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EXTERNAL SCIENTIFIC REPORT

Development of a *Salmonella* source-attribution model for evaluating targets in the turkey meat production[1]

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ABSTRACT

A *Salmonella* source attribution model based on a microbial-subtyping approach was developed to estimate the public health effect of setting a new target for the reduction of *Salmonella* in fattening turkey flocks in the European Union. The model considers the quantitative contribution and relevance of different *Salmonella* serovars found in turkeys to human salmonellosis and includes 25 Member States, four animal-food sources of *Salmonella* (turkeys, broilers, laying hens and pigs) and 23 *Salmonella* serovars. This turkey-target *Salmonella* attribution model (TT-SAM) employs prevalence and serovar distribution data from the EU statutory monitoring and EU-wide Baseline Surveys on *Salmonella* in animal-food sources, data on incidence and serovar distribution of human salmonellosis, and food availability data. It is estimated that around 2.6 %, 10.6 %, 17.0 % and 56.8 % of the human salmonellosis cases are attributable to turkeys, broilers, laying hens (eggs) and pigs, respectively. Of the turkey-associated human salmonellosis cases, around 63 % is estimated to be due to serovars other than the currently regulated *S.* Enteritidis and *S.* Typhimurium. Four serovars (*S.* Kentucky, *S.* Saintpaul, *S.* Senftenberg and *S.* Kottbus) had turkeys as the most important reservoir for human infections. Different scenarios are presented showing changes in the percentage of turkey-associated human salmonellosis cases under different prevalences of *Salmonella* in fattening turkey flocks. Comparing the situation in 2010 with a theoretical combined prevalence of 1 % for *S.* Enteritidis and *S.* Typhimurium (i.e. the current target), the expected reduction in number of turkey-associated cases is very small. Since, all MSs except one have already met the transitional target, this result is not unexpected. However, when adjusting the combined prevalence of all serovars to 1 %, a large reduction in the percentage of turkey-associated cases compared to the situation in 2010 is achieved. Uncertainty and data limitations are discussed thoroughly and a number of recommendations are provided.

KEY WORDS

Salmonella, source attribution, turkey meat production, target setting

DISCLAIMER

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SUMMARY

Following a request from the European Commission, the Scientific Panel on Biological Hazards (BIOHAZ) was asked to assess the relative public health impact if a new target for reduction of *Salmonella* is set in fattening turkey flocks being 1 % or less remaining positive for all *Salmonella* serovars with public health significance, compared to (1) the theoretical prevalence at the end of the transitional period (1 % or less flocks remaining positive for *Salmonella* Enteritidis and/or *Salmonella* Typhimurium), and (2) the real prevalence in 2010 reported by the Member States (MSs). This external scientific report describes the work conducted in order to support the BIOHAZ Panel in answering this request.

A turkey-target source attribution model (TT-SAM) was developed to provide estimates for the quantitative contribution of turkeys and other major animal-food sources to the estimated true burden of human salmonellosis in the EU. The mathematical model was based on the so-called microbial subtyping approach, which allows for distinguishing between the different *Salmonella* serovars. The basic principle is to compare the serovar distributions observed in different animal-food sources with the serovar distribution found in humans. A similar model has previously been applied to answer an equivalent question for *Salmonella* targets in the broiler production.

The TT-SAM model employed the following data: (i) the results from the harmonized EU monitoring in turkey, broiler and laying-hen flocks in 2010, (ii) the results from the EU-wide *Salmonella* Baseline Surveys on slaughter pigs, (iii) the reported cases of human salmonellosis in EU in 2010 as provided by the European Centre for Disease Prevention and Control (ECDC), and (iv) the amount of each food source available for consumption by MS as estimated from different data sources on production, import and export. The model included data from 25 MSs, four animal-food sources (turkeys, broilers, laying hens and pigs) and 23 individual serovars. To take account for differences in underreporting of human salmonellosis cases, MS-specific underreporting factors were applied in the model. Some sources of *Salmonella* (e.g. cattle/beef) were not included in the model due to lack of data. The possible influence of this is discussed.

First a baseline model applying reported prevalence data from the harmonized monitoring in turkey flocks in 2010 was developed. Then in order to answer the Terms of Reference, seven different scenarios, where the combined prevalences of specific serovars were changed, were developed and the results compared to the results of the baseline model.

The results of the baseline model indicated that 2.6 % (95 % CI: 1.2-5.2) of all human salmonellosis cases (i.e. estimated true number of cases when accounting for underreporting) in the EU were attributed to the turkey reservoir. This corresponds to 135 100 (95 % CI: 60 790-293 600 human cases in 2010. Around 63 % of the turkey-associated human salmonellosis cases were caused by serovars other than the currently regulated serovars *S.* Enteritidis and *S.* Typhimurium. Four serovars (*S.* Kentucky, *S.* Saintpaul, *S.* Senftenberg and *S.* Kottbus) had turkeys as the most important reservoir for human infections.

For the other animal-food sources included in the model, the attribution estimates were that 56.8 % (95 % CI: 48.2-65.8), 10.6 % (95 % CI: 5.1-18.3) and 17.0 % (95 % CI: 11.3-24.0) of the estimated number of human salmonellosis cases could be attributed to the pig, broiler and laying-hen reservoir, respectively. However, when looking at the relative risk between turkey meat and the other three sources weighted by the tonne of meat/eggs available for consumption, this picture changes, indicating that the risk of infection for the individual consumer is highest when consuming shell eggs closely followed by the consumption of pig meat, whereas the risk is lower for turkey and broiler meat.

For the scenario analyses, the largest reduction was found for the scenario, where the overall prevalence (i.e. the combined prevalence of all serovars) in turkey flocks per MSs is reduced to 1 %. Here a reduction in the number of turkey-associated human cases of 83.2 % (95 % CI: 79.0-87.4) compared to the baseline model was estimated. In absolute numbers, this corresponds to a reduction of 112 300 (95 % CI: 50 410-243 400) human salmonellosis cases. Overall, this scenario was estimated to reduce the percentage of human turkey-associated cases from 2.6 % to 0.4 %.

A combined prevalence of the top-6 serovars in turkeys that contribute most to human cases is reduced to 1 % or less in turkey flocks per MSs gave the next largest reduction in the number of turkey-associated human cases of 37.2 % (95 % CI: 19.2-54.0) compared to the baseline model. In absolute numbers, this corresponds to a reduction of 48 110 (95 % CI: 22 580-100 500) human salmonellosis cases. Overall, this scenario was estimated to reduce the percentage of human turkey-associated cases from 2.6 % to 1.7 %.

The least reduction was obtained in the scenario, where the achievement of the current target of the EU control programme of *Salmonella* in turkey flocks would be met. This analysis resulted in an estimated reduction in the number of turkey-associated human salmonellosis cases of only 0.4 % (95 % CI: 0.1-1.3) compared to the baseline model. In absolute numbers, this corresponds to an estimated reduction of 594 (95 % CI: 121-1 901) human cases. Since, all MSs except one have already met the transitional target, this result is not unexpected.

Several assumptions and factors contributing to the uncertainty and validity of the results are discussed. These 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 in both humans and animal-food sources. Such uncertainties cannot be statistically quantified, but should be kept in mind when interpreting the results.

The lower attribution estimate obtained for the laying-hen reservoir (i.e. shell eggs) by the TT-SAM model as compared to previous models is supported by data, since both the reported number of cases in EU (particularly *S.* Enteritidis cases) and the prevalence of *Salmonella* (particularly *S*. Enteritidis) in laying hen flocks have been decreasing from 2008 to 2010. The improved surveillance and control of *S*. Enteritidis in laying hens in many MSs is assessed to be responsible for a major part of this reduction.

The conclusions also emphasise that the reduction of the overall burden of human salmonellosis must be expected to change the attribution estimates, particular the relative estimates, following the logic that if one or more sources contribute significantly less to the overall burden other sources will contribute relative more. The high relative attribution estimate obtained for pig meat by the TT-SAM model, is believed to be partly explained by this.

Despite data limitations and the resulting uncertainty in the results, the source attribution estimates are considered to reflect the best current knowledge about which sources are most important for human salmonellosis in the EU, and highlight differences in the contribution of different food-animal sources for disease and on the efficiency of surveillance systems in place in EU MSs. The results are expected to be useful for the delineation of risk management strategies.

The report concludes with a number of recommendations, one of them being that based on the model results, pig meat is likely to be the most important source in a majority of MSs. Harmonised monitoring and control of *Salmonella* in pigs and pig meat should therefore be considered.

TABLE OF CONTENTS

BACKGROUND AS PROVIDED BY EFSA

EFSA has been working on a series of Scientific Opinions originated by a mandate received by the European Commission (EC) in July 2008 on the review of *Salmonella* targets in poultry primary production. The Opinions have been adopted by the BIOHAZ Panel and published on the EFSA website. Overall, they have provided a quantitative estimate of the public health impact of setting new targets for the reduction of *Salmonella* in poultry populations. Two of these Opinions, which have addressed in particular breeding flocks and laying hens of the species *Gallus gallus* have been published in March 2009 and 2010, respectively, while a third one on broilers of the same species (EFSA-Q-2008-00293) was adopted in March 2011.

A similar question for flocks of breeding and fattening turkeys was received by EFSA in June 2010 (EFSA-Q-2010-00899). Specifically, the EC has asked EFSA to assess the relative public health impact if a new target for reduction of *Salmonella* is set in fattening turkeys being 1 % or less of flocks remaining positive for all *Salmonella* serovars with public health significance compared to:

- the theoretical prevalence at the end of the transitional period (1 % or less of flocks remaining positive for *Salmonella* Enteritidis or *Salmonella* Typhimurium), and
- the real prevalence in 2010 to be reported by the Member States (MSs).

The above mandate has been assigned to the Scientific Panel on Biological Hazards (BIOHAZ), who has established an ad hoc Working Group (WG) to draft an Opinion which should be adopted by the BIOHAZ Panel, before the end of March 2012. Actually, EFSA was also asked to indicate and rank the *Salmonella* serotypes with public health significance according to Annex III of Regulation (EC) No 2160/2003[3] and to assess the impact of a reduction of the prevalence of *Salmonella* in breeding flocks of turkeys on the prevalence of *Salmonella* in flocks of fattening turkeys, but these questions are out of the scope of this assignment.

