Sources and trends of human salmonellosis in Europe, 2015–2019: An analysis of outbreak data

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A B S T R A C T

Salmonella remains a major cause of foodborne outbreaks in Europe despite the implementation of harmonized control programmes. Outbreak data are observed at the public health endpoint and provide a picture of the most important sources of human salmonellosis at the level of exposure. To prioritize interventions, it is important to keep abreast of the sources and trends of salmonellosis outbreaks. The objective of this study was to determine the main food sources and recent trends of Salmonella outbreaks in Europe. Salmonella outbreak data from 34 European countries in 2015–2019 were obtained from the European Food Safety Authority (EFSA). For the source attribution analysis, implicated foods were categorized according to EFSA's zoonosis catalogue classification scheme. An established probabilistic source attribution model was applied using the information on the implicated foods, overall and by region and serotype. To assess significant trends in outbreak occurrence, overall and by region and serotype, mixed-effects Poisson models were used. Overall, the most important food source of salmonellosis outbreaks was eggs (33 %, 95 % Uncertainty Interval [UI]: 31–36 %), followed by pork (7 %, 95 % UI: 6–8 %), and (general) meat products (6 %, 95 % UI: 5–8 %). While eggs were the most important food source in all regions, pork was the second most common food source in Northern and Western Europe, and (general) meat products in Eastern and Southern Europe. Outbreaks caused by S. Enteritidis (SE) and other known serotypes (other than SE and S. Typhimurium and its monophasic variant [STM]) were mostly attributed to eggs (37 %, 95 % UI: 34–41 % and 17 %, 95 % UI: 11–25 %, respectively), whereas outbreaks caused by STM were mainly attributed to pork (34 %, 95 % UI: 27–42 %). Overall, there was a significant increase in the number of outbreaks reported between 2015 and 2019, by 5 % on average per year (Incidence Rate Ratio [IRR]: 1.05, 95 % Confidence Interval [CI]: 1.01–1.09). This was driven by a significantly increased number of outbreaks in Eastern Europe, particularly those caused by SE (IRR: 1.15, 95 % CI: 1.09–1.22), whereas in Northern and Southern Europe, outbreaks caused by SE decreased significantly from 2015 to 2019 (IRR: 0.72, 95 % CI: 0.61–0.85; IRR: 0.70, 95 % CI: 0.62–0.79, respectively). Regional, temporal and serotype-associated differences in the relative contributions of the different sources were also observed.

1. Introduction

Although an integrated and harmonized approach to *Salmonella* control from farm to fork has been adopted across Europe, *Salmonella* remains the most common cause of foodborne outbreaks (FBOs) and the second most commonly reported zoonosis in Europe (EFSA and ECDC, 2021). In 2019, human salmonellosis amounted to 87,923 confirmed cases and was the cause of ~18 % of all FBOs in Europe (EFSA and ECDC, 2021). Indeed, contrary to other foodborne infections (e.g., campylobacteriosis), salmonellosis frequently occurs as part of

outbreaks (EFSA and ECDC, 2021). While most human salmonellosis generally manifest with mild, self-limiting gastrointestinal symptoms, they can also lead to chronic sequelae, such as reactive arthritis and irritable bowel disease (Esan et al., 2020; Trabulo et al., 2014), as well as become invasive and life-threatening in immunocompromised individuals (Balasubramanian et al., 2019).

After years of significant decrease between 2008 and 2014, the incidence of reported salmonellosis stabilized in most European countries from 2015 to 2019, with current incidence rates of around 20 cases per 100,000 inhabitants (EFSA and ECDC, 2021). This calls for

investigations of the reasons behind this stagnation, which may be found at the level of public health (e.g., changing exposure and risk factors, changes in surveillance systems and diagnostics, etc.), food production (e.g., premature relaxation of control measures, insufficient sampling efforts, etc.) or pathogen characteristics (e.g., emerge and spread of more virulent strains) (EFSA BIOHAZ, 2019). Human salmonellosis can be acquired from different sources, including food, direct contact with animals, through the environment and, to a limited extent, via person-to-person transmission (Dekker and Frank, 2015). However, the main source of human salmonellosis in Europe is food (Pires et al., 2014). Hence, identifying the main food products implicated in the acquisition of human salmonellosis is important to prioritize public health endeavors and to help reverse the stagnating trend in Europe.

Previous research showed that outbreak data, which are collected at the public health endpoint, provide an overview of the most important sources of human salmonellosis at the level of exposure (Adak et al., 2005; Painter et al., 2013; Pires et al., 2010). Furthermore, outbreak investigations provide insights into new, emerging vehicles of transmission (EFSA BIOHAZ, 2012; Pires et al., 2010). Therefore, using European outbreak data for recent years (2015–2019), the aim of this study was to estimate the relative contributions of different food sources to human salmonellosis and to assess trends in the occurrence and characteristics of human salmonellosis outbreaks over time, by European region, and most common *Salmonella* serotypes.

2. Methods

2.1. Data and study population

Data on FBO investigations reported by European countries to the European Food Safety Authority (EFSA) from January 2015 until December 2019 were analyzed. These data included information on the year and country of outbreak occurrence, implicated *Salmonella* serotype (if known), the strength of the evidence linking the outbreak to a specific source (strong or weak), the implicated food source, and the number of human cases involved. The strength of evidence implicating a particular food source in a given outbreak was determined based on the definitions proposed by the European Union Food-borne Outbreak Reporting System (EU-FORS) guidelines and the last published manual on FBO (EFSA, 2014), which include evidence from epidemiological, microbiological or product-tracing investigations. We considered only those outbreaks with more than one confirmed case reported and with strong evidence, because outbreaks with weak evidence were not reliable, as reported previously (EFSA BIOHAZ, 2020). Most FBOs in Europe are investigated and handled at the national level by the competent food safety and public health authorities. Individual countries are required to report data on FBOs every year (in compliance with Zoonoses Directive 2003/99/EC) to the EFSA, which is tasked with collecting, analyzing and describing FBO data annually. FBOs were grouped by European region: Eastern Europe (i.e., Albania, Bosnia and Herzegovina, Bulgaria, Czech Republic, Hungary, Montenegro, Poland, Republic of North Macedonia, Romania, Slovakia, Serbia), Northern Europe (i.e., Denmark, Estonia, Finland, Iceland, Latvia, Lithuania, Norway, Sweden, United Kingdom), Western Europe (i.e., Austria, Belgium, France, Germany, Luxembourg, Netherlands, Switzerland), and Southern Europe (i. e., Croatia, Greece, Italy, Malta, Portugal, Spain, Slovenia). We categorized serotypes as S. Enteritidis (SE), S. Typhimurium and its monophasic variant (STM), and unknown serotypes (i.e., serotypes that were neither determined nor reported along with the outbreak data, that is, serotyping information was unavailable). Because serotypes other than SE and STM had caused low numbers of outbreaks during the whole study period (i.e. <20 outbreaks per serotype), they were all grouped together as other known serotypes. Other known serotypes includes: *S.* 9,12:-:-, *S.* Abony, *S.* Agama, *S.* Agbeni, *S.* Agona, *S.* Bareilly, *S.* Bovismorbificans, *S.* Bredeney, *S.* Chester, *S.* Coeln, *S.* Derby, *S.* Dublin, *S.* Duesseldorf, *S.* Give, *S.* Goldcoast, *S.* group B, *S.* group C2, *S.* group D, *S.*

