Science of the Total Environment 985 (2025) 179591

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Swine production intensity and swine-specific fecal contamination of household surfaces at residences of industrial livestock operation workers and community residents, North Carolina, USA

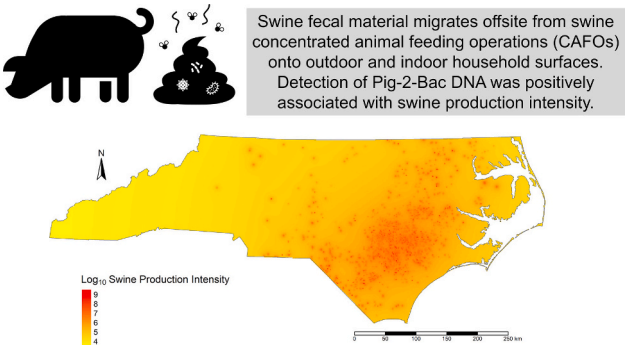
Kathleen M. Kurowski [a,b], Nora Pisanic [a,b], Kristoffer Spicer [a,b], Kate Kruczynski [a], Carolyn Gigot [a,b], Devon J. Hall Jr [c], Devon J. Hall Sr [c], Kyle T. Aune [a], Bonita Salmerón [a,b], Ana M. Rule [a], Christopher D. Heaney [a,b,d,e,*]

[a] Department of Environmental Health and Engineering, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA
[b] Community Science and Innovation for Environmental Justice Initiative, Center for a Livable Future, Department of Environmental Health and Engineering, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA
[c] Rural Empowerment Association for Community Help, Warsaw, NC, USA
[d] Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA
[e] Department of International Health, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA

HIGHLIGHTS

- Swine industrial livestock operations (ILOs) in NC produce large amounts of fecal waste.
- Nearby residents are concerned about fecal pollution from swine ILOs, which are regulated as non-discharge facilities.
- More Pig-2-Bac was detected on household surfaces in areas of higher swine production intensity.
- More Pig-2-Bac was detected outdoors compared to indoors, indicating an ambient environmental source.
- Pig-2-Bac has utility to quantify off-site migration of swine fecal matter to households proximal to ILOs.

GRAPHICAL ABSTRACT



ARTICLE INFO

Editor: Warish Ahmed

Keywords:
Concentrated animal feeding operations (CAFOs)
Hog production
Swine
Pig-2-Bac
Environmental justice

ABSTRACT

In North Carolina (NC), industrial livestock operations (ILOs) that produce swine concentrate fecal waste in lagoons and sprayfields, which are disproportionately located in low-income communities of color. Although swine-specific fecal contamination of surface waters proximal to swine ILOs has been documented, less is known about contamination of homes proximal to swine ILOs. Up to 6 outdoor and 6 indoor surface settled dust samples were collected from households: 1) with >= 1 ILO worker (ILO-W); 2) neighboring ILOs without occupational exposure to livestock (ILO-N); and 3) in metropolitan areas of NC (Metro). Using quantitative real-time PCR, the DNA copy number of Pig-2-Bac, a swine-specific fecal microbial source tracking (MST) marker, per square inch of household surfaces sampled was measured. We used permits of swine ILOs and steady state live weight to assign swine production intensity (SPI) exposure values to each household. We estimated associations between

* Corresponding author at: Department of Environmental Health and Engineering, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA.
E-mail address: cheaney1@jhu.edu (C.D. Heaney).

https://doi.org/10.1016/j.scitotenv.2025.179591
Received 13 October 2024; Received in revised form 7 April 2025; Accepted 30 April 2025
Available online 27 May 2025
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Fecal contamination
Microbial source tracking

household group (Metro as reference), outdoor versus indoor household surface, and $\log_{10}$ SPI with Pig-2-Bac DNA detection frequency (logistic) and quantity (linear) via regression modeling. Prevalence of household Pig-2-Bac positivity was 38 % (40/105) at ILO-W (159/536 swabs; 30 %); 44 % (47/107) at ILO-N (142/557 swabs; 25 %), and 1 % (1/81) at Metro (1/321 swabs; 1 %) households. Pig-2-Bac DNA was detected more often (odds ratio [OR] = 2.2; 95 % confidence interval [CI] = 1.6, 3.0) and in higher quantity ($\beta = 0.30$; 95 % CI = 0.19, 0.41) on outdoor compared to indoor surfaces. For every $\log_{10}$ unit increase in SPI, the Pig-2-Bac DNA detection frequency (OR = 5.4; 95 % CI = 2.8, 10.4) and quantity ($\beta = 0.21$; 95 % CI = 0.13, 0.29) increased. Results demonstrate the utility of Pig-2-Bac DNA measurement in household surface dust and suggest that swine ILOs contribute to the contamination of NC community residents' households with swine fecal material.

1. Introduction

Hog production in North Carolina (NC) is a multi-billion-dollar industry dominated by a small number of large, vertically integrated, transnational corporations, with one corporation controlling approximately 90 % of the state's hog production (https://ncglobaleconomy.com/hog/overview.shtml, n.d.). While most US-grown pork is consumed in the country, the US has also increasingly become a major exporter of pork, mainly to Japan, Mexico, China and Canada. While the product of these operations is shipped internationally, the adverse environmental impacts of industrial livestock production, including the approximately 10 billion gallons of liquid pig manure that NC's 18 million pigs produce each year (*North Carolina Annual Statistics Bulletin - Section 4: Livestock, Dairy, and Poultry Statistics*, 2022; Vilsack and Hamer, 2024), remain a local burden. Almost all swine in NC are raised in large-scale, vertically-integrated industrial livestock operations (ILO) designed to maximize outputs and minimize costs (Casey et al., 2015). Duplin and neighboring Sampson Counties, the two largest hog-producing counties in the United States, are home to about 4 million hogs that generate about half of the state's hog waste (Hamer et al., 2023). This waste is often stored in open pit lagoons and distributed over agricultural sprayfields nearby (*North Carolina Annual Statistics Bulletin - Section 4: Livestock, Dairy, and Poultry Statistics*, 2022; Hamer et al., 2023; Doherty, 2020).

Fecal material can be dispersed through air and runoff contaminating surface waters and watersheds nearby sprayfields and swine operations, but there is no acknowledgement of any air emissions from facilities. The NC Department of Environment and Natural Resources (NC DENR) permits swine concentrated animal feeding operations (CAFOs) as water non-discharge facilities. Measurements of surface waters near ILOs in NC showed poor water quality overall and higher swine fecal contamination downstream compared to upstream of ILOs (Heaney et al., 2015). To assess swine fecal contamination in water, the researchers had used the microbial source-tracking (Scott et al., 2002) marker Pig-2-Bac. Pig-2-Bac is a genomic DNA marker targeting *Bacteroidales*, a pig-specific gut microbe. *Bacteroidales* are anaerobic bacteria that decay rapidly under aerobic conditions, i.e. outside of the pig's gut, and are excellent candidates for host-specific fecal source tracking. Pig-2-Bac has been in use since 2009 and was evaluated by two independent studies, both showing 100 % sensitivity and 100 % specificity to swine feces (He et al., 2016; Mieszkin et al., 2009).

ILOs housing thousands of animals in confined spaces also release a variety of air pollutants including ammonia, hydrogen sulfide, particulate matter (PM), and volatile organic compounds into the environment, which can pose health risks to nearby residents (Burkholder et al., 2007; Schinasi et al., 2011; Thorne et al., 2009; Schiffman et al., 2005; Feilberg et al., 2017). Several studies have found that increased malodor and ammonia, hydrogen sulfide and PM were associated with adverse health effects among residents living near ILOs. Health effects described in these studies include symptoms of depression, anger and fatigue (Schiffman et al., 1995), headaches and nausea (Schiffman et al., 2005), increased acute blood pressure (Wing et al., 2013) and adverse respiratory outcomes including asthma among both adults and children (Schinasi et al., 2011; Pavilonis et al., 2013; Thu et al., 1997; Von Essen and Auvermann, 2005). Two large scale studies analyzed clinical health records and found that living in proximity to sprayfields and to ILOs was associated with increased odds of methicillin-resistant *Staphylococcus aureus* (MRSA) infection, skin and soft tissue infections and higher all-cause mortality and infant mortality (Kravchenko et al., 2018; Casey et al., 2013). Residents living near ILOs report poorer health and reduced quality of life (Villeneuve et al., 2009; Wing and Wolf, 2000; Cole et al., 2000) and have expressed concerns that, in addition to malodor, swine fecal matter may find its way into their homes. Swine fecal material from these operations could also be a vehicle for pathogens, including zoonotic viruses and antibiotic-resistant bacteria, and other contaminants like endotoxins (O'Shaughnessy et al., 2012) that may impact residents' health (Hellerstein and Fine, 2017). Even though evidence of swine fecal contamination on the outside walls of homes neighboring ILOs was presented in a nuisance trial against industrial hog corporations in North Carolina (Hellerstein and Fine, 2017), no research study has examined whether swine fecal matter enters the homes of community residents living near ILOs.