The three Opinions addressing *Gallus gallus* have employed a different approach in order to address the quantitative aspects of the questions received. Throughout these experiences, the BIOHAZ Panel and Unit have gained a good understanding of the limitations of the data available for the provision of quantitative estimates of the public health impact due to changes in *Salmonella* prevalence in poultry populations. The most recent of the Opinions related to *Salmonella* in broilers is supported by the work of a Contractor (CT/EFSA/BIOHAZ/2010/02) who provided quantitative estimates based on a broiler-target *Salmonella* source-attribution model (BT-SAM). It is based on the Hald model and uses a Bayesian approach employing microbial subtyping data (Hald et al., 2004). This type of model allows for the identification of the most important reservoirs of the zoonotic agent, assisting risk managers to prioritize interventions and focus control strategies at the animal production level. The model can provide estimates for the effect on the number of human cases originating from a particular reservoir, if the observed prevalence in that reservoir is changed or for specific subtypes e.g. specific serovars of *Salmonella* in that reservoir.

Up to now, this source-attribution approach has been considered by WG and Panel Experts as valid when addressing this type of questions, where the use of a classical quantitative risk assessment model (i.e. transmission model) would be impaired due to a lack of data and time limitations. A turkey-target *Salmonella* source-attribution model (TT-SAM) would support the BIOHAZ ad hoc Working Group

[3] Regulation (EC) No 2160/2003 of the European Parliament and of the Council of 17 November 2003 on the control of *salmonella* and other food-borne zoonotic agents. OJ L 325, 12.12.2003, p. 1-15.

dealing with turkey flocks (see above EFSA-Q-2010-00899) hereafter referred to as Working Group (WG).

TERMS OF REFERENCE AS PROVIDED BY EFSA

The purpose of the contract is to develop a turkey-target *Salmonella* source-attribution model (TT-SAM) providing results supporting the BIOHAZ ad hoc Working Group.

According to the Technical Specifications of the Negotiated Procurement Procedure NP/EFSA/BIOHAZ/2011/04, the tasks to be covered by this report:

to evaluate targets specifically answering the Terms of Reference of the *Salmonella* in turkey flocks mandate (EFSA-Q-2010-00899)

- The TT-SAM model should be built on the same mathematical principles as the BT-SAM model and fed with updated data to be discussed with the WG Experts. The data will mainly be provided to the Contractor by EFSA or obtained with the support of EFSA (e.g. human salmonellosis sporadic cases). Data will include for the various MSs (1) prevalences of various *Salmonella* serovars/serotypes in various animal-food sources (can be both baseline survey data and EU monitoring data), and related (2) food consumption and trade data, (3) data on food-borne outbreaks of *Salmonella*, and on (4) human salmonellosis cases reported to ECDC.

- The TT-SAM model needs to be checked to determine that it had resolved to produce stable results and a sensitivity analysis should be carried out. The Contractor needs to provide the expected rates of salmonellosis cases in the EU MSs (taking into account underreporting) and the percentages in terms of the EU expected rate (mean statistics, 2.5 % and 97.5 % statistics) by animal reservoir and serovar as done in the previous Contractor's report. The TT-SAM model should be used to evaluate targets specifically answering the Terms of Reference of the *Salmonella* in turkey flocks mandate (EFSA-Q-2010-00899). The WG will provide the Contractor with several scenarios that should be tested.

This contract/grant was awarded by EFSA to:

The National Food Institute, Technical University of Denmark, Denmark

Contract title: Development of a flexible user-friendly interface version of the *Salmonella* source-attribution model developed under CFT/EFSA/BIOHAZ/2010/02 for evaluating targets in turkey meat production (EFSA-Q-2010-00899) and use in future source-attribution assessments

Contract number: CT/EFSA/BIOHAZ/2011/02

OBJECTIVES

The overall objectives of the tasks covered by this report were to

- develop a mathematical model for attributing human cases of *Salmonella* to responsible food-animal reservoirs and/or food sources. The model is based on two existing *Salmonella* source-attribution models developed in the WinBUGS software as part of previous EFSA service contracts (CT/EFSA/BIOHAZ/2010/02 and CT/EFSA/ZOONOSES/2010/02).

- apply the model to evaluate the expected public-health effects (i.e. reduction in number of human salmonellosis cases) by setting specific targets for the occurrence of *Salmonella* in fattening turkey flocks in EU Members States (MSs) as requested by the mandate given by the EU Commission (EFSA-Q-2010-00899).

MATERIALS AND METHODS

1. Principle of the Bayesian subtyping approach for source attribution modelling

The microbial subtyping approach involves characterisation of isolates of the pathogen by phenotypic and/or genotypic subtyping methods. The principle is to compare the distribution of subtypes in potential sources (e.g. animals and food) with the subtype distribution in humans, and the approach is enabled by the identification of strong associations between some of the dominant subtypes and a specific food-animal reservoir, providing a heterogeneous distribution of subtypes among the sources. Subtypes exclusively or almost exclusively isolated from one source are regarded as indicators for the human health impact of that particular source, assuming that all human infections with these subtypes originate only from that source. Human infections caused by subtypes found in several reservoirs are then distributed relative to the prevalence of the indicator types.

The Bayesian model first described by Hald et al. (2004) attributes domestically acquired laboratory-confirmed human infections caused by different *Salmonella* subtypes (e.g. serovars, phage types, antimicrobial resistance profiles) as a function of the prevalence of these subtypes in animal and food sources and the amount of each food source consumed. However, the number of people being infected by a particular subtype in a particular food source supposedly depends on additional factors related to the subtype and food source in question. Therefore, a multi-parameter prior, which accounts for the presumed but undefined differences between subtypes and food sources with respect to cause human infections, was introduced.

The bacteria-dependent factor $\{q_i\}$ can be interpreted as combining survivability, virulence, and pathogenicity of the pathogen to estimate the ability of that subtype to cause disease, whereas the food source dependent factor $\{a_j\}$ estimates the ability of a food source to act as a vehicle for food-borne infections, as well as the sensitivity of the monitoring programme(s) used to obtain the data included in the model. It is, however, emphasised that the estimated values of the bacteria- and food-source-dependent factors are simply multiplication factors (comparable to regression coefficients in regression analyses) that helps us to arrive at the most likely solution given the observed data. Their relative size can provide an idea about the differences between subtypes and food types with respect to causing human infections, but estimates based on the results of a single model should be interpreted with care. However, by applying the model on a regular basis as new data becomes available, it may be possible to monitor the main sources and dynamics in the occurrence of human salmonellosis and to improve the estimation of the model parameters, including the bacteria- and food-dependent factors.

The basic equation used to estimate the number of human cases per source and type is defined as follows:

$$\lambda_{ij} = p_{ij} * M_j * a_j * q_i$$

where λ_{ij} is the expected number of cases per subtype *i* and source *j*, p_{ij} is the prevalence of subtype *i* in source *j*, M_j is the amount of source available for consumption in the country, a_j is the food source dependent factor for source *j*, and q_i is the bacteria dependent factor for type *i*. To avoid problems related to identifiability (i.e. overparameterisation) of the model described in Eq. 1, the number of estimated parameters needs to be reduced. The pooling of some subtypes or food sources into groups with similar characteristics is one way of addressing this problem. Depending on the available data, the model can be extended to include other dimensions such as time period (e.g. year) and country, which can also increase the robustness of the model and consequently improve the parameter estimation for instance by assuming that the q-values remain unchanged over at least shorter time periods (Pires and Hald, 2010) and are independent on country.

The model calculates the expected number of cases per subtype $\{\lambda_i\}$ according to the above equation. From this λ_i, a back-calculation is made by adding the number of travel- and outbreak-related cases with known subtype in order to get the expected number of reported cases. The observed data (i.e. the reported number of cases per subtypes) is then linked with the prior distribution by assuming that the number of cases per subtype is Poisson distributed (the likelihood function) with a parameter value equal to the expected number of cases. This results in posterior estimates for the unknown parameters q_i and a_j and consequently for the number of cases per subtype and source $\{\lambda_{ij}\}$, which can then be summarised over subtypes to get to the number of cases per source $\{\lambda_j\}$.

The microbial subtyping approach requires a collection of temporally and spatially related isolates from various sources and humans, and is consequently facilitated by an integrated food-borne disease surveillance programme focused on the collection of pathogen isolates from the major food animal reservoirs and from humans (Pires et al., 2009). The data quality and availability are considered the biggest limitation of this approach.

A strong advantage of the microbial subtyping approach is that it allows for the identification of the most important pathogen reservoirs, assisting risk managers to prioritize interventions and focus control strategies at the animal production level. Particularly, if repeated on a regular basis, the approach is regarded as a powerful tool to monitor the progress of control and follow the trends in the sources of human infections (Hald et al., 2004; Pires et al., 2009).

The results of this type of model can also provide estimates for the effect on the number of human cases originating from a particular reservoir (e.g. turkeys), if the observed prevalence in that reservoir is changed for instance following the implementation of a control program. Given the nature of the model, it will also be able to provide estimates on the expected change in human cases for specific subtypes, e.g. specific serovars of *Salmonella*.

However, in contrast to a "traditional" farm-to-consumption risk assessment model, the model does not give detailed insight into transmission routes and cannot provide estimates for the expected changes in human infections by the introduction of specific intervention strategies.

The Hald model described above was initially designed with two dimensions: *Salmonella* subtype and food source. In 2010, the model was extended by Pires and Hald (2010) to include a temporal dimension (year) for trend analyses within a single country. By including a temporal dimension, the model was able to produce more robust results and it was assessed that even with only serotyping data

available, the model would still produce meaningful results. This was considered to be useful for countries that use only serotyping in their national surveillance of *Salmonella*.

Through the EFSA service contracts CT/EFSA/BIOHAZ/2010/02 and CT/EFSA/ZOONOSES/2010/02, the Hald model was adapted to the EU level by including MS as a third dimension. The model produces attribution estimates at the overall EU level as well as MS-specific estimates, and allows for exploring the *Salmonella* contribution from food traded between MSs by accounting for export and import figures for the included food sources.

2. Development of a source attribution model for evaluating *Salmonella* targets in turkey flocks (EFSA mandate: EFSA-Q-2010-00899)

As described above, two mathematical models for *Salmonella* source-attribution at the EU level have been developed through two independent EFSA service contracts (the BT-SAM model from the CT/EFSA/BIOHAZ/2010/02 and the EU-*Salmonella* Source Attribution (EU-SSA) model from the CT/EFSA/ZOONOSES/2010/02). However, the two models are in principle addressing the same questions and employing the same type of data.

The specific model developed to answer the turkey target mandate is in the following referred to as: TT-SAM.