Indiana, *S.* Infantis, *S.* Kottbus, *S.* Livingstone, *S.* Mbandaka, *S.* Muenchen, *S.* Napoli, *S.* Newport, *S.* Paratyphi B, *S.* Poona, S. Rissen, *S.* Saintpaul, *S.* Senftenberg, *S.* Stanley, *S.* Thompson, *S.* Virchow, *S.* Weltevreden, *S.* 11:z41:e,n,z15, *S.* I, group O:9. Overall, there were 939 outbreaks caused by SE, 130 by STM, 107 by other known serotypes, and 332 by unknown serotypes. The general population size by year and country was retrieved from Eurostat (www.ec.europa.eu/eurostat/).

2.2. Food categorization

To categorize the food products implicated as sources of the FBOs, the food categorization scheme defined under the Zoonoses Catalogue applied by the EFSA was used (EFSA BIOHAZ, 2020). Simple foods were defined as those foods that contained only one single category/subcategory (e.g., salad contains vegetables, even if they contain various vegetables, steak contains beef, ham contains pork, etc.). Accordingly, only simple food commodities were considered in the analysis of the sources of human salmonellosis. Conversely, complex foods were considered as those foods that contain several ingredients that belong to different categories (e.g., bakery products contain eggs, dairy products, grains, sugar, etc.). For the purpose of this study, complex food categories that in the catalogue did not correspond to simple food ingredients, specifically 'bakery products', 'buffet meals', 'mixed food', 'other foods', 'sweets and chocolate', 'canned food products', and 'drinks, including bottled water', were all grouped together as unknown food sources in the analysis because it was not possible to pinpoint the exact components responsible for the infection. The sub-categorization within each main food category varied. For example, meat and meat products were subdivided if possible into 'bovine meat and products thereof', 'pig meat and products thereof' and 'broiler meat and products thereof', but all fruits and vegetables were grouped in one category 'vegetables, fruit and products thereof'. Type of processing or degree of cooking (i.e., raw, undercooked, well-done) were not included in the categorization scheme.

2.3. Data analysis

2.3.1. Source attribution model overview

An established source attribution model based on the analysis of outbreak data (Pires et al., 2012) was used to estimate the relative contributions of different food sources across all countries and the whole study period. In this model, the contribution of a specific source was estimated on the basis of the number of simple food outbreaks that were caused by that source. The proportion of outbreaks caused by each category was used to define the distribution representing the probability that an outbreak i was caused by source j (P_j). The number of ill people involved in the outbreaks was not considered in the analysis to avoid potential overestimation of the importance of infrequent sources that happened to have caused large outbreaks, as described in Pires et al. (2010). This probability was also estimated separately by year, region, and serotypes, as well as by serotype in each region, to explore potential differences in the attribution estimates.

The uncertainty in the probability for an outbreak to be caused by a source was quantified using a Dirichlet distribution, informed by S_i being the number of simple food outbreaks caused by a given source ι. To allow for the estimation of the uncertainty around the attribution (i. e., proportion) estimates for sources that were not implicated in any outbreak, the Dirichlet was parameterized with a uniform prior density function, which means that initially it is assumed that all potential sources of a *Salmonella* outbreak are equally likely as the source of a *Salmonella* outbreak before considering the actual outbreak data. Hence, the probability distribution was defined as Dirichlet ($S_i + 1, S_2 + 1, ..., S_k + 1$) for all k sources considered, with k corresponding to all food categories in the Zoonoses Catalogue (EFSA BIOHAZ, 2020). A Monte Carlo simulation approach was used to estimate the uncertainty around the attributable proportions. This simulation was implemented using the

computational environment R, version 4.2.0 (R Core Team, 2021); the source code is given in Annex 1 Appendix A of the supplementary material. The resulting uncertainty distribution was summarized using the mean and a 95 % uncertainty interval (UI).

2.3.2. Trend analysis

Because data was not over-dispersed and had to be analyzed as rates, and outbreak occurrence over the years varied across European regions and countries, mixed-effects Poisson models were used to assess the significance of inter-annual trends in outbreak occurrence. This analysis was performed overall, by region, serotype, and by serotype in each European region using separate mixed-effects Poisson models, accordingly. For the overall analysis, the model consisted of the annual number of outbreaks (response variable) with year as a fixed effect (predictor). To assess inter-annual changes by region and serotype, the model included a two-way interaction term between year and region, and between year and serotype, separately. To assess inter-annual changes by serotype in each region, a three-way interaction term was added between region, serotype and year. All models included country-specific data nested within the corresponding European region as random effects. The yearly country-specific population size was added as an offset term in each model. To assess the significance of each interaction term, the likelihood ratio test was used. The incidence rate ratio (IRR) with 95 % Confidence Interval (CI) along with *p*-values, were presented. The analysis was performed in R using the 'lme4' package v1.1–27 for linear mixed-effects models and the 'ggeffects' package v1.1.1 was used to plot the predicted counts of outbreaks by serotypes in each European region (Fig. 5).

3. Results

3.1. Descriptive data

In total, 1508 *Salmonella* outbreaks reported across 34 countries in 2015–2019 were included in the analysis. Of these outbreaks, 1040 (69 %) were caused by simple foods and 468 (31 %) by unknown food sources (hereafter referred to as unknown sources), which also included complex foods. A summary of the total number of outbreaks in simple and unknown sources and associated human cases by region, year, and by year in each European region with their respective number of inhabitants is presented in Table 1. The majority of outbreaks were reported in Eastern Europe (48 %), followed by Southern Europe (26 %), and most occurred in 2018 (25 %). The most commonly reported serotype associated with outbreaks was SE (62 %), followed by STM (9 %), whereas for 22 % of the outbreaks, serotyping information was not available.

