Salmonella enterica serotypes from human and nonhuman sources in Sao Paulo State, Brazil, 2004-2020

Sueli Aparecida Fernandes[1], Ana Terezinha Tavechio[1], Ângela Cristina Rodrigues Ghilardi[1], Elisabete Aparecida de Almeida[1], Josefa Maria Lopes da Silva[1], Carlos Henrique Camargo[1], Monique Ribeiro Tiba-Casas[1]

ABSTRACT

Salmonellosis ranks among the most frequently reported zoonosis worldwide and is often associated with foodborne outbreaks. Since the 1950s, the distribution of *Salmonella* serotypes in Sao Paulo State, Brazil, has been documented and periodically reported. In this study, we updated the data on the distribution of *Salmonella* serotypes received in our reference laboratory, isolated from human infections and nonhuman sources, from 2004 to 2020. In that period, a total of 9,014 *Salmonella* isolates were analyzed, of which 3,553 (39.4%) were recovered from human samples, mainly of stool (65%) and blood (25.6%), and 5,461 (60.6%) were isolated from nonhuman origins, such as animals (47.2%), food (27.7%) and animal environments (18.6%). In human isolates, a total of 104 serotypes were identified and the most frequent ones were Enteritidis, Typhimurium, *S*. I. 4,[5],12:i:-, Dublin and Typhi. A consistent reduction of the Enteritidis proportion was observed over the years. Among the 156 serotypes identified in isolates with nonhuman origins, Enteritidis, Mbandaka, Typhimurium, Agona and Anatum were ranked as the top five *Salmonella* serotypes; in more recent years, *S*. Heidelberg has increased in frequency. Although with different proportions, the top 10 prevalent serotypes were identified in both human and nonhuman origins, underscoring the role of animals, food products and environment as reservoirs of *Salmonella* with potential to cause human salmonellosis.

KEYWORDS: Salmonellosis. *Salmonella*. Human. Nonhuman. Serotype. Serotyping.

INTRODUCTION

Salmonella enterica is commonly acquired from contaminated food and non-typhoidal *Salmonella* (NTS) is an important worldwide cause of human foodborne infections, such as gastroenteritis and bacteremia[1,2]. Outbreaks of foodborne disease due to *Salmonella* are continually reported in many parts of the world[3,4]. Currently, more than 2,500 serotypes of *S. enterica* have been identified; however, most human infections are caused by a limited number of serotypes[5].

Changes in the prevalence of specific strain types and serotypes in human and animal populations may follow the introduction of the strain through international travel, human migration, food, animal feed, and livestock trade, underscoring the role of One Health in this pathogen[1]. The *Salmonella* serotypes may differ in their natural reservoirs, their geographic and seasonal distributions, and their ability to cause human infection[5]. Numerous reservoirs and the capacity for environmental persistence give *Salmonella* multiple entry points into the human population. A wide variety of animals, particularly animals for human nutrition, have been identified as reservoirs for non-typhoidal *Salmonella* (NTS) serotypes[1,6].

[1]Instituto Adolfo Lutz, Centro de Bacteriologia, São Paulo, São Paulo, Brazil

Correspondence to: Monique Ribeiro Tiba-Casas
Instituto Adolfo Lutz, Centro de Bacteriologia, Av. Dr. Arnaldo, 355, 9º Andar, CEP 01246-902, São Paulo, SP, Brazil.
Tel: +55-11-30682896

E-mail: monique.casas@ial.sp.gov.br

Most of the information regarding the prevalence of *Salmonella* has been provided by laboratorial surveillance, especially serotyping data that allow broad comparisons and identify trends, reservoirs and routes of transmission of *Salmonella* serotypes[5,7]. In Sao Paulo State, Brazil, the identification of *Salmonella* serotypes has been conducted by the Laboratory of Enteric Pathogens in Adolfo Lutz Institute since 1950, and the obtained data have been showing the significant changes in the epidemiology of salmonellosis in our region over the past years[7-9].

In this study, we evaluated the trends on distribution and prevalence of *Salmonella* serotypes isolated from clinical human and nonhuman sources in Sao Paulo State, Brazil, updating the data until 2020.

MATERIALS AND METHODS

Bacterial isolates

In this study, we analyzed 9,014 *Salmonella* isolates from human infections and nonhuman sources, received from 2004 to 2020 for serotyping at Institute Adolfo Lutz, a reference laboratory for public health in Brazil. These isolates had been isolated and presumptively identified in private and public hospitals, local public health, animal pathology and food microbiology laboratories from different geographic locations of the Sao Paulo State.

The 3,553 clinical non-duplicate *Salmonella* isolates were mainly from: stool (2,306), blood (913), cerebrospinal fluid (CSF) (28), urine (164) and other body fluids or unspecified origins (142). The other 5,461 *Salmonella* isolates were representative of the nonhuman sources, isolated from animals (2,578), mostly from poultry, pigs and bovine; food (1,510), including food-producing animals and other foodstuffs; environment (1,016), mainly poultry and pig environments; and other unspecified sources (357). The distribution of the human and nonhuman sources of *Salmonella* isolates are detailed in Figure 1.

