Attributing foodborne salmonellosis in humans to animal reservoirs in the European Union using a multi-country stochastic model

L. V. DE KNEGT*, S. M. PIRES AND T. HALD

National Food Institute, Division of Epidemiology and Microbial Genomics, Technical University of Denmark, Denmark

Received 14 January 2014; Final revision 25 June 2014; Accepted 8 July 2014; first published online 1 August 2014

SUMMARY

A Bayesian modelling approach comparing the occurrence of Salmonella serovars in animals and humans was used to attribute salmonellosis cases to broilers, turkeys, pigs, laying hens, travel and outbreaks in 24 European Union countries. Salmonella data for animals and humans, covering the period from 2007 to 2009, were mainly obtained from studies and reports published by the European Food Safety Authority. Availability of food sources for consumption was derived from trade and production data from the European Statistical Office. Results showed layers as the most important reservoir of human salmonellosis in Europe, with 42.4% (7903000 cases, 95% credibility interval 4181000–14510000) of cases, 95.9% of which was caused by S. Enteritidis. In Finland and Sweden, most cases were travel-related, while in most other countries the main sources were related to the laying hen or pig reservoir, highlighting differences in the epidemiology of Salmonella, surveillance focus and eating habits across the European Union.

Key words: Foodborne zoonoses, risk assessment, Salmonella, source attribution, surveillance.

INTRODUCTION

Unsafe food is related to several kinds of diseases, ranging from diarrhoeal syndromes to various forms of cancer. It has been estimated that foodborne or waterborne diarrhoeal diseases were responsible for 2.2 million deaths per year worldwide, 1.8 million of which were children [1]. Salmonella enterica is considered one of the leading causes of gastroenteritis and bacteraemia in the world [2, 3], being estimated to cause 93.8 million human cases and 155000 deaths every year [4]. In the European Union (EU), S. Enteritidis and S. Typhimurium are the most frequently reported serovars, but a wide range of other serovars frequently cause disease in humans and thus are of public health significance [3, 5]. Human infection is most often foodborne, but other routes of infection, namely contact with animals and environmental transmission, have been identified [6, 7].

To design and prioritize effective food safety interventions, it is important to identify which foods are vehicles for specific illnesses [8]. This process is called source attribution, and it can be based on different approaches, such as analysis of outbreak data, analysis of sporadic cases, microbial subtyping, comparative exposure assessment, intervention studies and expert elicitation [8]. Methods for source attribution are intended to provide countries with tools for priority setting in relation to human foodborne and
zoonotic diseases both at the national and regional level, being a critical tool for decision-making aimed at reducing human zoonotic infections faster and more effectively [9].

Hald et al. [10] developed a Bayesian approach based on microbial subtyping for attribution of human cases of salmonellosis to animal reservoirs in Denmark. It made use of Denmark’s extensive surveillance and data collection system to identify the main Salmonella subtypes responsible for human cases and compare them with those found in six animal-food sources. The model was further developed by Pires & Hald [11] to accommodate information from different time periods, and adapted by Mullner et al. [12] to apply it to Campylobacter.

Other EU Member States (MS) have performed Salmonella source-attribution studies based on the cited methods, e.g. Sweden [13] and The Netherlands [14]. A EU-wide source-attribution approach based on outbreak data was also developed [15]; this model attributed disease at the EU region level and did not provide estimates at country level. So, the relative contribution of different food sources for human salmonellosis in the remaining individual countries within Europe had still not been assessed.

This paper presents a study in which the Hald model was adapted to use EU-harmonized data reported by 24 MS to attribute human cases of salmonellosis to their respective animal reservoirs at both country and EU level.