2.1. The mathematics of the TT-SAM model

The TT-SAM model was set up in a Bayesian framework and estimates the number of human sporadic and domestic cases attributed to each source per country (λ_{cji}), assuming that the observed number of sporadic cases per subtype per country (o_{ci}) is Poisson distributed:

Poisson (o_{ci}) =$\sum \lambda_{ci}$, and

$$(1)\quad \lambda_{ckji} = p_{kij} * m_{ckj} * a_{cj} * q_i$$

where λ_{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*, p_{kij} is the prevalence of serovar *i* in source *j* in country *k*, m_{ckj} is the amount of source *j* available for consumption in country *c* produced in country *k*, a_{cj} is the source-dependent factor for source *j* in country *c*, and q_i is the subtype-dependent factor for serovar *i*. When *c* is equal to *k* the food originates from the country in which the case is reported.

The multi-parameter priors constituted a subtype-dependent factor (q_i) and food-source-dependent factor (a_{cj}) and were defined as uninformative prior distributions (uniform distributions). The subtype-dependent factor was estimated as a one-dimension parameter (q_i), meaning that it is a property of the *Salmonella* serovar and assumed independent of the country of infection. The q_i prior for *S.* Enteritidis was defined as 1, and all q_i values were estimated relatively to this one. q_i describes the differences in the ability of the various *Salmonella* serovars to cause human disease, accounting e.g. for differences in the serovars' survivability through the food chain and potential differences in pathogenicity. The food-source-dependent factor (a_{cj}) was assumed to vary between countries, accounting for variations in consumption patterns not captured by m_{ckj}. This factor may also include general variations between sources like the bacterial load/concentration in the food, and processing, handling or preparation practices. The model parameters are presented in Table 1.

Table 1: Input parameters applied in TT-SAM model to estimate the number of cases of human salmonellosis attributable to the animal sources

Notation	Description	Estimation
i	*Salmonella* serovar	-
j	Food-animal source	
c	Country where the human case was reported	
k	Country of origin of the food product[(a)]	
o_{ci}	Observed cases caused by serovar i in country c	Data
ob_{ci}	Observed cases caused by serovar i known to be outbreak related in country c. For each outbreak, one case was subtracted so that one outbreak contributed with one sporadic case.	Data
yt_{ci}	Observed cases caused by serovar i in country c that was reported as travel-related	Data
uf_c	Country-specific underreporting factor for human cases	dlnnorm(μ,σ)
p_{kji}	Prevalence of serovar i in source j in country k	Data
m_{ckj}	Amount of source j available for consumption in country c produced in country k[a]	Data
a_{cj}	Source-dependent factor for source j and country c	dunif(0,max a_{cj})
q_i	Subtype-dependent factor for serovar i	dunif(0,max q_i)

[a] If the food is produced and consumed in the same country, c=k

A Markov Chain Monte Carlo (MCMC) simulation, specifically the Gibbs sampler, was applied to arrive to the posterior distributions for a_{cj} and q_i. Three independent Markov chains of 40 000 iterations were run. For each chain, a different set of starting values for the priors, widely dispersed in the target distribution, were chosen. Convergence was monitored using the methods described by Gelman and Rubin (1992) 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.

The predictive ability of the model was assessed by estimating the ratio between the observed *Salmonella* cases (sporadic human cases reported in each country) and the number of cases predicted by the model.

The model was set up in WinBugs 1.4 (http://www.mrc-bsu.cam.ac.uk/bugs/).

2.2. Input data for the TT-SAM model

Data for the TT-SAM were provided by EFSA and by EFSA through ECDC. For some MSs, additional data were requested in case the data reported through the EU Summary Reports and the TESSy were considered insufficient. Data were in general provided as Excel files or SAS datasets, although some data were found in monitoring reports in the format of Word or PDF documents. Details of the data (i.e. choice of data and MSs to be included) were discussed thoroughly with the ad hoc BIOHAZ WG drafting the Scientific Opinion.

The following data were agreed upon:

2.2.1. Reported cases of human salmonellosis

The following data on the reported human salmonellosis were used as input to the model:

- number of reported cases per *Salmonella* serovar and MS in 2010
- number of reported travel-related cases per *Salmonella* serovar and MS in 2010
- number of reported outbreak-related cases per *Salmonella* serovar and MS in 2010

Data on human reported cases, including information on serovar and travel information were provided by EFSA through ECDC[4] (TESSy[5]). For some MSs, the serovar details in the TESSy data were insufficient and additional data were obtained by requests made by EFSA's BIOHAZ unit. *Salmonella* outbreak data were provided by EFSA's Biological Monitoring (BIOMO) unit. For one country, sufficient human data were not available/provided, and this MS was excluded from the model. Details of the data used for each MS is presented in Table 2.

The total number of reported cases included sporadic, travel and outbreak-related infections. Travel-related cases were reported as "imported". Information on imported cases varied in frequency and quality. The proportion of travellers varied greatly among MSs and for a few MSs, the travel-related cases represented the majority of all salmonellosis cases and for other MSs (9), no travel cases were reported. Data on domestic versus travel-related cases are, therefore, often incomplete. In the source attribution model, all records with missing or unknown travel information were considered domestically acquired in the reporting country.

The number of outbreak-related cases per serovar and country were identified and subtracted from the total number of domestically acquired cases to estimate the number of sporadic cases if this was not already done by the reporting country. One outbreak was assumed to contribute with one sporadic case.

Reported human isolates that were not classified to the serovar level or in which data were reported in aggregated form were reassigned to specific serovars according to proportions observed in the same dataset, in additional national datasets or in previous studies as indicated in Table 2. Isolates classified as serogroups were distributed among serovars pertaining to those serogroups, in accordance with the Kauffman-White-Le Minor Scheme 9th edition (WHOCC-Salm, 2007). Isolates classified as "*Salmonella*, serovar unknown", *Salmonella* Subspecies I, *Salmonella enterica* ssp. *enterica*, *Salmonella* spp. or "*Salmonella* spp., unspecified" were distributed among all serovars observed in the reference documents or datasets, also using the appropriate proportions. When some serovars were specifically reported and others were aggregated as "Others", the aggregated numbers were reassigned to serovars not specified in the original data, following the distributions observed in the reference documents or datasets. Isolates identified as *S.* 1,4,[5],12:i:- or *S.* 4,[5],12:i:- were reassigned to *S.* Typhimurium (EFSA Panel on Biological Hazards, 2010).

[4] ECDC has no responsibility for the results and conclusions when disseminating results of the work employing TESSy data supplied by ECDC.

[5] ECDC, TESSy Release on 06/10/2011. Validation of data based on draft Tables of 30/01/2012 to be included in draft EU SR.

Table 2: Data on the number of reported human cases of salmonellosis in 2010, the case numbers used in the model and data sources for the serovar distribution of the cases included in the model

	Reported cases in 2010 (EFSA, 2012)	Case numbers used in model[a]	Serovar details obtained through	Notes
Austria	2 179	2 186	ECDC	
Belgium	3 169	3 209	ECDC	
Bulgaria	1153	-	No data available	Excluded from the model
Cyprus	136	137	Additional national data	
Czech Republic	8 209	8 209	ECDC	
Denmark	1 608	1 612	ECDC	
Estonia	381	381	ECDC	
Finland	2 422	2 422	ECDC	
France	7 184	7 214	ECDC	
Germany	24 833	23 204	ECDC	
Greece	299	301	No data available	Data from 2009 from previous EU model was used (Pires et al., 2011)
Hungary	5 953	5 954	ECDC	
Ireland	349	350	ECDC	
Italy	2 730	3 533	ECDC	Number of cases reported as laboratory confirmed used in the model
Latvia	951	881	ECDC	
Lithuania	1 962	1 963	ECDC	
Luxembourg	211	211	ECDC	
Malta	160	-	ECDC	Excluded from the model
Poland	9 257	9 122	No data available	Data from 2009 from previous EU model was used (Pires et al., 2011)
Portugal	205	345	No data available	Data from 2009 from previous EU model was used (Pires et al., 2011)
Romania	1 285	1 137	ECDC	Cases with unknown serovars were re-distributed based on the cases with known serovars
Slovakia	4 942	4 943	ECDC	
Slovenia	363	363	ECDC	
Spain	4 420	4 422	Additional national data	Cases with unknown serovars were re-distributed based on the cases with known serovars
Sweden	3 612	3 612	ECDC	
The Netherlands	1 447	1 468	ECDC	Number of cases reported as laboratory confirmed used in the model
United Kingdom	9 670	11 893	ECDC	

a) Case numbers used in the model are derived from a raw dataset provided by ECDC through EFSA and therefore the numbers for some MS deviate from the reported number of cases in 2010 (EFSA and ECDC, 2012).

2.2.2. Underreporting factors

To take account for differences in human case underreporting between MSs, the TT-SAM model includes underreporting factors for the MSs. These underreporting factors were kindly provided by Prof. Arie Havelaar, a member of the BIOHAZ Working Group. The methodologies used for estimating the underreporting factors are described in Havelaar et al. (accepted). The underreporting factors are estimated based on data from 2009 and included as probability distributions in order to account for uncertainty around the data. A lognormal distribution was found to provide a good fit of the data and the estimated means and standard deviations were used as model input (Table 3).

Table 3: Estimated means and standard deviations for the underreporting factors applied in the TT-SAM model

	Mean(Ln)	Sdev(Ln)	Mean dist	Mean data
Austria	2.1	0.8	11.2	11
Belgium	0.9	0.9	3.6	3.5
Bulgaria	6.3	0.8	734.8	718.4
Cyprus	4.9	0.8	177.2	173.3
Czech Republic	3.1	0.8	29.6	28.9
Denmark	1.2	0.8	4.5	4.4
Estonia	2.5	0.8	17.4	16.9
Finland	-1.3	0.8	0.4	0.4
France	3	0.8	27.5	26.9
Germany	2	0.8	10	9.8
Greece	6.8	0.8	1257	1229
Hungary	3.9	0.8	68.3	66.8
Ireland	1.1	1.1	5.6	5.4
Italy	4	0.8	73.4	71.8
Latvia	3.5	0.8	45.4	44.3
Lithuania	3.8	0.8	60.5	59.1
Luxembourg	1	1	4.6	4.4
Malta	5.1	0.8	227.8	222.6
Poland	4.5	0.8	116.6	114
Portugal	7.4	0.8	2131.2	2083.8
Romania	5.5	0.8	358.4	350.2
Slovakia	3.7	0.8	54.3	53.1
Slovenia	3.4	0.9	41.7	40.5
Spain	5.1	0.8	219.1	214.2
Sweden	-1	0.8	0.5	0.5
The Netherlands	3	0.8	26.8	26.2
United Kingdom	1.7	0.8	7.5	7.3

2.2.3. Prevalence and serovar distribution for *Salmonella* in animal food sources

Prevalence data and serovar information were included for the following food sources:

- Slaughter pigs
- Broiler flocks
- Layer flocks
- Turkey flocks

Criteria for selecting which animal-food data to include in the model were agreed upon in the BIOHAZ WG and followed the principles in Table 4.