Biochemical identification and serotyping

First, all isolates were confirmed to be of the genus
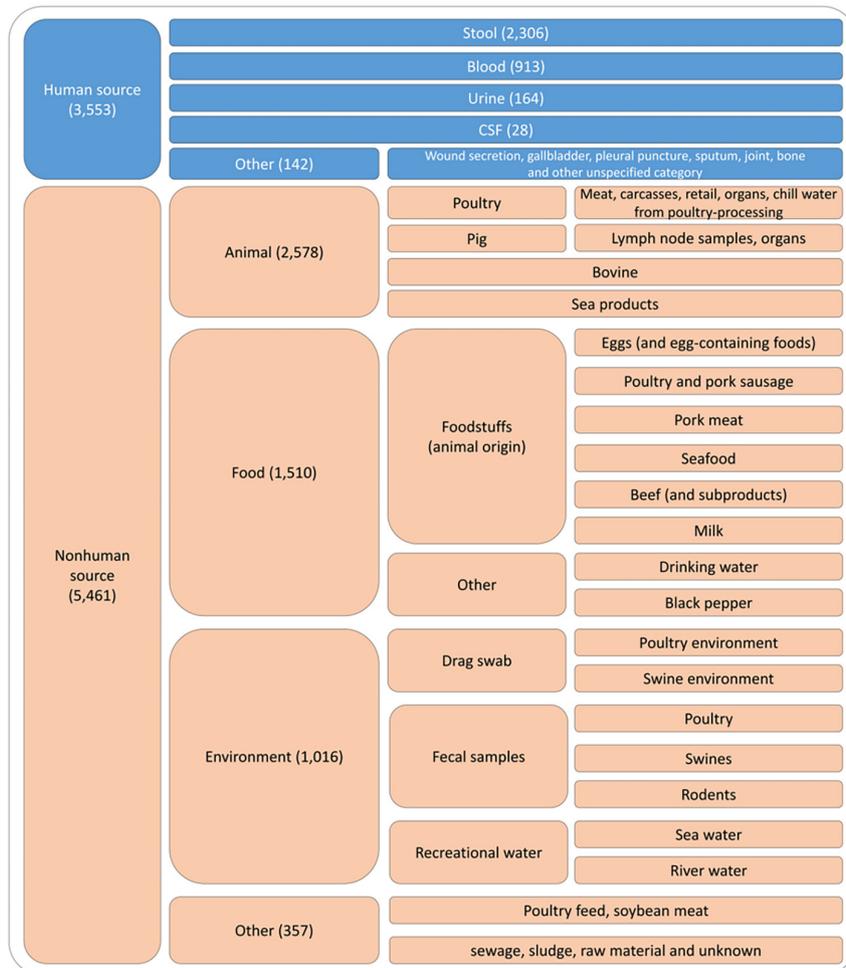
Figure 1 - Distribution of human and nonhuman sources of *Salmonella* isolates, 2004-2020 (n=9,014).

Salmonella based on conventional biochemical tests[10] and the subspecies level determination was based on biochemical characteristics of addition[11]. The *Salmonella* serotyping was performed according to the 9th edition of the White-Kauffmann-Le Minor scheme[11-13], on the basis of somatic O and H flagellar antigens by agglutination tests with antisera (prepared in the Laboratory of Enteric Pathogens, Adolfo Lutz Institute, Sao Paulo).

Data analysis

The results are presented in frequency and, for statistical analysis, three time periods were created: P1, comprising isolates from 2004-2008; P2, with isolates from 2009-2014; and P3, with isolates from 2015-2020. The chi-squared test was used to compare frequencies with the OpenEpi websever, and a P value < 0.05 was considered significant.

RESULTS

Salmonella serotypes from human sources

During the last 17-year laboratorial surveillance period, from 2004 to 2020, a total of 104 different serotypes were identified among 3,512 *Salmonella* isolates from human infection, another 41 "rough" strains were not serotyped (Supplementary Table S1).

The top ten identified serotypes: *S*. Enteritidis, *S*. Typhimurium, variant monophasic *S*. Typhimurium (*S*. I. 4,[5],12:i:-), *S*. Dublin, *S*. Typhi, *S*. Newport, *S*. Saintpaul,

S. Infantis, *S*. Panama and *S*. Javiana accounted for 2,464 (77.0%) of the strains.

These serotypes — except *S*. Typhi and *S*. Dublin, which were mostly detected in blood samples (93% and 81%, respectively) — were the most frequent serotypes identified from stool, blood, urine and CFS samples. The distribution of serotypes associated with human source isolation is presented in Figure 2.

S. Enteritidis was the most frequently reported *Salmonella* serotype in human infections, accounting for 41.9% (1,489) of all isolates, followed by *S*. Typhimurium with 11.4% (406), and *S*. I. 4,[5],12:i:- with 7.7% (275). By comparing the frequencies of main serotypes over the analyzed periods, a strong and significant decline was observed for *S*. Enteritidis (p < 0.05), while other serotypes presented a consistent growth in their frequencies (notably *S*. Typhimurium, *S*. Dublin, and *S*. Schwarzengrund – Figure 3, Supplementary Table S2).

Salmonella serotypes from nonhuman sources

A total of 156 different serotypes were identified among the 5,461 *Salmonella* isolates from nonhuman origins, excluding 107 "rough" *Salmonella* strains (Supplementary Table S3).