3.2. Source attribution estimates

3.2.1. Overall attribution estimates

Fig. 1 shows the overall attribution estimates. The most important source was 'eggs and egg products' (hereafter referred to as eggs) (33 %, 95 % UI: 31–36 %), followed by 'pig meat and products thereof' (hereafter referred to as pork) (7 %, 95 % UI: 6–8 %) and general 'meat and meat products' (hereafter referred to as meat) (6 %, 95 % UI: 5–8 %). 'Cereal products including rice and seeds/pulses (nuts, almonds)', 'herbs and spices', and 'tap water, including well water' were the sources with the lowest attribution proportions. Unknown sources accounted for 33 % of the outbreaks (Attribution estimates in supplementary material: Table 2 Appendix A).

3.2.2. Attribution estimates by year

Fig. 2 shows the attribution estimates by year. The highest attribution to eggs was estimated in 2018 and 2016, and the highest attribution to pork was estimated in 2015 and 2019. The attribution to cheese decreased from 7 % in 2015 to 1 % in 2019 and the attribution to 'fish

Table 1
Summary of human salmonellosis outbreaks and involved human cases in simple and unknown (including complex) food sources, overall, by year and European region, 2015–2019.

	Human cases, n (%)	Outbreaks, n (%)	Number of inhabitants
Total	23,318 (100)	1508 (100)	–
Year			
2015	3200 (14)	245 (16)	–
2016	4219 (18)	290 (19)	–
2017	4698 (20)	321 (21)	–
2018	5840 (25)	366 (25)	–
2019	5361 (23)	286 (19)	–
European region			
Eastern Europe	11,087 (48)	721 (48)	–
Northern Europe	3132 (13)	119 (8)	–
Western Europe	4429 (19)	273 (18)	–
Southern Europe	4670 (20)	395 (26)	–
2015			
Eastern Europe	1022 (32)	71 (29)	107,132,026
Northern Europe	491 (15)	29 (12)	97,795,685
Western Europe	844 (27)	66 (27)	193,943,701
Southern Europe	843 (26)	79 (32)	135,070,950
2016			
Eastern Europe	1619 (38)	127 (44)	106,753,391
Northern Europe	512 (12)	31 (11)	98,471,507
Western Europe	669 (16)	53 (18)	195,126,529
Southern Europe	1419 (34)	79 (27)	134,905,822
2017			
Eastern Europe	2579 (55)	178 (55)	106,557,327
Northern Europe	741 (16)	21 (7)	99,098,154
Western Europe	592 (13)	43 (13)	195,927,218
Southern Europe	786 (16)	79 (25)	134,849,164
2018			
Eastern Europe	3097 (53)	221 (60)	106,369,645
Northern Europe	765 (13)	15 (4)	99,660,050
Western Europe	1091 (19)	46 (13)	196,629,190
Southern Europe	887 (15)	84 (23)	134,885,612
2019			
Eastern Europe	2770 (51)	124 (43)	106,204,347
Northern Europe	623 (12)	23 (8)	100,194,515
Western Europe	1233 (23)	65 (23)	197,250,943
Southern Europe	735 (14)	74 (26)	134,531,416

European regions: Eastern Europe (Albania, Bosnia and Herzegovina, Bulgaria, Czech Republic, Hungary, Montenegro, Poland, Republic of North Macedonia, Romania, Slovakia, Serbia), Northern Europe (Denmark, Estonia, Finland, Iceland, Latvia, Lithuania, Norway, Sweden, United Kingdom), Western Europe (Austria, Belgium, France, Germany, Luxembourg, Netherlands, Switzerland), and Southern Europe (Croatia, Greece, Italy, Malta, Portugal, Spain, Slovenia).

and fish products' (hereafter referred to as fish) decreased from 3 % in 2015 to 0.4 % in 2019. The highest attribution to unknown sources was estimated in 2017 (Attribution estimates in supplementary material: Table 3 Appendix A).

3.2.3. Attribution estimates by region

Fig. 3 shows the attribution estimates by region. While eggs were the
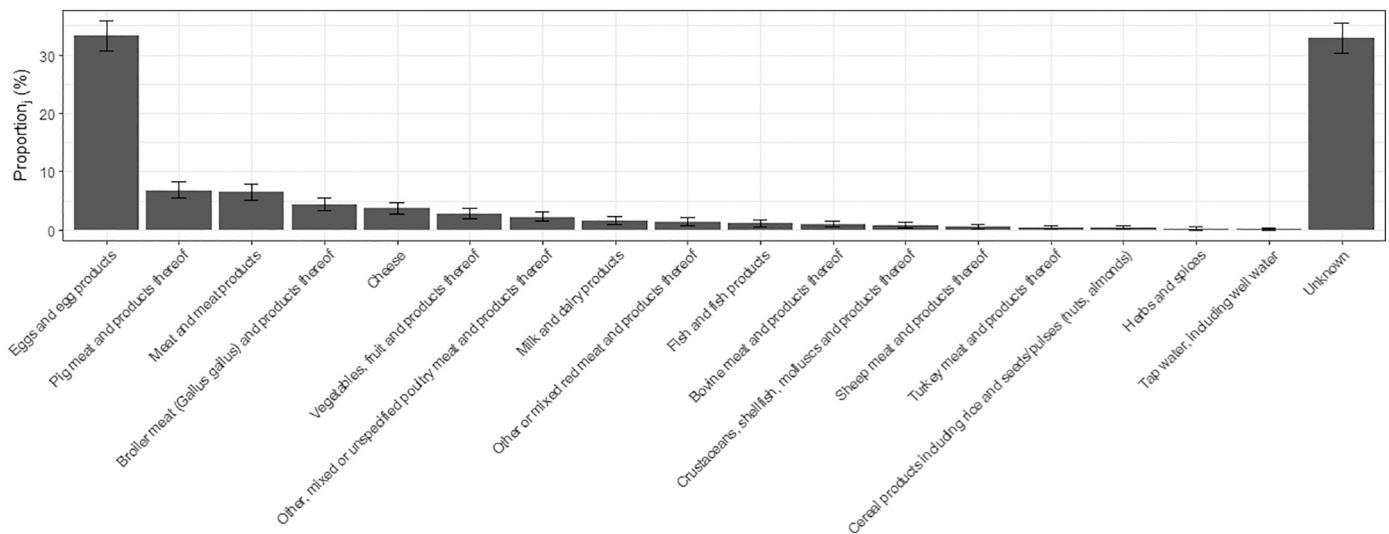
Fig. 1. Proportions of human salmonellosis outbreaks attributed to simple and unknown (including complex) food sources with their respective 95 % uncertainty intervals in Europe, 2015–2019.

most important food source in all regions, the second most important source in Northern and Western Europe was pork and in Eastern and Southern Europe was meat. Other less common food sources varied in each region. The proportion of outbreaks attributed to unknown sources were highest in Eastern Europe and lowest in Western Europe (Attribution estimates in supplementary material: Table 4 Appendix A).