Using Pig-2-Bac as a swine-specific fecal source-tracking marker, the goals of this study were to investigate (1) whether swine fecal matter contaminates indoor and outdoor household surfaces of ILO worker homes, residents living near ILOs without occupational livestock exposure, and residents of metropolitan areas in NC; and (2) how swine production intensity and spatial proximity to swine operations is related to household Pig-2-Bac contamination.

2. Methods

2.1. Study population and location

This study was conducted in collaboration between community organizers from the Rural Empowerment Association for Community Help (REACH) and researchers from the Johns Hopkins Bloomberg School of Public Health. We completed a pilot cross-sectional study between November 2017 and April 2018 (Study A), followed by a larger cross-sectional study between February 2021 and December 2022 (Study B). Both studies employed a snowball sampling approach, as described previously (Gigot et al., 2023). For Study A, households within a 10-km radius of a swine ILO in Duplin, Sampson or Bladen County, NC were eligible. Two types of households were enrolled: a) ILO worker (ILO—W) households with at least one adult (≥18 years of age) ILO worker; and b) ILO neighbor (ILO—N) households without occupational livestock exposure (including animal processing or rendering plants) within the last 12 months (Coffman et al., 2022). For Study B, the area of enrollment was enlarged and three types of households were eligible: 1) ILO-W households; 2) ILO-N households located near ILOs in livestock-dense regions of NC without occupational exposure to ILOs; and 3) Metro households in metropolitan areas of NC, including Raleigh, Durham, Chapel Hill, Greensboro, Charlotte and Wilmington, also without occupational exposure to ILOs as comparison group. At least one adult (≥18 years) participant in each household provided consent to participate in these studies. Fig. 1, made in collaboration with our community partners to protect the identities of participants, depicts the enrollment areas of both studies.

2.2. Surface swab and questionnaire data collection

Upon enrollment, participants responded to a baseline questionnaire administered by a community organizer or researcher. The baseline questionnaire assessed demographic information (self-reported age, sex, race/ethnicity, etc.), household-level and individual-level characteristics, occupation, job-related activities, and other non-job-related activities that could lead to livestock exposure. Household surface settled dust sampling was performed by community organizers (Study A) or by household members during the COVID-19 pandemic (Study B). In study B, community organizers instructed household members on how to collect a surface swab and then walked participants through the sampling procedure while on video call (FaceTime [Apple, Cupertino, CA]; Zoom [Zoom Video Communications, San Jose, CA], or other video conferencing applications).

Household surface settled dust samples in Study A were collected using standardized 12 in^2 templates on up to six indoor and six outdoor surfaces at each participating household. In Study B household surfaces were sampled by participants using standardized 10 cm^2 templates on two indoor and two outdoor surfaces. To account for the different surface areas sampled in Study A and B, Pig-2-Bac DNA copy number per in^2 is reported. Participants or organizers swabbed the surface horizontally and vertically in an "S" shaped pattern across the entire square surface with a sterile flocked swab (ESwab, COPAN Diagnostics Inc., Murrieta, CA) (Fig. S1). After sampling, swabs were stored in 1 mL Amies buffer and kept refrigerated until shipment to the researchers' laboratory. The average time from sample collection to receipt in the researchers' laboratory was 2 days in Study A and 5 days in Study B. Outdoor samples were collected from the A/C unit, vinyl/plank siding of residence, shed/roof overhang, window casing, underside of the porch or door casing. Indoor samples were collected from the A/C air intake or vent, top of the refrigerator, windowsill, chair headrest, top of TV/TV remote, or the refrigerator handle. For objects like the refrigerator handle and TV remote, the whole object (front and back) was swabbed and the area was estimated. Each household collected one outdoor and one indoor blank by briefly opening one swab outside and one swab inside the residence and placing the swabs directly into the Amies medium without touching any surfaces.

2.3. Quantification of Pig-2-Bac DNA

We followed the Minimum Information for Publication of Quantitative Real-Time PCR Experiments (MIQE) guidelines during analysis (Bustin et al., 2009). The sequence information for primers and probes can be found in Table S1 (Mieszkin et al., 2009). To quantify Pig-2-Bac DNA, 100 μL of each surface sample Amies medium was used for DNA extraction with a MagNA Pure LC 2.0 instrument (Roche, Basel, Switzerland). The DNA Isolation Kit III (Bacteria, Fungi) (Roche, Basel, Switzerland) was used according to manufacturer's instructions. Prior to extraction, each sample was spiked with 0.167 μL of mouse cDNA (Mouse Balbc Lung Total RNA, Zyagen, San Diego, CA) as a specimen processing control (SPC). DNA extracts were then assessed by real-time quantitative polymerase chain reaction (qPCR) for Pig-2-Bac DNA. Each well contained 5 μL of DNA extract as a template in each 20 μL qPCR reaction in addition to 10 μL of 2× reaction mix (TaqMan Fast Advanced Master Mix, Applied Biosystems, Foster City, CA), 500 nM Pig-2-Bac forward and reverse primer, and 250 nM probe (Mieszkin et al., 2009). All samples were analyzed on a QuantStudio 3 Real-Time PCR system (Applied Biosystems, Foster City, CA) using 40 amplification cycles. Each amplification cycle consisted of a denaturing step (15 s at 95 °C), an annealing step (20s at 60 °C) and an extension step (20s at 60 °C). A five-point quantitative standard curve using double stranded DNA fragments containing the Pig-2-Bac DNA sequence with DNA copy numbers, ranging from 300,000 copies to 30 copies per reaction, was included on every plate in duplicate (custom-made gBlocks, Integrated DNA Technologies, Coralville, IA). In addition, two wells of nuclease-free water were included on each qPCR plate as a negative control. A separate qPCR assay using a mouse beta actin DNA sequence (Mouse ACTB [Actin, Beta]) Endogenous Control (FAM Dye/MGB probe, Non-Primer Limited, Applied Biosystems, Waltham, MA) to detect the previously spiked in SPC was performed to ensure DNA extraction was successful. Additionally, an internal amplification control qPCR assay (IAC) was performed to assess potential inhibition in each DNA extract (PrimePCR Positive Control Probe Assay, Human, Bio-Rad, Hercules, CA). Control DNA was amplified using the same thermal cycling conditions as for the Pig-2-Bac DNA qPCR. Copy numbers per swab (1 mL) were calculated by multiplying the copy number per reaction (5 μL

