i>Veronica triloba</i>		Other	Both
			<i>Veronica</i> sp.		Unknown	Both
	Tetrachondraceae	<i>Polypremum</i>	<i>Polypremum procumbens</i>		Other	Both
	Verbenaceae	<i>Verbena</i>	<i>Verbena bonariensis</i>	purpletop vervain	Other	Both
			<i>Verbena</i> sp.		Unknown	Both
Magnoliales	Annonaceae	<i>Annona</i>	<i>Annona stenophylla</i>	dwarf custard apple	Other	Spring
Malpighiales	Euphorbiaceae	<i>Acalypha</i>	<i>Acalypha rhomboidea</i>	common three-seed mercury	Other	Both
		<i>Euphorbia</i>	<i>Euphorbia heterophylla</i>	Mexican fireplant	Other	Fall
			<i>Euphorbia oranensis</i>		Other	Both
			<i>Euphorbia serpens</i>	matted sandmat	Weed	Fall
			<i>Euphorbia</i> sp.		Unknown	Fall
	Linaceae	<i>Linum</i>	<i>Linum</i> sp.		Unknown	Both
	Phyllanthaceae	<i>Phyllanthus</i>	<i>Phyllanthus urinaria</i>	chamberbitter	Weed	Both
	Salicaceae	<i>Salix</i>	<i>Salix</i> sp.		Unknown	Both
	Violaceae	<i>Viola</i>	<i>Viola</i> sp.		Unknown	Fall
Malvales	Malvaceae	<i>Abelmoschus</i>	<i>Abelmoschus esculentus</i>	okra	Feed	Both
		<i>Abutilon</i>	<i>Abutilon</i> sp.		Other	Fall
		<i>Gossypium</i>	<i>Gossypium herbaceum</i>	Levant cotton	Feed	Both
			<i>Gossypium hirsutum</i>	upland cotton	Feed	Spring
			<i>Gossypium</i> sp.		Unknown	Both
		<i>Malva</i>	<i>Malva neglecta</i>	cheeseweed	Weed	Spring
		<i>Sida</i>	<i>Sida</i> sp.		Unknown	Both
Myrtales	Lythraceae	<i>Ammannia</i>	<i>Ammannia</i> sp.		Unknown	Both
		<i>Punica</i>	<i>Punica granatum</i>	pomegranate	Feed	Both
	Myrtaceae	<i>Eucalyptus</i>	<i>Eucalyptus</i> sp.		Unknown	Both
	Onagraceae	<i>Epilobium</i>	<i>Epilobium</i> sp.		Unknown	Both
		<i>Oenothera</i>	<i>Oenothera laciniata</i>	cutleaf evening primrose	Other	Both
			<i>Oenothera</i> sp.		Unknown	Both
Oxalidales	Elaeocarpaceae	<i>Sloanea</i>	<i>Sloanea</i> sp.		Other	Both
	Oxalidaceae	<i>Oxalis</i>	<i>Oxalis stricta</i>	common yellow woodsorrel	Weed	Both

			<i>Oxalis</i> sp.		Unknown	Both
Pinales	Pinaceae	<i>Pinus</i>	<i>Pinus</i> sp.		Unknown	Both
Poales	Cyperaceae	<i>Carex</i>	<i>Carex</i> sp.		Unknown	Both
	Juncaceae	Unknown	Unknown sp.		Unknown	Spring
	Poaceae	<i>Anthoxanthum</i>	<i>Anthoxanthum odoratum</i>	sweet vernal grass	Feed	Both
			<i>Anthoxanthum</i> sp.		Unknown	Both
		<i>Arrhenatherum</i>	<i>Arrhenatherum</i> sp.		Unknown	Both
		<i>Avena</i>	<i>Avena</i> sp.		Unknown	Both
		<i>Axonopus</i>	<i>Axonopus</i> sp.		Unknown	Both
		<i>Bromus</i>	<i>Bromus secalinus</i>	rye brome	Weed	Both
			<i>Bromus</i> sp.		Unknown	Both
