

Supplemental Table 1: Variables included in the multivariable analyses for *S. Infantis* vs. other *Salmonella* (2006–2020), REPJFX01 vs. other *Salmonella* (2016–2020), and REPJFX01 vs non-REPJFX01 (2016–2020)—Foodborne Diseases Active Surveillance Network (FoodNet)*, United States

Variables*	<i>S. Infantis</i> vs. other <i>Salmonella</i> † (2006–2020)		REPJFX01‡ vs. other <i>Salmonella</i> † (2016–2020)		REPJFX01‡ vs. non-REPJFX01 (2016–2020)	
	Univariable (Significant)	Multivariable (Included)	Univariable (Significant)	Multivariable (Included)	Univariable (Significant)	Multivariable (Included)
Serotype or strain category (as dependent variable)‡§						
Age (age group)	Yes	Yes	Yes	Yes	Yes	Yes
Sex	Yes	Yes	Yes	Yes	Yes	Yes
Race and ethnicity	Yes	Yes	No	Yes	Yes	Yes
Specimen source	Yes	Yes	Yes	Yes	Yes	Yes
Year or year group	Yes	Yes	Yes	Yes	Yes	Yes
Region	Yes	Yes	Yes	Yes	Yes	Yes
International travel	No	Yes	No	Yes	No	Yes
Outbreak associated	Yes	Yes	No	No	No	No
Hospitalization	Yes		No		Yes	
Hospitalization (as dependent variable¶)						
Serotype or strain category		Yes		Yes		Yes
Other variables¶¶		Yes		Yes		Yes

*FoodNet collects data on patient demographics, specimen source, hospitalization within 7 days of specimen collection, deaths, international travel in the 7 days before illness onset (since 2004), outbreak association, symptoms (since 2011), and selected comorbidities (since 2018). The 10 FoodNet sites were grouped using the 4 U.S. Census regions: Midwest (MN), Northeast (CT, NY), South (GA, MD, TN), and West (CA, CO, NM, OR). Odds ratios from logistic regression models that do not include 1.0 in the 95% confidence intervals were considered statistically significant.

†The 20 most common serotypes were determined from culture-confirmed infections reported during 1996–2020 and included *S. Infantis* and other *Salmonella* serotypes (in descending order): Enteritidis, Typhimurium, Newport, Javiana, I 4,[5],12:i:-, Heidelberg, Muenchen, Montevideo, Saintpaul, Braenderup, Oranienburg, Thompson, Mississippi, Bareilly, Agona, I 13,23:b:-, Paratyphi B var. L(+) Tartrate+, Hadar, and Poona.

‡REPJFX01 was defined as *S. Infantis* isolates related by core genome multilocus sequence typing within a range of 0–82 alleles, typically characterized by the presence of pESI megaplasmid harboring multiple resistance genes and *gyrA87* mutation conferring decreased susceptibility to ciprofloxacin.

§Eight variables that were significant in the univariable analyses or associated with *Salmonella* infections in previous studies were included in the final multivariable model for *S. Infantis* vs. other *Salmonella*, and similarly seven variables were included in the multivariable models for REPJFX01 (vs. other *Salmonella* and vs. non-REPJFX01).

¶¶The final models for REPJFX01 vs. other *Salmonella* and REPJFX01 vs non-REPJFX01 included all variables that were considered in the multivariable models with serotype or strain category as dependent variable. Although the initial model for *S. Infantis* vs. other *Salmonella* included outbreak associated, the final model shown in Supplemental Table 3 excluded this variable; results from the initial and final models were similar.

Supplemental Table 2: Demographic and other characteristics of REPJFX01 compared with non-REPJFX01 infection—Foodborne Diseases Active Surveillance Network (FoodNet), United States, 2016–2020

