Epidemiol. Infect. (2011), **139**, 1246–1253. © Cambridge University Press 2010
doi:10.1017/S0950268810002293

Source attribution of human *Salmonella* cases in Sweden

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(*Accepted 8 September 2010; first published online 14 October 2010*)

SUMMARY

The aim of this study was to identify the sources of sporadic domestic *Salmonella* cases in Sweden and to evaluate the usefulness of a source-attribution model in a country in which food animals are virtually free from *Salmonella*. The model allocates human sporadic domestic *Salmonella* cases to different sources according to distribution of *Salmonella* subtypes in the different sources. Sporadic domestic human *Salmonella* cases ($n=1086$) reported between July 2004 and June 2006 were attributed to nine food-animal and wildlife sources. Of all *Salmonella* cases, 82% were acquired abroad and 2·9% were associated with outbreaks. We estimated that 6·4% were associated with imported food, 0·5% with food-producing animals, and 0·6% with wildlife. Overall, 7·7% could not be attributed to any source. We concluded that domestic food-producing animals are not an important source for *Salmonella* in humans in Sweden, and that the adapted model is useful also in low-prevalence countries.

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

INTRODUCTION

The Swedish *Salmonella* strategy was implemented over 50 years ago, and today the *Salmonella* control programme covers the entire food chain, from feed to food. The programme's main aim is that animals sent for slaughter are free from *Salmonella*. Consequently, animal-derived food products will also be free from *Salmonella*. The programme has proven successful, and the prevalence of *Salmonella* in feed, live animals and animal products produced in Sweden is low. During 1996–2008, on average 0·02% of cattle, 0·01% of pig and 0·03% of poultry carcasses were found to be contaminated with *Salmonella* [1, 2]. Most of the reported human cases were acquired abroad. The average total incidence of *Salmonella* in humans during 1997–2008 was 47 cases/100 000 inhabitants, whereas the average domestic incidence only was 8·1/100 000 inhabitants [3].

The source of domestic *Salmonella* outbreaks may be established by outbreak investigations, but the sources of sporadic domestic cases in humans usually remain unknown. To improve appropriate *Salmonella* control strategies and further prioritize public health interventions in Sweden it is important to identify and investigate the relative role of sources of human infections. A source-attribution model to estimate the relative importance of the major sources of sporadic

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domestic cases of *Salmonella* has been developed [4] and has successfully been applied in countries where *Salmonella* is common in food-producing animals [5, 6]. The aim of this study was to obtain information on the sources of sporadic domestic human *Salmonella* cases in Sweden, as well as to evaluate the usefulness of a previously developed source-attribution model in a country where food-producing animals are virtually free from *Salmonella*.

Routine surveillance of animals, food and humans in Sweden

Notification and typing of isolates

Any finding of *Salmonella* in feed, feed mills, animals, food and humans is notifiable in Sweden. Each primary isolate from feed, feed mills or animals, and from the official control of food is sent to the National Veterinary Institute (SVA) for serotyping. All *Salmonella* Enteritidis and *S.* Typhimurium are phage-typed at the Swedish Institute for Infectious Disease Control (SMI). On a voluntary basis, positive findings in the in-house control in the food industry may also be serotyped and phage-typed. Until the end of 2004, all *Salmonella* strains from human cases were sent to the SMI for serotyping and phage-typing. However, from 1 January 2005 this only applies to domestic *Salmonella* cases.

Surveillance in animals

Food-producing animals are tested according to the *Salmonella* control programme. All samples taken are analysed by bacteriological methods (serological methods are not used). Commercial flocks of layers and breeder flocks of layers, broilers, turkeys and ratites are regularly tested during the production period. All slaughtered poultry, i.e. including ducks, geese, ratites or any other poultry are tested prior to slaughter. Annual testing is performed in pig-breeding herds and twice yearly in sow pools. At slaughterhouses, systematic sampling of lymph nodes is performed annually from about 3000 cattle, 3000 fattening pigs and 3000 adult pigs [1, 2]. If *Salmonella* infection is suspected in live animals, samples must be taken for further investigation. Furthermore, a trace-back/trace-forward investigation is always conducted for positive findings in an attempt to find the source or any possible spread of infection. Culture for *Salmonella* is also performed at sanitary slaughter and, if *Salmonella* is suspected, at necropsy. *Salmonella* in wildlife is surveyed passively. Dead diseased wild animals can be sent to SVA for autopsy without cost and, if relevant, bacteriological culture for *Salmonella* is performed.