The isolation source and annual distribution of the most prevalent serotypes are presented in Figures 4 and 5. Despite the high diversity of serotypes detected, the majority of isolates were limited to just a few serotypes. The top 10 most prevalent *Salmonella* serotypes (Enteritidis, Mbandaka, Typhimurium, Agona, Anatum, Senftenberg, Heidelberg,
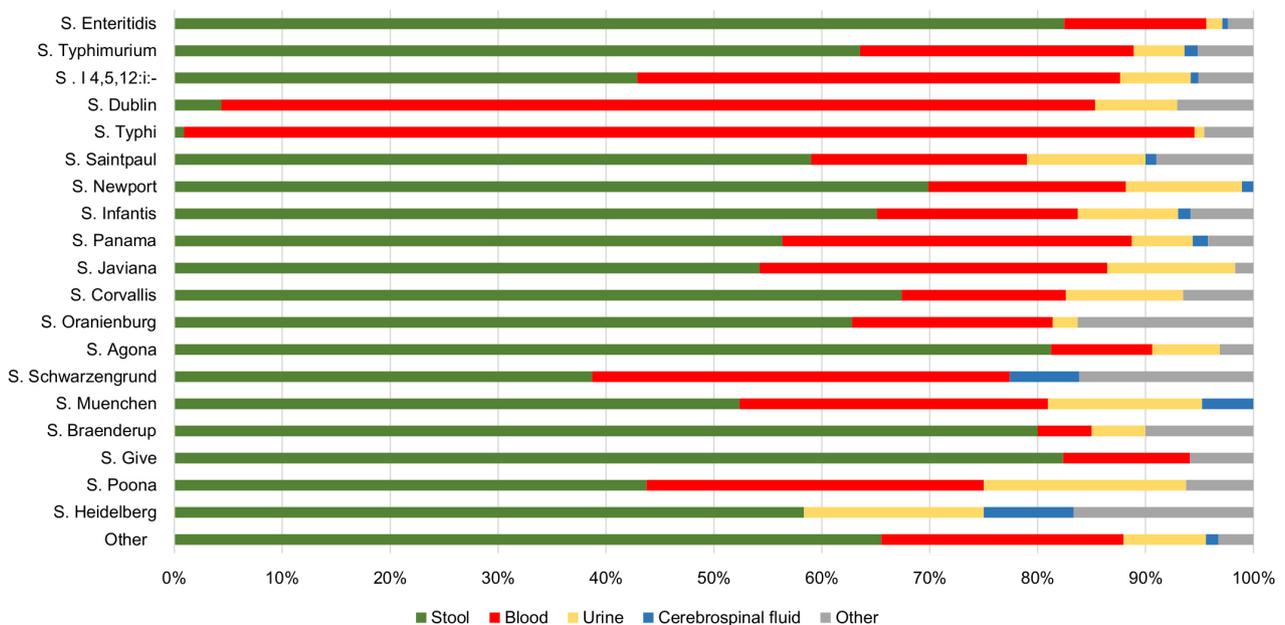
Figure 2 - Distribution of the most frequent *Salmonella* serotypes according to human sources.

S. I. 4,[5],12:i:-, Infantis and Saintpaul) accounted for 47.5% (2,592) of the total isolates recovered from food, animals, and the environment.

A strong reduction in the isolation ratio of *S*. Enteritidis was observed between the periods P1 and P2 ($p < 0.05$), and remained consistently low in the most recent years (P3). The

Human serotypes (n)	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	Total (%)
S. Enteritidis (1489)	58	68	74	59	53	40	39	35	40	34	20	9	17	18	12	10	18	42
S. Typhimurium (406)	10	8	8	8	11	14	13	14	10	12	13	23	12	11	13	16	7	11
S. I 4,[5],12:i:- (275)	5	5	1	7	6	6	7	14	11	13	12	8	12	8	6	8	11	8
S. Dublin (184)	2	0	2	2	5	5	7	3	4	10	16	10	5	9	11	6	7	5
S. Typhi (110)	2	2	2	5	3	1	1	1	1	1	1	3	0	14	9	8	8	3
S. Saintpaul (99)	3	1	0	2	3	5	2	3	2	2	5	3	6	7	3	3	2	3
S. Newport (93)	3	2	1	2	3	2	2	1	4	2	8	5	5	1	3	4	3	3
S. Infantis (86)	0	1	1	3	0	2	2	2	2	2	3	3	8	3	6	6	3	2
S. Panama (71)	1	1	1	0	3	1	2	3	2	2	0	3	4	2	3	6	8	2
S. Javiana (59)	1	1	1	1	1	1	1	0	1	1	3	3	3	1	3	6	6	2
S. Corvallis (46)	3	1	0	1	1	2	2	2	0	2	0	1	1	0	1	2	1	1
S. Oranienburg (43)	0	1	1	0	1	0	1	2	1	3	4	0	1	2	3	1	1	1
S. Agona (32)	0	2	0	1	2	0	0	2	1	0	1	1	2	0	2	2	0	1
S. Schwarzengrund (31)	0	0	0	0	0	1	2	1	1	0	0	2	1	2	4	3	1	1
S. Muenchen (21)	0	0	0	0	0	0	0	1	1	2	3	2	1	0	0	1	1	1
S. Mbandaka (14)	0	0	1	0	0	0	0	0	1	0	1	0	1	0	0	1	1	0
S. Heidelberg (12)	0	0	0	0	0	0	0	0	0	0	2	0	0	1	1	1	1	0
S. Anatum (10)	0	0	0	0	0	0	0	0	0	0	1	2	1	0	1	0	1	0
Other (472)	10	6	6	8	8	19	20	16	17	12	6	21	19	23	18	17	21	13
Total (3553) (%)	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100

