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Multistate outbreaks of salmonellosis linked to contact with backyard poultry—United States, 2015–2022

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Abstract

Aims: Contact with backyard poultry (i.e., privately-owned, non-commercial poultry) was first associated with a multistate outbreak of salmonellosis in 1955. In recent years, backyard poultry-associated salmonellosis outbreaks have caused more illnesses in the United States than salmonellosis outbreaks linked to any other type of animal. Here, we describe the epidemiology of outbreaks from 2015–2022 to inform prevention efforts.

Methods and Results: During 2015–2022, there were 88 multistate backyard poultry-associated salmonellosis outbreaks and 7866 outbreak-associated illnesses caused by 21 different *Salmonella* serotypes. *Salmonella Enteritidis* accounted for the most outbreaks ($n = 21$) and illnesses ($n = 2400$) of any serotype. Twenty-four percent (1840/7727) of patients with available information were <5 years of age. In total, 30% (1710/5644) of patients were hospitalized, and nine deaths were attributed to *Salmonella* infection. Throughout this period, patients reported behaviours that have a higher risk of *Salmonella* transmission, including kissing or snuggling poultry or allowing poultry inside their home.

Conclusions: Despite ongoing efforts to reduce the burden of salmonellosis associated with backyard poultry, outbreak-associated illnesses have nearly tripled and hospitalizations more than quadrupled compared with those in 1990–2014. Because this public health problem is largely preventable, government officials, human and veterinary healthcare providers, hatcheries, and retailers might improve the prevention of illnesses by widely disseminating health and safety

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CONFLICT OF INTEREST STATEMENT
The authors have no conflicts of interest to disclose.

ETHICS STATEMENT
These investigations were conducted consistent with applicable federal law and CDC policy: 45 C.F.R. part 46, 21 C.F.R. part 56; 42 U.S.C. §241(d); 5 U.S.C. §552a; 44 U.S.C. §3501 et seq.

SUPPORTING INFORMATION
Additional supporting information can be found online in the Supporting Information section at the end of this article.

recommendations to the public and by continuing to develop and implement prevention measures to reduce zoonotic transmission of *Salmonella* by backyard poultry.

Keywords

backyard poultry; one health; outbreak; *salmonella* ; zoonotic

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1 | INTRODUCTION

Non-typhoidal *Salmonella* infection causes approximately 1.4 million human illnesses, 26,000 hospitalizations, and 400 deaths annually in the United States (Collier et al., 2021). While *Salmonella* infections generally result in self-limited diarrhoea, fever, or abdominal pain, children <5 years of age or people who are >65 years of age, who have weakened immune systems, or who are pregnant have an increased risk of septicemia, meningitis, or death (Shane et al., 2017). Multistate outbreaks of salmonellosis are a persistent threat to public health, with outbreaks linked to food products or contact with animals or their environment occurring annually (CDC, 2022d; Marshall et al., 2020). Salmonellosis is a nationally notifiable disease in the United States (CDC, 2021b). Isolates obtained from patients are sequenced by state and local public health laboratories and analysed for genetic relatedness through PulseNet, the national molecular subtyping network for enteric disease surveillance, coordinated by the United States Centers for Disease Control and Prevention (CDC). In addition to analysing *Salmonella* isolates, public health officials routinely interview patients diagnosed with *Salmonella* infection to determine potential sources of exposure.

Approximately 11% of *Salmonella* infections in the United States result from contact with live animals (Beshearse et al., 2021; Hale et al., 2012). Contact with backyard poultry (BYP; i.e., privately-owned, non-commercial poultry,) such as chickens, ducks, turkeys, geese, guinea fowl, and quail, has been associated with more multistate salmonellosis outbreaks and outbreak-associated illnesses compared with any other type of animal (CDC, 2022d; Waltenburg et al., 2022). BYP-associated salmonellosis (BYPAS) outbreaks have been documented in the United States since 1955 (Anderson et al., 1955). Outbreaks have increased in size despite public health interventions and multitiered approaches to preventing illness (Basler et al., 2016; Behravesh et al., 2014). BYP ownership also continues to grow in the United States (AVMA, 2018; Nichols et al., 2021), suggesting that without disease prevention measures, BYPAS may be a persistent public health challenge.

Here, we present data collected during multistate BYPAS outbreaks investigated during 2015–2022 with the aims of describing the epidemiology of these outbreaks, characterizing trends in demographic characteristics and behaviours of patients, and informing actions that can be taken to reduce the impact of BYPAS on public health.

2 | METHODS

2.1 | Outbreak detection and case identification

We defined multistate BYPAS outbreaks as ≥2 culture-confirmed human *Salmonella* infections in the United States genetically related based on pulsed field gel electrophoresis (PFGE, for 2015–2018 outbreaks) or whole genome sequencing (WGS, for 2019–2022 outbreaks) and with epidemiologic or laboratory evidence linking illnesses to BYP during 2015–2022 (Basler et al., 2016; Waltenburg et al., 2022). We determined that isolates were genetically related based on presence of a matching PFGE pattern or relatedness within a given core genome multi-locus sequence typing (cgMLST) allele difference range (Table S1). For some outbreaks, we considered isolates part of the same outbreak even if the allele difference range was beyond the typical threshold used for foodborne outbreak investigations (e.g., 10 allele differences; Tolar et al., 2019) because outbreaks linked to animal contact are known to have greater genetic diversity (Gerner-Smidt et al., 2019). We defined a case as a laboratory-confirmed *Salmonella* infection with an isolate from an ill person, indistinguishable from the outbreak PFGE pattern or genetically related based on WGS and occurring during the outbreak investigation period (date of the first patient illness onset to date outbreak investigation was declared over by CDC). We defined BYP as chickens, ducks, turkeys, geese, guinea fowl, and quail that are sold to or owned by private individuals not for commercial food production or other commercial use. We defined contact with BYP to include any of the following within 7 days of illness onset: direct interaction with BYP or interaction with the environment where BYP live and roam, consumption of eggs or meat obtained from BYP, or residence with a household member who directly interacted with BYP. Data sources included the CDC Outbreak Response and Prevention Branch's outbreak management database; PulseNet; the System for Enteric Disease Response, Investigation, and Coordination (SEDRIC) (CDC, 2022c); and Epi Info™.

2.2 | Outbreak and patient characteristics

In the United States, public health officials routinely interview people with laboratory-confirmed *Salmonella* infections (or their caregiver/proxy) with a standardized questionnaire designed to collect demographic information and general food, animal, and other exposures the week prior to illness onset (Marshall et al., 2020). When patients are included in an ongoing multistate outbreak investigation, these data are shared with CDC. BYPAS outbreak patients (when available) were also asked a standardized set of BYP exposure questions, including type(s) and species of poultry contacted, type and location of contact, backyard poultry ownership and purchase information, and biosecurity and husbandry behaviours performed around BYP. Within a given year, the same BYP exposure questions were asked of patients, but these questions could be revised between different years. As such, some questions were only asked of patients during specific years. The data reported here are limited to information collected during all investigation years within the designated time frame unless indicated otherwise. Using a binomial probability analysis, we compared the proportion of patients reporting contact with BYP within 7 days of illness onset with the proportion of healthy individuals who reported contacting BYP in the 7 days before interview as part of the 2018–2019 Foodborne Diseases Active Surveillance Network (FoodNet) population survey (CDC, 2021a).

PulseNet transitioned from using PFGE to using WGS to detect outbreaks and outbreak-associated illnesses beginning in 2019 (Kubota et al., 2019). To describe how this transition might have affected the number of BYPAS outbreaks or illnesses detected, we determined the median and range for outbreak size and calculated the mean number of outbreaks that occurred during 2015–2018 and 2019–2022. We calculated frequencies for outbreak variables (e.g., *Salmonella* serotype) and patient variables (e.g., demographics, health outcomes, and biosecurity or husbandry behaviours around BYP) for each outbreak year. We compared select outbreak or patient characteristics between each outbreak serotype and a referent group (*Salmonella* Enteritidis, chosen as the referent because it was the most common serotype in BYPAS outbreaks) using chi-square, Fisher's exact test, or Wilcoxon Rank Sum test, as appropriate. Some *Salmonella* serotypes caused more than one outbreak during the analytic time frame, so we assessed whether the epidemiologic characteristics of different outbreaks within the same serotype were similar before deciding to report on epidemiologic characteristics aggregated at the serotype level. To do this, we used chi-square, Fisher's exact test, or Wilcoxon Rank Sum test, as appropriate, to determine if outbreaks of the same serotype shared similar epidemiologic characteristics before aggregating these variables for each serotype. For these comparisons, the outbreak with the most cases of a given serotype was used as the referent to compare to all other outbreaks of that serotype.