Surveillance in food

Domestic food of animal origin is tested according to the *Salmonella* control programme. Swab samples of carcasses are collected at slaughterhouses and about 3500 cattle, 3000 fattening pigs and 3000 adult pigs are sampled annually. From slaughtered poultry, about 3500 neck skins are collected annually. Sampling is also done at cutting plants; about 3500 samples from cutting plants handling beef and pork, and 1200 from plants handling poultry are collected annually [1, 2]. *Salmonella* is also an important parameter in in-house control programmes in both meat- and vegetable-processing enterprises. The results from these control programmes are available to the competent authority upon request. In addition, thousands of samples for *Salmonella* analyses in various food categories are collected annually in the official control performed by the 290 local competent authorities. The sampling protocols are decided by each local authority and the results are reported annually to the National Food Administration (SLV). National baseline studies, for example prevalence studies of *Salmonella* in vegetables, are also performed by the SLV in cooperation with local authorities.

Surveillance in humans

Testing for *Salmonella* may be performed on people seeking medical care due to gastroenteritis. A *Salmonella* case is considered to be of domestic origin if the patient has not travelled abroad during the incubation period. Investigations to identify the source of infection as well as any possible spread are conducted for all domestic cases. Usually, family members or any other persons suspected of having been infected from the same source are also sampled for *Salmonella*. Previously, testing for *Salmonella* was compulsory for people working with unpacked food when returning from visits of >5 days duration outside the Nordic countries. Although no longer compulsory, many food plants still require this testing. An increase in the number of reported cases of any *Salmonella* serovar or phage type (henceforth referred to as subtype) of domestic origin prompts an outbreak investigation. At county level, this surveillance is the responsibility of the County Medical Officer while SMI is responsible at

Table 1. *Notation, description and definition of parameters used to estimate the number of sporadic domestic cases of* Salmonella *per source*

Notation	Description	Estimation
i	Subscript for *Salmonella* type	—
j	Subscript for food source	—
P_{ij}	Number of isolates of *Salmonella* type i collected from source j	Data
a_j	Source-dependent factor for source j	Uniform (0,100)
q_i	Bacteria-dependent factor for type i,	Uniform (0,500)
λ_{ij}	Estimated expected number of sporadic cases infected by *Salmonella* type i and source j	$P_{ij} * q_i * a_j$
λ_i	Estimated expected number of sporadic cases infected by *Salmonella* type i	$\sum_j \lambda_{ij}$
o_i	Observed number of people infected with *Salmonella* type i, assumed to follow a Poisson distribution with mean λ_i	Poisson (λ_i)
λ_j	Estimated number of sporadic cases caused by source j	$\sum_i \lambda_{ij}$

national level. If any food or animals are suspected as a source of an outbreak, the relevant authorities are contacted and involved in the investigation.

MATERIAL AND METHODS

Model overview

The model is based on the method described by Hald *et al*. [4], where the distribution of *Salmonella* subtypes in animals and foods are compared with the subtypes' distribution in humans. The objective is to estimate the number of reported human cases of sporadic *Salmonella* infections that can be attributed to each of the nine different sources included in the current model. The model is built in a Bayesian framework and estimates the contribution of a set of unknown factors. These factors account for the differences in the ability of different *Salmonella* subtypes to cause disease (q_i), and of the different sources to act as a vehicle for infection with *Salmonella* (a_j). Both factors were defined as uninformative prior distributions as presented in Table 1. The iterative process, under a Markov Chain Monte Carlo simulation, allows for the estimation of posterior estimates for these factors with the model equation.

