EFSA Panel on Biological Hazards (BIOHAZ); Scientific Opinion on an estimation of the public health impact of setting a new target for the reduction of Salmonella in turkeys

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SCIENTIFIC OPINION

Scientific Opinion on an estimation of the public health impact of setting a new target for the reduction of *Salmonella* in turkeys[1]

EFSA Panel on Biological Hazards (BIOHAZ)[2, 3]

European Food Safety Authority (EFSA), Parma, Italy

ABSTRACT

The quantitative contribution of turkeys and other major animal-food sources to the burden of human salmonellosis in the European Union was estimated. A 'Turkey Target *Salmonella* Attribution Model' (TT-SAM) based on the microbial-subtyping approach was used. TT-SAM includes data from 25 EU Member States, four animal-food sources of *Salmonella* and 23 *Salmonella* serovars. The model employs 2010 EU statutory monitoring data on *Salmonella* in animal populations (EU baseline survey data for pigs), data on reported cases of human salmonellosis and food availability data. It estimates that 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. The top-6 serovars of fattening turkeys that contribute most to human cases are *S.* Enteritidis, *S.* Kentucky, *S.* Typhimurium, *S.* Newport, *S.* Virchow and *S.* Saintpaul. Comparing the prevalence of *Salmonella* in turkey flocks reported in 2010 with a theoretical combined prevalence for *S.* Enteritidis and *S.* Typhimurium of 1 % (i.e. the transitional target), a reduction of 0.4 % in the percentage of turkey-associated human salmonellosis cases would be achieved. However, when adjusting the combined prevalence of all serovars to 1 %, an 83.2 % reduction in the percentage of turkey-associated human salmonellosis cases, equivalent to 2.2 % of all human salmonellosis cases, is expected. Uncertainty and data limitations are discussed, including recommendations on how these could be overcome. Vertical transmission of *Salmonella* as well as hatchery acquired *Salmonella* contamination originating from breeding stock are very important sources for *Salmonella* infection in turkeys, and therefore controlling *Salmonella* in breeding flocks as well as in rearing and fattening flocks is necessary to minimise *Salmonella* in turkeys at slaughter.

KEY WORDS

Salmonella, poultry, turkeys, source attribution, microbial subtyping, targets.

[1] On request from the European Commission, Question No EFSA-Q-2010-00899, adopted on 8 March 2012.

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SUMMARY

Following a request from the European Commission, the Scientific Panel on Biological Hazards (BIOHAZ) was asked to deliver a Scientific Opinion on an estimate of the public health impact of setting a new target for the reduction of *Salmonella* in turkeys. Specifically, EFSA was asked to indicate and rank the *Salmonella* serovars with public health significance, 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 and to assess the relative public health impact if a new target for reduction of *Salmonella* is set in turkeys being 1 % or less of flocks 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).

In order to assess the impact of a reduction of *Salmonella* prevalence in breeding flocks of turkeys on the prevalence in flocks of fattening turkeys, information available in the literature and monitoring results about the presence of *Salmonella* serovars in turkey flocks at different level, were taken into account. From these data, it is clear that in some cases there is a coincidence between the serovars isolated in breeding flocks and the ones isolated in fattening flocks, but some of the serovars isolated in fattening flocks are not detected in breeding flocks, thus suggesting the relevance of other sources of infection, such as contaminated feed or turkey houses and breaches in biosecurity, not related to the concurrent presence of *Salmonella* in the parent stocks. The Panel therefore concluded that vertical transmission and hatchery acquired infection appear as most important sources for *Salmonella* infection in fattening turkeys. Controlling the infection in breeders is necessary, but not sufficient to control *Salmonella* in fattening flocks.

For the second task (to assess the relative public health impact of a new target for reduction of *Salmonella* in turkey flocks), the Panel was supported by the work of a contractor that developed a source attribution model providing 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 model was based on the so-called microbial-subtyping approach, where the serovar distributions observed in different animal-food sources is compared with the serovar distribution found in humans. The Technical Report submitted to EFSA by the contractor provides detailed information on the modelling approach and results.

The model considered the following data: (i) the results from the harmonised EU monitoring in turkeys, broiler and laying hen flocks in 2010, (ii) the EU-wide *Salmonella* baseline survey on slaughter pigs, (iii) the reported cases of human salmonellosis in EU in 2010 by MSs as provided by the European Centre for Disease Prevention and Control[4] (ECDC), and (iv) the amount of each food source available for consumption by MS as estimated from EUROSTAT data on production, import and export. The model included data from 25 MSs, four animal-food *Salmonella* sources (turkeys, broilers, laying hens and pigs) and 23 individual serovars. To take account for differences in underreporting of human salmonellosis cases between MSs, MS-specific underreporting factors were calculated and 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.

Initially, a model applying prevalence data from the harmonised EU monitoring conducted in turkey flocks in 2010 was developed. This model is referred to as the 'Turkey Target *Salmonella* Attribution Model' or TT-SAM model throughout the Opinion. In order to answer the Terms of Reference, seven different scenarios where *Salmonella* prevalences in turkey flocks were changed were developed and the results compared to the results of the TT-SAM model.

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

The Panel concluded that, based on the results of the TT-SAM model, in 2010, there were approximately 5.4 (95 % CI: 3.0-9.5) million true cases of human salmonellosis (i.e. estimated true number of cases when accounting for underreporting) in the EU, a 13 % decrease compared to 2009. 2.6 % (95 % CI: 1.2-5.2) of these human salmonellosis cases were attributed to turkeys. The top-6 serovars of fattening turkeys that contribute most to human cases are *S.* Enteritidis, *S.* Kentucky, *S.* Typhimurium, *S.* Newport, *S.* Virchow and *S.* Saintpaul.

For the other *Salmonella* sources considered, the model estimated that around 17.0 % (95 % CI: 11.3-24.0), 56.8 % (95 % CI: 48.2-65.8) and 10.6 % (95 % CI: 5.1-18.3) of the estimated number of human salmonellosis cases could be attributed to reservoirs relating to laying hens (eggs), pigs and broilers, respectively. However, when considering the risk between turkey meat and the other three sources weighted by the tonne of food available for consumption, the risk of infection is highest when consuming table eggs closely followed by the consumption of pig meat, whereas the risks associated with broiler and turkey meat were similar and approximately two-fold lower.

The Panel concluded that (1) considering that the current transitional target of the EU control programme of *Salmonella* in fattening turkey 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 per the 2010 harmonised monitoring in turkey flocks, an estimated reduction in the number of turkey-associated human salmonellosis cases of 0.4 % compared to the situation in 2010 is expected (in 2010 all MSs except one had already met the transitional target); (2) considering that an EU-wide target of maximum of 1 % of flocks remaining positive for the all the *Salmonella* serovars considered in the model would be met, an estimated reduction in the number of turkey-associated human salmonellosis cases of 83.2 % compared to the situation in 2010 is expected, corresponding to a 2.2 % reduction of all human salmonellosis cases. The Panel emphasised that the individual MS contributions to the estimated reductions vary greatly.

The Panel finally concluded that the main factors contributing to the uncertainty of the model results, apart from statistical uncertainties, are the lack of harmonised monitoring of human salmonellosis in the EU as well as the different levels of serovar detail reported in both the human and animal food source data. These uncertainties could not be statistically quantified with the model employed to support this Scientific Opinion.

The Panel makes a series of recommendations related to the establishment of active surveillance of human salmonellosis in all MSs including harmonised typing of human *Salmonella* isolates and efforts to quantify the level of under-ascertainment and underreporting. It is recommended to investigate the effectiveness of different sampling options at primary production, in order to ensure comparability of results, and to implement reliable tests, epidemiological studies and accurate reporting in order to identify emerging strains and antimicrobial use, and to apply targeted control measures. Comparable data on *Salmonella* in cattle would be necessary to obtain better estimates on the public health impact of different animal reservoirs.

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BACKGROUND AS PROVIDED BY THE EUROPEAN COMMISSION

The presence of *Salmonella* in poultry populations is considered as a risk factor for the presence of *Salmonella* in meat and eggs. Targets are being set for the reduction of certain *Salmonella* serotypes in different poultry populations within the framework of Regulation (EC) No 2160/2003[5] on the control of zoonoses. As a transitional measure, a limited number of serotypes have been considered for reduction during the first three years of the control programme. Before the end of this period, a review of the serotypes should be considered.

As regards turkeys, Regulation (EC) No 584/2008[6] sets a transitional target for reduction being less than 1 % of flocks remaining positive for *Salmonella* Enteritidis or *Salmonella* Typhimurium by the end of 2012 both in flocks of breeding and fattening turkeys. The Regulation also harmonises the monitoring in turkeys in all Member States from the beginning of 2010. Therefore, comparable prevalence data from all Member States will be available from this year onwards. These prevalence data will be forwarded by Member States to EFSA's Zoonoses Data Collection unit.

For the setting of a new target for reduction of *Salmonella* beyond 2012, a cost/benefit analysis should be carried out (See flow chart in next page). A first step is the assessment by EFSA of the benefit, which should be defined as a beneficial public health impact of a possible new target.

TERMS OF REFERENCE AS PROVIDED BY EUROPEAN COMMISSION

The EFSA is asked:

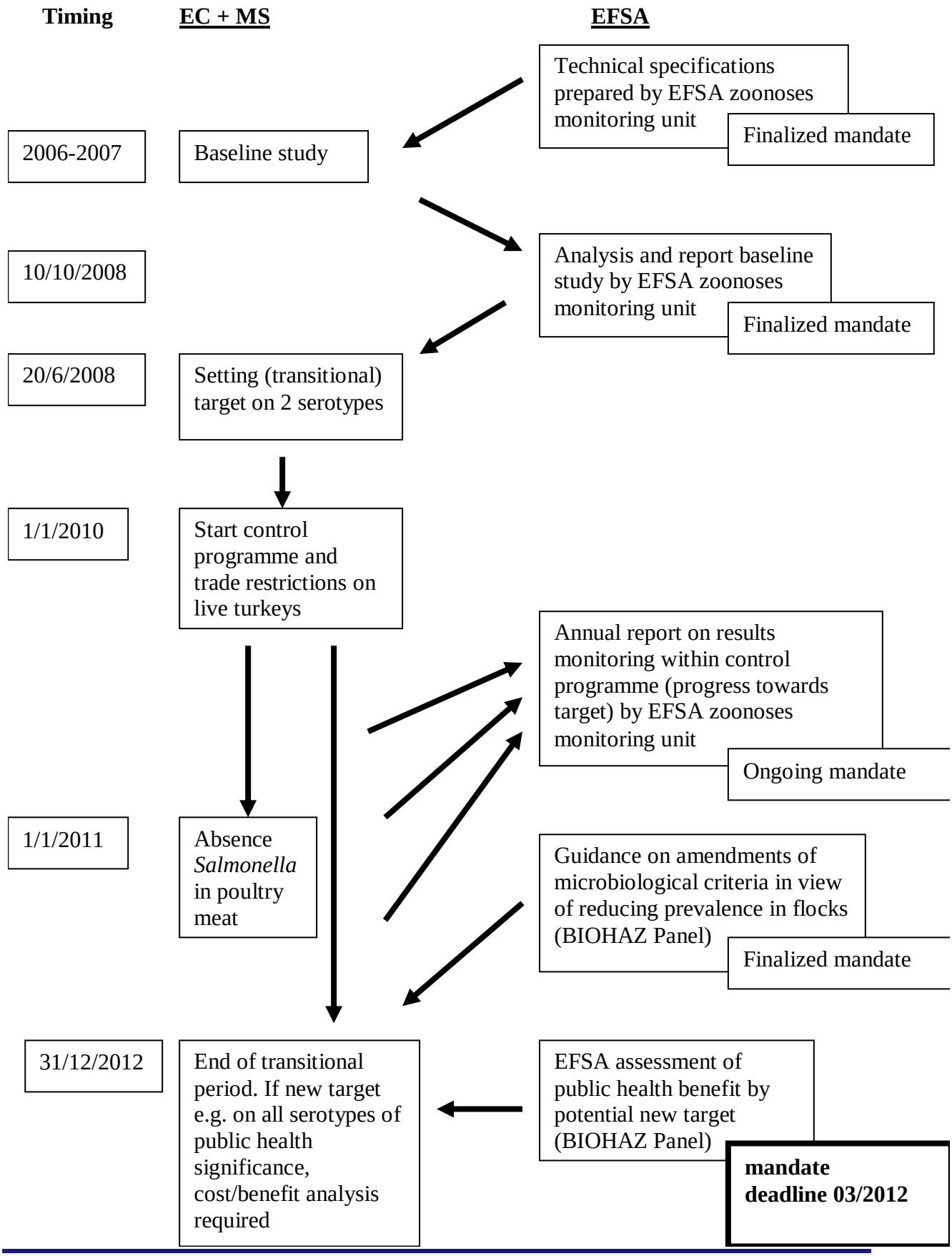
- To indicate and rank the *Salmonella* serotypes with public health significance according to Annex III of Regulation (EC) No 2160/2003,
- To assess the impact of a reduction of the prevalence of *Salmonella* in breeding flocks of turkeys on the prevalence of *Salmonella* in flocks of fattening turkeys,
- To assess the relative public health impact if a new target for reduction of *Salmonella* is set in turkeys being 1 % or less of flocks remaining positive for all *Salmonella* serotypes with public health significance.