When a *Salmonella* serotype caused more than one outbreak in a single year, we designated each outbreak strain based on the order in which the outbreak was detected (e.g., *Salmonella* Enteritidis Strain 1 and Strain 2 in 2018 indicates Strain 1 was identified first and Strain 2 was identified second in that year); numbering of outbreak strains does not indicate genetic relatedness between different years (e.g., *Salmonella* Enteritidis Strain 1 in 2018 is not necessarily genetically related to *Salmonella* Enteritidis Strain 1 in 2019). We applied a Bonferroni correction for multiple comparisons. Therefore, the significance threshold was set at $p < 0.0001$. Analyses and data visualization were performed using Stata (version 16; StataCorp., College Station, TX), SAS versions 9.4 (SAS Institute, Cary, NC, USA), or Microsoft Excel.

2.3 | Animal testing

Investigators with state or local governmental agencies collected samples from BYP or their habitats at the homes of patients or at the locations where patients reported purchasing poultry (USDA, 2014a). Types of samples collected were determined at the discretion of the investigator who took each sample and could include cloacal swabs of BYP, samples of fresh faeces in the environment, or swabs of potentially contaminated items in the BYP habitat such as bedding. The number of samples taken during each attempt to test BYP for *Salmonella*, the number of birds tested, and decisions regarding how to process and test samples were made by investigators and their affiliated laboratories following a recommended protocol (USDA, 2014a). We compared isolates from humans and animals (when available) and considered isolates detected in specimens collected from BYP or their habitats to be genetically related to isolates from ill people if they had a matching PFGE pattern or fell within the cgMLST allele range (as appropriate, Table S1).

3 | RESULTS

3.1 | Outbreak characteristics

From 2015 to 2022, there were 88 multistate BYPAS outbreaks and 7866 outbreak-associated illnesses caused by 21 different *Salmonella* serotypes (Table 1, Table S1); 2020 had the most outbreaks ($n = 17$) and outbreak-associated illnesses ($n = 1722$; Figure 1, Table 1). Median outbreak size was 46 cases (range: 8–848 cases), and the median number of outbreaks per year was 11 (range: 5–17 outbreaks/year; Figure 1, Table 1). From 2015 to 2018 there was an average of 8 outbreaks/year and 651 illnesses/year; from 2019 to 2022 there was an average of 14 outbreaks/year and 1316 illnesses/year. The onset of most outbreak-associated illnesses occurred during either April (23%) or May (24%, Figure 2). Ill people resided in 52 United States jurisdictions (all 50 states, the District of Columbia, and Puerto Rico; Figure 3), with most illnesses occurring in New York ($n = 417$, 5%), Ohio ($n = 391$, 5%), California ($n = 351$, 4%), Pennsylvania ($n = 313$, 4%), and Minnesota ($n = 311$, 4%; Table S2).

The five largest outbreaks were a 2020 *Salmonella* Hadar outbreak (848 cases), 2021 *Salmonella* Hadar outbreak (364 cases), 2022 *Salmonella* Enteritidis Strain 1 outbreak (322 cases), 2021 *Salmonella* Infantis Strain 1 outbreak (287 cases), and 2019 *Salmonella* Enteritidis Strain 1 outbreak (274 cases, Table S1). *Salmonella* Enteritidis accounted for the most outbreaks ($n = 21$) and illnesses $n = 2400$) during 2015–2022 (Figure S1). Compared with *Salmonella* Enteritidis, six *Salmonella* serotypes had a lower median age range and higher proportion of patients <5years of age ($p < 0.0001$ for each comparison, Table 2). The lowest median ages were observed for *Salmonella* Altona (median = <1 year), Alachua (median = 3 years), Indiana (median = 5 years), Agona (median = 8 years), and Typhimurium (median = 9 years). *Salmonella* Hadar caused more hospitalizations compared with *Salmonella* Enteritidis (38% vs. 29%, $p < 0.0001$). *Salmonella*-associated deaths were observed for *Salmonella* Infantis ($n = 3$), Enteritidis ($n = 2$), Hadar ($n = 1$), I 4,[5],12:i:- ($n = 1$), Mbandaka ($n = 1$), and Newport ($n = 1$, Table 2). The analysis performed to identify differences in demographic and health outcome variables between the outbreak strains of the same serotype identified only 1 of the 469 comparisons performed which were statistically significant, indicating that patients in outbreaks that were caused by the same serotype likely are similar by age, sex, and health outcomes (Table S3).

For 31 distinct outbreaks (35%), the strain of *Salmonella* associated with human illness was isolated from BYP (Table S1). These outbreak strains were isolated from cloacal swabs obtained from patients’ BYP or from specimens collected from the BYP habitat at patients’ residences or at retail locations where patients reported purchasing BYP.

3.2 | Patient characteristics

Of 7647 patients with information regarding sex available (97% of all patients), 4291 (56%) were female. Of 7727 patients with age information available, median age was 33 years (range: <1–106 years). Eight hundred and thirty-three (11%) patients were <1 year of age, 1007 (13%) were 1–4 years, and 583 (8%) were 5–10 years (Figure 4). Of 3845 patients with ethnicity information available, 443 (12%) were Hispanic. Of 4025 patients with race information available, 3749 (93%) were White, 89 (2%) were African American/Black, 46 (1%) were Native American or Alaska Native, 46 (1%) were Asian, 10 (0.2%) were Pacific Islander, and 31 (0.8%) reported more than one race. In total, 30% (1710/5644) of patients were hospitalized, with a median of 249 (range: 57–342) patients hospitalized/year (Table 1). The median age of hospitalized patients was 50 (range: <1–101) years (Figure 4). Of deaths reported to CDC, nine were attributed to *Salmonella* infection; the median age of patients that died was 63 (range: <1–77) years. The proportion of patients with *Salmonella* isolated from blood increased with age category (Figure 4). The median age of patients with *Salmonella* isolated from blood was 58 years (range: <1–102).

Among all outbreaks, 3452 (69%) of 4979 patients with information available reported contact with BYP, interaction with an environment where BYP live and roam, consumption of eggs or meat obtained from BYP, or residence with a household member who directly interacted with BYP (Figure 5). This was significantly higher than 6.2% (95% Confidence Interval: 5.3%–7.4%) of healthy people reporting contact with backyard poultry in 7 days prior to being surveyed in the 2018—2019 FoodNet Population Survey ($p < 0.01$). Patients most commonly reported contact with chicken (87%, 2313/2654) and ducks (34%, 891/2654; Figure S2). Of the 3452 patients who reported contact with BYP, 59% ($n = 2053$) reported that they owned BYP, whereas 6% ($n = 220$) denied owning BYP and 34% ($n = 1179$) did not provide information about whether they owned BYP. Of 1976 patients who specified where they contacted poultry, patients commonly reported BYP contact at their own residence (78%; 1550/1976); another person’s residence (13%; 260/1976); or at a store location (12%; 228/1976; Figure S3).

Of 1942 patients who provided additional details on their contact with BYP, most reported touching BYP (64%; 1249/1942), touching BYP enclosures (57%; 1112/1942), or providing feed or water to them (53%, 1046/1942; Figure 5b). Behaviours considered to have an increased risk of zoonotic *Salmonella* transmission including snuggling or kissing poultry were less frequently reported: 28% (551/1956) reported allowing their poultry inside their home, 21% (401/1942) reported snuggling poultry, and 7% (129/1942) reported kissing poultry. During 2022 only, patients were asked about eggs or meat that were consumed from BYP: 28% (147/509) reported consuming eggs from BYP, and 3% (14/494) reported consuming meat from BYP.