Table 4: Criteria for selecting animal-food data for TT-SAM model

	1st choice	2nd choice	3rd choice	4th choice
Turkey flocks	EU harmonised monitoring	EU reporting of serovars	Data from the request to the NRL[a]	EU baseline survey (2006/7)
Broiler flocks	EU harmonised monitoring	EU reporting of serovars	Data from the request to the NRL[a]	EU baseline survey (2008)
Laying hens flocks	EU harmonised monitoring	EU reporting of serovars	Data from the request to the NRL[a]	EU baseline survey (2004)
Slaughter pig herds	EU baseline survey (2006/7)	EU monitoring	-	-

[a] National Reference Laboratory

For the poultry sources, prevalence figures were obtained from the EU harmonised monitoring data for 2010 as reported by the MSs in EUSR (EFSA and ECDC, 2012). For four countries, no prevalence data were reported and the prevalence was assumed to be zero, because the production of the respective poultry species was very small. Three MSs reported not having commercial turkey flocks and one MS reported only 40 000 birds in the BS conducted in 2006/7 (Table 5). Data regarding serovar distribution were obtained using the selection criteria in Table 4. For a few MSs, it was necessary to use the serovar distribution from the Baseline Surveys (BS) in broilers (4th choice) (Table 5: Cyprus, Hungary and Slovakia). For Slovakia, also the overall prevalence in broilers was obtained from the BS, as the reported data for 2010 only included prevalence figures for *S.* Enteritidis and *S.* Typhimurium.

For prevalence and serovar distribution in slaughter pigs, data from the BS conducted in 2006/7 was used, since no EU-wide harmonised monitoring program is established for this species. Malta and Romania did not participate in this study and Malta was excluded from the model on this basis. For Romania, data from swabs of pig carcasses reported in EUSR 2010 were used (EFSA and ECDC, 2012).

In general for the distribution of serovars, aggregated data or isolates with no serotyping information (e.g. isolates reported as "Other serovars") were redistributed to specific serovars according to proportions observed in the same dataset, in additional national datasets or in previous studies as indicated in Table 5.

Based on the availability of human and animal food data, a total of 25 MSs were included in the model (Table 5).

Table 5: Data available and data choices on *Salmonella* prevalence and serovar distribution in turkey flock, broilers flocks, laying hen flocks and slaughter pigs herds

	Turkeys		Broilers		Layers		Pigs	
	Prevalence data	**Serovar data**	**Prevalence data**	**Serovar data**	**Prevalence data**	**Serovar data**	**Prevalence data**	**Serovar data**
Austria	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Belgium	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Bulgaria	EXCLUDED FROM THE MODEL DUE TO LACK OF SEROVAR SPECIFIC HUMAN DATA							
Cyprus	Small production. Assumed zero prev.		1st choice	4th choice	1st choice	1st choice	1st choice	1st choice
Czech Republic	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Denmark	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Estonia	Small production. Assumed zero prev.		1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Finland	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
France	1st choice	3rd choice	1st choice	1st choice	1st choice	3rd choice	1st choice	1st choice
Germany	1st choice	3rd choice	1st choice	3rd choice	1st choice	3rd choice	1st choice	1st choice
Greece	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Hungary	1st choice	3rd choice	1st choice	4th choice	1st choice	Other[a]	1st choice	1st choice
Ireland	1st choice	3rd choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Italy	1st choice	2nd choice	1st choice	2nd choice	1st choice	2nd choice	1st choice	1st choice
Latvia	Small production. Assumed zero prev.		1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Lithuania	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Luxembourg	Small production. Assumed zero prev.		Small production. Assumed zero prev.		1st choice	1st choice	1st choice	1st choice
Malta	EXCLUDED FROM THE MODEL DUE TO LACK OF DATA ON PIGS							
Poland	1st choice	2nd choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Portugal	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Romania	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	2nd choice	2nd choice[b]
Slovakia	1st choice	1st choice	4th choice	4th choice	1st choice	1st choice	1st choice	1st choice
Slovenia	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
Spain	1st choice	3rd choice	1st choice	3rd choice	1st choice	3rd choice	1st choice	1st choice
Sweden	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice	1st choice
The Netherlands	1st choice	3rd choice	1st choice	3rd choice	1st choice	3rd choice	1st choice	1st choice
United Kingdom	1st choice	3rd choice	1st choice	3rd choice	1st choice	3rd choice	1st choice	1st choice

[a] Data used for Hungary: Data from previous EU *Salmonella* Attribution model (Pires et al., 2011)

[b] Data used for Romania: Carcass swabs taken at slaughter (N=1 178; prevalence=2.4 %). Data reported in 2010 (EFSA and ECDC, 2012).

2.2.4. Serovars included in the model

Based on the top-15 serovars reported in humans and the top-5 in each of the four food-animal sources, the following serovars were selected to be included separately in the model:

1. Enteritidis	6. Kentucky	11. Saintpaul	16. Rissen	21. Livingstone
2. Typhimurium	7. Derby	12. Bovismorbificans	17. Senftenberg	22. Heidelberg
3. Infantis	8. Mbandaka	13. Braenderup	18. Bredeney	23. Anatum
4. Virchow	9. Hadar	14. Montevideo	19. Kottbus	
5. Newport	10. Agona	15. Brandenburg	20. London	

For each source and humans, remaining serovars were grouped into an "Others" category. It should be noted that it was decided to include the monophasic variants 1,4,[5],12:i:- or 4,[5],12:i:- in *S.* Typhimurium based on the conclusions from a recent EFSA opinion (EFSA Panel on Biological Hazards, 2010) and based on the fact that some countries report the monophasic variants as *S.* Typhimurium making a clear distinction impossible.

2.2.5. Production and trade data

Ideally, the TT-SAM model should employ consumption data of the specified food sources. However, national consumption data do not generally include information of the origin of the food (i.e. the country in which the food where produced), which is considered to be an essential part of the model because of the extensive trade of foods between MSs. Therefore, an approximation is used, where the amount available for consumption produced in a MS is estimated as:

Amount available for consumption = production – export

In addition, the amount of food imported to one MS from another MS was estimated as well in order to consider trade between MSs.

Data on production of the animal-food sources were extracted by EFSA from the EUROSTAT and provided as Excel files. Production data for broilers and turkeys were taken from the 2010 AVEC report (AVEC, 2011), as the EUROSTAT data does not provide information for the separate poultry species. For pig, the weight of slaughtered carcasses per MSs in 2010 was used as a measure of domestic production. Finally for eggs, data on the production of shell eggs were extracted from FAOSTAT[6], since these data were missing from many MSs in the EUROSTAT data.

All information on trade between MSs was extracted from EUROSTAT database[7] (dataset name: DS-016890-EU27 Trade Since 1988 By CN8). Export data as reported by the MSs were used for both estimating import and export. This was done in order to use only one table realising that there was a high degree of disagreement of the data reported in the export and import tables for each food source. The unit used for expressing the amount of food produced and exported was tonnes.

The amount available for consumption produced in a MS was as mentioned above estimated as: Production – export. In some instances, this resulted in negative production values i.e. the amount exported were larger than the amount produced within the country. In order to ensure that MSs would still have nationally produced food available in their own country, it was assumed that imported products could also be re-exported. Data availability and data used are presented in Appendix A.

[6] FAOSTAT data extracted 3. January 2010: http://faostat.fao.org/site/569/DesktopDefault.aspx?PageID=569#ancor
[7] http://epp.eurostat.ec.europa.eu/newxtweb/

2.3. Baseline model and scenario analysis

In order to answer the terms of references as provided by the EU Commission, the following baseline model (i.e. the model for which the different scenarios should be compared against) and scenarios were agreed upon in the WG:

- **Baseline.** The actual prevalence of all *Salmonella* serovars as reported by the MSs in 2010. The prevalence of *S.* Enteritidis and *S.* Typhimurium were used as reported in 2010 while the distribution of the other serovars took the ratio as reported elsewhere (see selection criteria in Table 4)
- **Scenario 1.** The transitional target, i.e. combined prevalence of *S.* Enteritidis and *S.* Typhimurium = 1 % (or less) using the current ratio
- **Scenario 2.** The prevalence of *S.* Enteritidis = 1 % (or less) and *S.* Typhimurium = 0 %
- **Scenario 3.** The prevalence of *S.* Enteritidis = 0 % and *S.* Typhimurium = 1 % (or less)
- **Scenario 4.** The overall prevalence, i.e. of all serovars = 1 % (or less)
- **Scenario 5.** The prevalence of the top-5 (i.e. *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Newport, and *S.* Kentucky) serovars in humans in 2010 = 1 % (or less)
- **Scenario 6.** The prevalence of the top-6 (i.e. *S.* Enteritidis, *S.* Kentucky, *S.* Typhimurium, *S.* Newport, *S.* Virchow, and *S.* Saintpaul) serovars of turkeys that contribute most to human cases (from the baseline model results) = 1 % (or less)
- **Scenario 7.** The prevalence of the *Gallus gallus* breeding hens regulated serovars (i.e. *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Virchow and *S.* Hadar) = 1 % (or less)

The baseline model estimated the number of human cases per MSs, serovar and animal reservoir (source) as explained in section 2.1. By summing these figures by MS and serovar, the estimated number of human cases per animal reservoir was calculated. The same model approach was used for the different scenarios, but here the prevalences of certain serovars were changed according to descriptions above and the results of the baseline model and the scenario in question were then compared. For all scenarios, the prevalences of *Salmonella* spp., *S.* Enteritidis and *S.* Typhimurium were kept as reported in 2010, if they were already below 1 %.

Since the baseline model took account for the amount available for consumption as well as trade between MSs, it is expected that food source with a relatively high consumption in most countries and where also large amounts are traded between MSs will contribute relatively more to the overall human salmonellosis burden. Because turkey meat is consumed relatively less often when compared to the other sources, we therefore decided also to calculate the relative risk per tonne of meat available for consumption in EU. This was simply done by taken the estimated number of case attributed to each reservoir and divide this with amount available for consumption. These figures were then presented as the relative risk compared to turkey meat.

RESULTS

3. Results of the baseline model

The results of the baseline model are presented in Table 6. As explained above, the baseline model applied to the extent possible reported monitoring data and human surveillance data from 2010 except for slaughter pigs, where the baseline survey data from 2006/7 were used.