METHODS

Data availability

All utilized data covered the period between 2007 and 2009. EU animal-food production and trade data were available as published by the Statistical Office of the European Union (EUROSTAT) [16]. Data on the prevalence of Salmonella serovars in animals and food were available from the EU-wide Baseline Studies (BS) conducted in different animal species [17–20] and from the European Union Summary Reports (EUSR) as published by the European Food Safety Authority (EFSA) from 2006 to 2009 [21–24]. Data on the number and serovar distribution of human cases reported to the European Surveillance System (TESSy) from 2007 to 2009 were extracted on 6 July 2010 and provided by the European Centre for Disease Prevention and Control (ECDC) through EFSA, except for Poland and Portugal, which directly provided additional datasets with more detailed serovar information. Human data included both case-based and aggregated data and were complemented with other data sources (e.g. national monitoring or laboratory surveillance data not published in the EUSR) when necessary and possible. One of the main obstacles for the use of these data is the underreporting of cases. It is generally understood that the real (and generally unknown) number of illnesses in the population is considerably larger than the number of cases reported in the surveillance system. Moreover, the level of underreporting varies strongly between countries, depending on differences in organization and effectiveness of local surveillance systems [25, 26]. This was taken into consideration by multiplying the country-specific underreporting factors (UFs) estimated by Havelaar et al. [27] to the reported sporadic cases. The UFs were fitted as lognormal distributions, following the methodology described in Hald et al. [28]. The number of cases originally reported in the datasets obtained, the UFs and the resulting adjusted totals can be seen in Table 1.

Data management

Isolates not classified up to the serovar level or reported in aggregated form were reassigned to specific serovars according to proportions observed in previous studies, in the same dataset or in other references, depending on the availability of data in each case. Isolates classified as serogroups were distributed among serovars pertaining to them, in accordance with the Kauffman–White–Le Minor scheme [29]. For sporadic human cases, the main reference dataset used to obtain the proportions for the reassignment was the WHO Global Foodborne Infections Network (GFN) Country Databank (CDB) [30], which contains the 15 most commonly identified Salmonella serovars among human and non-human sources in 84 countries. Animal isolates were reassigned based on proportions found in the BS datasets. Isolates identified as monophasic variants of S. Typhimurium (e.g. S.1,4,[5],12:i:- or S.4,[5],12:i:-) were reassigned to S. Typhimurium [31]. Outbreak-related cases were reassigned using the proportions observed in the outbreak dataset, because some serovars may be more prone to generate outbreaks than others, and thus the proportions observed in reported sporadic cases may not apply. At the EU level, a total of 9.1% of sporadic cases had to be reassigned to specific serovars, varying from zero in Portugal to 73.5% in...
Concerning the consumption data, the domestic amount of a product available in a country was estimated as domestic production minus export, whereas the amount of imported food available for consumption in MS A originating from MS B was estimated as import minus re-export (when re-export was relevant). That was done in order to consider the intra-community food trade and its impact on the incidence of human salmonellosis in importing countries. Trade between EU countries and third-party countries was not considered. To assess the assumption that the EUROSTAT trade could be used as an approximation for consumption data, the final trade dataset was compared with consumption data from the Food and Agriculture Organization (FAO) [32]. A proportional similarity index between the two datasets was calculated, obtaining 91% similarity. Thus, the data was considered appropriate for inclusion in the model.

Based on data quality, food-animal sources included in the final model were broilers, pigs, turkeys and laying hens (as the animal reservoir for eggs). Since neither harmonized EU monitoring data nor the amount of imported food available for consumption in MS A originating from MS B was estimated as import minus re-export (when re-export was relevant). That was done in order to consider the intra-community food trade and its impact on the incidence of human salmonellosis in importing countries. Trade between EU countries and third-party countries was not considered. To assess the assumption that the EUROSTAT trade could be used as an approximation for consumption data, the final trade dataset was compared with consumption data from the Food and Agriculture Organization (FAO) [32]. A proportional similarity index between the two datasets was calculated, obtaining 91% similarity. Thus, the data was considered appropriate for inclusion in the model.

Based on data quality, food-animal sources included in the final model were broilers, pigs, turkeys and laying hens (as the animal reservoir for eggs). Since neither harmonized EU monitoring data nor...
BS data were available for the cattle reservoir, this source was excluded from the final model due to poor data quality, which would significantly compromise the validity of the model results. As for MS, 24 were included in the model: Austria, Belgium, Cyprus, Czech Republic, Denmark, EE, Estonia, FI, Finland, FR, France, DE, Germany, GR, Greece, HU, Hungary, IE, Ireland, IT, Italy, LV, Latvia, LT, Lithuania, LU, Luxembourg, MT, Malta, NO, Norway, NL, The Netherlands, PL, Poland, RO, Romania, SK, Slovakia, SI, Slovenia, ES, Spain, SE, Sweden, UK.) FBO, Foodborne outbreaks.

