Geospatial Health 2025; volume 20:1416

One health review of recent *Salmonella* dynamics and human health outcomes in the United States

Geoffrey Kangogo,[1] Lavanya Sankaran,[2] Mitesh Rajpurohit,[1] Kate E. Trout[1]

[1]College of Health Sciences, University of Missouri, Columbia, Missouri; [2]College of Osteopathic Medicine, California Health Sciences University, California, United States of America

Abstract

This review assessed the combined impact of poultry production, climate variability, and agricultural environments on human salmonellosis risk across the United States. It considers whether regions with both high poultry production and notable climate variability show amplified infection patterns and whether environmental transmission pathways are becoming more prominent alongside direct poultry exposure. A comprehensive systematic literature review in PubMed was conducted following PRISMA guidelines for studies published between 2011 and 2025 addressing *Salmonella* in relation to human incidence, poultry processing and environmental exposure. Our search yielded 22 studies that met the inclusion criteria and it included a range of methods such as surveillance, epidemiological modeling, and intervention research across different U.S. regions. The key analytical variables included were serotype diversity, seasonal and regional distribution, antimicrobial resistance, and climate-related environmental transmission. The findings revealed significant geographic overlap between areas of intensive poultry production and high salmonellosis rates, especially in the southern states. A rise in multidrug-resistant serovars, such as *S. infantis* in poultry products, was found. Seasonal contamination patterns showed chicken cuts peaking in contamination during late winter, in contrast to the summer peak of human cases. We also observed that temperature extremes and heavy precipitation were linked to increased environmental contamination, particularly of water sources, and higher human exposure risk. These conditions also influenced serotype prevalence and the distribution of resistance genes. As a result, there is a need for integrated One Health strategies that should include adaptive poultry management, climate-responsive environmental monitoring with a focus on serotype-specific risk assessment to reduce the overall public health impact of *Salmonella*.

Correspondence: Kate Trout, Department of Health Sciences, College of Health Sciences, 707 Lewis Hall, Columbia, 65211 Missouri, United States of America.
Tel.: +1 573-882-9435
E-mail: kate.trout@health.missouri.edu

Key words: *Salmonella*, serotypes, foodborne illness, one health, climate and health, USA.

Conflict of interests: the authors declare no known financial interests or personal relationships that could have influenced the work reported in this paper.

Contributions: GK, Conceptualization, methodology, formal analysis, data curation, review & editing; LS, Literature search, data curation, formal analysis, writing original draft, visualization, review & editing, validation; MR, writing review & editing; KT, Supervision, conceptualization, writing review & editing, data interpretation, project administration.

Data availability: all data supporting the findings of this review are derived from publicly available sources as cited in the manuscript.

Acknowledgment: we would like to thank the SENS-D project team at the University of Missouri, Columbia. This work is supported by the National Science Foundation (NSF) Convergence Accelerator grants, Phase I (No. 0072474) and Phase II (No. 2344877).

Received: 26 June 2025.
Accepted: 9 November 2025.

Licensee PAGEPress, Italy
Geospatial Health 2025; 20:1416
doi:10.4081/gh.2025.1416

Introduction

Rising *Salmonella* prevalence and national responses

Salmonella infections represent a persistent and costly public health concern in the United States. The Centers for Disease Control and Prevention (CDC) estimates that *Salmonella* causes approximately 1.35 million infections each year in the U.S., *i.e.* about 15 cases per 100,000 population (Crim *et al.*, 2014; Pew, 2021; Punchihewage-Don *et al.*, 2022; CDC, 2024), making it one of the nation's leading causes of foodborne illness (CDC, 2024; U.S Food & Drug Administration - FDA, 2023). Non-Typhoidal (NTS) *Salmonella enterica,* especially serotypes *S. typhimurium* and *S. enteritidis*, is the primary agent of foodborne gastroenteritis linked to poultry products such as chicken and eggs (Algorri, 2019; CDC, 2024). Historically, contaminated poultry emerged as a predominant source of hospitalizations and deaths from food poisoning between 1998 and 2008. Contaminated poultry products accounted for 17% of foodborne-illness fatalities nationally, with *Salmonella* identified as the responsible pathogen in over one-quarter of those deaths (Painter *et al.*, 2013).

The rising infection burden from poultry contamination coincides with the substantial expansion of the U.S. broiler industry that increased by 21% between 2010 and 2020 (National Chicken Council - NCC, 2021a). Within the south-eastern region, which is the nation's primary poultry-producing region (Siceloff *et al.*, 2022), Georgia consistently tops in broiler output, producing more than 1.3 billion broilers annually (U.S. Department of Agriculture - USDA, 2021; Siceloff *et al.*, 2022), while Alabama and Arkansas follow closely behind with roughly 1.1 billion broilers each (USDA, 2021). The economic impact of this industry growth is substantial – in 2010, the value of broilers produced was $23.7 billion (USDA, 2011); by 2023, this value had risen to $42.6 billion (USDA, 2024), marking an 80% increase in ten years. Per-capita chicken consumption also saw a notable rise from approximately 82.6 pounds in 2010 (NCC, 2021b) to 102.6 pounds in 2024, reflecting a growing consumer preference for poultry (NCC, 2020). Southern states shoulder disproportionately high salmonellosis rates, compared to the national baseline of ~15 cases per 100,000 population (Crim *et al.*, 2014; Pew, 2021; Punchihewage-Don *et al.*, 2022). By 2019, Mississippi led with 36.7 cases per 100,000, followed by Florida (31.3), then Alabama, Arkansas, and Georgia (each approximately 20), respectively (FDA, 2024). Furthermore, FoodNet data reveal that *Salmonella* incidence trends have risen most sharply in Southern states over the past decades, with Georgia exhibiting the largest increase in prevalence of 140% within five years (Chai *et al.*, 2012). In response to these mounting threats, the USDA implemented updated performance standards aimed at reducing *Salmonella* contamination in the poultry processing supply chain nationwide (Food Safety and Inspection Service - FSIS, 2015, 2014). While the USDA's FSIS had been routinely sampling Ready-To-Eat (RTE) meat and poultry products for *Salmonella* contamination since 1996 (FSIS, 2015), the New Poultry Inspection System (NPIS) implemented in 2014 has modernized inspection of young-bird slaughter establishments to focus on controlling persistent pathogens like *Salmonella* (FSIS, 2014). Similarly, the USDA's FSIS launched sampling programs for raw chicken parts in 2015 (FSIS, 2015).

Although extensive control measures have been implemented at multiple points in the supply chain, national surveillance data indicate that *Salmonella* incidence in humans has not declined as expected and, in some reports, has shown an upward trend. The Federal Healthy People 2020 target aimed to reduce *Salmonella* infection rates nationwide to 11.4 per 100,000 (Pew, 2021). However, by 2019, the U.S. national average had instead increased to 17.1 cases (Pew, 2021; Tack *et al.*, 2020), exceeding both the target and the national incidence baseline to reflect the rising contemporary burden of Salmonellosis (Crim *et al.*, 2014).

Microbiology, taxonomy and key serovars

Salmonella enterica is a Gram-negative, motile bacterium from the Enterobacteriaceae family, able to survive in both animal hosts and the environment (Andino & Hanning, 2015; Jajere, 2019). It grows in diverse conditions, thriving between 5°C and 45°C and at neutral pH (Jajere, 2019; Galán-Relaño *et al.*, 2023). Its serovars are divided into typhoidal, like the *S. typhi*, *S. paratyphi,* which infect only humans causing systemic illness, and also NTS types, which are zoonotic and often linked to foodborne illness (Varma *et al.*, 2006; Fàbrega & Vila, 2013). In humans, typhoidal serovars lead to a systemic illness known as typhoid fever, which has an incubation period of 10 to 14 days and leads to symptoms such as high fever, headache, abdominal discomfort and mild gastrointestinal issues (Shaji *et al.*,2023). Conversely, NTS infections manifest much more rapidly within 6 to 72 hours, and usually present as acute gastroenteritis characterized by diahorrhea, vomiting, stomach cramps, and fever. Notably, among the NTS strains, *S. enteritidis* and *S. typhimurium* infect both animals and humans and can persist in chickens with little to no clinical symptoms, allowing for silent colonization of the intestines and reproductive tract that contaminates eggs and meat. Poultry is the main reservoir for NTS serovars like *S. enteritidis,* which is linked to eggs, *S. typhimurium*, and *S. infantis*, the latter of which is increasingly associated with multidrug resistance in broiler systems (Kosa *et al.*, 2015; Jajere, 2019; Punchihewage-Don *et al.*, 2022; Siceloff *et al.*, 2022; Shaji *et al.*, 2023; Montone *et al.*, 2023).

Transmission and pathogenesis

Poultry are the main source of *Salmonella* infections in humans, with transmission occurring both vertically, particularly through egg contamination before laying, and horizontally via contaminated feed, water and the environment (Liu *et al*., 2022; Shaji *et al.*, 2023) (Figure 1). Rodents and wild birds also spread the bacteria, while poor biosecurity increases flock transmission (Obe *et al.*, 2023; Huber *et al.*, 2024). Humans typically get infected by eating contaminated poultry products (Figure 2). After ingestion, *Salmonella* survives stomach acid and invades the intestines using a secretion system. This causes an inflammatory response, marked by the recruitment of neutrophils to the site of infection, resulting in symptoms like diarrhea, abdominal cramps and fever hours after ingestion. In healthy people, the infection usually resolves on its own and is confined to the gastrointestinal tract. However, in susceptible groups like infants, the elderly and immunocompromised individuals, *Salmonella* can lead to systemic dissemination and potential harm to organs such as the liver and spleen (Higginson *et al.*, 2016; Shaji *et al.*, 2023).

Environmental and climate factors heavily influence *Salmonella* prevalence. Warmer temperatures raise infection risk, especially in the southeast U.S., where poultry production is concentrated (Chai *et al.*, 2012; Jajere, 2019; Damtew *et al.*, 2024; FDA, 2024;). Heat stress increases shedding in broilers, contaminating litter and processing sites (Liu *et al.*, 2018; Huber *et al.*, 2024). Similarly, heavy rainfall after droughts elevates runoff contamination, introducing *Salmonella* into irrigation systems and production fields (Micallef *et al.*, 2012; Jiang *et al.*, 2015; Austhof *et al.*, 2024). In places like southern Georgia, pond contamination rates range from 15% to 85%, with warmer, wetter conditions supporting survival even in a dormant state (Luo *et al.*, 2015; Liu *et al.*, 2018; Billah & Rahman, 2024). Certain serovars thrive in specific regions of the U. S., like the *S. newport* and *S. javiana* that persist in humid Mid-Atlantic zones, while *S. infantis* is linked to heat-stressed broilers in the Southeast (Micallef *et al.*, 2012; Austhof *et al.*, 2024). In light of emerging spatiotemporal patterns, the objective of this study was to review recent literature through a PRISMA-guided format to identify the modern-day regional prevalence of *Salmonella* infections and pathogen dynamics on human infections across the U.S, applying a One Health lens to analyze the interconnectedness of human salmonellosis infection rates, poultry contamination, and climate dynamics.

Materials and Methods

This systematic review, guided by the ‘preferred reporting items for systematic reviews and meta-analyses’ PRISMA methodology, synthesized findings from 22 peer-reviewed studies to investigate the interconnected dynamics of *Salmonella* prevalence across human incidence, poultry processing and environmental reservoirs in the U.S., with particular attention to climatic influences. It was conducted according to the guidelines of 2020, which provide a comprehensive framework for ensuring transparency, completeness and reproducibility in systematic reviews (Page *et al*., 2021; Sarkis-Onofre *et al.*, 2021). A structured search was performed in PubMed to identify peer-reviewed articles published between 2011 and 2025 that examined *Salmonella* in relation to climate, poultry and regional patterns within the U. S. The search strategy employed operators to combine key concepts. Specifically, pathogen-related terms (“*Salmonella*” OR “Salmonellosis”) were combined with climate-related terms (“cli-

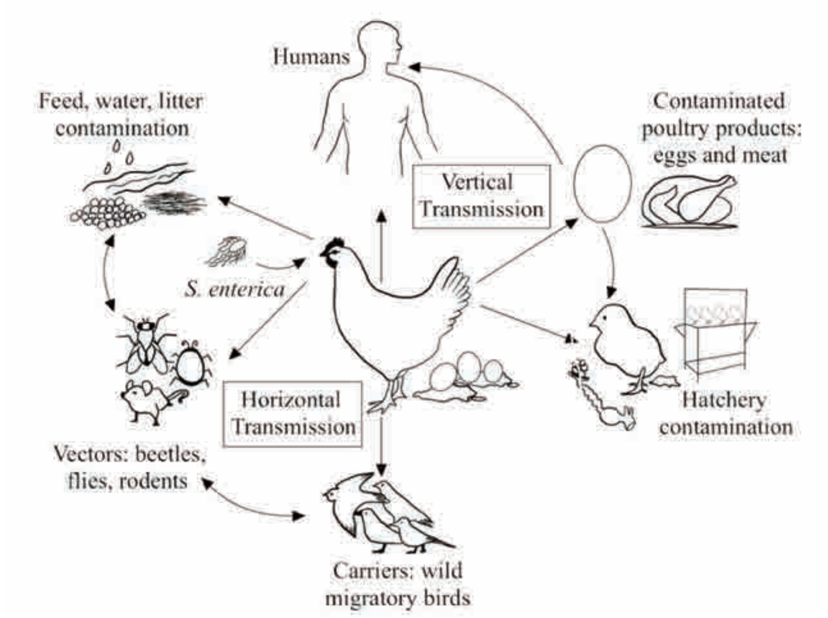

Figure 1. Overview of horizontal and vertical Salmonella transmission routes from poultry to humans. Image credit: Lavanya Sankaran.