The results indicate that 2.6 % (95 % CI: 1.2-5.2) of all human salmonellosis cases (i.e. estimated true number of cases when accounting for underreporting) in the EU were attributed to the turkey reservoir. This corresponds to 135 100 (95 % CI: 60 790-293 600) human cases in 2010.

For the other animal-food sources included in the model, the attribution estimates were that 56.8 % (95 % CI: 48.2-65.8), 10.6 % (95 % CI: 5.1-18.3) and 17.0 % (95 % CI: 11.3-24.0) of the estimated number of human salmonellosis cases could be attributed to the pig, broiler and laying hen reservoir, respectively.

Thirteen percent (692 600; 95 % CI: 336 200-1 281 000) of human cases could not be attributed to any of the included source. A proportion of these were reported as known travel-related.

Table 6: Estimated number and percent (%) of human cases in EU attributable to the four main animal reservoirs included in the baseline model

	Estimated number of human cases[a]				Percentage of human cases			
	mean	**median**	**2.5 %**	**97.5 %**	**mean**	**median**	**2.5 %**	**97.5 %**
Pigs	3 099 000	2 900 000	1 627 000	5 783 000	56.8 %	56.8 %	48.2 %	65.8 %
Broilers	559 300	515 100	267 100	1 112 000	10.6 %	10.2 %	5.1 %	18.3 %
Laying hens	928 000	847 700	443 100	1 878 000	17.0 %	16.7 %	11.3 %	24.0 %
Turkeys	135 100	121 000	60 790	293 600	2.6 %	2.3 %	1.2 %	5.2 %
Unknown/travel	692 600	742 200	366 200	1 281 000	-	-	-	-
Total cases	5 414 000	5 126 000	3 030 000	9 505 000	-	-	-	-

[a] Accounting for underreporting

The results presented in Table 7 shows the distribution of the estimated turkey-associated cases by serovar. Around 63 % of the turkey-associated human salmonellosis cases were caused by serovars other than the currently regulated serovars *S.* Enteritidis and *S.* Typhimurium. However, *S.* Enteritidis and *S.* Typhimurium were still among the most important serovars from turkeys. Four serovars (*S.* Kentucky, *S.* Saintpaul, *S.* Senftenberg and *S.* Kottbus) had turkeys as the most important reservoir for human infections (Appendix B), although the occurrence of these serovars in turkeys was limited to a minor number of MSs (4-10 MSs). It should be noted that among these, *S.* Kentucky was in 2010 among the top-5 serovars reported in humans.

Based on the results in Table 7, it was decided to include the top-6 serovars (i.e. *S.* Enteritidis, *S.* Kentucky, *S.* Typhimurium, *S.* Newport, *S.* Virchow and *S.* Saintpaul) from the turkey reservoir in the scenario 6 analysis.

Table 7: Estimated number of human cases by the serovars included in the model and originating from the turkey reservoir (baseline model)

Serovar	mean	median	2.5 %	97.5 %	% of cases	Cumulative %
S. Enteritidis	29 770	25 010	10 240	77 140	22.0 %	22.0%
S. Kentucky	22 970	20 640	10 290	49 500	17.0 %	39.0%
S. Typhimurium	20 010	16 060	6 180	57 880	14.8 %	53.8%
S. Newport	10 030	8 823	4 319	22 900	7.4 %	61.3%
S. Virchow	9 110	7 380	3 038	25 640	6.7 %	68.0%
S. Saintpaul	8 439	7 700	4 028	17 390	6.2 %	74.2%
S. Infantis	7 274	6 263	2 875	17 660	5.4 %	79.6%
S. Hadar	6 820	6 090	2 915	14 980	5.0 %	84.7%
S. Bredeney	4 924	4 444	2 142	10 520	3.6 %	88.3%
S. Agona	2 923	2 262	777	9 109	2.2 %	90.5%
S. Kottbus	2 907	2 367	993	8 090	2.2 %	92.6%
S. Derby	2 445	1 992	769	6 839	1.8 %	94.4%
S. Mbandaka	2 046	1 512	399	6 896	1.5 %	96.0%
S. Senftenberg	1 437	1 053	271	4 914	1.1 %	97.0%
S. Bovismorbificans	1 157	992	407	2 899	0.9 %	97.9%
S. Heidelberg	1 095	980	458	2 399	0.8 %	98.7%
S. Montevideo	850	634	187	2 829	0.6 %	99.3%
S. London	317	238	64	1 024	0.2 %	99.6%
S. Livingstone	307	223	52	1 062	0.2 %	99.8%
S. Anatum	143	108	32	457	0.1 %	99.9%
S. Brandenburg	112	82	19	388	0.1 %	100.0%
S. Rissen	39	29	7	135	0.0 %	100.0%
S. Braenderup	0	0	0	0	0.0 %	100.0%

From Table B1 (Appendix B), it can also be seen that the vast majority of human *S.* Typhimurium infection was estimated to be related to the pig reservoir. Pigs appeared to be the most important source of *S.* Enteritidis infections, but also laying hens (i.e. consumption of eggs) and broilers contributed significantly.

At the EU population level, the baseline model estimated the pig reservoir to be the most important source of human infections, followed by the laying hen and broiler reservoir. However, when looking at the relative risk between turkey meat and the other three sources weighted by the tonne of meat/eggs available for consumption, this picture changes, indicating that the risk of infection for the individual consumer is highest when consuming shell eggs (i.e. laying hen reservoir) closely followed by the consumption of pig meat, whereas the risk is lower for turkey and broiler meat (Table 8). The relative risks can be interpreted as the risk of salmonellosis for the individual consumer when consuming e.g. 100 g of shell eggs is 2 times higher than when eating 100 g of turkey meat.

Table 8: Estimated relative risk between turkey meat and the three other sources by tonne of food available for consumption

	Pigs	Broilers	Laying hens/ Shell eggs	Turkeys
Amount traded (tonnes)	24 505 213	10 508 293	6 967 907	2 060 755
No. of cases per tonne of food	0.1265	0.0532	0.1332	0.0656
Risk relative to turkey meat	1.93	0.81	2.03	1.00

4. Results of the scenario analysis

Table 9 and 10 present the estimated effects on human cases attributable to the turkey reservoir under the seven scenarios explored.

Not surprisingly scenario 4, where the overall prevalence (i.e. the combined prevalence of all serovars) in turkey flocks per MSs is reduced to 1 %, has the largest effect with an estimated reduction in the number of turkey-associated human cases of 83.2 % (95 % CI: 79.0-87.4) compared to the situation in 2010. In absolute numbers, this corresponds to an estimated reduction of 112 300 (95 % CI: 50 410-243 400) human salmonellosis cases (Table 10). Overall, this scenario was estimated to reduce the percentage of human turkey-associated cases from 2.6 % to 0.4 % (Table 9).

This scenario was followed by scenario 6, where the combined prevalence of the top-6 serovars of turkeys that contribute most to human cases is reduced to 1 % or less in turkey flocks per MSs. Under this scenario, an estimated reduction in the number of turkey-associated human cases of 37.2 % (95 % CI: 19.2-54.0) compared to the situation in 2010 was obtained. In absolute numbers, this corresponds to an estimated reduction of 48 110 (95 % CI: 22 580-100 500) human salmonellosis cases (Table 10). Overall, this scenario was estimated to reduce the percentage of human turkey-associated cases from 2.6 % to 1.7 % (Table 9).

The scenario with the least reduction was scenario 1, i.e. where the achievement of the current target of the EU control programme of *Salmonella* in turkey broiler flocks would be met (i.e. the combined prevalence of *S.* Enteritidis and *S.* Typhimurium being 1 % or less, and keeping the prevalence for the other 21 serovars as reported in 2010). This analysis resulted in an estimated reduction in the number of turkey-associated human salmonellosis cases of only 0.4 % (95 % CI: 0.1-1.3) compared to the situation in 2010. In absolute numbers, this corresponds to an estimated reduction of 594 (95 % CI: 121-1 901) human cases (Table 10). Since all MSs except one have already met the transitional target, this result is not unexpected.

For all scenarios, it should be noted that the individual MSs' contributions to the estimated reductions vary greatly depending on the turkey flock prevalence reported in 2010.

Table 9: Estimated number and percent of turkey-associated cases in EU under the different scenarios

	Number of cases[a]				Percentage of cases				Estimated total cases[a] from all sources in 2010 (mean)
		Credibility interval				Credibility interval			
	mean	median	2.5 %	97.5 %	mean	median	2.5 %	97.5 %	
Baseline	135 100	121 000	60 790	293 600	2.6 %	2.3 %	1.2 %	5.2 %	5 414 000
Scenario 1	134 500	120 400	60 570	292 400	2.5 %	2.3 %	1.2 %	5.2 %	5 413 400
Scenario 2	115 100	104 600	53 660	240 000	2.2 %	2.0 %	1.1 %	4.2 %	5 394 000
Scenario 3	104 800	95 240	49 240	216 600	2.0 %	1.9 %	1.0 %	3.9 %	5 384 000
Scenario 4	22 830	20 200	9 724	51 550	0.4 %	0.4 %	0.2 %	1.0 %	5 302 000
Scenario 5	97 260	83 330	39 360	238 000	1.9 %	1.6 %	0.8 %	4.5 %	5 376 000
Scenario 6	87 020	73 950	34 640	217 900	1.7 %	1.4 %	0.7 %	4.2 %	5 366 000
Scenario 7	111 400	98 150	48 980	252 800	2.1 %	1.9 %	1.0 %	4.7 %	5 390 000

[a] Accounting for underreporting

Table 10: Estimated reduction in the number and percentage of turkey-associated cases in EU when the results of the different scenarios are compared to the baseline model

	Reduction in number of cases[a]				Percentage (%) reduction of all turkey-associated cases		
		Credibility interval				Credibility interval	
	mean	median	2.5 %	97.5 %	mean	2.5 %	97.5 %
Baseline	0	0	-	-			
Scenario 1	594	448	121	1 901	0.4 %	0.1 %	1.3 %
Scenario 2	20 010	16 060	6 180	57 880	14.0 %	7.5 %	21.8 %
Scenario 3	30 360	25 540	10 530	78 410	21.6 %	13.6 %	28.4 %
Scenario 4	112 300	100 800	50 410	243 400	83.2 %	79.0 %	87.4 %
Scenario 5	37 870	34 350	17 570	78 780	29.6 %	13.0 %	44.8 %
Scenario 6	48 110	43 650	22 580	100 500	37.2 %	19.2 %	54.0 %
Scenario 7	23 740	21 210	10 070	52 980	18.1 %	9.4 %	28.4 %

[a] Accounting for underreporting

5. Goodness of fit of the model

Results of the goodness of fit test showed that the model fit was satisfactory for the vast majority of the countries (Figure 1). Poor fit was observed for countries with poor data availability or quality, in particular for two countries. The baseline model was therefore run without these two countries in order to assess the overall influences. The results showed that the relative attribution estimates changes very little (results not shown) and it was concluded that the poor data from these countries did not influence the results of the overall model.