3.2.4. Attribution estimates by serotype

Fig. 4 shows the attribution estimates by serotype. The food with the highest attribution proportion for SE was eggs (37 %, 95 % UI: 34–41 %), followed by meat (7 %, 95 % UI:5–9 %) and 'broiler meat (*Gallus gallus*) and products thereof' (hereafter referred to as chicken) (3 %, 95 % UI: 2–5 %). The most important contribution for STM was from pork (34 %, 95 % UI: 27–42 %), followed by eggs (11 %, 95 % UI: 6–16 %) and cheese (8 %, 95 % UI: 4–14 %). Most outbreaks caused by other known serotypes (i.e., other than SE and STM) were attributed to eggs (17 %, 95 % UI: 11–25 %), followed by pork (10 %, 95 % UI: 5–16 %). The most important source implicated in the outbreaks with missing serotyping information was eggs (34 %, 95 % UI: 29–40 %), followed by pork (9 %, 95 % UI: 6–13 %). The highest attributions to unknown sources were estimated for SE and by the unknown serotypes. Other less common food sources were attributed at lower proportions and varied among serotypes (Attribution estimates in supplementary material: Table 5 Appendix A).

3.2.5. Attribution estimates by serotype in each region

In the supplementary material: Appendix A.6 shows the attribution estimates for SE by European region. Eggs was the most important source for SE in all regions, with the highest proportion reported in Southern Europe, followed by Western Europe, Eastern Europe, and Northern Europe. The second most important source of SE in Eastern and Southern Europe was meat, whereas in Western Europe was cheese and in Northern Europe was chicken.

In the supplementary material: Table 7 Appendix A shows the attribution estimates for STM by European region. Pork was the most important source for STM in all regions, with the highest proportion in Western Europe, followed by Southern Europe, Northern Europe and Eastern Europe. The second most important source for STM was eggs in Eastern and Southern Europe, 'sheep meat and products thereof' (hereafter referred to as sheep meat) in Northern Europe, and cheese in Western Europe.

In the supplementary material: Table 8 Appendix A shows the attribution estimates for other known serotypes (i.e., other than SE and

STM) by European region. The most important source for the other known serotypes in Eastern and Southern Europe was eggs, followed by meat. The two most important sources for the other known serotypes varied between Western and Northern Europe.

In the supplementary material: Table 9 Appendix A shows the attribution estimates for unknown serotypes by European region. The highest attribution proportion for the unknown serotypes was to meat in Eastern and to eggs in Southern Europe, and to pork in Western and Northern Europe. The second highest attribution for the unknown serotypes was to eggs in Eastern and Western Europe, to chicken in Southern Europe, and to meat in Northern Europe.

3.3. Trends in outbreak occurrence

Table 2 shows counts and their respective percentage as well as the IRRs for all *Salmonella* outbreaks and by region and serotype during the whole study period. Overall, the number of reported outbreaks increased significantly over the study period, by 5 % on average per year (IRR: 1.05, 95 % CI: 1.01–1.09). Looking at the different regions, only Eastern Europe showed a significant increase in the number of outbreaks over the years, by 15 % on average per year (IRR: 1.15, 95 % CI: 1.09–1.21). Besides the unknown serotypes, only the known serotypes other than SE and STM showed a significant increase in the overall number of reported outbreaks, by 26 % on average per year (IRR: 1.26, 95 % CI: 1.10–1.44). The annual trends by serotype in each region are shown in Fig. 5 and the IRRs of *Salmonella* outbreaks by serotype in each European region are provided in the supplementary material (Table 2 in Appendix B). The number of SE outbreaks reported in Eastern Europe increased significantly over the years, by 15 % on average per year (IRR: 1.15, 95 % CI: 1.09–1.22), whereas in Northern and Southern Europe, this number declined significantly, by 28 % and 30 % on average per year, respectively (IRR: 0.72, 95 % CI: 0.61–0.85; IRR: 0.70, 95 %CI: 0.62–0.79, respectively). The number of outbreaks caused by the known serotypes other than SE and STM in Western Europe increased significantly by 35 % on average per year, respectively (IRR: 1.35, 95 % CI: 1.04–1.75). The outbreaks caused by the unknown serotypes increased significantly in Eastern and Southern Europe, by 19 % and 25 % on average per year, respectively (IRR: 1.19, 95 % CI:1.01–1.39; IRR: 1.25, 95 % CI: 1.13–1.38).