Figure 3 - Heatmap showing the annual frequency of the most prevalent human *Salmonella* serotypes.
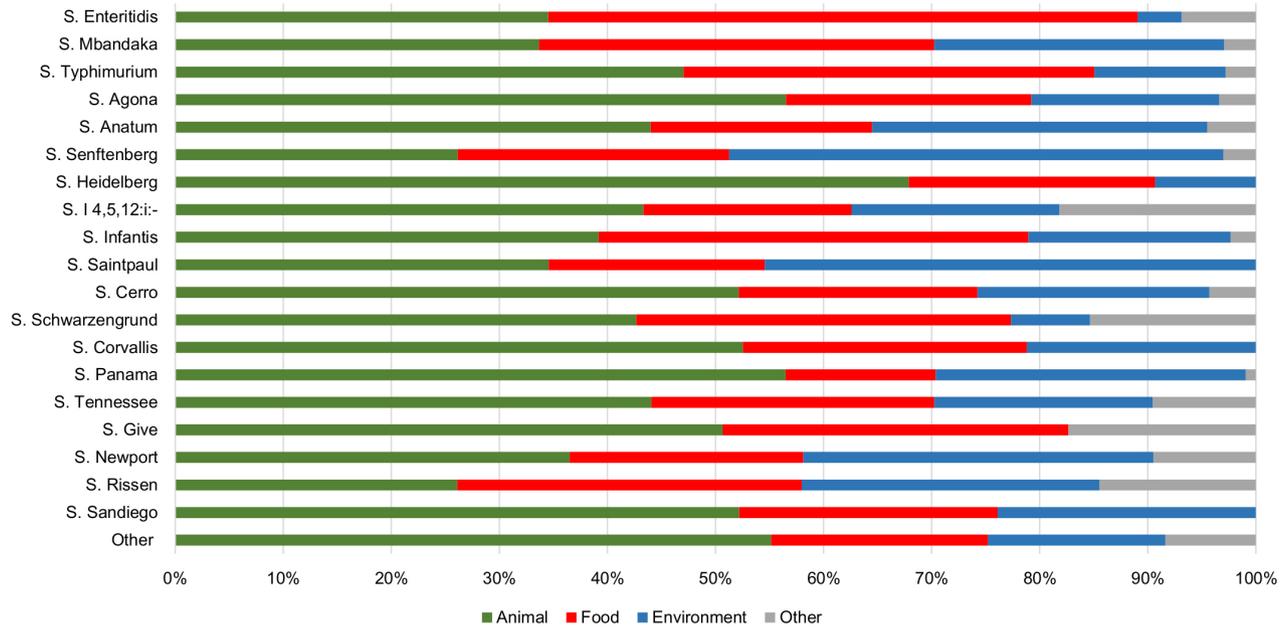

Figure 4 - Distribution of the most frequent *Salmonella* serotypes according to nonhuman sources.

Non-human serotypes (n)	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	Total (%)
S. Enteritidis (539)	24	12	13	15	11	6	6	1	8	4	3	1	20	7	2	0	3	10
S. Mbandaka (410)	10	17	5	8	8	12	6	6	5	3	2	1	2	1	9	18	16	8
S. Typhimurium (321)	2	8	5	8	7	8	6	4	3	4	9	15	5	3	5	4	1	6
S. Agona (207)	6	2	0	1	1	1	4	12	4	4	0	15	1	0	1	2	0	4
S. Anatum (200)	5	3	1	3	4	2	6	5	4	4	10	5	1	0	0	2	0	4
S. Senftenberg (199)	3	3	3	6	8	9	4	2	3	3	1	3	1	1	2	0	1	4
S. Heidelberg (193)	1	1	1	0	2	1	1	0	1	0	8	3	5	24	30	5	5	4
S. I 4,[5],12:i:- (187)	1	2	1	2	4	5	1	3	4	4	4	6	17	5	1	1	12	3
S. Infantis (171)	2	4	2	4	3	4	3	5	4	3	0	6	4	2	1	1	1	3
S. Saintpaul (165)	7	3	1	1	1	1	2	13	1	3	0	0	0	4	1	7	1	3
S. Cerro (163)	2	1	3	2	2	2	4	4	4	5	5	0	4	0	5	3	6	3
S. Schwarzengrund (150)	3	2	1	1	1	2	11	1	2	8	0	3	1	0	4	0	5	3
S. Corvallis (118)	0	3	1	2	2	4	0	6	2	5	6	1	0	0	1	3	2	2
S. Panama (108)	1	0	0	1	1	1	0	0	0	8	15	3	0	1	1	2	3	2
S. Tennessee (84)	1	2	3	4	1	2	2	1	1	1	1	0	0	0	1	2	0	2
S. Newport (74)	1	1	1	1	2	3	1	0	2	3	1	1	0	1	0	1	5	1
S. Gallinarum (59)	0	2	5	0	0	0	0	0	3	2	0	1	0	8	0	2	1	1
S. Muenchen (39)	1	0	0	0	1	0	0	0	2	1	0	0	0	1	0	5	8	1
S. Pullorum (28)	0	1	4	0	0	0	0	1	0	0	0	1	0	2	0	0	0	1
Other (2046)	27	36	48	40	41	37	42	37	47	35	34	36	38	40	37	45	29	37
Total (5461) (%)	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100

Figure 5 - Heatmap showing the annual frequency of the most prevalent nonhuman *Salmonella* serotypes.

same pattern was observed for *S*. Mbandaka. Conversely, the frequency of *S*. Typhimurium increased only in P3 compared to P2 and P1, as also observed for *S*. Heidelberg, the serotype with the highest increase in frequency among nonhuman sources (Figure 5, Supplementary Table S4).

