

Distribution of *Salmonella* serovars along the food chain in Poland, 2010–2015

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Abstract

Introduction: Data collection on the *Salmonella* occurrence is crucial in effective implementation of different actions or control programmes aiming to protect consumers' health and to reduce the level of *Salmonella* prevalence in farm animals. The goal was to describe *Salmonella* serovar distribution along the food chain in Poland during 2010–2015 and to identify their epidemiological importance. **Material and Methods:** Slide agglutination according to White-Kauffmann-Le Minor scheme was used to identify *Salmonella* serovars of 6,928 isolates originating from animals, food, feeds, and fertilisers. **Results:** In total, 160 *Salmonella* serovars were identified. Differences in serovar distribution were observed depending on animal species. Among isolates from hens, *S. Enteritidis* and *S. Infantis* were the most prevalent. Serovar pattern in turkeys differed from those in hens, with *S. Kentucky*, *S. Newport*, *S. Saintpaul* being the most prevalent. Monophasic *S. Typhimurium* was predominant in pigs. Serovars found in food reflected those observed among livestock animals. Nine out of the ten most prevalent serovars in animals and humans were also found in organic fertilisers. **Conclusion:** Serotyping of large number of isolates from different sources is essential for insight on emerging serovars and trends of *Salmonella* occurrence. This may increase the value of epidemiological data and result in updating of *Salmonella* control programmes to target further epidemiologically important serovars in animals and better protection of consumers' health.

Keywords: *Salmonella* serovars, salmonellosis, food chain, Poland.

Introduction

Salmonella infections, despite years of eradication, still constitute an important epidemiological and economic problem worldwide. According to data presented by the European Food Safety Authority (EFSA) in 2015, 94,625 cases of *Salmonella* infections were confirmed in humans, including 126 fatal, making salmonellosis the second most commonly reported zoonosis across the European Union. This was a 1.9% increase compared with 2014 (10, 11). *Salmonella* Enteritidis still remains the most prevalent serovar responsible for human salmonellosis, but epidemiological importance of other *Salmonella* serovars like monophasic *S. Typhimurium* 1,4,[5],12:i:- and *S. Infantis* increased during the study period (10, 11). In the USA salmonellosis was the most frequent bacterial foodborne illness in 2014 with 140 outbreaks out of 247 bacterial outbreaks noted (56.6%) and 2,395 cases constituting 27% of all illnesses (6).

Salmonella serovars differ in their ability to cause infections in humans (12, 23). Although a limited number of over 2,600 *Salmonella* serovars are of public health importance, all of them are potentially harmful and have a zoonotic potential (15, 31). It is worth pointing out that not only multidrug-resistant strains are responsible for human illnesses (4).

Contaminated food of animal origin is the main source of *Salmonella* for humans. Transmission of the pathogen to consumers is most often related to consumption of poultry products. Animals, often being asymptomatic pathogen carriers, are of particular importance in the spread of *Salmonella*. Travel and international trade also contribute to global increase of *Salmonella*-related risk (31). Information on the distribution of *Salmonella* serovars in food, feedingstuffs, animals and their environment is important to identify the sources and pathways of infections and can give insight into contamination routes. The ultimate aim of *Salmonella* control in

husbandry is to decrease pathogen prevalence along animal production chain and to reduce public health consequences of its spread to humans.

Our goal was to describe the distribution of *Salmonella* serovars along the food chain in Poland between 2010 and 2015 and to identify their importance to the epidemiology of human and animal salmonellosis.

Material and Methods

Between 2010 and 2015 a total of 10,422 *Salmonella* isolates were tested in the National Reference Laboratory for Salmonellosis (NRL) at the National Veterinary Research Institute (NVRI). *Salmonella* strains were either submitted to NRL by regional veterinary laboratories for confirmatory testing or isolated at the NVRI. The isolates were obtained under national *Salmonella* control programmes in poultry, official controls for compliance with feed and food law, research projects conducted at the NVRI, and routine commercial services. Duplicates and isolates without sufficient data on source of isolation were excluded and finally 6,928 strains were serotyped. They originated from food-producing animals and their environment, food of animal origin, feedingstuffs, and other sources, including fertilisers (Fig. 1).