		<i>Cenchrus</i>	<i>Cenchrus echinatus</i>	southern sandbar	Weed	Fall
		<i>Cynodon</i>	<i>Cynodon</i> sp.		Unknown	Both
		<i>Dactylis</i>	<i>Dactylis glomerata</i>	cat grass	Weed	Both
		<i>Dichanthelium</i>	<i>Dichanthelium</i> sp.		Unknown	Both
		<i>Digitaria</i>	<i>Digitaria violascens</i>	hairy crabgrass	Weed	Both
			<i>Digitaria</i> sp.		Unknown	Both
		<i>Echinochloa</i>	<i>Echinochloa</i> sp.		Unknown	Both
		<i>Eleusine</i>	<i>Eleusine</i> sp.		Unknown	Fall
		<i>Festuca</i>	<i>Festuca</i> sp.		Unknown	Spring
		<i>Glyceria</i>	<i>Glyceria</i> sp.		Unknown	Spring
		<i>Hordeum</i>	<i>Hordeum pusillum</i>	little barley	Other	Both
			<i>Hordeum vulgare</i>	barley	Feed	Both
			<i>Hordeum</i> sp.		Unknown	Both
		<i>Lolium</i>	<i>Lolium</i> sp.		Unknown	Both
		<i>Molinia</i>	<i>Molinia caerulea</i>	purple moor grass	Other	Both
		<i>Muhlenbergia</i>	<i>Muhlenbergia</i> sp.		Unknown	Both
		<i>Ottochloa</i>	<i>Ottochloa nodosa</i>		Other	Fall
		<i>Panicum</i>	<i>Panicum dichotomiflorum</i>	fall panicgrass	Weed	Spring
			<i>Panicum hirticaule</i>	Mexican panicgrass	Weed	Fall
		<i>Paspalum</i>	<i>Paspalum notatum</i>	bahiagrass	Feed	Both
			<i>Paspalum setaceum</i>	hairy beadgrass	Weed	Fall
			<i>Paspalum</i> sp.		Unknown	Both
		<i>Poa</i>	<i>Poa annua</i>	annual bluegrass	Weed	Both
			<i>Poa infirma</i>	weak bluegrass	Weed	Both
			<i>Poa trivialis</i>	rough bluegrass	Weed	Spring
			<i>Poa</i> sp.		Unknown	Both

		<i>Saccharum</i>	<i>Saccharum</i> sp.		Unknown	Both
		<i>Sacciolepis</i>	<i>Sacciolepis</i> sp.		Unknown	Fall
		<i>Schizachyrium</i>	<i>Schizachyrium scoparium</i>	little bluestem	Other	Fall
		<i>Secale</i>	<i>Secale</i> sp.		Unknown	Both
		<i>Setaria</i>	<i>Setaria parviflora</i>	marsh bristlegrass	Other	Both
			<i>Setaria</i> sp.		Unknown	Both
		<i>Sorghastrum</i>	<i>Sorghastrum nutans</i>	Indiangrass	Other	Both
		<i>Sorghum</i>	<i>Sorghum</i> sp.		Unknown	Both
		<i>Triticum</i>	<i>Triticum turgidum</i>	emmer wheat	Feed	Fall
			<i>Triticum</i> sp.		Unknown	Both
		<i>Zea</i>	<i>Zea</i> sp.		Unknown	Both
Proteales	Platanaceae	<i>Platanus</i>	<i>Platanus occidentalis</i>	American sycamore	Other	Both
			<i>Platanus orientalis</i>	Oriental pine	Other	Both
Ranunculales	Ranunculaceae	<i>Clematis</i>	<i>Clematis</i> sp.		Unknown	Fall
		<i>Ranunculus</i>	<i>Ranunculus parviflorus</i>	smallflower buttercup	Weed	Both
			<i>Ranunculus</i> sp.		Unknown	Both
Rosales	Cannabaceae	<i>Cannabis</i>	<i>Cannabis sativa</i>		Feed	Both