Comparison of *Salmonella* serotypes from different sources

When we compared the results of serotype prevalence in human and nonhuman *Salmonella* isolates (Figure 6), we observed that *S*. Enteritidis, *S*. Typhimurium, *S*. I. 4,[5],12:i:-, *S*. Saintpaul, *S*. Infantis, *S*. Newport and *S*. Panama were frequently detected in both origins. On the contrary, *S*. Mbandaka was the second most commonly isolated from nonhuman origins (7.5%), but only rarely isolated from humans (0.4%).

The additional statistical data analysis showed that *S*. Saintpaul, *S*. Panama, and *S*. Muenchen were homogeneously found in human and nonhuman sources (p > 0.05). While *S*. Enteritidis, *S*. Typhimurium, *S*. I 4,[5],12:i:-, and *S*. Newport were more frequently found in human specimens (p < 0.05), the other eight serotypes (*S*. Mbandaka, *S*. Infantis, *S*. Agona, *S*. Anatum, *S*. Heidelberg, *S*. Schwarzengrund, *S*. Corvallis, and *S*. Give) were mainly recovered from nonhuman sources (p < 0.05).

DISCUSSION

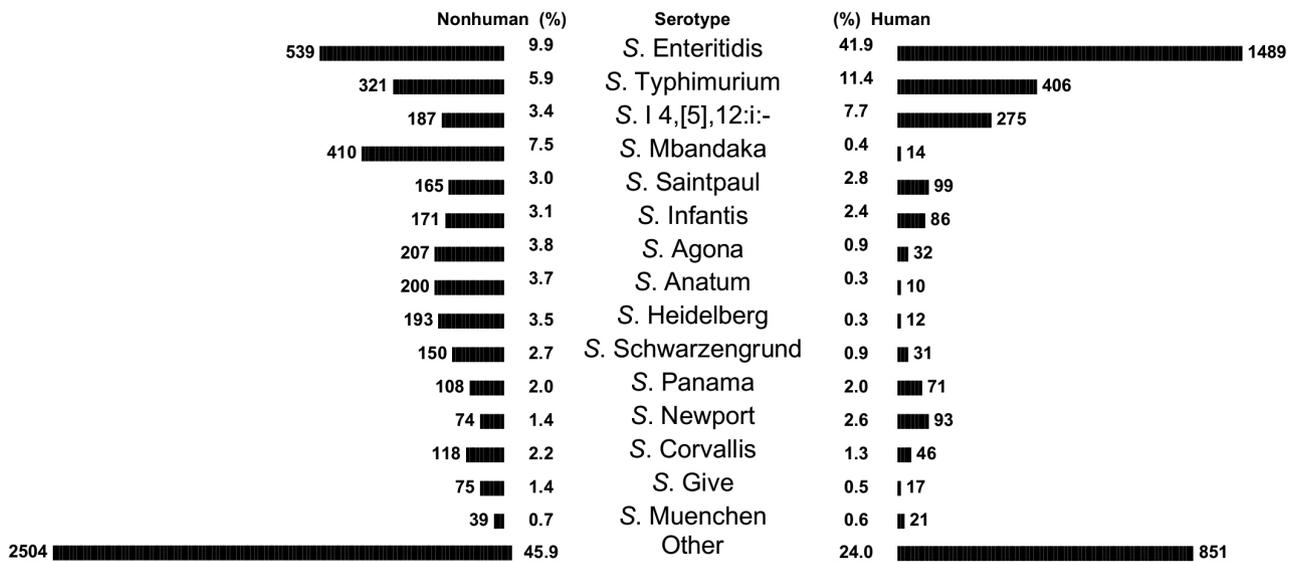This study integrates data of the distribution of *Salmonella enterica* serotypes identified among human infections, animals, food products and the environment in Sao Paulo State, Brazil.

Distribution of *Salmonella* serotypes from human infections

Our findings indicate that no significant change was detected in the prevalence of the three main serovars isolated from humans (*S*. Enteritidis, *S*. Typhimurium and *S*. I. 4,[5],12:i:-) when compared to previous studies in the State of Sao Paulo, Brazil[7,9]. *S*. Enteritidis and *S*. Typhimurium are the two most important NTS serotypes transmitted from animal to human infections reported in most parts of the world[3,6,14-17].

In Sao Paulo State, a remarkable increase of human *S*. Enteritidis frequency was observed in 1994, mainly associated with foodborne disease outbreaks and sporadic gastrointestinal disease[7,18]. *S*. Enteritidis remained the most commonly reported serotype worldwide, especially associated with foodborne outbreaks[19]. However, in this study, a major decrease in *S*. Enteritidis frequency was observed over the years, from 73.6% in 2006 to 19.9% in 2014. Similar patterns have been reported in the USA and Europe[1,20]. The decrease in the proportion of *S*. Enteritidis in humans may reflect the ongoing efforts made to control its spread through eggs by implementing quality-assurance programs.