The references for the two assessments mentioned above shall be:

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

[5] OJ L 325, 12.12.2003, p. 1. Regulation as last amended by Commission Regulation (EC) No 1237/2007 (OJ L 208, 24.10.2007, p. 5)
[6] OJ L 162, 21.6.2008, p. 3.

Flowchart *Salmonella* control programmes turkeys and needs for EFSA input



ASSESSMENT

1. Introduction

Three EFSA Scientific Opinions have dealt with quantitative estimates of the impact of setting new targets for the reduction of *Salmonella* in certain poultry populations (*Gallus gallus*), which were requested by the European Commission in a mandate in April 2008.

The first of the Opinions, which was published in April 2009, dealt with a request to provide a quantitative estimation of the impact of setting a new target for the reduction of the prevalence of *Salmonella* in breeding hens of *Gallus gallus* (EFSA, 2009b). A second Opinion, published in April 2010 provided an estimate of the public health impact of setting a new target for the reduction of *Salmonella* in laying hens (EFSA Panel on Biological Hazards, 2010a). The third Opinion was published in July 2011, and provided a quantitative estimate of the public health impact of setting a new target for the reduction of *Salmonella* in broilers (EFSA Panel on Biological Hazards, 2011a).

The present Opinion deals with the assessment of the public health impact of setting new targets for the reduction of *Salmonella* in two different populations: breeding and fattening turkeys. According to the Terms of Reference (ToR) provided by the European Commission, EFSA is asked to provide an estimate on the public health impact of different flock prevalence values (theoretical vs. reported for the year 2010) in turkeys of different *Salmonella* serovar groups (i.e. *S.* Enteritidis and *S.* Typhimurium vs. all *Salmonella* serovars with public health significance). EFSA is also asked 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.

The determination of the serovars with public health significance has been done following the criteria laid down in Annex III to Regulation (EC) No 2160/2003[7], as requested in the ToR. It follows a similar methodological approach as in the previous related Opinions (EFSA, 2009b; EFSA Panel on Biological Hazards, 2010a, 2011a), but in this case the particular context of turkey production is addressed.

The quantitative aspects considered in this Opinion have been supported by the work of a contractor selected by means of an EFSA negotiated procedure (CT/EFSA/BIOHAZ/2011/02), who has adapted the modelling approach developed as part of two negotiated procedures, CT/EFSA/BIOHAZ/2010/02 and used for the Opinion on *Salmonella* in broilers (referred to as the Broiler Target *Salmonella* Attribution Model or BT-SAM) (EFSA Panel on Biological Hazards, 2011a), and CT/EFSA/ZOONOSES/2010/02 (referred to as the EU-*Salmonella* Source Attribution or EU-SSA), in order to provide updated results concerning turkeys. The report of the work carried out by this contractor is published as a separate document (Hald et al., 2012) and should be read as part of the present Scientific Opinion.

2. *Salmonella* in humans in the EU

A total of 99 020 confirmed cases of human salmonellosis were reported from 27 EU Member States (MSs) through the European Surveillance System (TESSy) in 2010 (EFSA and ECDC, 2012). The EU notification rate was 21.5 cases per 100 000 population, ranging from 1.9 in Portugal to 91.1 confirmed cases per 100 000 population in Slovakia. As in previous years, *S.* Enteritidis and *S.* Typhimurium were the most frequently reported serovars (67.4 % of all reported cases where the information on serovars was provided) (EFSA and ECDC, 2012). This proportion is continuously decreasing (it was 75.6 % in 2009).

The five-year (2006-2010) EU-trend showed a statistically significant decrease in the reported incidence of human salmonellosis, although there were country-specific variations (EFSA and ECDC,

[7] 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.

2012). The decreasing trend is mainly explained by a downward trend in the number of *S.* Enteritidis infections. For 2010, a decrease was also noted for *S.* Typhimurium infections. However, comparison of the notification rates between countries should be made with caution because of the different degrees of underreporting that exist between MSs (EFSA Panel on Biological Hazards, 2011a). The importance of underreporting is discussed in more detail below. Comparison between years within a country is, in general, more valid.

The total number of reported cases includes sporadic, travel and outbreak-related infections. However, when assessing the public health importance of a given food source (e.g. turkey meat), and especially when assessing the expected reduction in human cases due to a certain control strategy, it is important to consider the proportion of cases that are associated with travel abroad and/or larger outbreaks. The effect of control efforts implemented at the EU level should be reflected in a decline in the total number of salmonellosis cases, including those acquired during intra-EU travelling. Cases acquired outside the EU cannot be expected to be reduced as a consequence of EU efforts to control *Salmonella* in primary production or processing. Large and possible international outbreaks may influence the total incidence in the EU as well as in individual MSs, but as they are often caused by failures in the production of a single or more (batches of) food product originating from the same producer, the EU and national control efforts may only affect such events to a minor degree. In other words, EU control efforts are in general expected only to have an effect on the number of sporadic cases acquired within the EU.

Overall, in 2010, the proportion of cases reported as acquired abroad was approximately 11 %, whereas the proportion of domestically acquired cases was around 63 %. However, these proportions varied greatly among MSs and for some countries such as Sweden and Finland, the travel-related cases represented the majority of all salmonellosis cases. The proportion of cases with an unknown origin represented around 26 % of confirmed cases, but in eight MSs the proportion of unknown location of origin is reported to be 100 % (EFSA and ECDC, 2012). Data on domestic vs. travel-related cases are, therefore, often incomplete, but should, as far as possible, be accounted for in the analysis of the public health impact of a given source.

New reporting specifications for food-borne outbreaks were implemented in 2010. These specifications are described in technical specifications for harmonised reporting of food-borne outbreaks through the EU reporting system in accordance with Directive 2003/99/EC[8] (EFSA, 2011a). As a consequence of the new specifications, the distinction between 'verified' and 'possible' food-borne outbreaks was abandoned and instead the MSs should report all food-borne outbreaks that meet the definition laid down by Directive 2003/99/EC.

The reported outbreaks are categorised based on the strength of evidence implicating a suspect food vehicle. In food-borne outbreaks where no particular food vehicle is suspected, and for food-borne outbreaks where the evidence implicating a particular food vehicle is weak, only a limited dataset is to be reported. Such datasets should include the number of outbreaks per causative agent and the number of human cases as well as the number of hospitalisations and deaths. For food-borne outbreaks, where the evidence implicating a particular food vehicle is strong, a more detailed dataset should be reported. These detailed datasets should include information on causative agents, food vehicles as well as the factors in food handling and preparation that contributed to the food-borne outbreaks. Furthermore, MSs should also report information on the nature of the evidence (microbiological or epidemiological) to support the link between human disease cases and the food vehicle.

In 2010, a total of 1 604 *Salmonella* outbreaks were reported, constituting approximately 31 % of the reported food-borne outbreaks. Of these, 341 were outbreaks with strong evidence, involving 5 212 confirmed cases, and the majority of the outbreaks (69.8 %) were reported by Poland, Spain and France (EFSA and ECDC, 2012). In total, 19 % of human cases in strong evidence outbreaks were

[8] Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EE. OJ L 325, 12.12.2003, p. 31-40.

hospitalised and the overall human case fatality rate was 0.17 %. The majority of strong evidence outbreaks were associated with foodstuffs of animal origin and eggs and egg products were the most common single foodstuff category reported as food vehicle (EFSA and ECDC, 2012). *S*. Enteritidis was the predominant serovar associated with the *Salmonella* outbreaks, which is similar to previous years (EFSA and ECDC, 2010, 2011, 2012). In 2010, *S*. Enteritidis accounted for 61.3 % of all strong evidence *Salmonella* outbreaks, 19.6 % of all human *Salmonella* cases, 39.0 % of all hospitalisations and 20.0 % of all case fatalities. *S*. Typhimurium was associated with 13.8 % of the strong evidence outbreaks, 10.9 % of all human cases, 14.3 % of all hospitalisations and 26.7 % of all deaths in 2010. In 18.8 % of the strong evidence outbreaks caused by *Salmonella*, the serovar was not reported or was unknown. Only 13.7 % of the outbreaks of *S*. Enteritidis or *S*. Typhimurium included information of the isolated phage type (EFSA and ECDC, 2012).

The reporting of outbreaks by the different MSs depends very much on the resources in place for handling these incidents. Furthermore, large outbreaks or those involving unusual serovars will have a greater probability of being detected by the surveillance systems in a MS than smaller outbreaks of common serovars. The chance for verifying the causative agent is also inherently associated with the incriminated food vehicle and source. If the combination of food vehicle and the causative agent is frequently linked and associated with outbreaks (e.g. *S*. Enteritidis in eggs) it may be anticipated that the chance for verifying the outbreak will be greater, since the possibly implicated food vehicle will most likely be included in epidemiological and microbiological investigations.

The previous Scientific Opinions dealing with a similar question, but related to laying hens and broilers, provide detailed information on underreporting of human salmonellosis (EFSA Panel on Biological Hazards, 2010a, 2011a). Details of the reporting system for human salmonellosis in the EU and the results up to 2007 can also be found in the previous Opinion relating to targets for breeding hens of *Gallus gallus* (EFSA, 2009b) and in the Community Summary Report (EFSA and ECDC, 2010). These documents also describe issues related to underreporting of human salmonellosis and indicate that the true incidence at population level may be considerably larger than the reported incidence, albeit that the level of underreporting varies strongly between MSs (de Jong and Ekdahl, 2006). 'Multipliers' (i.e. the ratio between true and reported cases) range from 4.7 for the UK (Tam et al., 2012), to 29.3 for the USA (Scallan et al., 2011).

