Salmonella serovars associated with human salmonellosis in Brazil (2011-2020)

Sorovares de *Salmonella* associados com Salmonelose humana no Brasil (2011-2020)

Serovariedades de *Salmonella* asociadas a salmonelosis humana en Brasil (2011-2020)

André Felipe das Mercês Santos
ORCID: https://orcid.org/0000-0002-7067-2852
Oswaldo Cruz Institute, Brazil
E-mail: andrefelipemercessantos@gmail.com
Laura Fabiana Vieira Amparo
ORCID: https://orcid.org/0000-0002-7444-3774
Oswaldo Cruz Institute, Brazil
E-mail: laurafabiana-amparo@hotmail.com
Simone da Costa Alves Machado
ORCID: https://orcid.org/0000-0002-4617-4239
Fluminense Federal University, Brazil
E-mail: machado.sca@gmail.com
Thomas Salles Dias
ORCID: https://orcid.org/0000-0001-8815-3316
Fluminense Federal University, Brazil
E-mail: thomassalles@id.uff.br
Lucia Helena Berto
ORCID: https://orcid.org/0000-0001-6653-0002
Ministry of Health, Brazil
E-mail: lucia.berto@saude.gov.br
Dayse Lima da Costa Abreu
ORCID: https://orcid.org/0000-0002-9705-1909
Fluminense Federal University, Brazil
E-mail: dayse.abreu@idd.uff.br
Maria Helena Cosendey de Aquino
ORCID: https://orcid.org/0000-0001-8729-909X
Fluminense Federal University, Brazil
E-mail: mhcaquino@idd.uff.br
Dália dos Prazeres Rodrigues
ORCID: https://orcid.org/0000-0003-1101-5518
Oswaldo Cruz Institute, Brazil
E-mail: daliarodrigues@yahoo.com.br
Virginia Léo de Almeida Pereira
ORCID: https://orcid.org/0000-0003-2197-8916
Fluminense Federal University, Brazil
E-mail: virginialeo@idd.uff.br

Abstract
Salmonella is one of the major foodborne pathogens worldwide. Domestic, wild animals, and a variety of food matrices can transmit *Salmonella* spp. to human*S*. Here, we report the top 10 *Salmonella* serovars isolated from human sources between 2011 and 2020 and received in the National Reference Laboratory for Enteric Disease*S*. Serotyping was performed according to the Kauffman-White scheme. 3113 isolates related to human cases belonging to 61 serogroups were received in the NRL between 2011 and 2020. The purpose of this article is the identification of circulating serotypes as the first step to understanding the epidemiology, and then, with this information, take actions to mitigate and control this pathogen.
Keywords: Foodborne disease; *Salmonella*; Serotyping.

Resumo
Salmonella é um dos principais patógenos de origem alimentar em todo o mundo. Animais domésticos, selvagens e uma variedade de matrizes alimentares podem transmitir *Salmonella* spp. aos humano*S*. Neste trabalho, relatamos os dez principais sorovares de *Salmonella* isolados de fontes humanas entre 2011 e 2020 recebidos no Laboratório de Referência Nacional de Enteroinfecções Bacterianas (LRNEB). A sorotipificação foi realizada de acordo com o esquema de Kauffman-White. 3.113 isolados relacionados a casos humanos pertencentes a 61 sorogrupos foram recebidos no LRNEB entre 2011 e 2020. O objetivo deste artigo é a identificação dos sorotipos circulantes como o primeiro passo para o entendimento da epidemiologia, e então, com essas informações, tomar ações para mitigar e controlar esse patógeno.
Palavras-chave: Doenças veiculada por alimentos; *Salmonella*; Sorotipagem.

Resumen

Salmonella es uno de los dos principales patógenos transmitidos por los alimentos en todo el mundo. Los animales domésticos, los animales salvajes y una variedad de fuentes de alimentos pueden transmitir *Salmonella* spp. años humano*S*. En este trabajo, reportamos los diez principales serovares de *Salmonella* aislados de fuentes humanas entre 2011 y 2020 recibidos en el Laboratorio de Referencia Nacional em Enteroinfección (LRNEB). La serotipificación se realizó según el esquema de Kauffman-White. Se recibieron 3.113 aislamientos relacionados con casos humanos pertenecientes a 61 serogrupos no LRNEB entre 2011 y 2020. El objetivo de este trabajo es la identificación de los serotipos circulantes como primer paso para conocer la epidemiología y, por tanto, con está información, tomar acciones para mitigar y controlar este patógeno.

