

Original Article

Comparison of the Serovars and Characteristics of *Salmonella* Isolated from Human Feces and Foods in the 1990s and 2010s in Tokyo

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ABSTRACT: *Salmonella* foodborne disease outbreaks have markedly decreased in recent years, and different *Salmonella* serovars have been isolated. To clarify the characteristics of *Salmonella* strains causing annual epidemics and to estimate the source, we conducted a serotyping test on 1,132 human-derived *Salmonella* isolates in the 1990s and 2010s, and 1,061 food-derived *Salmonella* isolates in the 2010s in Tokyo. The serovars commonly isolated from human feces in the 1990s and after 2012 were *S. Enteritidis*, *S. Typhimurium*, *S. Infantis*, *S. Thompson*, and *S. Agona*. The new main serovars isolated after 2012 were *S. Schwarzengrund*, *S. Enterica* serovar 4:i:-, and *S. Chester*. In contrast, the main serovars detected from foods after 2012 were *S. Infantis*, *S. Schwarzengrund*, *S. Agona*, *S. Manhattan*, *S. Typhimurium*, and *S. enterica* serovar UT: r:1,5. *S. Schwarzengrund* has recently been frequently isolated. These strains were mainly isolated from chicken meat and offal. It was suggested that the same serovars of human-derived isolates were also isolated from foods, especially chicken meat and offal, and that these were recently an important causative food of Salmonellosis.

INTRODUCTION

Foodborne outbreaks of *Salmonella* were the leading cause of foodborne illness in the 1990s worldwide (1,2), and more than 800 outbreaks were reported in 1999 in Japan. However, in recent years, such outbreaks have markedly decreased, with fewer than 50 outbreaks nationwide (3), and approximately 5 in Tokyo (4). The number of *Salmonella* outbreaks is markedly lower than that of *Norovirus* or *Campylobacter* foodborne outbreaks.

The major cause of foodborne outbreaks of *Salmonella* in the 1990s was eggs, because the chicks of *Salmonella*-contaminated egg-laying chickens were imported from Europe and the United States (5). The interior of the eggs was contaminated with *Salmonella*, and the contaminated eggs were distributed nationwide.

The major contributing serovar of foodborne outbreaks related to eggs is serogroup O9, *S. Enteritidis*, and the number of these isolates has increased since the latter half of the 1980s, becoming the main causative

serovar of *Salmonella* foodborne outbreaks.

Thereafter, the following prevention measures were implemented nationwide in Japan to reduce *Salmonella* foodborne illness: chicks of hens were inoculated with inactivated *Salmonella* vaccine, eggs were kept at a low temperature during distribution, expiration date labels were restricted, and hygiene management at poultry farms was promoted. As a result, *Salmonella* foodborne illnesses have been decreasing annually since the 2000s, and the number of outbreaks since 2008 has been less than 100 per year in Japan (3). The *Salmonella* contamination rate of eggs in Japan from 2004 to 2006 was 0.03%, but the rate from 2010 to 2011 was estimated to be 0.0029% (6). The decrease in the *Salmonella* contamination rate of eggs was thought to significantly reduced *Salmonella* foodborne illnesses.

Although, *Salmonella* foodborne outbreaks were significantly reduced, but the number of sporadic patients and asymptomatic pathogen carriers did not decrease yearly. *Salmonella* has also been isolated from raw chicken meat (7). It is important to understand the characteristics of isolated human- and food-derived *Salmonella* strains by comparing serovars, an epidemiological analysis method used to estimate the source and route of infection. However, as there are a few such reports, we serotyped human- and food-derived *Salmonella* strains isolated in the 1990s and the 2010s in Tokyo and compared them.