Underreporting values for human salmonellosis in the different EU MSs were estimated employing updated information on the risk from Swedish travellers in the EU in 2009 as described in detail in EFSA Panel on Biological Hazards (2011a). The underreporting values are presented in Table 1 of Appendix A together with the assumptions and limitations of this approach. Data were obtained from the Swedish Institute for Communicable Disease Control (Smittskyddsinstitutet, SMI, Solna, Sweden). The risk of salmonellosis in returning Swedish travellers in the EU was 8.44 per 100 000 travels (95 % CI 8.18-8.71), ranging between 0.13 for travel to Finland to 94.3 for travel to Bulgaria. Estimates of the true incidence were anchored to population-based estimates from the Netherlands, based on raw data from a Dutch case-control study (de Wit et al., 2001), where the incidence rates from these studies were applied to the population of 2009 and scaled to the observed average of laboratory-confirmed cases for these years in comparison to the year 1999 when the case-control study was performed. 31 700 (95 % CI 4 990-95 200) cases of salmonellosis per year were estimated to occur in the Netherlands in 2009.

For the EU-27, the estimated true incidence of salmonellosis in 2009 is 6.2 (95 % CI 1.0-19) million cases, which fits well in the range reported before. The underreporting factor at the EU-level is 57.5 (95 % CI 9.0-172). The estimated underreporting factors were provided to the contractor for their consideration in the model applied to support the quantitative aspects of this Scientific Opinion (Hald et al., 2012).

The disease burden of salmonellosis and its sequelae is 0.23 (0.05-0.6) million disability-adjusted life years (DALYs) per year and total annual costs were estimated at 2 (0.3-4) billion EURO (EFSA Panel on Biological Hazards, 2011a).

The establishment of active surveillance of human salmonellosis in all MSs, including harmonised typing of human *Salmonella* isolates and efforts to quantify the level of under-ascertainment and underreporting, would improve the estimation of the human health effects of interventions in primary food animal production. This would imply collaborative efforts to enumerate all cases identified in medical microbiological laboratories, so that underreporting is limited as much as possible. Population-based studies to identify the level of under-ascertainment would also be encouraged.

3. Turkey production in Europe

The poultry industry is the largest (in terms of animal numbers) and the most highly automated, vertically integrated, and intensive of the animal production industries. Various poultry species, mainly chickens (*Gallus gallus*), turkeys, duck and geese as well as guinea fowl, and ostriches are used in industrial and smaller scale meat production, and their importance varies with regions and food consumption habits.

The EU-27 turkey meat production in 2009 was estimated to be 1 644 133 tonnes (Table 1, Appendix B). In 2009, five countries (Germany, France, Italy, the UK and Hungary) produced almost 1 390 979 tonnes (i.e. 84.6 % of all EU production) (FAOSTAT, accessed 30 September 2011). According to the EU-wide baseline survey that was carried out between October 2006 and September 2007 to determine the prevalence of *Salmonella* in commercial turkey holdings with at least 250 birds for breeding turkeys and with at least 500 birds for fattening turkeys (EFSA, 2008b) the estimated numbers of breeding turkey flocks and birds in the EU and Norway in 2006-2007 were 406 and 3 831 537 respectively. In addition, the numbers of fattening turkey flocks and birds were 7 157 and 108 237 830 respectively (Table 1).

Table 1: Overview of the breeding and fattening turkeys in the EU and Norway, 2006-2007 (EFSA, 2008b)

MSs	Breeding turkey flocks[a]		Fattening turkey flocks[b]	
	No of holdings	No of birds	No of holdings	No of birds
Austria	0	0	115	1 380 000
Belgium	0	0	31	494 884
Bulgaria	1	11 823	4	80 704
Cyprus	0	0	10	40 000
Czech Republic	3	138 789	89	961 200
Denmark	0	0	27	756 000
Finland	9	50 688	77	1 139 600
France	209	2 119 260	2 591	20 106 160
Germany	23	150 558	670	17 688 000
Greece	10	27 750	70	175 000
Hungary	8	62 680	467	8 779 600
Ireland	2	30 000	103	1 472 076
Italy	53	451 560	848	17 180 480
Lithuania	0	0	12	249 696
Poland	19	123 823	729	14 580 000
Portugal	0	0	166	2 257 600
Slovakia	22	171 600	25	150 000
Slovenia	0	0	57	330 600
Spain	10	58 500	482	15 877 080
Sweden	1	3 310	9	336 150
The Netherlands	2	no data	55	1 980 000
The United Kingdom	29	384 076	460	1 656 000
EU	**401**	**3 784 417**	**7 097**	**107 670 830**
Norway	5	47 120	60	567 000

[a] with at least 250 birds.
[b] with at least 500 birds.

According to USDA Gain report (USDA, 2010), the EU-27 turkey production was expected to stabilize in 2010 and 2011, as declines in France, the UK, and Hungary were forecast to be outweighed by increases in Germany and Poland. EU-27 turkey imports in 2010 and 2011 were expected to remain stable under import quota controls. EU-27 turkey meat consumption was also expected to stabilize in 2010 and 2011. The total world production in 2011 was estimated to be 5 312 000 tonnes and out of these 1 940 000 tonnes were produced in the EU-27, 2 593 000 tonnes in USA and 505 000 tonnes in Brazil. The major producers for the remainder were Canada, Russia, Mexico, South Africa and China. The world total consumption was estimated to be 5 057 000 tonnes (Table 2, Appendix B).

The per capita consumption of turkey meat in all EU MSs is not available. According to AVEC (2011), turkey meat consumption in 2010 varied widely in the EU and ranged from 1.0 kg in the Netherlands to 6.4 kg in Austria, which is generally lower than in the USA, with a consumption of 7.4 kg per capita (Table 5, Appendix B).

According to Nunes (2008), the world turkey meat exports amounted to 5 540 000 tonnes in 2007. Only four turkey exporting countries/regions are worth noting: the USA, Brazil, EU and Canada. Brazil's market share jumped from 7.9 % of the global exports, in 2000, to 29.4 %, in 2007, a growth of 272 %. In the same period, the USA increased its market share by 25.6 %; the EU, the former leading exporting block, reduced its participation by almost 55 %, from 44.3 % to 19.9 %. The majority of the Brazilian turkey meat exports come to the EU, the second largest world importer, and most of this goes to Germany and Spain. Mexico is the world's largest importer of turkey meat. Brazilian poultry products, including turkey meat, are not allowed to be imported into North America, because of the current sanitary restrictions imposed on Brazilian products by the NAFTA guidelines.

According to AVEC (2010), world turkey meat exports are forecast to rise by 4 %. Both the USA and Brazil have expanded production and so should benefit from increased demand. Demands in Mexico are expected to increase by 10 % and in Canada by 4 %. Also in Russia, the demand has increased by 12 %, which is not entirely covered by an increase in the Russian production.

The turkey meat importation in the EU in 2010 for frozen boneless cuts of turkey was 12 814 tonnes, for prepared/preserved meat of turkeys was 83 797 tonnes and for preparations containing exclusively uncooked turkey meat (excl. sausages and similar products) was 78 940 tonnes (Table 3, Appendix B). In 2007 Germany imported 86 500 tonnes of fresh and frozen of turkey meat, followed by the Netherlands, Belgium and Austria with 44 900, 34 000 and 33 400 tonnes, respectively (Table 4, Appendix B)[9].

Available data from the EFSA Comprehensive European Food Consumption Database on consumption of turkey and broiler meat in the EU can be found in Table 6, Appendix B. An overview of the methodologies and protocols employed in the different national dietary surveys can be found in Merten et al. (2011). The consumption of turkey meat is variable, with the percentage of consumers ranging from 0.2 % (in Austria) to 47.9 % (in Denmark). As a comparison, the consumption of broiler meat ranges from 8.6 % (in Estonia) to 85.1 % (in Ireland). The quantity consumed (consumers only) ranges from 11.7 g/day to 261 g/day for turkey meat and from 19.7 g/day to 243 g/day for broiler meat. The consumption of preserved turkey and broiler meat is summarized in Table 7, Appendix B. In this case however, little data is available.

3.1. Structure of turkey industry

The production of turkey meat is based on the genetic selection of pure lineages of male and female birds using very precise genetically-influenced criteria, including productivity (growth rate), quality of products and resistance against disease. The selection methods ensure a uniform quality of bird for further multiplication and production. The turkey industry can be divided into the primary **breeding**

[9] http://www.thepoultrysite.com/focus/global-poultry-trends/2400/global-poultry-trends-region-select-track-poultry-trends-across-the-world

sector including pedigree as well as grandparent stock, and the **production sector**, which includes parent stock, hatcheries, fattening and processing.

3.1.1. Turkey breeding sector

The majority of **turkey primary breeding sector** supplies the production sector, although surplus production as well as imported hatching eggs and/or one day old poults from third countries, may also go directly for fattening. Currently, this sector is represented by a small number of companies in a limited number of countries.

The progeny comprise the great grandparent (GGP) and grandparent (GP) generations. The GP hatching eggs then produce parent stock (PS) that passes to the production sector and are the source of the final meat generation. They are usually housed on straw in semi-open naturally ventilated houses and eggs that are laid in ground-level nest boxes are manually collected several times a day. Most commercial turkey breeds are unable to mate naturally and are artificially inseminated at least once weekly using fresh semen collected from turkey toms.

3.1.2. Commercial meat turkey flocks

In intensive systems, meat turkey flocks are kept in most of the countries exclusively in partially open barns (curtains barns) with natural ventilation on floor on deep litter. The adjustable ventilation shutters (curtains) on the side of barn are controlled automatically, with the desired house temperature, which is adjusted using thermostatically controlled systems. To meet the high fresh air requirements of turkeys, additional ventilation may be provided during hot seasons. The barns are totally bedded and contain feeding and watering devices as well as a small department for sick birds. During the rearing an approximately 5 to 10 cm depth of soft wood shavings is usually used as litter, and may be covered in later stages by a layer of wheat straw or barley. In some countries turkeys are housed in closed fully controlled environment housing that is similar to that used for broilers.

One day old turkey chicks (poults) are transported after hatching in controlled climate vehicles to the farms. The transport of day-old poults poses few problems on short journeys because they are small and have yolk sac reserves. They are usually transferred by hand from the incubator to lightweight, disposable containers or re-usable plastic trays with ventilation holes. Newly hatched poults are not provided with food and water until they reach the rearing unit. During transportation, which may last up to two days on international journeys, poults are completely reliant on yolk sac metabolism. According to Council Regulation (EC) No 1/2005[10] is regulated, among other things that for poultry are allowed to be transported up to 72 h without water or feed supply (EFSA Panel on Animal Health and Welfare, 2011). According to this Regulation, when containers loaded with animals are placed one on top of the other on the means of transport, the necessary precautions shall be taken:

- to avoid, or in the case of poultry, rabbits and fur animals, to limit urine and faeces falling on the animals placed underneath;
- to ensure stability of the containers; and
- to ensure that ventilation is not impeded.