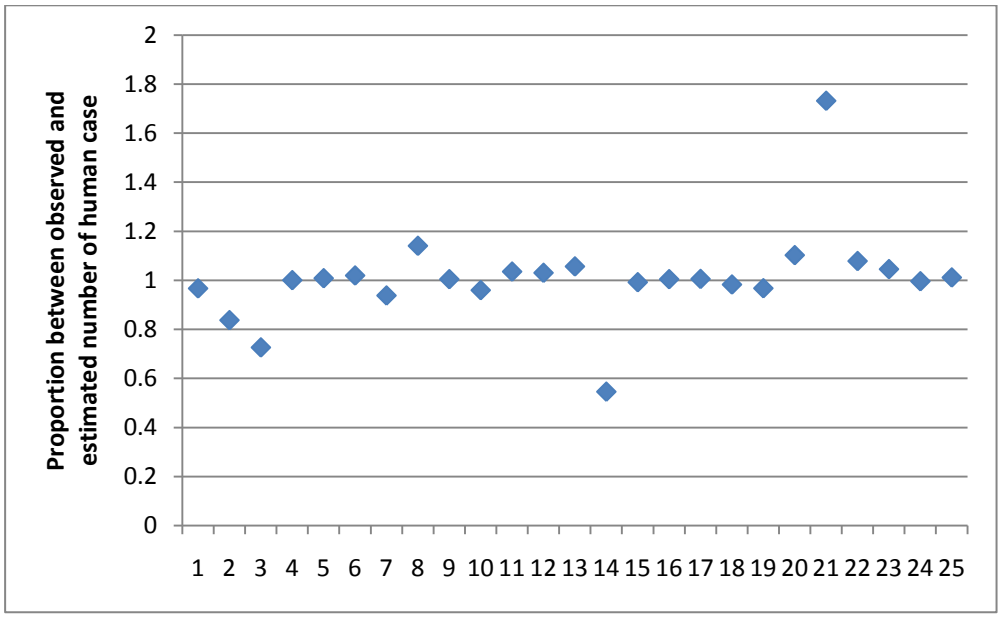

Figure 1: Ratio between the reported (observed) and estimated number of human salmonellosis cases by MS. A ratio around 1 indicates that the model fits the data well, whereas a ratio higher than 1 means that the model tends to underestimate the number of cases and an estimate below 1 reveals an overestimation.

DISCUSSION

6. Model assumptions and data uncertainty

The attribution of human *Salmonella* infections to food-animal sources in the EU on the basis of available data implied a number of assumptions:

- All major food sources of human salmonellosis in EU are included in the model;
- The sampling schemes and data collection of the EU harmonised monitoring programs in broilers, laying hens and turkeys, and the baseline survey of slaughter pigs generate data that are representative of animal reservoirs and MSs;
- The foodborne outbreak reporting system captures all large *Salmonella* outbreak with around the same detection sensitivity in each MSs;
- The TESSy generates data that are representative of the occurrence of human salmonellosis in each MSs as well as the serovar distribution;
- If no travel information was reported or if it was recorded as "Unknown", the human *Salmonella* infection was assumed to be acquired in the country where it was reported;
- The EUROSTAT production and trade data reflects the true flow of food in EU and food imported into a country is generally also consumed in that country, unless the amount produced in a country is less than the amount exported; in such cases re-exportation of imported food was assumed;

- The ability of a *Salmonella* serovar to cause infection (as represented by q) is a characteristic of the serovar and independent of time period and country of isolation;

- Food preparation practices and consumption patterns influence the estimated ability of a food source to act as a vehicle for infection, and so the source-dependent factor a_{cj} varies from country to country.

Due to data limitations and data uncertainty, it is obvious that some of the above assumptions can be questioned. It is not possible to quantify the effect these assumptions and data uncertainties may have on the model results, but some of the most important data issues identified include:

- ***Salmonella occurrence in animal reservoirs.*** The model includes only data on animal reservoirs for which there exist comparable data of reasonably good quality for the majority of MSs i.e. EU harmonised monitoring data for the poultry species and the baseline survey data for pigs. As mentioned above, it is assumed that these represent all the important sources of human salmonellosis, but food sources like beef, dairy products, and fruits and vegetables are not included, although they are known to act as vehicles for *Salmonella*.

  Omitting the cattle reservoir from the model due to lack of data, may have the consequence that a proportion of human cases were wrongly attributed to a reservoir with a similar serovar distributions i.e. pigs. An EU-wide baseline study of *Salmonella* in cattle or beef could be considered to investigate the role of the cattle reservoir as a source of human infections.

  It is emphasised that the subtyping approach employed is tracing human infections back to the animal reservoir of origin. This means that human infections caused by fruits and vegetables contaminated with faeces from an animal reservoir would be traced back to this reservoir, if produced in EU. For some type of risk management decisions (relating to control in primary production) this may be appropriate, whereas for other decisions (relating to control in later stages of the food chain), alternative attribution approaches may need to be explored.

  Salmonella contaminated foodstuffs imported from outside the EU are likely to be the source of some human salmonellosis cases in EU, and their importance are not accounted for by the model unless they resulted in outbreaks that were reported in the EU Summary Report in 2010. From the results of an attribution study using outbreak data, fruits and vegetables were estimated to contribute with 1.2-2.6 % to the burden of human salmonellosis in the EU in 2007-2009 (Pires et al., 2011).

- ***Food-borne outbreak data.*** There are differences in the level of detail in the reporting provided by the different EU MSs, which may reflect differences in the methodology and degree of outbreak-investigation carried out between MSs. In particular, the lack of harmonisation of food categories makes it difficult to apply the data for source attribution.

- ***Sporadic human salmonellosis.*** It is well-recognised that there are differences in the level of reporting of human foodborne infections in the EU MSs reflecting both differences in the methodologies used as well as the degree of reporting of human salmonellosis. To the extent possible, underreporting was accounted for in the model, but the estimation of the underreporting factors is based on Swedish travellers data, which in itself involves some degree of uncertainty by assuming that the incidence rate among travellers returning from a particular country is the same as the overall incidence rate in the country's native population (Havelaar et al., accepted).

- ***Level of subtyping detail.*** Another data limitation for the subtyping approach was linked to the reporting of aggregated data or data with no or sparse serotyping information by some countries. To overcome this, records were reassigned based on defined criteria and from some countries more complete data sets were obtained. These issues as well as the lack of further subtyping information (e.g. phage typing) on *S.* Enteritidis and *S.* Typhimurium may have resulted in attribution of some human cases to the wrong source. For instance, phage typing of *S.* Enteritidis would most likely have resulted in a better distinction between the pig, broiler and the laying hen reservoir in MSs, where *S.* Enteritidis is widely prevalent in two or more of these sources.

- ***Production and trade data.*** Ideally the same data source e.g. EUROSTAT should have been used to obtain information on the production of the different animal foods included in the model. However, as explained above the EUROSTAT production data for table eggs were insufficient and poultry meat is not reported by poultry species. Consequently, other data sources, where data are collected using different methodologies, were applied. This may have resulted in amounts of food available for consumption that is not representing the same level of aggregation for each of the animal food sources included in the model. For instance using the weight of slaughtered carcasses for pigs as an approximation for the amount available for consumption, may have resulted in an overestimation as compared to the other sources, as the whole pig carcass is obviously not consumed.

7. Model results compared to other attribution studies

As described in section 2, the TT-SAM model is based on the same mathematical principle as the two other models developed for EFSA in 2011; namely the BT-SAM model (Vose et al., 2011; EFSA Panel on Biological Hazards, 2011) and the EU-SSA model (Pires et al., 2011). However, the models are employing different datasets and it is therefore not possible to make a direct comparison of the models. First of all, the TT-SAM includes 25 MS, and thus more MSs than the BT-SAM (three more MSs) and the EU-SSA (one more MSs). Secondly, the TT-SAM model includes only 2010 data except for pigs, where the baseline survey data were used. The two other models are for the human data based on an aggregation of three years data (2007-2009) and for the animal reservoirs, the models are employing the baseline survey data for broilers (broiler carcasses), slaughter pigs and turkey flocks, and the 2008 monitoring data for laying hen flocks.

The results from the BT-SAM and the EU-SSA models are quite similar and, as explained, the models are based on almost the same data, except that the EU-SSA is including two more MSs. In contrast, the TT-SAM model estimates a substantial lower number of egg-related cases and a higher number of pig and broiler-meat related cases (Table 11).

Before discussing specific possible explanations for these discrepancies, it is important to note that the total number of reported human cases in EU has decreased in the period from 2007 to 2010. In 2007, approximately 154 000 cases were reported, which corresponds to around 8.85 million cases when accounting for underreporting. In 2010, these numbers were reduced to 99 000 reported cases and 5.41 million "true" cases. This reduction of the total burden of human salmonellosis must be expected to change the attribution estimates, particular the relative estimates, following the logic that if one or more sources contribute significantly less to the overall burden other sources will contribute relative more. The observed reduction in human cases is largely explained by a reduction in the number of *S.* Enteritidis cases, which are recognised to be particularly associated with shell-egg production. The EU harmonised monitoring put in place in 2008 and the setting of MS-specific targets for *S.* Enteritidis and *S.* Typhimurium occurrence in laying hens is assessed to be the main factor responsible for this development. This is strongly supported by the fact, that the prevalence of *S.* Enteritidis in laying hens

has decreased significantly in the same time period (i.e. 2007-2010) (EU SR, 2012). We believe that a part of the high increase (from around 28 % in the BT-SAM and EU-SAM model to 56 % in the TT-SAM) in the proportion of cases attributed to pig meat can be explained by this factor.

This is also supported by the results of the EU-SSA model when looking at the MS-level. In the EU-SSA model, laying hens/eggs were estimated to be the most important source of salmonellosis in Austria, Czech Republic, Estonia, Germany, Greece, Hungary, Latvia, Lithuania, Luxembourg, Slovenia, Slovakia, Spain and the United Kingdom, whereas pig meat was estimated to be most important source of *Salmonella* in Belgium, Cyprus, Finland, France, Ireland, Italy, Poland and Sweden. As the prevalence of *Salmonella* (and in particular *S.* Enteritidis) has decreased in laying hens in the majority of MSs since 2008, it is likely that pig meat is becoming the most important source in more MSs.