MATERIALS AND METHODS

Strains examined: A total of 1,132 *Salmonella*

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Table 1. Strains used in this study

Year	No. of strains isolated from:			
	Human feces		Foods	
	Sub-total		Sub-total	
1997	75		0	
1998	51	126	0	0
2012	80		80	
2013	93		112	
2014	115	288	116	308
2015	125		148	
2016	137		118	
2017	120	382	128	394
2018	139		134	
2019	143		143	
2020	54	336	82	359
Total	1,132		1,061	

strains isolated from foodborne outbreaks, sporadic cases, and asymptomatic pathogen carriers in Tokyo from 1997 to 1998 (the 1990s) and 9 years from 2012 to 2020 (the 2010s), were examined (Table 1). One representative strain was used when the serovars detected were the same in an outbreak to avoid bias due to the number of isolates in outbreak cases, while, one representative strain of each serovar was used when multiple serovars were detected in one outbreak. A total of 1,061 strains of *Salmonella* isolated from foods examined in outbreak investigations in the 2010s (2012–2020) were included (Table 1).

Identification of serovars: The O antigen was identified by the slide agglutination method using *Salmonella* immune serum (Denka, Tokyo, Japan), and the H antigen was identified by the tube agglutination method using *Salmonella* immune H serum (Denka). The serovars of isolates were determined by referring to “Antigenic Formulae of the *Salmonella* Serovars” (8) based on O and H antigens. Subspecies of *Salmonella* were also determined according to “Antigenic Formulae of the *Salmonella* Serovars” (8).

Ethics statement: This study was approved by the Ethics Review Committee of the Tokyo Metropolitan Institute of Public Health (30kenken782).

RESULTS

O serogroups of *Salmonella* isolates: The O serogroups of the *Salmonella* isolates from humans and food are shown in Table 2. Among the 1997–1998 human isolates, serogroup O9 had the largest proportion at 56.3%, followed by O7 at 19.0%, O4 at 15.9%, and O8 at 4.0%. On the other hand, among the 2018–2020 human isolates, serogroup O4 had the largest proportion at 41.7%, followed by O7 at 23.8%, O8 at 14.9%, and O9 at 8.9%. The most common serogroup of food isolates during the same period (2018–2020) was O4 at 63.8%, followed by O7 (24.0%), O8 (6.4%), and O9 (0.3%). Although the frequency of *Salmonella* O

serogroups isolated from humans and foods changed yearly, both human and food isolates exhibited similar tendencies.

Serovars of *Salmonella* isolated from human feces:

Among the 1,132 human isolates, 1,130 were subspecies I, one was subspecies II, and one was subspecies IIIa. In total, 1,123 strains were serotyped and classified into 99 serovars. Three strains were unable to be O-serotyped, and six were unable to be H-serotyped, including non-motility strains.

To clarify the characteristics of serovars of isolates, each year was summarized as years from 1997 to 1998 (1990s), and every three years from 2012 to 2014, 2015 to 2017, and 2018 to 2020. In the year groups, 23 serovars of 126 strains were isolated between 1997 and 1998, 50 serovars of 288 strains were isolated between 2012 and 2014, and 67 serovars of 382 strains were isolated between 2015 and 2017. Between 2018 and 2020, 62 serovars of 336 strains were detected; thus, more serovars were detected after 2012 than during the 1990s.

The top 20 serovars in each group are listed in Table 3. Serovars commonly isolated in the 1990s and the 2010s were *S. Enteritidis*, *S. Typhimurium*, *S. Infantis*, *S. Thompson*, and *S. Agona*. However, new serovars that were isolated after 2012 were *S. Schwarzengrund*, *S. enterica* serovar 4: i: -, and *S. Chester*.