Palabras clave: Enfermedades transmitidas por alimentos; *Salmonella*; Serotipificación.

1. Introduction

Salmonella enterica is a zoonotic pathogen of considerable concern to global human and animal health (CDC, 2019; EFSA & CDC, 2021; Knodler & Elfenbein, 2019). Over 2500 serotypes have been described for *Salmonella* however, less than 100 serotypes account for most human infections (Bjelland et al., 2020; Jajere, 2019). Non-typhoidal *Salmonella* infections are self-limiting diarrhoeal illness with low fatality cases, but in some cases can trigger an invasive disease with higher fatality cases when compared to non-invasive infection (Global Burden of Disease Non-Typhoidal Salmonella Invasive Disease Collaborators, 2019; Trotta et al., 2021). A wide variety of domestic and wild animals, and a variety of food matrices can transmit *Salmonella* spp. to humans. The transfer often occurs when these microorganisms are introduced into food preparation areas, as well as through direct contact with infected animals or humans (Yu et al., 2021). Most of the data related to human salmonellosis in Brazil come from scientific research, since the Ministry of Health does not disclose annual reports as it occurs in North America and Europe. In Brazil, the National Reference Laboratory for Enteric Diseases, Oswaldo Cruz Institute – FIOCRUZ (NRL) receives *Salmonella* strains from Public Health Laboratories, Universities, Food Production Industries, and other Brazilian sectors for serotyping and genotyping. This allows tracing the profile of the serovars involved in human salmonellosis over time. Here, we report the top 10 *Salmonella* serovars isolated from human sources between 2011 and 2020.

2. Methodology

Isolates were received in NRL in Nutrient Agar and then inoculated in Costa and Vernin media, Lysine Iron Agar and sulphide-indole-motility and incubated at 37°C for 24 hours for confirmation as *Salmonella enterica*; serotyping was performed according to the Kauffman-White scheme (Issenhuth-Jeanjean et al., 2014).

3. Results and Discussion

3113 isolates related to human cases were received in NRL between 2011 and 2020. In all, 61 different serogroups were identified, although most occurred occasionally.

Compared to other countries, we had a low frequency of *Salmonella enterica* associated with human cases of human origin (CDC, 2019; EFSA & CDC, 2021). Due to the lack of mandatory notification, which only became necessary in a food-borne outbreak in October 2017, and the lack of accounting for gastroenteritis cases compared to other countries (Panzenhagen et al., 2016).

From a public health perspective, according to the World Health Organization (WHO), *Salmonella* spp. is among the 31 pathogens presenting the highest capability of triggering intestinal or systemic disease in humans among diarrheal and/or invasive agents (viruses, bacteria, protozoa, helminths, and chemicals) and the third leading cause of death among food-transmitted diseases (Criscuolo et al., 2019; Gong et al., 2022).

Annual culture-confirmed human infection surveys regarding *Salmonella* indicate that the five most prevalent serovars in Brazil, in decreasing order were Enteritidis and Typhimurium from 2011 to 2014. From 2015 onwards, the observed order of serovars prevalence was Typhimurium, Enteritidis, or Infantis according to the year, followed by Newport. In the United States, it was Typhimurium, Enteritidis followed by Newport, and monophasic Typhimurium 4,[5],12:i−. *S.* Enteritidis, Typhimurium, monophasic Typhimurium 1,4,[5],12:i−, Infantis, and Newport in the European Union (Centers for Disease Control and Prevention (CDC), 2018; European Food Safety Authority, 2018). Although the role of animal-based foods in the transmission of this pathogen to humans has been previously demonstrated, the prevalence of *Salmonella* serovars in these products is not yet fully understood. The prevalence in different food matrices varies according to countries and regions, influenced both by culture and food production practices, as well as by geographic location and economic power. Furthermore, production animals are often asymptomatic carriers, and after entering the slaughterhouse, *Salmonella* can be transferred to other substrates during industrial processing (Bell et al., 2021; Issenhuth-Jeanjean et al., 2014).