Still, when looking in Table 11, there also seems to be an absolute increase in the number of pig-related cases. Possible explanations for this include that in the TT-SAM model the monophasic variants (1,4,[5],12:i:-) of *S.* Typhimurium are included in the group of *S.* Typhimiurium. Since the monophasic strains are emerging rapidly in many MSs and pig meat is associated with *S.* Typhimurium infections, pig meat related infections should be expected to increase.

Table 11: Comparison of the results from the TT-SAM, BT-SAM and EU-SAM models. For the sake of comparison, the attribution estimates for the BT-SAM and EU-SSA models have been manipulated to obtain roughly the same number of MSs and time period

A. Comparison of the TT-SAM, BT-SAM and EU-SSA models adding results from the TT-SAM model for those MSs not included in the BT-SAM and the EU-SSA

25 MSs	Pigs	Broilers	Layers	Turkeys	Total number of estimated case per year	Percentage explained by the four sources
TT-SAM	3 099 000	559 300	928 000	135 100	5 414 000	87 %
BT-SAM[a]	2 251 897	184 769	2 243 992	174 571	~6 075 129	80 %
EU-SSA[b]	2 010 893	712 010	2 050 478	195 820	~5 900 000	84 %

a Divided by 3 to obtain the estimates per year and then added 2010 estimates from PL, PT and RO from TT-SAM, as these countries were not in the BT-SAM model

b Divided by 3 and added 2010 estimates from RO, that were not included in the EU-SSA model

B. Comparison of the TT-SAM, BT-SAM and EU-SSA models for the 22 MSs common for all three models

22 MSs	Pigs	Broilers	Layers	Turkeys
TT-SAM	1 631 043	431 442	639 389	89 674
BT-SAM	824 838	69 063	1 901 027	130 969
EU-SSA	886 779	55 032	1 688 575	165 501

Other explanations that are linked to the availability and quality of data as also described above include:

- Other potentially important sources of human salmonellosis like beef and dairy products are not included in the model. Some infections related to the cattle reservoir are therefore likely to have been wrongly attributed to pigs.
- In MSs, where *S.* Enteritidis is prevalent in both slaughter pigs and laying hens, the lack of further subtyping data (e.g. phage typing) makes it difficult for the model to distinguish between the two sources. Some *S.* Enteritidis cases may therefore have been wrongly attributed to pigs instead of laying hens (shell eggs). In fact, it is also likely that the number of broiler-related *S.* Enteritidis infections has been overestimated for the same reason.
- Finally, in MSs with reasonably good travel data it can be seen that a large proportion of the *S.* Enteritidis infections are linked to travel. It is assumed that this would also be the case in many of the MSs with poor or no travel data. Unfortunately, it is not possible for the countries with travel data to distinguish between infections acquired within and outside EU. However, if a substantial number of these are acquired outside EU, they will wrongly have been attributed to one of the sources included in the model, and mainly pig meat and laying hens/shell eggs.

Denmark and the Netherlands have for many years used microbial subtyping to estimate the relative importance of different sources to human salmonellosis. Comparing these national estimates with the MS-specific estimates coming out of the TT-SAM model is another way of validating the model results. For Denmark, the TT-SAM model estimates that for the human cases reported in Denmark, 19 %, 2 %, 8 % and 5 % can be attributed to pigs, broilers, eggs and turkeys, respectively. Data from Denmark show that the same estimates based on the national model in 2010 were 22 % for pigs, 0.7 % for broilers, 1.8 % for eggs and 1 % for turkeys (Anonymous, 2011). The somewhat lower estimate for eggs may be explained by the fact that the Danish model does not consider the impact of imported eggs, whereas this is included in the present model through the use of trade data.

For the Netherlands, the present model estimates that 20 %, 14 %, 23 % and 6 % of cases can be attributed to pigs, broilers, eggs and turkeys, respectively. In comparison, the national estimates for the Netherlands for 2010 were 19 % for pigs, 18 % for broilers, and 29 % for eggs (Aalten et al., 2011). It should be noted that turkeys are not included as a putative source in the Dutch model. Both the Danish and Dutch model uses subtyping for further distinction between sources, employs better travel data and includes additional sources such as the bovine reservoir. Still, the TT-SAM model provides MS-specific estimates for these two countries that are in accordance with published national estimates. Unfortunately, only a few MSs produce such data.

The EU-wide baseline survey data are in general considered valid and provide the best available data for comparison between countries. The main issues are that not all MSs participated in all surveys, that the surveys differ in time and that the surveys are becoming outdated. Particular the latter makes the use of the baseline survey data for future attribution studies questionable, as the *Salmonella* situation in both human and animal reservoirs is dynamic and must be expected to change over a period of time, particularly when targeted control programs are implemented. Data reported as part of the EU harmonised monitoring are therefore going to be the primary data used for these kind of models, but they suffer from the fact that even though the minimum requirement for the monitoring is harmonised, national surveillance systems still differs with respect to e.g. sampling frequencies and the detail with which the serovar distribution is reported.

In conclusion, despite data limitations and the resulting uncertainty in the results, the source attribution estimates are considered to reflect the best current knowledge about which sources are most important for human salmonellosis in the EU, and highlight differences in the contribution of different food-animal sources for disease and on the efficiency of surveillance systems in place in EU MSs. The results are expected to be useful for the delineation of risk management strategies.

CONCLUSIONS AND RECOMMENDATIONS

CONCLUSIONS

- The TT-SAM model estimated that 2.6 % (95 % CI: 1.2-5.2) of all human salmonellosis cases (i.e. estimated true number of cases when accounting for underreporting) in the EU were attributed to the turkey reservoir. This correspond to 135 100 (95 % CI: 60 790-293 600) human cases in 2010.
- For the other animal-food sources included in the model, the attribution estimates were that 56.8 % (95 % CI: 48.2-65.8), 10.6 % (95 % CI: 5.1-18.3) and 17.0 % (95 % CI: 11.3-24.0) of the estimated number of human salmonellosis cases could be attributed to the pig, broiler and laying hen reservoir, respectively.
- However, when looking at the relative risk between turkey meat and the other three sources weighted by the tonne of meat/eggs available for consumption, this picture changes, indicating that the risk of infection for the individual consumer is highest when consuming shell eggs closely followed by the consumption of pig meat, whereas the risk is lower for turkey and broiler meat.
- Around 63 % of the turkey-associated human salmonellosis cases were caused by serovars other than the currently regulated serovars *S.* Enteritidis and *S.* Typhimurium. However, *S.* Enteritidis and *S.* Typhimurium were still among the most important serovars from turkeys. Four serovars (*S.* Kentucky, *S.* Saintpaul, *S.* Senftenberg and *S.* Kottbus) had turkeys as the most important reservoir for human infections.
- In the situation, where the overall prevalence (i.e. the combined prevalence of all serovars) in turkey flocks per MSs is reduced to 1 % (scenario 4), a reduction in the number of turkey-associated human cases of 83.2 % (95 % CI: 79.0-87.4) compared to the situation in 2010 was estimated. In absolute numbers, this corresponds to a reduction of 112 300 (95 % CI: 50 410-243 400) human salmonellosis cases. Overall, this scenario was estimated to reduce the percentage of human turkey-associated cases from 2.6 % to 0.4 %.
- In the situation, where the combined prevalence of the top-6 serovars of turkeys that contribute most to human cases is reduced to 1 % or less in turkey flocks per MSs (scenario 6), a reduction in the number of turkey-associated human cases of 37.2 % (95 % CI: 19.2-54.0) compared to the situation in 2010 was estimated. In absolute numbers, this corresponds to a reduction of 48 110 (95 % CI: 22 580-100 500) human salmonellosis cases. Overall, this scenario was estimated to reduce the percentage of human turkey-associated cases from 2.6 % to 1.7 %.
- The least reduction was obtained in the situation, where the achievement of the current target of the EU control programme of *Salmonella* in turkey flocks would be met (i.e. scenario 1). This analysis resulted in an estimated reduction in the number of turkey-associated human salmonellosis cases of only 0.4 % (95 % CI: 0.1-1.3) compared to the situation in 2010. In absolute numbers, this corresponds to an estimated reduction of 594 (95 % CI: 121-1 901) human cases. Since, all MSs except one have already met the transitional target, this result is not unexpected.
- Some *Salmonella* reservoirs (e.g. cattle/beef) were not included in the model due to poor data availability and quality. It is therefore likely that the contribution of the human salmonellosis cases allocated to the animal reservoirs included in the model, particularly pigs, have been overestimated.
- Besides the statistical uncertainty reflected in the credibility intervals in the model results, other factors contributed to the uncertainty of the validity of the results. These 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 in both the human and animal food source data. Such uncertainties cannot be statistically quantified, but should be kept in mind when interpreting the results.

- The lower attribution estimate obtained for the laying hen reservoir (i.e. shell eggs) by the TT-SAM model as compared to previous models is supported by data, since both the reported number of cases in EU (particularly *S.* Enteritidis cases) and the prevalence of *Salmonella* (particularly *S.* Enteritidis) in laying hen flocks have been decreasing from 2008 to 2010. The improved surveillance and control of *S.* Enteritidis in laying hens in many MSs is assessed to be responsible for a major part of this reduction.
- The reduction of the overall burden of human salmonellosis must be expected to change the attribution estimates, particular the relative estimates, following the logic that if one or more sources contribute significantly less to the overall burden other sources will contribute relative more. The high relative attribution estimate obtained for pig meat by the TT-SAM model, is believed to be partly explained by this.
- Despite data limitations and the resulting uncertainty in the results, the source attribution estimates are considered to reflect the best current knowledge about which sources are most important for human salmonellosis in the EU, and highlight differences in the contribution of different food-animal sources for disease and on the efficiency of surveillance systems in place in EU MSs. The results are expected to be useful for the delineation of risk management strategies.

RECOMMENDATIONS

- The role of the pig reservoir presumable through the consumption of pig meat was estimated by the TT-SAM model to have increased both relatively and absolutely when compared to the results from the BT-SAM and the EU-SSA models. Although, the number of cases attributed to pig meat may have been overestimated, pig meat is likely to be the most important source in a majority of MSs. Harmonised monitoring and control of *Salmonella* in pigs and pig meat should therefore be considered.
- Some of the uncertainty in the results presented in this report occurred as a consequence of the lack of harmonized *Salmonella* subtyping in EU countries. It is recommended to provide more comparable subtyping data (e.g. phage typing, molecular typing and antimicrobial resistance testing) from both human and animal-food sources from all MSs. This would improve future source attribution studies and trend analyses.
- The systems for reporting of human salmonellosis cases vary considerably between MSs making it difficult to compare incidences and the effect of EU-wide *Salmonella* control. A continuous effort to provide comparable and harmonized data on human salmonellosis in all MSs is therefore recommended. This should include efforts to quantify the level of underreporting.
- The cattle reservoir is recognized as a source of human salmonellosis, but was not included in the subtyping approach due to lack of comparable data. It may be considered to conduct an EU-wide baseline survey of *Salmonella* in cattle or beef to investigate the role of beef as a source of human infections.
- The microbial subtyping approach should be repeated on a regular basis (e.g. every 3 to 5 years) in order to evaluate the effect of *Salmonella* control in the various food-animal sources and to follow the trends and dynamic changes in the sources of human salmonellosis.