Among isolates in the 1990s, *S. Enteritidis* was the most frequently detected serovar, accounting for 56.3% of the isolates. The next frequently detected serovar was *S. Typhimurium* (10.3%), and these top two serovars accounted for 66.6% of 1990s isolates. The isolation rate of *S. Enteritidis* was dramatically decreased since 2012, accounting for 18.4% ($P < 0.01$, Fisher’s exact test) of the isolates in the three years from 2012 to 2015, 10.5% in the years from 2015 to 2017, and in the years from 2018 to 2020 was 7.4%. No strain of *S. Schwarzengrund* was isolated in the 1990s, but 17 strains (5.9%, $P < 0.01$) were isolated from 2012 to 2014, 34 strains (8.9%) from 2015 to 2017, and 42 strains (12.5%) from 2018 to 2020. The detection frequency increased significantly in each year. No strain of *S. enterica* serovar 4:i:- was isolated in the 1990s, but 13 strains (4.5%, $P < 0.05$) were isolated from 2012 to 2014, 22 strains (5.8%) from 2015 to 2017, and 24 strains (7.1%) from 2018 to 2020. The detection frequency increased in each year. *S. Chester* has been isolated since 2014. In particular, 11 strains were isolated during 2014, and 13 in 2016, all of which were isolated from sporadic patients.

Serovars of *Salmonella* isolated from foods: Foods were examined for bacteriological pathogens, including *Salmonella*, to detect the causative pathogens of foodborne outbreaks in Tokyo. The most common origin of the 1,061 *Salmonella* isolates used in the present study included chicken meat and chicken offal (1,018 strains), followed by pork offal (15 strains), beef offal (6 strains), unknown meat type (3 strains), and other foods (5 strains).

Only 11 food-derived strains of *Salmonella* were revealed in foodborne outbreaks, and the causative foods were cold vegetable soup, vegetable pickles, white fish meatballs, vegetable salads, raw eggs, grilled pork, green onions, seasoned eggs, and pork fat (Table 4). All 1,061 strains of *Salmonella* isolated from foods

Table 2. O-groups of *Salmonella* isolated from human feces and foods

O-group	No. of isolates from human feces (%)				No. of isolates from foods (%)		
	1997–1998 ¹⁾	2012–2014	2015–2017	2018–2020	2012–2014	2015–2017	2018–2020
O4	20 (15.9)	105 (36.5)	177 (46.3)	140 (41.7)	97 (31.5)	193 (49.0)	229 (63.8)
O7	24 (19.0)	69 (24.0)	85 (22.3)	80 (23.8)	157 (51.0)	131 (33.2)	86 (24.0)
O8	5 (4.0)	37 (12.9)	47 (12.3)	50 (14.9)	21 (6.8)	34 (8.6)	23 (6.4)
O9	71 (56.3)	56 (19.4)	45 (11.8)	30 (8.9)	8 (2.6)	3 (0.8)	1 (0.3)
O3,10	0	7 (2.4)	14 (3.7)	17 (5.1)	1 (0.3)	2 (0.5)	3 (0.8)
O13	0	1 (0.4)	5 (1.3)	8 (2.4)	2 (0.6)	0	0
O1,3,19	1 (0.8)	6 (2.0)	2 (0.5)	3 (0.9)	2 (0.6)	1 (0.3)	0
Others	5 (4.0)	7 (2.4)	7 (1.8)	8 (2.4)	20 (6.6)	30 (7.6)	17 (4.7)
Total	126 (100)	288 (100)	382 (100)	336 (100)	308 (100)	394 (100)	359 (100)

¹⁾: Years for isolation of *Salmonella*.

Table 3. Serovars of *Salmonella* isolated from human feces (Top20) in each year groups