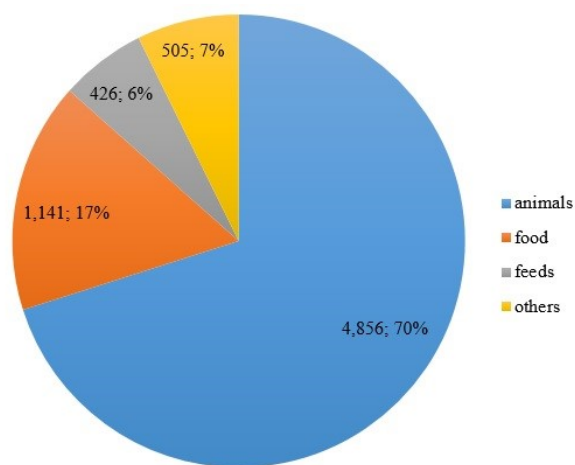


Fig. 1. The origin of tested *Salmonella* strains

Salmonella detection was carried out in the country-wide network of official veterinary diagnostic laboratories according to procedures compliant with PN-EN ISO 6579:2003 standard (26). Serotyping was performed by slide agglutination method according to White-Kauffmann-Le Minor scheme (15), using commercial sera manufactured by: Immunolab (Poland), Biomed (Poland), Sifin (Germany), Statens Serum Institut (Denmark), and Mast Group (U.K.). Monophasic *S. Typhimurium* strains (1,4,[5],12:i:-) were confirmed with PCR method recommended by the EFSA (16, 33). The variability of serovars observed in various sources was measured with Simpson's diversity index (21).

Table 1. Sample types and number of *Salmonella* isolates from food, animals, and feedingstuffs

Food (n = 1,141)		% (numbers)
Sample type		
broiler meat		42.2% (482)
samples from food processing plant		15.3% (175)
poultry meat and poultry meat products (unspecified)		15.3% (175)
pork and pork products		12.3% (140)
turkey meat		8.6% (98)
meat (other, mixed, unspecified)		2.9% (33)
beef and beef products		2.3% (26)
others and unspecified		1.1% (12)
Animals (n = 4,856)		
Sample type		
livestock environment (farm)		55.5% (2697)
secretions / excretions (faeces)		31.1% (1511)
internal organs and tissues		6.9% (335)
transportation environment		1.4% (70)
swabs / washes / scrapings		0.5% (25)
poultry hatching facility		0.4% (17)
others and unspecified		4.1% (201)
Feedingstuffs (n = 426)		
Sample type		
feed production plant environment		22.8% (97)
plant feed materials		21.4% (91)
animal feed materials		14.1% (60)
pet feed		13.4% (57)
compound feed for poultry		8.9% (38)
compound feed for swine		4.2% (18)
compound feed for ruminants		4.0% (17)
others and unspecified		11.3% (48)

Results

Among 6,928 isolates, 160 *Salmonella* serovars were identified as follows: 124 in animals, 44 in food, 73 in animal feeds, and 15 in fertilisers. The majority of serovars (n = 146) were rarely (less than 53 isolates) noted during the study (data not shown).

Differences in *Salmonella* serovars distribution were observed depending on animal species (Table 2).

Among 3,191 isolates from hens 52 *Salmonella* serovars were identified. *S. Enteritidis* was the most prevalent (54,7%). High contributions of *S. Infantis* (14.0%) and *S. Mbandaka* (8.4%) were noted. *S. Typhimurium*, *S. Virchow*, *S. Newport*, and rough strains were also reported among the top serovars in hens (3.5%, 3.2%, 2.6%, and 2.4%, respectively). Other serovars were involved in 11.1% of total cases. Similar serovar distribution was observed in broilers, laying hens, and breeding flocks of *Gallus gallus* (data not presented). Simpson's diversity ratio calculated for hen isolates was the lowest amongst analysed sources and it was undoubtedly connected with limited number of predominant serovars (D = 0.670, Table 2).