4 | DISCUSSION

During 2015–2022, contact with BYP caused more multistate *Salmonella* outbreaks and outbreak-associated illnesses than contact with any other type of animal (CDC, 2022d; Waltenburg et al., 2022). Although BYPAS has been a recognized public health problem for decades, outbreaks have continued to occur annually (Basler et al., 2016; Behravesh et al., 2014). BYPAS outbreak-associated illnesses have nearly tripled and hospitalizations more than quadrupled compared with BYPAS multistate outbreaks during 1990–2014, resulting in greater demands on medical and public health resources (Basler et al., 2016). The upward trends in illnesses and outbreaks have persisted despite widespread outreach to BYP owners and education about *Salmonella* (Behravesh et al., 2014; CDC, 2022a, 2022b; Varela et al., 2022); dissemination of guidance to reduce *Salmonella* spread at hatcheries and retail stores (Nichols et al., 2018; USDA, 2014b); research to identify BYP owner knowledge gaps, refine biosecurity practice recommendations, and improve public health communication strategies (Ayala et al., 2022; Elkhoraibi et al., 2014; Gollarza, 2022; Kauber et al., 2017; Larsen et al., 2022; Madsen et al., 2013; McDonagh et al., 2019; Paphitis et al., 2023); and investigation of annual outbreaks to track and mitigate outbreak strains.

4.1 | Impacts of changes in Salmonella surveillance on BYPAS

Certain factors could have contributed to the observed increase in BYPAS outbreaks and illnesses. Improvements in public health surveillance systems, such as the implementation of WGS to detect outbreaks (Kubota et al., 2019), have improved outbreak detection. Notably, the average number of BYPAS outbreak-associated illnesses doubled and the average number of outbreaks increased for the 4 years following implementation of WGS in PulseNet laboratories compared to the 4 years prior. WGS has also enabled greater resolution for different strains of *Salmonella* within serotypes that were previously indistinguishable by PFGE. For example, prior to 2019, all *Salmonella* Enteritidis isolates were considered part of one to two outbreaks each year; with WGS it was possible to identify highly related *Salmonella* Enteritidis isolates and further distinguish outbreaks.

4.2 | Factors influencing BYP exposure and ownership

Additionally, the number of BYP owners in the United States is growing (AVMA, 2018; Nichols et al., 2021). The Foodborne Diseases Active Surveillance Network (FoodNet) estimated that 6.2% (95% Confidence Interval: 5.3%–7.4%) of people in FoodNet's surveillance area—which represents 15% of the US population—had contact with BYP in the week prior to interview during 2018–2019 (CDC, 2021a). More recent market research from the American Pet Product Association suggests that BYP contact could be even more common in the United States, with 13% of surveyed households reporting BYP ownership in 2020 (APPA, 2022). BYP are most widely available in retail stores in the United States beginning in early spring and throughout spring and summer months, which aligns with when most BYPAS is detected each year (Basler et al., 2016; Behravesh et al., 2014). BYP ownership offers the opportunity for the public, even those living in urban environments, to reap the benefits of producing their own food and engaging in the human-animal bond (CDC, 2022a). Ownership has become more popular in the US, particularly in times of social and economic change, such as during the onset of the SARS-CoV-2 pandemic in 2020 (Nichols et al., 2021) or amidst increasing prices for eggs during 2022–2023 as a result of highly pathogenic avian influenza affecting the United States (Smialek & Swanson, 2023). As the number of people who have contact with BYP increases, BYPAS might be expected to increase; 2020 resulted in the highest number of BYPAS outbreaks and outbreak-associated illnesses of any year reported to date (Nichols et al., 2021). This demonstrates the ongoing need for partners across public health, industry, and academia to inform the public about zoonotic diseases like *Salmonella* transmitted from BYP to people. Similarly, these groups should work to implement data-driven solutions to mitigate *Salmonella* spread along the distribution chain of BYP from hatchery to backyard.

4.3 | Serotype-specific findings

Some BYPAS serotypes represent a greater public health burden. Serotypes such as *Salmonella* Enteritidis, Hadar, and Infantis caused the highest number of BYPAS outbreak-associated illnesses annually during 2015–2022. *Salmonella* Hadar also resulted in the highest proportion of BYPAS hospitalizations compared with other serotypes, an observation previously documented among BYPAS patients >65 years of age (Whitehill et al., 2022). *Salmonella* Enteritidis and Infantis caused the most BYPAS deaths. In addition to these serotypes, *Salmonella* Mbandaka, Braenderup, Indiana, Muenchen, I 4,[5],12:i:-, and Typhimurium have caused multiple outbreaks over several years. WGS data analysis has suggested that some serotypes have closely genetically related strains that persistently cause BYPAS illnesses over time or recurrently lead to BYPAS outbreaks. Identifying, describing, and tracking these reoccurring and persisting strains will enable public health investigators and industry partners to better understand the sources of these strains and potentially hone in on specific interventions to reduce their spread or address reservoirs that allow these strains to persist within the BYP industry (CDC, 2023b).

4.4 | Age-specific considerations for BYPAS

Similar to other salmonellosis outbreaks linked to animal contact, children are disproportionately affected by BYPAS outbreaks, with 24% of BYPAS illnesses occurring in children <5 years of age (Marus et al., 2019; Nichols et al., 2022; Waltenburg et al., 2022). As such, CDC recommends that children <5 years of age not directly interact with BYP, and caregivers who interact with poultry should properly wash their hands between interacting with BYP and children (Varela et al., 2022). However, research has shown that BYP owners infrequently limit their children’s interactions with BYP flocks (Kauber et al., 2017; Larsen et al., 2022; McDonagh et al., 2019). This evidence collectively demonstrates that improved approaches to informing parents and caregivers about BYPAS to motivate them to follow public health recommendations are warranted to reduce BYPAS illnesses in young children. Additionally, people >65 years of age were more likely to be hospitalized, develop septicemia, or die because of BYPAS. People >65 years old or those with weakened immune systems should exercise caution when contacting BYP because of their risk for severe health outcomes from salmonellosis (Behravesh et al., 2014; Varela et al., 2022; Whitehill et al., 2022).

4.5 | *Testing BYP for* Salmonella *outbreak strains*

A crucial aspect of confirming, tracing, and mitigating BYPAS outbreaks is collecting samples from BYP to test for *Salmonella*. Outbreak strains were detected via sampling in 35% of BYPAS outbreaks during 2015–2022. Several factors limit the detection of outbreak strains from BYP. First, not all patients agree to have their BYP tested by public health officials; this could be associated with concern about harm to the birds or other consequences following positive test results, even though sampling can just be limited to obtaining swabs of BYP habitats without having to handle the birds (USDA, 2014a). Second, BYP can shed *Salmonella* intermittently (Rukambile et al., 2019), and therefore, investigators can expect that some collected samples will test negative. *Salmonella* surveillance studies in BYP have reported between 1.7% to 19% positivity in animals sampled (Clothier et al., 2018; Larsen et al., 2022; Manning et al., 2015; McDonagh et al., 2019). Finally, multistate investigations rely on individual state, local, and territorial governmental agencies or academic partners to conduct sampling on behalf of the broader investigation, and not all agencies have dedicated funding, trained and available personnel, or laboratory capacity to conduct testing on animal or environmental specimens.

To improve the quantity and quality of laboratory data collected from BYP during outbreak investigations, public health officials should train staff—using pre-prepared talking points—to explain sampling for *Salmonella* when interviewing patients to increase the number who are willing to allow their BYP to be tested. Because sampling from BYP can include cloacal swabbing, sampling of fresh faeces in the environment, or swabbing heavily soiled areas of the environment, staff can also be easily trained to collect samples (NWCPHP, 2023). Collecting multiple samples from different birds in a flock and different areas in their environment can increase the chances of isolating *Salmonella* despite intermittent *Salmonella* shedding. Public and animal health agencies can collaboratively develop partnerships with backyard poultry hatcheries and retail stores in order to conduct sampling for outbreak strains at points of purchase (Sidge et al., 2019). Similarly, previous work has demonstrated the utility of partnerships between academic and public health groups as a helpful approach for sampling poultry and discovering sources of *Salmonella* strains linked to BYPAS outbreaks (Habing et al., 2015). Testing BYP for *Salmonella* during outbreak investigations will continue to be important for confirming future outbreak vehicles and tracing sources of outbreak strains. Furthermore, identifying *Salmonella* serotypes that are shed by BYP and are persistent concerns for public health can direct *Salmonella* surveillance conducted by BYP hatcheries as well as inform their efforts to mitigate these strains such as through vaccination of poultry.

4.6 | Prevention of BYPAS using a multitiered approach

Prevention of BYPAS has been ongoing for decades in response to outbreak investigations and through general efforts led by industry, academic, and governmental partners (Gaffga et al., 2012; Loharikar et al., 2012; Nichols et al., 2018; Robertson et al., 2019). There are no federal regulations specifically pertaining to control of non-typhoidal *Salmonella* of consequence to human health within the BYP industry, but BYP hatcheries can voluntarily participate in the United States Department of Agriculture National Poultry Improvement Plan, which has some programs that include requirements for monitoring of *Salmonella* strains of consequence to public health in addition to *Salmonella* strains that impact poultry health like *Salmonella* Gallinarum and Pullorum (USDA, 2020). Some hatcheries also reportedly vaccinate poultry against *Salmonella* serotypes that impact human health, though the prevalence, consistency, and efficacy of these vaccination programs across BYP hatcheries are not documented. Retail stores have also provided educational materials to their customers about risks of BYPAS, though, again, the prevalence and consistency of these practices across retail stores are not documented.