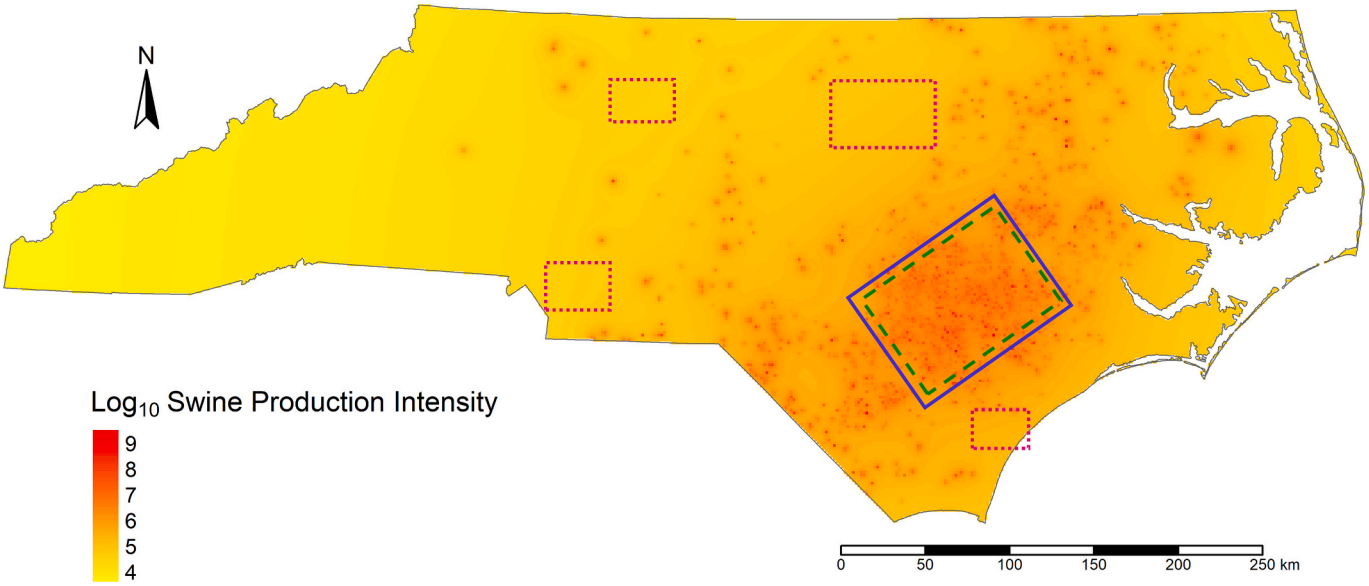


Fig. 1. Locations of households participating in this study and summary of the $\log_{10}$ swine production intensity (SPI) across North Carolina. Note. Green dashed line box: Approximate locations of industrial livestock operation worker (ILO-W) households; purple solid line box: Industrial livestock operation neighbor (ILO-N) households; pink dashed line boxes: Metro households. Study A (2017–2018) only included households from within the green/purple square and Study B included households from all squares (green/purple and pink). Sum of inverse distance weighting, using the distance between grid points and swine operations and steady state live weight (SSLW), was performed based on a 1.6 km by 1.6 km grid.

extracted DNA template) by 200. Copy numbers per surface swab were divided by the area of the household surface settled dust template used in in^2, to obtain the Pig-2-Bac DNA copy number per in^2.

2.4. Spatial analysis

Home addresses of participants were recorded during enrollment. Addresses were geolocated for further analysis, generating a single point based on the centroid for the property. Out of the 293 households included in this study, 42 (14 %) households (30 ILO—W, 10 ILO-N and 2 Metro households) did not have addresses that could be geocoded and had to be excluded from spatial analyses. Study B households with and without spatial data had similar prevalences of Pig-2-Bac DNA detection, both indoors and outdoors and between study groups (Table S2).

CAFO location coordinates and operation information, such as permit type, allowable hog count and steady state live weight (SSLW) were obtained from records of permitted North Carolina swine facilities operating in 2015 from the publicly available animal operation facilities map from the North Carolina Division of Water Quality (DWQ) (North Carolina Department of Environmental Quality, n.d.). Data from 2015 were used as it is a better representation of the swine population during our study time period (2017–2022). Industrial hog operations are defined as feedlots with >250 swine and liquid waste management systems (North Carolina Environmental Management Commission, 2019). Facilities report information on the number of hogs, hog species and life stage, as well as coordinates of the facility and the name of the corporate integrator. The SSLW of each facility, used in the estimate of swine spatial intensity, is calculated by DWQ using the number of hogs of each type and life stage and the average weight for that life stage. This spatial analysis used data from 2190 permitted swine CAFOs.

Three different spatial analysis methods were used to categorize exposure to swine fecal waste and intensity of swine production. First, buffers of 5 km, 3 km and 1 km were created around each geocoded household. Counts of swine CAFOs that fell within each distance buffer were calculated as one measure of exposure to swine CAFOs. Second, the Euclidean distance between each household and the nearest swine CAFO was used. Third, a swine CAFO intensity variable to indicate swine production intensity (SPI) exposure value was calculated for each household using the summed inverse-distance weighted (IDW) exposure described by Eq. (1):

$$\textit{Swine production intensity exposure for household } j = \sum_{i=1}^{n} \frac{a_i}{d_{ij}^2} \quad (1)$$

where n is the number of swine CAFOs, a_i is the SSLW of the swine CAFO i, and d_{ij}^2 is the distance squared between the swine CAFO i and household j (Casey et al., 2013). The SPI values were $\log_{10}$ transformed since the variable was not normally distributed. The same summed IDW method was also used on a 1.6 km resolution grid across the state for visualization purposes. Spatial data management and map construction were conducted in ArcGIS Pro version 2.9.5 (Esri, 2021) and R (version 4.2.2, R Foundation for Statistical Computing, Vienna, Austria (R Core Team, 2022)).

2.5. Statistical analysis

All qPCR Pig-2-Bac DNA copy number estimates per in^2 were $\log_{10}$ transformed prior to analysis. Our outcomes of interest were Pig-2-Bac DNA detection on at least one surface (outdoors and indoors) and $\log_{10}$ Pig-2-Bac DNA copy number per in^2. The lowest detected value in our sample set was 8.6 copies per sample. We defined the limit of detection of our assay at half of this value (4.3 copies per sample), which was imputed for swabs without detectable Pig-2-Bac DNA. We performed a sensitivity analysis using two additional imputation values (2.15 copies per sample; and 0.1 copies per sample) to test the robustness of the associations between: 1) distance to nearest swine CAFO in km; 2) swine production intensity (SPI) value; and 3) household group with the change in $\log_{10}$ Pig-2-Bac DNA copy number per in^2. Differences in the beta coefficient and 95 % confidence interval estimates were minimal when the lower limit of detection imputed value was decreased. With similar estimates across imputation values, we selected 4.3 copies per sample, half the lowest detected Pig-2-Bac DNA copy number per sample (8.6 copies) (Table S3).

The SPI values were evaluated as a continuous variable. Questions that assessed work in ILOs (CAFOs, processing plants, rendering facilities) and a composite binary variable that used reported occupation title, reported hog contact, and reported poultry contact to assess occupational hog or poultry exposure were used in models that explored associations between Pig-2-Bac outcomes of interest and potential occupational exposures. Questions used to gather information about personal protective equipment (PPE) use at work and habits surrounding its use were used to create binary variables for PPE use at work and for bringing PPE home after work.

To explore differences in SPI, Pig-2-Bac copy number per in^2 and number of CAFOs between household type, a Mann-Whitney U test was used since the distributions of these variables were skewed. We used logistic regression models to estimate the odds ratios (OR) and 95 % confidence intervals (CIs) of associations between swine spatial variables (intensity and distance to nearest swine CAFO), sampling location, household type, occupational factors and presence or absence of Pig-2-Bac. We used linear regression models to estimate β coefficients and 95 % CIs of the associations between swine spatial variables (distance to nearest swine CAFO and SPI), sampling location (outdoor vs indoor), household type (ILO-W, ILO-N vs Metro), and occupational factors with $\log_{10}$ Pig-2-Bac DNA copy number per in^2 estimates. To account for repeated measures and non-independence of multiple swabs at each household, we used generalized estimating equations (GEE) with an exchangeable working correlation. To account for any potential confounding due to differences between Study A and B, logistic and linear regression models were adjusted for Study A vs. Study B as a binary independent variable. To explore the impact occupational swine exposure could have on associations between SPI and Pig-2-Bac outcomes, the ILO-W group was stratified into ILO workers with vs. without occupational swine exposure (Table S4 and S5). However, due to the small number of non-swine workers, the primary analyses presented involve pooling of ILO-W with and without occupational exposure to swine. To explore the potential influence of season of swab collection on associations (Table S6), models examining the association of distance to nearest swine CAFO and SPI with Pig-2-Bac DNA detection were adjusted for season in addition to Study A vs Study B (Table S7). Since we found minimal changes in magnitude or precision of estimates when adjusting for season, we chose to omit season in the primary analysis. To explore the potential influence of study designation on associations, we estimated the association of distance to nearest swine CAFO and SPI with Pig-2-Bac DNA detection for each study independently (Table S8 and S9). Since we found minimal changes in precision of estimates, we chose to present the pooled estimates of both Study A and Study B, while adjusting for study. Because this was not a randomized study, statistical significance cannot be interpreted as the probability that observed difference would occur by chance if there were no differences between groups being compared. However, 95 % confidence intervals (CIs) are presented for easy comparison with other studies. All analyses were performed in R (version 4.2.2, R Foundation for Statistical Computing, Vienna, Austria (R Core Team, 2022)).