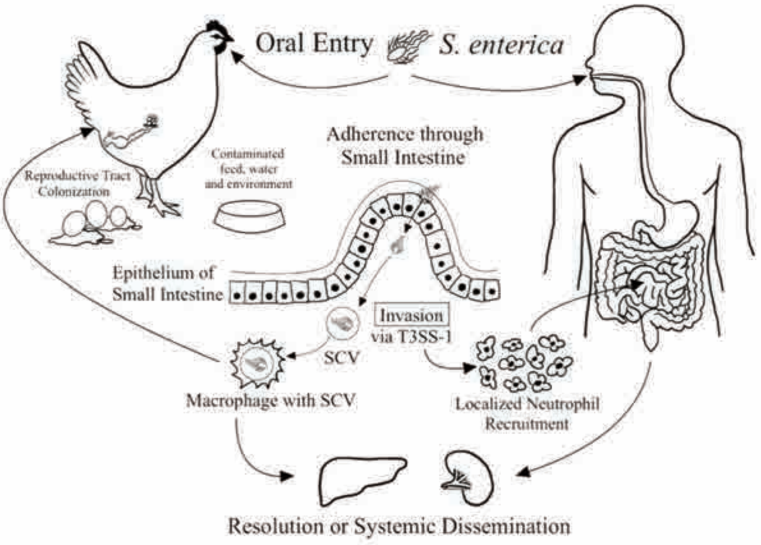

Figure 2. Pathogenesis of *Salmonella* infection in chickens and humans. Image credit: Lavanya Sankaran.

mate” OR “temperature” OR “rainfall” OR “precipitation” OR “humidity” OR “weather” OR “flood” OR “storm” OR “season”), agriculture-related terms (“poultry” OR “chicken” OR “eggs” OR “foodborne” OR “food” OR “agriculture”), and geographic qualifiers (“regional” OR “region” OR “geographic” OR “state”) using the AND operator. To restrict the scope to U.S.-focused studies, search strings also required that at least one of the geographic identifiers (“USA” OR “U.S.” OR “United States”) appeared in the title or abstract fields.

All records retrieved (n = 70) were imported into a reference manager and duplicates were removed. Initial screening of titles and abstracts was conducted independently by two reviewers based on predefined eligibility criteria. This dual-review process enhances the reliability of findings and minimizes potential bias in data interpretation (Page *et al.*, 2021; Sarkis-Onofre *et al.*, 2021). Inclusion criteria consisted of primary research articles conducted within the U. S., published between 2011–2025 examining *Salmonella* in relation to climate, poultry or agriculture. Studies conducted outside the U. S., publications outside the date range, quasi-experimental study designs, literature reviews, meta analyses, commentary pieces and studies not involving *Salmonella* incidence with climate, poultry or agriculture (n=43), were excluded.

The remaining 27 articles underwent full-text review to confirm eligibility. An additional five articles (n=5) were excluded during full-text screening since they had outcomes not grounded in the One Health model examining the interconnected roles of human health, animal health, and the environment in the spread of *Salmonella*. Discrepancies in the eligibility decisions were resolved through consensus or consultation with a third reviewer. A final total of 22 articles was included in the synthesis and a formal quality assessment of all included studies was conducted using the ‘strengthening the reporting of observational studies in epidemiology’ (STROBE) checklist to evaluate reporting transparency and methodological rigor. The study selection process is summarized in the PRISMA flow diagram (Figure 3).

Due to heterogeneity in study designs, populations and outcome measures, we conducted a narrative synthesis of the included studies. Extracted data were thematically organized to identify key patterns, similarities and discrepancies across studies. Variables included study location, population, *Salmonella* serovars assessed, environmental or climatic exposures, poultry-related risk factors and major findings related to contamination trends or climate associations. Reported serovar names were recorded to assess diversity across contexts and serovar diversity was explicitly captured to identify cross-study patterns. Quantitative outcomes, such as prevalence rates, odds ratios and statistical significance of analysis were tabulated when available. Study limitations related to methodology, sampling, and generalizability were noted during synthesis. Given the interconnected nature of poultry, environment and human health, the synthesis was conducted with a One Health approach, emphasizing the integration of data across these domains to capture complex, interdependent risk pathways.

The 22 studies included in this review generally demonstrated high reporting quality based on the STROBE checklist, with most clearly stating their objectives, data sources, and design. However, limitations in reporting potential biases and justifications for study size were noted. These studies examined the influence of poultry contamination, environmental exposures, and climate-related factors such as rainfall, temperature, humidity, and extreme weather events on the prevalence of *Salmonella* in humans. To facilitate

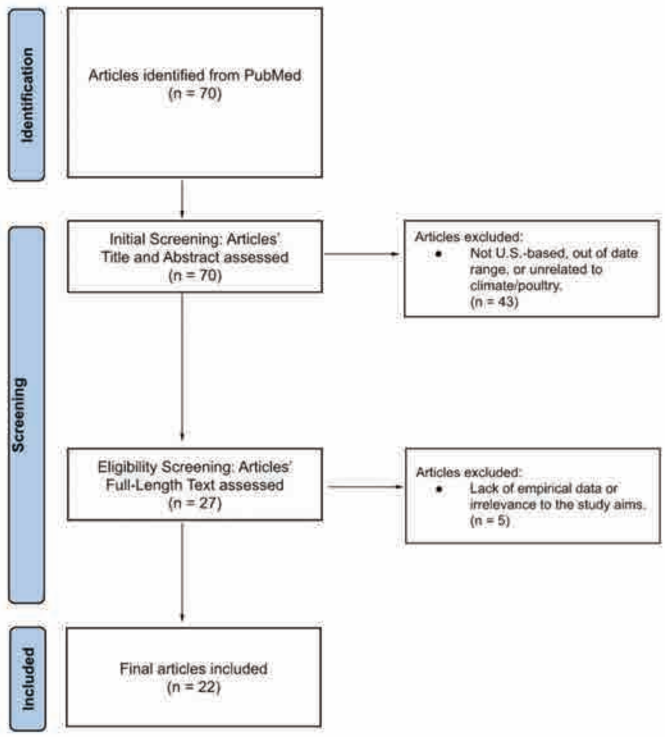

Figure 3. PRISMA diagram demonstrating screening and review process. Image credit: Lavanya Sankaran.

meaningful comparisons using a One Health approach, studies were categorized into three main groups based on their study population: i) human incidence, ii) poultry processing and iii) environmental transmission presenting a summarized overview by group and year of publication (Table 1).

Results

Geographically, eight studies (36.4%) drew upon national datasets to provide broad coverage of human salmonellosis trends (Crim *et al.*, 2018; Snyder *et al.*, 2019; Judd *et al.*, 2019; Simpson *et al.*, 2020; Morgado *et al.*, 2021), while three of them examined poultry contamination (Mamber *et al.*, 2018; Beczkiewicz & Kowalcyk, 2021; Williams *et al.*, 2022). Seven studies (31.8%) centred on the U.S. South, spanning poultry-based Antimicrobial Resistance (AMR) surveillance (Glaize *et al.*, 2021), produce farm irrigation water quality (Agga *et al.*, 2023; Hwang *et al.*, 2020), environmental pathogen reservoirs in soil and ponds (Lee *et al.*, 2019), storm-runoff impacts (Harris *et al.*, 2018), and both single-state and multi-state climate-linked salmonellosis modelling (Akil, 2021; Akil *et al.*, 2014). Three studies (13.6%) focused on the Northeast, examining irrigation water quality (Jones *et al.*, 2014), microbial contamination (Deaven *et al.*, 2021), and small-scale produce farms (Marine *et al.*, 2015). Two studies (9.1%) in the West and Midwest surveyed surface waters and microbiomes in arid growing regions (Mukherjee *et al.*, 2019; Gorski *et al.*, 2022;) and another two (9.1%) employed multiregional surveillance methods covering three of four U.S. Census regions (Haack *et al.*, 2016; Malayil *et al.*, 2022). Together, these 22 articles employ diverse investigative tools to elucidate how environmental, agricultural and climatic factors drive *Salmonella* enterica persistence and transmission throughout the U.S. food system, setting the stage for a One Health comparison of human incidence, poultry processing, and environmental transmission in the sections that follow.

Human Salmonella incidence

Amongst the twenty-two articles identified in this literature review, eight (36%) specifically address human *Salmonella* incidence across the U.S. providing contemporary insights into serotype distribution, transmission routes, seasonality, regional

Table 1. Classification of systematic review results by study population.

Study population	Year	Author	U.S. Census Region	Sample (size)	Study design
Human incidence (n = 8)	2014	Akil *et al.*	South (MS, TN, AL)	Monthly reported state-level cases (N/A)	Ecological, retrospective, observational
	2018	Crim *et al.*	Nationwide	Laboratory-confirmed Newport cases (7,630)	Descriptive, retrospective, observational
	2019	Judd *et al.*	All 4 U.S. census regions (Northeast, Midwest, South, West)	LEDS data on human infections by serotype (690,479)	Analytical, retrospective, observational
	2019	Mukherjee *et al.*	Midwest (MI)	Clinical isolates from hospitals (198)	Cross-sectional, retrospective, observational
	2019	Snyder *et al.*	Nationwide	National FDOSS outbreak data (2,447)	Descriptive, retrospective, observational
	2020	Simpson *et al.*	All 4 U.S. census regions (10 states)	FoodNet human cases and data (99)	Time-series, retrospective, observational
	2021	Akil	South (MS)	State Department of Health data (15,484)	Descriptive, retrospective, observational
	2021	Morgado *et al.*	All 4 U.S. census regions (7 states)	FoodNet surveillance of human infections by serovar (32,951)	Time-series, retrospective, observational
Poultry (n = 3)	2018	Mamber *et al.*	Nationwide	RTE poultry products (91,038)	Descriptive, retrospective, observational
	2021	Beczkiewicz & Kowalcyk	Nationwide	Whole chicken carcasses from USDA FSIS plants (40,497)	Analytical, retrospective, observational
	2022	Williams *et al.*	Nationwide	Chicken parts from FSIS and retail chicken from NARMS (n = 83,976)	Analytical, retrospective, observational
Environment (n = 11)	2014	Jones *et al.*	Northeast (NY)	Surface water from agricultural irrigation sites (123)	Descriptive, cross-sectional, observational
	2015	Marine *et al.*	Northeast (MD, DE, NJ)	Organic samples from small farms (577)	Descriptive, cross-sectional, observational
	2016	Haack *et al.*	Multiregional: Midwest, Northeast, South	Animal waste, stream water, and streambed sediment (N/A)	Analytical, longitudinal, observational (cohort)
	2018	Harris *et al.*	South (GA)	Surface water from storm runoff and irrigation ponds (107)	Descriptive, cross-sectional, observational
	2019	Lee *et al.*	South (GA)	Soil and splash water (120)	Experimental, cross-sectional, Interventional
	2020	Hwang *et al.*	South	Soil and fecal samples from pasteurized poultry farms (1,472)	Analytical, longitudinal, observational
	2021	Deaven *et al.*	Northeast (PA)	Freshwater used in agricultural irrigation (112)	Descriptive, cross-sectional, observational
	2021	Glaize *et al.*	South (NC)	Produce, fecal, and environmental samples (1,536)	Experimental, cross-sectional, interventional
	2022	Gorski *et al.*	West (CA)	Surface water in agricultural fields (2,979)	Descriptive, longitudinal, observational
	2022	Malayil *et al.*	Multiregional: Northeast, South, West	Recycled and surface water used in agricultural irrigation (410)	Descriptive, cross-sectional, observational
	2023	Agga *et al.*	South (KY and FL)	Groundwater (488)	Analytical, cross-sectional & longitudinal, observational

MS, Mississippi; TN, Tennessee; AL, Alabama; MI, Michigan; NY, New York; MD, Maryland; DE, Delaware; NJ, New Jersey; GA, Georgia; PA, Pennsylvania; NC, North Carolina; CA, California; KY, Kentucky; FL, Florida; RTE, ready to eat; FSIS, Food Safety and Inspection Service; NARMS, National Antimicrobial Resistance Monitoring System; FDOSS, Foodborne Disease Outbreak Surveillance System; LEDS, Laboratory-based Enteric Disease Surveillance.

patterns, climate impacts, antimicrobial resistance and demographic associations. Reported prevalence varied considerably across different studies depending on period, geographic scope and reporting methods. A nationwide analysis of *Salmonella* outbreaks between 1998 and 2015 documented 2,447 salmonellosis outbreaks involving a total of 65,916 individual cases, with an average of 27 cases per outbreak (Snyder *et al.*, 2019). This period overlapped with a FoodNet surveillance conducted from 2004 to 2014, which identified 32,951 culture-confirmed cases of *Salmonella* infection from four key serovars (*S. enteritidis, S. javiana, S. newport, and S. typhimurium*) across seven states (Mukherjee *et al.*, 2019; Morgado *et al.*, 2021). In parallel, a broader national analysis reported that *Salmonella* consistently ranked among the most common foodborne pathogens from 1996 to 2017, with an average monthly infection rate of 12.68 cases per million population (cpm), one of the highest observed among tracked enteric infections (Simpson *et al.*, 2020).

The nationwide analysis of *Salmonella* outbreaks found that *S. enterica* was the confirmed pathogen in 98.6% of the 2,447 outbreaks reported (Snyder *et al.*, 2019). Among outbreaks with identified serotypes, *S. enteritidis* (29.1%), *S. typhimurium* (12.6%), and *S. newport* (7.6%) were the most common (Snyder et al., 2019). These findings align with smaller-scale studies, such as one conducted across Michigan, which found *S. enteritidis* to be the most prevalent serovar (36.9%), followed by *S. typhimurium* (19.5%) and *S. newport* (9.7%) (Mukherjee *et al.*, 2019). However, a broader surveillance revealed that while common serotypes dominate outbreak reports, the greatest serotype diversity exists among rare strains. For instance, a comprehensive serotype analysis identified 618 distinct serotypes, with very rare and rare serotypes comprising nearly 95% of observed diversity but less than 10% of total cases (Judd *et al.*, 2019). Notably, this diversity included emerging serotypes like *S. braenderup* and *S. infantis*, which showed statistically significant increases in prevalence over the study period (Judd *et al.*, 2019), highlighting the ongoing evolution of the *Salmonella* serotype landscape in the U.S. (Snyder *et al.*, 2019). Food vehicle analysis showed eggs (12.5%), chicken (12.4%), and pork (6.5%) as the leading sources of *Salmonella* outbreaks, with *S. enteritidis* strongly linked to eggs and *S. enteritidis*, *S. heidelberg*, and *S. typhimurium* common in poultry-related cases (Snyder *et al.*, 2019; Varma *et al.*, 2006; Kosa *et al.*, 2015; Montone *et al.*, 2023; Shaji *et al.*, 2023). Over time, egg-associated outbreaks declined sharply, from 14 to 3.4 per five-year period (Snyder *et al.*, 2019).