4. Discussion
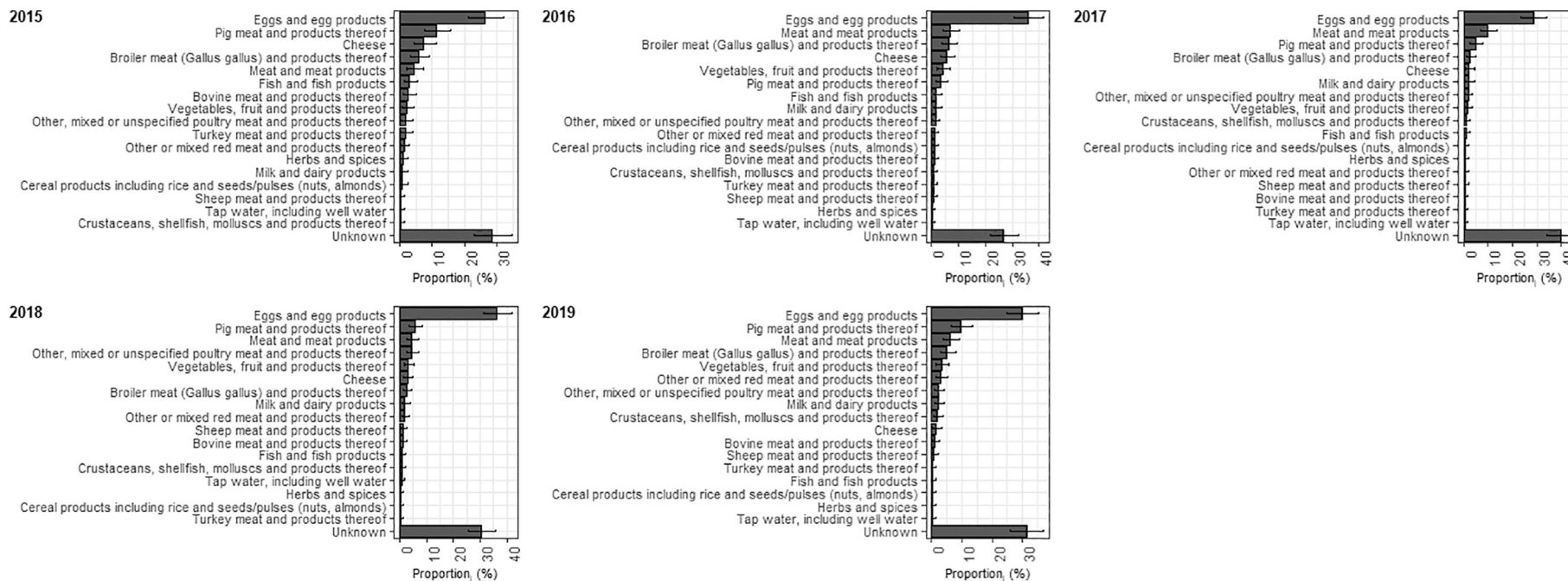
Our results showed that, among 18 simple food sources, the

Fig. 2. Proportions of human salmonellosis outbreaks attributed to simple and unknown (including complex) food sources by year with their respective 95 % uncertainty intervals in Europe, 2015–2019.
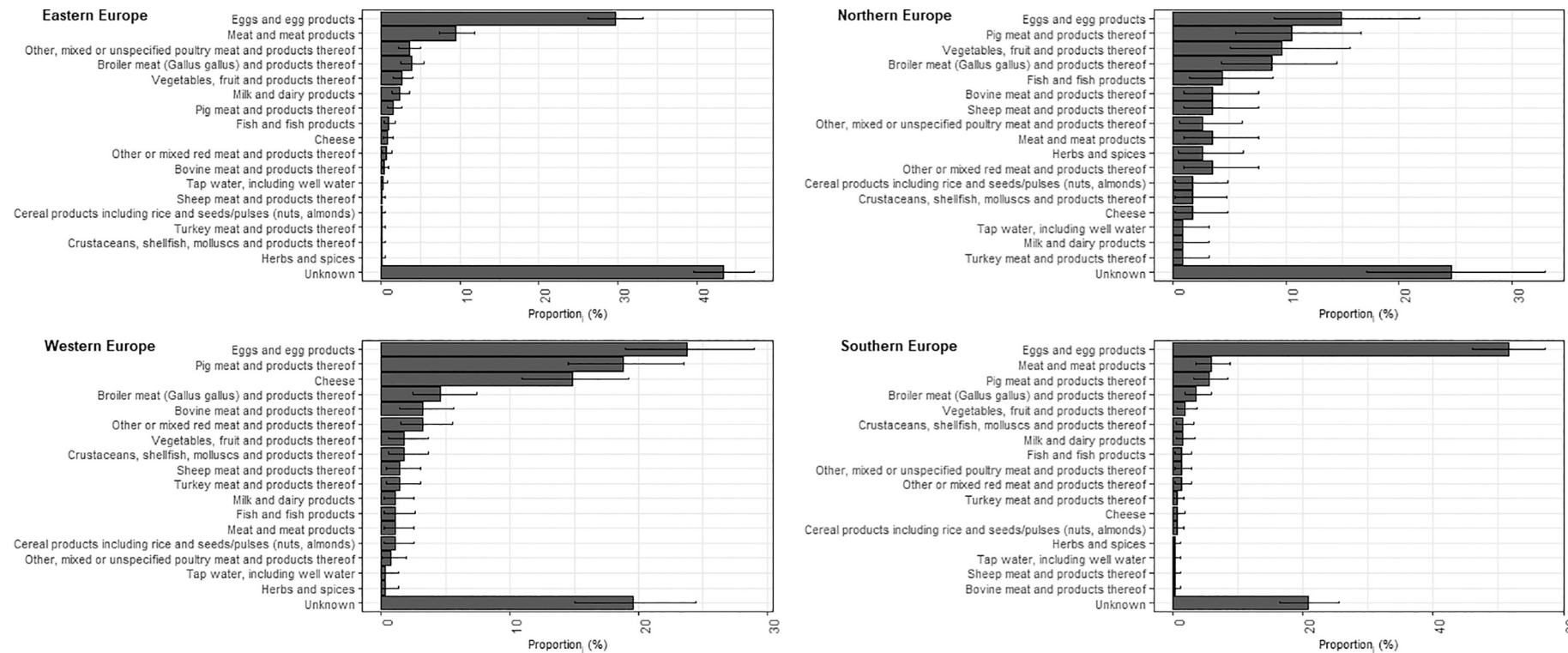
Fig. 3. Proportions of human salmonellosis outbreaks attributed to simple and unknown (including complex) food sources by European region with their respective 95 % uncertainty intervals, 2015–2019.
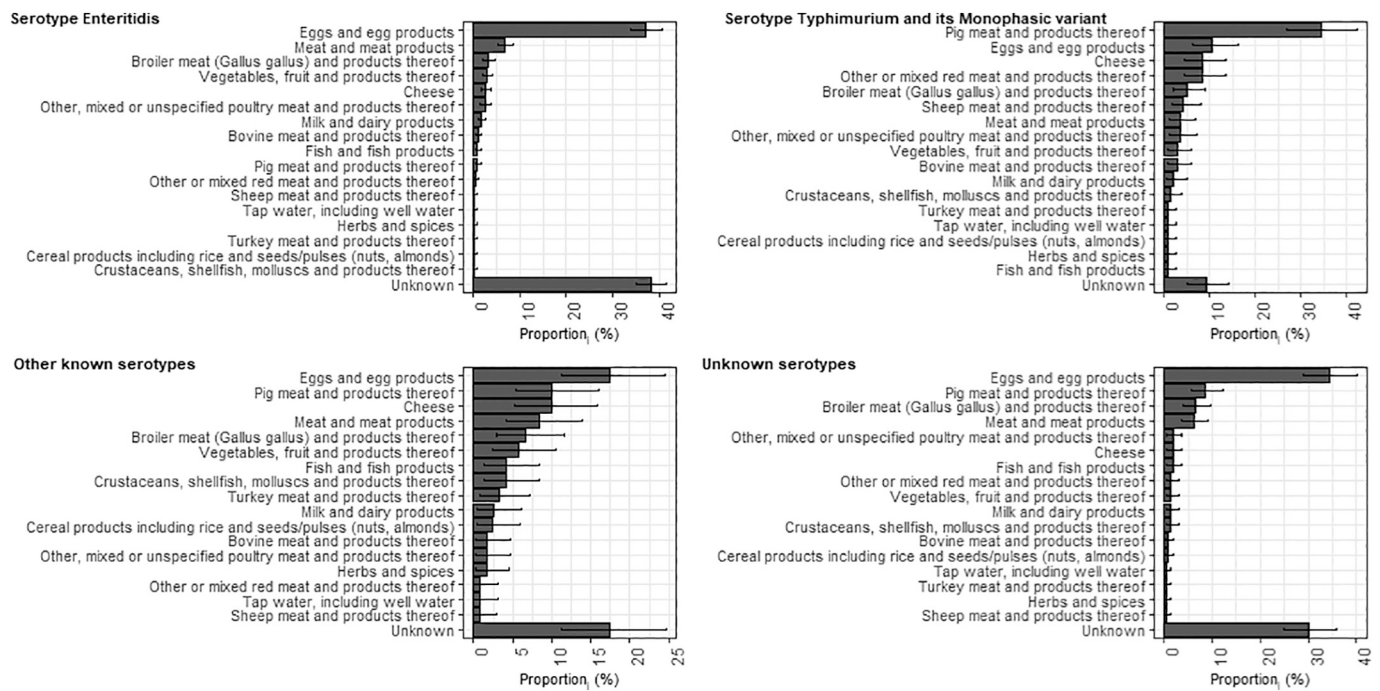
Fig. 4. Proportions of human salmonellosis outbreaks attributed to simple and unknown (including complex) food sources by the most common serotypes reported with their respective 95 % uncertainty intervals in Europe, 2015–2019.