Serovars not included in the above list were aggregated as ‘Others’.

Data management was performed using SAS Enterprise Guide, SAS/STAT® User’s Guide, v. 8 (SAS Institute Inc., USA). Data origin and countries providing information for each food-animal reservoir, reported human cases and cases related to foodborne Salmonella outbreaks are summarized in Figure 1. A detailed description and discussion of the data management steps, challenges and appraisal of the final quality appear in de Knegt et al. [33].
Model overview

The presented approach for source attribution by microbiological subtyping works by comparing the number of human cases caused by different subtypes of a pathogen with the distribution of the same subtypes in different food-animal sources, utilizing a collection of temporally and spatially related isolates from multiple sources and humans.

The model attributes sporadic domestic cases to food-animal sources. A sporadic case is defined as a subject that could not be associated with a recognized foodborne disease outbreak. Outbreak-related cases are added to the final results of the model, being attributed to the source implicated in the outbreak, if that is known. If not, they are considered outbreaks attributed to the source implicated in the outbreak, clonally distributed among animal hosts [10], the food-animal sources. A sporadic case is defined as a subject that could not be associated with a recognized foodborne disease outbreak.

Model parameters and specifications

The model takes into account the number of cases caused by a serovar, the prevalence of each serovar in each source in each country, the underreporting multipliers in each country, and relative impact of a set of unknown factors, as described in Hald et al. [10]. The unknown factors were included as multi-parameter priors, and account for the differences in the ability of different subtypes to cause disease and of different sources to act as vehicles for infection. Multiple loops were included to accommodate data from the 24 countries. An overview of the model parameterization can be drawn as:

\[ a_{ij} \sim \text{Uniform}(0, 100), \]
\[ q_i \sim \text{Uniform}(0, 100), \]
\[ \lambda_{ci} \sim \text{Poisson}(\alpha_{ci}), \]
\[ \lambda_{cijkl} = \sum_{j=1}^{n} \lambda_{ckji}, \]
\[ \lambda_{ckji} = p_{kij} \times m_{kij} \times a_{ij} \times q_i, \]

where: (1) \( \lambda_{ckji} \) is the expected number of cases per serovar \( i \) and source \( j \) reported in country \( c \) and caused by food produced in country \( k \); (2) \( p_{kij} \) is the prevalence of serovar \( i \) in source \( j \) in country \( k \); (3) \( m_{kij} \) is the amount of source \( j \) available for consumption in country \( c \) produced in country \( k \); when a source is domestically produced in the country of attribution, \( c=k \); (4) \( a_{ij} \) is the source-dependent factor for source \( j \) in country \( c \); (5) \( q_i \) is the subtype-dependent factor for serovar \( i \). The source-dependent factor \( a_{ij} \) was assumed to vary between countries, accounting for variability in consumption patterns and preferences not captured by \( m_{kij} \) also including general variations between sources, e.g. bacterial load/concentration in the food and processing, handling or preparation practices. The subtype-dependent factor \( q_i \) is a one-dimensional parameter, meaning that it is a property of the \textit{Salmonella} serovar and assumed independent.
of the country of infection. The $q_i$ prior for S. Enteritidis is defined as 1, and all other $q_i$ values are estimated relatively to this one. The amount of food source available for consumption in the country where a Salmonella case was reported considers both domestically produced and imported foods ($m_{kj}$). The number of human sporadic and domestic cases attributed to each source per country ($y_{cji}$) is estimated assuming a Poisson distribution of the observed number of sporadic cases per subtype per country ($o_{cji}$). After attribution, sporadic reported cases were multiplied by the correspondent UF in each MS. Model parameters are presented in Table 2.

The model was built in WinBUGS 1.4 (http://www.mrc-bsu.cam.ac.uk/bugs/), which uses Markov Chain Monte Carlo (MCMC) with Gibbs sampling as a default to obtain summary values for posterior distributions. Five independent chains ran for 40,000 iterations each to obtain the values for $a_{ij}$ and $q_i$. Each chain had a different set of starting values for the priors, widely dispersed in the target distribution. Chain convergence was monitored using the methods described by Gelman & Rubin [34] and was considered to have occurred when the variance between the different chains was no larger than the variance within each individual chain, and when the chains had reached a stable level.