Regional differences were also linked to serovar type. Analysis of FoodNet data from 2004 to 2014 found that cases of salmonellosis were reported more frequently in rural settings for most serovars, with the notable exception of *S. enteritidis*, which showed a higher rate in urban areas (2.8 per 10,000 in urban vs. other serovars generally higher in rural) (Morgado *et al.*, 2021). This is supported by the findings of another study revealing that *S. enteritidis* cases across Michigan were significantly more likely to occur in urban areas, while *S. typhimurium* cases were associated with animal contact and rural residents (Mukherjee *et al.*, 2019). Urban residence was linked to both higher rates of *S. enteritidis* infections and greater odds of hospitalization with *S. enteritidis*, reflecting the unique risk of this serovar in densely populated areas with higher poultry consumption and retail exposure (Morgado *et al.*, 2021; Mukherjee *et al.*, 2019). Notably, *S. enteritidis* was also associated with consumption of retail bottled water (64.7%) relative to municipal (37.0%) and even well water (52.6%) (Mukherjee *et al.*, 2019), which may correlate to the high urban prevalence of the serotype. This pattern is further supported by findings from Mississippi, which reported higher rates of *Salmonella* in highly populated regions of the state from 2010 to 2018 (Akil, 2021), aligning with the broader observation that urban settings present distinct risk profiles for certain serovars (Morgado *et al.*, 2021; Mukherjee *et al.*, 2019).

Antimicrobial resistance patterns in *Salmonella* isolates varied significantly across studies, with notable regional and serovar-specific differences. In one study of NTS *Salmonella* isolates, 15.2% were resistant to at least one antibiotic (Mukherjee *et al.*, 2019), and 7.5% were classified as multidrug-resistant, meaning they were resistant to three or more antimicrobial classes. *S. typhimurium* isolates were particularly prone to resistance, with 21% showing resistance to at least one antibiotic, followed by 5.6% of *S. enteritidis* isolates (Mukherjee *et al.*, 2019). An increasing trend in tetracycline, ampicillin, and cephalosporin resistance was also observed among key serovars, with resistant infections associated with significantly longer hospital stays, averaging 5.9 days compared to 4.0 days for patients with susceptible infections (Mukherjee *et al.*, 2019). In contrast, an analysis of *S. newport* isolates using the National Antimicrobial Resistance Monitoring System (NARMS) found a substantially lower prevalence of AMR from the southern census region, with 60% of these isolates classified as pansusceptible (Crim *et al.*, 2018), meaning that they lacked resistance to any tested antibiotics. This pansusceptible rate was significantly three times higher in the South than in other regions (Crim *et al.*, 2018), suggesting a regional concentration of strains that remain fully susceptible to treatment.

The southern census region accounted for the largest share of *Salmonella* cases nationally, contributing 33.5% of reported infections between 1996 to 2016 – a significantly higher proportion than the Midwest, Northeast, or West (Judd *et al.*, 2019). This regional pattern aligns with FoodNet data, which identified Georgia as having the highest average incidence among seven surveillance states with 23.4 cases per 100,000 population (Morgado *et al.*, 2021), while the remaining states averaged approximately 13.8 cases per 100,000 population. Georgia's high case burden is further supported by another analysis, which found monthly infection rates in the state were approximately 17.8 cases per million population (cpm) (Simpson *et al.*, 2020), nearly double the rate observed in Oregon (8.56 cpm), highlighting significant geographic variation in infection risk. At the state level, there is also considerable variation in outbreak rates for specific food vehicles. Alaska reported the highest number of egg-associated outbreaks per 100,000 population (0.137) and the highest number of outbreak-associated cases (0.959) (Snyder *et al.*, 2019), while Hawaii had the highest rate of chicken-associated outbreaks (0.143 per 100,000 population) and Pennsylvania had the highest number of outbreak-associated cases for chicken (2.687). Despite this high burden, Hawaii had the third-highest standardized number of *Salmonella* outbreaks overall but did not report comparably high rates for other foodborne pathogens (Snyder *et al.*, 2019).

The stability of seasonal outbreaks varies significantly across regions. National analyses found that infections with generally high rates, like *Salmonella*, exhibited stable seasonality, indicating consistent national seasonal patterns over time (Simpson *et al.*, 2020). However, more localized analyses reveal substantial regional variation. For example, states like New York and Minnesota had a greater tendency for random, high-intensity outbreaks, while Colorado, New Mexico and Oregon had more pronounced, pattern-like infections during certain periods (Simpson *et al.*, 2020). By comparison, studies from Mississippi, Tennessee and Alabama found no significant change in temperature or precipitation rates over the study period (Akil *et al.*, 2014).

Two studies by the same lead author offer complementary insights into *Salmonella* dynamics in the southern United States, highlighting both climatic and regional drivers of infection that contribute to the high prevalence documented. The first study examined the impact of temperature and precipitation on *Salmonella* incidence across Mississippi, Tennessee and Alabama from 2002 to 2011 (Akil *et al.*, 2014), focusing on the potential influence of climatic factors on infection risk. This study reported a significant positive correlation between temperature and *Salmonella* incidence, estimating that a 1°F increase would correspond to an approximate four additional cases per 100,000 population, or a 3% rise above the baseline incidence (Akil *et al.*, 2014). However, no significant association was identified between monthly average precipitation and *Salmonella* cases. Seasonal trends were also evident, with the highest incidence observed in the summer months from July through September (Akil *et al.*, 2014). In contrast, the second study focused more narrowly on Mississippi from 2010 to 2018 (Akil, 2021), evaluating the broader epidemiological landscape of foodborne diseases within the state. This analysis confirmed *Salmonella* as the leading pathogen accounting for approximately 80% of all reported foodborne illness cases (Akil, 2021), significantly higher than other pathogens like Campylobacter and Shigella. The study reported an annual average *Salmonella* incidence of 32.3 cases per 100,000 population in Mississippi (Akil, 2021), nearly double the national average of 16.7 cases per 100,000 population during the same period.

This seasonal variation in *Salmonella* incidence is consistently reported across multiple studies, with most identifying clear summer peaks, though the specific timing and intensity can vary by serovar and region. One study analyzing state-level infection data across Michigan found that 70.2% of *Salmonella* cases occurred in the summer and fall, with pronounced serovar-specific patterns (Mukherjee *et al.*, 2019). *S. enteritidis*, for example, exhibited a strong summer peak, with 47.2% of cases reported during this period, compared to 15.3% in fall and 13.9% in winter (Mukherjee *et al.*, 2019). *S. newport* displayed an even more pronounced seasonal trend, with 74% of cases occurring in summer, while *S. typhimurium* showed a similar bias, with 42.1% of cases occurring in summer compared to only 15.8% in winter (Mukherjee *et al.*, 2019). National-level analyses of infection timing also support this seasonal clustering. An evaluation of monthly infection rates for multiple enteric pathogens, including *Salmonella*, demonstrated tight clustering of peak infection periods in mid-to-late July (Simpson *et al.*, 2020), reflecting the influence of summer heat on pathogen transmission dynamics. This national pattern was further supported by heatmaps showing synchronous summer peaks for multiple pathogens (Simpson *et al.*, 2020), including Campylobacter, Shigella and Cryptosporidium, underscoring the shared climatic drivers of these enteric infections. Further investigation into seasonal case distribution found that overall *Salmonella* case counts peaked in summer (38.6%) and reached their lowest levels in winter (14.5%) (Judd *et al.*, 2019). However, this study also noted a contrasting trend in serotype diversity, with the greatest overall serotype richness observed in winter, when rare and very rare serotypes accounted for more than 10% of all cases (Judd *et al.*, 2019). Another study examining outbreak data from 1998 to 2015 further reinforced these findings, documenting the highest frequency of *Salmonella* outbreaks in summer (June to August), with distinct seasonal variation in outbreak-associated foods (Snyder *et al.*, 2019). For example, egg-related outbreaks peaked in summer (Snyder *et al.*, 2019), but the highest number of outbreak-associated cases for eggs occurred in winter, while chicken outbreaks were most common in summer but had the highest case counts in spring. Turkey outbreaks and cases, by contrast, both peaked in autumn, illustrating that the seasonal dynamics of poultry transmission can vary significantly depending on the serovar and food vehicle involved.

Seasonal peaks in *Salmonella* incidence during summer are likely driven by higher temperatures that promote bacterial growth and persistence. A multi-state study in Mississippi, Tennessee, and Alabama found that each 1°F increase corresponded to about four additional cases per 100,000 population, while precipitation showed no significant effect (Akil *et al.*, 2014). In contrast, FoodNet data revealed that extreme weather influenced serovar-specific risks, with heat waves linked to higher *S. newport* incidence in Maryland and Tennessee, and precipitation events increasing *S. javiana* in Connecticut and *S. enteritidis* in New Mexico (Morgado *et al.*, 2021). Overall, temperature strongly drives general *Salmonella* incidence, but extreme precipitation amplifies risks for certain serovars, especially those tied to environmental or plant-based reservoirs. Thus, while temperature appears to be a strong driver of general *Salmonella* incidence, extreme precipitation may play a critical role in amplifying the risk for certain serovars, particularly those associated with environmental or plant-based reservoirs. Ultimately, these key findings across the eight studies identified in relation to human *Salmonella* incidence are summarized in Table 2.

Poultry processing vectors

Drawing upon the twenty-two selected articles, the findings from three studies specifically focused on *Salmonella* contamination in poultry products regulated by the USDA's FSIS. These nationwide samples include whole chicken carcasses, raw chicken parts, and RTE meat and poultry products. It's crucial to view these results through the lens of the evolving FSIS oversight over the past 10 years, particularly the implementation of the 'New Poultry Inspection System' (NPIS) starting in 2014 and the specific FSIS performance standards for poultry processing in 2016 (Mamber *et al.*, 2018; Beczkiewicz & Kowalcyk, 2021; Williams *et al.*, 2022).

Salmonella prevalence is highest early in the poultry supply chain and declines substantially through processing to retail. FSIS sampling (2005-2012) showed very low contamination in ready to eat products, averaging 0.05-0.06% (Mamber *et al.*, 2018). The highest positives were limited to a few items, such as fermented sausages and powdered chicken broth at 2.5% (Mamber *et al.*, 2018). In contrast, raw poultry products, particularly whole chicken carcasses, demonstrate a substantially higher prevalence of *Salmonella*. One study assessing whole carcasses after the 2014 (NPIS) implementation found that 4.26% (1,725/40,497) of samples tested positive for *Salmonella* (Beczkiewicz & Kowalcyk, 2021). The impact of more recent regulatory changes is even more pronounced at the retail level – a separate study evaluated the national impact of the 2016 FSIS performance standards for chicken parts and found a dramatic reduction in contamination rates, with *Salmonella*-positive samples declining by more than 75% following the implementation of these standards far exceeding the 30% reduction initially predicted by FSIS risk assessments (Williams *et al.*, 2022). Independent testing by the FDA's surveillance program at retail locations confirmed reductions of a similar scale (Williams *et al.*, 2022), meaning that the improvements seen at the processing level were found to be translating effectively to the final products available to consumers.

Analysis of serotypes across the different product types highlights both common strains and shifting dynamics. In the study of RTE products sampled from 2005-2012, despite the low number of positives, 27 distinct serotypes were found, with *S. infantis* and *S. typhimurium* being the most common, each accounting for five isolates (Mamber *et al.*, 2018). Other notable serotypes in the RTE study included *S. derby*, *S. enteritidis*, and *S. johannesburg*, each accounting for four isolates (Mamber *et al.*, 2018). This aligns with the results from the whole chicken carcasses sampled between 2015-2019, the most frequently identified serotypes were *S. ken-*

Table 2. Summary of articles related to Salmonella human incidence (n = 8).

Year	Author	Region	Sample (size)	Serovar	Major finding
2014	Akil et al.	South U.S. (MS, TN, AL)	Monthly reported state-level cases (N/A)	S enterica (general)	• Increase of 1°F associated with 3% increase in MS and three-states model. • *Salmonella* infections peaked in summer: highest rates observed from July-September. • Unlike other studies, no significance found between precipitation and Salmonella outbreaks.
2018	Crim *et al.*	Nationwide	Laboratory-confirmed Newport cases (7,630)	Newport	• 60% of NARMS Newport isolates were pansusceptible from the South. • The rate of pansusceptible isolates in the South was 3x times that of the rest of the country. • 70% of pansusceptible outbreaks in NORS were produce-associated.
2019	Judd *et al.*	4 U.S. census regions	LEDS data on human infections by serotype (690,479)	*Salmonella* spp. (general)	• Identified 618 distinct Salmonella serotypes. • Overall case counts peaked in summer and were lowest in winter, but serotype richness was highest in winter. • South had the highest prevalence but lowest serotype richness, while the West had the highest diversity of serotypes across most age groups.
2019	Mukherjee *et al.*	Southern MI	Clinical isolates from hospitals (198)	35 total: Enteritidis, Typhimurium, Newport, etc.	• Top 3 serovars: *S. enteritidis, S. typhimurium* and *S. newport*, found to have seasonal summer trend. • 15.2% of isolates were resistant to at least one antibiotic, and 7.5% had MDR. S. typhimurium more commonly resistant than S. enteritidis. • Enteritidis cases more likely in urban areas, while *S. typhimurium* common in rural settings.
2019	Snyder *et al.*	Nationwide	National FDOSS outbreak data (2,447)	Enteritidis, Typhimurium, Newport, Braenderup, Infantis	• Top 3 serovars: *S. enteritidis* (29.1%), *S. typhimurium* (12.6%) and *S. newport* (7.6%). • Common food vehicles: eggs (12.5%), chicken (12.4%), and pork (6.5%). • Outbreaks common in summer, but outbreak-associated cases significant in winter or spring.
2020	Simpson *et al.*	Nationwide and 10 states.	FoodNet human cases and data (99)	Salmonella spp. (general)	• *Salmonella* had the one of the highest average monthly rates amongst pathogens at 12.68 cpm • Nationally and at the state level, *Salmonella* peaked in summer (July). • Georgia showed ~2x the infection rate of Oregon.
2021	Akil	MS	State Department of Health data (15,484)	S enterica (general)	• *Salmonella* accounted for 80% of reported foodborne illnesses in MS. • Significant summer peak, with the highest rates observed from July-September. • Infection rates higher in regions with dense populations and urban zones.
2021	Morgado *et al.*	7 States covering 4 U.S. census regions	FoodNet surveillance of human infections by serovar (32,951)	4 total: Enteritidis, Newport, Javiana, Typhimurium	• Newport infections increased by 7% in MD and 6% in TN following extreme heat events. • Javiana infections rose by 22% in CT and 5% in GA following extreme precipitation events. • Areas with dense animal farming showed highest climate-driven increases in *Salmonella* infections.