Other known serotypes include: *S.* 9,12:-:-, *S.* Abony, *S.* Agama, *S.* Agbeni, *S.* Agona, *S.* Bareilly, *S.* Bovismorbificans, *S.* Bredeney, *S.* Chester, *S.* Coeln, *S.* Derby, *S.* Dublin, *S.* Duesseldorf, *S.* Give, *S.* Goldcoast, *S.* group B, *S.* group C2, *S.* group D, *S.* Indiana, *S.* Infantis, *S.* Kottbus, *S.* Livingstone, *S.* Mbandaka, *S.* Muenchen, *S.* Napoli, *S.* Newport, *S.* Paratyphi B, *S.* Poona, *S.* Rissen, *S.* Saintpaul, *S.* Senftenberg, *S.* Stanley, *S.* Thompson, *S.* Virchow, *S.* Weltevreden, *S.* 11:z41:e,n,z15, *S.* I, group O:9.

Table 2

Annual incidence of *Salmonella* outbreaks, by European region and serotype from the mixed-effects Poisson regression model, 2015–2019.

Predictors	N (%)	Years (2015–2019)	P
		Adjusted IRR	
Overall[¥]	1508 (100)	1.05 (1.01–1.09)	0.007
European region[a]			
Eastern Europe	721 (48)	1.15 (1.09–1.21)	<0.001
Northern Europe	119 (8)	0.89 (0.78–1.01)	0.070
Western Europe	273 (18)	0.98 (0.90–1.07)	0.342
Southern Europe	395 (26)	0.99 (0.93–1.06)	0.813
Serotype[b]			
Enteritidis	939 (62)	1.00 (0.96–1.05)	0.981
Typhimurium/Monophasic[ŧ]	130 (9)	1.04 (0.92–1.17)	0.539
Other known serotypes	107 (7)	1.26 (1.10–1.44)	0.001
Unknown serotypes	332 (22)	1.16 (1.07–1.25)	<0.001

European regions: Eastern Europe (Albania, Bosnia and Herzegovina, Bulgaria, Czech Republic, Hungary, Montenegro, Poland, Republic of North Macedonia, Romania, Slovakia, Serbia), Northern Europe (Denmark, Estonia, Finland, Iceland, Latvia, Lithuania, Norway, Sweden, United Kingdom), Western Europe (Austria, Belgium, France, Germany, Luxembourg, Netherlands, Switzerland), and Southern Europe (Croatia, Greece, Italy, Malta, Portugal, Spain, Slovenia). Other known serotypes include: *S.* 9,12:-:-, *S.* Abony, *S.* Agama, *S.* Agbeni, *S.* Agona, *S.* Bareilly, *S.* Bovismorbificans, *S.* Bredeney, *S.* Chester, *S.* Coeln, *S.* Derby, *S.* Dublin, *S.* Duesseldorf, *S.* Give, *S.* Goldcoast, *S.* group B, *S.* group C2, *S.* group D, *S.* Indiana, *S.* Infantis, *S.* Kottbus, *S.* Livingstone, *S.* Mbandaka, *S.* Muenchen, *S.* Napoli, *S.* Newport, *S.* Paratyphi B, *S.* Poona, *S.* Rissen, *S.* Saintpaul, *S.* Senftenberg, *S.* Stanley, *S.* Thompson, *S.* Virchow, *S.* Weltevreden, *S.* 11:z41:e,n,z15, *S.* I, group O:9.

[ŧ] Typhimurium and its monophasic variant.

[¥] Crude incidence rate ratio (IRR).

[a] *P*-value of the two-way interaction term between years and European regions: 0.001.

[b] *P*-value of the two-way interaction term between years and *Salmonella* serotypes: <0.001.

consumption of eggs was the most important one among all human salmonellosis outbreaks reported in Europe between 2015 and 2019, followed by pork and other meat products. The importance of these sources has already been highlighted in previous analyses based on the same type of data from 2005 to 2009 (Pires et al., 2011; Pires et al., 2010).