The basic model equation is

$$\lambda_{ij} = P_{ij} * q_i * a_j, \quad (1)$$

where λ_{ij} is the expected number of human cases per *Salmonella* type i and source j, P_{ij} is the number of isolates of *Salmonella* type i collected from source j, q_i is the bacteria-dependent factor for type i and a_j is the food source-dependent factor for source j.

The bacteria-dependent factor q_i describes differences in the ability of the different *Salmonella* subtypes to cause disease, accounting for differences in the ability to survive of the subtypes in the food chain and potential differences in pathogenicity. The food source-dependent factor (a_j), may account for characteristics of the food item that influence its ability to act as a vehicle for exposure to the pathogen and infection (e.g. general differences in the pathogen load, food characteristics influencing growth factors, or preparation and handling procedures). It also reflects differences in the epidemiology, sensitivity of the surveillance programmes, randomness of the sampling schemes, and differences in exposure to the sources. In the current model, differences in consumption patterns of the investigated foods in the population are also accounted for in a_j. The prior estimate of q_i for the serovar *S*. Enteritidis was defined as 1. All remaining q_i estimates are relative to this value.

The model was ran with five independent Markov chains of 40 000 iterations each, which proved able to provide appropriate convergence as monitored by the method described by Gelman & Rubin [7].

Data used in the model

The study period was 2 years, from 1 July 2004 to 31 June 2006.

Salmonella findings in humans

Data, including serovars and phage types, on all human cases were obtained from a database at SMI. In all, 1296 domestic cases including 227 outbreak cases

https://doi.org/10.1017/S0950268810002293 Published online by Cambridge University Press

(originating from 17 outbreaks) were reported during the study period. All *Salmonella* outbreak-associated cases except one case per outbreak were subtracted from the dataset, and consequently domestic outbreaks were represented with one single case in the model. In total, 1086 (1296 minus 210) sporadic domestic human *Salmonella* cases were included in the model (see Appendix, available online). If two different serovars or phage types were reported from the same person, these may have been registered as two cases, but this situation is regarded as unusual. The remaining outbreak cases ($n=210$) and travel-related cases ($n=5859$) were added to the output of the model after the attribution was performed. A total of 39 cases were excluded (whether they were domestic or travel-related) as data was missing.

Salmonella findings in animals and food

Data for food-producing animals (pigs, cattle and poultry) and wild animals (small passerine birds, seagulls, hedgehogs) were obtained from the National Board of Agriculture. From food-producing animals, only the primary isolates (the first isolate from an infected herd) were included. Furthermore, positive samples from surveillance at slaughterhouses and cutting plants were also included.

Data on *Salmonella* findings in food were collected by SLV from the following sources: (i) official control by local authorities, (ii) official control by SLV, (iii) in-house control performed by food establishments, (iv) import control, (v) outbreak data reported to SLV and SMI; and (vi) results from bacteriological analysis of food items performed at the SVA or SMI.

Due to lack of representative data on *Salmonella* occurrence in imported foods, source data were found to be of insufficient input information for the model. As a substitute, travel-related human cases were included in the model as a source reflecting imported foods, and were assumed to reflect undetected *Salmonella*-contaminated imported food. Because serotyping and phage-typing of travel-related cases ceased at the end of 2004, used data ($n=6470$) was obtained from an earlier period (1 January 2003 to 31 December 2004). This was not considered to severely affect the output of the model, as the serovar distribution was rather stable over time.

In all, data on 6688 isolates from different sources were collected, including imported foods ($n=132$), travel-related cases (proxy for imported foods) ($n=6470$), pigs ($n=17$), cattle ($n=29$), layers ($n=3$), broilers ($n=1$), geese ($n=2$), passerine birds ($n=21$), seagulls ($n=10$) and hedgehogs ($n=3$). After exclusion of subtypes where no human domestic cases were reported, a total of 6161 isolates from sources remained, imported foods ($n=117$), travel-related cases (proxy for imported foods) ($n=5977$), pigs ($n=17$), cattle ($n=26$), layers ($n=3$), broiler ($n=1$), geese ($n=1$), passerine birds ($n=21$), seagulls ($n=10$) and hedgehogs ($n=2$) (see Appendix). Cases were allocated to these 10 sources, and cases allocated to imported foods and travel-related cases (proxy for imported foods) were summarized to represent total number of cases allocated to imported foods.