2.6. Ethics statement

Both studies were a collaboration between the Johns Hopkins Bloomberg School of Public Health (BSPH) and REACH. The BSPH Institutional Review Board approved both studies (IRB00014420 and IRB00005253). Before participation, adult participants provided written or oral informed consent.

3. Results

3.1. Participant characteristics

Two hundred and ninety-three households participated in this study. Of those, 105 were industrial livestock operation worker (ILO—W) households, 107 were ILO neighbor (ILO—N) households, and 81 were NC metropolitan area (Metro) households (Table 1). Among the 293 households, 38 were enrolled between 2017 and 2018, and 255 were enrolled between 2021 and 2022 (Table 1). Across all household groups, the majority of participants identified as Black/African American (83 % overall) (Table S10). The mean distance to nearest swine CAFO was similar between the ILO-W group (3.59 km) and the ILO-N group (2.92 km), whereas the mean distance of Metro households to nearest swine CAFO was significantly larger (18.05 km; Table 1). ILO-N households had more swine CAFOs within a 5 km radius of their home with a mean of 12.26 swine CAFOs, compared to 9.60 swine CAFOs in the ILO-W group (Table 1). In both studies, ILO-W and ILO-N households were located in overlapping regions of North Carolina. Although participation criteria were slightly different, household characteristics were similar. Among the 105 ILO-W households, 71 % (75/105) reported occupational swine exposure and 26 % (27/105) reported occupational chicken exposure. Most of the participants enrolled in the worker group worked in livestock production (raising livestock) (74 %, 78/105) compared to working in livestock processing and rendering plants (21 %, 22/105). Ninety-nine percent of workers reported using some form of personal protective equipment (PPE), including face, eye, hand and foot protection. Over half (65 %) of workers report bringing some PPE home from their work (Table S11).

3.2. Pig-2-Bac DNA detection at the household- and swab-level

Among the 293 enrolled households, 30 % (88 households) had at least one positive Pig-2-Bac surface, either indoors or outdoors. ILO-N households had the highest proportion of Pig-2-Bac detected on at least one surface, 44 % (47/107 households), followed by ILO-W households (38 %, 40/105 households) (Table 1). Out of the 1456 swabs collected, 42 swabs (~3 %) had insufficient sample volume for testing due to leakage during shipment. Out of 1414 surface swabs analyzed 695 (49 %) were outdoor and 719 (51 %) were indoor samples (Table 2). ILO-W household samples had the highest prevalence of Pig-2-Bac DNA detection (30 %), followed by ILO-N household samples (25 %); only one Metro household sample (1 %) tested positive for Pig-2-Bac. The ILO-W and ILO-N groups contributed approximately the same number of swabs, 536 swabs and 557 swabs respectively, while the Metro group contributed fewer swabs overall (321 swabs) (Table 2). Twenty-one percent of all swabs collected, both indoors and outdoors, were Pig-2-Bac positive. Among all outdoor swabs, 26 % (179/695) were positive; 35 % (91/262) for the ILO-W group, 32 % (87/273) for the ILO-N group, and 0.1 % (1/160) for the Metro group were positive (Table 2). Among the indoor swabs, 17 % (123/719) were positive overall; 28 % (68/247) for the ILO-W group, 19 % (55/284) for the ILO-N group, and 0 % (0/161) for the Metro group were positive. The ILO-N group had the highest mean Pig-2-Bac DNA copy number per in^2 with 63.85 copies (SD = 868.48) followed by the ILO-W group with a mean of 35.75 copies per in^2 (SD = 131.17), and lastly the Metro group with a mean of 0.63 copies per in^2 (SD = 7.06). All three household groups had higher Pig-2-Bac copy numbers per in^2 on outdoor surfaces compared to indoor surfaces (Table 2).

3.3. Associations between Pig-2-Bac DNA detection and swab location

ILO-W households with any livestock exposure, ILO-W households with occupational swine exposure, and ILO-N households all had elevated odds of Pig-2-Bac DNA detection on outdoor compared to indoor surfaces. The only Pig-2-Bac positive surface detected in the Metro group (n = 1/321) was an outdoor surface. Outdoor surfaces were 2.2 (95 % CI = 1.6, 3.0) times more likely to test Pig-2-Bac positive than indoor surfaces across all household groups (Table 3, Fig. 2). The odds of Pig-2-Bac DNA detection outdoors compared to indoors was 2.1 (95 % CI = 1.3, 3.3) in the ILO-W group and 2.4 (95 % CI = 1.5, 3.8) in the ILO-N group. Outdoor surfaces harbored 0.30 $\log_{10}$ Pig-2-Bac DNA copy numbers more per in^2 (95 % CI = 0.19, 0.41) than indoor surfaces. This trend was consistent for the ILO-W households (β = 0.33; 95 % CI = 0.14, 0.51) and the ILO-N households (β = 0.36; 95 % CI = 0.16, 0.57) (Table 3, Fig. 2). The single Metro household Pig-2-Bac DNA positive sample from an outdoor surface contained 2029.2 Pig-2-Bac DNA copies per in^2. Among outdoor surfaces, ILO-W and ILO-N Pig-2-Bac positivity was similar (OR = 1.1, 95 % CI = 0.7, 1.9), but among indoor surfaces, Pig-2-Bac was higher in ILO-W compared to ILO-N households (OR = 1.5, 95 % CI = 0.9, 2.5).

3.4. Associations between Pig-2-Bac DNA detection and study group assignment

We also examined associations of Pig-2-Bac DNA presence and

Table 1
Household-level distance to nearest swine CAFO, swine production intensity (SPI), and Pig-2-Bac DNA swab positivity overall and by household group and surface location (outdoor vs indoor), North Carolina, 2017–2022.

	Overall	ILO-W	ILO-N	Metro
Households enrolled, n	293	105	107	81
Study A (2017–2018)	38	18	20	0
Study B (2021–2022)	255	87	87	81
Distance to nearest swine CAFO (km)				
Mean ± SD	7.88 ± 9.97	3.59 ± 4.70[a,c]	2.92 ± 2.42[b,c]	18.05 ± 11.7
Mean ± SD number of swine CAFOs within 5 km of household	7.67 ± 9.15	9.60 ± 7.43[a,c]	12.26 ± 10.88[b,c]	0.22 ± 0.61
Mean ± SD number of swine CAFOs within 3 km of household	2.34 ± 3.89	2.97 ± 3.34[a]	3.69 ± 5.18[b]	0.07 ± 0.33
Mean ± SD number of swine CAFOs within 1 km of household	0.17 ± 0.50	0.23 ± 0.57[a]	0.26 ± 0.64[b]	0.00 ± 0.00
Mean ± SD swine production intensity (SPI) value	5.85 ± 0.74	6.26 ± 0.35[a,c]	6.31 ± 0.35[b,c]	4.89 ± 0.36
Households with ≥1 Pig-2-Bac DNA positive surface swab, n (%)	88/293 (30)	40/105 (38)	47/107 (44)	1/81 (1)
Households with ≥1 Pig-2-Bac DNA positive outdoor surface swab, n (%)	75/293 (26)	34/105 (32)	40/107 (37)	1/81 (1)
Households with ≥1 Pig-2-Bac DNA positive indoor surface swab, n (%)	55/293 (19)	27/105 (26)	28/107 (26)	0/81 (0)

Note: ILO-W = industrial livestock operation workers. ILO-N = industrial livestock operation neighbors. Metro = metropolitan area residents. SD = standard deviation. CAFO = confined animal feeding operation. km = kilometer. All differences were tested using a Mann Whitney *U* test.
[a] ILO-W and Metro group means are significantly ($p < 0.05$) different from each other.
[b] ILO-N and Metro group means are significantly ($p < 0.05$) different from each other.
[c] ILO-W and ILO-N group means are significantly ($p < 0.05$) different from each other.

Table 2
Swab-level Pig-2-Bac DNA detection frequency and copy number per in^2 within household surface settled dust samples, overall and by household group, North Carolina, 2017–2022.

