

Occurrence and human exposure assessment of enteric bacteria and their antimicrobial resistance in North Carolina farmers

Canadian Journal of Agriculture and Crops

Vol. 11, No. 2, 14–28, 2026

e-ISSN: 2518-6655



Corresponding Author

Kimberly Bower¹

Emily S. Bailey²

Victor Varela³

Vera Luther^{3,4}

Christopher Ohl^{3,4}

Mark D. Sobsey¹

¹Department of Environmental Sciences and Engineering, Gillings School of Global Public Health, the University of North Carolina at Chapel Hill, 135 Dauer Drive, CB#7431, Chapel Hill, North Carolina 27599, United States.

¹Email: k_blauth13@yahoo.com

¹Email: mark_sobsey@unc.edu

²Department of Public Health, College of Pharmacy & Health Sciences, Campbell University, 217 Main Street, Buies Creek, North Carolina, 27506, United States.

²Email: ebailey@campbell.edu

³Section on Infectious Diseases, Department of Internal Medicine, Wake Forest School of Medicine, Winston-Salem, North Carolina, United States.

³Email: vvarela@charter.net

^{3,4}Email: vera.p.luther@hitchcock.org

^{3,4}Email: chris.ohl@dartmouth.edu

⁴Geisel School of Medicine at Dartmouth and Dartmouth Health, Hanover, New Hampshire, United States.

ABSTRACT

Purpose: Antibiotic use in high density animal agriculture, such as confined animal feeding operations (CAFOs), is a potential source of human exposure to enteric bacteria and antibiotic resistant (AR) bacteria. This pilot study was intended to assess the impacts of CAFOs on human pathogens (*Salmonella*) and AR enteric bacteria (*E. coli* and *Enterococcus*) occurrence in people living near or working on these facilities. **Design/Approach:** People associated with eleven swine CAFOs were compared with those of six row crop farms for occurrence and frequency of AR enteric bacteria. Fecal samples were collected from 87 people associated with both farm types, to assess AR enteric bacteria carriage. **Findings:** AR bacteria carriage was higher in people associated with CAFOs (RR= 1.42 [95% CI =1.17 1.72]). **Conclusion:** The AR bacteria in human stool samples could not be specifically attributed to the farms. **Practical Implications:** Further analysis on additional CAFOs and row crop farms and their people is recommended to increase statistical power and attempt to determine if there are or are not differences in the prevalence of AR bacteria found in the environment and in people on swine farms compared to row crop farms.

Keywords: Antimicrobial resistance, Enteric bacteria, Exposure assessment, Farmers, Quantitative Microbial Risk Assessment (QMRA).

DOI: 10.55284/cjac.v11i2.1993

Citation | Bower, K., Bailey, E. S., Varela, V., Luther, V., Ohl, C., & Sobsey, M. D. (2026). Occurrence and human exposure assessment of enteric bacteria and their antimicrobial resistance in North Carolina farmers. *Canadian Journal of Agriculture and Crops*, 11(2), 14–28.**Copyright:** © 2026 by the authors. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).**Funding:** This work was supported by the North Carolina Department of Health and Human Services and the United States Centers for Disease Control and Prevention.**Institutional Review Board Statement:** This study was approved by the Institutional Review Board of Wake Forest University Baptist Medical Center (WFUBMC) in February 2004 (Protocol No. BG04-022). All participants provided informed verbal consent, and the collected data were anonymized to ensure participant confidentiality.**Transparency:** The authors confirm that the manuscript is an honest, accurate, and transparent account of the study; that no vital features of the study have been omitted; and that any discrepancies from the study as planned have been explained. This study followed all ethical practices during writing.**Competing Interests:** The authors declare that they have no competing interests.**Authors' Contributions:** All authors contributed equally to the conception and design of the study. All authors have read and agreed to the published version of the manuscript.**History:** Received: 17 August 2026/ Revised: 17 September 2026/ Accepted: 5 October 2026/ Published: 19 October 2026**Publisher:** Online Science Publishing

Highlights of this paper

- Evidence in North Carolina farms that there is a greater risk of carriage of antibiotic resistant enteric bacteria in swine farm workers than in row crop workers.
- There is a research gap in the evaluation of anti biotic resistant bacteria exposure at the human animal interface.
- Further investigation is required to understand differences in prevalence of antibiotic resistant bacteria in farm workers.

1. INTRODUCTION

Animal agriculture is a growing industry worldwide. In North Carolina alone, there are about 8.3 million pigs and 23.8 million chickens (layers, 20 weeks old or older) [1]. As increases in human population has increased the demand for meat and other animal food products, the available land for production facilities has decreased. As a result, many facilities increasingly house thousands of animals at a single location called confined animal feeding operations (CAFOs). Swine CAFOs, especially those in NC, are very large farms with many thousands of animals confined in crowded buildings. This type of swine production system is considered efficient and economical and can be managed with relatively few workers. Hence, such production systems are widely used in the USA and worldwide.

The swine waste from the buildings housing these animals is collected typically through slatted floors and is conveyed by periodic flushing and then discharge to earthen lagoons. However, the management of swine wastes from such productions systems can pose environmental and human health risks. In NC, many such farms are located in the coastal plains that are subjected to periotic flooding caused by hurricanes and tropical storms that can inundate entire farms by flooding and cause the release of swine waste from storage lagoons. In the lagoons the liquid waste typically undergoes several months of treatment by anaerobic digestion before spray irrigating it onto adjacent fields. Such waste still contains high concentrations of enteric bacteria, including those that are antibiotic resistant. It is well-documented that water, soil and air on or near swine farms usually contains comparatively high concentrations of AR enteric bacteria, which has been well-documented in NC [2].

With high concentrations of animals at a single location, it is essential that facility operators maintain conditions that promote animal health and growth. Antibiotic use at sub-therapeutic levels enables faster animal growth with less feed to maintain the overall health of the animals [3]. However, in 2017, the U.S. Food and Drug Administration implemented new regulations to eliminate over-the-counter status for in-feed antibiotics that are medically important in human medicine and require additional veterinary oversight for on-farm applications [4]. Antibiotic use is now limited to prevention, treatment and control of disease. Prior to 2017, including at the time this study was conducted, antibiotics were often introduced into animal facilities during the production process and global use of antibiotics for swine growth promotion is still widespread [5].

While many studies have demonstrated that AR bacteria and antibiotic residues are present in animal agriculture facilities [6-13] fewer studies have evaluated the impact of this presence on humans and human health [14-17]. In

previous studies that have evaluated the human health effects of AR bacteria exposure, they have primarily focused on the consumption of animal products that may contain antibiotic resistant bacteria. Specifically, the evaluation of consumer meat products has led to the identification of AR bacteria in commercially available food products [18-20]. Outbreak identifications in Denmark have also linked the consumption of pork contaminated with multi-drug-resistant *Salmonella enterica* serotype Typhimurium with human infections as well as to secondary transmission from slaughterhouse workers who worked with the infected animals [21]. Work examining environmental exposures has been conducted both within and outside of the U.S. that reports increased prevalence of AR bacteria colonization in farm workers in direct contact with animal feces, specifically on chicken or swine farms [22-27]. Despite the links between exposure to animals and animal feces and AR bacteria colonization, information on infection and carriage risks for individuals who live near animal agriculture locations or in the surrounding community is still limited.