Characteristics*	REPJFX01† (n=248) No. (%)	Non-REPJFX01 (n=455) No. (%)	Odds ratio (95% CI)	Adjusted odds ratio (95% CI)‡
Age group (y)				
0–4	18 (7.3)	85 (18.7)	Ref	Ref
5–17	16 (6.5)	47 (10.3)	1.61 (0.75, 3.44)	1.23 (0.49, 3.08)
18–44	64 (25.8)	128 (28.1)	2.36 (1.31, 4.26)§	1.59 (0.76, 3.30)
45–64	76 (30.7)	120 (26.4)	2.99 (1.67, 5.36)§	1.93 (0.94, 3.95)
≥ 65	74 (29.8)	75 (16.5)	4.66 (2.55, 8.50)§	2.45 (1.16, 5.15)§
Sex				
Male	74 (30.0)	197 (43.3)	Ref	Ref
Female	173 (70.0)	258 (56.7)	1.79 (1.28, 2.48)§	1.51 (0.99, 2.31)
Race and ethnicity				
White, non-Hispanic (NH)	161 (71.2)	261 (62.7)	Ref	Ref
Black, NH	37 (16.4)	37 (8.9)	1.62 (0.99, 2.66)	1.32 (0.69, 2.53)
Asian, Pacific Islander, NH	3 (1.3)	34 (8.2)	0.14 (0.04, 0.47)§	0.19 (0.05, 0.70)§
Native American, NH	1 (0.4)	5 (1.2)	0.32 (0.04, 2.80)	0.81 (0.09, 7.58)
Multiple, other, unknown race, NH	5 (2.2)	17 (4.1)	0.48 (0.17, 1.32)	0.44 (0.12, 1.67)
Hispanic or Latino	19 (8.4)	62 (14.9)	0.50 (0.29, 0.86)§	0.65 (0.34, 1.27)
Specimen source				
Stool	160 (64.5)	387 (85.2)	Ref	Ref
Blood	8 (3.2)	15 (3.3)	1.29 (0.54, 3.10)	1.63 (0.57, 4.63)
Urine	65 (26.2)	42 (9.3)	3.74 (2.44, 5.75)§	3.33 (1.89, 5.87)§
Other	15 (6.0)	10 (2.2)	3.63 (1.60, 8.25)§	4.24 (1.49, 12.09)§
Year				
2016	5 (2.0)	48 (10.5)	Ref	Ref
2017	35 (14.1)	81 (17.8)	4.15 (1.52, 11.31)§	4.91 (1.52, 15.86)§
2018	63 (25.4)	100 (22.0)	6.05 (2.29, 16.01)§	6.28 (2.02, 19.51)§
2019	88 (35.5)	139 (30.5)	6.08 (2.33, 15.86)§	6.94 (2.27, 21.21)§
2020	57 (23.0)	87 (19.1)	6.29 (2.36, 16.75)§	4.84 (1.53, 15.29)§
Region of residence¶				
Midwest (MN)	36 (14.5)	116 (25.5)	Ref	Ref
Northeast (CT, NY)	103 (41.5)	90 (19.8)	3.69 (2.31, 5.89)§	3.73 (2.12, 6.57)§
South (GA, MD, TN)	63 (25.4)	120 (26.4)	1.69 (1.04, 2.74)§	1.94 (1.05, 3.57)§
West (CA, CO, NM, OR)	46 (18.6)	129 (28.4)	1.15 (0.70, 1.90)	1.09 (0.58, 2.05)
International travel				
No	189 (89.2)	376 (91.5)	Ref	Ref
Yes	23 (10.8)	35 (8.5)	1.31 (0.75, 2.28)	1.63 (0.85, 3.14)
Hospitalized‡				
No	168 (69.4)	341 (77.3)	Ref	
Yes	74 (30.6)	100 (22.7)	1.50 (1.06, 2.14)§	

*The total number of infections (n) are shown for years included; the total number with known data was used as denominator to calculate the percentage of infections for each category. Missing data (shown in **Supplemental Table 6**) were excluded in the univariable and multivariable analyses. Infections were categorized as missing race-ethnicity if ethnicity was missing regardless of race data. International travel was defined as travel outside the United States within the 7 days before illness onset.

†REPJFX01 was defined as *S. Infantis* isolates related by core genome multilocus sequence typing within a range of 0–82 alleles, typically characterized by the presence of pESI megaplasmid harboring multiple resistance genes and *gyrA87* mutation conferring decreased susceptibility to ciprofloxacin.

‡Six variables (age group, sex, race-ethnicity, specimen source, region, and year) that were significant in the univariable analysis and international travel, which has been associated with *Salmonella* infections in previous studies, were considered in the multivariable model. The final model included the 7 variables. Multivariable analyses with hospitalization as dependent variable are shown in **Supplemental Table 3**.

§Odds ratios that do not include 1.00 in the 95% confidence intervals (CIs) were considered statistically significant.

¶The 10 sites in FoodNet were grouped using the 4 U.S. Census regions.