	Overall	ILO-W	ILO-N	Metro
Surface swabs collected, n	1414	536	557	321
Outdoor surface swabs, n	695	262	273	160
Indoor surface swabs, n	719	274	284	161
Pig-2-Bac DNA positive surface swabs				
Overall; n+/total, (%)	302/1414 (21)	159/536 (30)	142/557 (25)	1/321 (1)
Outdoor; n+/total, (%)	179/695 (26)	91/262 (35)	87/273 (32)	1/160 (0.1)
Indoor; n+/total, (%)	123/719 (17)	68/247 (28)	55/284 (19)	0/161 (0)
Pig-2-Bac DNA copy number per in^2				
Overall				
Mean ± SD	38.85 ± 551.27	35.75 ± 131.17[a,c]	63.85 ± 868.48[c]	0.63 ± 7.06
Geometric mean (SD)	0.57 (11.86)	0.87 (15.63)	0.65 (15.40)	0.23 (1.63)
Outdoor				
Mean ± SD	60.04 ± 781.88	48.39 ± 165.42[a]	105.8 ± 1236.62[b]	1.06 ± 10.01
Geometric mean (SD)	0.82 (13.17)	1.28 (17.16)	1.01 (17.36)	0.27 (1.62)
Indoor				
Mean ± SD	18.37 ± 79.36	23.67 ± 85.18[a]	23.54 ± 93.47	0.21 ± 0.07
Geometric mean (SD)	0.41 (10.17)	0.60 (13.58)	0.43 (12.84)	0.19 (1.54)

Note. in = inches. SD = standard deviation. ILO-W = industrial livestock operation workers. ILO-N = industrial livestock operation neighbors. Metro = metropolitan area residents. All values below the limit of detection were assigned a value of 0.63 Pig-2-Bac DNA copies per in^2 (Study A) or 0.27 Pig-2-Bac DNA copies per in^2 (Study B). All differences were tested using a Mann Whitney U test.
[a] ILO-W and Metro group means are significantly ($p < 0.05$) different from each other.
[b] ILO-N and Metro group means are significantly ($p < 0.05$) different from each other.
[c] ILO-W and ILO-N group means are significantly ($p < 0.05$) different from each other.

Table 3
Associations between household surface sampling location (outdoor versus indoor) and Pig-2-Bac DNA detection and log_{10} copy number per in^2, North Carolina, 2017–2022.

	N+/total (%)	Odds of Pig-2-Bac DNA detection		GM (SD) Log_{10} Pig-2-Bac DNA copy number per in^2	Log_{10} Pig-2-Bac DNA copy number per in^2	
		Indoor	Outdoor		Indoor	Outdoor
		OR (95 % CI)	OR (95 % CI)		β (95 % CI)	β (95 % CI)
Overall	302/1414 (21)	Ref	2.2 (1.6, 3.0)	0.82 (13.17)	Ref	0.30 (0.19, 0.41)
Industrial livestock operation workers (ILO-W)	159/536 (30)	Ref	2.1 (1.3, 3.3)	1.28 (17.16)	Ref	0.33 (0.14, 0.51)
Industrial livestock operation neighbors (ILO-N)	142/557 (25)	Ref	2.4 (1.5, 3.8)	1.01 (17.36)	Ref	0.36 (0.16, 0.57)
Metro residents	1/321 (1)	–	–	0.27 (1.62)	–	–

Note. OR = odds ratio. GM = geometric mean. SD = standard deviation. in = inches. Ref = reference. Overall category includes the contribution of the Metro group. Models are adjusted for Study A (2017–2018) vs Study B (2021–2022). All values below the limit of detection were assigned a value of 0.63 Pig-2-Bac DNA copies per in^2 (Study A) or 0.27 Pig-2-Bac DNA copies per in^2 (Study B).

quantity with household study group and sampling location (outdoor versus indoor). ILO-W household surfaces were 40.1 times (95 % CI = 5.5, 293) more likely and ILO-N household surfaces were 31.2 times (95 % CI = 4.3, 228) more likely to contain Pig-2-Bac traces than Metro household surfaces (Table S12). Compared to the Metro household surfaces, the Pig-2-Bac concentration on ILO-W household surfaces was 0.39 log_{10} copies (95 % CI = 0.19, 0.42) higher per in^2 and 0.23 log_{10} copies (95 % CI = 0.12, 0.34) higher on ILO-N household surfaces (Table S12).

3.5. Associations between occupational swine exposure among ILO-W participants and Pig-2-Bac DNA detection

We also examined the effect of occupational swine exposure on Pig-2-Bac presence and quantity indoors and outdoors. Pig-2-Bac was more frequently detected outdoors at ILO-W households who reported working with swine (42 %, 85/205) compared to ILO-W households who reported work with other animals (11 %, 6/57). Indoor surfaces of households with swine worker exposure were 8.3 (95 % CI = 1.9, 35.2) times more likely to test Pig-2-Bac positive than indoor surfaces of other livestock worker households (Table S13). Swine worker compared to other livestock worker households were also more likely to test Pig-2-Bac positive outdoors (OR = 3.4, 95 % CI = 1.2, 9.7), although this difference was less pronounced (Table S13). The difference in log_{10} Pig-2-Bac DNA copy number per in^2 on outdoor (β = 0.30, 95 % CI = −0.04, 0.64) and indoor (β = 0.33, 95 % CI = 0.11, 0.56) surfaces was similar, comparing those with occupational swine exposure to those without (Table S14). Taking any PPE home from work compared to leaving PPE at work, increased the odds of Pig-2-Bac DNA detection both on outdoor (OR = 1.8, 95 % CI = 0.7, 4.4) and indoor surfaces (OR = 1.5, 95 % CI = 0.6, 3.5), although not statistically significant (Table S15). Differences in mean Pig-2-Bac DNA copy number per in^2 reflected this trend (Table S16).

3.6. Associations between Pig-2-Bac DNA detection and swine production intensity (SPI)

We examined associations of Pig-2-Bac DNA detection with different measures of the intensity of exposure to swine CAFOs. The SPI values were highest in the southeastern portion of North Carolina (Fig. 1). Mean log_{10} SPI exposure was 6.26, 6.31, and 4.89 in the ILO-W, ILO—N, and Metro household groups, respectively (Table 1). Among all

households, each 1 log_{10} increase in SPI was associated with a 5.4-fold (95 % CI = 2.8, 10.4) higher likelihood of Pig-2-Bac DNA detection on all household surfaces (Table 4). Each log_{10} increase in SPI among ILO-W households was associated with a 13.1-fold (95 % CI = 2.8, 60.2) higher likelihood for Pig-2-Bac detection; ILO-N household surfaces were 2.2 (95 % CI = 0.7, 7.2) times more likely to harbor Pig-2-Bac contamination with each log_{10} increase in SPI (Table 4). Among the ILO-W households, those with occupational swine exposure were 10.4 (95 % CI = 2.5, 43.4) more likely to have Pig-2-Bac DNA on any household surface with each unit increase in SPI (Table S4). Each 1 log_{10} unit increase in SPI was associated with an increase of 0.21 log_{10} Pig-2-Bac DNA copies per in^2 (95 % CI = 0.13, 0.29) among all households combined and a 0.68 log_{10} Pig-2-Bac DNA copies per in^2 increase (95 % CI = 0.21, 1.14) among ILO-W households (Table 5). The increase in Pig-2-Bac DNA copy number per in^2 per SPI unit was highest among workers with self-reported occupational swine exposure (β = 0.72, 95 % CI = 0.18, 1.26) (Table S5). These associations are also represented in Fig. 2 for visual comparison. Increasing SPI exposure was associated with higher Pig-2-Bac DNA copy number per in^2 across all household surfaces at ILO-W and ILO-N households. This trend was more pronounced outdoors compared to indoors (Fig. 3). Detection of Pig-2-Bac DNA on household surfaces was most strongly associated with the number of swine CAFOs within a 1 km buffer surrounding each household among the ILO-W group (OR = 1.8, 95 % CI = 1.2, 2.9), followed by the number of swine CAFOs within a 3 km buffer (Table S17), demonstrating that swine CAFOs in closer proximity to residences increase the odds of Pig-2-Bac DNA detection. The magnitude of increase in Pig-2-Bac DNA copies per in^2 was highest when estimating associations with the number of swine CAFOs within a 1 km buffer, but the direction of the association was consistent albeit lower in magnitude when considering all CAFOs within a 3 km or 5 km buffer zone (Table S18).