In research evaluating AR bacteria near animal agriculture locations, resistant bacteria have been detected in aerosol samples downwind of swine CAFOs [28] and in ground water beneath swine lagoons [7, 29]. Studies evaluating manure or manure slurry applied to fields or on-farm spray irrigation with lagoon waste document an increased prevalence of AR bacteria in the farm environment [30, 31]. Often the spread or spraying of the manure or manure slurry is close to the animal facilities themselves. Therefore, people who live on or near these facilities may have an increased risk of acquiring resistant bacteria by being exposed to them from soil or contact or consumption of contaminated produce or by consuming contaminated water [32]. In Figure 1, we display graphically proposed relationships between antibiotics introduced via animal feed or through therapeutic antimicrobials in animal farming or through treatment for row crops, compared to the locations at which AR bacteria are detected along the food processing chain. These relationships have been established through a review of the currently available literature evaluating the distribution of antibiotics through the food production system. Although there is a difference in the way in which antibiotics are introduced for animal farmers and for row crop farmers, AR bacteria are detectable in a variety of sources, wastes and wastewaters [7], surface waters [33], ground waters [2] and the food crops produced for public consumption [30].

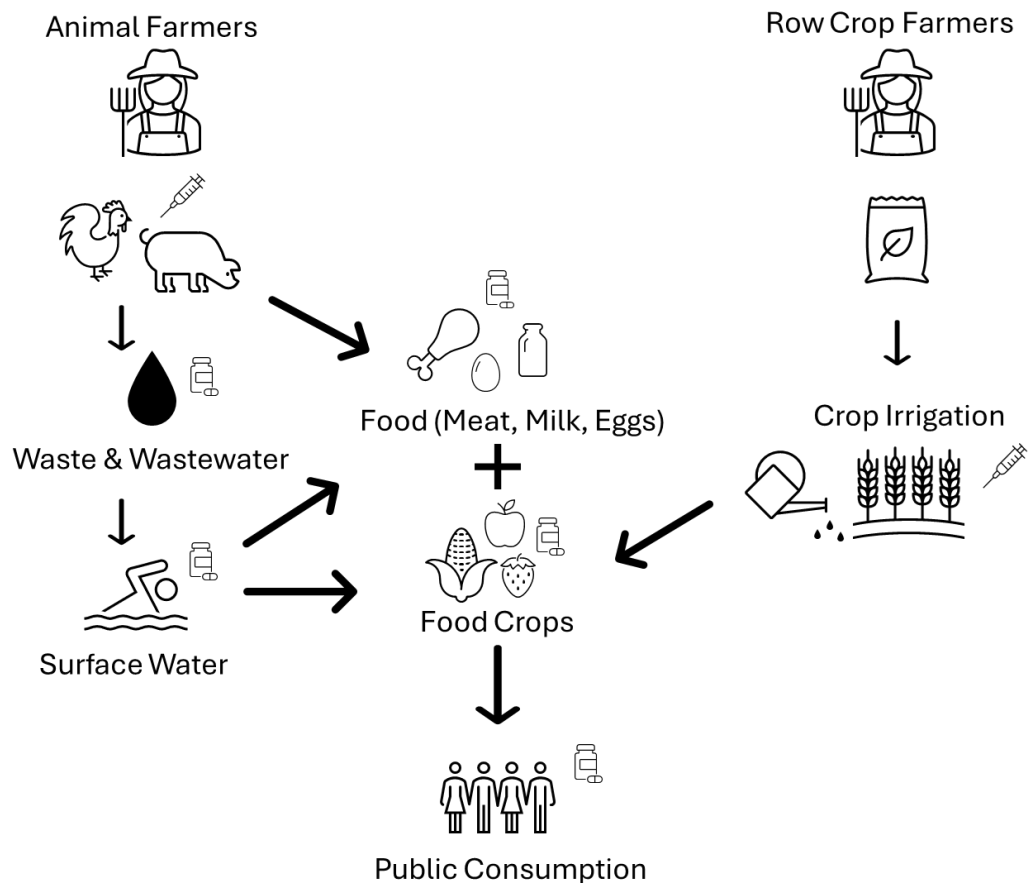


Figure 1. Pathways of antibiotic resistance through the two farming modalities by introduced antibiotics () and detected antibiotics ().

This study is intended to examine the differences in the prevalence of antibiotic resistant enteric bacteria and *Salmonella* from two different types of farm exposures in farm workers in North Carolina. The objective of this study is to determine if human exposure to animal-related, specifically swine-related, agriculture environments results in an increased risk of acquiring or carrying antibiotic resistant bacteria or *Salmonella* when compared to those exposed to non-animal agriculture facilities.

2. MATERIALS AND METHODS

2.1. Ethics Approval

This study was approved by the institutional review board at Wake Forest University Baptist Medical Center (WFUBMC) protocol number BG04-022 and the United States Centers for Disease Control (the funding source of the project). All recruited participants signed an informed consent form prior to enrollment into the study.

2.2. Participant recruitment

Farmers of animal agriculture (swine farm) and non-animal agriculture (row crop farm) facilities and neighbors living within one mile of farms in eastern North Carolina were recruited to participate in this study between 2005 and 2007. Swine farmers were the exposed group and non-animal farmers were the unexposed (or control) group.

Upon enrollment in the study, each participant received and signed informed consent and completed an in person questionnaire which included questions regarding occupation, personal antibiotic use, contact with animals, water exposures (e.g., contact with environmental surface water for recreation or work, and source of drinking water), travel history, as well as other personal information that could potentially impact their acquisition of antimicrobial resistant bacteria or *Salmonella* infection.

Each participant was asked to submit a fecal sample once monthly for one year. Participants were also asked to submit additional fecal samples if they were sick with a diarrheal illness during the year of participation. Follow up questionnaires accompanied each fecal sample to ensure there was no change in exposure to antibiotics or resistant bacteria.

Fecal samples were collected using a unique method, called the biowipe method, developed by Dr. Chris Ohl and colleagues at Baptist Medical Center, Wake Forest University and then used by this lab for other studies of antimicrobial resistant bacteria in humans that allows the participant to collect his/her own sample and send it to the laboratory [34, 35]. Each participant was asked to soil a plastic backed absorbent fabric with fecal matter (at least the size of a quarter in diameter), fold it in half and place it in a plastic bag containing a gauze layer saturated with transport medium (Cary-Blair medium [Thermo Fisher Scientific, Waltham, MA] that encouraged bacterial survival until the specimen reached the laboratory). The bag along with a monthly questionnaire was mailed to the Wake Forest University Baptist School of Medicine (WFUBMC) laboratory for further processing.