Salmonella remains the most important cause of FBOs in Europe and identifying the main food sources is essential for guiding public health interventions (EFSA and ECDC, 2021). This has become even more important since the (pre-COVID19) long-term declining trend of salmonellosis incidence in Europe has stagnated in recent years (EFSA and ECDC, 2021). In this study, we inferred the relative contributions of different sources of salmonellosis using data from documented outbreak investigations in 34 European countries over a longer timeframe (five years) than previous analyses of this kind (Pires et al., 2011; Pires et al., 2010). These data also allowed us to explore inter-annual trends in both outbreak occurrence and the relative importance of the different sources, as well as potential differences across European regions and serotypes. Pires et al. (2010) compared the attribution estimates derived from the analysis of outbreak data reported to the EFSA during 2005–2006, considering also the number of ill people implicated in these outbreaks, as well as the number of outbreaks themselves, and concluded that the former approach is likely to lead to an overestimation of the importance of some sources when extrapolating to the whole population. This can occur when the data are sparse, if some of the reported outbreaks are very large, or if the sources causing outbreaks and sporadic cases are generally different. We circumvented some of these issues by focusing only on strong evidence outbreaks, regardless of the number of cases involved.

While our results mainly confirm previous evidence on the main sources of salmonellosis based on outbreak data, we observed two main differences. First, the data of the present study provided more information to identify those food sources that might be relevant for the
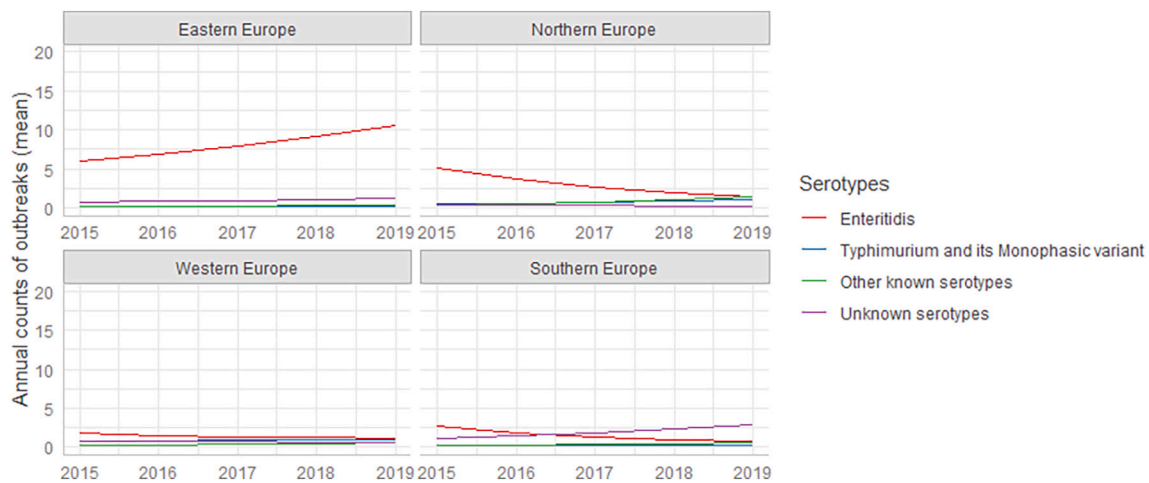
Fig. 5. Annual trends of human salmonellosis outbreaks by serotype per each European region based on the mixed-effects Poisson regression model with a three-way interaction term between year, European region, and serotype (2015–2019).
Other known serotypes include: *S.* 9,12:-:-, *S.* Abony, *S.* Agama, *S.* Agbeni, *S.* Agona, *S.* Bareilly, *S.* Bovismorbificans, *S.* Bredeney, *S.* Chester, *S.* Coeln, *S.* Derby, *S.* Dublin, *S.* Duesseldorf, *S.* Give, *S.* Goldcoast, *S.* group B, *S.* group C2, *S.* group D, *S.* Indiana, *S.* Infantis, *S.* Kottbus, *S.* Livingstone, *S.* Mbandaka, *S.* Muenchen, *S.* Napoli, *S.* Newport, *S.* Paratyphi B, *S.* Poona, *S.* Rissen, *S.* Saintpaul, *S.* Senftenberg, *S.* Stanley, *S.* Thompson, *S.* Virchow, *S.* Weltevreden, *S.* 11:z41:e,n,z15, *S.* I, group O:9. *P*-value of the three-way interaction term: <0.001.

observed improvements in outbreak investigation and reporting, including source tracing, over the last decade in Europe. Second, in our study, the proportion of outbreaks attributed to unknown sources was largest in Eastern Europe, mainly due to the contribution of five new countries in this region (i.e., Albania, Bosnia and Herzegovina, Montenegro, Macedonia, and Serbia). Whereas, previously, the largest proportion of outbreaks attributed to unknown sources occurred in Northern Europe.

The proportion of salmonellosis attributed to eggs did not differ substantially over the study period, which is in agreement with the stable prevalence of the *Salmonella* 'target serotypes', including SE, in flocks of breeding hens, laying hens, and broilers in the EU since 2015 (EFSA and ECDC, 2021). It is known that certain EU member states did not meet their target for reduction of the target serovars in laying hens during 2015–2019, and in some countries, the reported prevalence of SE in layer flocks was considerably high (EFSA and ECDC, 2016, 2017, 2018, 2019, 2021). For example, in 2016, Poland reported that 7 % of layer flocks (i.e., 169 out of 2362) were positive to SE, compared to the target of 2 % or a proportionate target of reduction compared to previous years (EFSA and ECDC, 2017). While eggs from those farms may not be put on the market, it is also likely that not all positive flocks were detected. These findings are also likely to explain why the number of SE outbreaks in Eastern Europe increased.

The proportion of salmonellosis attributed to other, less common sources, varied over the years without a clear tendency during the study period, except for the contributions of cheese and fish, which decreased steadily over the years. Regional differences were also observed. While eggs were the most important source in all European regions, they accounted for a higher proportion of outbreaks in Southern and Eastern Europe. Conversely, pork had a higher proportion of outbreaks attributed to in Western and Northern European countries. This concurs with recent source attribution reports on sporadic salmonellosis cases in countries such as the Netherlands and Denmark, where pork was identified as the important food source in 2019 (DTU, 2020; RIVM, 2020). A previous analysis performed at the European level found that poultry meat ranked second in terms of the most important sources of human salmonellosis outbreaks in Eastern and Southern Europe (Pires et al., 2011). This seems to have changed in more recent years, as we found that (general) meat products have become the second most important source of salmonellosis outbreaks in these regions, indicating a less detailed specification of the sources implicated in the outbreaks, as

reported by the countries in these regions during 2015–2019. Other sources had fairly similar attributions between Southern/Eastern and Northern/Western Europe and their contributions were generally lower and varied across regions. Possible reasons for these differences have been indicated previously (Pires et al., 2011; Pires et al., 2010) and include differences in food consumption habits, *Salmonella* prevalence, and FBO data quality and/or availability across countries.