The female and male day old poults are brought separately from the hatchery directly to the farm, where they are normally kept for the first weeks in heated barns with spot heaters. On these farms, male and female birds may sometimes be placed in brooding houses for the first 5-6 weeks of age, while older male birds from previous flocks are in adjacent houses. When those older male birds are sent to slaughter and after cleaning and disinfection of the barn, the brooding male birds from the new flock are moved to the vacated houses. More modern rearing farms will, however, operate an 'all in/all out' policy and in some cases rearing and fattening is carried out in the same house ('day old to death' production). The feed provided to growing turkeys is arranged in multiple stages (beginning with a

[10] Council Regulation (EC) No 1/2005 of 22 December 2004 on the protection of during transport and related operations and amending Directives 64/432/EEC and 93/119/EC and Regulation (EC) No 1255/97. OJ L 3, 5.1.2005, p. 1-44.

crumb type formulation and continuing with small pellets) so that a sequence of rations of decreasing protein content, digestibility and cost can be fed to birds as they grow older as they become more capable of utilising lower quality rations. The ration changes, as well as frequent changes in sources and the range of ingredients to provide least cost rations act as a digestive stress factor which may precipitate intestinal disorders, including increased *Salmonella* colonisation and excretion if it is present in the feed or in the birds or their environment (EFSA, 2008f). The water supply for most commercial scale turkey production is from the main municipal supply, but some farms may use private sources from bore holes on the site.

Hens are marketed between 16 and 17 weeks of age. At this age hens will typically weigh 10-11 kg. Toms (males) are often marketed between 20 and 21 weeks of age and will weigh 20-21 kg (Hafez, 1997).

3.2. Preparation for transport to slaughter

Preparations for turkey processing start in the shed. Standardization of the feed withdrawal period of 6 to 12 h is advised. This protocol allows emptying of the gastro-intestinal tract without exhausting the birds before processing and reduces gut rupture during evisceration and the faecal contamination of carcass and processed products. The length of the time of feed withdrawal should be carefully planned according to the catching, transport and holding time before processing.

The Regulation No 853/2004[11], Annex III Section II indicates some basic requirements concerning the transport of live animals: 1) animals must be handled carefully without causing unnecessary stress; and 2) crates and other equipment must be easy to clean and disinfect, and all equipment must be cleaned, washed and disinfected immediately after emptying and, if necessary, before re-use.

Another requirement concerns animals showing symptoms of disease or originating in flocks known to be contaminated with agents of public health importance; these birds may only be transported to the slaughterhouse when permitted by the competent authority.

It is essential that loading and transport of the birds is carried out by trained personnel, who handle the birds carefully and do not cause them distress.

Upon arrival at the processing plant the animals are left to recuperate for at least 2 h in a conditioned lairage area as laid down in Council Regulation (EC) No 1099/2009[12]. During this period, they recover from transport stress, predominantly anxiety and physical stress. Their body temperature, blood circulation and respiration return to normal, which is a prerequisite for optimal stunning (Kranen, 2005).

Poultry slaughter and dressing may involve different technologies, dependent mainly on the commercial strategy of the company. In general, birds are placed on the line and stunned using electrical or gas methods, followed by bleeding by neck-cutting. None of the slaughterhouses processing turkey have fully automated bleeding systems. This is due to the wide variation in the age, size and weight of turkeys slaughtered for human consumption[13]. Electrical techniques are more prevalent having been in commercial use for longer.

The **stunning and killing** stages have few microbiological implications, although electrical water-bath stunning has been shown to be a source of cross-contamination. Modern developments in gas stunning may avoid this problem (Mead et al., 1997).

[11] Regulation (EC) No 853/2004 of the European Parliament and of the Council of 29 April 2004 laying down specific hygiene rules for food of animal origin. OJ L 226, 25.6.2004, p. 22-82.

[12] Council Regulation (EC) No 1099/2009 of 24 September 2009 on the protection of animals at the time of killing. OJ L 303, 18.11.2009, p. 1-30.

[13] Study on stunning/killing practices in slaughterhouses and their economic, social end environmental consequences. Final Report - Part II: Poultry. DG SANCO Evaluation Framework Contract Lot 3 (Food Chain). http://www.civic-consulting.de/reports/slaughter_study_part2.pdf

Turkeys are usually **scalded/plucked (defeathered)** at 50-56 °C for 2.5 to 4 min. Scald water is usually indirectly heated by steam or hot water and the temperature controlled by thermostat[14]. Plucking (defeathering) with automatic machinery causes considerable dissemination of microorganisms which leads to cross-contamination of carcasses.

Evisceration involves removal of the internal organs. Lines are usually automated except where bird size varies such as at turkey processors where the male and female birds differ in size. The most critical points during processing for cross-contamination are scalding, plucking and evisceration, mainly as a result of damage to the intestines as well as contact between intestines and carcasses. Heads are macerated at some sites (Hafez, 1999; Hafez et al., 2001).

At the end of the line the carcases are washed using spray water, cooled (24-72 h at 0 to 2 °C with a final temperature on the carcass surface of 0 °C and about 3 °C in the deep breast muscles) and finally cut. In many turkey plants, portioning lines undertake a range of further cutting and trimming and these operations are performed by a combination of automated and manual lines. In addition, this may be followed by the addition of other ingredients to the meat (e.g. bread-crumbs, herbs etc.) and/or by cooking to produce ready meals and cooked meats (DEFRA, 2007). Most sites undertake vacuum shrink wrapping using hot air, hot water or steam and add a gas flush to extend shelf life. Packing units should be insulated to conserve heat and have interlocks to switch them off when no product is passing through.

Packaging of poultry meat and products protects them from undesirable factors such as contamination during distribution, moisture, light, oxygen and can also be used as a means of providing information for the consumer. Several developments in the area of food packaging to extend shelf life and improve the quality of the product have been achieved. For fresh and frozen poultry polyethylene wrapping is normally used. Further possibilities are the use of vacuum or modified atmosphere packaging (MAP). MAP provides a gas atmosphere in the package without a vacuum or pressure change. The procedures include replacement of oxygen with carbon dioxide and/or nitrogen gas. By altering the gas composition, a bacteriostatic or bacteriocidal effect can be achieved, especially against certain Gram-negative bacteria. There are a considerable number of publications on the advantages and disadvantages of this method (e.g. Bolder (1993), Hafez (1999), Farber (1991)).

4. *Salmonella* contamination of turkeys and turkey meat along the processing chain

An overview of the main potential contamination routes in turkey breeding and production is given in Figure 1, Appendix C. Meat contamination by *Salmonella* is directly related to the flock contamination via the slaughtering process and the contamination of carcasses mainly during evisceration. A study aiming to assess the risk of *Salmonella* contamination of turkey carcasses, showed that the risk of meat contamination at the slaughterhouse and cutting plant is associated with the carriage rate of *Salmonella* in live animals: a group with a low carriage rate represents a moderate risk (0 to 4 % contaminated meat), while one with a high carriage rate represents a higher risk (11 to 40 % contaminated meat) (Petton et al., 2003).

Hafez et al. (1997) examined seven meat turkey flocks, which tested negative for *Salmonella* during the entire rearing period, directly after harvest and through the whole processing procedure. Directly after the transport and on arrival to slaughterhouse, *S.* Saintpaul was present in faecal samples collected from one flock. During processing, salmonellae could not be detected in faecal samples from flocks slaughtered prior to the monitored flocks. Examination of scalding water revealed positive results in four cases. In all flocks, one or two *Salmonella* serovars were isolated from skin samples after evisceration. Examination of liver samples revealed a lower isolation rate. Additional contamination with other serovars can take place during further processing (cooling and cutting). Examination of meat samples after cutting revealed a high contamination rate of 71 % (Tables 2 and

[14] The Environment Agency – making your environment a better place Sector Performance. Review 2010 Slaughterhouses and Animal By-Products Industries. May 2010. www.environment-agency.gov.uk

3). Furthermore, the isolation of more than one serovar, which was not detected during the rearing period, indicates that cross-contamination can take place during processing.

Table 2: Results of *Salmonella* serovars isolated in processing plant from seven *Salmonella*-negative fattening turkey flocks (Hafez et al., 1997)

Flock No	Gender	After transport	Flock slaughtered prior to monitored flock	Scalding water	Skin after evisceration	Liver after evisceration	Skin after cooling	Skin after cutting	Muscle after cutting
1[a]	male	n[c]	-[e]	n[c]	Newport Agona	Newport	Newport Agona	Bredeney	Bredeney
2[a]	male	n.d.[d]	n.d.[d]	Saintpaul	Saintpaul	Saintpaul	Saintpaul	Saintpaul	Saintpaul
3[a]	male	n[c]	n[c]	Newport	Hadar	Newport	Saintpaul Newport	Newport	Saintpaul Newport
4[a]	male	n[c]	n[c]	n[c]	Saintpaul Duisburg	n[c]	n[c]	n[c]	n[c]
5[a]	female	n[c]	n[c]	Saintpaul	Indiana	n[c]	Newport Reading	Reading	Newport Reading
6[b]	female	n[c]	n[c]	Newport	Newport	Newport	n[c]	n[c]	n[c]
7[b]	female	Saintpaul	n[c]	n[c]	Typhimurium[f] Newport	n[c]	Typhimurium[f]	Chester	Saintpaul

[a] manual cutting.
[b] mechanical cutting.
[c] n = negative.
[d] n.d. = not done.
[e] - = no flock prior to monitored flock.
[f] *S.* Typhimurium var. cop.

Table 3: Summary of *Salmonella* isolation in processing plant from seven *Salmonella*-negative fattening turkey flocks (Hafez et al., 1997)

Samples	Results[a]	% of positive
Scalding water	4/19	21.05
Skin after evisceration	67/158	58.77
Liver after evisceration	11/148	7.43
Skin after cooling	28/70	40.00
Skin after cutting	29/70	41.43
Muscles after cutting	23/70	32.86

[a] *Salmonella* positives/No of samples tested.

5. *Salmonella* in turkeys and turkey meat in the EU

5.1. Monitoring of *Salmonella* in breeding and fattening turkeys

5.1.1. Legal background

Directive 2003/99/EC[15] provides for the monitoring of zoonoses in animal populations in Europe. The purpose of this Directive is to ensure that zoonoses, zoonotic agents and related antimicrobial resistance are properly monitored, and that food-borne outbreaks receive proper epidemiological

[15] Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EE. OJ L 325, 12.12.2003, p. 31-40.

investigation, to enable the collection in the Community of the information necessary to evaluate relevant trends and sources (art. 1).

According to art. 4, monitoring shall be based on the systems in place in MSs. However, where necessary to make data easier to compile and compare, detailed rules for the monitoring of zoonoses and zoonotic agents listed in Annex I may be laid down.

Such detailed rules shall define minimum requirements for the monitoring of certain zoonoses or zoonotic agents. They may, in particular, specify:

- the animal population or subpopulations or stages in the food chain to be covered by monitoring;
- the nature and type of data to be collected;
- case definitions;
- sampling schemes to be used;
- laboratory methods to be used in testing; and
- the frequency of reporting, including guidelines for reporting between local, regional and central authorities.

The first indications on criteria for *Salmonella* monitoring have been laid down in Regulation 2160/2003[16], which in Annex II lists minimum requirements that food business operators have to respect having samples taken and analysed for the control of *Salmonella* in different animal species and categories. As far as turkey flocks are concerned, the Regulation requires all *Salmonella* strains with public health significance to be monitored, by sampling birds leaving for slaughter. As for broilers, the Regulation states that the results of the analyses of samples must be known before the animals leave for the slaughterhouse. No other details are given in this Regulation concerning the kind or number of samples to be taken, or the laboratory methods to be used for the analysis. No criteria are defined for official control.

Before setting the targets for the reduction of the prevalence of certain *Salmonella* serotypes both in breeding and in fattening flocks of turkeys, a baseline survey was organised in all EU MSs and took place between October 2006 and September 2007, according to Commission Decision No 2006/662/EC[17].

With Commission Regulation No 584/2008[18], Commission has set the targets for the reduction of the prevalence of *S.* Enteritidis and *S.* Typhimurium in turkeys, and has described the testing scheme necessary to verify their achievement.

