



Top 10 *Salmonella* Serovars Associated with Human Salmonellosis in Brazil (2011-2020)

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Abstract

Salmonella is one of the major foodborne pathogens worldwide. Domestic, wild animals and a variety of food matrices can transmit *Salmonella* spp. to humans. 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 Diseases. Serotyping was performed according to the Kauffman-White scheme. Three thousand one hundred and thirteen isolates related to human cases belonging to 61 serogroups were received in the NRL between 2011 and 2020. The identification of circulating serotypes is the first step to understanding the epidemiology, and then, with this information, takes actions to mitigate and control this pathogen.

Keywords: Foodborne disease; *Salmonella*; Serotyping

Introduction

Salmonella enterica is a zoonotic pathogen of considerable concern to global human and animal health [1-3]. Over 2500 serotypes have been described for *Salmonella* however, less than 100 serotypes account for most human infections [4]. Non-typhoidal *Salmonella* infections are self-limiting diarrheal illness with low fatality cases, but in some cases can trigger an invasive disease with higher fatality cases when compared to non-invasive infection [5]. 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. 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.

Material and Methods

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 hr for confirmation as *Salmonella enterica*; serotyping was performed according to the Kauffman-White scheme [6].

Results and Discussion

Three thousand one hundred and thirteen 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 [1,2]. Due to the lack of mandatory notification, which only became necessary in a foodborne outbreak in October 2017, and the lack of accounting for gastroenteritis cases compared to other countries [7].

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Table 1: Top 10 *Salmonella enterica* serovars isolated from human source in Brazil from 2011 to 2021.

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	<i>enterica</i>	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	<i>enterica</i> (4,12)	3	Saintpaul	6	Muenchen	5	Dublin	6	<i>enterica</i>	7
Total	578		521		359		386		279	
Top 10 serovars	2016		2017		2018		2019		2020	
	Serovar	N	Serovar	N	Serovar	N	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	<i>enterica</i> (O:4,5)	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	Akufo	4	Montevideo	3	<i>enterica</i> (O:4,5)	5
10	Dublin	4	Schwarzengrund	7	Anatum	3	Orion	3	Heidelberg	4
Total	266		220		179		130		195	

N: Number of strains

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.

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 *S. 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 [8,9]. 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 [10].

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 [8] and third in the United States [9] in reports of human salmonellosis. 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. It's followed by *S. Infantis* with 5.1% (159/3,113 isolates). Table 1 details the top 10 serovars of each year in the analyzed 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 eggs. Seafood, fruits and vegetables can also serve as vehicles [1]. Several countries reported *S. typhimurium*, *S. enteritidis*, and *S. Infantis* as being the most related to enteric and invasive diseases in humans [1]. 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.

In conclusion we present important data on the main *Salmonella* serotypes that have caused human salmonellosis in Brazil over the past ten years. Tracing the profile of circulating serotypes is the first step to understanding the epidemiology, and with this data produces actions to mitigate and control this pathogen.

Author Contributions

Conceptualization, methodology, research, resources, data retention, writing, original draft preparation, writing, review and editing. All authors have read and accepted the published version of the manuscript.

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