No.	1997–1998		2012–2014		2015–2017		2018–2020	
	Serovar	No. of isolates (%)	Serovar	No. of isolates (%)	Serovar	No. of isolates (%)	Serovar	No. of isolates (%)
1	Enteritidis	71 (56.3)	Enteritidis	53 (18.4)	Infantis	47 (12.3)	Schwarzengrund	42 (12.5)
2	Typhimurium	13 (10.3)	Infantis	40 (13.9)	Enteritidis	40 (10.5)	Enteritidis	25 (7.4)
3	Infantis	7 (5.6)	Typhimurium	27 (9.4)	Schwarzengrund	34 (8.9)	Serovar 4: i : -	24 (7.1)
4	Thompson	5 (4.0)	Schwarzengrund	17 (5.9)	Saintpaul	26 (6.8)	Infantis	22 (6.5)
5	Singapore	3 (2.4)	Saintpaul	14 (4.9)	Chester	23 (6.0)	Typhimurium	19 (5.7)
6	Virchow	3 (2.4)	Serovar 4: i : -	13 (4.5)	Serovar 4: i : -	22 (5.8)	Agona	18 (5.4)
7	Corvallis	3 (2.4)	Chester	11 (3.8)	Typhimurium	20 (5.2)	Thompson	18 (5.4)
8	Agona	2 (1.6)	Manhattan	11 (3.8)	Stanley	19 (5.0)	Newport	16 (4.8)
9	Brandenburg	2 (1.6)	Thompson	10 (3.5)	Agona	17 (4.5)	Chester	11 (3.3)
10	Othmarschen	2 (1.6)	Agona	8 (2.8)	Thompson	17 (4.5)	Stanley	9 (2.7)
11	Champaign	2 (1.6)	Senftenberg	6 (2.1)	Newport	11 (2.9)	Braenderup	9 (2.7)
12	Waycross	2 (1.6)	Litchfield	5 (1.7)	Manhattan	9 (2.4)	Corvallis	7 (2.1)
13	Bredeney	1 (0.8)	Nagoya	5 (1.7)	Anatum	8 (2.1)	Mbandaka	6 (1.8)
14	Derby	1 (0.8)	Bareilly	4 (1.4)	Litchfield	7 (1.8)	Manhattan	6 (1.8)
15	Haifa	1 (0.8)	Braenderup	4 (1.4)	Bareilly	5 (1.3)	Saintpaul	5 (1.5)
16	Mikawasima	1 (0.8)	Newport	4 (1.4)	Blockley	4 (1.0)	Bareilly	5 (1.5)
17	Montevideo	1 (0.8)	Derby	3 (1.0)	Brandenburg	3 (0.8)	Oranienberg	5 (1.5)
18	Potsdam	1 (0.8)	Serovar 4: ch : -	3 (1.0)	Reading	3 (0.8)	Bovismorbificans	5 (1.5)
19	Tennessee	1 (0.8)	Montevideo	3 (1.0)	Virchow	3 (0.8)	Panama	5 (1.5)
20	Hadar	1 (0.8)	Rissen	3 (1.0)	Muenchen	3 (0.8)	Anatum	5 (1.5)
	Others	3 (2.4)	Others	44 (15.3)	Others	61 (16.0)	Others	74 (22.0)
	(3 serovars)		(30 serovars)		(47 serovars)		(42 serovars)	
	Total	126 (100)		288 (100)		382 (100)		336 (100)

were subspecies I. Among them, 992 strains were classified into 38 serovars, 65 strains could not be typed for the O-serogroup, and 4 strains were unable to be H-typed because of non-motility.

Regarding the serovars of *Salmonella* detected in year groups, 23 types were detected in 2012–2014, 23 types were detected in 2015–2017, and 27 types were detected in 2018–2020. The top 20 serovars of each 3-year group are shown in Table 5. The serovars commonly detected in all year groups were *S. Infantis*, *S. Schwarzengrund*, *S. Agona*, *S. Manhattan*, *S. Typhimurium*, and *S. enterica* serovar UT: r: 1,5.

The number of isolations or the isolation rate of *S. Schwarzengrund* was 41 (13.3%) from 2012 to 2014, 125 (31.7%) from 2015 to 2017, and 184 (51.3%) from 2018 to 2020, markedly increasing each year groups ($P < 0.01$).

The number of isolations or the isolation rate of *S. Infantis*, which was the most frequently detected strain accounting for 152 (49.4%) from 2012 to 2014, decreased to 125 (31.7%, $P < 0.01$) from 2015 to 2017, and to 76 (21.2%, $P < 0.05$) from 2018 to 2020.