MS, Mississippi; TN, Tennessee; AL, Alabama; MI, Michigan; MD, Maryland; CT, Connecticut; GA, Georgia; FDOSS, Foodborne Disease Outbreak Surveillance System; LEDS, Laboratory-based Enteric Disease Surveillance; NARMS, National Antimicrobial Resistance Monitoring System; NORS, National Outbreak Reporting System; MDR, multidrug resistant.

tucky (50.6%), *S. enteritidis* (14.2%), *S. infantis* (9.8%), and *S. typhimurium* (9.7%) (Beczkiewicz & Kowalcyk, 2021). In contrast, the analysis of data from chicken parts collected from April 2015 through December 2020 highlighted rapid and dramatic changes in the composition of these common serotypes, while *S. enteritidis* and *S. kentucky* were common serotypes in chicken parts as well, *S. infantis* became dominant and showed a rapid and substantial increase, rising from less than 4% of positive samples in 2015 to nearly 25% in 2020 (Williams *et al.*, 2022). Concurrently, the prevalence of *S. kentucky* and *S. typhimurium* decreased in chicken parts during this period, both falling below 25% by 2020 (Williams *et al.*, 2022). This study also found that serotypes *S. enteritidis* and *S. typhimurium* are the only ones frequently isolated in both chicken samples and humans (Williams *et al.*, 2022). Predictions based on the serotype trends observed in chicken parts suggested that without new interventions, such as broader serotype vaccinations, *S. infantis* was likely to become the dominant serotype in chicken parts by 2021-2023 (Williams *et al.*, 2022). This projected increase in *S. infantis* was expected to be offset by larger decreases in *S. enteritidis* and Kentucky, for which specific vaccines are available. However, the study authors emphasized that despite the rapid increase in the proportion of *S. infantis*-positive samples, the overall reduction in *Salmonella* prevalence in chicken parts has likely limited consumer exposure to this specific serotype (Williams *et al.*, 2022).

Resistance patterns in *Salmonella* isolates from chicken parts present a mixed but concerning picture. An analysis of these isolates found that slightly less than half were pan-susceptible, meaning they did not exhibit antibiotic resistance (Williams *et al.*, 2022). However, a more troubling trend identified was the increase in the proportion of *Salmonella* isolates resistant to one or more antibiotics classified as critically important, with the estimated fraction of such isolates increasing by double (Williams *et al.*, 2022). Authors attribute this rise in resistance to critically important antibiotics primarily to the change in the composition of *Salmonella* serotypes, specifically the rapid increase in the prevalence of *S. infantis,* isolates noted to have a larger proportion classified as MDR. Their growing prominence in the chicken parts population could have a disproportionate effect on overall antimicrobial resistance patterns (Williams *et al*., 2022). In contrast to the trend driven by *S. infantis*, predictions for 2021–2023 suggested that, without new interventions, AMR trends in other serotypes were generally improving for critically and highly important antibiotic categories (Williams *et al.*, 2022).

In poultry processing, the establishment size and production focus were indeed found to be associated with *Salmonella* contamination. The RTE study found that nearly all *Salmonella*-positive samples were obtained from small establishments based on the number of employees following hazard analysis procedures (Mamber *et al.,* 2018). When analyzed by production volume (in pounds per year), positive RTE samples were most commonly found in establishments producing between 10,000 and 10 million lbs per year (Mamber *et al*., 2018). Moreover, another study found that establishments slaughtering more than 10 million birds per year had significantly lower odds of contamination compared to those slaughtering less (Beczkiewicz & Kowalcyk, 2021).

Seasonal patterns were observed with new considerations. For whole chicken carcasses, the odds of contamination were higher in the summer than in winter, a trend consistent with historical observations for many meat and poultry products (Beczkiewicz & Kowalcyk, 2021). However, in the study of chicken parts, the peak in contamination was found to occur in late winter, with peaks occurring in January to February and in early summer (Williams *et al.*, 2022). This pattern is noted as being almost completely reversed from the seasonal pattern in human cases of salmonellosis, which has a more pronounced July-August peak and February nadir (Williams *et al.*, 2022). This shift in seasonality for chicken parts was highlighted as one of the most surprising findings of the study. The seasonal trend observed in retail chicken parts lagged behind the FSIS trend, consistent with the expected delay between production and retail and the aggregation of samples into months (Williams *et al.*, 2022). In contrast, the study on RTE products found no significant seasonal effect with respect to *Salmonella* detection and may have resulted from a lack of seasonal patterns in RTE products that were expected and reflected the regulated control over pathogens in the post-processing environment (Mamber *et al.*, 2018).

Geographic region was associated with *Salmonella* contamination, though findings varied across product types. In the study of RTE meat and poultry products, *Salmonella* was detected in samples from all geographic regions (Mamber *et al.*, 2018). The south-eastern region had the highest percentage of positive samples (0.11%), while the North Central region had the lowest (0.02%), and these regional differences in RTE contamination were statistically significant (Mamber *et al.*, 2018). The south-eastern region in this study included the states of Alabama, Florida, Georgia, Kentucky, Mississippi, North Carolina, South Carolina, Tennessee, Virginia, West Virginia, Puerto Rico and the U.S. Virgin Islands (Mamber *et al.*, 2018). The finding of higher contamination in the Southeast for RTE products aligns with the broader observation that the southern census region accounted for the largest share of human *Salmonella* cases nationally (Judd *et al.*, 2019). In contrast, the study of whole chicken carcasses found that contamination odds were actually the lowest in the Mid-East Central region (Beczkiewicz & Kowalcyk, 2021). The Mid-East Central region included the states of Alabama, Kentucky, Mississippi, and Tennessee, and was used as the reference group due to having the highest concentration of poultry processing establishments among all other regions (Beczkiewicz & Kowalcyk, 2021). As such, the regional findings across these two studies do not agree when considering different product types (RTE *vs.* whole carcasses); states grouped into a lower-risk category in one study appear in a higher-risk category in the other (Mamber *et al.*, 2018; Beczkiewicz & Kowalcyk, 2021). These key findings on poultry processing are summarized in Table 3.

Environmental and agricultural transmission

Within the 22 articles identified in this literature review, 11specifically address environmental or agricultural vectors linked to *Salmonella* transmission across the U. S. These vectors include sources such as surface water, groundwater, streams, ponds, storm runoff, soil, sediment, animal feces, plants and fresh produce. Water sources, including surface and recycled water, irrigation ponds, streams, storm runoff and ditches are recognized as significant environmental reservoirs for *Salmonella*. Despite variation in prevalence across diverse geographic contexts in these studies, surface water and surface water-derived sources specifically demonstrate a high-risk environmental reservoir for *Salmonella* prevalence (Jones *et al.*, 2014; Harris *et al.*, 2018; Deaven *et al.*, 2021; Gorski *et al.*, 2022; Malayil *et al.*, 2022; Agga *et al.*, 2023). In a survey of 2,979 public-access surface water samples, including rivers, streams, lakes and ponds from a Central

California leafy-green region, *Salmonella* was recovered from 56.4% of samples, with watershed-specific rates ranging from 43.7% to 78.1% (Gorski *et al.*, 2022). Studies in the eastern U.S. reported comparable prevalence rates. In New York State, *Salmonella* was detected in 43% of surface water samples overall (n = 123), with the highest incidence observed in irrigation ponds (46%), followed by canals (40%) and creeks (26%) (Jones *et al.*, 2014), while 49% of freshwater samples from Pennsylvania river basins tested positive for *Salmonella* (Deaven *et al.*, 2021). An identical 49% of water samples from southern Georgia produce farms were *Salmonella*-positive, including 100% of storm-flow collections (Harris *et al.*, 2018). Similarly, a culture-independent metagenomic survey of recycled and surface irrigation waters in the Mid-Atlantic and Southwest detected *Salmonella enterica* in 100% of the tested water types (Malayil *et al.*, 2022). By contrast, studies on groundwater report substantially lower prevalence. In Bowling Green, Kentucky, 14.5% of groundwater samples tested positive for *Salmonella*, compared to just 4.4% in Florida (Agga *et al.*, 2023). Within Kentucky, *Salmonella* was detected across all sampled sites, with surface-fed groundwaters notably showing the highest prevalence (26.1%) among different sources (Agga *et al.*, 2023). While water sources show high prevalence, other matrices such as faeces and soil contribute to environmental contamination, but at generally lower and more variable rates (Marine *et al.*, 2015; Haack *et al.*, 2016; Lee *et al.*, 2019; Hwang *et al.*, 2020; Glaize *et al.*, 2021). In a longitudinal study conducted on small-scale sustainable farms with dairy and poultry operations, only 5 out of 1,133 samples (0.44%) collected over 15 months tested positive for *Salmonella* (Glaize *et al.*, 2021). Of these, three were faecal samples from the dairy pasture, while the remaining positives included one romaine lettuce sample and one soil sample near a poultry operation (Glaize *et al.*, 2021). Similarly, a study comparing soil and faecal samples from pasturized poultry farms reported higher prevalence in feces (16%) than in soil (8.1%) (Hwang *et al.*, 2020), though both were low. Another survey in southern Georgia also reported low soil contamination, with only 1 out of 120 soil samples testing positive (Lee *et al.*, 2019). However, experimental data from the same study demonstrated that *Salmonella* could transfer from inoculated soil to produce (Lee *et al*., 2019). Several studies have also explored the presence of *Salmonella* in sediment and stream-associated environments. In Mid-Atlantic U.S., one study assessing farming systems detected *Salmonella* in 1 of 13 pond and river sediment samples (7.7%) and confirmed its presence in 8 out of 369 leafy greens samples (2.2%) (Marine *et al.*, 2015). In contrast, another survey using genomic analysis found that *Salmonella* genes, including invA and spvC, were rarely detected or not detected at all in streambed sediment samples, even after enrichment (Haack *et al.*, 2016). However, discriminant analysis of gene patterns showed a tendency for stream water samples to group according to animal type, with poultry and swine gene profiles being most distinctive, and beef and dairy overlapping (Haack *et al.*, 2016).

There are key similarities that are evident in the presence of specific *Salmonella* serovars across different water reservoirs. In the Susquehanna River Basin, serovars *S. give*, *S. typhimurium*, *S. thompson* and *S. infantis* were consistently identified throughout the watershed and across multiple seasonal collections (Deaven *et al.*, 2021). Over the two-year sampling period, *S. give* emerged as the most prevalent serovar, comprising 43% of positive samples and dominating over half (54%) of those in which it was detected (Deaven *et al.*, 2021). This aligns with findings from the central California coastal survey, where *S. give* ranked as the second most frequent serovar (17.3%) across five years (Gorski *et al.*, 2022). Likewise, *S. give* was among the top six serotypes detected in urban karst groundwater systems in Bowling Green, Kentucky (9.1% of 176 isolates) (Agga *et al.*, 2023) and was frequently isolated from irrigation pond water and storm runoff in southern Georgia (Harris *et al.*, 2018). *S. typhimurium* also demonstrated broad geographic distribution, ranking among the top eight human illness-associated serovars in the Susquehanna study (Deaven *et al.*, 2021) and appearing as the third most common serovar in the Central California dataset (11.7%, 227 isolates) (Gorski *et al.*,

Table 3. Summary of articles related to poultry processing vectors (n = 3).

Year	Author	Region	Sample (size)	Serovar	Major finding
2018	Mamber *et al.*	Nationwide	RTE poultry products (91,038)	26 total: *S. infantis,* *S.typhimurium,* *S. derby,* *S.enteritidis,* etc.	• Only 0.06% (ALLRTE) and 0.05% (RTE001) tested positive for *Salmonella.* • 27 distinct serotypes were detected: Infantis and Typhimurium being the most common. • Southeast had the most positive samples, while the North Central region had the least.
2021	Beczkiewicz & Kowalcyk	Nationwide	Whole chicken carcasses from USDA FSIS plants (40,497)	4 total: *S. kentucky,* *S. enteritidis,* *S. infantis,* *S. typhimurium*	• Establishments processing >10 million birds annually had lower odds of contamination compared birds annually had lower odds of contamination compared to smaller processors. • Contamination was significantly higher in summer than in winter. • Mideast central region selected as the reference group, but had the lowest contamination odds
2022	Williams *et al.*	Nationwide	Chicken parts from FSIS and retail chicken from NARMS (83,976)	*S. enteritidis,* *S. kentucky,* *S.infantis,* *S.schwarzengrund,* *S. typhimurium*	• Seasonal contamination peaks in chicken parts shifted from summer to winter in recent years. • Infantis prevalence rose from less than 4% in 2015 to nearly 25% in 2020. • Nearly half of *Salmonella* isolates were pansusceptible, but the estimated fraction of MDR isolates doubled, especially *S. infantis.*

RTE, ready to eat; FSIS, Food Safety and Inspection Service; NARMS, National Antimicrobial Resistance Monitoring System; USDA, United States Department of Agriculture; MDR, multidrug resistant; ALLRTE, all RTE poultry products; RTE001, specific RTE poultry product category.

2022). The California survey additionally reported *S. enteritidis* among its top ten most abundant serovars (Gorski *et al.*, 2022). However, traditional culture-based detection methods failed to identify either *S. typhimurium* or *S. enteritidis* in water samples from the Little River watershed in southern Georgia despite their known association with human illness in that region (Harris *et al.*, 2018).This discrepancy was also echoed in the Susquehanna study, where advanced genomic analyses revealed that *S. typhimurium* and *S. enteritidis* were frequently masked by more abundant serovars in mixed populations, specifically in 78% and 71% of detections (Deaven *et al.*, 2021), respectively.