2.3. Sample Processing

Upon receipt, fecal specimens were assigned a specimen and laboratory number. The fecal matter was removed from the absorbent paper by swab, as per the biowipe method [34, 35] (if only a small amount of fecal matter was present, the soiled portion was cut out). The swab or absorbent paper cut out was placed into Tryptic Soy Broth (TSB) [Becton Dickinson, Franklin Lakes, NJ] with 20% glycerol. The samples were sonicated in a water bath for one minute at approximately 20kHz. Next the samples were vortexed on high speed for at least two minutes. The broth was then transferred into a 5ml polypropylene culture tube and frozen at -80°C. Samples were analyzed in batches for *E. coli*, *Enterococcus* sp. and *Salmonella* and processed within 48 hours of receipt at the laboratory. As this study was conducted between 2005 and 2007, samples may have been analyzed at any point during this time.

Samples were processed for *E. coli* using the Colilert™ system by IDEXX. Samples were analyzed using quantitrays and the Colilert medium, with incubation for 24 hours; the first 3 hours at 37°C then the remaining time at 44.5°C (the elevated temperature for fecal coliforms). Positive wells were counted (yellow color for fecal coliforms and blue fluorescence under long wavelength UV light for *E. coli*) and the most probable number (MPN) concentration was determined using a table provided by IDEXX. Aliquots of 10µl from several *E. coli*-positive wells per sample were removed aseptically, placed on EC agar medium with MUG, over which was a 0.45µm pore size filter, and streaked to isolate colonies. The plates were incubated for 24 hours at 44.5°C, and colonies that fluoresced blue under UV light were selected for archiving and further characterization.

Enterococcus sp. were analyzed using the Enterolert™ system by IDEXX. Samples were added to quantitrays with the Enterolert medium and incubated for 24 hours at 41°C. Wells that fluoresce were scored positive for *Enterococcus*, tallied and quantified using the MPN table of IDEXX. Then, 10µl aliquots from positive wells were streaked on Bile Esculin Azide agar plates that were incubated at 37 °C for 24 hours. Brownish black colonies with a halo indicative of *Enterococcus* were selected for archiving and further characterization.

Salmonella sp. were analyzed using the 3-volume x 3-replicates per volume broth enrichment-colony isolation MPN method for water sample volumes of 900ml, 90 ml and 9 ml; and samples that were likely to have higher *Salmonella* concentrations were 10-fold serially diluted. Samples were pre-enriched in Buffered Peptone Water by incubating for 18-24 hours at 37°C. The larger water sample volumes (900, 90, 9) were added to 100, 10 and 1 ml of 10X Buffered Peptone Water, respectively; 10ml/10g lagoon samples were added to 10mls of 2X Buffered Peptone Water; and the 1 ml volumes of undiluted or serial dilutions of samples were added to 1X buffered Peptone Water. In each instance, the final concentration of the pre-enrichment medium was a 1X solution. After the 24-hour incubation period, 100µl of pre-enrichment culture was transferred into 10ml of Rappaport-Vassiliadis broth and incubated at 41°C for 24 hours for selective enrichment. From the enrichment cultures, approximately 10 µl were streaked onto Salmonella/Shigella agar using a sterile loop, and the plates were incubated at 37°C for 24 hours. Black

colonies with a clear halo were counted as presumptive positive and several were selected for archiving. *Salmonella* MPNs were computed using the Thomas [36] or standard 3 volume-3 dilution MPN tables.

E. coli and *Enterococcus* sp. with antibiotic resistance were pre-screened using selective agar media impregnated individually with low concentrations of clinically significant antibiotics (Table 1). Any *E. coli* or *Enterococcus* sp. that were able to grow on these selective agars were isolated, collected and archived for further analyses. *Salmonella* sp. was of interest regardless of their resistance traits, and therefore, these organisms were screened with selective agar without antibiotics.

Table 1. Concentrations of Prescreening Antibiotics for Human Bacterial Isolation.

For <i>E. coli</i> :	For <i>Enterococcus</i> Sp.
Ciprofloxacin 2 µg/ml	Ampicillin 8 µg/ml
Gentamicin 4 µg/ml	Gentamicin 250 µg/ml
Norfloxacin 4 µg/ml	Streptomycin 250 µg/ml
Tetracycline 4 µg/ml	Quinupristin/dalphopristin 2 µg/ml
	Vancomycin 8 µg/ml
	Tetracycline 4 µg/ml

All archived isolates were purified and then biochemically identified using Enterotubes® for *E. coli* (Becton Dickinson, Franklin Lakes, NJ) or APi20 strep strips for presumptive *Enterococcus* sp. (BioMérieux, Marcy-l'Étoile, France). Confirmed *E. coli*, and *Enterococcus* sp. were analyzed for antimicrobial sensitivity by standard methods using the Sensititre AST system (ThermoFisher Scientific, Waltham, MA).

2.4. Antibiotic Resistance Testing

Antibiotic resistance profiles were determined using Minimum Inhibitory Concentration (MIC) break points as set by the National Committee for Clinical Laboratory Standards [37] (formerly NCCLS – National Committee of Clinical Laboratory Standards) and the National Antibiotic Resistance Monitoring System (NARMS). For antibiotics for which there are no established breakpoints, MIC₅₀ and MIC₉₀ values were reported.

Sensititre™ multi-well MIC plats by TREK Diagnostics® were used to determine antibiotic resistance profiles, using previously described methods [38]. Veterinary plate layouts were used (CMV1AGNF and CMV1AGPF) according to standard microdilution methods, with each well inoculated with a standard concentration of bacteria (10-200 cfu/µL) and after incubation scoring for growth. Using the MIC breakpoints (or for strictly veterinary drugs, MIC₅₀ and MIC₉₀ – the point at which growth was inhibited for 50% or 90% of the bacterial isolates respectively), the isolate was determined to be susceptible, intermediate, or resistant [39]. Supplemental Table 1 and 2 outline antibiotics tested, concentrations analyzed, and breakpoints used.

2.5. Data Analysis

All information provided by the participants in the introduction (initial) questionnaire was recorded electronically using EpiInfo®. The database was then imported into STATA® (Version 10) and GraphPad® (Version 5) by Instat™ for further data analysis. Using assigned study numbers, all personal information was linked to specimens and bacterial profiles of those bacteria isolated from the specimens.

Initial epidemiologic-microbiologic analysis examined the specimens received and scored them as positive or negative based upon bacterial isolation and antibiotic resistance screening. Specifically, if one or more bacterial isolates from a single specimen was found to be resistant to at least one clinically significant antibiotic upon subsequent antibiotic resistance screening for MIC, the specimen was scored positive. If a single individual had at least one specimen that was positive for resistant bacteria, that person was scored to be positive for the outcome (carriage of antibiotic resistant bacteria).