Table 2. Diversity of *Salmonella* serovars found in animals and their environment, in food of animal origin, animal feedingstuffs, and fertilisers

Source and serovar	% (numbers)	Source and serovar	% (numbers)	Source and serovar	% (numbers)	Source and serovar	% (numbers)
hens (n = 3,191; D = 0.670)		turkeys (n = 486; D = 0.887)		geese (n = 381; D = 0.736)		ducks (n = 226; D = 0.772)	
Enteritidis ^H	54.7(1744)	Kentucky ^H	22.4 (109)	Typhimurium ^H	38.1 (145)	Enteritidis ^H	42.9 (97)
Infantis ^H	14.0 (447)	Newport ^H	16.0 (78)	Enteritidis ^H	33.1 (126)	Typhimurium ^H	17.7 (40)
Mbandaka ^H	8.4 (269)	Saintpaul ^H	13.2 (64)	Newport ^H	6.6 (25)	Indiana ^H	8.4 (19)
Typhimurium ^H	3.5 (113)	Typhimurium ^H	9.1 (44)	Indiana ^H	6.3 (24)	Newport ^H	5.3 (12)
Virchow ^H	3.2 (102)	Enteritidis ^H	7.2 (35)	Mbandaka ^H	5.0 (19)	S. sp. (rough)	4.0 (9)
Newport ^H	2.6 (83)	Lexington	5.8 (28)	Hadar ^H	1.3 (5)	Give	3.5 (8)
S. sp. (rough)	2.4 (78)	Stanley ^H	3.5 (17)	Kottbus	1.0 (4)	Kottbus	3.5 (8)
Senftenberg	1.9 (60)	Agona ^H	3.1 (15)	1,4,[5],12:i:- ^H	1.0 (4)	Anatum	2.7 (6)
Indiana ^H	1.6 (50)	Anatum	2.5 (12)	Agona ^H	0.8 (3)	Infantis ^H	1.8 (4)
Hadar ^H	0.7 (23)	1,4,[5],12:i:- ^H	1.9 (9)	Infantis ^H	0.8 (3)	Saintpaul	1.8 (4)
Tennessee	0.6 (19)	Mbandaka	1.6 (8)	Virchow ^H	0.8 (3)	Senftenberg	1.3 (3)
Agona ^H	0.5 (17)	Bredeney	1.4 (7)	Anatum	0.5 (2)	Hadar ^H	0.9 (2)
Kottbus	0.5 (17)	Indiana	1.4 (7)	Oranienburg	0.5 (2)	London	0.9 (2)
Braenderup ^H	0.4 (14)	Infantis ^H	1.2 (6)	Schleissheim ^H	0.5 (2)	Tennessee	0.9 (2)
Coeln	0.4 (14)	Virchow	1.2 (6)	S. sp. (rough)	0.5 (2)	1,4,[5],12:i:- ^H	0.4 (1)
other	4.4 (141)	other	8.4 (41)	other	3.1 (12)	other	4.0 (9)
Source and serovar		Source and serovar		Source and serovar		Source and serovar	
swine (n = 224; D = 0.724)		food (n = 1,141; D = 0.881)		feedingstuffs (n = 426; D = 0.954)		fertilisers (n = 31; D = 0.912)	
1,4,[5],12:i:- ^H	47.8 (107)	Infantis ^H	23.4 (267)	Mbandaka ^H	10.8 (46)	Infantis ^H	7
Derby ^H	19.6 (44)	Enteritidis ^H	17.6 (201)	Infantis ^H	8.9 (38)	Virchow ^H	5
Typhimurium ^H	8.9 (20)	Indiana ^H	10.8 (123)	Agona ^H	8.0 (34)	Enteritidis ^H	4
Infantis ^H	4.5 (10)	Newport ^H	9.8 (112)	Derby ^H	6.6 (28)	Schleissheim ^H	3
Choleraesuis	2.7 (6)	Typhimurium ^H	7.2 (82)	Senftenberg	6.1 (26)	Newport ^H	2
Enteritidis ^H	2.2 (5)	Kentucky ^H	4.8 (55)	Enteritidis ^H	5.2 (22)	1,4,[5],12:i:- ^H	1
Rissen	2.2 (5)	Saintpaul ^H	3.0 (34)	Typhimurium ^H	4.5 (19)	Bredeney	1
S. sp. (rough)	1.8 (4)	Virchow ^H	2.8 (32)	Lexington	3.8 (16)	Derby ^H	1
6,7:-:1,5	0.9 (2)	Derby ^H	2.7 (31)	Livingstone	3.3 (14)	Kentucky ^H	1
Agona ^H	0.9 (2)	Mbandaka ^H	2.6 (30)	4:d:-	2.1 (9)	London	1
Brandenburg ^H	0.9 (2)	1,4,[5],12:i:- ^H	2.4 (27)	Anatum	2.1 (9)	Mbandaka ^H	1
Give	0.9 (2)	Agona ^H	2.2 (25)	Bredeney	2.1 (9)	Poona	1
Indiana	0.9 (2)	S. sp. (rough)	1.2 (14)	Indiana ^H	2.1 (9)	Putten	1
London	0.9 (2)	London	1.1 (12)	Newport ^H	2.1 (9)	Senftenberg	1
Ohio	0.9 (2)	Bardo	0.9 (10)	Saintpaul ^H	1.9 (8)	Typhimurium ^H	1
other	4.0 (9)	other	7.5 (86)	other	30.5 (130)	other	0