BYPAS outbreaks have affected people in all 50 states, Washington DC, and Puerto Rico, though some states—including several in the Midwest and Northeast regions of the country—report higher numbers of BYPAS. Factors not captured in this study could contribute to the observed incidence of BYPAS in specific states and regions such as availability of BYP for purchase in those regions or social and cultural factors influencing the prevalence of BYP ownership. Nevertheless, the size and widespread geographic range of these outbreaks demand public health resources across many agencies and make identifying sources of outbreak strains challenging. The diverse nature of the backyard poultry industry and the numerous hatcheries, breeders, suppliers, and retailers that market BYP across the United States contributes to the widespread distribution of BYPAS outbreaks. Though details of traceback efforts implemented during outbreak investigations are beyond the scope of this article, it is important to recognize the challenges of tracing sources of BYP amidst this complex industry as a barrier to mitigating the spread of outbreak strains (Behravesh et al., 2014). Previous BYPAS investigations have successfully identified source hatcheries of few outbreak strains (Gaffga et al., 2012; Loharikar et al., 2012; Robertson et al., 2019), but this is not always possible.

Therefore, it is crucial for public health officials to implement other strategies to prevent outbreaks and illnesses in people who have contact with BYP. For example, informing BYP owners of the risks of *Salmonella* and other zoonoses can bolster adherence to at-home biosecurity practices such as routine handwashing after handling or interacting with BYP, refraining from higher risk behaviours such as kissing or snuggling the birds, restricting young children’s access to BYP, and keeping BYP outdoors as opposed to inside the home (Varela et al., 2022). While we report that the proportion of patients that kissed, snuggled, or allowed backyard poultry inside their home declined over time or remained at a low, consistent level compared with previous reports (Basler et al., 2016), these behaviours have not been eliminated among BYP owners and have even been observed at higher rates in other studies (Larsen et al., 2022; McDonagh et al., 2019). Recent focus groups with BYP owners demonstrated that some owners are unwilling to forego physical contact with their birds despite knowing about the potential for *Salmonella* transmission (Gollarza, 2022). BYP owners reported that they were likely to ignore messaging perceived as paternalistic or fear-mongering, suggesting that educational outreach to BYP owners could have more impact when conveyed in a positive tone and utilizing visually appealing images and graphics (Gollarza, 2022). Further research examining the diverse beliefs and perceptions of BYP owners could uncover gaps in our understanding of attitudes and perceptions toward sources of information for prevention of BYP-associated zoonoses and potentially identify additional strategies for successful messaging. Such research could similarly identify if there are other unique partnerships or programs that public health could utilize to improve the public’s receptivity of health and safety recommendations regarding BYP.

In addition to interventions focused on interactions with BYP, further work can be done to understand the impact of *Salmonella* reduction strategies within the BYP industry. Current interventions that BYP hatcheries implement to reduce the transmission of *Salmonella* among poultry need to be systematically documented across all BYP hatcheries in the United States, and the efficacy of these actions needs to be assessed for their impact on public health. This information would allow for best practices to be refined and implemented across all BYP hatcheries consistently. Furthermore, BYP retailers need to be systematically assessed regarding the information they provide to the public about BYPAS. This would allow for identification of stores that do not routinely provide such education to customers so that these stores can be equipped with resources to do so. Ideally, all retailers would provide information to all customers purchasing BYP about the risks of BYPAS.

4.7 | Limitations of this analysis

Additional limitations to this analysis should be considered. First, not all patients were available for interview by public health officials, and some that were interviewed could not recall requested exposure information. As a result, the epidemiologic information presented here is a subset of the overall outbreak population. Second, health outcome data—particularly the incidence of *Salmonella*-associated deaths—were not systematically collected and reported and might not be completely characterized by available data. Third, opportunities and resources to collect samples from BYP for *Salmonella* testing were limited during investigations. Most outbreak strains were never isolated from BYP to aid in confirming BYP as the source of the outbreak, but it was not systematically documented for which outbreaks had samples from BYP tested for *Salmonella* and which did not have these types of samples available. Fourth, this analysis was limited to multistate BYPAS outbreaks. Single-state BYPAS outbreaks also occur annually, though they represent a relatively small proportion of outbreak-associated illnesses (CDC, 2023a). Additionally, the identification of patients as part of an outbreak necessitates those ill individuals to seek medical care, healthcare providers to order appropriate diagnostic testing, and positive test results to be reported to public health departments. Thus, the outbreak-associated illnesses reported here are likely an underestimate of the true number of people that were affected by BYPAS (Collier et al., 2021; Hale et al., 2012; Scallan et al., 2011). Finally, BYP represent multiple species of domesticated birds such as chickens, ducks, turkeys, geese, guinea fowl, and quail. Different types of birds might come into contact with one another during processing or order fulfilment at hatcheries, when shipped or sold at stores, or at private residences. All BYP can carry non-typhoidal *Salmonella* that can be transmitted to people, allowing for spread of this pathogen between poultry species. As a result, this precludes the ability of public health officials to determine if a given species or breed of bird is the source of *Salmonella* strains in every outbreak.

5 | CONCLUSIONS

Outbreaks and illnesses linked to BYP in the United States have grown in size, though this public health problem is preventable. Public health and animal health governmental officials, human and veterinary healthcare providers, BYP breeders and retailers, researchers, and extension agents should continue to collaborate and implement approaches to reduce the spread of *Salmonella* and ensure health and safety recommendations pertaining to BYP are disseminated widely. Novel, evidenced-based, and audience tested strategies to reaching and educating the public are encouraged and might be more likely to succeed in preventing illnesses. Outbreak investigators should continue to collect robust epidemiologic and laboratory evidence to inform outbreak mitigation and communication strategies. Collaboration between industry representatives and public and animal health officials can identify opportunities for *Salmonella* surveillance that can detect outbreak strains early and potentially identify opportunities to eliminate these strains from recurrently causing outbreaks. The persisting problem of BYPAS outbreaks and illnesses necessitates ongoing interventions and refinement of diverse strategies to prevent further expansion of this public health threat.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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DISCLAIMER

The findings and conclusions of this study are those of the authors and do not necessarily represent the official position of the US Centers for Disease Control and Prevention (CDC).

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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Impacts

- Backyard poultry is the most common type of animal linked to multistate human salmonellosis outbreaks in the United States and were the source of 88 multistate outbreaks and 7866 illnesses in 2015–2022.
- Children <5 years of age were disproportionately impacted in these outbreaks, indicating that focused prevention efforts for parents and caregivers are needed to reduce infections.
- Prevention of backyard poultry-associated salmonellosis requires an integrated approach necessitating engagement across industry, veterinary, medical, agricultural, and public health sectors to implement effective strategies to investigate, mitigate, and prevent outbreaks.