The isolation or the isolation rate of *S. Typhimurium* also decreased to 21 (6.8%) from 2012 to 2014, to 9

The Serovars and Characteristics of *Salmonella*

Table 4. *Salmonella* foodborne outbreaks in which same serovar of *Salmonella* isolated both from patients and associated foods

Outbreak No.	Year	Serovar of <i>Salmonella</i>	Associated food
1	2013	Typhimurium	Cold vegetable soup, vegetable pickles
2	2013	Enteritidis	White fish meatball
3	2014	Enteritidis	Vegetable salads
4	2014	Enteritidis	Raw eggs
5	2015	Stanley	Grilled pork, green onions, seasoned egg
6	2016	Serovar 4: i: -	Pork fat ¹⁾

¹⁾: *S. Bredeney* and *S. Derby* were also isolated.

Table 5. Serovars of *Salmonella* isolated from foods (Top20) in each year groups

No.	2012–2014		2015–2017		2018–2020	
	Serovar	No. of isolates (%)	Serovar	No. of isolates (%)	Serovar	No. of isolates (%)
1	Infantis	152 (49.4)	Schwarzengrund	125 (31.7)	Schwarzengrund	184 (51.3)
2	Schwarzengrund	41 (13.3)	Infantis	125 (31.7)	Infantis	76 (21.2)
3	Agona	24 (7.8)	Agona	45 (11.4)	Agona	24 (6.7)
4	Typhimurium	21 (6.8)	Serovar UT: r : 1,5	26 (6.6)	Manhattan	12 (3.3)
5	Serovar UT: r : 1,5	18 (5.8)	Manhattan	17 (4.3)	Serovar UT: r : 1,5	10 (2.8)
6	Manhattan	17 (5.5)	Blockley	16 (4.1)	Serovar 4: i : -	7 (1.9)
7	Enteritidis	8 (2.6)	Typhimurium	9 (2.3)	Blockley	7 (1.9)
8	Derby	4 (1.3)	Heidelberg	4 (1.0)	Typhimurium	6 (1.7)
9	Bredeney	3 (1.0)	Derby	3 (0.8)	Thompson	4 (1.1)
10	Serovar 4: i : -	3 (1.0)	Stanley	3 (0.8)	Serovar UT:d:1.7	4 (1.1)
11	Oranienberg	2 (0.6)	Colindale	3 (0.8)	Serovar 4: -	3 (0.8)
12	Corvallis	2 (0.6)	Enteritidis	3 (0.8)	Rissen	3 (0.8)
13	Senftenberg	2 (0.6)	Serovar UT: d:1,7	3 (0.8)	Anatum	3 (0.8)
14	Havana	2 (0.6)	Serovar 4: i : -	2 (0.5)	Brandenburg	2 (0.6)
15	Saintpaul	1 (0.3)	Anatum	2 (0.5)	Stanley	2 (0.6)
16	Braenderup	1 (0.3)	Bredeney	1 (0.3)	Bredeney	1 (0.3)
17	Montevideo	1 (0.3)	Serovar 4: -	1 (0.3)	Derby	1 (0.3)
18	Singapore	1 (0.3)	Tennessee	1 (0.3)	Bareilly	1 (0.3)
19	Dusseldorf	1 (0.3)	Virchow	1 (0.3)	Hato	1 (0.3)
20	Yovokome	1 (0.3)	Serovar 7: - : 1,5	1 (0.3)	Corvallis	1 (0.3)
	Others (3 serovars)	3 (1.0)	Others (3 serovars)	3 (0.8)	Others (7 serovars)	7 (1.9)
	Total	308 (100)	Total	394 (100)	Total	359 (100)

(2.3%, $P < 0.01$) from 2015 to 2017, and to 6 (1.7%) from 2018 to 2020.