2.6. Exposure Assessment

Individuals associated with swine farms (the “exposed” group) were compared with those associated with row crop farms (the “unexposed” group) using log-linear regression analysis to determine if risk of harboring antibiotic-resistant bacteria in their fecal microbial flora (outcome) was higher based upon exposure to animal agriculture. To assess risk, we compared the prevalence proportion of carriage in the two exposure groups:

$$(A_1/N_1)/(A_0/N_0) \quad (1)$$

Where A_1 is the number of people in the exposed group, N_1 is the total number of people in the exposed group, A_0 is those with the outcome in the non-exposed group and N_0 is the total number of people in the non-exposed group. A log linear model was then used to assess risk between the two populations where the outcome was carriage of AR bacteria, and the prediction variable is association with animal agriculture. This model compares the prevalence proportion of the exposed group to the unexposed group:

$$\text{Probability of Outcome} = \alpha + \beta_1(X_1) + \beta_2(X_2) \dots \beta_n(X_n) \quad (2)$$

Where β_1 is the regression coefficient for the exposure variable and $\beta_{2...n}$ are the regression coefficients for other variables that may be included in the model such as age, gender, race/ethnicity, etc. To understand the potential impacts of each of these variables, exposure risk estimates were calculated (data not shown) based on each of the variables being the exposure rather than the farm type with which the individual was associated. This model was:

$$\text{Outcome} = \alpha + \beta_1(\text{assessed variable}) \quad (3)$$

An adjusted log linear model was used to determine a risk ratio for each variable along with outcome and exposure:

$$\text{Outcome} = \alpha + \beta_1(\text{exposure}) + \beta_2(\text{assessed variable}) \quad (4)$$

To determine the potential for confounding, the risk ratios (RR) of the adjusted models (not shown) were compared with the crude model and the impact of any variable was determined by a ten percent change in the natural log of the risk estimates. The percent change was calculated using:

$$\% \text{change} = (\ln(\text{modified}) - \ln(\text{crudeRR})) / \ln(\text{crudeRR}) \quad (5)$$

Six variables resulted in a 10% change in estimate ([Table 2](#)) and the adjusted model was:

$$\text{Prob}(\text{outcome}) = \alpha + \beta_1(\text{exposure}) + \beta_2(\text{drinking water source}) + \beta_3(\text{chronic illness}) + \beta_4(\text{pets}) + \beta_5(\text{antibiotic use}) + \beta_6 - \beta_{10}(\text{age category}) \quad (6)$$

Table 2. Risk Ratio Estimates, 95% Confidence Limits, p-value and % Change in Estimates for Models including Different Variables that may Impact the Risk Estimation of Carriage of Resistant Bacteria.

Model Variables	Risk ratio	95% Confidence Interval (Precision)*		P-value	% change
Exposure (Crude model)	1.31	1.05- 1.63	(1.55)	0.017	--
Exposure + Farmer	1.28	1.04-1.58	(1.77)	0.020	-7.5%
Exposure + Age (Categorical)	1.25	1.06-1.48	(1.40)	0.008	-15.9%
Exposure + Age (Dichotomous)	1.28	1.03 -1.58	(1.53)	0.026	-8.9%
Exposure +Gender	1.32	1.06 -1.65	(1.56)	0.013	4.3%
Exposure + Race	1.31	1.05-1.64	(1.56)	0.019	0.6%
Exposure + Doctor visit	1.29	1.03-1.61	(1.56)	0.025	-5.3%
Exposure + Antibiotic usage	1.27	1.02-1.58	(1.55)	0.034	-11.0%
Exposure + Antacid use	1.35	1.09 -1.67	(1.53)	0.06	3.0%
Exposure +Steroid use	1.29	1.04-1.60	(1.54)	0.021	-5.1%
Exposure +Chronic illness	1.34	1.07-1.68	(1.57)	0.011	10.0%
Exposure + Pets	1.35	1.08-1.69	(1.56)	0.007	13.2%
Exposure +Foreign travel	1.28	1.02-1.60	(1.57)	0.030	-7.2%
Exposure + Immigration	1.33	1.06-1.65	(1.56)	0.012	5.5%
Exposure + Water source	1.39	1.12-1.71	(1.53)	0.002	21.9%
Exposure +Recreational water use	1.27	1.03-1.58	(1.53)	0.026	-9.6%
Exposure + Eat soft cheese	1.27	1.03-1.57	(1.52)	0.027	-10.9%
Exposure +Eat raw/Rare meat	1.31	1.06-1.64	(1.55)	0.014	2.3%

Note: * Precision is the confidence interval width (Upper Limit / Lower limit).

The age variable was categorical and dummy variables were used to account for each age category. The risk estimate for this model was assessed using a backwards elimination approach to determine if all variables were required. This technique begins with the full model and removes one variable at a time. As done above in comparing the crude to the adjusted models, the percent change in estimate was assessed as each variable was removed from the model. In this case the full model is compared with that of the removed covariate. The final model was:

$$\text{Prob}(\text{outcome}) = \alpha + \beta_1(\text{exposure}) + \beta_2(\text{drinking water source}) + \beta_3(\text{antibiotic use}) + \beta_4(\text{pets}) \quad (7)$$

3. RESULTS

3.1. Participants

A total of 126 farmers and neighbors of eleven animal agriculture facilities and six row crop farms in six North Carolina counties were enrolled in the study. There was a significant loss to follow up of the recruited participants, because of the 126 people who enrolled, only 87 (69%) sent at least one fecal specimen during the study period. Only 15 people (12%) submitted all 12 of the requested specimens. Of the 87 people that submitted at least one specimen, 15 only sent one (1) specimen, 12 sent only two (2) to three (3) specimens, 25 sent four (4) to eight (8) specimens and 35 sent nine to 12 specimens. All participants who submitted at least one specimen were included in the risk analysis. This resulted in a total of 578 specimens among the 126 participants, 87 of which sent at least one fecal specimen.

Of the 87 active participants, who submitted at least one specimen, 47 (54%) were employees or neighbors of an animal agriculture facility, and 40 (46%) were employees or neighbors of a row crop farm. The participants were not matched based upon demographic characteristics. However, for comparison purposes, it was important to characterize similarities or differences between these two groups.

There was no statistically significant difference between the two populations in gender ($p=0.4680$), age ($p=0.817$), or household income ($p=0.092$). However, race/ethnicity was the only variable for which there was a significant difference between the exposure groups. The proportion of minorities in the row crop communities was significantly lower than the proportion in CAFO communities ($p = 0.015$). Of those associated with the row crop farms, 98% of the participants were Caucasian/White, one was African American/Black and none were Hispanic. In the group associated with animal agriculture, 72% were Caucasian/White, 17% (eight people) were African American/Black and 11% (five people) were Hispanic. Upon closer examination of the three race/ethnicity categories (White/Caucasian, Black/African American and Hispanic) there were disparities in those that submitted specimens.

Seventy percent (70%, 12 people) of Hispanics that were recruited did not submit any specimens. Comparatively, only 26% (25 people) of White/Caucasian enrollees and 18% (2 people) Black/African American participants did not submit any samples. Calculating an odds ratio, recruited Hispanic participants were 10.8 times higher odds of not submitting any specimens (95% CI 1.35-125.132) than the recruited participants that were White/Caucasian. In other words, there was a statistically higher proportion of Hispanics that were lost to follow up than those who were White/Caucasian ($p=0.0068$). Comparing the Black/African American recruits to their White/Caucasian counterparts, there was no increase in the odds of submission of specimens ($OR = 1.54$, $[0.29 \text{ } 15.55]$, $p = 0.5934$).