Supplemental Table 3: Multivariable analyses to assess association between hospitalization (as dependent variable) and serotype or strain category, *S. Infantis*, REPJFX01, non-REPJFX01, and other *Salmonella* infections—Foodborne Diseases Active Surveillance Network (FoodNet), 2006–2020

Characteristics*	Adjusted odds ratio (95% CI)*: hospitalized as dependent variable (yes, no) <i>S. Infantis</i> vs. other <i>Salmonella</i> † (2006–2020)	Adjusted odds ratio (95% CI)*: hospitalized as dependent variable (yes, no) REPJFX01‡ vs. other <i>Salmonella</i> † (2016–2020)	Adjusted odds ratio (95% CI)*: hospitalized as dependent variable (yes, no) REPJFX01‡ vs. non-REPJFX01 (2016–2020)
Serotype or strain category			
<i>S. Infantis</i>	0.89 (0.79, 1.00)	-	-
REPJFX01	-	0.97 (0.69, 1.35)	1.27 (0.78, 2.08)
Non-REPJFX01	-	-	Ref
Other <i>Salmonella</i>	Ref	Ref	-
Age group (y)			
0–4	Ref	Ref	Ref
5–17	0.97 (0.91, 1.04)	0.94 (0.83, 1.06)	0.67 (0.24, 1.83)
18–44	1.22 (1.15, 1.30)§	1.18, (1.06, 1.31)§	0.88 (0.40, 1.95)
45–64	2.34 (2.20, 2.48)§	2.33 (2.10, 2.58)§	1.42 (0.67, 3.00)§
≥ 65	4.75 (4.43, 5.08)§	4.21 (3.77, 4.71)§	3.76 (1.76, 8.03)§
Sex			
Male	Ref	Ref	Ref
Female	0.93 (0.90, 0.97)§	0.92 (0.86, 0.98)§	0.65 (0.41, 1.03)
Race and ethnicity			
White, non-Hispanic (NH)	Ref	Ref	Ref
Black, NH	1.57 (1.48, 1.66)§	1.79 (1.62, 1.97)§	1.39 (0.68, 2.84)
Asian, Pacific Islander, NH	0.99 (0.88, 1.10)	1.11 (0.90, 1.35)	0.67 (0.20, 2.26)
Native American, NH	1.76 (1.42, 2.17)§	2.20 (1.56, 3.11)§	0.61 (0.06, 6.67)
Multiple, other, unknown race, NH	0.95 (0.83, 1.09)	1.01 (0.81, 1.26)	1.75 (0.49, 6.21)
Hispanic or Latino	1.44 (1.35, 1.53)§	1.53 (1.38, 1.71)§	0.95 (0.45, 2.00)
Specimen source			
Stool	Ref	Ref	Ref
Blood	11.75 (10.60, 13.02)§	14.03 (11.70, 16.83)§	107.23 (12.17, 944.46)§
Urine	0.37 (0.33, 0.41)§	0.33 (0.28, 0.40)§	0.59 (0.30, 1.17)
Other	3.07 (2.66, 3.55)§	2.42 (1.99, 2.94)§	1.30 (0.46, 3.72)
Region of residence¶			
Midwest (MN)	Ref	Ref	Ref
Northeast (CT, NY)	1.25 (1.16, 1.35)§	1.50 (1.32, 1.71)§	2.10 (1.11, 3.98)§
South (GA, MD, TN)	1.48 (1.39, 1.58)§	1.62 (1.45, 1.81)§	1.60 (0.82, 3.11)
West (CA, CO, NM, OR)	0.89 (0.83, 0.96)§	1.00 (0.88, 1.14)	0.94 (0.46, 1.93)
International travel			
No	Ref	Ref	Ref
Yes	0.45 (0.41, 0.49)§	0.49 (0.43, 0.56)§	0.25 (0.08, 0.80)§
Year group			
2006–2010	Ref	-	-
2011–2015	0.96 (0.91, 1.01)	-	-
2016–2020	0.95 (0.90, 0.99)§	-	-
Year			
2016	-	Ref	Ref
2017	-	0.95 (0.86, 1.06)	0.43 (0.17, 1.05)
2018	-	0.93 (0.84, 1.03)	0.43 (0.18, 1.01)
2019	-	0.97 (0.88, 1.08)	0.39 (0.17, 0.89)§
2020	-	1.05 (0.94, 1.17)	0.77 (0.33, 1.79)

*Categories for missing data (shown in **Supplemental Tables 4 and 6**) were excluded in the multivariable analyses. Infections were categorized as missing race-ethnicity if ethnicity was missing regardless of race data. International travel was defined as travel outside the United States within the 7 days before illness onset. Multivariable analyses to assess association between hospitalization (as dependent variable) and serotype or strain category adjusted for 6 variables (age group, sex, race-ethnicity, specimen source, region, and year or year group) that were significant in the univariable analyses and international travel, which has been associated with *Salmonella* infections in previous studies.