S. Typhimurium and *S*. I. 4,[5],12:i:-, a variant of *S*. Typhimurium, were respectively the second and third most prevalent serotypes detected in clinical samples in this study. *S*. Typhimurium has a well-characterized ability to infect various species which can survive for a long time in

Nonhuman	(%)	Serotype	(%)	Human
539	9.9	*S*. Enteritidis	41.9	1489
321	5.9	*S*. Typhimurium	11.4	406
187	3.4	*S*. I 4,[5],12:i:-	7.7	275
410	7.5	*S*. Mbandaka	0.4	14
165	3.0	*S*. Saintpaul	2.8	99
171	3.1	*S*. Infantis	2.4	86
207	3.8	*S*. Agona	0.9	32
200	3.7	*S*. Anatum	0.3	10
193	3.5	*S*. Heidelberg	0.3	12
150	2.7	*S*. Schwarzengrund	0.9	31
108	2.0	*S*. Panama	2.0	71
74	1.4	*S*. Newport	2.6	93
118	2.2	*S*. Corvallis	1.3	46
75	1.4	*S*. Give	0.5	17
39	0.7	*S*. Muenchen	0.6	21
2504	45.9	Other	24.0	851

Figure 6 - Frequency of the common serotypes identified in *Salmonella* isolates recovered from human and nonhuman sources in Sao Paulo, Brazil, 2004-2020 (n=9,014).

the environment, enhancing its ability to be one of the most common causes of salmonellosis[15]. *S.* Typhimurium are important foodborne pathogens in all parts of the world[6,20].

S. I 4,[5],12:i:- was first reported in the 1980s, with an increased prevalence since the late 1990s in humans and animals, especially in Europe and the Unites States[21], and also in Brazil[7,22]. *S.* I. 4,[5],12:i:- has been responsible for an increasing number of foodborne outbreaks, attributed to pigs and pork products and frequently associated with the emergence of the multidrug-resistant phenotype[21,23].

The majority of the NTS isolates evaluated in this study were recovered from gastrointestinal diseases (64.9%). However, a significant percentage (32.1%) of *Salmonella* infections was recovered from extra intestinal sources. The frequency of serotypes *S.* Dublin, *S.* Typhimurium and *S.* I. 4,[5],12:i:- were notably high in extra intestinal sources, which may require antimicrobial treatment. This fact is of public health concern, considering that over the years an increasing proportion of *Salmonella enterica* have acquired antimicrobial resistance — especially the extended-spectrum B-Lactamases (ESBL) that produces *Salmonella* serotypes from both clinical and nonhuman sources, as also reported in our region[24-26], indicating a reduction in the available drug options for patient treatment..

The typhoidal *Salmonella* serotypes are known to cause different clinical manifestations in comparison to NTS infections. Here, we identified that *S.* Typhi, ranked as the fifth most prevalent serotype from human sources, is mainly isolated from septicemia infections. Although the proportion of isolates has decreased over the years (2004-2016), *S.* Typhi re-emerged in 2017, when cluster cases of typhoidal fever were reported in Sao Paulo city, Brazil, affecting 14 people, including infants[26]. *S.* Typhi remains endemic in developing countries typically associated with poor sanitation and a weaker healthcare system[1,7,8]. *S.* Saintpaul rose from tenth to sixth position; *S.* Newport and *S.* Javiana appeared among the ten most identified serotypes, while *S.* Agona and *S.* Corvallis are out of this rank when compared to those reported in the last period (1996-2003)[7]. A distinct difference between the isolates in this new period was the increase of the *S.* Newport and *S.* Javiana serotypes among the human isolates.

Distribution of *Salmonella* serotypes from nonhuman sources

Among the various 156 serotypes identified in nonhuman isolates of this study, *Salmonella* Enteritidis was the most frequent, but with a decline in its frequency in recent years. *S.* Enteritidis is the most frequent cause of salmonellosis worldwide, which can be associated with eggs and contaminated poultry consumption, as identified in Europe and the USA[14,17]. However, recent studies have revealed that, in addition to eggs, foodstuffs including meat, chicken, vegetables, and dairy products played a significant role in causing SE disease outbreaks all over the USA between 1990 and 2015[27].

Salmonella Mbandaka, the second most prevalent serotype in this study, was extensively detected in poultry meat, particularly poultry carcasses, as well as in isolates from animals environment. This finding is in agreement with previous reports that described the presence of this serotype in such sources, as well as in connection with foodborne outbreaks[28,29]. In our region, *S.* Senftenberg was the second most detected serotype strain in the 1990s, losing its position to *S.* Mbandaka which is currently the second most detected serotype. *Salmonella* Mbandaka has been identified by the CDC as an important outbreak-causing serotype of *Salmonella* and it has been reported as a cause of human salmonellosis in several countries, making this serotype globally important for human and animal health[28,30]. Studies have shown that this serotype has rarely been reported and is currently adapted for multi-host propagation[30]. According to outbreak investigation reports, *S.* Mbandaka can originate from both live animals and processed food. The increase of *S.* Mbandaka in this last period of 2004-2020, ranking second among animal, food and environmental strains, showed evidence that the increase of this serotype requires epidemiological monitoring. Thus, efforts should be focused on the elaboration of efficient strategies in order to control the expansion of this serovar, to substantially avoid economic loss. These results also provide a baseline for future comparisons.

The Typhimurium serotype – which is not only known for infecting poultry and pigs, but also acts as a potential agent for human gastroenteritis – was found to be the third most prevalent serovar during the study period. As in other studies, *S.* Typhimurium and *S.* I. 4,[5],12:i:- were also detected in both animal and food samples[14], and ranked from fifth to third when comparing the present results with our previous studies on nonhuman strains.

S. Heidelberg, which was not frequently detected, is now among the top ten frequently identified serotypes, mainly associated with poultry samples. *Salmonella* Heidelberg ranks among the most prevalent causes of human salmonellosis in the United States[16] and Canada[31]. In the last few years, the *S.* Heidelberg serotype has also emerged in various countries such as Argentina[32], Brazil[33] and Europe[20]. This serotype has been observed in other studies[32,33] and has also been involved in foodborne outbreaks[34]. The increasing isolation of *S.* Heidelberg, as well as its antimicrobial

resistance in our region[35], highlights its emergence, spread and maintenance in the environment, and reinforces the need to improve measures for prevention and surveillance.