RESULTS

The most important source of human salmonellosis at the EU level was estimated to be the laying hen reservoir (i.e. eggs), with 42.4% [7903000 cases, 95% credibility interval (CrI) 4181000–1451000] of cases, followed by 31.1% attributed to pigs (5800000 cases, 95% CrI 2973000–1110000). Broilers and turkeys were estimated to be less important sources of Salmonella, contributing with 12.6% (2350000 cases, 95% CrI 736300–6194000) and 3.8% (702400 cases, 95% CrI 325500–1590000), respectively. A total of 1.6% (292400 cases, 95% CrI 150700–562700) of all salmonellosis cases were reported as being travel-related, and 0.1% (13848) of cases were reported as being part of outbreaks with unknown source. Cases which could not be attributed to any of the sources included in the model corresponded to 8.5% of the total (1578000 cases, 95% CrI 828400–2951000).

The most important serovars contributing to human salmonellosis originating from the animal reservoirs are presented in Table 3. Of all S. Enteritidis infections, 63% (7504000 cases, 95% CrI 3964000–1377000) were attributed to laying hens, whereas 90.8% of S. Typhimurium originated from pigs (2950000 cases, 95% CrI 1510000–5663000). Compared to infections attributed to layers and pigs, a large proportion of cases were caused by other serovars in other sources, such as 4.5% S. Infantis in broilers (106600 cases, 95% CI 32560–284500) and 9.2% S. Newport (226296 cases, 95% CrI 84379–567930) or 4.5% S. Saintpaul (33580 cases, 95% CrI 18052–62443) in turkeys. In those sources, these serovars were not the most frequently associated with cases, but still constituted a significant burden.

Table 2. Parameters used to estimate the number of sporadic cases of salmonellosis attributable to the animal sources

<table>
<thead>
<tr>
<th>Notation</th>
<th>Description</th>
<th>Estimation</th>
</tr>
</thead>
<tbody>
<tr>
<td>$i$ (1–22)</td>
<td>Salmonella serovar</td>
<td>—</td>
</tr>
<tr>
<td>$j$ (1–4)</td>
<td>Food-animal source</td>
<td>—</td>
</tr>
<tr>
<td>$c$ (1–24)</td>
<td>Country where the human case was reported</td>
<td>—</td>
</tr>
<tr>
<td>$k$ (1–24)</td>
<td>Country of origin of the food product*</td>
<td>—</td>
</tr>
<tr>
<td>$o_{cji}$</td>
<td>Observed cases caused by serovar $i$ in country $c$</td>
<td>Data</td>
</tr>
<tr>
<td>$ob_{cji}$</td>
<td>Observed cases caused by serovar $i$ known to be outbreak related in country $c$.</td>
<td>Data</td>
</tr>
<tr>
<td>$y_{cji}$</td>
<td>Observed cases caused by serovar $i$ in country $c$ that was reported as travel-related</td>
<td>Data</td>
</tr>
<tr>
<td>$p_{kji}$</td>
<td>Prevalence of serovar $i$ in source $j$ in country $k$</td>
<td>Data</td>
</tr>
<tr>
<td>$m_{kj}$</td>
<td>Amount of source $j$ available for consumption in country $c$ produced in country $k$*</td>
<td>dunif(0,max $a_{ij}$)</td>
</tr>
<tr>
<td>$a_{ij}$</td>
<td>Source-dependent factor for source $j$ and country $c$</td>
<td>dunif(0,max $q_i$)</td>
</tr>
<tr>
<td>$q_i$</td>
<td>Subtype-dependent factor for serovar $i$</td>
<td>—</td>
</tr>
<tr>
<td>$uf_c$</td>
<td>Underreporting factor for country $c$</td>
<td>dlnorm($q_i$,σ)</td>
</tr>
<tr>
<td>$spdoci$</td>
<td>Total number of sporadic cases caused by serovar $i$ in country $c$</td>
<td>$o_{cji}−y_{cji}−ob_{cji}+1$</td>
</tr>
</tbody>
</table>

* If the food is produced and consumed in the same country, $c=k$. 