S. newport was the most prevalent serotype in Bowling Green's urban karst groundwater and surface waters, accounting for 17.6% of 31 isolates and exhibiting wide spatial distribution (Agga *et al.*, 2023). It also appeared among the top eight illness-associated serovars in the Susquehanna River basin (Deaven *et al.*, 2021) and was listed among the top 24 serovars in the Central California survey (Gorski *et al.*, 2022). Likewise, *S. muenchen* was found frequently across regions, ranking fourth in Central California (8.2% of 158 isolates) and emerging as the most common serovar (21.0%) when including potentially monophasic variants like I 6,8:d:- (Gorski *et al.*, 2022). *S. muenchen* was also prevalent in Kentucky (9.1%) (Agga *et al.*, 2023) and was the most frequently identified serovar across water samples from southern Georgia farms (Harris *et al.*, 2018). Importantly, MDR strains of *S. muenchen* were reported in both surface and groundwater sources in Mid-Atlantic and Southwest U.S. (Agga *et al.*, 2023), with specific prevalence in Kentucky urban karst systems (Malayil et al., 2022). *S. infantis* exhibited similar environmental persistence, consistently detected throughout the Susquehanna watershed (Deaven *et al.*, 2021), and found among the most abundant serovars in surface waters over multiple years in central California (Gorski *et al.*, 2022). Despite some overlaps in the presence of certain *Salmonella* serovars across different studies, regional differences in serovar presence were evident. For instance, *S. montevideo* was among the six most frequently isolated serovars in the Central California coastal water survey with 4.0% prevalence (Gorski *et al.*, 2022). In contrast, while *S. montevideo* was noted as being among the most common serovars associated with human illness in southern Georgia, it was not found in any samples from irrigation ponds and storm runoff/flow in that region (Harris *et al.*, 2018). Similarly, both *S. javiana* and *S. enteritidis* were also common human pathogens in the study region but were not detected in the southern Georgia samples surveyed (Harris *et al.*, 2018). Beyond water sources, studies have identified important serovars in other environmental matrices and animal sources. In the longitudinal survey of dairy and poultry operations, the five positive samples across faeces, produce and soil yielded isolates of four serovars: *S. agona, S.* give, *S. typhimurium* and *S. newport* (Glaize *et al.*, 2021). *S. agona* and *S. give* isolates were recovered from the positive dairy fecal samples, and *S. typhimurium* and *S. newport* isolates were recovered from soil and lettuce samples collected near the poultry operation. Experimental studies confirmed the ability of S. *typhimurium* to survive in soil for up to 8 to 10 days post-inoculation (Lee *et al.*, 2019). In parallel, *Salmonella* was isolated from eight leafy green samples collected in the Mid-Atlantic region in Fall 2012 and finding *S. mbandaka* to be predominant, followed by *S. braenderup* and *S. newport* (Marine *et al.*, 2015).

Studies across different regions reveal both consistent and contrasting seasonal patterns in *Salmonella* prevalence and serovar distribution in hydrous environmental sources. In central California Coastal region, where a study of surface waters between 2011 and 2016 demonstrated significant seasonality in *Salmonella* prevalence, with the overall prevalence higher in spring (64.3%) than in both autumn (49.4%) and winter (52.1%) (Gorski *et al.*, 2022). Seasonality was also observed for specific serovars in this region; among the most abundant serovars, which were I 6,8:d:-, *S. give*, S. *oranienburg,* and *S. infantis* that were most often isolated in the spring months. *S. montevideo* was most often isolated during the summer, *S. enteritidis* in the autumn and serovars *S. typhimurium*, *S. muenchen, S. heidelberg and S. senftenberg* were most identified in isolates from the winter months (Gorski *et al.*, 2022). Consistent with higher spring prevalence in California, investigations in the Susquehanna River Basin over two years found that overall *Salmonella* prevalence was significantly greater in spring (~85% across the study timeframe) than summer (~30%) (Deaven *et al.*, 2021). Seasonal differences in serovar identity were also evident: S. give was particularly abundant in the spring collections but rarely found during the summer collections. Conversely, *S. infantis* was more frequently identified in the summer collections than the spring collections (Deaven *et al.*, 2021). *S. typhimurium* was noted as more abundant in the spring in the Susquehanna Basin (Deaven *et al.*, 2021), which also differs from its higher prevalence in winter in the California study (Gorski *et al.*, 2022). In Bowling Green, Kentucky, a study of karst groundwater and predominantly groundwater-fed surface waters found that *Salmonella* prevalence varied by season, increasing in the spring and peaking during the summer (Agga *et al.*, 2023). This aligns with the higher prevalence in spring seen in other studies and introduces a summer peak. However, in contrast to the expected, the highest prevalence overall in this study was observed in surface water in the month of November (Agga *et al.*, 2023). Serotype distribution also varied seasonally in Bowling Green, with different serotypes explored like *S. meleagridis* (June), *S. newport* (July), and *S. bareilly* (August) peaking in summer months, while *S. paratyphi B* var. *S. java* and S. hartford were mostly obtained in November (Agga *et al.*, 2023). The Kentucky study notably exhibited the most diverse serotypes in the summer months in, averaging 10 serotypes per sample collected during that time (Agga *et al.*, 2023). Additional findings reveal consistent seasonal patterns in *Salmonella* prevalence and serovar distribution in environmental sources such as produce, soil, and animal feces, with warmer months (spring, summer, and autumn) generally showing higher prevalence than winter. In the Mid-Atlantic region, a study found a significant association between *Salmonella* recovery on leafy greens and the autumn growing season (Marine *et al.*, 2015), but not farming season or region. Investigations in the Southeast U.S. involving pastured poultry farms found that the prevalence of *Salmonella* in soil samples was highest in summer (11%) (Hwang *et al.*, 2020), while the highest number of positive faeces samples were observed in spring (22%). Another longitudinal study have shown that samples from soil, produce and animal faeces during summer and spring seasons have also tested positive for *Salmonella* (Glaize *et al.*, 2021).

Rainfall and runoff have been linked to higher *Salmonella* detection in environmental sources. In California, it was noted that five days of rain increased surface water prevalence from nearly 50% to 72% (Gorski *et al.*, 2022). Irrigation ponds in Georgia showed higher concentrations after rain, with 100% positivity in storm flow samples (Harris *et al.*, 2018). Similar patterns were observed in Pennsylvania, where high river discharge during spring coincided with peak *Salmonella* frequency (Deaven *et al.*, 2021). Multi-state poultry and dairy watershed studies also found that rainfall increased fecal material contaminated with *Salmonella* (Haack *et al.*, 2016), while soil splash during rain transferred *Salmonell*a to crops (Lee *et al.*, 2019). However, effects were not uniform, where a study in New York found that less rainfall was associated with higher prevalence (Jones *et al.*, 2014), and after Hurricane Sandy, despite heavy flooding, no pathogen increase was observed (Marine *et al.*, 2015).

Environmental conditions involving temperature dynamics plays a complex role in *Salmonella* ecology across the agricultural landscape. The surface irrigation water survey in New York found no strong correlations between water temperature and the presence or concentration of *Salmonella* (Jones *et al.*, 2014). Similarly, the Susquehanna River study observed the greatest frequency of *Salmonella* in spring when water temperatures were lowest and did not find a positive correlation with warmer temperatures and *Salmonella* prevalence (Deaven *et al.*, 2021). For soil and faecal samples, temperature was considered more influentialin soil, microcosm experiments indicated that *Salmonella* survival during the first 45 days was greater at 4°C than at 25°C (Lee *et al.*, 2019), with authors suggesting that the more extreme and oscillating temperatures in field conditions may have contributed to increased decay compared to consistent laboratory temperatures. On produce and plant surfaces, a study in the Mid-Atlantic region found that temperature fluctuations and near-freezing conditions, such as those following a major storm event, likely hindered bacterial growth, observing lower counts of indicator bacteria (total *coliforms* and aerobic plate counts) on produce and soil samples during a colder sampling period compared to a warmer one (Marine *et al.*, 2015). In contrast, a study of pastured poultry farms found that average temperature was not found as a primary driver for soil models; however, for faecal samples in the same study, authors identified average temperature seven days prior to sampling as an important meteorological variable, with its strongest impact associated with *Salmonella* prevalence when temperature exceeded 28°C (Hwang *et al.*, 2020).

At a much lower scale, humidity emerged as a significant meteorological factor, particularly for *Salmonella* associated with animal faeces and soil. Studies have shown that humidity plays a key role in *Salmonella* presence in soil and faeces from pastured poultry farms, with detection more likely when humidity ranges between 20% and 70% (Hwang *et al.*, 2020). Wind also played a crucial role, with gusts of over 11 m/s strongly linked to *Salmonella* in faeces samples (Hwang *et al.*, 2020). It was also observed that vegetation barriers help to limit wind-driven pathogen spread to produce fields (Glaize *et al.*, 2021).

Additional studies highlighted significant findings regarding the presence of *Salmonella* and associated Antimicrobial Resistance (AMR), Multidrug Resistance (MDR) and specific genes in environmental matrices, including water, soil and animal waste (Haack *et al.*, 2016). Upon screening of enriched animal wastes from nationwide watersheds, the authors of this study targeted and tested two specific *Salmonella* genes: invA, a key marker for *Salmonella* presence due to its role in bacterial invasion of host cells and spvC, a gene associated with *Salmonella* virulence and systemic infection (Haack *et al.*, 2016). The plasmid-encoded spvC marker was co-detected with invA in the dairy and swine wastes, but importantly and by contrast, spvC was also uniquely identified in two beef and one poultry sample lacking invA (Haack *et al.*, 2016). The authors concluded that the invA-only assays may underestimate the presence of *Salmonella* in poultry production environments, suggesting that detection of both genes provides a more comprehensive picture of harmful strains in environments like poultry production (Haack *et al.*, 2016). Investigations in terrestrial environments have also revealed notable patterns in AMR among *Salmonella* isolates, particularly in poultry-dense regions. A study on pastured poultry and dairy farms isolated four *Salmonella* serovars: *S. agona* and *S. give* isolates were recovered from the positive dairy faecal samples, while *S. typhimurium* and *S. newport* isolates were recovered from soil and lettuce samples collected near the poultry operation (Glaize *et al.*, 2021). Specifically, authors of this study noted that *S. newport* and *S. typhimurium* were of concern in their study population due to their tendency to harbor multiple AMR genes (Glaize *et al.*, 2021). The study also detected naturally occurring rifampicin-resistant *Salmonella S. typhimurium* in soil samples collected near poultry operations during a challenge trial; however, these positive samples did not match the banding pattern of the laboratory strains used in the inoculums (Glaize *et al.*, 2021). This potentially represents the distribution of naturally occurring organisms already present in the environment. These key findings on environmental vectors are summarized in Table 4.

Discussion

The results consistently highlight the substantial public health burden of salmonellosis and reveal complex, interdependent risk pathways that necessitate a One Health approach for effective understanding and mitigation. *Salmonella* prevalence was found to exhibit a clear gradient across sectors and geographies, with human incidence remaining stubbornly high, particularly in the southern regions where environmental surface waters posed the greatest risk, followed by raw poultry and RTE products, in that order.

Salmonella prevalence by region and facility

National surveillance data show that human *Salmonella* incidence has remained elevated for more than two decades, consistently exceeding public health targets. Recent FoodNet data highlight the highest recorded incidence in 2022, well above the Healthy People 2030 benchmark (Delahoy, 2023; OASH, 2022). This recent trajectory aligns with earlier FoodNet data from 2004–2014, which likewise fell into a similarly elevated range among seven states (Morgado *et al.*, 2021), and with a 1996–2017 analysis demonstrating that *Salmonella* consistently ranked among enteric pathogens with the highest monthly incidence (Simpson *et al.*, 2020). Thus, for over twenty years, human *Salmonella* incidence has remained stubbornly high and largely resistant to incremental interventions, aligning with previous understandings that incidence has persistently exceeded public health objectives for over a decade (NCC, 2020; Painter *et al.*, 2013; Tack *et al.*, 2020).

Geographic analyses uniformly identify the South census region as the nation's *Salmonella* hotspot. From 2004 to 2014, Georgia (America's largest broiler producer) reported the highest incidence among seven states (Morgado *et al.*, 2021), and between 2010-2018, Mississippi's annual incidence nearly doubled the national average (Akil, 2021). These state-level trends mirror national incidence patterns found, as the South consistently records the largest share of cases year after year (Crim *et al.*, 2018; Judd *et al.*, 2019; Snyder *et al.*, 2019). While national *Salmonella* incidence peaks during summer, southern incidence curves often rise earlier and remain elevated longer throughout the year than other

Table 4. Summary of articles related to *Salmonella* in the environment (n = 11).

Year	Author	Region	Sample (size)	Serovar	Major finding
2014	Jones *et al.*	NY	Surface water from agricultural irrigation sites. (123)	Salmonella spp. (general)	• 43% of samples tested positive for Salmonella, with higher rates in ponds (46%) compared to creeks (26%). • Samples collected after >0.64 cm of rainfall had higher levels than those collected after <0.64 cm of rainfall • Detection rates were higher in low-rainfall periods when irrigation water was used.
2015	Marine *et al.*	Mid-Atlantic U.S. MD, DE, NJ)	Sediment, irrigation water, and leafy greens from small farms. (577)	4 total: *S. mbandaka,* *S. braenderup,* *S. newport,* *S. thompson*	• Found prevalence in river sediment samples (7.7%) and leafy greens samples (2.2%). • Significant association between recovery on leafy greens and the fall growing season (P = 0.006) • No association between rainfall and recovery.
2016	Haack *et al.*	12 states across the U.S.	Animal waste, stream water, and streambed sediment. (N/A)	*Salmonella* spp. (general)	• *Salmonella* genes were detected in dairy and swine waste but not poultry. • Despite targeted sampling, no Salmonella was detected in directly preserved stream water or sediment samples. • Pathogen gene detection varied significantly by waste type; dairy and swine waste posed the highest contamination risk.
2018	Harris *et al.*	Little River watershed (Southern GA)	Surface water from storm runoff and irrigation ponds. (107)	*S. bareilly,* *S. saintpaul,* *S. muenchen,* *S. rubislaw,* *S. gaminara*	• *Salmonella* concentrations in pond water were significantly higher after rain events and in storm flow from streams and ditches. • Serovars found in water samples matched those causing human illnesses in the region, such as S. muenchen. • *Salmonella* levels were consistently highest in storm flow compared to pond water.
2019	Lee *et al.*	Southern GA	Soil and splash water. (120)	*S. typhimurium*	• *Salmonella* was not detectable in soil after 8-10 days, regardless of moisture content. • Contamination levels were significantly higher in wet plots compared to dry plots (P = 0.04). • *Salmonella* transfer from soil to produce was significantly influenced by splash events.
2020	Hwang *et al.*	Southeastern US	Soil and fecal samples from pasturized poultry farms (n = 1,472)	*Salmonella* spp. (general)	• Overall Salmonella prevalence was 8.1% in soil samples and 16.0% in feces samples from pastured poultry farms. • Highest soil prevalence occurred in summer (11%), while fecal prevalence peaked in spring (22%). • Humidity and wind speed were key predictors of presence, with rapid increases in risk above 28°C.
2021	Deaven *et al.*	U.S. Mid-Atlantic (PA)	Freshwater used in agricultural irrigation. (112)	25 total: *S. enteritidis,* *S. give,* *S. typhimurium, S. thompson,* *S.infantis,* etc.	• Higher river discharge during spring, ~4x that of summer, was primary driver of Salmonella presence. • Each positive sample contained three serovars, with 80% of positive samples containing multiple serovars. • The most common serovar was Give, present in 43% of samples.
2021	Glaize *et al.*	NC	Produce, faecal, and environmental samples (1536)	4 total: Agona, Typhimurium, Give, Newport	• No Salmonella was detected in produce plots located 61 or 122 meters from poultry operations, suggesting effective vegetative buffer zones. • Four serovars were detected: Agona, Typhimurium, Give, and Newport. • Only 0.44% of environmental samples tested positive for *Salmonella* over the two-year study.
2022	Gorski *et al.*	Central CA Coast	Surface water in agricultural fields (2979)	91 total: *S. infantis,* *S. give,* *S. muenchen,* *S. typhimurium*, etc.	• Salmonella prevalence in surface waters reached 56.4%, with higher levels detected in spring than fall or winter. • Prevalence increased significantly (72.0%) after heavy rain events, compared to 50.8% before rainfall. • Analysis revealed 91 different serovars, with S. infantis, S. give and *S. typhimurium* among the most common.
2022	Malayil *et al.*	U.S. Mid-Atlantic and Southwest	Recycled and surface water used in agricultural irrigation (410)	S. enterica (general)	• *Salmonella* detected in all tested water types, but prevalence was highest in surface waters in the Mid-Atlantic region. • Fluoroquinolone resistance genes were identified in recycled water samples, indicating potential AMR hotspots. • Metagenomic methods detected Salmonella using 500 mL samples, a significantly lower volume than traditional culture methods.
2023	Agga *et al.*	Bowling Green, KY and Tampa, FL	Groundwater (488)	18 total: *S. newport,* *S. javania,* *S.hartford,* *S.give, S.agona,* etc.	• *Salmonella* was detected in 14.4% of water samples from Kentucky and 4.4% from Florida. • 12.5% of isolates were resistant to multiple antibiotics, with 81.8% of resistant isolates being MDR. • Common serotypes: *S. newport, S. paratyphi b var. S. java,* and *S. hartford.*