Eggs were the primary source of SE and pork of STM. This is consistent with previous evidence (Pires et al., 2011; Pires et al., 2010), as SE is a poultry-adapted serotype that is strongly associated with laying hens, whereas STM is strongly associated with red meat-producing animals, such as pigs and cattle (Mughini-Gras et al., 2014). Eggs were also the first and second most important source among outbreaks caused by other known serotypes and by STM, respectively. Although attribution estimates for each serotype included in the category 'other known serotypes' were not generated due to the lower number of outbreaks caused by these serotypes, the attribution to eggs can be expected to vary across the serotypes in this group (Pires et al., 2010). Conversely, the relatively higher attributions of STM to eggs can be expected to vary between European regions (Pires et al., 2010), as also observed in our analysis. We observed that eggs were the second most important source among outbreaks caused by STM in Eastern and Southern Europe, whereas cheese and sheep meat were the second most important sources in Western and Northern Europe, respectively. The relatively higher contribution of pork to the outbreaks caused by the other known serotypes, such as serotype Derby among others, found in this study, was also documented in recent studies where a link between this serotype and pigs was evidenced using either outbreak or sporadic case data (Arnedo-Pena et al., 2016; De Knegt et al., 2015; Rettenbacher-Riefler et al., 2015; Sevellec et al., 2020; Simon et al., 2018). Moreover, food products like vegetables and cheese were also the main sources in the same group of serotypes, mainly in Northern and Western European countries, as also shown in previous studies (Pires et al., 2011; Pires et al., 2010).

The overall number of reported *Salmonella* outbreaks in Europe has increased significantly over the study period and this was driven by the observed increase in the occurrence of outbreaks caused by SE and reported from Eastern Europe. SE was also the predominant serotype causing outbreaks in our study, accounting for over 60 % of the outbreaks. This might be related, to some extent, to the largest European multi-country outbreak of SE ever document so far, which was linked to

contaminated eggs from Poland and involved (recurrently) 14 European countries since 2016 (ECDC and EFSA, 2017; Pijnacker et al., 2019). Indeed, even though actions were taken to control this outbreak already in 2016, the number of cases started to increase again at the end of 2017, with indications that the outbreak went on until at least 2019 (EFSA and ECDC, 2021). In addition, the significantly increasing trend in *Salmonella* outbreaks we observed can also be explained by the increasingly widespread use of advanced molecular methods, such as whole-genome sequencing (WGS), for outbreak detection and source tracing, which has been gradually replacing other typing methods and has become the standard for *Salmonella* typing in several European countries in the last years. This has likely helped in identifying more clusters of cases in routinely collected *Salmonella* surveillance data, improving trace-back and our understanding of the evolution of FBOs (Franz et al., 2016). Yet, whether the increase in reported outbreaks is genuine (i.e., caused by increased exposure to the pathogen) or is the result of enhanced public health surveillance, including routine application of WGS, remains to be clarified further.

The observed decrease in the number of *Salmonella* outbreaks caused by SE in Northern and Southern European countries might be the result of the strong measures applied to reduce SE in these countries. However, it is also important to emphasize that there was a significant increase in *Salmonella* outbreaks caused by unknown serotypes, especially in Eastern and Southern Europe. From the results of the attribution analysis, one-third of the outbreaks caused by unknown serotypes were attributed to eggs, which might be an indication that a number of outbreaks caused by SE in Eastern and Southern Europe were actually 'hidden' among the outbreaks reported with unknown serotyping information in the study period.

Typically, the use of outbreak data for source attribution of foodborne diseases provides an epidemiological picture that may not be fully representative of all infections occurring in the general population. This is because most infections are sporadic, i.e. not all infections occur as part of outbreaks, and outbreaks are generally more likely to 'make the news' and be thoroughly investigated. In addition, reported outbreaks depend on the level of the trace-back, which might provide an incorrect picture when focusing only on the final vehicle of transmission (i.e., food item consumed) because of cross-contamination. Moreover, some food sources are more likely to be associated with reported outbreaks than others, which may lead to an overestimation of their contribution (Pires et al., 2011). These can be relatively more common food sources or sources that are more likely to be investigated. Data on complex foods were included as unknown sources in the analyses. Certainly, to be informative and comparable, the inclusion of complex foods as such in the analysis would have required partitioning their ingredients into simple food categories with the highest likelihood of causing the outbreaks and estimating the underlying uncertainty, which was not possible here. Additional limitations and uncertainties of the model used in the present study have been discussed previously (Pires et al., 2019; Pires et al., 2012; Pires et al., 2010). For instance, the analyses cannot fully account for the differences in the surveillance systems, including laboratory capacity, as well as underreporting in human and food source data across countries. Nevertheless, efforts have been made to harmonize the reporting of outbreaks across European countries in the past decade. Hence, foodborne outbreak data are more comparable nowadays than ten years ago. Future research needs to explore illness attributed to other points of contamination along the farm-to-fork continuum and should consider the role of other transmission routes, i.e. direct contact with animals and the environment, using other source attribution methods, such as the microbial subtyping approach used for sporadic cases (Pires et al., 2014; Pires et al., 2012; Pires et al., 2010).

5. Conclusion

Based on outbreak data, the most important source of human salmonellosis in Europe from 2015 to 2019 was eggs, followed by pork.

Regional, temporal and serotype-associated differences in the relative contributions of the different sources were also observed. Evidence that salmonellosis outbreaks have increased in occurrence in Eastern European countries during the study period, particularly those caused by SE, was also provided. As outbreaks depict only a specific, albeit important, side of salmonellosis epidemiology, comparisons of these results with those based on source attribution of sporadic cases at different points in the transmission chain would provide a complete picture of where human salmonellosis is mainly acquired from.

CRediT authorship contribution statement

Linda Chanamé Pinedo: Conceptualization, Methodology, Formal analysis, Visualization, Writing – original draft, Writing – review & editing. **Lapo Mughini-Gras:** Conceptualization, Methodology, Supervision, Writing – review & editing. **Eelco Franz:** Writing – review & editing. **Tine Hald:** Writing – review & editing. **Sara M. Pires:** Conceptualization, Methodology, Supervision.

Declaration of competing interest

The authors report no conflicts of interest.

Data availability

Data will be made available on request.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ijfoodmicro.2022.109850.

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