Only 8 strains (2.6%) of *S. Enteritidis*, which was in the top position in the 1990s, were isolated from 2012 to 2014, 3 strains (0.8%) were in 2017. *S. Enteritidis* was not isolated between 2018 and 2020. *S. Enteritidis* was detected in the foods during 2012–2017, including white fish meatballs, vegetable salads, eggs, minced chicken balls, seasoned chicken thighs, chicken offal (liver and cartilage), and pork tongue.

DISCUSSION

Although the number of *Salmonella* strains isolated or collected in one year varies, 51–143 human-derived strains and 80–148 food-derived strains have been

examined each year. Especially, in 2020, both human- and food-derived strains decreased significantly to 37.8% and 57.3% of the previous year's isolation numbers, respectively. As many people refrained from eating at restaurants due to the new coronavirus infection (COVID-19) epidemic, the decrease in foodborne illness in Tokyo similar to Japan (3), reduced the number of foodborne bacterial diseases isolates. In addition, the decrease in the number of outbreak investigations also affected the number of isolates.

In the latter half of the 1990s, *Salmonella* foodborne outbreaks occurred frequently worldwide, and the number of *Salmonella* outbreaks in Japan exceeded 500 in one year (3). In Tokyo, 26 outbreaks occurred in 1997 and 21 in 1998 (4). Many of the causative foods of *Salmonella* foodborne illness are related to eggs, such

as the consumption of raw eggs (Tamagokake-gohan, Japanese dish), homemade mayonnaise, yams with raw eggs (Tororo imo, Japanese dish), insufficiently heated processed egg dishes, or secondary contamination from eggs (9). The causative organism of most *Salmonella* foodborne outbreaks related to eggs was *S. Enteritidis*, and 56.3% of human-derived strains in the 1990s were *S. Enteritidis* in this study. *S. Enteritidis* still accounts for the highest rate of isolates based on the isolation status of human-derived strains since 2012, but its proportion is decreasing yearly. This tendency was consistent with the "Infectious Agents Surveillance Report" by the National Institute of Infectious Disease, Japan (10).

After 2012, human-derived strains were classified into more than 50 serovars each year, which was greater than the number of serovars in the 1990s when *S. Enteritidis* was mainly isolated. On the other hand, the food-derived strains after 2012 were classified into less than 27 serovars each year, with fewer than human-derived strains. They were mainly isolated from raw chicken meat or chicken offal, and the serovars of the *Salmonella* isolates were specific. *Salmonella* serovar Schwarzengrund, *S. Infantis*, *S. Agona*, *S. Manhattan*, *S. enterica* serovar UT: r:1,5, and *S. Typhimurium* were ranked high and were always included in the top 10 serovars among food-derived strains. The strains of these six serovars accounted for 86.9% to 88.6% in all year groups since 2012. In a study of isolates from chicken meat in Tokyo during 1992–2012 by Katoh et al., *S. Infantis* was the most prevalent (65.4%), but the isolation rates of *S. Typhimurium* (4.2%), *S. Manhattan* (2.5%), *S. Schwarzengrund* (1.9%), and *S. Agona* (1.5%) were low (7).

As the recent reports on the serovars of *Salmonella* isolates from food-producing animals are scarce. Nippon AMR One Health Report (NAOR) 2020 showed that the serovars of *Salmonella* isolated from diseased food-producing animals between 2014 and 2018 were as follows: the most prevalent serovars were *S. enterica* serovar 4:i:- (33.8%) and *S. Typhimurium* (33.8%) in cattle, *S. Typhimurium* (42.4%) and *S. enterica* serovar 4:i:- (22.1%) in pigs, and *S. Schwarzengrund* (31.3%) and *S. Infantis* (18.8%) in chickens, respectively (11). Serovars such as *S. Infantis*, *S. Schwarzengrund*, and *S. Typhimurium* were frequently isolated from foods in this study, mainly raw chicken meat and chicken offal, and were also ranked high among human-derived strains. In particular, the appearance and increase in *S. Schwarzengrund* in both food- and human-derived strains after 2012 were characteristic. These results suggest that chicken meat and offal are important causative foods of *Salmonella* foodborne illnesses.