NY, New York; MD, Maryland; DE, Delaware; NJ, New Jersey; GA, Georgia; PA, Pennsylvania; NC, North Carolina; CA, California; KY, Kentucky; FL, Florida; spp., multiple species within a genus; AMR, antimicrobial resistance; MDR, multidrug resistant; °C, degrees Celsius.

regions (Snyder *et al.*, 2019; Simpson *et al*., 2020;), reflecting the region's higher baseline burden throughout the warmer months. This agrees with current understandings of temperature and precipitation-driven seasonality of salmonellosis, whereby warmer, more humid conditions prolong transmission windows in the South beyond those of cooler regions. For example, the South experiences average July temperatures above 85°F compared to around 75°F in the Northeast and records an average of 20 heavy-precipitation days each summer (Austhof *et al*., 2024; Damtew *et al.*, 2024). Indeed, environmental persistence plays a crucial role in sustaining the South's elevated *Salmonella* risk, amplifying exposures beyond traditional poultry-related pathways. Surface waters in agricultural regions, including southern Georgia and the Susquehanna River Basin, exhibit consistently high *Salmonella* prevalence, with studies detecting it in nearly half of irrigation pond samples and increased presence linked to higher river discharge (Harris *et al.*, 2018; Deaven *et al.*, 2021; Gorski *et al.*, 2022). Storm runoff from poultry farms and surrounding fields can mobilize bacteria into irrigation reservoirs, as shown by 100% of storm flow samples testing positive and post-storm *Salmonella* loads spiking sharply (Harris *et al.*, 2018). Critically, during drought periods when surface water availability decline, growers increasingly rely on irrigation ponds fed by storm runoff from poultry farms and surrounding fields. Contaminated soils also act as a vector for crop contamination; soil-to-produce splash experiments conducted in Georgia field microcosms demonstrated that *Salmonella* can persist in soil for up to ten days after inoculation and transfer onto crop foliage as high as 80 cm away during modest splash events (Lee *et al.*, 2019). These findings underscore how environmental reservoirs, such as surface water and soil, contribute to the persistent Salmonella burden in agricultural areas (Akil *et al.*, 2014; Harris *et al.*, 2018; Morgado *et al.*, 2021). Since the south-eastern states produce over 60% of U.S. broilers, with Georgia alone generating 16.4 billion pounds annually (USDA, 2021), it can be said that climatic, agricultural and poultry factors jointly amplify regional exposure risk.

Cross analysis revealed that poultry processing characteristics further shape the geographic prevalence gradient, linking small-scale operations and product type to complexities in the high southern human burden. RTE poultry products tested positive for *Salmonella* at very low rates overall (Mamber *et al.*, 2018), with FSIS surveillance confirming that raw poultry products harbour substantially more *Salmonella* than RTE items (Beczkiewicz & Kowalcyk, 2021; Williams *et al.*, 2022). However, results diverged when RTE products showed the highest odds of contamination in the Southeast (Mamber *et al.*, 2018), whereas whole chicken carcass surveillance identified the Mid-East Central region, which served as the reference group due to its high concentration of poultry processing establishments and included several high-production Southeastern states, as having the lowest odds of carcass contamination (Beczkiewicz & Kowalcyk, 2021). These findings reflect both the efficacy of RTE post-processing lethality steps and the heterogeneity of processing practices across product streams. Supporting literature helps contextualize this contrast: although the Southeast remains the nation's largest poultry-producing region and has historically generated the highest raw-product *Salmonella* prevalence, it was the only region to achieve sustained declines in contamination across a five-year sampling period, culminating in the lowest regional incidence among processing establishments for both carcasses and parts in 2020 (Siceloff *et al.*, 2022). A 75% decline in chicken-part contamination from 2015–2020 (Williams *et al.*, 2022) signals positive change in southern processing facilities, though RTE contamination remains a concern. Nationwide studies show that small scale processing facilities handling fewer than ten million birds have higher odds of *Salmonella* contamination in both carcasses and RTE products (Mamber *et al.*, 2018; Beczkiewicz & Kowalcyk, 2021). Also, processing plants producing both raw and RTE poultry reported lower contamination on raw carcasses, likely due to stricter controls required for RTE production (Beczkiewicz & Kowalcyk, 2021). These findings highlight that smaller operations face greater risks and that cross-stream interventions can reduce contamination and regional disparities (Siceloff *et al.*, 2022).

Conventional wisdom links these southern burdens to rural agricultural exposures. Indeed, attribution modeling estimated that contact with livestock commodities and, particularly, poultry accounts for a substantial share of sporadic *Salmonella* cases (Painter *et al.*, 2013), reinforcing the traditional farm-to-fork paradigm in these broiler-heavy regions. However, three recent investigations challenge that assumption by demonstrating rising urban risk. Analysis of FoodNet data showed that most serovars were reported more frequently in rural settings, with the notable exception of *S. enteritidis*, which exhibited a higher urban incidence compared to other serovars (Morgado *et al.*, 2021). Similarly, a Michigan case–control found that urban residence significantly predicted *S. enteritidis* infections, while *S. typhimurium* remained tied to animal contact and rural residency (Mukherjee *et al.*, 2019). Importantly, that same study linked urban *S. enteritidis* cases to both increased hospitalization odds and a higher prevalence of retail-bottled water consumption versus municipal or well water (Mukherjee *et al.*, 2019), suggesting unique urban exposure pathways through retail and water systems. Likewise, statewide data from Mississippi documented higher salmonellosis rates in highly populated urban counties than in surrounding rural areas (Akil, 2021), further underscoring this emerging urban burden. Together, these findings indicate that urban environmental and retail dynamics,particularly those affecting serovar *S. enteritidis*, rival traditional exposures related to farming.

Serotype diversity and distribution

The sources reveal a varied landscape of *Salmonella* serotypes across different domains, with both commonalities and differences in the most prevalent types. Eggs and chicken remain the most frequently implicated vehicles in human outbreak investigations, with *S. enteritidis*, *S. typhimurium* and *S. newport* continuing to dominate investigations (Mukherjee *et al.*, 2019; Morgado *et al.*, 2021). Indeed, egg-linked outbreaks were dominated by *S. enteritidis* (Snyder *et al*., 2019), while chicken and turkey outbreaks were frequently tied to *S. typhimurium* and *S. newport* (Mamber *et al.*, 2018; Beczkiewicz & Kowalcyk, 2021; Morgado *et al*., 2021) reflecting well-established host–reservoir associations (Varma *et al.*, 2006; Kosa *et al*., 2015; Montone *et al*., 2023; Shaji *et al.*, 2023 Although *S. enteritidis* remains widespread (Mukherjee *et al.*, 2019; Morgado *et al.*, 2021), egg-associated outbreaks linked to it have declined significantly over the past decade (Snyder *et al.*, 2019), suggesting changing transmission dynamics in food systems. Importantly, rare or very rare serovars, each representing a small fraction of cases, collectively accounted for nearly 95% of total serotype diversity during long-term surveillance (Judd *et al.*, 2019), indicating a substantial reservoir of genetically diverse strains with potential for future emergence. This underlying variability reflects the genomic and ecological plasticity of

Salmonella, supported by molecular evidence of broad environmental tolerance and diverse virulence mechanisms (Andino & Hanning, 2015; Jajere, 2019). One of the most notable recent trends is the emergence of *S. infantis* as a leading serovar in poultry and a rising concern in human health. Historically less dominant in clinical settings (Jajere, 2019; Punchihewage-Don *et al.*, 2022; Siceloff *et al.*, 2022; Montone *et al.*, 2023), *S. infantis* has shown a marked increase in both human and poultry surveillance. The significance of this trend is amplified by *S. infantis*' frequent MDR phenotype, which compounds its risk to public health and complicates outbreak control (Montone *et al*., 2023). Based on its increasing prevalence, modelling studies predicted that *S. infantis* could become the dominant serovar in chicken parts by 2021–2023 in the absence of expanded serotype-targeted interventions(Williams *et al.,* 2022).Though reductions in overall *Salmonella* contamination in chicken parts may mitigate some consumer exposure, the relative rise of *S. infantis* highlights the limits of current control strategies focused on traditional serovars like *S. enteritidis*, which is better covered by available vaccines (Williams *et al*., 2022).

Environmental reservoirs act as hidden sources of *Salmonella* diversity, often revealing serovars less common in clinical cases. For example, *S. muenchen* has been repeatedly detected in irrigation waters and karst groundwater and shows multidrug resistance, raising concern about its future public health significance (Gorski *et al*., 2022; Agga *et al*., 2023; Harris *et al*., 2018). Other surveys highlight serovars such as *S. give* and *S. infantis* that can mask dominant strains, underscoring how environmental niches maintain a genetic pool that may later influence poultry systems and human infections (Deaven *et al*., 2021; Gorski *et al*., 2022; Glaize *et al*., 2021). Consequently, the recurrent co-occurrence of *S. enteritidis* and *S. typhimurium* alongside lesser-known serovars like *S. give* illustrates how environmental reservoirs can incubate emergent strains, providing a pool of genetic diversity that poultry operations and human exposures subsequently draw from (Deaven *et al*., 2021; Gorski *et al.*, 2022).

Regional analyses further defy expectations. Although the South consistently bears the highest human incidence, its serotype richness among clinical cases is paradoxically lower than that of the West, which exhibits greater serovar diversity across age groups (Judd *et al*., 2019). This may reflect the southern region's strong poultry production infrastructure, which promotes the dominance of a few well-adapted serovars such as *S. enteritidis* and *S. newport* (Punchihewage-Don *et al*., 2022) reinforced by intensive vertical integration and high environmental persistence (Siceloff *et al*., 2022). The South also sustains the lowest proportion of pansusceptible *S. newport* isolates (Crim *et al*., 2018) suggesting localized selection pressures that favor resistant or emerging strains. In contrast, the Western U.S. supports a wider array of serovars (Gorski *et al*., 2022), likely due to more diverse environmental reservoirs, produce types, and transmission pathways (Micallef *et al*., 2012). These regional contrasts imply that interventions should be tailored: in the South, addressing the entrenched dominance of a few high-risk serovars, and in the West, mitigating a broader array of potential threats.

Finally, wildlife and subsurface pathways further enrich this serovar mosaic. In the Mid-Atlantic region, wild birds foraging in produce fields have been shown to introduce *S. typhimurium*, *S. infantis* and *S. newport*, mirroring serovars detected in nearby soil, sediment, and surface water (Lee *et al*., 2019; Marine *et al.*, 2015). This supports the understanding that avian vectors can intermittently reseed agricultural environments with clinically relevant serovars (Micallef et al., 2012). Concurrently, urban groundwater systems in regions such as Kentucky and the Southeast have yielded frequent detections of *S. enteritidis* and *S. infantis*, likely introduced through subsurface leaching from poultry litter, septic effluent, or wildlife waste (Agga *et al*., 2023; Harris *et al*., 2018). The recovery of MDR phenotypes from both rural and urban groundwater systems raises concern that environmental pathways may sustain not only *Salmonella* viability, but also resistance profiles typically associated with poultry operations (Gorski *et al*., 2022; Agga *et al*., 2023).

Seasonality

Seasonality remains one of the most consistent features of *Salmonella* epidemiology, with U.S. human incidence reliably peaking between July and September (Akil *et al*., 2014; Mukherjee *et al*., 2019; Simpson *et al*., 2020; Akil, 2021). Southern states experience particularly steep midsummer spikes (Akil *et al*., 2014; Akil, 2021), where temperatures frequently surpass 90°F and humidity remains persistently high (Austhof *et al*., 2024; Damtew *et al*., 2024). Longitudinal analyses confirm that this summer peak has remained stable for over two decades, despite extensive public health interventions (Mukherjee *et al*., 2019; Snyder *et al*., 2019; Simpson *et al*., 2020). This summertime amplification in human disease parallels findings in poultry production, where the warmest months consistently coincide with the highest odds of *Salmonella* contamination on raw whole chicken carcasses (Beczkiewicz & Kowalcyk, 2021). These findings underscore the climate-sensitive amplification of *Salmonella* transmission, as elevated heat and humidity enhance bacterial replication on food surfaces, in live animals, and across environmental reservoirs. Yet several unexpected seasonal dynamics emerge when examining serotype-specific and environmental patterns more closely. Notably, while total case counts peak in summer, human serotype richness reaches its highest levels during winter months, when overall incidence is lowest (Judd *et al*., 2019). During this lower-incidence period, rare serovars that are typically overshadowed by dominant strains become more visible (Beczkiewicz & Kowalcyk, 2021). This inverse relationship, likely driven by storage and processing delays that carry summer-amplified contamination into winter retail channels (Chai *et al*., 2012; Jajere, 2019), suggests that cooler seasons may allow rare serovars to emerge, free from competitive dominance.