---

Downloaded from https://www.cambridge.org/core. IP address: 54.70.40.11, on 30 Sep 2019 at 09:14:39, subject to the Cambridge Core terms of use, available at https://www.cambridge.org/core/terms . https://doi.org/10.1017/S0950268814001903
When looking at attribution within specific countries, 13 MS (Austria, Czech Republic, Estonia, Germany, Greece, Hungary, Latvia, Lithuania, Luxembourg, Slovenia, Slovakia, Spain, UK) had the laying hen reservoir estimated as the most important source of salmonellosis. Pigs were the larger contributor for salmonellosis in eight (Belgium, Cyprus, Finland, France, Ireland, Italy, Poland, Sweden) MS, and the proportion of disease attributed to layers and pigs were similar in The Netherlands. Imported turkey meat and domestic broilers had a localized importance in Denmark and Portugal, respectively. The majority of Salmonella infections in Finland, Sweden and, to a lesser extent, Denmark, Ireland and the UK were reported as travel-related (Fig. 2). Online Appendix A contains the country-specific attribution tables.

As mentioned earlier, a feature of this model is its ability to estimate the country of origin of cases attributed in other countries, as country-specific prevalences and amounts are used. When considering all sources together, Poland was estimated to be the most important source country for human salmonellosis in the EU, contributing 21.3% of cases (3,563,710 cases, 95% CrI 21.1–21.5) and pigs to Poland (24.2% or 1,402,000 cases, 95% CrI 23.9–24.5) and Spain (22.5% or 1,306,000 cases, 95% CrI 22.1–23.0). The majority of cases attributed to layers originated from Greece (21.5% or 1,701,000 cases, 95% CrI 21.2–21.7) and Spain (17.9% or 1,414,000 cases, 95% CrI 17.6–18.2) and Portugal this occurred for broilers. The highest values of $a_{ij}$ for pigs, whereas in Portugal this occurred for broilers. The highest values of $q_i$ were estimated for S. Kentucky, S. Newport, S. Virchow and S. Typhimurium. Values estimated for $a_{ij}$ and $q_i$ are shown in online Appendices C and D.

**DISCUSSION**

This study represents the first attempt to conduct source attribution of human salmonellosis in most European countries. Results suggest that layers were the most important source of salmonellosis in the EU in the study period, being responsible for over

<table>
<thead>
<tr>
<th>Animal source associated with cases</th>
</tr>
</thead>
<tbody>
<tr>
<td>Broilers</td>
</tr>
<tr>
<td>Serovar</td>
</tr>
<tr>
<td>Enteritidis</td>
</tr>
<tr>
<td>Infantis</td>
</tr>
<tr>
<td>Typhimurium</td>
</tr>
<tr>
<td>Virchow</td>
</tr>
<tr>
<td>Kentucky</td>
</tr>
<tr>
<td>Others</td>
</tr>
<tr>
<td>Total cases</td>
</tr>
</tbody>
</table>
40% of all *Salmonella* infections. At the country level, layers were estimated as the most important source in 13/24 countries, followed by pigs, which were the most important source in eight countries. Turkeys were revealed as particularly important only in Denmark and broilers in Portugal. The identification of the most important sources of salmonellosis is a step for prioritization of actions and interventions aimed at reducing the public health burden of disease.

These attribution estimates took into account the amount of food produced and traded between countries as reported to the EUROSTAT database. The underlying assumption was that these data reflected the real flow of foodstuffs and consequent exposure in the countries. However, the dataset used was built based on production, imports, exports and poultry trade datasets, and their quality and consistency depend on factors such as the recording and reporting of information by the countries. It is an important feature in this model that the relative contribution of food-animals produced in different countries is dependent not only on the *Salmonella* prevalence in a source in an exporting country, but also on the amount imported from that country. This is a point in which the EU model differs from the way single-country models work: in a single-country model, $m_j$ works as a subset of $a_j$, as they have the same dimensions [10, 11, 13]; for each source, there is only one value of $m$ and one value for the prevalence of a subtype in that source. The $m_j$, therefore, has the role of weighting the contribution of the different sources, which is, up to a point, already reflected in $a_j$. In the multi-country model, $m$ in a reporting country is composed by subsets of $m$ from different countries or origin of the food sources, each one with its own prevalence. For that reason, even if an exporting country has a very high prevalence in a source, this prevalence will have little impact in an importing country if the amount imported is very small, particularly if another country with a low prevalence exports very large amounts which can, ultimately, ‘dilute’ the high prevalence found in the first country. In short, the amount imported ultimately drives the $m^*p$ in the model formula, particularly when large differences
in trade volume are observed, and so the quality of the trade data has a large impact on the observed results. Trade data may also not necessarily reflect the primary origin of the food. It is not uncommon to import food products into one country in which the foods are then repacked and relabelled and exported to other countries. This may also happen for food products imported from third-party countries. A consequence of this will be that cases are attributed to EU countries, which may not be the primary producers of the food in question. Unfortunately, it is not possible to quantify the impact of this since the information necessary to assess this is not available at the EU level.