†The 20 most common serotypes were determined from culture-confirmed infections reported during 1996–2020 and included *S. Infantis* and other *Salmonella* serotypes (in descending order): Enteritidis, Typhimurium, Newport, Javiana, I 4,[5],12:i:-, Heidelberg, Muenchen, Montevideo, Saintpaul, Braenderup, Oranienburg, Thompson, Mississippi, Bareilly, Agona, I 13,23:b:-, Paratyphi B var. L(+) Tartrate+, Hadar, and Poona.

‡REPJFX01 was defined as *S. Infantis* isolates related by core genome multilocus sequence typing within a range of 0–82 alleles, typically characterized by the presence of pESI megaplasmid harboring multiple resistance genes and *gyrA87* mutation conferring decreased susceptibility to ciprofloxacin.

§Odds ratios that do not include 1.00 in the 95% confidence intervals (CIs) were considered statistically significant.

¶The 10 sites in FoodNet were grouped using the 4 U.S. Census regions.

Supplemental Table 4: Number and percentage of infections caused by *Salmonella* ser. Infantis and other common *Salmonella* serotypes with missing data on demographic, clinical, and other characteristics—Foodborne Diseases Active Surveillance Network (FoodNet), United States, 2006–2020

Characteristics*	S. Infantis (n=2,363)* No. (%)	Other <i>Salmonella</i> † (n=80,559)* No. (%)
Age group (2006–2020)	0 (0)	33 (0.04)
Sex	3 (0.1)	157 (0.2)
Race and ethnicity	314 (13.3)	13,650 (16.9)
Specimen source	4 (0.2)	377 (0.5)
Year	0 (0)	0 (0)
Region of residence‡	0 (0)	0 (0)
International travel	379 (16.0)	17,944 (22.3)
Hospitalized	91 (3.9)	2,856 (3.5)
Died	88 (3.7)	3,019 (3.7)
Outbreak associated	0 (0)	0 (0)
History of comorbidities (2018–2020), S. Infantis n=630, other <i>Salmonella</i> n=15,034*		
Abdominal surgery	309 (49.0)	6,627 (44.1)
Cancer	249 (39.5)	5,851 (38.9)
Diabetes	252 (40.0)	5,895 (39.2)
Symptoms (2011–2020), S. Infantis n=1,854, other <i>Salmonella</i> n=53,552*		
Fever	430 (23.2)	15,132 (28.3)
Diarrhea	318 (17.2)	11,864 (22.2)
Bloody diarrhea	436 (23.5)	14,802 (27.6)
Antimicrobial use (2017–2020), S. Infantis n=803, other <i>Salmonella</i> n=20,274*	344 (42.8)	9,915 (48.9)

*The total number of infections (n) are shown for years included; the total number with known data was used as denominator to calculate the percentage of infections for each category. Missing data shown here were excluded in the univariable and multivariable analyses comparing S. Infantis vs. other common serotypes. Infections were categorized as missing race-ethnicity if ethnicity was missing regardless of race data. International travel was defined as travel outside the United States within the 7 days before illness onset. The infection was categorized as outbreak associated if the case-patient was part of a recognized outbreak. History of selected comorbidities within the 6 months before illness onset was defined for the following: abdominal surgery (e.g., removal of appendix or gallbladder, any surgery of the stomach or large intestine); diagnosis or treatment for cancer (including leukemia/lymphoma); and diagnosis or treatment for diabetes.

†The 20 most common serotypes were determined from culture-confirmed infections reported during 1996–2020 and included S. Infantis and other *Salmonella* serotypes (in descending order): Enteritidis, Typhimurium, Newport, Javiana, I 4,[5],12:i:-, Heidelberg, Muenchen, Montevideo, Saintpaul, Braenderup, Oranienburg, Thompson, Mississippi, Bareilly, Agona, I 13,23:b:-, Paratyphi B var. L(+) Tartrate+, Hadar, and Poona.

‡The 10 sites in FoodNet were grouped using the 4 U.S. Census regions: Midwest (MN), Northeast (CT, NY), South (GA, MD, TN), and West (CA, CO, NM, OR).