A similar seasonal shift appears in poultry surveillance. While contamination on whole carcasses peaks in midsummer (Beczkiewicz & Kowalcyk, 2021), the highest prevalence in chicken parts now occurs during the January–February period (Williams *et al.*, 2022). Egg-associated outbreaks surprisingly cluster in late winter (January through March), even though total *Salmonella* outbreaks are most frequent in midsummer (Snyder *et al*., 2019). This winter spike aligns with production and processing rhythms in layer facilities, where birds often shed higher loads of *S. enteritidis* during cooler months while housed indoors (Gantois *et al*., 2009; Liu *et al.,* 2022). Chicken-associated outbreaks, by contrast, concentrate in spring (April to June), preceding but not coinciding with the peak in human cases (Akil *et al*., 2014; Mukherjee *et al.*, 2019). The spring timing corresponds to broiler production cycles: flocks hatched in cooler months reach slaughter size in early spring, thus elevating contamination risks at processing plants and during subsequent distribution (Punchihewage-Don *et al*., 2022). These findings challenge the assumption that warm months are the exclusive driver of *Salmonella* diversity and burden and underscore how distribution, processing lag, and ecological competition all interact to shape risk across seasons. Meanwhile, RTE poultry products, which are subject to cooking and stringent post-lethality controls, show no significant seasonal variation (Mamber *et al.*, 2018), demonstrating how effective processing steps can decouple seasonality at this point in the supply chain.

Environmental reservoirs present their own complex seasonality. In Mid-Atlantic and south-eastern watersheds, spring water sampling often yields higher *Salmonella* prevalence than summer, despite lower ambient temperatures (Harris *et al*., 2018; Deaven *et al*., 2021). Moderate spring precipitation and runoff mobilize sediment-associated *Salmonella* into rivers and irrigation channels, creating elevated risk before high-heat amplification in summer (Jiang *et al*., 2015; Luo *et al*., 2015). Similarly, in leafy-green growing regions of central California, *Salmonella* prevalence peaks in spring due to winter storms that flush pathogens from upstream sources into surface waters used for irrigation (Gorski *et al*., 2022; Malayil *et al*., 2022). These patterns emphasize that season-specific hydrologic events, not just ambient temperature, can initiate seasonal exposure through water systems.

Climate and weather specific factors

Beyond predictable seasonal rhythms, acute weather events and long-term climate trends exert powerful, sometimes unexpected influences on *Salmonella* dynamics across interconnected domains. While summer heat elevates human and poultry burden (Mukherjee *et al*., 2019; Beczkiewicz & Kowalcyk, 2021), extreme heat events can trigger serovar-specific responses. In the Mid-Atlantic and southern coastal regions, analyses linking FoodNet data with meteorological records show that high heat waves correlate with notable increases in S. *newport* cases (Crim *et al*., 2018; Deaven *et al*., 2021; Morgado *et al*., 2021). This aligns with laboratory findings demonstrating that *S. newport* can tolerate higher temperatures in stream environments, allowing it to proliferate under heat stress when competing flora diminish (Jajere, 2019; Jiang *et al*., 2015).

Precipitation's role can be equally, if not more, consequential than temperature. Mid-Atlantic watershed studies demonstrate that river discharge, used as a proxy for daily rainfall, emerges as the dominant predictor of *Salmonella* presence in surface water, often eclipsing temperature as a driver during late winter and early spring runoff events (Harris *et al*., 2018; Deaven *et al*., 2021). These spring flows seed irrigation systems and downstream drinking water intakes, producing environmental risk far removed from midsummer heat (Liu *et al.*, 2018; Luo *et al*., 2015).Therefore, the mobilization of pathogens from soil, wildlife droppings, and adjacent poultry operations during storms create acute environmental hotspots for *Salmonella*.

Floods and hurricanes can rapidly reshape *Salmonella* risk across broad geographies, intersecting poultry, produce, and municipal systems. In both coastal and Mid-Atlantic regions, post-hurricane monitoring showed that surface waters and municipal waste sites were inundated with *Salmonella* serovars within hours of storm surges (Harris *et al*., 2018; Deaven *et al*., 2021). These high-water events triggered late-fall spikes in human infections, diverging from the typical midsummer seasonal peak observed in national surveillance (Morgado *et al.*, 2021). The floods flushed mobilized bacteria from benthic sediments and livestock-influenced soils into irrigation systems and downstream drinking water intakes, demonstrating how a single extreme event can propagate contamination through multiple domains almost simultaneously. Contrary to assumptions that droughts uniformly reduce waterborne risk, several studies show that scarcity can concentrate *Salmonella* in the remaining water supplies, thereby elevating exposure. In parts of the Southwest, extended drought conditions forced small produce growers to rely heavily on recycled water, or water stored through the dry season after having received run-off from livestock operations and urban landscapes. Testing of these recycled reservoirs revealed elevated *Salmonella* loads, particularly of *S. newport* and *S. typhimurium* strains commonly associated with livestock (Jones *et al*., 2014; Malayil *et al*., 2022). During consecutive drought years, human cases of *S. newport* infection rose in regions served by these irrigation systems (Crim *et al.*, 2018; Judd *et al*., 2019), suggesting that drought-driven reliance on limited, contaminated water sources can concentrate pathogen exposure even in the absence of flooding.

Antimicrobial Resistance (AMR) trends

Resistance to critical antibiotics in *Salmonella* is emerging across human, poultry, and environmental domains, with serotype shifts and reservoir interactions driving much of the observed AMR landscape. In human surveillance from Michigan, roughly one in six clinical isolates exhibited resistance to at least one antibiotic, and nearly eight percent qualified as MDR (Mukherjee *et al*., 2019). Within those isolates, *S. typhimurium* carried resistance more frequently than *S. enteritidis*, and resistance to tetracyclines and third-generation cephalosporins rose steadily over the study period. Infections caused by resistant strains also corresponded with significantly longer hospital stays underscoring both increased clinical severity and healthcare burdens when patients contract AMR *Salmonella*. These human-level AMR patterns closely mirror serotype dynamics in poultry processing. From 2015 through 2020, chicken-part sampling detected a dramatic surge of *S. infantis* (Williams *et al*., 2022), a serovar inherently prone to multidrug resistance (Montone *et al.*, 2023). As *S. infantis*'s proportion of positive samples grew from single digits to almost 25%, overall rates of resistance to clinically important antibiotics likewise climbed. Crucially, when *S. infantis* was removed from the dataset, there was no upward trend in resistance among the remaining serovars, indicating that *S. infantis* was the primary driver of rising AMR in poultry. By contrast, resistance among *S. enteritidis*, *S. typhimurium*, and Kentucky either remained flat or declined. In tandem, human surveillance in this period recorded *S. infantis* as a fast-growing contributor to clinical cases; its expansion through the poultry production chain thus served as an indicator for emerging AMR risk in humans.

Environmental sources both reflect and amplify these AMR dynamics. In Mid-Atlantic irrigation waters, recycled water sources, often used for preharvest irrigation, consistently carried higher abundances of antibiotic-resistance genes (ARGs) associated with tetracyclines, β-lactams, and sulfonamides than surface water (Malayil *et al*., 2022), suggesting that treated wastewater inputs can elevate baseline resistance loads in agricultural environments. Surface-water sources, in turn, contained a broader mix of ARGs, including streptomycin and chloramphenicol resistance, reflecting runoff from livestock operations and wildlife (Punchihewage-Don *et al.*, 2022). During heavy rainfall events in southern Georgia, storm run-off that inundated irrigation ponds not only mobilized *Salmonella* but delivered strains harbouring ARGs for aminoglycosides, tetracyclines, and macrolides, matching resistance profiles found in poultry, litter, and soil (Harris *et al*., 2018; Lee *et al*., 2019).

Limitations and contextual factors

Despite these insights, the studies reviewed had notable limitations. Most human *Salmonella* data come from passive surveillance, which depends on people seeking care and being tested, leading to underreporting, especially of mild or asymptomatic cases. This can underestimate true infection rates and serotype diversity, particularly for rare strains (Snyder *et al*., 2019; Morgado *et al*., 2021). Delays between symptom onset and testing may also affect how accurately we understand seasonal patterns. Environmental studies face similar challenges. Many rely on a few water or soil samples collected at a single time point, which may miss temporary spikes caused by events like heavy rain (Deaven *et al*., 2021). For example, California irrigation studies often focus on select sites, leaving gaps in geographic coverage (Gorski *et al*., 2022). In order to improve future research, there is a need for a more consistent and frequent sampling, alongside the integration of clinical, environmental and food system data. Also, active human surveillance and standardized methods across clinical processing and environmental domains would better capture emerging risks and support a stronger One Health response.

Conclusion

The explicit adoption of a One Health framework was fundamental for this research, particularly for the recognition of *Salmonella* risk as a product of intricate interactions between human health outcomes, animal agriculture (particularly poultry), environmental conditions (like water quality and climate) and human behaviour. The core objective was to understand how these overlapping dynamics influence the national *Salmonella* burden and whether regions with high poultry contamination or significant climatic variability showed amplified patterns of human infection. Overall, human salmonellosis remains a significant burden, with serotypes like *S. enteritidis* and *S. typhimurium* continuing to dominate. However, emerging serotypes such as MDR *S. infantis* are shifting the risk landscape. The findings have crucial implications, especially the unexpected seasonal patterns and regional differences in contamination between poultry products and human illness. In addition, we established that facility characteristics, such as processing both raw and ready-to-eat poultry, were surprisingly linked to lower contamination rates, likely due to stricter safety measures. Environmental transmission plays a larger role than previously thought, with water sources showing both pathogen presence and antimicrobial resistance signals. Ultimately, the complex and sometimes counterintuitive dynamics revealed in this review demonstrate that addressing salmonellosis effectively requires unified, transdisciplinary interventions that integrate insights and actions across human, animal, and environmental health domains under a unified One Health framework.

References

Agga GE, Kaiser R, Polk J, Allard M, 2023. Prevalence and whole-genome sequencing characterization of Salmonella in urban karst groundwater and predominantly groundwater□fed surface waters for serotypes and antimicrobial resistance. J Environ Qual 52:691–705.

Akil L, 2021. Trends of foodborne diseases in mississippi: association with racial and economic disparities. Diseases 9, 83.

Akil L, Ahmad HA, Reddy RS, 2014. Effects of climate change on Salmonella infections. Foodborne Pathog Dis 11:974–80.

Algorri, R., 2019. Foodborne Illness Part 3: How Does Salmonella Make Us Sick?. ASM.org. Accessed 5.28.25. Available from: https://asm.org:443/articles/2019/april/foodborne-illness-part-3-how-does-salmonella-make

Andino A, Hanning I, 2015. Salmonella enterica: survival, colonization, and virulence differences among serovars. Sci World J 2015;520179.

Austhof E, Pogreba-Brown K, White AE, Jervis RH, Weiss J, Davis SS, Moore D, Brown HE, 2024. Association between precipitation events, drought, and animal operations with Salmonella infections in the Southwest US, 2009–2021. One Health 19:100941.

Beczkiewicz ATE, Kowalcyk BB, 2021. Risk Factors for salmonella contamination of whole chicken carcasses following changes in U.S. regulatory oversight. J Food Prot 84:1713–21.

Billah MM, Rahman MS, 2024. Salmonella in the environment: A review on ecology, antimicrobial resistance, seafood contaminations, and human health implications. J Hazard Mater Adv 13:100407.

Boston University, 2020. Salmonella enterica species (S. typhimurium and S. enteriditis serotypes) Agent Information Sheet | Office of Research. Accessed 5.29.25. Available from: https://www.bu.edu/research/ethics-compliance/safety/rohp/agent-information-sheets/salmonella-typhimurium-agent-information-sheet/

CDC, 2024. About Salmonella Infection. US CDC. Available from: https://www.cdc.gov/salmonella/about/index.html (accessed 5.28.25).

Chai SJ, White PL, Lathrop SL, Solghan SM, Medus C, McGlinchey BM, Tobin-D'Angelo M, Marcus R, Mahon BE, 2012. Salmonella enterica Serotype Enteritidis: increasing incidence of domestically acquired infections. Clin Infect Dis 54:S488–97.

Crim SM, Chai SJ, Karp BE, Judd MC, Reynolds J, Swanson KC, Nisler A, McCullough A, Gould LH, 2018. Salmonella enterica Serotype Newport Infections in the United States, 2004–2013: Increased Incidence Investigated Through Four Surveillance Systems. Foodborne Pathog Dis 15, 612–20.

Crim SM, Iwamoto M, Huang JY, Griffin PM, Gilliss D, Cronquist AB, Cartter ., Tobin-D'Angelo M. Blythe D, Smith K, Lathrop S, Zansky S, Cieslak PR, Dunn J, Holt KG, Lance S, Tauxe R, Henao OL, 2014. Incidence and Trends of Infection with Pathogens Transmitted Commonly Through Food – Foodborne Diseases Active Surveillance Network, 10 U.S. Sites, 2006–2013. Morb Mortal Wkly Rep 63:328–32.

Damtew YT, Tong M, Varghese BM, Anikeeva O, Hansen A, Dear K, Driscoll T, Zhang Y, Capon T, Bi P, 2024. The impact of temperature on non-typhoidal Salmonella and Campylobacter infections: an updated systematic review and meta-analysis of epidemiological evidence. eBioMedicine 109:105393.

Deaven AM, Ferreira CM, Reed EA, Chen See JR, Lee NA, Almaraz E, Rios PC, Marogi JG, Lamendella R, Zheng J, Bell RL, Shariat NW, 2021. Salmonella Genomics and Population Analyses Reveal High Inter- and Intraserovar Diversity in Freshwater. Appl Environ Microbiol 87:e02594-20.

Delahoy MJ, 2023. Preliminary incidence and trends of infections caused by pathogens transmitted commonly through food – foodborne diseases active surveillance network, 10 U.S. sites, 2022. MMWR Morb Mortal Wkly Rep 72:26a1.

Fàbrega A, Vila J, 2013. Salmonella enterica serovar typhimurium skills to succeed in the host: virulence and regulation. Clin Microbiol Rev 26:308–41.