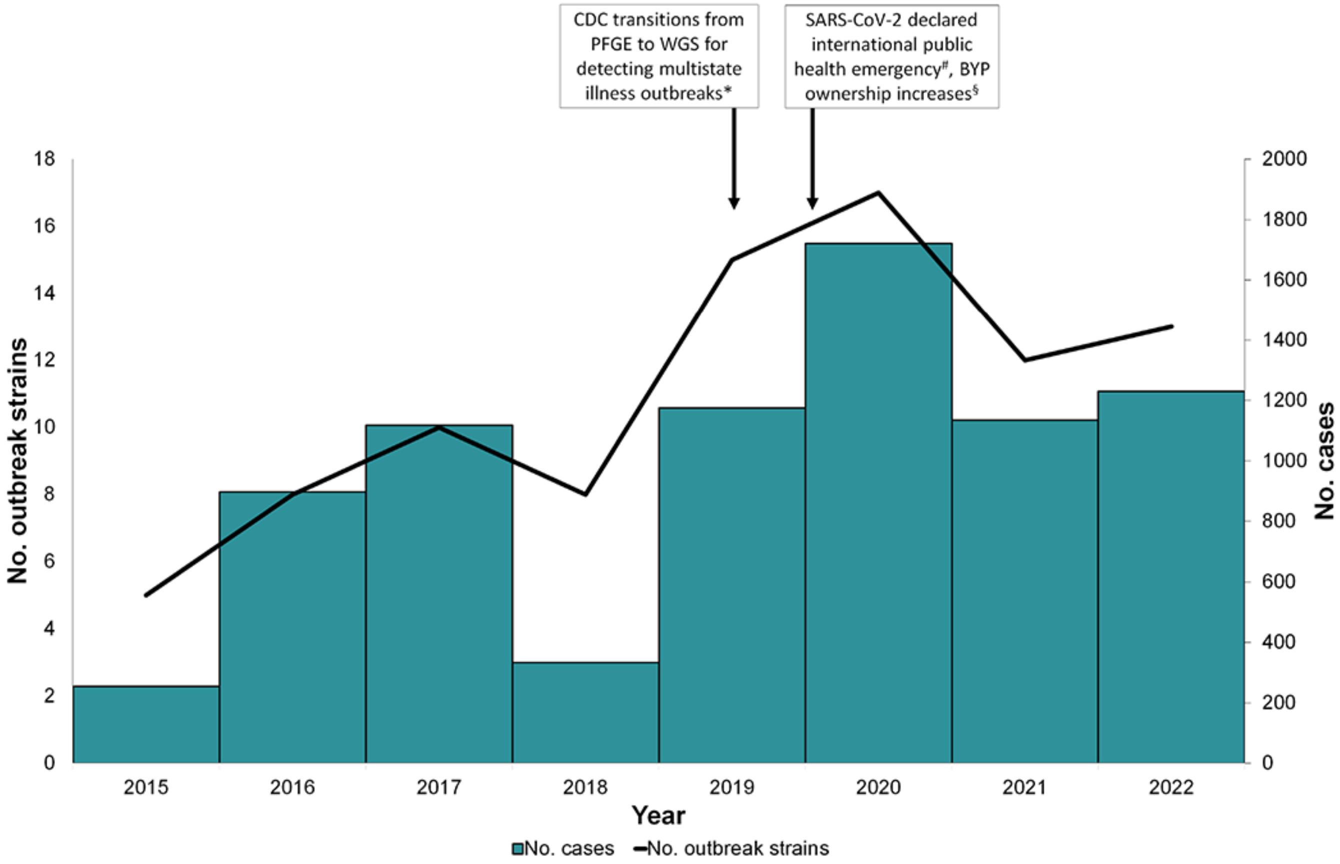


FIGURE 1.

Number of backyard poultry (BYP)-associated salmonellosis outbreaks and outbreak-associated illnesses by year of the first illness onset–United States, 2015–2022. PFGE, Pulsed-field gel electrophoresis; WGS, whole genome sequencing; *Kubota et al. (2019); #WHO (2020); §Nichols et al. (2021).

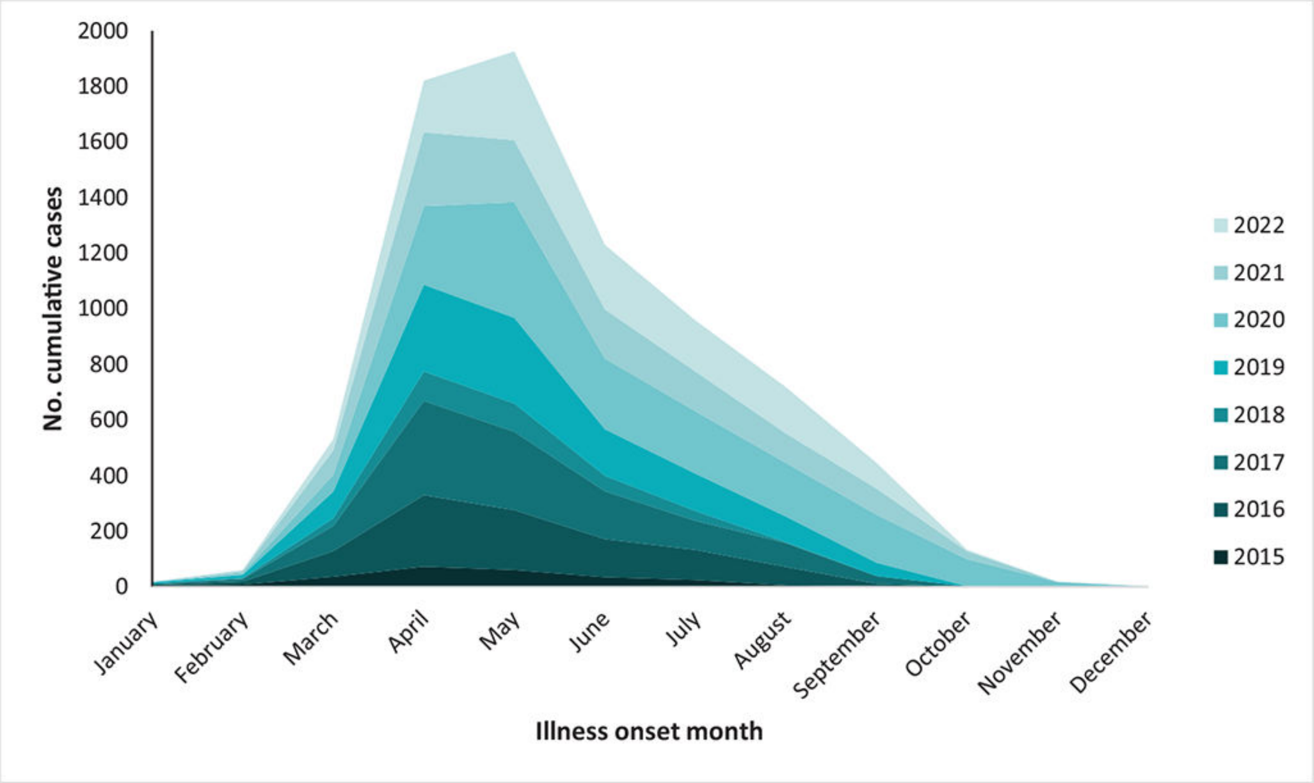


FIGURE 2.

Cumulative number of backyard poultry-associated *Salmonella* illnesses by month of illness onset—United States, 2015–2022. The number of cases identified each month in a given year is indicated by the area shaded by each different colour, with the overall curve demonstrating the cumulative number of cases during 2015–2022 for each month. When patient illness onset date was not reported, an estimated onset date was determined as 3 days before the reported isolation date.