Salmonella Typhimurium represented 29.4% of the total (918/3,113 isolates) being the main serovar agent of salmonellosis in Brazil. The results reported here confirm that the Typhimurium serovar shows a cosmopolitan profile. It is considered an example of a generalist serovar. Therefore, these results corroborate those associated with *S.* Typhimurium and its monophasic variant from a global point of view confirming that pork meat is the main source of this serovar. Thus, it is not surprising that it ranks second in Europe (European Food Safety Authority, 2018) and third in the United States (Centers for Disease Control and Prevention (CDC), 2018; Tack et al., 2020) in reports of human salmonellosi*S*. Despite the decrease in the number of diseases caused by *S.* Enteritidis this serovar ranked second with 20.8% (647/3,113 isolates) of the total. In this study, *S.* Enteritidis was found to be the most prevalent serovar associated with human cases up to 2014. This is in agreement with the global increase in the incidence of this serovar since the 1980s associated with consumption of eggs and poultry and its decrease in the 2010s, a fact reported in other countries, such as the USA (Wright et al., 2016; Tang et al., 2019). It´s followed by *S.* Infantis with 5.1% (159/3,113 isolates). which is commonly found in chickens and broiler flocks. Outbreaks caused by *S.* Infantis have been associated with pet food and treats, and the main animal reservoirs of serovar Infants are poultry and swine. It is a common serovar in a number of countries and recognizes as invasive serovar specially for children (Gorski et al., 2022). Table 1 details the top 10 serovars of each year in the analysed period. Most of these serovars have a wide host range that can colonize several animals and are primarily transmitted to humans by foods of animal origin, such as raw meat, pork, poultry, and egg*S*. Seafood, fruits and vegetables can also serve as vehicles (EFSA & CDC, 2021). Several countries reported *S.* Typhimurium, *S.* Enteritidis, and *S.* Infantis as being the most related to enteric and invasive diseases in humans (EFSA & CDC, 2021; Guard et al., 2021). In 2015 *S.* Heidelberg emerged among the main serotypes causing human salmonellosis with the peak of cases in 2016, becoming the second most common serovar. However, as of 2017, the frequency of serotyped strains such as *S.* Heidelberg from humans began to decrease, thus leaving the ranking of the 5 most frequently isolated serovars in humans as of 2019.

4. Final Considerations

The prevalence and serovar diversity of *Salmonella enterica* from human sources were evaluated for 10 years. Until 2014 *S.* Enteritidis was the prevalent serovar in Brazil both in human and non-human source*S*. From 2015 onwards, *S.* Typhimurium which was the second increased its prevalence, occupying a prominent position and showing the occurrence of other serovars in human source*S*. However, it is necessary to evaluate the intraserovar diversity using subtyping methods such as PFGE and WG*S*. These will allow understanding the wide prevalence and diversity of *Salmonella* serovars, recognizing those prevalent in foodborne diseases. These data will help in the elaboration of efficient control strategies to intervene in the occurrence of salmonellosis and reduce the economic burden on health systems.

Table 1 – Top 10 *Salmonella* enterica serovars isolated from human source in Brazil from 2011 to 2020.

Top 10 serovars	2011		2012		2013		2014		2015	
	Serovar	N	Serovar	N	Serovar	N	Serovar	N	Serovar	N
1	Enteritidis	171	Enteritidis	167	Enteritidis	105	Enteritidis	103	Typhimurium	85
2	Typhimurium	118	Typhimurium	165	Typhimurium	95	Typhimurium	101	Infantis	22
3	Typhi	110	Infantis	24	Infantis	19	Infantis	37	Agona	17
4	Panama	16	Panama	13	Newport	16	Panama	14	Belem	13
5	Schwarzengrund	6	Muenchen	12	Typhi	13	Agona	11	Enteritidis	13
6	Branderup	17	Schwarzengrund	11	Saintpaul	11	Saintpaul	10	Newport	11
7	Corvallis	4	Newport	10	*enterica*	9	Typhi	10	Heidelberg	8
8	Saintpaul	3	Typhi	9	Panama	9	Hadar	7	Panama	8
9	Dublin	3	Braenderup	7	Dublin	6	Schwarzengrund	7	Schwarzengrund	8
10	*enterica*	3	Saintpaul	6	Muenchen	5	Dublin	6	*enterica*	7
Total	578		521		359		386		279	