Travel-related cases had a localized importance in Northern Europe, notably in Scandinavian countries. Although data quality issues underline any interpretations of the travel data, these results are corroborated by other studies for at least two countries. A previous source attribution study in Sweden allocated 82% of Salmonella infections as travel-related [13], and results of the Danish source account for the same period [35] found a proportion of travel-related Salmonella cases varying between 22 and 46%, which, although higher than estimated by the EU model, accounted for the probability of a case with unknown travel information having been travelling abroad before onset of symptoms, and so add more ‘possible’ travelers. Other countries, such as Spain, had zero cases attributed to international travel, as no travel information was reported. For this model, cases that were reported as acquired outside the country were considered as travel-related cases, and all cases without specific information otherwise were assumed to be domestically acquired. That resulted in the data available being dependent on the patients being asked whether they had been travelling abroad before onset of symptoms, and the information being registered centrally. For that reason, travel-related disease is expected to be underestimated. Differences between patients travelling within or outside Europe were not assessed, as this information was only available for a few MS.

The use of UFs has proved important when considering the effect of source and country contributions at the EU level. This is particularly clear for broilers: this reservoir was the most important only in Portugal, but the use of an UF multiplied its impact within the EU by 2082·9 (mean value), increasing both the relative contribution of broilers and of Portugal to the total cases of salmonellosis, when compared to the original numbers. A similar effect can be observed for the contribution of Greece to the total cases attributed to layers. It should therefore be noted that most of the cases ‘originated’ by countries with large UFs were reported in those same countries, so one should be careful when interpreting these results as countries ‘exporting’ cases to the rest of the EU. Limitations of the use of the UFs include the fact that they have been calculated based on incidence data from returning Swedish travellers [25] and on a burden of illness study from The Netherlands [27]. Therefore, they bring along a set of assumptions related to the eating habits and exposures of Swedish travellers and to the current Salmonella incidence in The Netherlands. Some of the values seem extreme, like for Portugal (2082·9) and Sweden (0·5), and may require a more careful interpretation when used for countries standing alone. However, as a measure of relative contribution among countries within the EU, the UF-adjusted numbers were considered a better reflection of reality than the raw reported data. Further considerations about the limitations of UFs are described in the original paper [27], as well as de Knegt et al. [33].

As there was a large variation in the availability of data from the EFSA BS or EU-harmonized monitoring and surveillance of food sources between MS, only broilers, laying hens, pigs and turkeys could be included in the model. This can result in the misplacing of some cases when their ‘correct’ source is not included. As an example, it is expected that some cases that should be attributed to beef could be attributed to pigs instead, as S. Typhimurium is a common serovar in both sources. However, it should be noted that when the Danish model started being applied, it only included five sources, and it was still a powerful tool in guiding the decisions for the targeted actions regarding broilers, pigs and table eggs that markedly decreased the prevalence of Salmonella in these sources in the last decade [36, 37]. Fruits and vegetables, which are also recognized as sources of salmonellosis, were not included. This happened because the approach employed attributes cases to the original animal reservoirs, meaning that infections caused by fruits and vegetables contaminated with faeces from production animals would be traced to the animal reservoir.