		<i>Celtis</i>	<i>Celtis occidentalis</i>	hackberry	Other	Both
	Moraceae	<i>Morus</i>	<i>Morus</i> sp.		Unknown	Fall
	Rhamnaceae	<i>Ceanothus</i>	<i>Ceanothus</i> sp.		Unknown	Fall
	Rosaceae	<i>Aphanes</i>	<i>Aphanes</i> sp.		Other	Both
		<i>Fragaria</i>	<i>Fragaria virginiana</i>	Virginia strawberry	Other	Both
			<i>Fragaria</i> sp.		Unknown	Fall
		<i>Malus</i>	<i>Malus hupehensis</i>	tea crabapple	Feed	Both
			<i>Malus rockii</i>		Other	Spring
			<i>Malus tschonoskii</i>	pillar apple	Other	Fall
			<i>Malus</i> sp.		Unknown	Both
		<i>Potentilla</i>	<i>Potentilla indica</i>	mock strawberry	Other	Both
			<i>Potentilla</i> sp.		Unknown	Spring
		<i>Prunus</i>	<i>Prunus grayana</i>	Gray's bird cherry	Other	Both
			<i>Prunus serotina</i>	black cherry	Other	Spring
			<i>Prunus</i> sp.		Unknown	Both
		<i>Pyrus</i>	<i>Pyrus</i> sp.		Unknown	Both
		<i>Rosa</i>	<i>Rosa acicularis</i>	prickly wild rose	Other	Spring
		<i>Rubus</i>	<i>Rubus trivialis</i>	Southern dewberry	Other	Both
			<i>Rubus</i> sp.		Unknown	Both
	Ulmaceae	<i>Ulmus</i>	<i>Ulmus alata</i>	winged elm	Other	Both

	Urticaceae	<i>Laportea</i> <i>Urtica</i>	<i>Laportea canadensis</i> <i>Urtica</i> sp.	Canadian wood nettle	Other Unknown	Spring Both
Santalales	Santalaceae	Unknown	Unknown sp.		Unknown	Both
	Anacardiaceae	<i>Rhus</i>	<i>Rhus copallinum</i>	shining sumac	Other	Spring
	Rutaceae	<i>Citrus</i>	<i>Citrus</i> sp.		Unknown	Fall
	Sapindaceae	<i>Acer</i>	<i>Acer negundo</i>	boxelder maple	Other	Spring
			<i>Acer pseudoplatanus</i>	sycamore maple	Other	Both
			<i>Acer rubrum</i>	red maple	Other	Both
			<i>Acer saccharinum</i>	silver maple	Other	Both
			<i>Acer</i> sp.		Unknown	Spring
		<i>Koelreuteria</i>	<i>Koelreuteria paniculata</i>	golden raintree	Other	Both
Saxifragales	Altingiaceae	<i>Liquidambar</i>	<i>Liquidambar</i> sp.		Unknown	Both
Solanales	Convolvulaceae	<i>Convolvulus</i>	<i>Convolvulus arvensis</i>	field bindweed	Weed	Both
			<i>Convolvulus</i> sp.		Unknown	Fall
		<i>Dichondra</i>	<i>Dichondra</i> sp.		Other	Both
		<i>Ipomoea</i>	<i>Ipomoea quamoclit</i>	quamoclit	Other	Spring
	Solanaceae	<i>Capsicum</i>	<i>Capsicum</i> sp.		Unknown	Both
		<i>Lycium</i>	<i>Lycium</i> sp.		Unknown	Both
		<i>Nicotiana</i>	<i>Nicotiana</i> sp.		Unknown	Both
		<i>Solanum</i>	<i>Solanum pseudocapsicum</i>	Jerusalem cherry	Other	Fall
			<i>Solanum</i> sp.		Unknown	Both
Zingiberales	Musaceae	<i>Musa</i>	<i>Musa</i> sp.		Unknown	Spring