3.2. Human Specimens

Of the 87 participants who submitted a total of 578 specimens., 285 (49%) did not yield *E. coli* or *Enterococcus* sp. when isolated on selective agar media (MacConkey Agar and Enterococcus Agar, respectively) impregnated with low level antibiotics. Of the remaining fecal specimens, 106 (18%) had at least one *E. coli* that was resistant to the prescreening antibiotics and 200 specimens had at least one *Enterococcus* isolate with resistance to one of the six prescreening drugs. A total of 148 *E. coli* and 265 *Salmonella* isolates were biochemically confirmed from human specimens.

The number of resistant isolates per specimen ranged from one to five *E. coli*, *Enterococcus* or both; however, the majority of the specimens only had one isolate. There was a total of 154 positive specimens submitted by people associated with CAFOs and 143 positive specimens submitted by people associated with row crop farms. Specimens with multiple isolates were submitted by people in both groups.

Of the 87 people who submitted specimens, only 16 people had no growth of antibiotic resistant bacteria in their stool samples. Twelve (12) of these individuals were associated with row crop farms and four were associated with swine farms. There were 13 people for which all of their specimens had at least minimally resistant targeted enteric bacteria present. For all other participants, more than one of the specimens had resistant bacteria and at least one specimen did not contain any bacteria with resistance.

3.3. Risk analysis

3.3.1. Risk of Carriage

Assessing only risk of carriage, those associated with animal agriculture had a higher risk of antibiotic resistance than those associated with row crop farms ($RR_{crude} = 1.31$, 95% CI=1.05, 1.63, $Prob>|z| = 0.017$). This estimate implies that those who live near or work on animal agriculture facilities are 1.31 times (30%) more likely to carry antibiotic-resistant bacteria in their gastrointestinal bacterial flora than those who live near or work on row crop farms. As many factors outside of exposure could impact this result, the 18 potential confounders considered in the analysis and are shown in Table 2. Using a backwards elimination approach and a 10% change in estimate technique, the final model included three covariates: antibiotic use, drinking water and having pets. Considering all the factors, the final model estimates had a Risk Ratio of 1.42 (95% CI = 1.17-1.72). This estimate is statistically significant as the confidence interval does not include the null value of 1.0. The precision of this estimate as determined by the confidence interval width (Upper limit/Lower limit) is 1.47. Furthermore, adjusting for the covariates did make the estimate more precise than the crude model (precision = 1.55) or adjusting for any of the three covariates alone in an adjusted model. For the three variables the precision was greater than 1.60 in the adjusted models.

While in this analysis, farmer status did not have an impact on the overall risk analysis, there is interest in understanding the potential risk of working in animal agriculture as opposed to working in a non-animal agriculture setting. In this study 23 farmers submitted at least one specimen: nine row crop farmers and 14 animal agriculture growers. When comparing these two groups, utilizing log-linear regression, the Risk Ratio is 1.93 (0.90 – 4.13). While the risk appears to be larger among growers than that among the community as a whole, ($RR_{crude}=1.31$), the confidence interval includes the null value and therefore the result is not statistically significant. However, the

precision of this estimate is relatively large (4.59 compared with 1.55 of the overall study). A larger population size would likely increase the precision of the estimate, in which case a better estimate of the risk could be calculated.

3.3.2. Risk Based On Magnitude of Antibiotic-Resistant Isolates

Resistant *E. coli* isolates were collected from people who lived near or worked on CAFOs as well as those associated with row crop farms. Of the 148 isolates collected from the stool samples, 89 of them (60%) were isolated from people in the animal agriculture communities and 59 isolates (40%) were collected from people associated with the row crop farms. *E. coli* isolates collected from those people who live near or work on row crop farms (no exposure) had a statistically different frequency distribution of multi-drug resistance than the *E. coli* isolates collected from people associated with swine CAFOs (Kolmogrov-Smirnov $p < 0.0001$) (Figure 2). Overall, isolates collected from people associated with row crop farms have a higher frequency of multi-drug resistance ($p = 0.004$) as well as a higher proportion of isolates resistance to higher numbers of antibiotics. The highest number of antibiotics to which *E. coli* isolates had resistance was nine (9) for people associated with CAFOs and 10 for people in row crop communities. When comparing proportions of the two exposure groups for *E. coli* resistance to four (4) or more antibiotics and six (6) or more antibiotics, the proportion of isolates collected from people in row crop communities had higher frequencies of resistance to the multiple drugs than those isolates collected from CAFO communities ($p = 0.0007$ & $p < 0.0001$). In other words, *E. coli* isolates collected from people in row crop communities had resistance to more antibiotics and at a higher frequency than those *E. coli* isolates collected from people in animal agriculture communities.

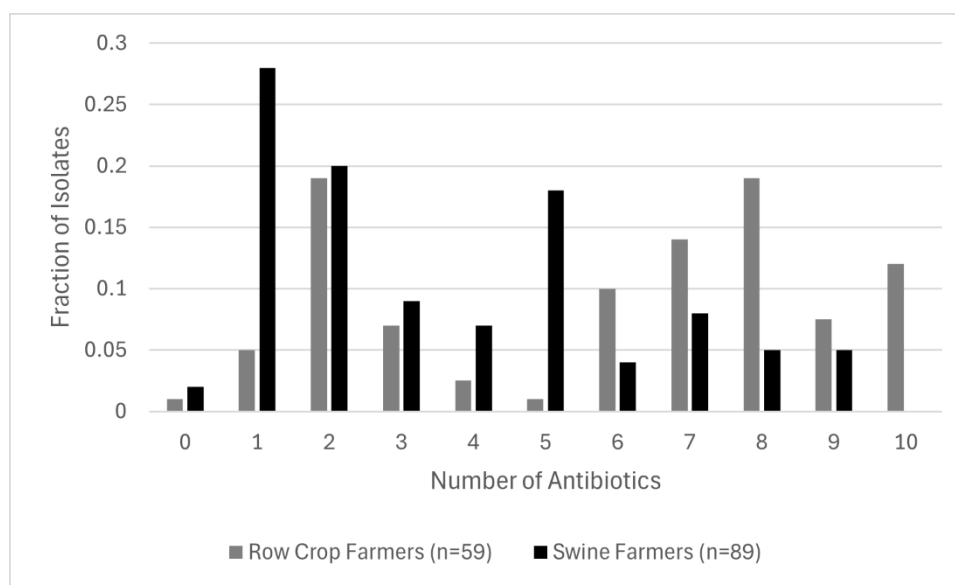


Figure 2. Proportion of *E. coli* Isolates from Human Study Participants Resistant to Different Numbers of Antibiotics by Row Crop Farmers (No exposure group) and Swine Farmers (Exposure group).