Supplemental Table 5: International travel and destinations of patients with REPJFX01, non-REPJFX01, and other *Salmonella* infections—Foodborne Diseases Active Surveillance Network (FoodNet)*, United States, 2016–2020

International travel and destination*	REPJFX01†	Non- REPJFX01	P value*	Other <i>Salmonella</i> ‡	P value‡
International travel	248	455		25,602	
Yes	23 (10.8)	35 (8.5)	0.34	2,222 (10.5)	0.89
No	189 (89.2)	376 (91.5)		18,849 (89.5)	
Missing*	36 (14.5)	44 (9.7)		4,531 (17.7)	
Destination (yes, n)	23	35		2,222	
Dominican Republic	10 (45.5)	0 (0)	<0.001*	307 (13.9)	<0.001*
South America	9 (40.9)	1 (2.9)		39 (1.8)	
Ecuador, Peru	9	0		15	
Other	0	1		24	
Other§	3 (13.6)	34 (97.1)		1,868 (84.3)	
Missing*	1 (4.4)	0 (0)		8 (0.4)	

*Values are no. (%) or p values unless indicated. The total number of infections with known data was used as denominator to calculate the percentage of infections (i.e., yes, no) for each category. Missing data were excluded (number and percentage shown in italics) to calculate p values using Pearson's chi-square; p <0.5 was considered statistically significant. International travel was defined as travel outside the United States in the 7 days before illness onset. The 10 sites in FoodNet include CA, CO, CT, GA, MD, MN, NM, NY, OR, and TN. The p values shown here were calculated for the comparisons between REPJFX01 and non-REPJFX01 infections.

†REPJFX01 was defined as *S. Infantis* isolates related by core genome multilocus sequence typing within a range of 0–82 alleles, typically characterized by the presence of pESI megaplasmid harboring multiple resistance genes and *gyrA87* mutation conferring decreased susceptibility to ciprofloxacin.

‡The 20 most common serotypes were determined from culture-confirmed infections reported during 1996–2020 and included *S. Infantis* and other *Salmonella* serotypes (in descending order): Enteritidis, Typhimurium, Newport, Javiana, I 4,[5],12:i:-, Heidelberg, Muenchen, Montevideo, Saintpaul, Braenderup, Oranienburg, Thompson, Mississippi, Bareilly, Agona, I 13,23:b:-, Paratyphi B var. L(+) Tartrate+, Hadar, and Poona. The p values shown here were calculated for the comparisons between REPJFX01 and other *Salmonella* infections.

§The 3 other destinations reported among REPJFX01 cases included Cambodia, Canada, and Ghana. The 34 other destinations reported among non-REPJFX01 cases included Mexico (15) and 2 each for Costa Rica, Cuba, Jamaica, and Spain.

Supplemental Table 6: Number and percentage of infections caused by REPJFX01, non-REPJFX01, and other common *Salmonella* serotypes with missing data on demographic, clinical, and other characteristics —Foodborne Diseases Active Surveillance Network (FoodNet), United States, 2016–2020

Characteristics*	REPJFX01† (n=248)* No. (%)	Non-REPJFX01 (n=455)* No. (%)	Other <i>Salmonella</i> ‡ (n=25,602)* No. (%)
Age group (2016–2020)	0 (0)	0 (0)	0 (0)
Sex	1 (0.4)	0 (0)	74 (0.3)
Race and ethnicity	22 (8.9)	39 (8.6)	2,523 (9.9)
Specimen source	0 (0)	1 (0.2)	35 (0.1)
Year	0 (0)	0 (0)	0 (0)
Region of residence§	0 (0)	0 (0)	0 (0)
International travel	36 (14.5)	44 (9.7)	4,531 (17.7)
Hospitalized	6 (2.4)	14 (3.1)	892 (3.5)
Died	7 (2.8)	19 (4.2)	706 (2.8)
Outbreak associated	0 (0)	0 (0)	0 (0)
History of comorbidities (2018–2020), REPJFX01 n=208, non-REPJFX01 n=326, other <i>Salmonella</i> n=15,034*			
Abdominal surgery	128 (61.5)	134 (41.1)	6,627 (44.1)
Cancer	91 (43.8)	111 (34.0)	5,851 (38.9)
Diabetes	89 (42.8)	114 (35.0)	5,895 (39.2)
Symptoms (2016–2020)			
Fever	36 (14.5)	53 (11.6)	4,331 (16.9)
Diarrhea	32 (12.9)	40 (8.8)	3,509 (13.7)
Bloody diarrhea	49 (19.8)	57 (12.5)	4,531 (17.7)
Antimicrobial use (2017–2020), REPJFX01 n=243, non-REPJFX01 n=407, other <i>Salmonella</i> n=20,274*			
	96 (39.5)	148 (36.4)	9,915 (48.9)

*The total number of infections (n) are shown for years included; the total number with known data was used as denominator to calculate the percentage of infections for each category. Missing data shown here were excluded in the univariable and multivariable analyses comparing REPJFX01 vs. other common serotypes. Infections were categorized as missing race-ethnicity if ethnicity was missing regardless of race data. International travel was defined as travel outside the United States within the 7 days before illness onset. The infection was categorized as outbreak associated if the case-patient was part of a recognized outbreak. History of selected comorbidities within the 6 months before illness onset was defined for the following: abdominal surgery (e.g., removal of appendix or gallbladder, any surgery of the stomach or large intestine); diagnosis or treatment for cancer (including leukemia/lymphoma); and diagnosis or treatment for diabetes.