Cases where (i) information on the serovar and/or phage type was missing, (ii) the *Salmonella* subtype was not found in any of the sources, and (iii) information in sources was not sufficient for the model to estimate the q_i values for these subtypes, were merged into one group '*Salmonella* others'. The final dataset consisted of 78 different *Salmonella* subtypes and the group '*Salmonella* others' (see Appendix).

RESULTS

Only sporadic domestic human cases of *Salmonella* were modelled and attributed to the sources, but results are expressed as the proportion of the total number of reported human *Salmonella* cases caused by different sources, including travel- and outbreak-related cases (Table 2, Fig. 1). The majority 5859 (82%) of notified *Salmonella* cases in humans were acquired abroad and 210 (2·9%) were associated with outbreaks. Sporadic domestic human cases accounted for 1086 (15%) of all reported cases. The model identified imported food as the most important source for sporadic domestic cases, responsible for 458 (6·4%) of all reported cases. Of these, 449 (6·3%) were allocated to the proxy for imported food (travel-related human cases) and nine (0·13%) to findings in imported food. Food-producing animals and wildlife each accounted for 34 (0·5%) and 44 (0·6%) cases. Pigs, cattle, layers, broilers, and geese each accounted for six (0·08%), seven (0·1%), 11 (0·16%), seven (0·09%) and three (0·04%) cases. Small passerine birds, seagulls, and hedgehogs each accounted for 16 (0·22%), six (0·09%) and 22 (0·3%) human sporadic cases; 7·7% could not be attributed to any source.

The food source-dependent factor a_i varied between 0·01 and 25, whereas wild animals, broilers and layers presented the highest values (>1). The bacteria-dependent factor q_i varied between 0·5 and 282, the

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Table 2. *Human domestic sporadic* Salmonella *cases reported between 1 July 2004 and 31 June 2006 (mean percent and 95% credibility interval) attributed to nine different sources and an unknown source. Cases attributed to groups of sources (food-producing animals and wildlife) are also detailed. Percent travel-related cases and cases due to domestic outbreaks are also given*

	Attributed human cases (mean and 95% credibility interval)		
Source	Mean (%)	2·5%	97·5%
Imported food	6·4	5·8%	7·1%
Food-producing animals			
Pigs	0·08	0·002%	0·28%
Cattle	0·10	0·003%	0·30%
Layers	0·16	0·08%	0·27%
Broilers	0·09	0·01%	0·19%
Geese	0·04	0·01%	0·10%
Wild life			
Small passerine birds	0·22	0·05%	0·37%
Seagulls	0·09	0·02%	0·17%
Hedgehogs	0·30	0·04%	0·49%
Unknown source	7·7	7·1%	8·3%
Outbreaks	2·9	—	—
Travel-related cases	82	—	—
Total	100		
All food-producing animals	0·5	0·3%	0·8%
All wildlife	0·6	0·3%	0·9%

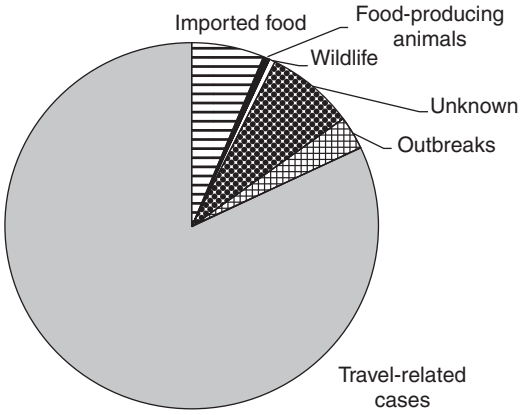

Fig. 1. Sources of *Salmonella* in humans in Sweden, 1 July 2004 to 31 June 2006 ($n=7155$). Estimated major sources for sporadic cases ($n=1086$), number of outbreak cases ($n=210$) and cases contracted abroad ($n=5859$).

median value being 12% and 92% of the subtypes presenting a value <100.