FDA, 2023. Get the Facts about Salmonella. U.S Food &Drug Administration. Available from: https://www.fda.gov/animal-veterinary/animal-health-literacy/get-facts-about-salmonella. Accessed 05.10.2025

FDA, 2024. Release of 2019 Annual Report on the Sources of Foodborne Illness by the Interagency Food Safety Analytics Collaboration. Accessed 5.15.25. Available from: https://www.fda.gov/food/hfp-constituent-updates/release-2019-annual-report-sources-foodborne-illness-interagency-food-safety-analytics-collaboration.

FSIS, 2014. Modernization of Poultry Slaughter Inspection. Accessed 5.28.25. Available from: https://www.federalregister.gov/documents/2014/08/21/2014-18526/modernization-of-poultry-slaughter-inspection

FSIS, 2015. Changes to the Salmonella and Campylobacter Verification Testing Program: Proposed Performance Standards for Salmonella and Campylobacter in Not-Ready-to-Eat Comminuted Chicken and Turkey Products and Raw Chicken Parts and Related Agency Verification Procedures and Other Changes to Agency Sampling. Available from: https://www.federalregister.gov/documents/2015/01/26/2015-01323/changes-to-the-salmonella-and-campylobacter-verification-testing-program-proposed-performance (accessed 5.28.25).

Galán-Relaño Á, Valero Díaz A, Huerta Lorenzo B, Gómez-Gascón L, Mena Rodríguez MÁ, Carrasco Jiménez E, Pérez Rodríguez F, Astorga Márquez RJ, 2023. Salmonella and Salmonellosis: an update on public health implications and control strategies. Anim Open Access J 13:3666.

Gantois I, Ducatelle R, Pasmans F, Haesebrouck F, Gast R, Humphrey TJ, Van Immerseel F, 2009. Mechanisms of egg contamination by Salmonella Enteritidis. FEMS Microbiol Rev 33:718–38.

Glaize A, Young M, Harden L, Gutierrez-Rodriguez E, Thakur S, 2021. The effect of vegetation barriers at reducing the transmission of Salmonella and Escherichia coli from animal operations to fresh produce. Int J Food Microbiol 347:09196.

Gorski L, Liang AS, Walker S, Carychao D, Aviles Noriega A, Mandrell RE, Cooley MB, 2022. Salmonella enterica Serovar Diversity, Distribution, and Prevalence in Public-Access Waters from a Central California Coastal Leafy Green-Growing Region from 2011 to 2016. Appl Environ Microbiol 88:e01834-21.

Haack SK, Duris JW, Kolpin DW, Focazio MJ, Meyer MT, Johnson HE, Oster RJ, Foreman WT, 2016. Contamination with bacterial zoonotic pathogen genes in U.S. streams influenced by varying types of animal agriculture. Sci Total Environ 563–564:340–50.

Harris CS, Tertuliano M, Rajeev S, Vellidis G, Levy K, 2018. Impact of storm runoff on Salmonella and Escherichia coli prevalence in irrigation ponds of fresh produce farms in southern Georgia. J Appl Microbiol 124:910–21.

Higginson EE, Simon R, Tennant SM, 2016. Animal models for salmonellosis: applications in vaccine research. Clin. Vaccine Immunol. CVI 23, 746–756. https://doi.org/10.1128/CVI.00258-16

Huber N, Meester M, Sassu, EL, Waller ESL, Krumova-Valcheva G, Aprea G, D'Angelantonio D, Zoche-Golob V, Scattolini S, Marriott E, Smith RP, Burow E, Carreira GC, 2024. Biosecurity measures reducing Salmonella spp. and hepatitis E virus prevalence in pig farms – a systematic review and meta-analysis. Front Vet Sci 11:1494870

Hwang D, Rothrock MJ, Pang H, Guo M, Mishra A, 2020. Predicting Salmonella prevalence associated with meteorological factors in pastured poultry farms in southeastern United States. Sci Total Environ 713:136359.

Jajere SM, 2019. A review of Salmonella enterica with particular focus on the pathogenicity and virulence factors, host specificity and antimicrobial resistance including multidrug resistance. Vet World 12:504–21.

Jiang C, Shaw KS, Romeo C, Blythe D, Mitchell C, Murtugudde R, Sapkota AR, Sapkota A, 2015. Climate Change, Extreme Events and Increased Risk of Salmonellosis in Maryland, USA: Evidence for Coastal Vulnerability. Environ. Int. 83:58–62.

Jones LA, Worobo RW, Smart CD, 2014. Plant-pathogenic oomycetes, Escherichia coli strains, and Salmonella spp. frequently found in surface water used for irrigation of fruit and vegetable crops in New York State. Appl Environ Microbiol 80:4814–20.

Judd MC, Hoekstra RM, Mahon BE, Fields PI, Wong KK, 2019. Epidemiologic patterns of human Salmonella serotype diversity in the USA, 1996–2016. Epidemiol Infect 147:e187.

Kosa KM, Cates SC, Bradley S, Godwin S, Chambers D, 2015. Consumer shell egg consumption and handling practices: results from a national survey. J Food Prot 78:1312–9.

Lee D, Tertuliano M, Harris C, Vellidis G, Levy K, Coolong T, 2019. Salmonella survival in soil and transfer onto produce via splash events. J Food Prot 82:2023–37.

Liu B, Zhang X, Ding X, Bin P, Zhu G, 2022. The vertical transmission of Salmonella Enteritidis in a One-Health context. One Health 16:100469.

Liu H, Whitehouse CA, Li B, 2018. Presence and Persistence of Salmonella in Water: The Impact on Microbial Quality of Water and Food Safety. Front. Public Health 6:159.

Luo Z, Gu G, Ginn A, Giurcanu MC, Adams P, Vellidis G, van Bruggen AHC, Danyluk MD, Wright AC, 2015. Distribution and Characterization of Salmonella enterica Isolates from Irrigation Ponds in the Southeastern United States. Appl Environ Microbiol 81:4376–87.

Malayil L, Ramachandran P, Chattopadhyay, S, Allard SM, Bui A, Butron J, Callahan MT, Craddock HA, Murray R, East C, Sharma M, Kniel K, Micallef S, Hashem F, Gerba CP, Ravishankar S, Parveen S, May E, Handy E, Kulkarni P, Anderson-Coughlin B, Craighead S, Gartley S, Vanore A, Duncan R, Foust D, Haymaker J, Betancourt W, Zhu L, Mongodin EF, Sapkota A, Pop, M, Sapkota AR, 2022. Variations in bacterial communities and antibiotic resistance genes across diverse recycled and surface water irrigation sources in the mid-atlantic and southwest United States: A CONSERVE two-year field study. Environ Sci Technol 56:15019–33.

Mamber SW, Mohr T, Leathers C, Mbandi E, Bronstein P, Barlow K, 2018. Occurrence of Salmonella in Ready-to-Eat Meat and Poultry Product Samples from U.S. Department of Agriculture–Regulated Producing Establishments. I. Results from the ALLRTE and RTE001 Random and Risk-Based Sampling Projects, from 2005 to 2012. J Food Prot 81:1729–36.

Marine SC, Pagadala S, Wang F, Pahl DM, Melendez MV, Kline WL, Oni RA, Walsh CS, Everts KL, Buchanan RL, Micallef SA, 2015. The Growing Season, but Not the Farming System, Is a Food Safety Risk Determinant for Leafy Greens in the Mid-Atlantic Region of the United States. Appl Environ Microbiol 81:2395–407.

Micallef SA, Rosenberg Goldstein RE, George A, Kleinfelter L, Boyer MS, McLaughlin CR, Estrin A, Ewing L, Jean-Gilles Beaubrun J, Hanes DE, Kothary MH, Tall BD, Razeq JH, Joseph SW, Sapkota AR, 2012. Occurrence and antibiotic resistance of multiple Salmonella serotypes recovered from water, sediment and soil on mid-Atlantic tomato farms. Environ Res 114:31–9.

Montone AMI, Cutarelli A, Peruzy MF, La Tela I, Brunetti R, Pirofalo MG, Folliero V, Balestrieri A, Murru N, Capuano F, 2023. Antimicrobial resistance and genomic characterization of Salmonella Infantis from different sources. Int J Mol Sci 24:5492.

Morgado ME, Jiang C, Zambrana J, Upperman CR, Mitchell C, Boyle M, Sapkota AR, Sapkota A, 2021. Climate change, extreme events, and increased risk of salmonellosis: foodborne diseases active surveillance network (FoodNet), 2004-2014. Environ Health 20:105.

Mukherjee S, Anderson CM, Mosci RE, Newton DW, Lephart P, Salimnia H, Khalife W, Rudrik JT, Manning SD, 2019. Increasing frequencies of antibiotic-resistant non-typhoidal Salmonella infections in Michigan and risk factors for disease. Front Med 6:250.

NCC, 2020. National Chicken Council | Chicken Processors Redoubling Efforts to Keep Essential Workers Safe and Healthy. Accessed 5.29.25. Available from: https://www.nationalchickencouncil.org/chicken-processors-redoubling-efforts-to-keep-essential-workers-safe-and-healthy/

NCC, 2021a. National Chicken Council | 2020 U.S. Broiler Chicken Industry Sustainability Report. Accessed 5.29.25. Available from: https://www.nationalchickencouncil.org/industry/sustainabilityreport/

NCC, 2021b. National Chicken Council | Per Capita Consumption of Poultry and Livestock, 1965 to Forecast 2022, in Pounds. Accessed 5.29.25. Available from: https://www.nationalchickencouncil.org/about-the-industry/statistics/per-capita-consumption-of-poultry-and-livestock-1965-to-estimated-2012-in-pounds/

OASH, 2022. Reduce infections caused by Salmonella – FS-04 - Healthy People 2030 | odphp.health.gov [WWW Document]. Accessed 6.3.25. Available from: https://odphp.health.gov/healthypeople/objectives-and-data/browse-objectives/foodborne-illness/reduce-infections-caused-salmonella-fs-04

Obe T, Boltz T, Kogut M, Ricke SC, Brooks LA, Macklin K, Peterson A, 2023. Controlling Salmonella: strategies for feed, the farm, and the processing plant. Poult Sci 102:103086.

Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, Shamseer L, Tetzlaff JM, Akl EA, Brennan SE, Chou R, Glanville J, Grimshaw JM, Hróbjartsson A, Lalu MM, Li T, Loder EW, Mayo-Wilson E, McDonald S, McGuinness LA, Stewart LA, Thomas J, Tricco AC, Welch VA, Whiting P, Moher, D, 2021. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. BMJ 372:n71.

Painter, J.A., Hoekstra, R.M., Ayers, T., Tauxe, R.V., Braden, C.R., Angulo, F.J., Griffin, P.M., 2013. Attribution of Foodborne Illnesses, Hospitalizations, and Deaths to Food Commodities by using Outbreak Data, United States, 1998–2008 - Volume 19, Number 3 – March 2013 - Emerging Infectious Diseases journal - CDC. Available from: https://doi.org/10.3201/eid1903.111866

Pew, 2021. 12 Charts Explore America’s Salmonella Problem – and Steps to Solve It. https://pew.org/3k2FfDz (accessed 5.29.25).

Punchihewage-Don AJ, Hawkins J, Adnan AM, Hashem F, Parveen S, 2022. The outbreaks and prevalence of antimicrobial resistant Salmonella in poultry in the United States: An overview. Heliyon 8:e11571.

Sarkis-Onofre R, Catalá-López F, Aromataris E, Lockwood C, 2021. How to properly use the PRISMA Statement. Syst Rev 10:117.

Shaji S, Selvaraj RK, Shanmugasundaram R, 2023. Salmonella infection in poultry: a review on the pathogen and control strategies. Microorganisms 11:2814.

Siceloff AT, Waltman D, Shariat NW, 2022. Regional Salmonella differences in United States broiler production from 2016 to 2020 and the contribution of multiserovar populations to Salmonella surveillance. Appl Environ Microbiol 88:e0020422.

Simpson RB, Zhou B, Naumova, EN, 2020. Seasonal synchronization of foodborne outbreaks in the United States, 1996–2017. Sci Rep 10:17500.

Snyder TR, Boktor SW, M’ikanatha NM, 2019. Salmonellosis Outbreaks by Food Vehicle, Serotype, Season, and Geographical Location, United States, 1998 to 2015. J Food Prot 82:1191–9.

Tack DM, Ray L, Griffin PM, Cieslak PR, Dunn J, Rissman T, Jervis R, Lathrop S, Muse A, Duwell M, Smith K, Tobin-D’Angelo M, Vugia DJ, Zablotsky Kufel J, Wolpert BJ, Tauxe R, Payne DC, 2020. Preliminary Incidence and Trends of Infections with Pathogens Transmitted Commonly Through Food – Foodborne Diseases Active Surveillance Network, 10 U.S. Sites, 2016–2019. MMWR Morb Mortal Wkly Rep 69:509–14.

USDA, 2011. Poultry - Production and Value 2010 Summary. USDA, National Agricultural Statistics Service. Available from: https://efaidnbmnnnibpcajpcglclefindmkaj/ https://www.aphis.usda.gov/sites/default/files/demographics2011.pdf . Accessed 5.10.25

USDA, 2021. Poultry - Production and Value 2020 Summary. USDA, National Agricultural Statistics Service. Available from: https://efaidnbmnnnibpcajpcglclefindmkaj/ https://www.nass.usda.gov/Publications/Todays_Reports/reports/plva0421.pdf. Accessed 06.04.25

USDA, 2024. Poultry - Production and Value 2023 Summary. USDA, National Agricultural Statistics Service. Available from: https://efaidnbmnnnibpcajpcglclefindmkaj/ https://downloads.usda.library.cornell.edu/usda-esmis/files/m039k491c/b2775j31b/9k4213149/plva0424.pdf. Accessed 06.04.25

Varma JK, Marcus R, Stenzel SA, Hanna SS, Gettner S, Anderson BJ, Hayes T, Shiferaw B, Crume TL, Joyce K, Fullerton KE, Voetsch AC, Angulo FJ, 2006. Highly Resistant Salmonella

Newport-MDRAmpC Transmitted through the Domestic US Food Supply: A FoodNet Case-Control Study of Sporadic Salmonella Newport Infections, 2002–2003. J Infect Dis 194:222–30.

Williams MS, Ebel ED, Golden NJ, Saini G, Nyirabahizi E, Clinc N, 2022. Assessing the effectiveness of performance standards for Salmonella contamination of chicken parts. Int J Food Microbiol 378:109801.