4. Discussion

The results of our study suggest that swine fecal matter from swine CAFOs is contributing to the contamination of indoor and outdoor household surfaces of nearby community residents. The Pig-2-Bac prevalence was highest in the ILO-N group (44 % or 47/107 households had ≥1 Pig-2-Bac DNA positive surface), followed by the ILO-W group (38 %; 40/105 households with ≥1 Pig-2-Bac DNA positive surface), and lowest in the Metro group (1 %; 1/81 households). At the swab level, Pig-2-Bac was most frequently detected in ILO-W household surface samples (30 % Pig-2-Bac positive) followed by ILO-N household surface samples (25 % Pig-2-Bac positive), with only a single outdoor surface from a Metro household that tested positive (0.3 %). We observed higher Pig-2-Bac prevalence outdoors compared to indoors, but no significant difference between ILO-W and ILO-N household outdoor surfaces (ILO—W: 91/262 [35 %]; ILO—N: 87/273 [32 %]). We did see higher detection frequency on ILO-W compared to ILO-N indoor surfaces (ILO—W: 68/247 [28 %]; ILO—N: 55/284 [19 %]). Significantly more ILO-W and ILO-N households had ≥1 Pig-2-Bac positive outdoor compared to indoor surface. This suggests an environmental source of Pig-2-Bac and that ILO work take home exposure could contribute to the presence of Pig-2-Bac indoors among ILO-W households, e.g., through shoes worn during ILO work or other PPE that is brought home. Higher swine production intensity and the number of ILOs within a 1- or 3-km radius of the home were correlated with significantly higher likelihood of Pig-2-Bac detection on household surfaces, respectively, indicating that areas of dense swine production are contributing the most swine fecal contamination to residents' homes, including to homes of residents without any occupational exposure to swine.

The microbial source tracking marker Pig-2-Bac has been used to detect swine fecal contamination in water, nasal swabs and on surfaces (Heaney et al., 2015; Pisanic et al., 2015; Schiaffino et al., 2021). Several studies have examined water quality in North Carolina and beyond using Pig-2-Bac as part of their assessment, e.g., Heaney et al. and Christenson et al. showed higher concentrations of swine fecal contamination in surface water and watersheds, respectively, downstream of swine CAFOs and sprayfields compared to upstream (Heaney et al., 2015; Malajacan et al., 2023; Christenson et al., 2022; Browning et al., 2023; Vadde et al., 2019). Around the US and rest of the world, Pig-2-Bac has been detected in streams in the Ozarks (Browning et al., 2023), rivers in France (Mieszkin et al., 2009) and China (Vadde et al., 2019), as well as lakes in the Philippines (Malajacan et al., 2023), indicating offsite migration of swine fecal waste. We previously examined Pig-2-Bac as a biomarker of recent occupational exposure to swine or swine waste (Pisanic et al., 2015). Pig-2-Bac was present in 61 % of nasal swabs of swine ILO workers and was found to decline in copy number with time away from hog ILO work. Pig-2-Bac in this context was used as a marker for recent human exposures to swine, demonstrating the utility of Pig-2-Bac outside of water contamination research.

In North Carolina, swine CAFOs are concentrated in the rural southeastern region of the state, which includes both rural and more urban areas from which participants were recruited. Additionally, the cities of Raleigh and Charlotte have sub-urban portions of their metropolitan area that extend out into, and are adjacent to, areas that are closer to a swine CAFO and/or swine production-related activities such

Table 4
Associations between distance to nearest swine CAFO and swine production intensity (SPI) and Pig-2-Bac DNA detection on any surfaces, North Carolina, 2017–2022.

	Pig-2-Bac DNA detection N+/total (%)	Distance to nearest swine CAFO in km	Swine production intensity (SPI)
		OR (95 % CI)	OR (95 % CI)
Overall	280/1238 (23)	0.8 (0.7, 0.9)	5.4 (2.8, 10.4)
Industrial livestock operation workers (ILO-W)	147/415 (35)	0.8 (0.6, 1.1)	13.1 (2.8, 60.2)
Industrial livestock operation neighbors (ILO-N)	132/510 (26)	0.9 (0.7, 1.1)	2.2 (0.7, 7.2)
Metro residents	1/313 (1)	–	–

Note: km = kilometer. CAFO = concentrated animal feeding operation. Overall category includes the contribution of the Metro group. Models are adjusted for Study A (2017–2018) vs Study B (2021–2022).

Table 5
Associations between distance to nearest swine CAFO and swine production intensity (SPI) and change in log_{10} Pig-2-Bac DNA copy number per in^2 on any surfaces, North Carolina, 2017–2022.

	GM (SD) log_{10} Pig-2-Bac DNA copy number per in^2	Distance to nearest swine CAFO in km	Swine production intensity (SPI)
		β (95 % CI)	β (95 % CI)
Overall	0.57 (11.86)	−0.01 (−0.01, −0.006)	0.21 (0.13, 0.29)
Industrial livestock operation workers (ILO-W)	0.87 (15.63)	−0.02 (−0.04, −0.005)	0.68 (0.21, 1.14)
Industrial livestock operation neighbors (ILO-N)	0.65 (15.40)	−0.01 (−0.06, 0.03)	0.16 (−0.23, 0.55)
Metro residents	0.23 (1.63)	–	–

Note: SD = standard deviation. GM = geometric mean. in = inches. km = kilometers. CAFO = concentrated animal feeding operation. Overall category includes the contribution of the Metro group. Models are adjusted for Study A (2017–2018) vs Study B (2021–2022). All values below the limit of detection were assigned a value of 0.63 Pig-2-Bac DNA copies per in^2 (Study A) or 0.27 Pig-2-Bac DNA copies per in^2 (Study B).

