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Presence of animal feeding operations and community socioeconomic factors impact salmonellosis incidence rates: An ecological analysis using data from the Foodborne Diseases Active Surveillance Network (FoodNet), 2004–2010

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ABSTRACT

Nontyphoidal *Salmonella* spp. are a leading cause of foodborne illness. Risk factors for salmonellosis include the consumption of contaminated chicken, eggs, pork and beef. Agricultural, environmental and socioeconomic factors also have been associated with rates of *Salmonella* infection. However, to our knowledge, these factors have not been modeled together at the community-level to improve our understanding of whether rates of salmonellosis are variable across communities defined by differing factors. To address this knowledge gap, we obtained data on culture-confirmed *Salmonella* Typhimurium, *S.* Enteritidis, *S.* Newport and *S.* Javiana cases (2004–2010; n=14,297) from the Foodborne Diseases Active Surveillance Network (FoodNet), and socioeconomic, environmental and agricultural data from the 2010 Census of Population and Housing, the 2011 American Community Survey, and the 2007 U.S. Census of Agriculture. We linked data by zip code and derived incidence rate ratios using negative binomial regressions. Multiple community-level factors were associated with salmonellosis rates; however, our findings varied by state. For example, in Georgia (Incidence Rate Ratio (IRR)=1.01; 95% Confidence Interval (CI)=1.005–1.015) Maryland (IRR=1.01; 95% CI=1.003–1.015) and Tennessee (IRR=1.01; 95% CI=1.002–1.012), zip codes characterized by greater rurality had higher rates of *S.* Newport infections. The presence of broiler chicken operations, dairy operations and cattle operations in a zip code also was associated with significantly higher rates of infection with at least one serotype in states that are leading producers of these animal products. For instance, in Georgia and Tennessee, rates of *S.* Enteritidis infection were 48% (IRR=1.48; 95% CI=1.12–1.95) and 46% (IRR=1.46; 95% CI=1.17–1.81) higher in zip codes with broiler chicken operations compared to those without these operations. In Maryland, New Mexico and Tennessee, higher poverty levels in zip codes were associated with higher rates of infection with one or more *Salmonella* serotypes. In Georgia and Tennessee, zip codes with higher percentages of the population composed of African Americans had significantly higher rates of infection with one or more *Salmonella* serotypes. In summary, our findings show that community-level agricultural, environmental and socioeconomic factors may be important with regard to rates of infection with *Salmonella* Typhimurium, Enteritidis, Newport and Javiana.

1. Introduction

Nontyphoidal *Salmonella* spp. are a leading cause of bacterial foodborne illness, responsible for an estimated 1.2 million cases of acute gastroenteritis in the United States each year, including approximately 23,000 hospitalizations and 450 deaths (Scallan et al., 2011). Salmonellosis is characterized by diarrhea, fever and abdominal cramping following a 6–72 h incubation period and typically self-resolves in 5–7 days (Crump et al., 2015; Hohmann, 2001). However, *Salmonella* infections involving sequelae (e.g. bacteremia and septic arthritis), as well as cases occurring among infants, the elderly and immunocompromised individuals, can require antimicrobial therapy and other medical treatment

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(Crump et al., 2015; Hohmann, 2001).

Salmonella are frequently detected in broiler chickens (Adell et al., 2014; Clemente et al., 2014; Madden et al., 2011; Sapkota et al., 2014), eggs (Van Hoorebeke et al., 2011; Wales and Davies, 2011), pigs (Arnold et al., 2015; Pires et al., 2014a; Tamang et al., 2015), and cows (Hanson et al., 2015); therefore, the consumption of contaminated broilers, eggs, pork and beef have been identified as significant exposure pathways for both sporadic cases and outbreaks (Mughini-Gras et al., 2014; Pires et al., 2014b). Direct contact with infected animals and their production environments, as well as exposure to fecally-contaminated water, have also been shown as possible environmental exposure pathways (Pires et al., 2014b). For example, untreated poultry litter (waste) from animal feeding operations is often land applied as a soil amendment, and, if the litter is *Salmonella*-positive, proximal surface water and groundwater can become contaminated during runoff events, serving as a potential environmental source of exposure to *Salmonella* spp. (Haley et al., 2009; Jenkins et al., 2006; Maurer et al., 2015; Vereen et al., 2013). In addition, several studies have provided evidence that socioeconomic factors can influence rates of infection with *Salmonella* (Chang et al., 2009; Newman et al., 2015).

However, to our knowledge, agricultural, environmental and socioeconomic factors at the community-level have not been modeled together to improve our understanding of whether community transmission of *Salmonella* may be more likely in areas defined by specific factors. Chang et al. (2009) conducted a county-level, ecological analysis of the influence of sociodemographic factors on the incidence of salmonellosis and showed that race, ethnicity, location of residence, age and socioeconomic factors may affect *Salmonella* incidence (Chang et al., 2009); however, they did not focus on agricultural or environmental risk factors that may also impact rates of infection.