The use of serovar as subtyping level, which resulted from the scarcity or absence of data on further subtyping levels (phage typing, antimicrobial resistance profiles), can also result in misattribution of cases. A good example is S. Enteritidis, which is present in all sources [17–20]. Without more specific
differentiation between subtypes found in each reservoir, cases are likely to be ‘cross-attributed’ among sources. In countries where travel information was not provided, the misattribution of *S. Enteritidis* cases may include the attribution of cases which are actually travel-related to the animal reservoirs. In MS with reasonably good travel data it can be seen that a large proportion of the *S. Enteritidis* infections are linked to travel, indicating that the same situation could be found in MS with poor or no travel data. In that scenario, travel-related cases would be wrongly attributed to one of the sources included in the model, as also observed by Hald et al. [28]. A large proportion of cases was attributed to ‘unknown sources’ in some countries. This category receives cases caused by serovars not found in any of the animal reservoirs in the country, and where there was no positive information on travel. Large differences between countries are therefore explained by the assumption that cases with no travel information were domestic and by the lack of outbreak data in some countries. Finally, the limited number of sources included in the model undoubtedly also explains a proportion of the cases in the unknown category, since cases infected with serovars from reservoirs not included in the model will go to this category as well.

The values of *q* and *a* can be regarded as multiplication factors that indicate the impact a specific subtype and food source has on the number of human cases. For *q*, this may be interpreted as a way of accounting for ‘theoretical’ differences in the subtypes’ virulence and/or their ability to survive in the food chain. As for *a*, it may account for general differences in bacterial load in the product and preparation habits before consumption [8, 11]. Based on the data available, the posterior values are estimated as

\[ a_{ij} \times q_i = (\lambda_{ckji} / (p_{kij} \times m_{ckj})), \]

Because *q* and *a* are estimated considering each food/subtype combination (i.e. a multi-parameter prior), the ranking of results for each parameter alone may not correspond to findings of studies which focused specifically on virulence factors or survival of *Salmonella* in food sources [3, 38].

Despite data limitations and the consequent uncertainty in the results, the source-attribution estimates are considered valid as a first indication of which sources are most important for human salmonellosis in several countries. Limitations include the variability in the human surveillance systems in place in the countries, as well as the different details with which serovar information is reported for both human and animal-food sources. Such uncertainties cannot be statistically quantified, but should be borne in mind when interpreting the results. The relative importance of different food-animal sources was found to vary between countries according to differences in prevalences, trade and consumption patterns and preferences, as well as animal and food production systems, also highlighting regional differences in the focus of surveillance systems in place in EU MS. The results are expected to be useful for the delineation of risk management strategies in the EU. An application of the methods presented here was recently published in an EFSA report [39], where the EU model was used with data collected after the implementation of the EU-harmonized reporting of *Salmonella* in breeding and layer hens. The obtained estimates clearly show the impact of such programmes, when compared to our results [39]. Therefore, the application of the model on a regular basis and the analysis of its results over the years allows, for example, for the evaluation of the impact of implemented control activities, which would also be a way of validating the results.

**SUPPLEMENTARY MATERIAL**

For supplementary material accompanying this paper visit http://dx.doi.org/10.1017/S0950268814001903.

**ACKNOWLEDGEMENTS**

The staff of EFSA’s Task Force of Zoonoses Data Collection are acknowledged for providing the original datasets necessary to conduct this study. The views or positions expressed in this publication do not necessarily represent in legal terms the official position of the European Food Safety Authority. The European Food Safety Authority assumes no responsibility or liability for any errors or inaccuracies that may appear.

The views and opinions of the authors expressed herein do not necessarily state or represent those of the ECDC. The accuracy of the authors’ statistical analysis and the findings they report are not the responsibility of ECDC. ECDC is not responsible for conclusions or opinions drawn from the data provided. ECDC is not responsible for the correctness of the data and for data management, data merging and data collation after provision of the data. ECDC shall not be held liable for improper or incorrect use of the data.
DECLARATION OF INTEREST

The initial version of the EU model was developed with partial funding from contract CT/EFSA/Zoonoses/2010/02 (contract value 45000 Euros) between EFSA and the DTU National Food Institute, in relation to Question No. EFSA-Q-2010-00685.

REFERENCES

31. European Food Safety Authority. Panel on biological hazards (BIOHAZ); Scientific opinion on monitoring and assessment of the public health risk of ‘Salmonella Typhimurium-like’ strains. EFSA Journal 2010; 8: 1826.