Top 10 serovars	2016		2017		2018		2019		2020	
	Serovar	N	Serovar	N	Serovar		Serovar	N	Serovar	N
1	Typhimurium	64	Typhimurium	63	Typhimurium	56	Typhimurium	45	Typhimurium	62
2	Heidelberg	30	Enteritidis	20	Enteritidis	20	Newport	9	Enteritidis	20
3	Infantis	19	Agona	13	Newport	17	Dublin	6	Infantis	10
4	Agona	17	Infantis	13	Infantis	11	Saintpaul	6	Muenchen	10
5	Enteritidis	14	Panama	12	Heidelberg	10	Typhi	5	Newport	8
6	Panama	13	Javiana	8	Agona	9	Enteritidis	4	Minnesota	6
7	*enterica*	8	Saintpaul	8	Derby	5	Heidelberg	4	Saintpaul	6
8	Hadar	7	Typhi	8	Typhi	5	Infantis	4	Typhi	5
9	Typhi	5	Anatum	7	Akuafo	4	Montevideo	3	*enterica*	5
10	Dublin	4	Schwarzengrund	7	Anatum	3	Orion	3	Heidelberg	4
Total	266		220		179		130		195	

N- number of strains. Source: Authors.

References

Centers for Disease Control and Prevention (CDC). (2018). National Enteric Disease Surveillance: *Salmonella* Annual Report, 2016. *US Department of Health and Human Services, Centers for Disease Control and Prevention: Atlanta, GA, USA*.

Centers for Disease Control and Prevention (CDC). (2019). Surveillance for Foodborne Disease Outbreaks, United States, 2017, Annual Report. *Atlanta, Georgia: U.S. Department of Health and Human Services, CDC*.

Bell, R. L., Kase, J. A., Harrison, L. M., Balan, K. V., Babu, U., Chen, Y., Macarisin, D., Kwon, H. J., Zheng, J., Stevens, E. L., Meng, J., & Brown, E. W. (2021). The Persistence of Bacterial Pathogens in Surface Water and Its Impact on Global Food Safety. *Pathogens, 10*(11). 10.3390/pathogens10111391

Bjelland, A. M., Sandvik, L. M., Skarstein, M. M., Svendal, L., & Debenham, J. J. (2020). Prevalence of *Salmonella* serovars isolated from reptiles in Norwegian zoo*S. Acta Vet Scand, 62*(1), 3. 10.1186/s13028-020-0502-0

Global Burden of Disease Non-Typhoidal Salmonella Invasive Disease Collaborators.(2019). The global burden of non-typhoidal *Salmonella* invasive disease: a systematic analysis for the Global Burden of Disease Study 2017. *Lancet Infect Dis, 19*(12), 1312-1324. 10.1016/S1473-3099(19)30418-9

Criscuolo, A., Issenhuth-Jeanjean, S., Didelot, X., Thorell, K., Hale, J., Parkhill, J., Thomson, N. R., Weill, F. X., Falush, D., & Brisse, S. (2019). The speciation and hybridization history of the genus *Salmonella. Microb Genom, 5*(8). 10.1099/mgen.0.000284

European Food Safety Authority (EFSA) & Centers for Disease Control and Prevention (CDC). (2018). The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2017. *16*(12), e05500. https://doi.org/10.2903/j.efsa.2018.5500

European Food Safety Authority (EFSA) & Centers for Disease Control and Prevention (CDC). (2021). The European Union One Health 2019 Zoonoses Report. *EFSA J, 19*(2), e06406. 10.2903/j.efsa.2021.6406

Gong, B., Li, H., Feng, Y., Zeng, S., Zhuo, Z., Luo, J., Chen, X., & Li, X. (2022). Prevalence, Serotype Distribution and Antimicrobial Resistance of Non-Typhoidal *Salmonella* in Hospitalized Patients in Conghua District of Guangzhou, China. *Front Cell Infect Microbiol, 12*, 805384. 10.3389/fcimb.2022.805384