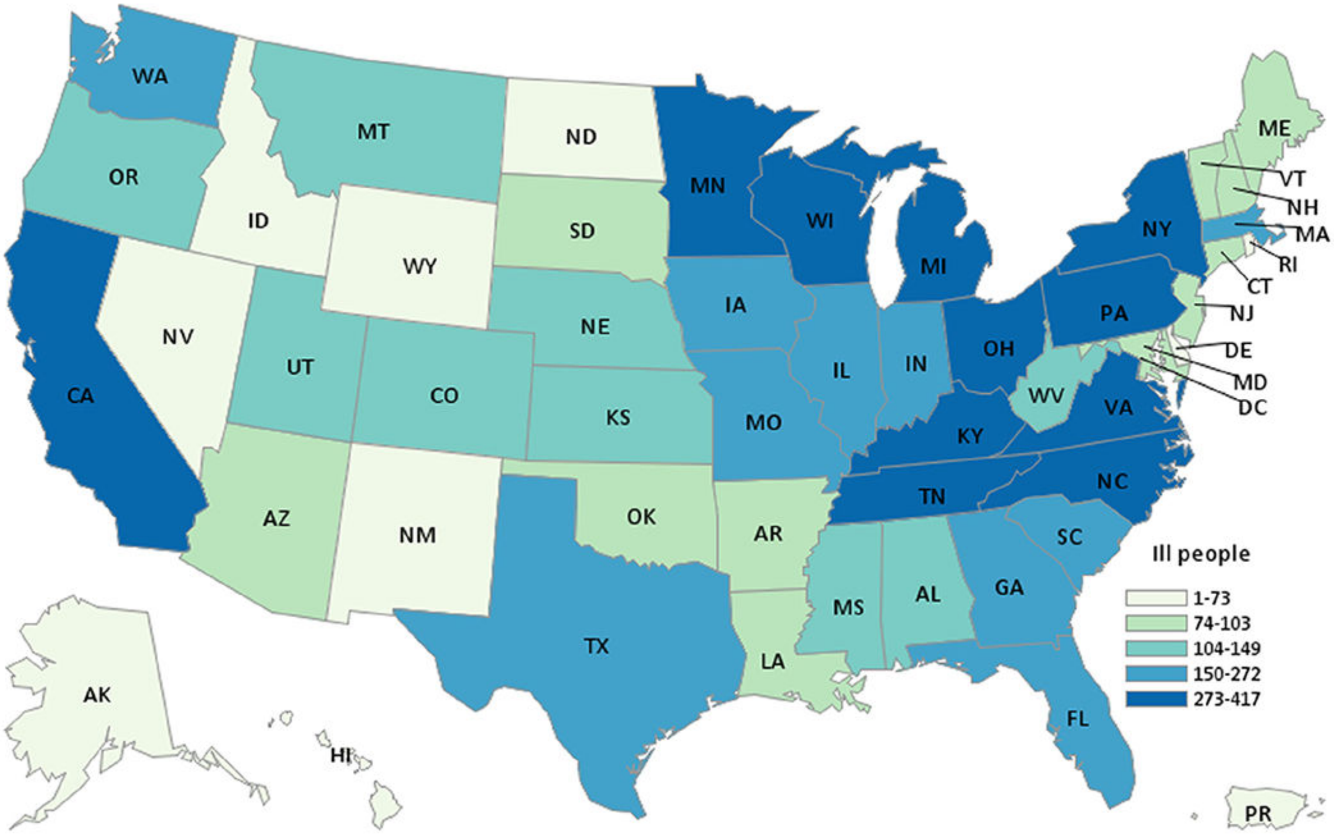


FIGURE 3.

Number of backyard poultry-associated salmonellosis outbreak patients by state or territory of residence–United States, 2015–2022. Thresholds for categorizing jurisdictions were determined based on equivalent quantiles for illness count.

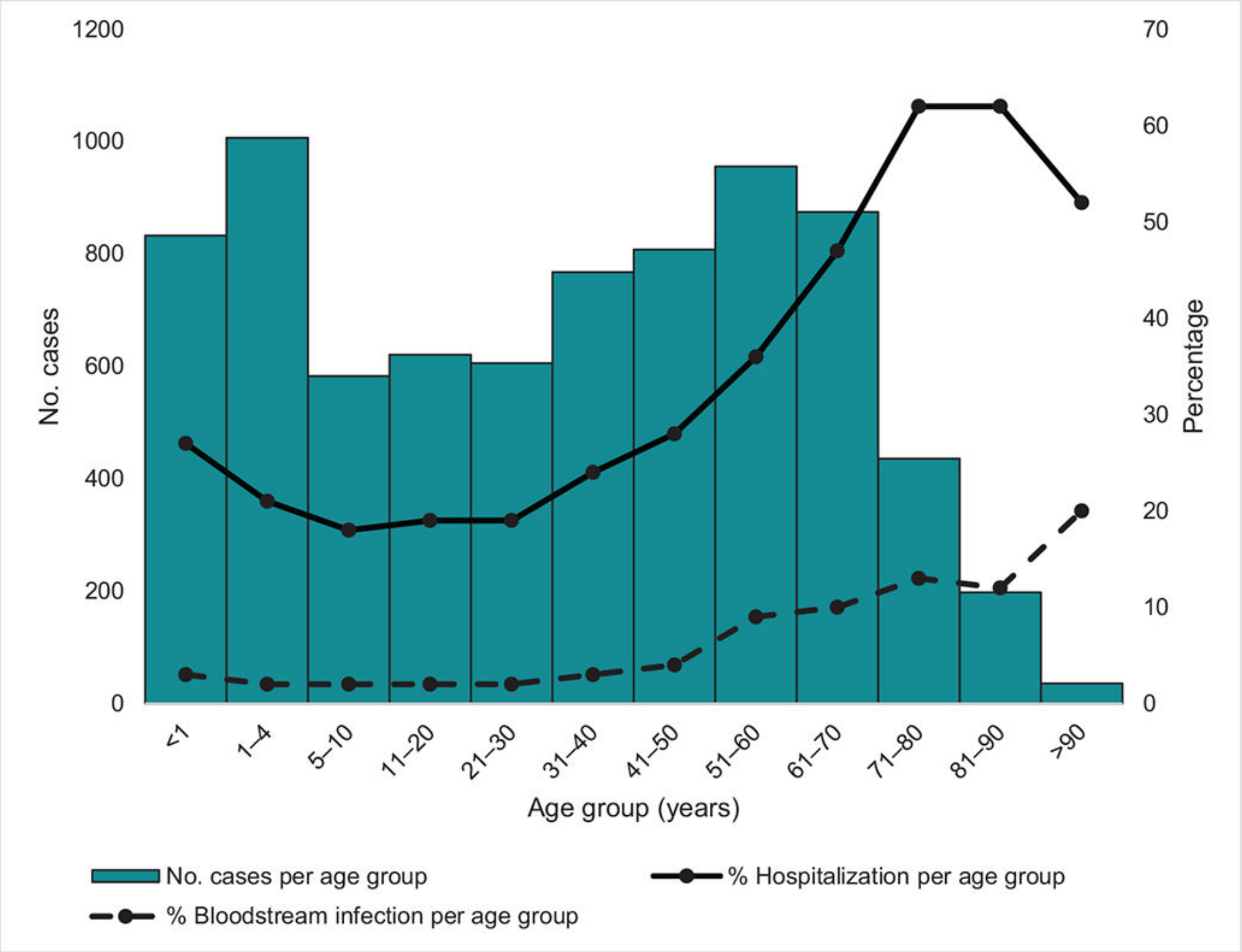
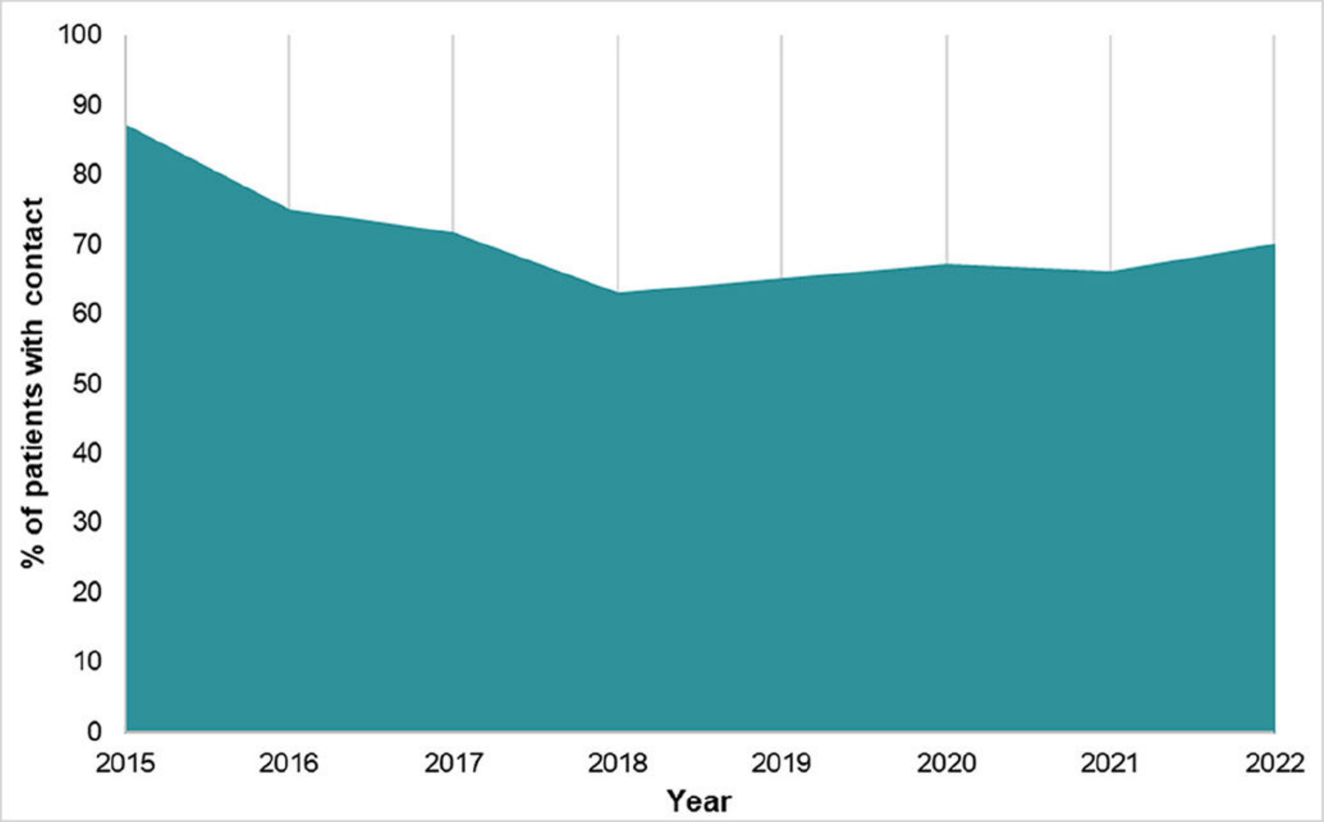


FIGURE 4.