DISCUSSION

In this study, a source-attribution model was applied to Swedish data, and results show that the most important source for domestic sporadic human cases was imported food, accounting for 6·4% of all human *Salmonella* cases (Table 2, Fig. 1). The results suggest that the most efficient way to decrease the number of sporadic domestic human *Salmonella* cases is to decrease the prevalence of *Salmonella* in imported food. However, the use of data from travel-related cases as a complement to available data for imported food can be questioned. Nevertheless this approach was considered the best available option for the model used. The reasoning behind the use of this approach was that both imported food and travel-related human cases are contaminated/infected abroad. The serovar distribution in different countries may vary, and although the countries of origin of contaminated food may not be exactly the same as the countries where travel-related cases contract *Salmonella*, it was assumed that this did not severely affect the output of the model. However, it cannot be excluded that cases secondary to travel-related cases could have been assigned to the source 'proxy for imported food'. Previous studies have estimated that about 4% of reported *Salmonella* cases correspond to secondary cases [Y. Andersson (SMI), personal communication]. Thus, we can expect that a similar proportion of the cases attributed to the proxy for imported food might be cases secondary to travel-related cases. It was concluded that better data on imported food and on fresh

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produce are needed for future source-attribution studies. The need for better data is also supported by the fact that a similar proportion of cases (7·7%) could not be attributed to any source. Nevertheless, it is probable that a substantial proportion of domestic cases were caused by imported food. This is hypothesized because despite the control measures in place for some imported foods of animal origin, imports of *Salmonella*-contaminated consignments cannot always be prevented. Additionally, vegetables are an increasing source of *Salmonella* infections for humans [8], and there is no requirement to test fresh produce imported to Sweden for *Salmonella*. Furthermore, the majority (90%) of *Salmonella* outbreaks attributed to defined food commodities between 1992 and 2009 ($n=40$), were considered to be due to imported food (SLV, unpublished results). In summary, we concluded that although misclassification may have occurred, our estimate of 6·4% of all domestic cases being attributed to imported food is not an overestimation.

Our results suggest that domestic food-producing animals are not an important source for *Salmonella* in humans in Sweden. Pigs, cattle, layers, broilers, and geese each accounted for $<0{\cdot}2\%$ of the *Salmonella* cases in humans). Swedish food-producing animals are practically free from *Salmonella* [2, 9–11]. These low levels contrast with most other European countries, where the prevalence of *Salmonella* in food-producing animals is much higher [9–11], as well as with source-attribution studies performed in other countries, which have identified food-producing animals as an important source for *Salmonella* [5, 6].

Interestingly, similar proportions of cases were attributed to each of the included wildlife sources, where $\leqslant 0{\cdot}3\%$ was attributed to each of the sources small passerine birds, hedgehogs, and seagulls. Each of these sources seems to act as a reservoir for specific subtypes. *S*. Typhimurium DT40 and U277 are usually found during winter in small passerine birds submitted for autopsy and at bird-feeding places [12]. *S*. Typhimurium DT40 and U277 are also the most common *Salmonella* subtype isolated in cats, probably acquired when eating infected birds [13]. In humans, these phage types are usually found in children, mostly also in late winter [14], and the source of infection is probably also contaminated bird-feeding places or infected outdoor cats. *S*. Typhimurium DT41 is the most common subtype in seagulls in Sweden, and *S*. Typhimurium DT1 in hedgehogs.

To our knowledge, wildlife has not been included in any source-attribution study of *Salmonella* infections elsewhere, which may be explained by the smaller contribution of wildlife to human salmonellosis compared to food-producing animals in most countries. However, in countries where the major sources of infection for a specific pathogen has been reduced or eliminated, as is the case in Sweden, Norway, and Finland, other minor sources may be detected. This is in accordance with what has been observed for bovine tuberculosis. Before eradication of this disease in Sweden, infected cattle were the major source of infection. However, after eradication of the disease in cattle, humans infected with *Mycobacterium bovis* were identified as an important source for infection in cattle [15]. Another example is the contribution of feed as a source of *Salmonella* in pig production. In countries where *Salmonella* in pig herds is common, feed may not be considered to be an important source, but it becomes more evident as a source for infection in countries where pig herds are practically free from *Salmonella* [16, 17].