Regarding foodborne outbreaks caused by *Salmonella* in recent years in Japan, foods other than eggs such as grilled eel, sashimi (raw fish), vegetable salads with chicken meat, cherry tomatoes, and salads, have been identified. The serovars of the causative strains included *S. Typhimurium*, *S. Enteritidis*, *S. Agona*, *S. Stanley*, *S. Saintpaul*, *S. Bredeney*, *S. Derby*, and *S. enterica* serovar 4:i:-. Different foods have been considered the cause of foodborne outbreaks in recent years, rather than the widespread distribution of specific causative foods, such as eggs in the 1990s, and are related to the diversity of serovars of human-derived strains.

In the United States, foodborne illness source attribution estimates for *Salmonella* using multi-year outbreak surveillance data (12) were as follows: over 75% of cases were attributed to seven food categories: chicken meat; seeded vegetables such as tomatoes, pork, fruits, other produce, eggs, and turkey. The credibility intervals for each of the seven food categories that accounted for 75.6% of all cases overlapped. The trends in Japan are similar to those in the United States.

S. enterica serovar 4 [5], 12: i: - strain, was reported as a monophasic mutant of *S. Typhimurium* (13), and its incidence has increased in Spain, Asia, and the United States since the late 1990s (10,14,15). In Tokyo, several strains of this serovar have been isolated every year since its first isolation in 1998, and there have been three outbreaks of foodborne illness and sporadic cases caused by this serovar in 2009. Although the causative food was not identified, it was presumed to be pork offal because it was detected at a high rate in pork offal (16). Since 2012, the detection rate of this serovar has increased, but the source of the infection remains unclear.

Although serovar Chester was not isolated from humans between 1997 and 1998, 11 strains (3.8%) were isolated between 2012 and 2014, 23(6.0%) between 2015 and 2017, 11(3.3%) between 2018 to 2020, respectively. An increase in the incidence of this serovar has been observed. However, no common sources of infection have been identified in epidemiological studies. In addition, Ando et al. (17) conducted a detailed analysis using whole genome sequencing (WGS) because the isolation rates of *S. Chester* increased in the Kanto region, including Tokyo, Chiba, Ibaraki Prefectures, and Yokohama City, between 2014 and 2016. Based on their analysis, the infection had not spread via human-human transmission, but possible foods causing the disease have not been identified. Although an epidemic of this serovar of salmonellosis associated with travel to Morocco was also reported in Europe at the same time (18), the strains causing the epidemic in the Kanto region differed from those in Moroccan.

Since 1999, the Tokyo Metropolitan Government has been conducting the "Enteropathogenic Bacteria Carrier Surveillance" as one of its own projects. The target organisms for this surveillance were enterohemorrhagic *Escherichia coli* and *Salmonella*. In the asymptomatic pathogen carrier survey of food handlers, 547,992 stool samples were examined for *Salmonella* during the 10 years from 2011 to 2020, and the number of positive samples was 237 (0.043%) (19). Although *Salmonella* foodborne outbreaks have reduced, the number of asymptomatic pathogen carriers of *Salmonella* has not significantly decreased, and the source of infection in asymptomatic persons is unknown. Other than food, companion animals such as dogs and cats are also considered sources of infection. Some sporadic patients were suspected of being infected by companion animals, but the infection route was unclear.

As gastroenteritis caused by *Salmonella* is not a controlled disease under Japan's Infectious Diseases Control Law, the number of infected persons each year is unclear. Although more than 100 isolates are collected annually in Tokyo, the number of collected

strains is considered a part of the actual number of infected persons. It is also important to compare the overseas distribution status and epidemic serovars. For a more detailed analysis of organisms, it is necessary to perform a WGS analysis. However, as much information can be obtained from serovars, it is necessary to continue conducting serotyping analyses and collecting information on *Salmonella* isolated from humans and foods.

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Conflict of interest None to declare.

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