A total of 265 *Enterococcus* isolates were collected from the submitted specimens. Of these isolates, 86 (32%) were isolated from people associated with row crop farms and 179 (68%) were isolated from people associated with swine animal agriculture. Unlike the *E. coli* isolates, the frequency distributions of drug resistance in *Enterococci* by exposure were not significantly different (Kolmogrov-Smirnov $p = 0.65$). Furthermore, there were no significant differences in the proportions of multi-drug resistance, based on conducted proportion analyses comparing frequency of resistance to two or more drugs ($p = 0.87$) (including human and veterinary drugs), four or more drugs ($p = 0.89$) and six or more drugs ($p = 0.81$) in the two exposure groups.

4. DISCUSSION

Antibiotic resistant bacteria are found in people associated with animal agriculture and row crop farming. Overall, there was a higher proportion of drug resistant bacteria (both *E. coli* and *Enterococcus*) found in people associated with animal agriculture than those associated with row crop farms. However, when examining the magnitude of the number of antibiotics to which the individual bacteria are resistant, there was no difference among the *Enterococcus* isolates collected from people associated with row crop farms compared with those isolates collected from people associated with swine CAFOs. In contrast, the *E. coli* isolates collected from people associated with row crop farms had a higher proportion of multi-drug resistant bacteria than the isolates collected from people in swine CAFO communities.

The reasons for why *E. coli* isolates collected from people associated with row crop farms had a higher proportion of multi-drug resistant bacteria than the isolates collected from people in swine CAFO communities is unknown and deserves further study. However here are some plausible reasons for this difference:

- Antibiotic use in crops: While not as common as in animal agriculture, antibiotics can be used on crops to control certain bacterial diseases. This creates a selective pressure for resistant bacteria in the environment, which people can then be exposed to.
- Manure application: Even on row crop farms, manure from CAFOs or other livestock operations might be used as fertilizer or soil amendment. This can introduce additional resistant bacteria into the environment to which people get exposed.
- Water contamination: Runoff from fields can carry bacteria, including multi-resistant *E. coli*, into waterways. People who use this water for irrigation or even recreation could be exposed.
- Diversity of resistant strains: Row crop farms might have a wider variety of environmental sources for antibiotic-resistant bacteria compared to CAFOs with a more controlled environment, due to the use of only specific antibiotics. This diversity could lead to a higher chance of encountering multi-drug resistant strains present on row crop farms.
- Other sources of exposure: People in both types of farm communities could have additional but different sources of exposure to resistant bacteria, such as travel or contact with healthcare facilities.

The results of this study yielded valuable data on antibiotic-resistant bacteria presence on intensive swine agriculture and row crop farms and in people working on and living near these farms that provide a much better understanding of antibiotic resistant bacteria human carriage in rural communities in eastern North Carolina. It was possible to analyze the two exposure groups, people working on or near intensive swine agriculture farms and people associated with row crop farms, with regard to carriage of antibiotic-resistant bacteria. The risk of antibiotic-resistant bacteria carriage was significantly higher in people associated with swine agriculture farms compared to those associated with row crop farms (unadjusted RR = 1.31, 95% CI = 1.05 to 1.63). However, the sources of the antibiotic-resistant bacteria harbored by the participants of this study are unclear based on the study findings.

Comparing the two study populations, there was a higher occurrence of antibiotic-resistant bacteria carriage among those people who live near or worked on intensive swine agriculture facilities when compared to those who are associated with non-animal agriculture (row crop) facilities. This relationship held true in the crude model in which only exposure status and outcome was assessed, as well as in models for which other potentially confounding variables were included, such as source of drinking water, medication usage, having pets and overall health of the participant.

After assessing all the potential cofounders and relevant demographic variables, it was found that a model including the outcome, type of farm association (exposure), the source of drinking water, having pets and use of antibiotics during the study was the most appropriate. Using this modeling approach, there is a risk ratio estimate of 1.42 (95% CI = 1.17 -1.72). As the confidence limits do not include the null value, this estimate is considered to be statistically significant. Given this estimate, it is concluded that there is an increased risk of antibiotic resistant

bacteria carriage in those who are associated with animal agriculture when compared with those associated with non-animal agriculture. In other words, people who live near or work on intensive animal agriculture facilities are 1.4 times more likely to carry antibiotic resistant bacteria in their fecal material than those who live near or work on row crop farms. An important consideration in this risk estimate is also the interaction between the participants and prescription antibiotics. It is well known that the over prescription of antibiotics results in an abundance of AR bacteria in humans. However, this is an understudied and undervalued area of antibiotic exposure and use concerning the understanding of AR use and occupational exposures. In our population we do not have specific medical histories of the participants, as we are evaluating occupational exposures. Despite this, it is possible that infections, antibiotic prescriptions, and individual resistance to antibiotics and the presence of AR through other means could be a confounder in the risk of AR bacterial carriage.

Although there are few other studies that evaluate the trend in antimicrobial resistance related to individuals who live near or work on row crop farms, there is increasing evidence that there are high levels of environmental resistance that contribute to human disease and health outcomes [39, 40]. In studies that evaluated antimicrobial resistance in humans and animals, and in particular the widespread use of antimicrobials on animal farms, indiscriminate use of antibiotics is known to increase the prevalence of AR bacteria in both humans and animals [41, 42]. In studies examining the difference between industrial livestock operations and antibiotic free livestock operations, industrial livestock operation workers were significantly more likely to carry AR *Staphylococcus aureus* [32]. As seen in our results, although animal exposure does increase the number of detected AR bacteria, AR continues to be prevalent in agricultural settings and in environments downstream of areas where antimicrobials are used.

As this was only a pilot study involving a relatively small number of farms and farm workers or neighbors and was of limited and variable duration, not all of the initial research questions could be adequately addressed with sufficient analytical power to determine if there were clear differences in risks in carriage of antibiotic resistant enteric bacteria, based on the types and frequencies of bacterial carriage and the properties of these resistant bacteria in the exposed and unexposed study groups. Another limitation of this study is that it did not include molecular genetic analysis of the identified antibiotic resistant bacteria. Such molecular genetic analysis could have potentially revealed other difference or similarities between the antimicrobial resistant bacteria of people associated with swine farms (the exposed) compared people associated with row crop farms (the unexposed). However, because some statistically significant differences were observed in this pilot study, notably antibiotic resistant carriage frequencies, it is recommended that larger studies of this type involving more farms and people be conducted to better understand the risks and their possible exposure sources of antibiotic resistant bacteria in these agricultural communities and their people.

5. CONCLUSIONS

Only limited research has been conducted to evaluate the AR bacteria exposure at the human animal interface on farms. The results of our work in North Carolina indicate that there is a greater risk of carriage of AR enteric bacteria in swine farm workers when compared to row crop workers. However, further investigation of additional CAFOs and row crop farms is recommended to increase statistical power in determining if there are or are not differences in the prevalence of AR bacteria found in the environment and in people on swine farms compared to row crop farms. Such studies can more fully assess impacts of swine agriculture on human carriage, infection, and possibly health effects associated with AR exposure to enteric bacteria.