The source-dependent factor a_i reflects characteristics of the source, the frequency/intensity of exposure and the sensitivity of the surveillance system for that source [4]. In our study, consumption data were not used, and thus a_i also reflects differences in consumption and exposure patterns. Because these factors vary between sources, further comparison of a_i values were not made.

The q_i values represent several factors describing a complex system that is not fully understood [18]. Besides differences in survivability of different serovars along the food chain and potential differences in their pathogenicity [18], other factors such as an undetected outbreak can affect the q_i value. As the 95% credibility intervals hardly showed any significant difference between the q_i value, an analysis setting equal q_i values and thereby omitting estimating q_i from the model was done. The number of cases allocated to travel (proxy for food) was lower compared to the default model and the number of cases allocated to imported food items was higher compared to the default model, but the total number of cases allocated to food animals, wild life and imported food groups (including both sources, i.e. imported cases and food) did not differ significantly from the default model (results not shown). Furthermore, as the deviance information criterion (DIC) value was lower for the default model compared to the model with fixed q_i values (results not shown) the default model was considered to be the best model.

In the current study, the prior estimates of q_i for all *S*. Enteritidis phage types were assumed to be equal,

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as this decreased the number of parameters that had to be estimated by the model. There is no reason to believe that q_i should be different for different *S*. Enteritidis phage types, and similar assumptions have been made previously [4]. In the paper by Hald *et al*. [4], the q_i for all *S*. Typhimurium were also assumed to be equal. However, as multi-resistant *S*. Typhimurium are probably included in the data, we chose to use this approach only for *S*. Enteritidis phage types. The results of this study demonstrate that further evaluation of the interpretation of the q_i values is needed, for example by comparison of the output of different source-attribution studies.

Outbreak investigations may be successful in identifying the original source of the *Salmonella* infections. Yet little is known about the source of sporadic domestic cases. Source attribution has successfully been used to identify sources of sporadic cases in countries where *Salmonella* is common in food-producing animals [5, 6]. To the best of our knowledge, this paper is the first attempt to apply source attribution to sporadic *Salmonella* cases in a country where food-producing animals are virtually free from *Salmonella*. The main problem identified in our study was lack of data. In the source-attribution study by Hald *et al*. [4], 2611 sporadic human cases (1976 domestic cases and 962 with unknown place of infection) were attributed to nine different sources represented by 1455 *Salmonella* isolates for one year (1999). In our study, the annual number of sporadic cases was about 500, and from the nine sources slightly more than 100 *Salmonella* isolates per year were reported. To increase the amount of data available for the analysis, we expanded the study period to 2 years. This may lead to errors because the timespan between the attributed cases and the finding of a specific type of *Salmonella* in sources may increase from at the most 1 year, as in the study by Hald *et al*. [4], to 2 years as in the current study. A new three-dimensional model, using year as a third dimension (in addition to subtype and source), has been recently developed [18]. This model provides more robust estimates, particularly of the bacteria-dependent factors, because data from several years can be used. However, it does not solve the problem of artificial division of time periods into 12-month intervals. This division prevents the attribution of human cases occurring early in one year to *Salmonella*-contaminated sources identified late the previous year. Despite this deficiency, it is our intention to collect data of higher quality, especially concerning imported food, and for a longer time period (at least 5 years) and apply this new source-attribution approach to these data.

Despite the shortcomings of the model, we conclude that the presented approach is useful to attribute human sporadic salmonellosis in Sweden and acknowledge the utility of a future application of the model to more complete and accurate data.

NOTE

Supplementary material accompanies this paper on the Journal's website (http://journals.cambridge.org/hyg).

ACKNOWLEDGMENTS

This work was supported by Med-Vet-Net, a European Network of Excellence for Zoonoses research, working for control and prevention of zoonoses and foodborne diseases.

DECLARATION OF INTEREST

None.

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