†REPJFX01 was defined as *S. Infantis* isolates related by core genome multilocus sequence typing within a range of 0–82 alleles, typically characterized by the presence of pESI megaplasmid harboring multiple resistance genes and *gyrA87* mutation conferring decreased susceptibility to ciprofloxacin.

‡The 20 most common serotypes were determined from culture-confirmed infections reported during 1996–2020 and included *S. Infantis* and other *Salmonella* serotypes (in descending order): Enteritidis, Typhimurium, Newport, Javiana, I 4,[5],12:i:-, Heidelberg, Muenchen, Montevideo, Saintpaul, Braenderup, Oranienburg, Thompson, Mississippi, Bareilly, Agona, I 13,23:b:-, Paratyphi B var. L(+) Tartrate+, Hadar, and Poona.

§The 10 sites in FoodNet were grouped using the 4 U.S. Census regions: Midwest (MN), Northeast (CT, NY), South (GA, MD, TN), and West (CA, CO, NM, OR).

Supplemental Table 7: Adjusted odds ratios for race-ethnicity stratified by region in the multivariable model* with race-ethnicity and region interaction term, comparing *S. Infantis* infections with other *Salmonella* infections†—Foodborne Diseases Active Surveillance Network (FoodNet)‡, 2006–2020

Race-ethnicity	Adjusted odds ratio (95% CI)			
	Midwest‡ (n=9,003)	Northeast‡ (n=10,625)	South‡ (n=45,776)	West‡ (n=17,518)
White, Non-Hispanic (NH)	Ref	Ref	Ref	Ref
Black, NH	2.34 (1.55, 3.53)§	0.90 (0.60, 1.36)	0.79 (0.62, 1.00)	1.49 (0.96, 2.32)
Asian, Pacific Islander, NH	5.03 (3.56, 7.11)§	1.81 (0.97, 3.39)	0.64 (0.29, 1.45)	4.89 (3.92, 6.10)§
American Indian, NH	0.70 (0.17, 2.85)	1.00 (0.13, 7.58)	1.84 (0.25, 13.59)	1.01 (0.54, 1.87)
Multiple or other/unknown race, NH	2.40 (1.28, 4.52)§	0.74 (0.34, 1.59)	1.51 (0.93, 2.44)	1.99 (1.31, 3.02)§
Hispanic or Latino	2.36 (1.61, 3.44)§	1.42 (1.03, 1.96)§	1.41 (1.03, 1.93)§	1.17 (0.94, 1.45)
Missing, n (% of total for the region)	705 (7.8)	1,524 (14.3)	9,187 (20.1)	2,548 (14.5)

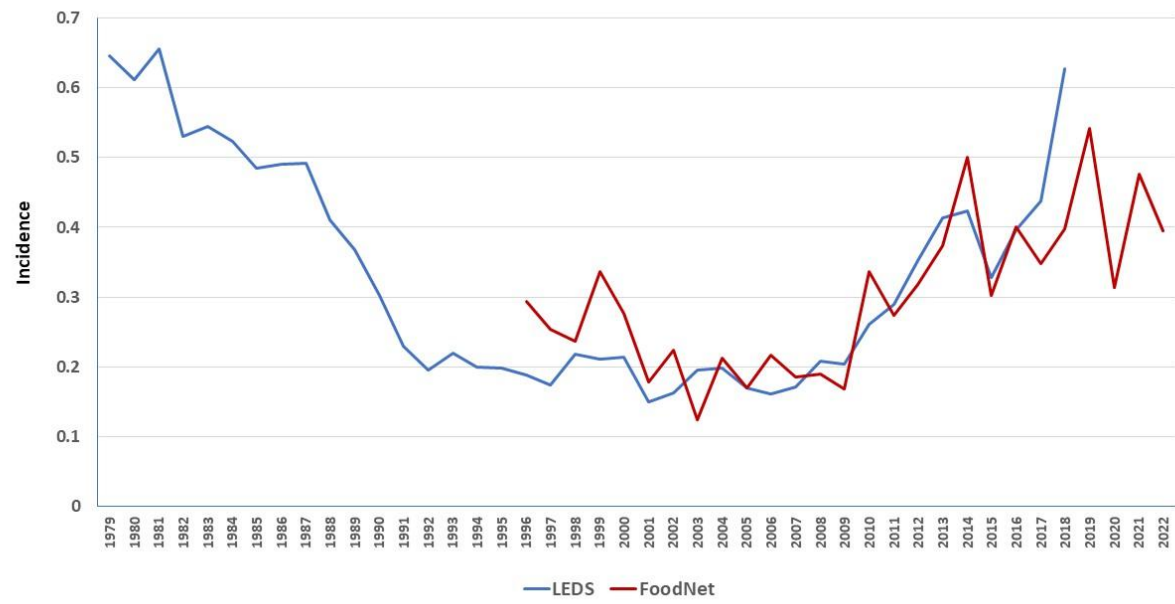
*Model includes age group, sex, race-ethnicity, specimen source, year, region, international travel, outbreak associated, and race-ethnicity and region interaction term. Infections were categorized as missing race-ethnicity if ethnicity was missing regardless of race data.