REFERENCES

- [1] North Carolina Department of Agriculture and Consumer Services & United States Department of Agriculture National Agricultural Statistics Service, "2023 North Carolina agricultural statistics, Publication No. 224, North Carolina

- Department of Agriculture and Consumer Services, 2023," 2023. https://data.nass.usda.gov/Statistics_by_State/North_Carolina/Publications/Annual_Statistical_Bulletin/AgStat2023.pdf
- [2] M. E. Anderson and M. D. Sobsey, "Detection and occurrence of antimicrobially resistant *E. coli* in groundwater on or near swine farms in eastern North Carolina," *Water Science and Technology*, vol. 54, no. 3, pp. 211-218, 2006. <https://doi.org/10.2166/wst.2006.471>
- [3] I. Phillips *et al.*, "Does the use of antibiotics in food animals pose a risk to human health? A critical review of published data," *Journal of Antimicrobial Chemotherapy*, vol. 53, no. 1, pp. 28-52, 2004. <https://doi.org/10.1093/jac/dkg483>
- [4] U.S. Food and Drug Administration Center for Veterinary Medicine, "New animal drugs and new animal drug combination products administered in or on medicated feed or drinking water of food-producing animals: Recommendations for drug sponsors for voluntarily aligning product use conditions with GFI #209, Guidance for Industry No. 213, U.S. Department of Health and Human Services," 2013. <https://www.fda.gov/media/83488/download>
- [5] A. Lekagul, V. Tangcharoensathien, and S. Yeung, "Patterns of antibiotic use in global pig production: A systematic review," *Veterinary and Animal Science*, vol. 7, p. 100058, 2019. <https://doi.org/10.1016/j.vas.2019.100058>
- [6] B. A. Wiggins, "Discriminant analysis of antibiotic resistance patterns in fecal streptococci, a method to differentiate human and animal sources of fecal pollution in natural waters," *Applied and Environmental Microbiology*, vol. 62, no. 11, pp. 3997-4002, 1996. <https://doi.org/10.1128/aem.62.11.3997-4002.1996>
- [7] J. C. Chee-Sanford, R. I. Aminov, I. J. Krapac, N. Garrigues-Jeanjean, and R. I. Mackie, "Occurrence and diversity of tetracycline resistance genes in lagoons and groundwater underlying two swine production facilities," *Applied and Environmental Microbiology*, vol. 67, no. 4, pp. 1494-1502, 2001. <https://doi.org/10.1128/AEM.67.4.1494-1502.2001>
- [8] E. R. Campagnolo *et al.*, "Antimicrobial residues in animal waste and water resources proximal to large-scale swine and poultry feeding operations," *Science of the Total Environment*, vol. 299, no. 1-3, pp. 89-95, 2002. [https://doi.org/10.1016/S0048-9697\(02\)00233-4](https://doi.org/10.1016/S0048-9697(02)00233-4)
- [9] S. Donabedian, L. A. Thal, P. Bozigar, T. Zervos, E. Hershberger, and M. Zervos, "Antimicrobial resistance in swine and chickens fed virginiamycin for growth promotion," *Journal of Microbiological Methods*, vol. 55, no. 3, pp. 739-743, 2003. <https://doi.org/10.1016/j.mimet.2003.07.002>
- [10] L. Garcia-Migura, E. Pleydell, S. Barnes, R. H. Davies, and E. Liebana, "Characterization of vancomycin-resistant *Enterococcus faecium* isolates from broiler poultry and pig farms in England and Wales," *Journal of Clinical Microbiology*, vol. 43, no. 7, pp. 3283-3289, 2005. <https://doi.org/10.1128/jcm.43.7.3283-3289.2005>
- [11] R. M. Travis *et al.*, "Chloramphenicol and kanamycin resistance among porcine *Escherichia coli* in Ontario," *Journal of Antimicrobial Chemotherapy*, vol. 58, no. 1, pp. 173-177, 2006. <https://doi.org/10.1093/jac/dkl207>
- [12] C. R. Jackson, P. J. Fedorka-Cray, J. B. Barrett, L. M. Hiott, and T. A. Woodley, "Prevalence of streptogramin resistance in enterococci from animals: Identification of vatD from animal sources in the USA," *International Journal of Antimicrobial Agents*, vol. 30, no. 1, pp. 60-66, 2007. <https://doi.org/10.1016/j.ijantimicag.2007.03.010>
- [13] P. M. da Costa, M. Oliveira, A. Bica, P. Vaz-Pires, and F. Bernardo, "Antimicrobial resistance in *Enterococcus* spp. and *Escherichia coli* isolated from poultry feed and feed ingredients," *Veterinary Microbiology*, vol. 120, no. 1-2, pp. 122-131, 2007. <https://doi.org/10.1016/j.vetmic.2006.10.005>
- [14] V. Economou and P. Gousia, "Agriculture and food animals as a source of antimicrobial-resistant bacteria," *Infection and Drug Resistance*, vol. 8, pp. 49-61, 2015. <https://doi.org/10.2147/IDR.S55778>
- [15] P. R. Randad *et al.*, "Transmission of antimicrobial-resistant *Staphylococcus aureus* clonal complex 9 between pigs and humans, United States," *Emerging Infectious Diseases*, vol. 27, no. 3, pp. 740-748, 2021. <https://doi.org/10.3201/eid2703.191775>