According to this Regulation, the Community target shall be:

- a reduction of the maximum percentage of fattening turkey flocks remaining positive of *S.* Enteritidis and *S.* Typhimurium to 1 % or less by 31 December 2012; and
- a reduction of the maximum percentage of adult breeding turkey flocks remaining positive of *S.* Enteritidis and *S.* Typhimurium to 1 % or less by 31 December 2012.

[16] 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.

[17] Commission Decision No 2006/662/EC of 29 September 2006 concerning a financial contribution from the Community towards a baseline survey on the prevalence of *Salmonella* in turkeys to be carried out in the Member States. OJ L 272, 3.10.2006, p. 22-26.

[18] Commission Regulation (EC) No 584/2008 of 20 June 2008 implementing Regulation (EC) No 2160/2003 of the European Parliament and of the Council as regards a Community target for the reduction of the prevalence of *Salmonella enteritidis* and *Salmonella typhimurium* in turkeys. OJ L 162, 21.6.2008, p. 3-8.

According to Commission Regulation No 584/2008[19], flocks of turkeys shall be sampled on the initiative of the food business operator and by the competent authority.

(i) Sampling of flocks of fattening and breeding turkeys on the initiative of the food business operator shall take place within three weeks before the birds are moved to the slaughterhouse.

(ii) Additionally, sampling of flocks of breeding turkeys on the initiative of the food business operator shall take place:

- in rearing flocks: at day-old, at four weeks of age and two weeks before moving to the laying phase or laying unit, and
- in adult flocks: at least every third week during the laying period at the holding or at the hatchery.

(iii) Sampling by the competent authority shall include at least:

- once a year, all flocks on 10 % of holdings with at least 250 adult breeding turkeys between 30 and 45 weeks of age but including in any case all holdings where *S.* Enteritidis or *S.* Typhimurium was detected during the previous 12 months, and all holdings with elite, GGP and GP breeding turkeys; this sampling may also take place at the hatchery,
- all flocks on holdings in case of detection of *S.* Enteritidis or *S.* Typhimurium from samples taken at the hatchery by food business operators or within the frame of official controls, to investigate the origin of infection,
- once a year, all flocks on 10 % of the holdings with at least 500 fattening turkeys, but in any case:
    - all flocks on the holding when one flock tested positive for *S.* Enteritidis or *S.* Typhimurium in samples taken by the food business operator, unless the meat of the turkeys in the flocks is destined for industrial heat treatment or another treatment to eliminate *Salmonella*,
    - all flocks on the holding when one flock tested positive for *S.* Enteritidis or *S.* Typhimurium during the previous round in samples taken by the food business operator, and
    - each time the competent authority considers it necessary.

In fattening turkeys, the sampling protocol requires that at least two pairs of boot/sock swabs shall be taken. For free range flocks of turkeys, samples shall only be collected in the area inside the house. All boot/sock swabs must be pooled into one sample. In flocks with less than 100 turkeys, where it is not possible to use boot/sock swabs as access to the houses is not possible, they may be replaced by hand drag swabs, where the boot swabs or socks are worn over gloved hands and rubbed over surfaces contaminated with fresh faeces, or if not feasible, by other sampling techniques for faeces fit for the intended purpose.

Each year MSs have to prepare their National Control Programme (NCP), and submit it to the European Commission in order to get approval and possible co-financing. NCPs must include monitoring schemes and control measures foreseen by the legislation, but further samples or specific methods can be added if considered appropriate according to the national epidemiological situation. The effectiveness of control measures applied is measured through the achievement of the defined community targets. Details of NCPs are reported in Appendix D, Tables 1, 2 and 3.

[19] Commission Regulation (EC) No 584/2008 of 20 June 2008 implementing Regulation (EC) No 2160/2003 of the European Parliament and of the Council as regards a Community target for the reduction of the prevalence of *Salmonella enteritidis* and *Salmonella typhimurium* in turkeys. OJ L 162, 21.6.2008, p. 3-8.

In breeding flocks of turkeys, the sampling protocol is the same applied in breeding flocks of *Gallus gallus* (Commission Regulation (EC) No 213/2009[20]) and the monitoring can be applied either at farm level or in the hatcheries.

Before 2010 there was no harmonised monitoring and reporting system for *Salmonella* in turkeys in the EU. Although some MS and some individual turkey integrations had in place monitoring programmes that were similar to those used in chickens, the intensity of monitoring has typically been lower, sampling protocols have been highly variable and many operators have carried out no testing at all, apart from that required by Food Hygiene legislation on turkey meat and products, for which serovar data is not available.

5.1.2. Baseline survey

An EU-wide baseline survey was carried out to determine the prevalence of *Salmonella* in commercial turkey holdings with at least 250 birds for breeding turkeys and with at least 500 birds for fattening turkeys. The sampling of turkey flocks took place between October 2006 and September 2007. A total of 539 breeding turkey flocks and 3 769 fattening turkey flocks, with validated results, from the EU and Norway, were included in the survey analyses.

A detailed description of the design of the baseline survey, including descriptions of the sample design and size as well as the bacteriological testing is found in SANCO/2083/2006[21].

In breeding flocks of turkeys, environmental faecal samples were taken on holdings with at least 250 birds within nine weeks before leaving the selected holding for slaughter. In most MSs, only one flock per holding was sampled even though two flocks with birds of eligible age could have been reared during the survey period. Five pooled environmental faeces samples were taken in every selected flock. Each pooled sample comprised faecal material fixed to a pair of boot swabs (or sock samples which were considered equivalent). This sampling procedure should theoretically have provided 95 % confidence of detection of 1 % within-flock prevalence assuming the analytical method was 100 % sensitive. Environmental faecal samples were taken from flocks with fattening turkeys with at least 500 birds (the sampling frame covered primarily holdings representing at least 80 % of the total population of turkey meat finishing flocks). The fattening turkey flocks were sampled within three weeks before leaving the selected holding for slaughter. On each selected fattening holding, one flock with turkeys of the appropriate age was to be sampled. However, in MSs where the calculated number of flocks to be sampled was greater than the number of available holdings with at least 500 birds, up to four flocks could have been sampled on the same holding in order to achieve the calculated number of flocks. Where possible, the additional flocks from a single holding were to originate from different turkey houses and samples taken in different seasons. If the number of flocks to be sampled was still not sufficient, progressively smaller holdings were to be selected, focussing preferably on holdings with more than 250 birds. Five pooled environmental faeces samples were taken in every selected flock. Each pooled sample comprised faecal material fixed to a pair of boot swabs (or sock samples which were considered equivalent). This sampling procedure should theoretically have provided 95 % confidence of detection of 1 % within flock prevalence assuming the analytical method was 100 % sensitive. For all production types the same sampling approach was applied. For free-range flocks, samples were to be collected in the area inside the house.

The number of flocks to be sampled was stratified according to the flock size and region in the MS, meaning that a representative number of flocks in different size categories of flocks as well as in different regions had to be sampled. Samples were taken by the competent authority in each MS or

[20] Commission Regulation (EC) No 213/2009 of 18 March 2009 amending Regulation (EC) No 2160/2003 of the European Parliament and of the Council and Regulation (EC) No 1003/2005 as regards the control and testing of *Salmonella* in breeding flocks of *Gallus gallus* and turkeys. OJ L 73, 19.3.2009, p. 5-11.

[21] European Commission, Health & Consumer Protection Directorate (DG SANCO). Baseline survey on the prevalence of *Salmonella* in flocks of turkeys in the EU: Technical specifications. SANCO/2083/2006. Presented at the meeting of the Standing Committee on the Food Chain and Animal Health on 18 July 2006.

under its supervision and were tested by the National Reference Laboratory (or an authorised laboratory) using the ISO 6579:2002 Annex D method[22].

5.1.3. Monitoring systems in the EU

It is desirable to monitor breeding flocks at the holding frequently enough to detect *Salmonella* infection and to withdraw eggs from the hatchery before hatching and further dissemination of infection or contamination (Pomeroy and Fenstermacher, 1943). Since the incubation period for turkey eggs is 28 days, but eggs are transferred to the hatching stage three days before hatch, a three-week sampling interval during lay provides optimal detection, as well as sufficient time to identify the serovar present in the flock before diverting eggs from hatching. Within the EU, the EC and the MSs have agreed on testing hatcher basket liners for this purpose. The agreement was based on studies in France that had shown this method to be at least equivalent to sampling 300 faeces from the breeding flock, providing a detection threshold of 1 % within flock prevalence with 95 % confidence. Since sampling of hatcher basket liners could be impractical in some large hatcheries with automated systems, and various additional alternative options were agreed for hatchery sampling, i.e. hatcher basket liners, broken eggshells, chiffonette swabs from hatchers after hatching or chiffonette swabs from hatcher baskets. In previous studies, such samples have been shown to give an accurate indication of egg contamination and infection[23] of progeny (Cox et al., 1990; Davies and Bedford, 2001; Davies and Wray, 1994; Gauger and Greaves, 1946) but their relative sensitivity and specificity in relation to each other and to sampling at the holding is not known. Hatchery-based monitoring may also detect cross-contamination of eggs by *Salmonella* from other breeding flocks hatched in the same airspace (Byrd et al., 1998; Cason et al., 1991) or persistent contamination of hatchers (Chen et al., 2002; Christensen et al., 1997). The potential for cross-contamination means that all breeding flocks that supplied eggs hatched in the airspace where positive samples were obtained must be visited and sampled to accurately confirm infection of breeding birds.

Options for sampling at the holding include boot swabs or sock swabs (or hand held fabric chiffonette swabs in small houses when boot swabbing is not possible. Boot swabs have been shown to be simple and effective for detection of *Salmonella* excretion in chicken flocks (Gradel et al., 2002; Skov et al., 1999) and proved superior to US-style drag swabs (Buhr et al., 2007; Caldwell et al., 1994; McCrea et al., 2006; McCrea et al., 2005; Opengart et al., 1991). Comparative sampling studies in turkey flocks confirmed the efficiency of boot swabbing (Mueller-Doblies et al., 2009) in turkey flocks, but additional sensitivity could be gained, allowing a reduction in the number of boot swabs from five to one pair, if an additional large dust sample was taken (Arnold et al., 2009). The dust sample was particularly valuable in breeding farms where *Salmonella* may be more difficult to detect because a low within-flock prevalence (Davies et al., 1998; Mueller-Doblies et al., 2009) results in apparent false negative test results (Davies, 2004) in flocks identified as positive by intensive sampling (Davies and Wray, 1996). Limitations of test sensitivity may, in part, be responsible for failure to control persistence of *Salmonella* between flocks (Danguy des Deserts et al., 2010; Featherstone et al., 2010; Mueller-Doblies et al., 2010; Nayak and Stewart-King, 2008; Nayak et al., 2004). Additional detection sensitivity may be gained by carrying out serological monitoring (Danguy Des Deserts et al., 2010; Featherstone et al., 2010; Mueller-Doblies et al., 2010; Nayak and Stewart-King, 2008; Nayak et al., 2004) but serology is not an approved method for statutory monitoring and may be affected by false positive results. It can, however, be a useful additional voluntary procedure that flock owners can use to enhance detection and to guide more intensive bacteriological confirmatory sampling.