^H – Top-10 *Salmonella* serovars noted in humans according to the National Public Health Institute (28)**Table 3.** Distribution of *Salmonella* serovars by food items

Serovar	Food sample type (number of isolates)							
	Food processing plant	Broiler meat	Poultry meat and poultry products (unspecified)	Pork and pork products	Turkey meat	Meat (other, mixed, unspecified)	Beef and beef products	Others and unspecified
	(n = 175)	(n = 482)	(n = 175)	(n = 140)	(n = 98)	(n = 33)	(n = 26)	(n = 12)
Infantis	37	172	35	12	3	7	1	0
Enteritidis	26	100	45	11	2	6	6	5
Indiana	11	96	13	3	0	0	0	0
Newport	18	41	28	3	16	3	1	2
Typhimurium	12	7	12	32	9	4	6	0
Kentucky	14	5	3	0	33	0	0	0
Saintpaul	10	2	2	3	15	0	2	0
Virchow	3	18	4	3	0	4	0	0
Derby	4	0	4	21	1	1	0	0
Mbandaka	5	11	10	4	0	0	0	0
1,4,[5],12:i:-	5	1	0	15	1	2	3	0
Agona	6	4	5	2	6	1	1	0
S.sp. (rough)	4	1	7	2	0	0	0	0
London	4	0	0	6	0	1	1	0
Bardo	4	4	2	0	0	0	0	0
other	12	20	5	23	12	4	5	5

Table 4. Distribution of *Salmonella* serovars by feed items

Serovar	Feedingstuff sample type (number of isolates)							
	Feed production plant environment	Plant feed materials	Animal feed materials	Pet feed	Compound feed for poultry	Compound feed for swine	Compound feed for ruminants	Others and unspecified
	(n = 97)	(n = 91)	(n = 60)	(n = 57)	(n = 38)	(n = 18)	(n = 17)	(n = 48)
Mbandaka	9	18	0	1	5	2	5	6
Infantis	6	4	13	8	2	0	0	5
Agona	4	14	3	2	4	3	2	2
Derby	5	4	10	6	0	1	0	2
Senftenberg	3	16	2	0	2	1	1	1
Enteritidis	1	2	0	3	5	2	3	6
Typhimurium	1	3	3	7	0	1	0	4
Lexington	8	3	0	0	4	1	0	0
Livingstone	3	4	3	0	2	0	2	0
4:d:-	4	0	3	2	0	0	0	0
Anatum	3	0	2	1	1	0	2	0
Bredeney	2	1	6	0	0	0	0	0
Indiana	0	0	0	4	1	1	0	3
Newport	1	1	0	2	0	0	0	5
Saintpaul	0	0	0	6	0	0	0	2
other	47	21	15	15	12	6	2	12

Diversity of serovar pattern in turkey isolates ($D = 0.887$) was higher than in those recovered from geese ($D = 0.736$), ducks ($D = 0.772$), or swine ($D = 0.724$). The most commonly observed serovars in turkeys were *S. Kentucky* (22.4%), *S. Newport* (16.0%), *S. Saintpaul* (13.2%), and *S. Typhimurium* (9.1%).

The same four serovars, but at different frequencies, were observed among isolates from geese and ducks. In geese *S. Typhimurium* (38.1%) and *S. Enteritidis* (33.1%) prevailed, but in ducks both serovars occurred in the opposite order (*S. Enteritidis* at 42.9% followed by *S. Typhimurium* with 17.7%). The occurrence of *S. Indiana* was noted more often in ducks (8.4%) than in geese (6.3%).

Monophasic *S. Typhimurium* was the predominant serovar in pigs (47.8%). High contributions of *S. Derby* (19.6%) and *S. Typhimurium* (8.9%) were observed. Other serovars were rarely noted, with percentages ranging from 0.9% to 4.5%.