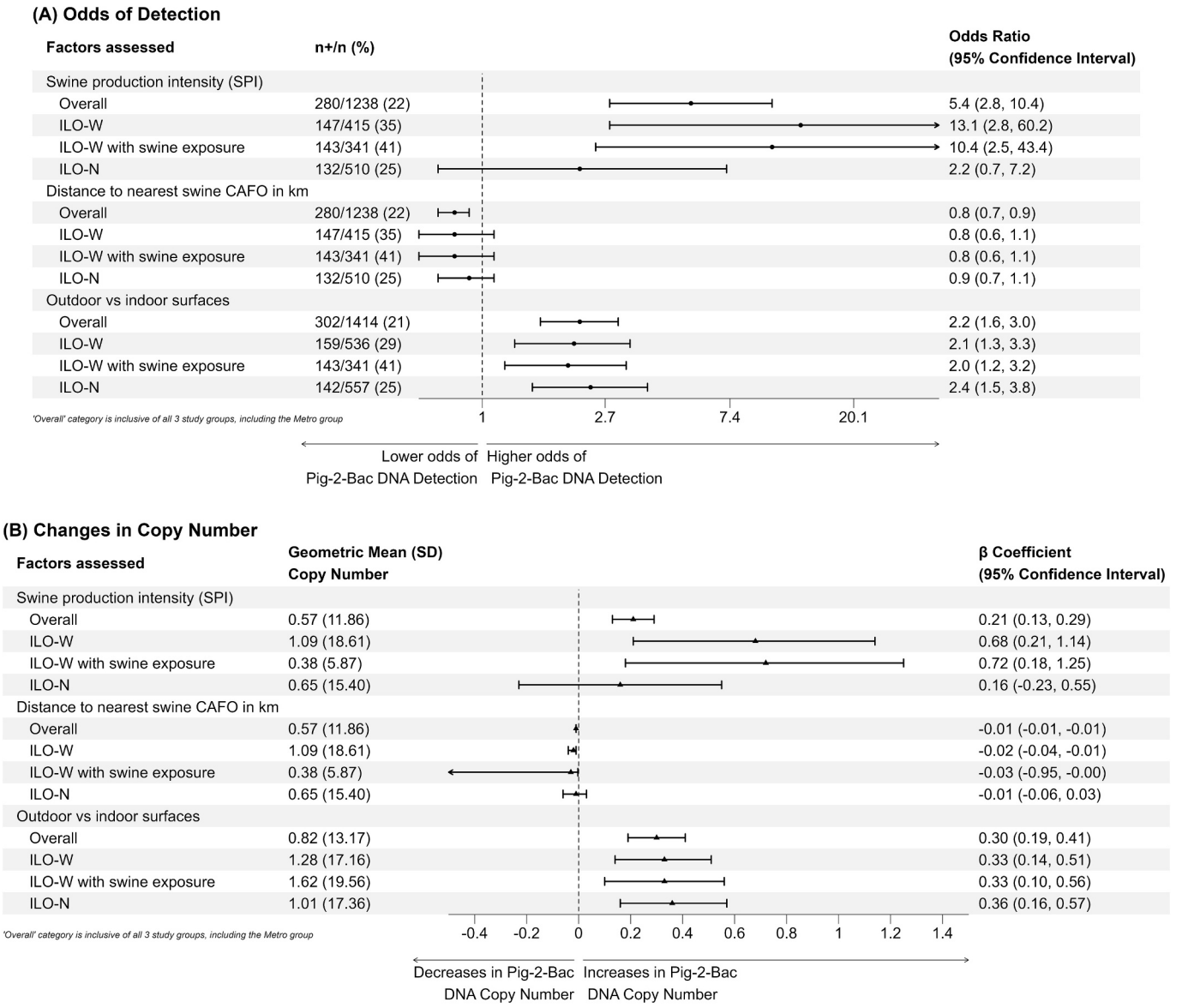


Fig. 2. Associations between exposure factors (including occupational swine exposure) and Pig-2-Bac DNA detection or changes in $\log_{10}$ Pig-2-Bac DNA copy number per in^2. (A) Each dot represents the odds ratio (OR) for the presence of Pig-2-Bac DNA and the line represents the 95 % confidence interval. The vertical dashed line at 1 indicates the OR null value. (B) Each triangle represents the β coefficient for the change in $\log_{10}$ Pig-2-Bac DNA copy number per in^2 and the line represents the 95 % confidence interval. The vertical dashed line at 0 represents the β null value. In both figures, "ILO-W with swine exposure" refers to ILO-W participants who self-reported occupational swine exposure.

as swine trucking routes to pork processing facilities, which could explain the detection of Pig-2-Bac on the single outdoor surface that tested positive among the Metro household group.

Residents of color and low-income residents in southeastern North Carolina have long been disproportionately impacted by proximity of hog CAFOs (Bob Edwards, 2000; Lewis et al., 2023; Son et al., 2021; Wing and Johnston, 2014; Nicole, 2013; Ladd and Edward, 2002), and have been vocal about the impact these facilities have on their lives. Complaints of residents are often ignored or not taken seriously, but tools such as Pig-2-Bac MST can be used to validate and demonstrate the conditions neighbors experience, as was the case in past nuisance lawsuits against the swine industry (Rodgers, 2018). In 2018, approximately 500 southeastern NC residents filed nuisance lawsuits against the industrial hog corporations that oversee these facilities with the argument that the environmental pollutant emissions, odor, flies, trucks and noise from these operations adversely affected their quality of life and health, thereby unreasonably interfering with their use and enjoyment of personal property (Addison, 2023; Shaffer, 2018). While residents were successful in these trials, North Carolina lawmakers fought to make it more difficult for neighbors of these operations to sue industrial swine companies in the future (Blythe, 2018; Doran, 2019; Barnett, 2018; Jackson et al., n.d.-a). With the amendment of right-to-farm laws that further limited the already restricted recovery of damages in nuisance actions, the ability of residents to use legal action to fight against the multi-national corporations that pollute the air they breathe and the land they live on was severely limited, much to the dismay of the neighbors and the general public (Jackson et al., n.d.-b; Dixon et al., 2017).

Strengths of this study include the use of spatial and molecular methods to assess swine fecal contamination and the inclusion of different household types (ILO—W, ILO—N, Metro) with varying swine production intensity exposure. The highly sensitive and specific Pig-2-Bac marker has been a proven way to estimate contamination with swine fecal filth (Heaney et al., 2015; Pisanic et al., 2015), and its

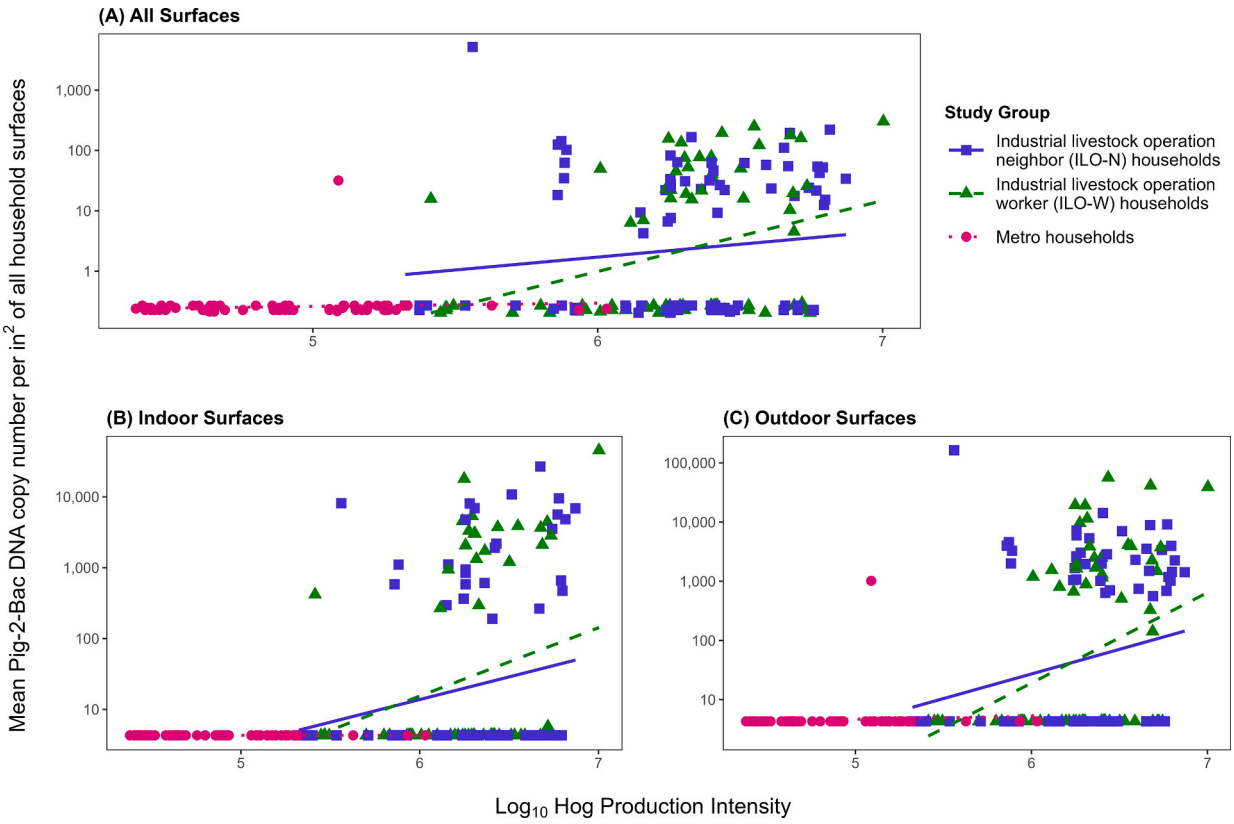


Fig. 3. Relation of $\log_{10}$ swine production intensity (SPI) value and household-level mean Pig-2-Bac DNA copy number per in^2 by household group on (A) all household surfaces; (B) on indoor surfaces; and (C) on outdoor surfaces. Note. All surfaces in each household were averaged for (A). Blue squares represent industrial livestock operation worker (ILO-N) households; solid blue line represents a line of best fit. Green triangles represent industrial livestock operation neighbor (ILO-W) households; dashed green line represents a line of best fit. Pink circles represent Metro households; dotted pink line represents line of best fit.

application in this setting provides a quantitative way to substantiate neighbors' complaints of contamination and quality-of-life disruption. This study provides scientific evidence for allegations of nuisance and adverse health impacts imposed on communities living in proximity of the hog farming industry in the United States, as in previous expert testimony in nuisance lawsuits that were successful for the neighbors of swine operations (Rodgers, 2018).

The use of spatial analysis techniques to assign SPI exposure values to each residence is another strength of this study. Previous studies have used community-level exposure to industrial food animal production in North Carolina, but few studies estimated nearby swine exposure at the household level using individual ILO characteristics to assign exposure burden. Often, CAFO exposure is measured to the census tract or census block, or is characterized by the distance between the residence and nearest CAFO (Quist et al., 2022; Schinasi et al., 2014; Kalkowska et al., 2018). While these metrics are useful, the method employed in this study gives a more precise household-level estimate of SPI exposure. Other studies have also used an inverse distance weighted approach but didn't factor in life stage and waste impact of the animals. Using other spatial metrics, such as distance to nearest swine CAFO and number of swine CAFOs within household buffers of different sizes, we observed trends consistent with the more granular SPI metric. Additionally, our SPI metric could provide a surrogate measure of exposure to swine fecal material when molecular lab methods are infeasible.