Fattening turkeys are required to be monitored either with two pairs of boot swabs or a single pair of boot swabs combined with a dust swab sample to be taken within three weeks before slaughter. In fattening turkeys the high level of spread and excretion of *Salmonella* within a flock (Harbaugh et al., 2006; Hoover et al., 1997) and persistence in older birds, unlike broilers (Cox et al., 2000; Eblen et al.,

[22] ISO 6579:2002. Microbiology of food and animal feeding stuffs – Horizontal method for the detection of *Salmonella* spp. – Amendment 1: Annex D: Detection of *Salmonella* spp. in animal faeces and in environmental samples from the primary production stage. International Organization for Standardization.

[23] Infection refers to subclinical infection or colonisation, rather than infection resulting in clinical disease.

2005; Nayak et al., 2003; Rostagno et al., 2006; Santos et al., 2005), means that detection is not normally difficult and can be achieved to an acceptable level with one pair of boot swabs walked round the whole house (Mueller-Doblies et al., 2009). Sensitivity analysis in the EU baseline survey (EFSA, 2008b) showed that almost all MSs had a large proportion of positive flocks with all five pairs of boot swabs positive. A theoretical calculation suggested that a reduction of five pairs to two pairs of boot swabs per flock could have reduced the overall prevalence estimate from 3.8 % to 2.8 %, but this does not take into account the fact that each pair of boot swabs was only used over one-fifth of the area of the house in the baseline survey. Whatever the sampling or culture method chosen, it is always possible to increase detection of infected flocks further by applying more complex or intensive protocols (Carrique-Mas and Davies, 2008; Davies et al., 2001).

The test method to be used for all statutory monitoring in primary production in the EU is ISO 6579:2002 Annex D[24]: Detection of *Salmonella* spp. in animal faeces and in samples of the primary production stage. This involves a non-selective pre-enrichment stage to revitalise *Salmonella* that may be in a stressed condition and to increase the number of organisms before transfer of an inoculum (0.1 ml after 16-20 h incubation at 37 °C) to modified semi-solid Rappaport-Vassiliadis medium (MSRV), supplemented by novobiocin to reduce Gram-positive competing organisms. *Salmonella* normally migrates more quickly than competing organisms in the malachite green/magnesium chloride based inhibitory medium at 41.5 °C and can be preferentially recovered from the margin of the zone of turbid growth. A loop of this growth is plated on to two selective indicator agars, Xylose Lysine Decarboxylase agar (XLD) and a second media of choice, although the value of the second media is often debatable (Carrique-Mas et al., 2009) and greater detection could normally be achieved by testing more samples with a single plate method (Carrique-Mas and Davies, 2008). Suspect colonies are confirmed biochemically and/or by slide agglutination tests and isolates can then be submitted for serotyping and further characterisation.

There may be potential in the future for improving detection and confirmation of *Salmonella* by the use of molecular methods such as PCR or microarray (Bailey, 1998; Eyigor and Carli, 2003; Fratamico, 2003) but these do not always perform reliably in all laboratories, especially in a faecal matrix, and such alternative methods have to be validated according to European EN/ISO 16140:2003[25] standards.

Other sample and culture techniques, such as the 'egg moulding method' described by Baxter-Jones and Wilding (1982), have shown increased isolation rates of *Salmonella* in turkey hatching eggs in comparison with conventional culture methods. Hafez et al. (1986) described a further modification using enrichment media in empty eggshells. The re-isolation rate of *S.* Senftenberg using this method was always higher than examination of yolk and/or albumen alone from artificially contaminated broiler chicken, turkey and quail hatching eggs. Investigation on isolation of *S.* Enteritidis from experimentally contaminated chicken hatching eggs (layer type) using pre-enrichment of empty eggshell samples led to significantly higher detection rates in comparison with the same samples cultured without pre-enrichment after contamination with 10^2 cfu/ml *S.* Enteritidis (Hafez and Jodas, 1992). It is therefore important to test whole eggshells and not just swabs for maximum detection of egg-borne contamination, but since it is hatched eggs or embryonic mortalities that are tested in the case of breeding birds the sampling methods that are designated in EU Regulations are appropriate. Additional voluntary monitoring of dust (at the farm or hatchery), faeces, meconium or hatchery macerator waste is sometimes carried out by turkey breeders and can provide valuable epidemiological information and improved detection of *Salmonella*. It is important that serotyping, ideally with appropriate additional phage typing and harmonised antimicrobial susceptibility testing, is carried out to assist epidemiological investigations and inform control actions.

[24] ISO 6579:2002. Microbiology of food and animal feeding stuffs – Horizontal method for the detection of *Salmonella* spp. – Amendment 1: Annex D: Detection of *Salmonella* spp. in animal faeces and in environmental samples from the primary production stage. International Organization for Standardization.

[25] ISO 16140:2003. Microbiology of food and animal feeding stuffs – Protocol for the validation of alternative methods. International Organization for Standardization.

In conclusion, it can be difficult to detect *Salmonella* in breeding flocks because of the low within-flock prevalence, intermittent excretion of serovars with low virulence and clustering of infection resulting from distribution of birds in multiple small pens. In both breeding flocks and fattening flocks inclusion of dust and care when taking, despatching and testing samples is necessary for optimal detection.

5.1.4. Results of monitoring

5.1.4.1. Results of monitoring breeding turkeys

In the baseline survey, in each MS, the number of reported holdings was combined with the number of birds annually reared in each holding (as evaluated from this survey) to estimate turkey breeders population size. The geographical distribution of breeding turkeys in the EU was highly heterogeneous. In fact, France accounted for 56.0 % of the breeding population, followed by Italy (11.9 %) and the UK (10.1 %). The remaining MSs contributed with less than 5 % of the total breeding population.

The weighted *Salmonella* prevalences in turkey breeding flocks in each MS, at EU level and in Norway are presented in Table 4. Although in some MSs all breeding flocks that were available at the time of the visit were sampled (census sampling), it was decided to report 95 % confidence intervals (CI) of prevalence for MSs where at least one flock was found *Salmonella* infected. In this way, inference was attempted to the turkey production beyond the time of the data collection. Conversely, it was decided not to report CIs for countries where no flocks were found infected. The *Salmonella* prevalence in these flocks varied widely amongst the MSs, from 0 % to 82.9 %. *Salmonella* spp. was found in six out of 14 MSs providing data on flocks of breeding turkey. No positive flocks were found in Norway. The weighted EU-level prevalence (13.6 %) was higher than the raw, unweighted prevalence (7.2 %). This difference is due to the large weights that were assigned to flocks from Slovakia and Italy (because of relatively large numbers of holdings and of flocks per holding) combined with relatively high prevalence of infection in these MSs.

S. Enteritidis and/or *S.* Typhimurium were found in breeding turkey flocks from only three MSs (Table 4). The estimated EU observed prevalence was 1.7 % for these two serovars, varying from 0 % to 8.3 % within the MSs. The raw, unweighted prevalence was 0.9 %. At the MS-level, prevalence was highest in Italy and it was low in France and the UK. *Salmonella* serovars other than *S.* Enteritidis or *S.* Typhimurium were found in the breeding flocks from six MSs. No single *Salmonella* serovar was isolated in more than three of the 14 reporting MSs.

In total, 135 *Salmonella*-positive samples were found (5.0 % of 2 695 samples) originating from 40 positive breeding turkey flocks. Only one *Salmonella* serovar was isolated from each of the *Salmonella*-positive sample. The frequency distribution of isolated *Salmonella* serovars in the EU is listed in Table 5. This table is ranked based on the percentages of specific *Salmonella* serovar-positive flocks, as flock was the epidemiological unit of interest. *S.* Saintpaul was the most frequently reported serovar from the breeding turkey flocks, found in 42.5 % of the *Salmonella* positive flocks, followed by *S.* Kottbus and *S.* Typhimurium (17.5 % and 10.0 % of the *Salmonella* positive flocks, respectively). *S.* Kottbus was the serovar most commonly isolated in terms of number of MSs (three MSs). The distribution of the reported serovars varied amongst the MSs. Isolation of *S.* Saintpaul in breeding turkey flocks was only reported by Slovakia. The fact that it was isolated in 17 flocks in this MS resulted in S. Saintpaul being the most frequently reported serovar, at EU breeding flock level. For MSs reporting more than one breeding turkey flock positive for specific serovars, *S.* Kottbus was the most frequently reported serovar for Hungary (two flocks), and the UK (four flocks positive). *S.* Typhimurium was the most frequently reported serovar for Italy (three flocks positive).

In the harmonised monitoring of 2010, data on *Salmonella* in adult turkey breeding flocks were reported by 13 MSs and one non MS. Six MSs reported *Salmonella* in their flocks, ranging from 2.8 % in the UK to 52.9 % in Spain. Of the two target serovars (*S.* Enteritidis and *S.* Typhimurium), only *S.* Typhimurium was found; in four flocks in France and in one flock in Spain.

Table 4: Results of the EU monitoring of *Salmonella* in breeding turkey flocks for 2010 (harmonised monitoring) and from the baseline survey carried out in breeding flocks in the EU and Norway, 2006-2007 (EFSA, 2008b)

	2010 Monitoring[a]			BSL flocks 2006-2007[b]		
	N	% pos (all)	% pos (*S.* Enteritidis and/or *S.* Typhimurium)	N	% pos (all)	% pos (*S.* Enteritidis and/or *S.* Typhimurium)
Bulgaria	-	-	-	7	0	0
Czech Republic	12	50.0	0	4	0	0
Finland	10	0	0	15	0	0
France[b, c]	785	4.3	0.5	205	1.6 (0.5 - 5.2)	0.5 (0.1 - 3.3)
Germany	141	0	0	98	0	0
Greece	4	0	0	6	0	0
Hungary	118	0	0	13	4.1 (0.5 - 26.3)	0
Ireland	14	0	0	2	0	0
Italy	177	26.6	0	28	21.5 (8 - 46.3)	8.3 (2.5 - 24.4)
Poland	66	13.6	0	6	0	0
Slovakia	21	0	0	21	82.9 (47.1 - 96.3)	0
Spain	17	52.9	5.9	10	5.3 (0.6 - 32.4)	0
Sweden	4	0	0	1	0	0
The United Kingdom	249	2.8	0	116	4.4 (1.6 - 11.4)	0.5 (0.1 - 3.2)
EU Total	**1 618**	**6.9**	**0.3**	**532**	**13.6 (8.1 - 21.8)**	**1.7 (0.6 - 4.9)**
Norway	15	0	0	7	0	0

[a] Austria, Belgium, Bulgaria, Cyprus, Denmark, Estonia, Latvia, Lithuania, Luxembourg, Malta, Portugal, Romania, Slovenia, and the Netherlands did not report data in the 2010 monitoring of breeding flocks of turkeys.

[b] Weighted prevalence estimate. The 95 % CI is given between brackets. For details see reference original EFSA Report (EFSA, 2008b). Austria, Belgium, Cyprus, Denmark, Estonia, Latvia, Lithuania, Luxemburg, Portugal, Slovenia, and the Netherlands did not report data on flocks with breeding turkey flocks in the baseline survey. Malta and Romania did not participate in the baseline survey.

[c] In the 2010 monitoring, *S.* Typhimurium result includes the reporting of monophasic variants.