During 2010–2015 only few isolates from cattle were available (*S. Typhimurium* $n = 2$, monophasic *S. Typhimurium* $n = 5$, *S. Dublin* $n = 3$, *S. Enteritidis* $n = 1$).

The most frequent serovars found among isolates from food of animal origin were in decreasing order: *S. Infantis* (23.4%) and *S. Enteritidis* (17.6%) followed by *S. Indiana* (10.8%), *S. Newport* (9.8%), and *S. Typhimurium* (7.2%) (Table 2). The first three serovars were also the most often recovered from broiler meat samples, whereas *S. Typhimurium* was most common in pork and pork meat products (Table 3).

Among 73 serovars from feedingstuffs, there was no visibly predominant serovar, but *S. Mbandaka* (10.8%), *S. Infantis* (8.9%) and *S. Agona* (8.0%) were relatively often recovered. *S. Infantis*, *S. Typhimurium*, and *S. Derby* were often noted in pet feed (Table 4). That source of isolation along with fertilisers showed the

highest variability ($D > 0.9$) of the serovars observed during the study.

Thirty-one isolates from fertilisers covered 15 serovars. Noteworthy is the fact that identified serovars like *S. Infantis*, *S. Enteritidis*, *S. Virchow*, *S. Newport*, *S. Typhimurium*, monophasic *S. Typhimurium*, *S. Derby*, *S. Kentucky*, and *S. Mbandaka* were also the most commonly found in animals, foods, and humans.

Discussion

Data collection on the occurrence of *Salmonella* is a crucial element in control of the pathogen in animals and provides a possibility to evaluate the efficiency of national *Salmonella* control programmes. Products of animal origin are considered to be the main source of *Salmonella* for humans. *Salmonella*-contaminated feed, a possible vector of new *Salmonella* serovars to animals, via food of animal origin, may finally affect consumers' health. Each year *Salmonella* serovars different than those targeted in national *Salmonella* control programmes cause several human illnesses. Comparison of top serovars noted in the USA and EU clearly demonstrates geographical differences in *Salmonella* epidemiology (7, 11). Monitoring of the distribution of *Salmonella* serovars from various sources is relevant for the detection of national and global *Salmonella* outbreaks and supports good insight into current epidemiological status (11, 30).

As far as we know, this study is one of the most extensive presentations on the occurrence of *Salmonella* serovars from a national perspective and provides detailed data on serovar distribution, wide spectrum of serovars, and a variety of *Salmonella* sources.

Many serovars noted along the food chain in Poland were also responsible for human infections (27, 28).

Finding the same *Salmonella* serovars in humans, animals, food of animal origin, and feedingstuffs might indicate their epidemiological linkages. As shown in the study, some currently spotted tendencies might result in serious epidemiological consequences.

In the present study *S. Enteritidis*, which is responsible for the greatest proportion of human salmonellosis cases in Poland (78.6% in 2014), along with *S. Infantis* and *S. Mbandaka* (27, 28), represented also serovars most frequently observed in animals. It was particularly demonstrated in poultry, where in the case of hens and geese dominating serovars proved to be *S. Enteritidis*, *S. Infantis*, and *S. Mbandaka*, but in ducks – *S. Enteritidis* and *S. Infantis*. Similar distribution pattern of these three serovars in broilers, laying hens, and breeding flocks of *Gallus gallus* (data not shown) might result from farm environment contamination and vertical transmission of the infection inside the breeding flocks. *Salmonella* serovars found in food of animal origin reflect the distribution of serovars among livestock. *S. Enteritidis* and *S. Infantis*, as the most prevalent in food of animal origin, represent a good example as we noted a significant increase in *S. Infantis* presence in food compared to our previous study (from 12.2% up to 23.4%), whereas, at the same time *S. Enteritidis* decreased from 26.3% down to 17.6% (17). It can be assumed that this shift in predominant serovars is the effect of *Salmonella* control programmes in poultry aiming at limited number of serovars. Broiler and unspecified poultry meat seem to be the main source of these two serovars for humans in Poland and the same situation is observed across the EU (10, 11). Franco *et al.* (14) reported spread of multidrug-resistant *S. Infantis* causing infections in humans in Italy between 2011 and 2014, and the outbreak clone strain was associated with broilers and broiler meat. In our study all three poultry-associated serovars were noted in feedingstuffs: poultry feed – *S. Enteritidis* and *S. Mbandaka*, feed materials and pet feed – *S. Infantis*. This finding is a cause for concern and it indicates the role of feedingstuffs as a source of *Salmonella* transmission to humans. It is worth emphasising that contaminated feeds may affect consumer health in a direct way – by *Salmonella* infected pet feed and not only *via* infected animals. In 2012, documented outbreak of human salmonellosis caused by *S. Infantis* transmitted from “Dry Dog Food” was reported in the United States and Canada (5). Feed-associated outbreak noted in Austria in 2010 showed the indirect way of *Salmonella* transfer to humans. Eggs obtained from flocks fed *S. Mbandaka*-contaminated feed were the main cause of human illness (1). Epidemiological success and public health consequences of *S. Mbandaka* ST413 spread in Poland were addressed elsewhere (19). Currently ongoing egg-related multi-country *S. Enteritidis* outbreak was traced back to a packing centre and multiple laying hen farms in Poland (8).