Gorski, L., Liang, A. S., Walker, S., Carychao, D., Aviles Noriega, A., Mandrell, R. E., & Cooley, M. B. (2022). *Salmonella* enterica Serovar Diversity, Distribution, and Prevalence in Public-Access Waters from a Central California Coastal Leafy Green-Growing Region from 2011 to 2016. *Appl Environ Microbiol, 88*(3), e0183421. 10.1128/AEM.01834-21

Guard, J., Rivers, A. R., Vaughn, J. N., Rothrock, J., Michael J., Oladeinde, A., & Shah, D. H. (2021). AT Homopolymer Strings in *Salmonella* enterica Subspecies I Contribute to Speciation and Serovar Diversity. *9*(10), 2075.

Issenhuth-Jeanjean, S., Roggentin, P., Mikoleit, M., Guibourdenche, M., de Pinna, E., Nair, *S.*, Fields, P. I., & Weill, F.-X. (2014). Supplement 2008–2010 (no. 48) to the White–Kauffmann–Le Minor scheme. *Research in Microbiology, 165*(7), 526-530. https://doi.org/10.1016/j.resmic.2014.07.004

Jajere, S. M. (2019). A review of *Salmonella* enterica with particular focus on the pathogenicity and virulence factors, host specificity and antimicrobial resistance including multidrug resistance. *Vet World, 12*(4), 504-521. 10.14202/vetworld.2019.504-521

Knodler, L. A., & Elfenbein, J. R. (2019). *Salmonella* enterica. *Trends Microbiol, 27*(11), 964-965. 10.1016/j.tim.2019.05.002

Panzenhagen, P. H. N., Aguiar, W. S., da Silva Frasão, B., de Almeida Pereira, V. L., da Costa Abreu, D. L., dos Prazeres Rodrigues, D., do Nascimento, E. R., & de Aquino, M. H. C. (2016). Prevalence and fluoroquinolones resistance of Campylobacter and *Salmonella* isolates from poultry carcasses in Rio de Janeiro, Brazil. *Food Control, 61*, 243-247. https://doi.org/10.1016/j.foodcont.2015.10.002

Tack, D. M., Marder, E. P., Griffin, P. M., Cieslak, P. R., Dunn, J., Hurd, S., Scallan, E., Lathrop, S., Muse, A., Ryan, P., Smith, K., Tobin-D'Angelo, M., Vugia, D. J., Holt, K. G., Wolpert, B. J., Tauxe, R., & Geissler, A. L. (2019). Preliminary Incidence and Trends of Infections with Pathogens Transmitted Commonly Through Food - Foodborne Diseases Active Surveillance Network, 10 U.*S.* Sites, 2015-2018. *MMWR Morb Mortal Wkly Rep, 68*(16), 369-373. 10.15585/mmwr.mm6816a2

Tang, Y., Davies, R., & Petrovska, L. (2019). Identification of Genetic Features for Attenuation of Two *Salmonella* Enteritidis Vaccine Strains and Differentiation of These From Wildtype Isolates Using Whole Genome Sequencing. *Front Vet Sci, 6*, 447. 10.3389/fvet*S.*2019.00447

Trotta, A., Del Sambro, L., Galgano, M., Ciccarelli, S., Ottone, E., Simone, D., Parisi, A., Buonavoglia, D., & Corrente, M. (2021). *Salmonella* enterica Subsp. houtenae Associated with an Abscess in Young Roe Deer (Capreolus capreolus). *Pathogens, 10*(6). 10.3390/pathogens10060654

Wright, A. P., Richardson, L., Mahon, B. E., Rothenberg, R., & Cole, D. J. (2016). The rise and decline in *Salmonella* enterica serovar Enteritidis outbreaks attributed to egg-containing foods in the United States, 1973-2009. *Epidemiol Infect, 144*(4), 810-819. 10.1017/s0950268815001867

Yu, C. H., Wang, C. C., Hu, C. F., & Wang, C. C. (2021). A rare case of *Salmonella* enterica serotype Weltevreden osteomyelitis in Taiwan. *Pediatr Neonatol, 62*(5), 571-572. 10.1016/j.pedneo.2021.05.013