†20 most common serotypes were determined from culture-confirmed infections reported during 1996–2020 and included *S. Infantis* and other *Salmonella* serotypes (in descending order): Enteritidis, Typhimurium, Newport, Javiana, I 4,[5],12:i:-, Heidelberg, Muenchen, Montevideo, Saintpaul, Braenderup, Oranienburg, Thompson, Mississippi, Bareilly, Agona, I 13,23:b:-, Paratyphi B var. L(+) Tartrate+, Hadar, and Poona.

‡The 10 sites in FoodNet were grouped using the 4 U.S. Census regions: Midwest (MN), Northeast (CT, NY), South (GA, MD, TN), and West (CA, CO, NM, OR).

§Odds ratios that do not include 1.00 in the 95% confidence intervals (CIs) were considered statistically significant.

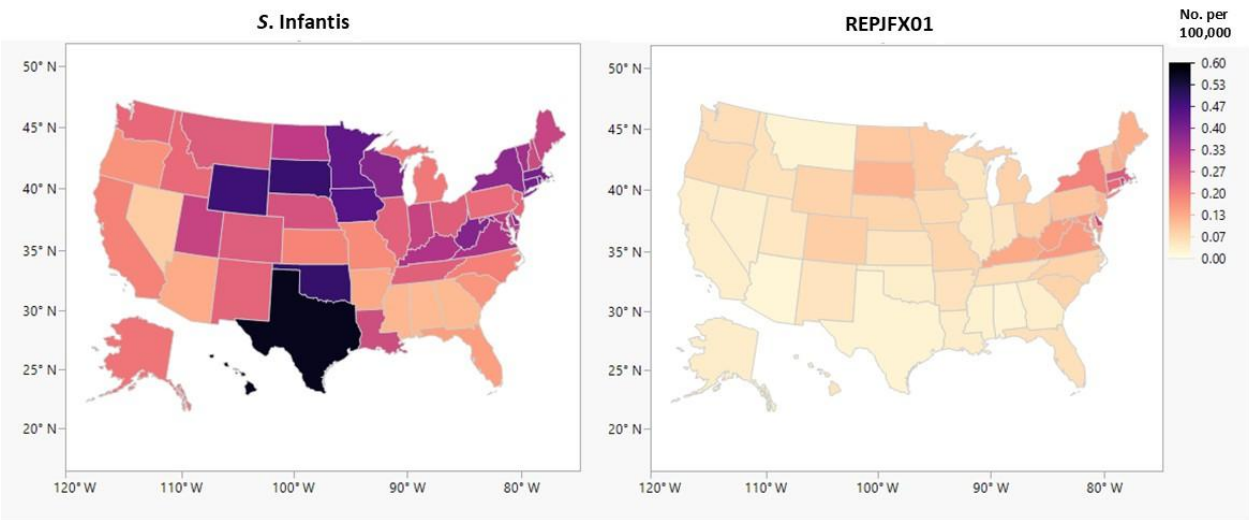
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Supplemental Figure 1: Annual incidence (per 100,000 persons) of *Salmonella ser. Infantis* infections—Laboratory-Based Enteric Disease Surveillance (LEDS) and Foodborne Diseases Active Surveillance Network (FoodNet), 1979–2022. LEDS, established in 1967, receives reports of laboratory-confirmed *Salmonella* infections from public health laboratories in 50 states and participating regional public health laboratories. FoodNet began active surveillance for laboratory-confirmed *Salmonella* infections in 5 sites in 1996 and gradually expanded until 2004 when it stabilized to its current 10-site catchment (CA, CO, CT, GA, MD, MN, NM, NY, OR, TN).