Table 5: Frequency distribution of isolated *Salmonella* serovars in the breeding turkey flocks baseline survey in the EU and Norway, 2006-2007 (EFSA, 2008b)

Serovar	Samples with serovars (N=135)		Holdings with serovars (N=26)		Flocks with serovars (N=40)		Countries with serovars
	N	%	N	%	N	%	N
Saintpaul	54	40.0	8	30.8	17	42.5	1
Kottbus	21	15.6	4	15.4	7	17.5	3
Typhimurium	10	7.4	4	15.4	4	10.0	2
Heidelberg	11	8.1	2	7.7	3	7.5	2
Derby	11	8.1	2	7.7	3	7.5	2
Blockley	5	3.7	1	3.8	1	2.5	1
Senftenberg	5	3.7	1	3.8	1	2.5	1
Corvallis	5	3.7	1	3.8	1	2.5	1
Bredeney	5	3.7	1	3.8	1	2.5	1
Bradford	4	3.0	1	3.8	1	2.5	1
Enteritidis	3	2.2	1	3.8	1	2.5	1
Thompson	1	0.7	1	3.8	1	2.5	1
Total isolates	135						

[a] Source 14 MSs: Bulgaria, Czech Republic, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Poland, Slovakia, Spain, Sweden, and the United Kingdom.

5.1.4.2. Results of monitoring in fattening turkeys

In the baseline survey, in each MS, the number of reported holdings was combined with the number of birds annually reared in each holding (as evaluated from this survey) to estimate fattening turkey population size. The geographical distribution of fattening turkeys was less heterogeneous compared to that of the turkey breeding flocks. Still, five MSs accounted for 79.3 % of the fattening bird population, namely, France (18.7 %), Germany (16.4 %), Italy (16.0 %), Spain (14.7 %), and Poland (13.5 %).

The weighted *Salmonella* prevalences in turkey fattening flocks in each MS, at EU level, and in Norway are presented in Table 6. *Salmonella* spp. was found in 19 out of 22 MSs providing data on fattening turkey flocks. No positive flock was found in Norway. The EU-level weighted prevalence of *Salmonella* spp. (30.7 %) was close to the unweighted prevalence (30.4 %), meaning that approximately one in three fattening turkey flocks, raised over the one year period of the baseline survey, were *Salmonella*-positive. The *Salmonella* prevalence in these flocks also varied widely amongst the MSs, from 0 % to 78.5 %. In individual MSs, prevalence was highest in Hungary followed by Cyprus and Spain. In general, *Salmonella* infections were more widespread in fattening turkey flocks within MS, than in breeding turkey flocks.

S. Enteritidis and/or *S.* Typhimurium were found in fattening turkey flocks from 13 MSs (Table 6). The EU level, weighted prevalence estimate (3.8 %) was almost equal to the unweighted prevalence (3.9 %). The MS specific observed flock prevalence of *S.* Enteritidis and/or *S.* Typhimurium varied from 0 % to 18.4 % in fattening turkeys. MS-level prevalence peaked in the Czech Republic followed by Belgium and Italy. *Salmonella* serovars other than *S.* Enteritidis and/or *S.* Typhimurium were found in 19 MSs.

The five most frequently isolated *Salmonella* serovars from fattening turkey flocks in the EU, in decreasing order, were: *S.* Bredeney, *S.* Hadar, *S.* Derby, *S.* Saintpaul and *S.* Kottbus (Table 7). Out of these, only *S.* Hadar and *S.* Derby are frequent causes of *Salmonella* infections in humans within the EU. The serovar distribution varied amongst the MSs, with serovars tending towards specific distribution patterns of their own.

Table 6: Results of the EU monitoring of *Salmonella* in fattening turkey flocks for 2010 (harmonised monitoring) and from the baseline survey carried out in fattening flocks in the EU[b] and Norway, 2006-2007 (EFSA, 2008b)

	2010 Monitoring[a]			BSL flocks 2006-2007[b]		
	N	**% pos (all)**	**% pos (*S.* Enteritidis and/or *S.* Typhimurium)**	**N**	**% pos (all)**	**% pos (*S.* Enteritidis and/or *S.* Typhimurium)**
Austria[c]	355	8.5	0.3	202	25.5 (15.5 - 38.9)	0.4 (0.1 - 2.7)
Belgium	146	0.7	0	74	17.8 (7.1 - 38)	7.1 (1 - 36.3)
Bulgaria	-	-	-	17	0	0
Cyprus	-	-	-	14	57.6 (23.9 - 85.5)	0 (0 - 0)
Czech Republic[c]	283	19.1	0.7	194	42.7 (33.8 - 52.1)	18.4 (12.4 - 26.4)
Denmark	24	4.2	0	59	4.0 (0.6 - 22.2)	0 (0 - 0)
Finland	348	0	0	133	0	0
France[d,e]	9 394	7.7	0.6	326	13.3 (9.4 - 18.4)	3.8 (1.9 - 7.4)
Germany[d]	971	1.0	0.6	295	9.2 (6.2 - 13.4)	2.6 (1.3 - 5.2)
Greece	14	7.1	0	43	16.5 (6.7 - 35.1)	0 (0 - 0)
Hungary	2 997	29.9	0.2	289	78.5 (70.7 - 84.6)	3.6 (1.7 - 7.3)
Ireland	103	1.0	0	259	27.6 (18.1 - 39.7)	0 (0 - 0)
Italy	2 468	17.7	0.2	268	38.8 (31.8 - 46.4)	6.1 (3.5 - 10.2)
Lithuania	6	16.7	0	63	5.3 (1.2 - 19.9)	1.5 (0.2 - 9.1)
Poland	3 434	5.2	0.7	322	26.9 (19.9 - 35.4)	4.2 (2.4 - 7.2)
Portugal	25	0	0	105	6.3 (2.9 - 13.2)	0 (0 - 0)
Romania	54	13.0	0	-	-	-
Slovakia	24	0	0	25	22.9 (19 - 27.4)	0 (0 - 0)
Slovenia	112	0.9	0	131	21.1 (13.1 - 32.2)	4.7 (1.7 - 12.1)
Spain	1 316	19.8	1.7	380	56.3 (50.1 - 62.4)	2.8 (1.5 - 4.9)
Sweden	155	0	0	14	0	0
The Netherlands	229	2.6	0	172	14.1 (7.5 - 24.9)	1.5 (0.3 - 6.9)
The United Kingdom	3 078	15.4	0.1	317	32.2 (24.7 - 40.6)	4.6 (2.2 - 9)
EU Total	**25 536**	**12.1**	**0.5**	**3 702**	**30.7 (28.2 - 33.2)**	**3.8 (3.0 - 5.0)**
Norway	385	0	0	67	0	0
Switzerland	60	3.3	0	-	-	-

[a] Bulgaria, Cyprus, Estonia, Latvia, Luxembourg, and Malta did not report data in the 2010 monitoring of fattening flocks of turkeys.

[b] Weighted prevalence estimate. The 95 % CI is given between brackets. For details see reference original EFSA Report (EFSA, 2008b). Estonia, Latvia, Luxemburg reported not having commercial turkey flocks in the baseline survey. Malta and Romania did not participate in the baseline survey.

[c] In the 2010 monitoring, one flock positive for two serovars.

[d] In the 2010 monitoring, *S.* Typhimurium result includes the reporting of monophasic variants.

[e] In the 2010 monitoring, the number of flocks tested is an underestimate as all flocks are tested but not all negative flocks are recorded.

Table 7: Frequency distribution of isolated *Salmonella* serovars in the fattening turkey flocks baseline survey in the EU[a] and Norway, 2006-2007 (EFSA, 2008b)

Serovar	Samples with serovars (N=135)		Holdings with serovars (N=26)		Flocks with serovars (N=40)		Countries with serovars
	N	%	N	%	N	%	N
Bredeney	633	16.5	157	16.8	186	17.2	6
Hadar	494	12.9	146	15.6	152	14.0	10
Saintpaul	417	10.9	105	11.2	112	10.3	12
Derby	377	9.8	122	13.1	123	11.3	11
Kottbus	286	7.5	88	9.4	90	8.3	9
Typhimurium	272	7.1	84	9.0	86	7.9	12
Orion	231	6.0	29	3.1	66	6.1	2
Infantis	204	5.3	55	5.9	72	6.6	4
Enteritidis	117	3.1	54	5.8	55	5.1	8
Agona	99	2.6	20	2.1	31	2.9	8
Newport	95	2.5	30	3.2	33	3.0	9
Blockley	86	2.2	39	4.2	40	3.7	7
Indiana	71	1.9	26	2.8	32	3.0	8
London	70	1.8	31	3.3	31	2.9	1
Heidelberg	46	1.2	17	1.8	18	1.7	3
Kedougou	44	1.1	12	1.3	12	1.1	2
Senftenberg	35	0.9	15	1.6	15	1.4	7
Montevideo	34	0.9	11	1.2	13	1.2	3
Zanzibar	25	0.7	11	1.2	12	1.1	2
Virchow	23	0.6	11	1.2	11	1.0	2
Others	191	5.0					
Salmonella untypeable	2	0.1	2	0.2	2	0.2	2
Total isolates	3 852						

[a] Source 22 MSs: Austria, Belgium, Bulgaria, Cyprus, Czech Republic, Denmark, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Lithuania, Poland, Portugal, Slovakia, Slovenia, Spain, Sweden, the Netherlands, and the United Kingdom.

In the harmonised monitoring in 2010, information on *Salmonella* in turkey fattening flocks was provided by 21 MSs and two non MSs. No *Salmonella* was found in samples tested in Finland, Portugal, Slovakia, Sweden and Norway. In the 17 MSs reporting positive findings, the percentage of positive samples ranged from 0.7 % to 29.9 %. Figures 1 and 2 show the individual MS prevalence (% positive flocks tested) of *Salmonella* spp. and the prevalence of *S.* Enteritidis and *S.* Typhimurium combined of both the 2010 statutory monitoring and the baseline survey in turkey flocks carried out between 2006 and 2007 in the different EU MSs.

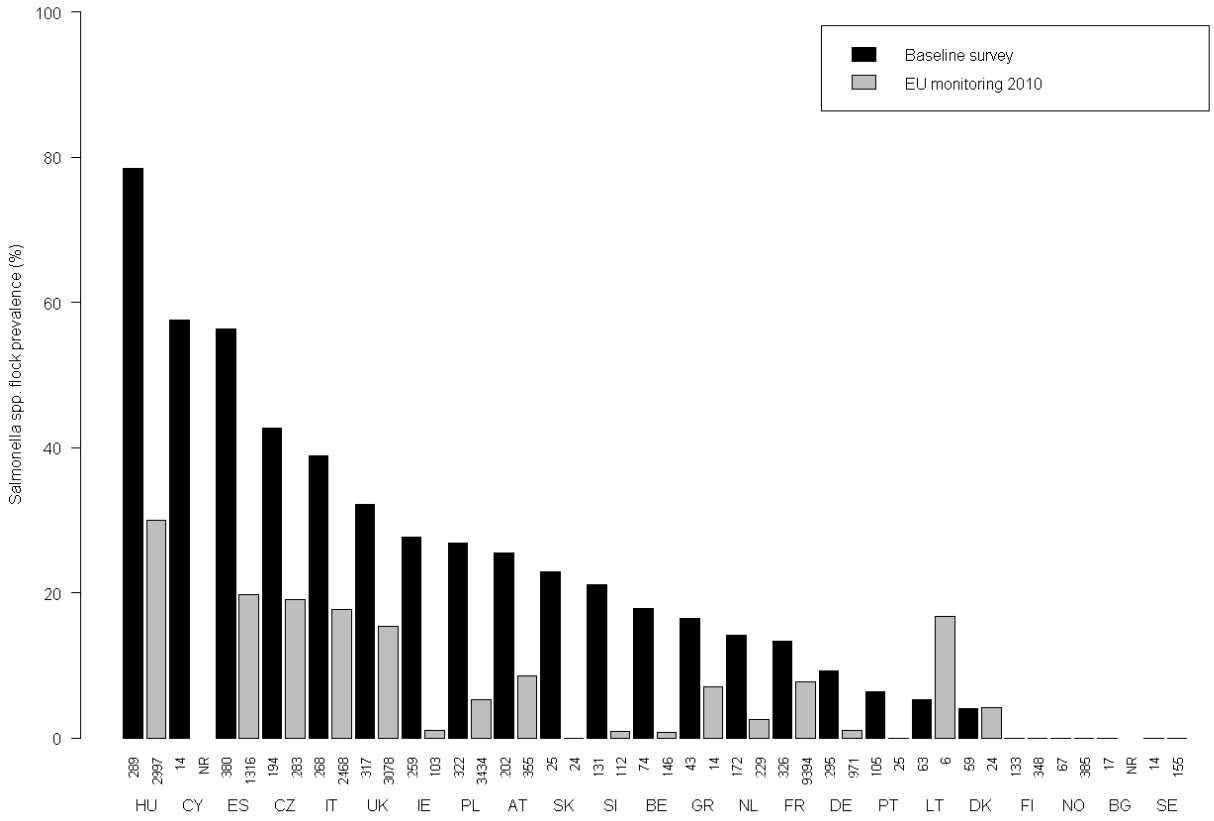


Figure 1: Prevalence (%) of *Salmonella* spp. in the different EU MSs as reported through EU harmonised monitoring (EFSA and ECDC, 2012) and through the baseline survey (weighted prevalence) in turkey fattening flocks in the EU[a] and Norway carried out between 2006 and 2007.