When comparing the present results with our previous studies[7,9,18] we see, over the years, especially more recently, an increase in the prevalence of *Salmonella* serotypes among nonhuman isolates in Sao Paulo State such as *S.* Mbandaka, *S.* Anatum, *S.* Heidelberg and *S.* Saintpaul, with the decline of *S.* Senftenberg and *S.* Hadar. These results also provide a baseline for future comparisons for *Salmonella* epidemiological surveillance.

CONCLUSION

Regarding the results detected in both human infection and nonhuman sources, *S.* Enteritidis and *S.* Typhimurium remain the most frequent in Sao Paulo State, Brazil, which are the two most important NTS serotypes transmitted from animal to human in most parts of the world. The top five serotypes most commonly found in nonhuman sources – *S.* Enteritidis, *S.* Typhimurium, *S.* I. 4,[5],12:i:-, *S.* Infantis and *S.* Saintpaul – were also ranked as the most frequent, associated with more than 65% of human disease over the period studied. Nevertheless, other serotypes common in nonhuman sources, such as *S.* Anatum, *S.* Agona, *S.* Schwarzengrund, *S.* Corvallis, *S.* Muenchen and *S.* Heidelberg, were also detected in human infections, but in a comparative reduced frequency.

The data presented here support the established importance of animals, food products and the environment as sources of salmonellosis. The overall similarity between the types and frequencies of serotypes isolated in humans and nonhuman sources is consistent with other studies that hypothesize that animals might serve as reservoirs for salmonellosis. *Salmonella* serotyping remains an important laboratory tool that helps public health researchers to better understand and define the epidemiology of salmonellosis in a geographic area. The measurement of trends in serovars over time can provide information about emerging serotypes and about the efficacy of prevention and control measures.

CONFLICT OF INTERESTS

The authors declare no conflict of interests.

FUNDING

REFERENCES

1. Hendriksen RS, Vieira AR, Karlsmose S, Lo Fo Wong DM, Jensen AB, Wegener HC, et al. Global monitoring of Salmonella serovar distribution from the World Health Organization Global Foodborne Infections Network Country Data Bank: results of quality assured laboratories from 2001 to 2007. Foodborne Pathog Dis. 2011;8:887-900.

2. Scallan E, Hoekstra RM, Angulo FJ, Tauxe RV, Widdowson MA, Roy SL, et al. Foodborne illness acquired in the United States: major pathogens. Emerg Infect Dis. 2011;17:7-15.

3. Majowicz SE, Musto J, Scallan E, Angulo FJ, Kirk M, O'Brien SJ, et al. The global burden of nontyphoidal Salmonella gastroenteritis. Clin Infect Dis. 2010;50:882-9.

4. European Food Safety Authority, European Centre for Disease Prevention and Control. The European Union One Health 2018 Zoonoses Report. EFSA J. 2019;17:5926.

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

6. Simpson KM, Hill-Cawthorne GA, Ward MP, Mor SM. Diversity of Salmonella serotypes from humans, food, domestic animals and wildlife in New South Wales, Australia. BMC Infect Dis. 2018;18:623.

7. Fernandes SA, Tavechio AT, Ghilardi AC, Dias AM, Almeida IA, Melo LC. Salmonella serovars isolated from humans in São Paulo State, Brazil, 1996-2003. Rev Inst Med Trop Sao Paulo. 2006;48:179-84.

8. Taunay AE, Fernandes SA, Tavechio AT, Neves BC, Dias AM, Irino K. The role of public health laboratory in the problem of salmonellosis in São Paulo, Brazil. Rev Inst Med Trop Sao Paulo. 1996;38:119-27.

9. Tavechio AT, Ghilardi AC, Peresi JT, Fuzihara TO, Yonamine EK, Jakabi M, et al. Salmonella serotypes isolated from nonhuman sources in São Paulo, Brazil, from 1996 through 2000. J Food Prot. 2002;65:1041-4.

10. Ewing WH. Edwards and Ewing's identification of Enterobacteriaceae. 4th ed. New York: Elsevier Science; 1986.

11. Grimont PA, Weil FX. Antigenic formulae of the Salmonella serovars. 9th ed. Paris : Institut Pasteur; 2007.

12. Guibourdenche M, Roggentin P, Mikoleit M, Fields PI, Bockemühl J, Grimont PA, et al. Supplement 2003-2007 (No. 47) to the White-Kauffmann-Le Minor scheme. Res Microbiol. 2010;161:26-9.

13. Issenhuth-Jeanjean S, Roggentin P, Mikoleit M, Guibourdenche M, Pinna E, Nair S, et al. Supplement 2008-2010 (no. 48)

to the White-Kauffmann-Le Minor scheme. Res Microbiol. 2014;165:526-30.

14. Dewey-Mattia D, Manikonda K, Hall AJ, Wise ME, Crowe SJ. Surveillance for foodborne disease outbreaks: United States, 2009-2015. MMWR Surveill Summ. 2018;67:1-11.

15. Powell MR, Crim SM, Hoekstra RM, Williams MS, Gu W. Temporal patterns in principal Salmonella serotypes in the USA: 1996-2014. Epidemiol Infect. 2018;146:437-41.