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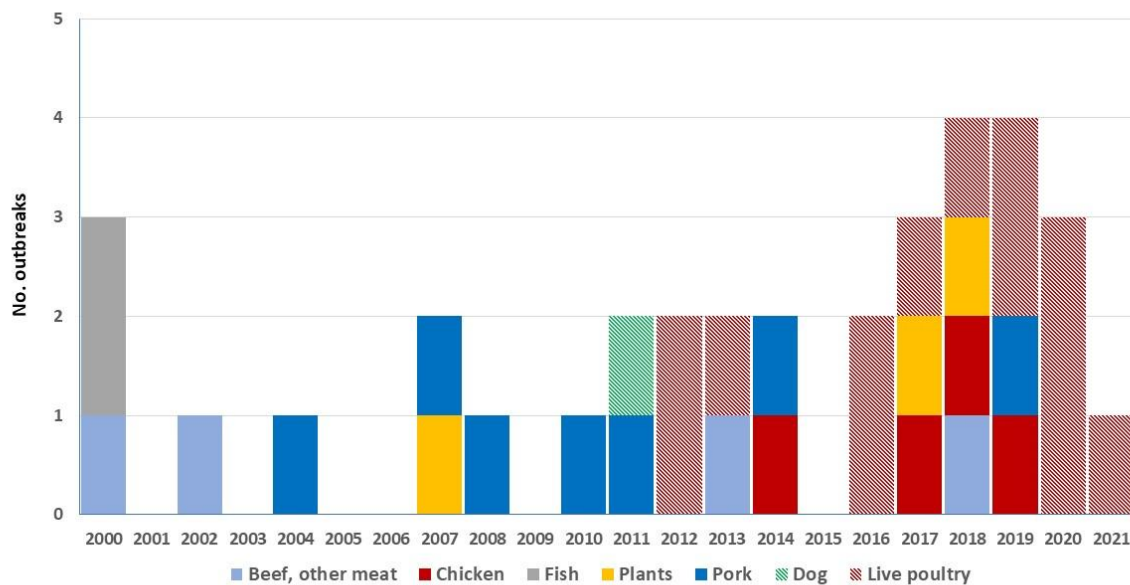
Supplemental Figure 2: Mean annual number of sequenced *Salmonella* ser. *Infantis* and REPJFX01 isolates per 100,000 persons, by state—PulseNet, 2012–2022. REPJFX01 was defined as *Salmonella* *Infantis* isolates related by core genome multilocus sequence typing within a range of 0–82 alleles, typically characterized by the presence of pESI megaplasmid harboring multiple resistance genes and *gyrA87* mutation conferring decreased susceptibility to ciprofloxacin. By state, the mean annual number of *S. Infantis* sequence uploads per 100,000 persons during 2012–2022 ranged from 0.09 (Nevada) to 0.57 (Texas, Hawaii). The mean annual number of REPJFX01 sequence uploads per 100,000 persons ranged from 0.02 (Arizona, Montana) to 0.30 (Rhode Island, Delaware).

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Supplemental Figure 3: Number of sequenced *Salmonella* ser. Infantis isolates and percentage of REPJFX1 isolates, by year— National Antimicrobial Resistance Monitoring System (NARMS), 2012–2022. REPJFX1 was defined as *Salmonella* Infantis isolates related by core genome multilocus sequence typing within a range of 0–82 alleles, typically characterized by the presence of pESI megaplasmid harboring multiple resistance genes and *gyrA87* mutation conferring decreased susceptibility to ciprofloxacin. Percentages of REPJFX1 are not shown for 2012 and 2013 (only 1 isolate was sequenced).



Supplemental Figure 4: Number of *Salmonella* ser. Infantis outbreaks linked to a single food or animal category, by year—National Outbreak Reporting System (NORS), 2000–2021. CDC has received reports of foodborne disease outbreaks to the Foodborne Disease Outbreak Surveillance System electronically since 1998. The reporting platform NORS launched in 2009 to integrate outbreak reporting and includes data on all foodborne and waterborne outbreaks and enteric disease outbreaks transmitted by contact with environmental sources, infected persons or animals, or unknown modes. Information on outbreaks of human enteric illness linked to contact with animals or their environments has been collected through the Animal Contact Outbreak Surveillance System (ACOSS) since 2009. Foodborne outbreaks are shown in solid bars and animal contact outbreaks in hashed bars. Year was based on the earliest date of reported illness onset.