Number of backyard poultry-associated *Salmonella* outbreak patients, proportion of hospitalization, and proportion with bloodstream infection by age group—United States, 2015–2022.


100
90
80
70
60
50
40
30
20
10
0
% of patients with contact
2015
2016
2017
2018
2019
2020
2021
2022
Year

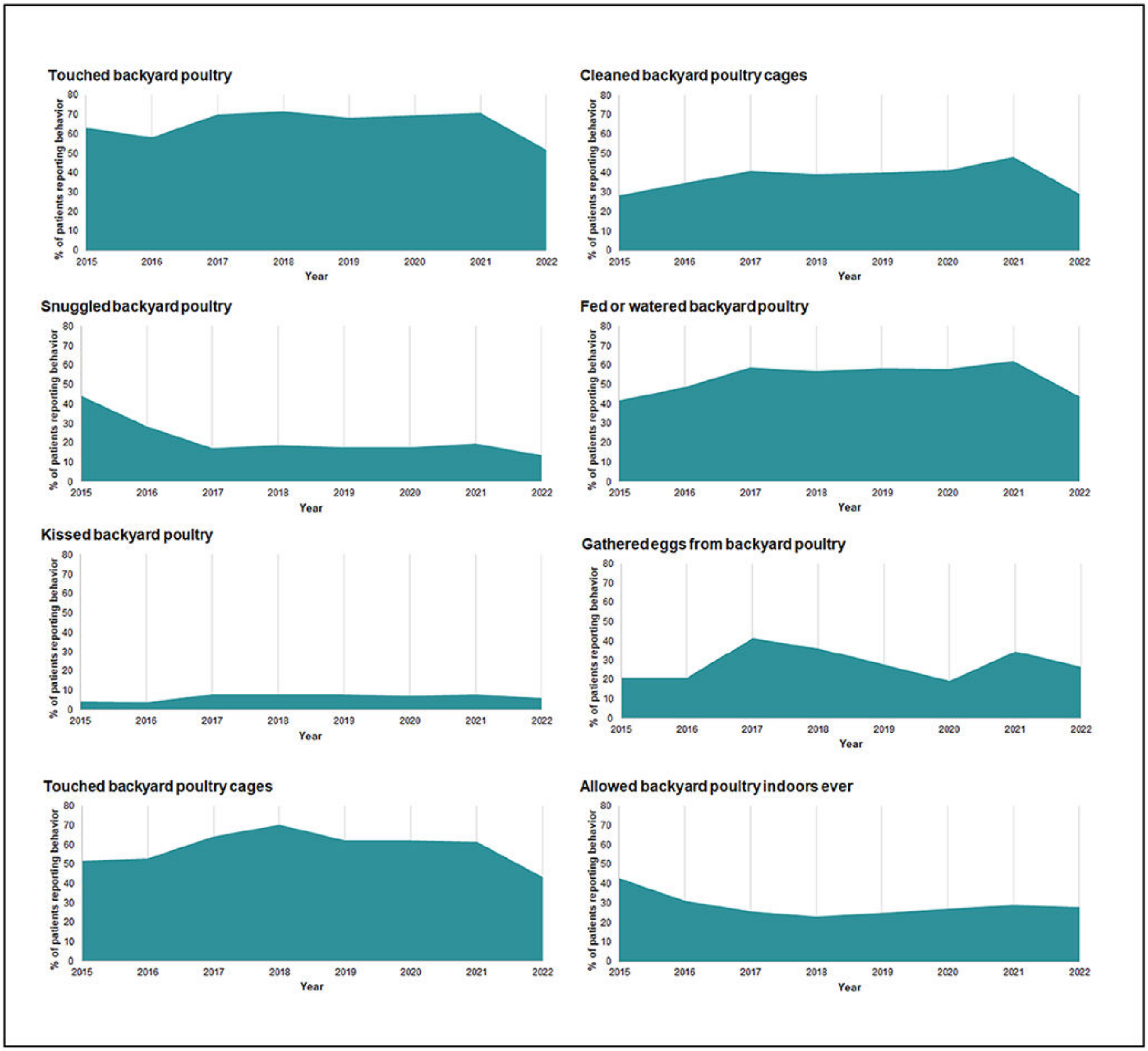


FIGURE 5.

(a) Proportion of patients with available information reporting contact* with backyard poultry (BYP)—United States, 2015–2022. Overall, 3452 of 4979 (69%) people with available information reported contact with BYP. *Contact was defined as directly interacting with BYP or the environment where they live and roam, consumption of eggs or meat obtained from BYP, or residing with a household member that has direct interaction with BYP. (b) Proportion of patients reporting they practiced specific biosecurity or husbandry behaviours —United States, 2015–2022. Of patients reporting contact with BYP, some provided information on the specific behaviours performed when interacting with poultry. Patients could designate that they performed more than one behaviour in the questionnaire.

TABLE 1

Number of backyard poultry (BYP)-associated *Salmonella* outbreaks, outbreak-associated illnesses, and patient characteristics by year of first illness onset-United States, 2015–2022.

Year	No. outbreak strains	No. cases	*Salmonella* serotypes (No. of outbreak strains if >1/ serotype)	Median age in years (minimum-maximum age)	No. <5 years of age (%)[a]	No. >65 years of age (%)[a]	No. female (%)[a]	No. bloodstream infection[b] (%)[a]	No. hospitalized (%)[a]	No. died (%)[a]	No. contact[c] with BYP (%)[a]
2015	5	255	Enteritidis, Hadar, Indiana, Muenchen, Muenster	19 (<1–89)	84/252 (33)	25/252 (10)	126/252 (50)	9/255 (4)	63/170 (37)	0/174 (0)	156/180 (87)
2016	8	897	Braenderup, Enteritidis, Hadar, Indiana, Infantis (2) Mbandaka, Muenster	27 (<1–106)	225/894 (25)	109/894 (12)	458/880 (52)	23/887 (3)	210/763 (28)	1/758 (0.1)	567/754 (75)
2017	10	1118	Braenderup, Enteritidis, Hadar, I 4,[5],12:i:-, Indiana, Infantis, Litchfield, Mbandaka, Muenchen, Typhimurium	28 (<1–101)	304/1108 (27)	126/1108 (11)	606/1101 (55)	29/1096 (3)	258/913 (28)	1/869 (0.1)	583/820 (71)
2018	8	333	Enteritidis (2), Indiana, Infantis, Litchfield, Montevideo (2), Senftenberg	36 (<1–90)	69/327 (21)	44/327 (13)	179/310 (58)	9/326 (3)	57/247 (23)	0/235 (0)	132/210 (63)
2019	15	1176	Agona, Alachua, Altona, Anatum, Braenderup (2), Enteritidis (2), Infantis (2), Manhattan, Montevideo, Muenchen, Newport, Oranienburg	34 (<1–99)	232/1075 (22)	140/1075 (13)	634/1122 (57)	48/1146 (4)	239/828 (29)	2/771 (0.3)	451/690 (65)
2020	17	1722	Agona, Anatum, Braenderup, Enteritidis (4), Hadar, I 4,[5],12:i:-, Infantis (2), Mbandaka, Muenchen, Newport, Thompson, Typhimurium (2)	35 (<1–95)	403/1708 (24)	270/1708 (16)	977/1666 (59)	99/1689 (6)	342/1028 (33)	1/977 (0.1)	600/905 (66)
2021	12	1135	Enteritidis (6), Hadar, Indiana Infantis (2), Mbandaka, Muenchen	37 (<1–97)	270/1134 (24)	183/1134 (16)	647/1109 (58)	68/1124 (6)	277/843 (33)	2/853 (0.2)	449/677 (66)
2022	13	1230	Enteritidis (4), Hadar, I 4,[5],12:i:, Indiana, Infantis (2), Mbandaka (2), Typhimurium (2)	36 (<1–102)	253/1229 (21)	193/1229 (16)	664/1207 (55)	79/1222 (6)	264/852 (31)	2/762 (0.4)	514/743 (69)
Total	88	7866	Agona (2), Alachua, Altona, Anatum (2), Braenderup (5), Enteritidis (21), Hadar (6), I 4,[5],12:i:- (3), Indiana (6), Infantis (12), Litchfield	33 (<1–106)	1840/7727 (24)	1090/7727 (14)	4291/7647 (56)	364/7745 (5)	1710/5644 (30)	9/5399 (0.2)	3452/4979 (69)