Limitations of this study include potential differences in swab collection technique between Study A and Study B. Community organizers and researchers at JHU made in-person home visits to collect surface samples in Study A, while a household member was trained to collect settled dust samples in Study B while on video call with a community organizer or study team member due to contact-less protocol requirements during the COVID-19 pandemic. In Study A (2017–2018), a larger template was used for sample collection compared to in Study B (2021−2022). The difference in template size between the studies could have led to an underestimate of detection prevalence in Study B. The time between sample collection and sample processing was shorter in Study A, which could have contributed to an underestimate of Pig-2-Bac in Study B, too. To adjust for the potential confounding influence of differences between Study A and B, study was included as covariate in all statistical models. Additionally, a sensitivity analysis was conducted (Table S8 and S9) to examine outcomes for each study independently, which confirmed all trends observed after combining data from both studies. Additionally, swabs were collected at different times of the year. Differences in temperature, rainfall, UV exposure and other meteorological variables could affect the detection of Pig-2-Bac DNA. While swabs were collected during all seasons, the distribution was not equal across seasons (Table S6). Study A did not collect swabs during the summer, only Study B did, which led to fewer total swabs collected in summer. Study B also had lower detection frequencies and a lower mean Pig-2-Bac DNA copy number per in^2 overall, which could be why prevalence and quantity were lower in the summer. Although our overall findings were consistent even after including season as a covariate in regression models, future work should assess potential seasonal differences. Past studies that have reported temporal stability of Pig-2-Bac DNA did not necessarily test seasonal differences (Mieszkin et al., 2009). Future studies could also evaluate differences in Pig-2-Bac detection by surface type to assess if there are differences based on sampling location/orientation and surface material; surface material was not recorded here. Additionally, we were not sufficiently powered examine the effect of mask and other PPE usage, as most of the workers in our study reported PPE usage, including masks, at work. Lastly, information about swine CAFO lagoon waste sprayfields, trucking routes and other potential mechanisms of hog fecal movement were not

collected and incorporated into the SPI in this study as they were not publicly available. Geospatial source data for the swine CAFO location from public permit records does not provide information about where the fecal waste from specific swine CAFOs is disposed of, such as sprayfield information. This could lead to an underestimate of associations between SPI and Pig-2-Bac, as a more refined SPI would incorporate sprayfields and locations of open swine waste lagoons. Additionally, future studies could incorporate updated swine CAFO permit location data, as there were issues with repeat coordinates of operations in the 2022 permit data that made use of that data not possible for spatial analysis. We chose to use the 2015 data due to completeness, the time period of Study A (2017/2018) and lack of significant difference in total swine production in NC (Hamer et al., 2023; Reilly et al., 2015).

Future studies should also assess contamination from other livestock industries in the area, particularly poultry. Incorporating poultry fecal contamination could provide a more complete picture of the cumulative effects of residential proximity and occupational intensity of exposure to industrial food animal production in North Carolina. In southeastern North Carolina, swine and poultry production are often co-located, contributing to the cumulative environmental burden of communities impacted by these CAFOs (Graddy and Rabine, 2024). This combination of exposures could lead to increased risk of zoonotic disease transmission, particularly among those with contact to both swine and poultry and/or their waste products. The triangle of humans, swine and poultry is a potential biosecurity concern for epidemic and pandemic influenza reassortment as well as potential spillover and transmission of other pathogens between swine, poultry, and humans (Zhou et al., 1999; McLean and Graham, 2022; Abdelwhab and Mettenleiter, 2023; Miller et al., 2017; Hollenbeck, 2016; Moore et al., 2021). Influenza has spilled over from swine to humans in the past, causing influenza epidemics and pandemics (McLean and Graham, 2022; Junqueira et al., 2023; Trovão and Nelson, 2020; Markin et al., 2023; Freidl et al., 2017; Brockwell-Staats et al., 2009; Richard et al., 2014), and human-livestock contact can increase risk of pathogen and disease transmission (Klous et al., 2016). Additionally, evidence of bioaerosol transmission, in particular transmission of infectious viruses, as far as tens of kilometers away from animal operations make understanding the extent of the cumulative exposure risks to community residents and their home environments important (Kumar et al., 2024).

This study showed that that swine fecal material is present in household surface settled dust, more often and at higher levels on outdoor compared to indoor surfaces. Detection of Pig-2-Bac DNA on outdoor surfaces of residents' homes living near hog CAFOs, whether in the ILO worker group or neighbor group, along with the near absence of Pig-2-Bac on Metro household surfaces, indicates that swine fecal material is very likely – either directly from the operation or from nearby spray fields – discharged from CAFOs, which are regulated as "non-discharge facilities" in NC. Migration of pig specific fecal *Bacteroidales*, a bacterium living in the pig digestive tract, is likely indicative of spillover of other zoonotic pathogens from ILOs onto nearby residents' properties. While pig *Bacteroidales* may primarily be a nuisance, zoonotic viruses, antibiotic resistant bacteria, and fungi that are detrimental to human health are likely spread alongside. Characterizing such co-exposures would help close the gap between SPI and health effects that ILO neighbors and workers report and experience.

5. Conclusions

Our findings show that swine fecal matter is ubiquitous on household surfaces of communities in regions with high density swine production and suggest that fecal matter from swine CAFOs migrates offsite and contaminates the outdoor and – to a lesser extent – indoor home environments of those living nearby. This study contributes to the growing evidence that swine CAFOs, which are regulated as non-discharge facilities, can indeed contaminate off-site water, air, and land, including the private properties of nearby residents with swine fecal filth. The detection of swine fecal matter on community homes demonstrates the negative impact the vertically-integrated swine industry has on neighbors, providing scientific evidence in support of the community's lived experiences. Future studies should also include markers of poultry fecal contamination and measurements of air pollutants to better capture cumulative impacts of swine and poultry CAFO co-location along with measures of exposure and respiratory, enteric, and zoonotic infections to improve our understanding of adverse health effects related to industrial livestock production.

CRediT authorship contribution statement

Kathleen M. Kurowski: Writing – original draft, Visualization, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Nora Pisanic:** Writing – review & editing, Project administration, Methodology, Investigation, Data curation, Conceptualization. **Kristoffer Spicer:** Writing – review & editing, Investigation, Data curation. **Kate Kruczynski:** Writing – review & editing, Project administration, Data curation. **Carolyn Gigot:** Writing – review & editing, Project administration, Data curation. **Devon J. Hall:** Writing – original draft, Project administration, Investigation, Conceptualization. **Kyle T. Aune:** Writing – review & editing, Software, Methodology. **Bonita Salmerón:** Writing – review & editing, Software. **Ana M. Rule:** Writing – review & editing, Supervision, Methodology. **Christopher D. Heaney:** Writing – review & editing, Resources, Project administration, Methodology, Funding acquisition.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

We would like to thank the community organizers at the Rural Empowerment Association for Community Help (REACH), especially Margaret Carr, Clesha Hall, Unique Hall, Angela Matthews, Arika Miller, Helen Santizo, Phyla Holmes, Norma Mejia, and Sherneka Smith. This study would not have been possible without the strong partnership that REACH has with members of communities in areas of dense industrial hog production. We would like to thank all the participants who agreed to be part of this study. We would also like to thank Will Hendrick for his review, input and sharing of informational resources during the drafting of the manuscript. We would also like to acknowledge Carly Ordak, Caryn Kok and Eric Xu for their assistance with household surface settled dust swab testing.

Funding for this study was provided in part by an anonymous gift and the E.W. "Al" Thrasher Award 10287 from the Thrasher Research Fund. KK and CDH were supported by the National Institute for Occupational Safety and Health (NIOSH) Education and Research Center (ERC) grant T42 OH0008428. CDH, BS, KS, AR, and NP were supported by the Community Science and Innovation for Environmental Justice (CSI EJ) Initiative of the Johns Hopkins Center for a Livable Future. CDH and NP were supported by National Institute of Allergy and Infectious Diseases (NIAID) grant number R21AI139784 and National Institute of Environmental Health Sciences (NIEHS) grant number R01ES026973. CDH and BS were supported by NIEHS P30 Center for Community Health: Addressing Regional Maryland Environmental Determinants of Disease (CHARMED) grant number P30ES032756.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.scitotenv.2025.179591.

Data availability

Data will be made available on request.

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