- [16] J. P. Graham *et al.*, "The animal-human interface and infectious disease in industrial food animal production: Rethinking biosecurity and biocontainment," *Public Health Reports*, vol. 123, no. 3, pp. 282-299, 2008. <https://doi.org/10.1177/003335490812300309>
- [17] M. Aziz *et al.*, "Pediatric urinary tract infections caused by poultry-associated *Escherichia coli*," *Microbiology Spectrum*, vol. 12, no. 7, pp. e03415-23, 2024. <https://doi.org/10.1128/spectrum.03415-23>
- [18] C. M. Schroeder *et al.*, "Antimicrobial resistance of *Escherichia coli* O157 isolated from humans, cattle, swine, and food," *Applied and Environmental Microbiology*, vol. 68, no. 2, pp. 576-581, 2002. <https://doi.org/10.1128/AEM.68.2.576-581.2002>
- [19] P. Messi, E. Guerrieri, S. de Niederhausern, C. Sabia, and M. Bondi, "Vancomycin-resistant enterococci (VRE) in meat and environmental samples," *International Journal of Food Microbiology*, vol. 107, no. 2, pp. 218-222, 2006. <https://doi.org/10.1016/j.ijfoodmicro.2005.08.026>
- [20] S. M. D. Bearson, "Salmonella in swine: Prevalence, multidrug resistance, and vaccination strategies," *Annual Review of Animal Biosciences*, vol. 10, no. 1, pp. 373-393, 2022. <https://doi.org/10.1146/annurev-animal-013120-043304>
- [21] K. Mølbak *et al.*, "An outbreak of multidrug-resistant, quinolone-resistant *Salmonella enterica* serotype Typhimurium DT104," *New England Journal of Medicine*, vol. 341, no. 19, pp. 1420-1425, 1999. <https://doi.org/10.1056/NEJM199911043411902>
- [22] S. B. Levy, "Emergence of antibiotic-resistant bacteria in the intestinal flora of farm inhabitants," *The Journal of Infectious Diseases*, vol. 137, no. 5, pp. 688-690, 1978. <https://doi.org/10.1093/infdis/137.5.688>
- [23] A. E. van den Bogaard, N. London, C. Driessen, and E. E. Stobberingh, "Antibiotic resistance of faecal *Escherichia coli* in poultry, poultry farmers and poultry slaughterers," *Journal of Antimicrobial Chemotherapy*, vol. 47, no. 6, pp. 763-771, 2001. <https://doi.org/10.1093/jac/47.6.763>
- [24] A. E. van den Bogaard, R. Willems, N. London, J. Top, and E. E. Stobberingh, "Antibiotic resistance of faecal enterococci in poultry, poultry farmers and poultry slaughterers," *Journal of Antimicrobial Chemotherapy*, vol. 49, no. 3, pp. 497-505, 2002. <https://doi.org/10.1093/jac/49.3.497>
- [25] H. Aubry-Damon *et al.*, "Antimicrobial resistance in commensal flora of pig farmers," *Emerging Infectious Diseases*, vol. 10, no. 5, pp. 873-879, 2004. <https://doi.org/10.3201/eid1005.030735>
- [26] C. Xu, L. Kong, H. Gao, X. Cheng, and X. Wang, "A review of current bacterial resistance to antibiotics in food animals," *Frontiers in Microbiology*, vol. 13, p. 822689, 2022. <https://doi.org/10.3389/fmicb.2022.822689>
- [27] A. O. Ajayi, A. T. Odeyemi, O. J. Akinjogunla, A. B. Adeyeye, and I. Ayo-Ajayi, "Review of antibiotic-resistant bacteria and antibiotic resistance genes within the one health framework," *Infection Ecology & Epidemiology*, vol. 14, no. 1, p. 2312953, 2024. <https://doi.org/10.1080/20008686.2024.2312953>
- [28] D. D. Ferguson, T. C. Smith, B. M. Hanson, S. E. Wardyn, and K. J. Donham, "Detection of airborne methicillin-resistant *Staphylococcus aureus* inside and downwind of a swine building, and in animal feed: Potential occupational, animal health, and environmental implications," *Journal of Agromedicine*, vol. 21, no. 2, pp. 149-153, 2016. <https://doi.org/10.1080/1059924X.2016.1142917>
- [29] F.-Z. Gao *et al.*, "Swine farm groundwater is a hidden hotspot for antibiotic-resistant pathogenic *Acinetobacter*," *ISME Communications*, vol. 3, no. 1, p. 34, 2023. <https://doi.org/10.1038/s43705-023-00240-w>
- [30] L. M. Johnston and L.-A. Jaykus, "Antimicrobial resistance of *Enterococcus* species isolated from produce," *Applied and Environmental Microbiology*, vol. 70, no. 5, pp. 3133-3137, 2004. <https://doi.org/10.1128/AEM.70.5.3133-3137.2004>
- [31] G. Sengeløv, Y. Agersø, B. Halling-Sørensen, S. B. Baloda, J. S. Andersen, and L. B. Jensen, "Bacterial antibiotic resistance levels in Danish farmland as a result of treatment with pig manure slurry," *Environment International*, vol. 28, no. 7, pp. 587-595, 2003. [https://doi.org/10.1016/S0160-4120\(02\)00084-3](https://doi.org/10.1016/S0160-4120(02)00084-3)

- [32] J. L. Rinsky *et al.*, "Livestock-associated methicillin and multidrug resistant *Staphylococcus aureus* is present among industrial, not antibiotic-free livestock operation workers in North Carolina," *PLoS One*, vol. 8, no. 7, p. e67641, 2013. <https://doi.org/10.1371/journal.pone.0067641>
- [33] L. M. Casanova, V. R. Hill, and M. D. Sobsey, "Antibiotic-resistant *Salmonella* in swine wastes and farm surface waters," *Letters in Applied Microbiology*, vol. 71, no. 1, pp. 117-123, 2020. <https://doi.org/10.1111/lam.13242>
- [34] E. Sozzi *et al.*, "The BioWipe: A non-invasive method to detect intestinal carriage of multi-drug resistant GRAM-negative bacteria," *Journal of Chemotherapy*, vol. 34, no. 3, pp. 203-205, 2022. <https://doi.org/10.1080/1120009X.2021.2008643>
- [35] J. Mans *et al.*, "Applicability of Bio-wipes for the collection of human faecal specimens for detection and characterisation of enteric viruses," *Tropical Medicine & International Health*, vol. 19, no. 3, pp. 293-300, 2014. <https://doi.org/10.1111/tmi.12251>
- [36] H. A. Thomas, "Bacterial densities from fermentation tube tests," *Journal (American Water Works Association)*, vol. 34, no. 4, pp. 572-576, 1942. <https://doi.org/10.1002/j.1551-8833.1942.tb19721.x>
- [37] National Committee for Clinical Laboratory Standards, *Performance standards for antimicrobial susceptibility testing: Twelfth informational supplement (NCCLS document M100-S12)*. Wayne, PA: National Committee for Clinical Laboratory Standards, 2002.
- [38] D. Cole *et al.*, "Free-living Canada geese and antimicrobial resistance," *Emerging Infectious Diseases*, vol. 11, no. 6, pp. 935-938, 2005. <https://doi.org/10.3201/eid1106.040717>
- [39] A. Scherer, H. R. Vogt, E. M. Vilei, J. Frey, and V. Perreten, "Enhanced antibiotic multi-resistance in nasal and faecal bacteria after agricultural use of streptomycin," *Environmental Microbiology*, vol. 15, no. 1, pp. 297-304, 2013. <https://doi.org/10.1111/1462-2920.12028>
- [40] E. O. Ager, T. Carvalho, E. M. Silva, S. C. Rieke, and J. L. Hite, "Global trends in antimicrobial resistance on organic and conventional farms," *Scientific Reports*, vol. 13, p. 22608, 2023. <https://doi.org/10.1038/s41598-023-47862-7>
- [41] K. Lunha *et al.*, "Antimicrobial resistance in fecal *Escherichia coli* from humans and pigs at farms at different levels of intensification," *Antibiotics*, vol. 9, no. 10, p. 662, 2020. <https://doi.org/10.3390/antibiotics9100662>
- [42] G. Ström *et al.*, "Antimicrobials in small-scale urban pig farming in a lower middle-income country—arbitrary use and high resistance levels," *Antimicrobial Resistance & Infection Control*, vol. 7, p. 35, 2018. <https://doi.org/10.1186/s13756-018-0328-y>

Online Science Publishing is not responsible or answerable for any loss, damage or liability, etc. caused in relation to/arising out of the use of the content. Any queries should be directed to the corresponding author of the article.