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APPENDICES

A. PRODUCTION, EXPORT AND IMPORT DATA USED IN THE TT-SAM MODEL

Table A1: Estimated national production available for consumption in 2010 for turkey meat, broiler meat, pig meat and shell eggs. Estimates are based on the data presented in Tables B2-B5.

	TURKEY MEAT in tonnes	BROILER MEAT in tonnes	PIGS MEAT in tonnes	SHELL EGGS in tonnes
AT	22,000	88,856	542,131	93,000
BE	4,000	0	587,588	189,000
BG	1,000	77,000	37,346	85,096
CY	1,000	27,000	57,059	9,910
CZ	3,000	181,000	275,905	122,132
DE	439,000	1,030,000	5,069,726	664,268
DK	0	175,000	932,478	76,376
EE	0	14,000	31,930	11,366
ES	25,000	1,022,000	2,686,409	733,419
FI	9,000	85,398	202,392	53,080
FR	372,024	1,045,000	2,010,326	946,600
GR	3,000	160,000	113,717	99,800
HU	77,755	240,000	416,146	151,804
IE	0	109,000	198,846	45,000
IT	242,781	754,844	1,632,715	736,800
LT	0	60,871	54,814	36,470
LU	0	0	9,509	1,274
LV	0	23,000	23,327	32,745
MT	0	5,000	6,960	5,091
NL	27,000	158,347	901,794	188,010
PL	208,145	873,124	1,741,425	484,453
PT	39,000	267,000	384,201	131,000
RO	0	380,000	234,195	297,535
SE	4,000	63,447	263,478	103,200
SI	6,000	54,541	24,902	21,618
SK	0	74,000	68,599	72,447
UK	162,000	1,379,000	774,466	619,000

Table A2: Production, import and export of turkey meat in EU MSs in 2010.

TURKEY	AVEC production data 2010 in tonnes[1]	Total import (from export sheet) EUROSTAT External Trade 2010 in tonnes[2]	Total export EUROSTAT traces 2010 in tonnes[2]
AT	22,000	38,604	13,229
BE	4,000	36,557	2,540
BG	1,000	10,393	144
CY	1,000	784	19
CZ	3,000	11,011	488
DE	439,000	95,195	81,855
DK	0	10,599	2,565
EE	0	1,168	191
ES	25,000	22,268	16,032
FI	9,000	1,134	984
FR	412,000	32,501	72,477
GR	3,000	7,288	1,217
HU	100,000	11,297	33,542
IE	6,000	9,871	18,227
IT	279,000	9,386	45,605
LT	0	3,983	985
LU	0	3,463	27
LV	0	1,190	36
MT	0	267	0
NL	27,000	41,100	27,794
PL	280,000	8,995	80,850
PT	39,000	13,534	645
RO	0	9,110	332
SE	4,000	3,416	343
SI	6,000	3,743	399
SK	0	6,064	356
UK	162,000	33,931	25,967

[1] AVEC (Association of Poultry Processors and Poultry Trade in the EU Countries), 2011. 2011 Annual Report. Available at http://www.avec-poultry.eu/Default.aspx?ID=4731, 52 pp.

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Table A3: Production, import and export of broiler meat in EU MSs in 2010.

BROILERS	AVEC production data in tonnes[1]	Total import (from export sheet) EUROSTAT traces 2010 in tonnes[2]	Total export EUROSTAT traces 2010 in tonnes[2]
FR	1,045,000	311,466	84,335
NL	663,000	314,180	818,833
DE	1,030,000	445,637	213,510
IT	780,000	33,517	58,673
UK	1,379,000	320,953	172,700
IE	109,000	70,502	24,332
DK	175,000	75,354	52,326
GR	160,000	48,563	8,071
PT	267,000	25,197	3,829
ES	1,022,000	64,623	56,475
BE	255,000	80,584	336,435
LU	0	5,918	213
SE	79,000	23,879	39,432
FI	88,000	4,142	6,744
AT	90,000	35,354	36,497
MT	5,000	4,195	0
EE	14,000	19,473	5,767
LV	23,000	24,840	5,672
LT	67,000	16,178	22,307
PL	1,070,000	22,763	219,639
CZ	181,000	72,293	23,415
SK	74,000	48,311	26,390
HU	240,000	56,928	40,241
RO	380,000	138,109	51,274
BG	77,000	69,848	33,825
SI	57,000	6,073	8,532
CY	27,000	11,728	1,141

[1] AVEC (Association of Poultry Processors and Poultry Trade in the EU Countries), 2011. 2011 Annual Report. Available at http://www.avec-poultry.eu/Default.aspx?ID=4731, 52 pp.

[2] http://epp.eurostat.ec.europa.eu/newxtweb/ extracted on 13th December 2011, codes 02071110, 02071130, 02071190, 02071210, 02071290, 02071310, 02071320, 02071330, 02071340, 02071350, 02071360, 02071370, 02071391, 02071399, 02071410, 02071420, 02071430, 02071440, 02071450, 02071460, 02071470, 02071491, 02071499.

Table A4: Production of pig carcasses and import and export of pig meat in EU MSs in 2010.

PIGS	Slaughtered animals 2010, in tonnes carcasses. EUROSTAT[1].	Total import (from export sheet) EUROSTAT External Trade 2010 in tonnes[2]	Total export EUROSTAT External Trade 2010 in tonnes[2]
AT	542,131	147,266	130,180
BE	1,123,769	84,856	621,037
BG	37,346	87,669	1,450
CY	57,059	42,397	4,628
CZ	275,905	187,461	35,105
DK	1,666,300	109,510	843,333
EE	31,930	25,242	6,947
FI	203,068	13,902	14,579
FR	2,010,326	404,401	384,480
DE	5,443,166	961,605	1,335,045
GR	113,717	208,201	3,765
HU	416,146	121,712	110,469
IE	214,129	64,702	79,985
IT	1,632,715	945,394	61,322
LV	23,327	31,009	1,468
LT	54,814	52,585	2,545
LU	9,509	6,234	1,914
MT	6,960	2,235	0
NL	1,288,274	287,268	673,748
PL	1,741,425	495,468	144,545
PT	384,201	116,781	9,863
RO	234,195	178,915	2,763
SK	68,599	109,421	7,911
SI	24,902	42,142	1,260
ES	3,368,921	75,810	758,323
SE	263,478	80,487	14,654
UK	774,466	475,793	107,148

[1] http://appsso.eurostat.ec.europa.eu/nui/show.do?dataset=food_in_pagr2&lang=en, extracted on 2nd December 2012, slaughtered pigs for meat consumption.

[2] http://epp.eurostat.ec.europa.eu/newxtweb/, extracted on 13th December 2011, codes 02031110, 02031190, 02031211, 02031219, 02031290, 02031911, 02031913, 02031915, 02031955, 02031959, 02031990, 02032110, 02032190, 02032211, 02032219, 02032290, 02032911, 02032913, 02032915, 02032955, 02032959, 02032990.

Table A5: Production, import and export of shell eggs in EU MSs in 2010

EGGS	Production of shell eggs 2010, in tonnes. FAOSTAT[1]	Total import (from export sheet) EUROSTAT traces 2010 in tonnes[2]	Export TRACES data eggs in tonnes[2]
AT	93,000	14,877	5,417
BE	189,000	37,825	0
BG	89,264	2,978	7,146
CY	9,910	414	0
CZ	122,132	30,668	4,387
DK	76,376	16,841	1,709
EE	11,366	5,556	848
FI	61,500	46	8,466
FR	946,600	62,770	41,666
DE	664,268	628,299	96,775
GR	99,800	4,112	104
HU	151,804	11,537	5,993
IE	45,000	1,723	1,704
IT	736,800	38,714	22,123
LV	44,990	6,236	18,481
LT	42,804	4,274	10,609
LU	1,274	2,428	69
MT	5,091	217	0
NL	631,000	102,276	545,266
PL	618,496	13,826	147,870
PT	131,000	7,400	6,678
RO	297,535	16,998	5,778
SK	74,646	9,948	12,146
SI	21,618	1,253	21
ES	840,000	2,731	109,312
SE	103,200	6,945	2,017
UK	619,000	27,038	3,347

1 FAOSTAT data extracted 3. January 2010: http://faostat.fao.org/site/569/DesktopDefault.aspx?PageID=569#ancor
2 http://epp.eurostat.ec.europa.eu/newxtweb/ extracted on 13th December 2011, codes 04070030.

B. SEROVAR DISTRIBUTION AMONG THE ESTIMATED NUMBER HUMAN OF HUMAN CASES

Table B1: Number of human cases by serovar and animal reservoir as estimated by the TT-SAM model.

	Pigs	Broilers	Layers	Turkeys
S. Enteritidis	1 313 000	459 600	806 000	29 770
S. Typhimurium	1 543 000	15 440	17 030	20 010
S. Infantis	29 500	36 170	29 650	6 820
S. Virchow	13 270	4 250	20 540	9 110
S. Newport	33 170	4 470	6 878	10 030
S. Kentucky	0	2 347	8 207	22 970
S. Derby	30 400	187	48	2 445
S. Mbandaka	5 620	12 800	6 362	2 046
S. Hadar	14 780	11 270	4 930	7 274
S. Agona	9 136	873	2 481	2 923
S. Saintpaul	293	662	39	8 439
S. Bovismorbificans	25 420	557	2 288	1 095
S. Braenderup	5 840	316	7 227	0
S. Montevideo	5 615	1 214	7 371	850
S. Brandenburg	12 200	441	19	112
S. Rissen	33 530	295	462	39
S. Senftenberg	134	269	206	1 437
S. Bredeney	6 669	2 180	680	4 924
S. Kottbus	2 495	389	265	2 907
S. London	9 867	0	671	317
S. Livingstone	1 706	2 428	4 209	307
S. Heidelberg	177	2 703	2 313	1 157
S. Anatum	3 686	421	78	143
Total	3 099 508	559 281	927 955	135 125