Similarly to above-mentioned serovars, *S. Virchow*, listed among the main causes of human infections, was also associated mostly with hens and broiler meat (11,

28). Occurrence of this serovar in other animal species and feedingstuffs was low. That is consistent with previous findings showing that *S. Virchow* is rarely isolated from sources other than humans and chickens (29).

S. Typhimurium, the second most prevalent serovar among the human salmonellosis cases in Poland (6.2% in 2014) and across the EU (15.8% in 2015) (11, 28), occurred very often in hens, geese, ducks, turkeys, and pigs in Poland. Notifiable decline of *S. Typhimurium* incidents in hens (from 5.6% to 3.5%) and in foods (from 14.3% to 7.2%) was observed during this study compared to 2005–2010 (17). We assume that this reduction might result from implementation of national *Salmonella* control programmes in poultry, similarly to a decrease in *S. Enteritidis* infection. *S. Typhimurium* was the most frequently recovered from pork and poultry meat, the same as it was observed in food-associated *Salmonella* outbreaks across the EU and in the USA (11, 20, 22).

Interestingly, in comparison to our previous study, the number of *S. Typhimurium* pig isolates decreased from 27.4% to 8.9% and it was replaced by monophasic *S. Typhimurium* (17). Similarly to Poland, monophasic strains of *S. Typhimurium* (*Salmonella* 1,4,[5],12:i:- and *S. 1,4,12:i:-*) represented a significant number of pig isolates in Spain, Malta, the United Kingdom, and Italy (10, 11). Monophasic *S. Typhimurium* – the worldwide emerging pathogen – has been occurring in Poland since 2008 (16, 33). In 2015, it was the third most frequently reported serovar in pigs and the second serovar recovered from pork across the EU (11). In comparison to other European countries, where monophasic *S. Typhimurium* was the third most important serovar associated with human salmonellosis, epidemiological significance of this serovar in humans seems to be limited in Poland (11). In 2014 it took the 9th place on the list of the top human serovars (28).

S. Derby, another serovar associated with pork production worldwide, consistently persists among serovars responsible for human salmonellosis (11, 28). Seven percent increase in the number of this serovar in pigs was noted compared to the previous period (17). We found only few *S. Derby* isolates coming from other animal species (data not presented). *S. Derby* and *S. Typhimurium* were recovered in pet feed. This is another proof that feed might be the possible direct or indirect source of *Salmonella* infections.

Serovars *S. Newport*, *S. Kentucky*, and *S. Saintpaul* were found most frequently among isolates from turkeys and turkey meat. This serovar pattern was different than those observed in other poultry species in Poland. The rationale for that could be an import of breeding material for turkey fattening flocks. We noted a change in *Salmonella* serovars distribution in turkeys in comparison to the previous years when *S. Saintpaul*, *S. Typhimurium*, and *S. Newport* were the most frequent serovars (17). The epidemic spread of multiresistant *S. Kentucky* in turkey flocks in Poland has been observed since 2010 (32).

S. Kentucky and *S. Newport* were listed among the top ten serovars in human salmonellosis across the EU, causing 0.7% and 1.0% of all reported cases in 2015 (11). Turkey associated *Salmonella* outbreaks were repeatedly reported. Previously described epidemic spread of *S. Saintpaul* in a cluster of EU countries (34) presumably continues since it caused a multi-country outbreak in 2012. This led *S. Saintpaul* to become the fifth most commonly reported serovar in 2012 in humans across the EU (9). During the study, a similar turkey-related outbreak affecting hundreds of people in several countries was caused by *S. Stanley* (24).