Year	No. outbreak strains	No. cases	*Salmonella* serotypes (No. of outbreak strains if >1/ serotype)	Median age in years (minimum-maximum age)	No. <5 years of age (%)[a]	No. >65 years of age (%)[a]	No. female (%)[a]	No. bloodstream infection[b] (%)[a]	No. hospitalized (%)[a]	No. died (%)[a]	No. contact[c] with BYP (%)[a]
			(2), Manhattan, Mbandaka (6), Montevideo (3), Muenchen (5), Muenster (2), Newport (2), Oranienburg, Senftenberg, Thompson, Typhimurium (5)								

[a] Percentages are calculated based on the number of patients each year with available information regarding each variable.

[b] Bloodstream infection was determined based on whether the patient’s isolate was obtained from blood instead of another source site (e.g., stool, urine).

[c] Contact was defined as directly interacting with BYP or the environment where they live and roam, consumption of eggs or meat obtained from BYP, or residing with a household member that has direct interaction with BYP.

TABLE 2

Comparison of patient demographic characteristics by outbreak serotype: backyard poultry-associated *Salmonella* outbreaks–United States, 2015–2022.

Serotype	No. cases	No. years serotype caused outbreak	Median age (minimum-maximum age)	*p*-value[b]	No. under 5 years old (%)[a]	*p*-value[c]	No. over 65 years old (%)[a]	*p*-value[c]	No. female (%)[a]	P-value[c]	No. bloodstream[d] infection (%)[a]	*p*-value[c]	No. hospitalized (%)[a]	*p*-value[c]	No. died (%)[a]	*p*-value[c]
Enteritidis	2400	8	37 (<1–94)	Ref	315/2350 (13)	Ref	344/2350 (15)	Ref	1288/2332 (55)	Ref	140/2367 (6)	Ref	514/1762 (29)	Ref	2/1625 (0.1)	Ref
Agona	102	2	8 (<1–87)	**<0.0001**	43/102 (42)	**<0.0001**	8/102 (8)	**<0.0001**	56/100 (56)	0.961	9/102 (9)	0.319	20/67 (30)	0.999	0/64 (0)	0.999
Alachua	17	1	3 (<1–81)	0.030	8/13 (62)	**<0.0001**	3/13 (23)	0.422	6/13 (46)	0.706	1/16 (6)	0.999	5/15 (33)	0.777	0/14 (0)	0.999
Altona	8	1	<1 (<1–74)	0.028	5/8 (63)	**<0.0001**	1/8 (13)	1.000	5/8 (63)	0.955	0/8 (0)	0.999	0/6 (0)	0.190	0/6 (0)	0.999
Anatum	135	2	38 (<1–99)	0.446	28/126 (22)	0.009	20/126 (16)	0.801	80/133 (60)	0.307	2/133 (2)	0.032	23/84 (27)	0.818	0/86 (0)	0.999
Braenderup	634	4	34 (<1–101)	0.008	114/610 (19)	0.001	70/610 (11)	0.0522	357/622 (57)	0.358	14/618 (2)	**<0.0001**	111/445 (25)	0.087	0/419 (0)	0.999
Hadar	1861	6	39 (<1–97)	0.026	473/1851 (26)	**<0.0001**	306/1851 (17)	0.101	1061/1806 (59)	0.034	88/1827 (5)	0.136	496/1300 (38)	**<0.0001**	1/1259 (0.1)	0.395
I 4,[5],12:i:-	109	3	21 (<1–87)	0.001	32/109 (29)	**<0.0001**	13/109 (12)	0.518	46/106 (43)	0.022	6/108 (6)	0.999	29/81 (36)	0.248	1/80 (1)	0.216
Indiana	263	6	5 (<1–89)	**<0.0001**	126/261 (48)	**<0.0001**	22/261 (8)	0.008	127/256 (50)	0.099	19/262 (7)	0.469	48/188 (26)	0.311	0/186 (0)	0.999
Infantis	1147	7	30 (<1–106)	**<0.0001**	328/1129 (29)	**<0.0001**	161/1129 (14)	0.807	632/1114 (57)	0.423	46/1132 (4)	0.026	225/849 (27)	0.170	3/833 (0.4)	0.999
Litchfield	27	2	56 (<1–82)	0.150	3/27 (11)	0.949	7/27 (26)	0.170	13/27 (48)	0.588	0/25 (0)	0.397	8/23 (35)	0.721	0/22 (0)	0.999
Manhattan	47	1	43 (<1–83)	0.918	10/44 (23)	0.117	7/44 (16)	0.983	23/43 (53)	0.942	2/47 (4)	0.868	12/36 (33)	0.720	0/35 (0)	0.999
Mbandaka	256	5	21 (<1–92)	**<0.0001**	101/253 (40)	**<0.0001**	35/253 (14)	0.802	142/249 (57)	0.635	11/255 (4)	0.367	51/184 (28)	0.743	1/182 (0.5)	0.999
Montevideo	78	2	30 (<1–77)	0.008	19/77 (25)	0.008	3/77 (4)	0.005	38/72 (53)	0.770	1/78 (1)	0.130	15/63 (24)	0.435	0/59 (0)	0.999
Muenchen	87	5	27 (<1–88)	0.012	28/87 (32)	**<0.0001**	14/87 (16)	0.824	54/86 (63)	0.202	5/87 (6)	0.999	19/66 (29)	1.000	0/67 (0)	0.999
Muenster	48	2	12 (<1–77)	**<0.0001**	23/48 (48)	**<0.0001**	3/48 (6)	0.143	17/47 (36)	0.014	0/48 (0)	0.154	15/35 (43)	0.116	0/39 (0)	0.999

Serotype	**No. cases**	**No. years serotype caused outbreak**	**Median age (minimum-maximum age)**	***p*-value**[b]	**No. under 5 years old (%)**[a]	***p*-value**[c]	**No. over 65 years old (%)**[a]	***p*-value**[c]	**No. female (%)**[a]	**P-value**[c]	**No. bloodstream**[d] **infection (%)**[a]	***p*-value**[c]	**No. hospitalized (%)**[a]	***p*-value**[c]	**No. died (%)**[a]	***p*-value**[c]
Newport	118	2	40 (<1–88)	0.214	15/110 (14)	0.999	18/110 (16)	0.718	64/114 (56)	0.925	3/117 (3)	0.155	19/67 (28)	0.995	1/65 (0)	0.999
Oranienburg	10	1	56 (<1–74)	0.025	0/10 (0)	0.376	2/10 (20)	0.648	7/10 (70)	0.527	1/10 (10)	0.458	3/4 (75)	0.078	0/2 (0)	0.999
Senftenberg	33	1	42 (<1–86)	0.354	3/29 (10)	0.836	5/29 (17)	0.604	24/29 (83)	0.002	0/30 (0)	0.327	2/22 (9)	0.068	0/19 (0)	0.999
Thompson	22	1	31 (<1–67)	0.028	8/21 (38)	0.003	1/21 (5)	0.347	15/22 (68)	0.317	0/22 (0)	0.472	3/17 (18)	0.439	0/14 (0)	0.999
Typhimurium	464	3	9 (<1–102)	**<0.0001**	158/462 (34)	**<0.0001**	47/462 (10)	0.014	236/458 (52)	0.160	16/453 (4)	0.335	92/330 (28)	0.683	0/323 (0)	0.999

[a] Percentages are calculated based on the number of patients each year with available information regarding each variable. **Bold font** indicates *p*-values below a significance threshold of $p < 0.0001$ based on Bonferroni correction for multiple comparisons.

[b] Determined by the Wilcoxon Rank Sum test.

[c] Determined by the chi square or two-tailed Fisher’s exact test, as appropriate.

[d] Bloodstream infection was determined based on whether the patient’s isolate was obtained from blood instead of another source site (e.g., stool and urine).