In this study, we explored associations between zip code level agricultural, environmental and socioeconomic factors and zip code level incidence of nontyphoidal *Salmonella* infections at multiple surveillance sites in the U.S. We focused on infections with four major *Salmonella* serotypes–Enteritidis, Typhimurium, Newport and Javiana–that accounted for 54% of all culture-confirmed *Salmonella* infections reported to the U.S. Foodborne Diseases Active Surveillance Network (FoodNet) in 2014 (Crim et al., 2015). Findings from this study will further our knowledge regarding community factors that may be influential with regard to the incidence of salmonellosis.

2. Methods

2.1. Data sources

FoodNet is a collaboration between the Centers for Disease Control and Prevention (CDC), 10 state health departments, the U.S. Department of Agriculture's Food Safety and Inspection Service (USDA-FSIS), and the U.S. Food and Drug Administration (FDA) (CDC, 2016). Ten states comprise the FoodNet surveillance region, which represents 15% of the total U.S. population. FoodNet conducts active, population-based surveillance for laboratory-confirmed infections caused by nine pathogens transmitted commonly through food, including *Salmonella.* For this study, we restricted our analyses to data on culture-confirmed cases of *Salmonella* Typhimurium, *Salmonella* Enteritidis, *Salmonella* Javiana and *Salmonella* Newport reported between 2004 and 2010 to the FoodNet sites that included complete states: Connecticut, Georgia, Maryland, Minnesota, New Mexico, Oregon, and Tennessee.

In addition to the FoodNet data, we obtained socioeconomic and environmental data from the 2010 Census of Population and Housing (United States Census Bureau, 2010) and the 2011 American Community Survey (United States Census Bureau, 2011) (5-year estimates) by 5-digit zip code tabulation area (ZCTA) as previously described (Zappe Pasturel et al., 2013). Animal feeding operation data were obtained from the 2007 U.S. Census of Agriculture, National Agricultural Statistics Service (USDA, 2015).

2.2. Descriptive analyses

FoodNet *Salmonella* case count data by serotype were linked with the socioeconomic, environmental and agricultural data by zip code and 5-digit ZCTA. After linking the data, we calculated incidence rates by serotype per 100,000 population for each zip code using zip code population estimates from the 2010 Census (United States Census Bureau, 2010).

2.3. Negative-binomial regressions

To explore associations between incidence rates for each of the four serotypes (Typhimurium, Enteritidis, Javiana and Newport) and socioeconomic, environmental and agricultural factors (at the zip code level), we employed regression models. First, we used the inverse of the variance inflation factor to evaluate collinearity among our predictor variables, and highly collinear variables were excluded using a stepwise approach. We then compared several regression models for count data and tested models with and without zero inflation and with and without spatial covariate structure. The negative-binomial regression models without spatial covariate structures were the most appropriate for these data.

The final negative binomial models for each serotype included the zip code level variables described in Table 1. Cases reported in Georgia between 2004 and 2008 (n=4750) and 318 cases from the other FoodNet sites were excluded from the final models because either zip code information was missing for these cases or socioeconomic Census variables were not available for the given zip code. We ran state-specific regression models for each serotype because the states differed so greatly with regard to some characteristics (particularly the animal feeding operation variables and the related level of animal production occurring in each state) that including all states in one model masked important findings. All modeling was performed using SAS version 9.3. *P*-values of ≤ 0.05 were used to determine statistical significance.

3. Results

Between 2004 and 2010, 19,365 cases of culture-confirmed *Salmonella* Typhimurium, *S.* Enteritidis, *S.* Newport and *S.* Javiana infections were reported to FoodNet by Connecticut, Georgia, Maryland, Minnesota, New Mexico, Oregon, and Tennessee. Of those cases, 14,297 had valid zip codes (n=2343 zip codes), for which Census data were available, and were included in subsequent analyses. The number of zip codes included per state was as follows: Connecticut, 229; Georgia, 501; Maryland, 316; Minnesota, 483; New Mexico, 151; Oregon, 207; and Tennessee, 456. The majority of Enteritidis (52.3%), Newport (39.2%) and Typhimurium (34.6%) cases were 20–59 years old; however, the majority of Javiana (37.6%) cases were 0–4 years old (Table 2). In terms of race and ethnicity, the majority of cases across all serotypes were White and Non-Hispanic (Table 2).

3.1. Community environmental and agricultural factors

Our negative binomial regression results provided evidence that multiple community-level environmental and agricultural factors are associated with rates of salmonellosis (Figs. 1 and 2;