It is noteworthy that in Poland, unlike in other European countries, *S. Indiana* and *S. Agona* persist among top serovars responsible for human salmonellosis. In 2014, these two serovars caused 0.37% and 0.83% of all human *Salmonella* cases respectively (28). Still there were some reports on outbreaks associated with these serovars in other countries, for example a large *S. Agona* outbreak in England in 2013 (13), caused by contaminated food of plant origin, namely curry leaves. Most of our *S. Indiana* and *S. Agona* isolates were associated with poultry. We noted an increase in the number of *S. Indiana* originating from geese and ducks (17). Similar situation was observed in Great Britain where *S. Indiana* became the most prevalent serovar in ducks during 2012 and 2013 (2). The number of *S. Indiana* isolates from food increased dramatically compared to our previous study (17). Interestingly, we found *S. Indiana* occurring almost as frequently as *S. Enteritidis* in broiler meat samples (Table 3). High percentage of this serovar in broiler meat compared to its presence in hens may suggest cross-contamination during slaughter or the fact that the serovar is not targeted in control programmes. It is disturbing that there are several reports on *S. Indiana* carrying quinolones resistance genes widespread in chickens and ducks in China (3, 25).

The presented data show a variety of possible *Salmonella* sources. We indicate that geese and ducks might also be relevant source of epidemiologically important *Salmonella* serovars to humans and more attention should be paid to this infection route. The epidemiological situation in bovine salmonellosis in Poland has not been part of this study. Nevertheless, the importance of serovars found in cattle and beef indicates the need for further investigation. The varieties of serovars found in feeds confirm their role as *Salmonella* introduction route to animal flocks (18). The most common *Salmonella* serovars found in feedingstuffs were also noted among serovars isolated from animals and humans. A large diversity of serovars isolated from feeds and feed products could have been associated with the import of contaminated feeds and raw feed materials coming from different geographic regions of the world (18).

Since the number of studied *Salmonella* isolates obtained from fertilisers was small, it is difficult to draw a substantive conclusion. However, top nine *Salmonella* serovars associated with human and animal infections

were noted, including *S. Enteritidis*, multiresistant *S. Kentucky*, and monophasic variant of *S. Typhimurium*. This implicates the role of animals in *Salmonella* circulation in the environment and also points that fertilisers, similarly to feedingstuffs, might be a threat to humans. It also indicates that fertilisers can play an important role in the spread of *Salmonella* by contaminated food of plant origin.

Our study focused on *Salmonella* serovars along the food chain, but we should bear in mind other reservoirs of *Salmonella* such as wildlife or pet animals. In terms of *Salmonella* infections, reptile pets, whose popularity continues to grow, are of particular importance (35).

Salmonella serovars vary in their pathogenic potential and have different entryways into human population. That is why talking about *Salmonella* epidemiology is a significant simplification. In order to gain a better perspective, further molecular typing studies, including whole genome sequencing (WGS), pulsed field gel electrophoresis (PFGE), multilocus sequence typing (MLST), antimicrobial resistance testing, and identification of specific resistance mechanisms are needed to explore specifics of spread of particular *Salmonella* serovars along the food chain in Poland.

Monitoring of *Salmonella* occurrence and definite serovar identification are essential for determination of infection sources and reduction of salmonellosis in humans (17). The observed continuous decrease in infection rate during the study period presumably results from *Salmonella* control programmes in poultry across the EU, targeting *S. Enteritidis*, *S. Typhimurium*, *S. Hadar*, *S. Infantis*, and *S. Virchow* in *Gallus gallus* breeding flocks, and *S. Enteritidis* and *S. Typhimurium* in other poultry populations covered by the programmes (11, 20). However, decrease in occurrence of one serovar is often associated with an increase in the other serovars that may also cause foodborne outbreaks. This suggests that the applied control measures are not equally efficient against all *Salmonella* serovars and that more attention should be paid to different sources of infection. Therefore, *Salmonella* control programmes should be updated to target other epidemiologically important serovars. It is essential to serotype a number of isolates from different sources for an insight on emerging serovars and trends of *Salmonella* infections. This could increase the value of epidemiological data and result in prompt actions leading to efficient protection of consumers' health.

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