16. Luvsansharav UO, Vieira A, Bennett S, Huang J, Healy JM, Hoekstra RM, et al. Salmonella serotypes: a novel measure of association with foodborne transmission. Foodborne Pathog Dis. 2020;17:151-5.

17. Sarno E, Pezzutto D, Rossi M, Liebana E, Rizzi V. A review of significant European foodborne outbreaks in the last decade. J Food Prot. 2021;84:2059-70.

18. Tavechio AT, Fernandes SA, Neves BC, Dias AM, Irino K. Changing patterns of Salmonella serovars: increase of Salmonella Enteritidis in São Paulo, Brazil. Rev Inst Med Trop Sao Paulo. 1996;38:315-22.

19. Zhang Y, Liu K, Zhang Z, Tian S, Liu M, Li X, et al. A Severe gastroenteritis outbreak of salmonella enterica serovar enteritidis linked to contaminated egg fried rice, China, 2021. Front Microbiol. 2021;12:779749.

20. European Food Safety Authority, European Centre for Disease Prevention and Control. The European Union One Health 2019 Zoonoses Report. EFSA J. 2021;19:6406.

21. Elnekave E, Hong S, Mather AE, Boxrud D, Taylor AJ, Lappi V, et al. Salmonella enterica serotype 4,[5],12:i:- in swine in the United States Midwest: an emerging multidrug-resistant clade. Clin Infect Dis. 2018;66:877-85.

22. Tavechio AT, Ghilardi AC, Fernandes SA. Multiplex PCR identification of the atypical and monophasic Salmonella enterica subsp. enterica serotype 1,4,5,12:i:- in São Paulo State, Brazil: frequency and antibiotic resistance patterns. Rev Inst Med Trop Sao Paulo. 2004;46:115-7.

23. Tavechio AT, Fernandes SA, Ghilardi AC, Soule G, Ahmed R, Melles CE. Tracing lineage by phenotypic and genotypic markers in Salmonella enterica subsp. enterica serovar 1,4,[5],12:i:- and Salmonella Typhimurium isolated in state of São Paulo, Brazil. Mem Inst Oswaldo Cruz. 2009;104:1042-6.

24. Fernandes SA, Paterson DL, Ghilardi-Rodrigues AC, Adams-Haduch JM, Tavechio AT, Doi Y. CTX-M-2-producing Salmonella Typhimurium isolated from pediatric patients and poultry in Brazil. Microb Drug Resist. 2009;15:317-21.

25. Fernandes SA, Camargo CH, Francisco GR, Bueno MF, Garcia DO, Doi Y, et al. Prevalence of extended-spectrum β-Lactamases CTX-M-8 and CTX-M-2-producing salmonella serotypes from clinical and nonhuman isolates in Brazil. Microb Drug Resist. 2017;23:580-9.

26. Tiba-Casas MR, Sacchi CT, Gonçalves CR, Almeida EA, Soares FB, Bertani AM, et al. Molecular analysis of clonally related Salmonella Typhi recovered from epidemiologically unrelated cases of typhoid fever, Brazil. Int J Infect Dis. 2019;81:191-5.

27. Sher AA, Mustafa BE, Grady SC, Gardiner JC, Saeed AM. Outbreaks of foodborne Salmonella enteritidis in the United States between 1990 and 2015: an analysis of epidemiological and spatial-temporal trends. Int J Infect Dis. 2021;105:54-61.

28. Hoszowski A, Zając M, Lalak A, Przemyk P, Wasyl D. Fifteen years of successful spread of Salmonella enterica serovar Mbandaka clone ST413 in Poland and its public health consequences. Ann Agric Environ Med. 2016;23:237-41.

29. Bonifait L, Thépault A, Baugé L, Rouxel S, Le Gall F, Chemaly M. Occurrence of salmonella in the cattle production in France. Microorganisms. 2021;9:872.

30. Antony L, Fenske G, Kaushik RS, Nagaraja TG, Thomas M, Scaria J. Population structure of Salmonella enterica serotype Mbandaka reveals similar virulence potential irrespective of source and phylogenomic stratification. F1000Res. 2020;9:1142.

31. Dutil L, Irwin R, Finley R, Ng LK, Avery B, Boerlin P, et al. Ceftiofur resistance in Salmonella enterica serovar Heidelberg from chicken meat and humans, Canada. Emerg Infect Dis. 2010;16:48-54.

32. Dominguez JE, Viñas MR, Herrera M, Moroni M, Gutkind GO, Mercado EC, et al. Molecular characterization and antimicrobial resistance profiles of Salmonella Heidelberg isolates from poultry. Zoonoses Public Health. 2021;68:309-15.

33. Voss-Rech D, Kramer B, Silva VS, Rebelatto R, Abreu PG, Coldebella A, et al. Longitudinal study reveals persistent environmental Salmonella Heidelberg in Brazilian broiler farms. Vet Microbiol. 2019;233:118-23.

34. Paphitis K, Pearl DL, Berke O, McEwen SA, Trotz-Williams L. Detection of spatial and spatio-temporal Salmonella Heidelberg and Salmonella Typhimurium human case clusters focused around licensed abattoirs in Ontario in 2015, and their potential relation to known outbreaks. Zoonoses Public Health. 2021;68:609-21.

35. Tiba-Casas MR, Camargo CH, Soares FB, Doi Y, Fernandes SA. Emergence of CMY-2-producing salmonella Heidelberg associated with IncI1 plasmids isolated from poultry in Brazil. Microb Drug Resist. 2019;25:271-6.