[a] Bulgaria, Cyprus, Estonia, Latvia, Luxembourg, and Malta did not report data in the 2010 monitoring of fattening flocks of turkeys. Estonia, Latvia, Luxemburg reported not having commercial turkey flocks in the baseline survey. Malta and Romania did not participate in the baseline survey. NR=not reported.

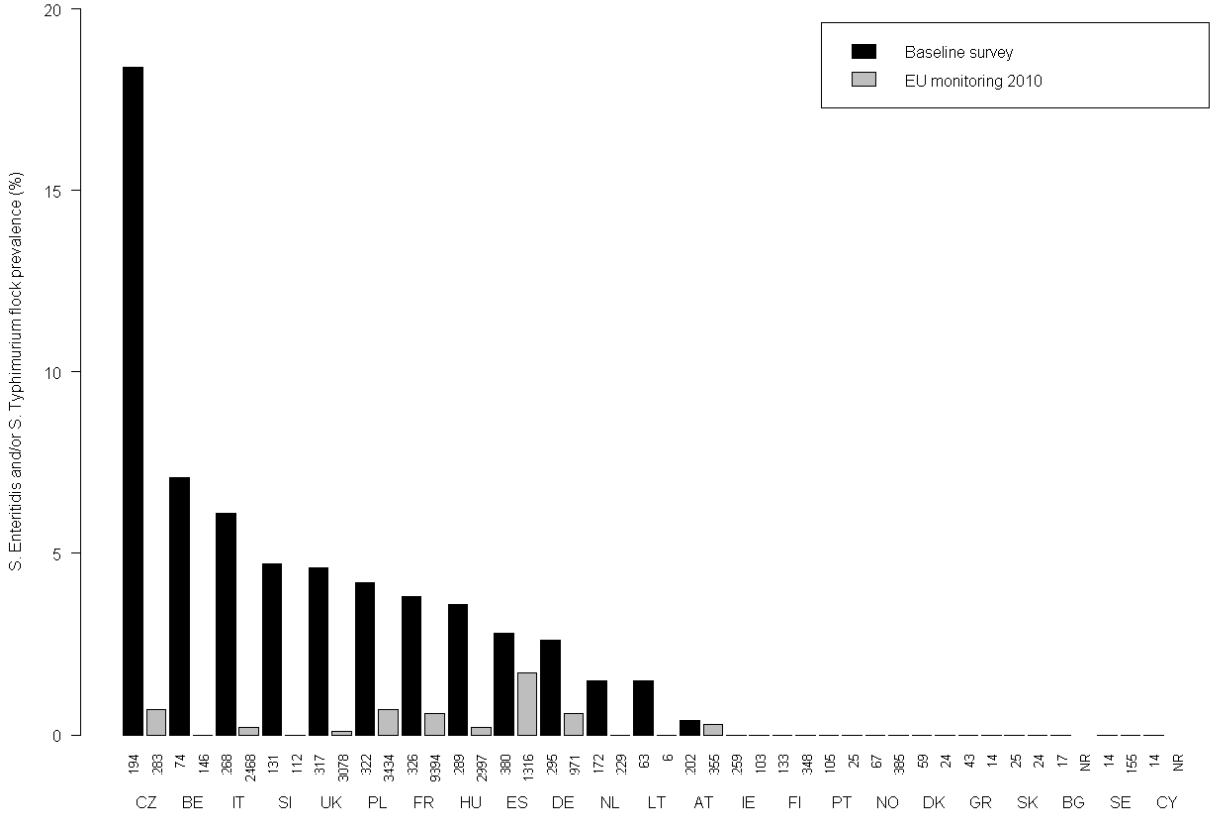


Figure 2: Prevalence (%) of *S.* Enteritidis and *S.* Typhimurium in turkey fattening flocks in the different EU MSs as reported through EU harmonised monitoring (EFSA and ECDC, 2012) and through the baseline survey (weighted prevalence) in turkey fattening flocks in the EU[a] and Norway carried out between 2006 and 2007.

[a] Bulgaria, Cyprus, Estonia, Latvia, Luxembourg, and Malta did not report data in the 2010 monitoring of fattening flocks of turkeys. Estonia, Latvia, Luxemburg reported not having commercial turkey flocks in the baseline survey. Malta and Romania did not participate in the baseline survey. NR=not reported.

With few exceptions, higher prevalences of *Salmonella* spp. and *S.* Enteritidis and/or *S.* Typhimurium were observed in the baseline survey than through the statutory monitoring. This is in line with observations made in other baseline surveys, and may be attributable to the application of control measures in the period between the two sampling schemes, as well as to the different sensitivity of sampling and testing schemes applied.

Commission Regulation (EC) No 584/2008[26] states that no more than 1 % of fattening and adult breeding turkey flocks are to remain positive for *S.* Enteritidis and *S.* Typhimurium by 31 December 2012. It is noteworthy that in 2010, only one out of the 21 MSs and two non MSs providing *Salmonella* data for fattening flocks reported a *S.* Enteritidis and/or *S.* Typhimurium prevalence above the 1 % prevalence target (EFSA and ECDC, 2012).

[26] Commission Regulation (EC) No 584/2008 of 20 June 2008 implementing Regulation (EC) No 2160/2003 of the European Parliament and of the Council as regards a Community target for the reduction of the prevalence of *Salmonella enteritidis* and *Salmonella typhimurium* in turkeys. OJ L 162, 21.6.2008, p. 3-8.

5.1.5. Factors influencing the detection of *Salmonella* in breeding and fattening turkey flocks

5.1.5.1. Factors influencing the detection of *Salmonella* in breeding turkey flocks

Experience from breeding turkey flocks suggests that the within-flock sample prevalence is likely to be lower than in fattening flocks (Mueller-Doblies et al., 2009). Flocks, especially at elite or GP level or toms, are likely to be sub-divided into small groups with separate feeders and water supply which limits lateral spread and recycling of infection resulting in a non-uniform distribution, especially in the case of serovars with limited virulence that have originated from contaminated feed production (Davies et al., 1998). Any detection method has a limited sensitivity and this is related to the within-flock prevalence and number of organisms present in the sample, the ability of the *Salmonella* strain to survive in the presence of competing flora during pre-enrichment and the ability of competing flora to grow in the selective culture media (Arnold et al., 2009; Davies et al., 2001; Sherrod et al., 1995). This varies between flocks but can lead to a dilution effect in which *Salmonella* fails to be detected against a background of competing organisms. Atypical salmonellae may also be encountered occasionally (Hall et al., 1978) and these may be difficult to identify. Detection of *Salmonella* in breeding flocks is improved by the inclusion of a dust sample as well as a faeces sample (Mueller-Doblies et al., 2009). Dust can be a valuable sample as most *Salmonella* strains survive desiccation well compared with competing organisms and dust accumulates over time, so is likely to include faecal components from periods between sampling where levels of *Salmonella* excretion may have been higher (Carrique-Mas and Davies, 2008). Sensitivity analysis carried out by EFSA (EFSA, 2008b) using data from the baseline survey of breeding flocks showed that in several MSs with positive flocks only one or two pairs of the five pairs of boot swabs that were taken were found to be positive. This suggests that some positive flocks would be likely to be missed if a smaller number of samples were taken, especially if the samples are combined into a smaller number of pooled samples (Arnold et al., 2009), as occurs in the routine monitoring programme. On the other hand routine monitoring of breeding flocks is carried out every three weeks during lay, so the cumulative detection level should be relatively high, as long as operator sampling and testing is working correctly. In some countries there appears to be a large difference between the detection sensitivity of official and operator sampling. The reason for this has not been fully elucidated but could include less robust sampling materials, less thorough sampling, less attention to temperature effect and time delays before testing and less efficient laboratory procedures in private laboratories. More investigation of the reasons for these differences is warranted, especially as only 10 % of commercial turkey breeding and fattening houses, representing around 5 % of flocks, are officially sampled each year.

Interventions such as vaccination (Tenk et al., 2000; Thain et al., 1984), antibiotic treatment (Reynolds et al., 1997), acidification of feed or water (Wales et al., 2010a) or adding inhibitory substances such as lime to litter (Bennett et al., 2005) may also reduce the level of *Salmonella* in faeces or the sampled environment, making detection more difficult. In the antimicrobial hatchery treatment of breeding flocks or use of formaldehyde during hatching may also inhibit detection (Cadirci, 2009).

5.1.5.2. Factors influencing the detection of *Salmonella* in fattening turkey flocks

Similar limiting factors apply to the detection of *Salmonella* in fattening turkey flocks to those described above for breeding turkey flocks. In large flocks or holdings preventive or therapeutic antimicrobial treatment may be regularly required and there is a chance that this may interfere with detection, depending on the products used and susceptibility of the particular *Salmonella* strains present. In the EU baseline survey there did not appear to be a statistically significant effect of medicating birds within two weeks before sampling (EFSA, 2008d). Routine use of antimicrobials may actually favour colonisation of young poults or breeding birds after placement as a result of perturbation of intestinal flora (Sekirov et al., 2008), but it is desirable to avoid periods of medication when samples are taken, or to take repeat samples where this is unavoidable. Hafez et al. (1997) monitored 24 fattening turkey flocks for *Salmonella* during the entire rearing period (day one to week 20 weeks). Although in 20 out of 24 monitored flocks antibiotics and chemotherapeutics were applied to treat respiratory disease condition and coccidiosis, shedding of salmonellae in faeces seemed not to be influenced and in *Salmonella* infected flocks, *Salmonella* could be detected during the entire

rearing period. The development of a reliable method for detecting all relevant antimicrobials in the tissues, or ideally in the faeces of treated birds is highly recommended (Huet et al., 2010).

As in breeding birds there also appears to be a discrepancy between the results of official and operator sampling, and the reasons for this should be investigated in detail by MS where this occurs.

In conclusion, the theoretical detection capability of five or two pairs of boot swabs may be compromised by pooling of samples for pre-enrichment, but more work is needed to fully quantify this effect which is likely to compromise detection of breeding flocks in particular because of the lower numbers of *Salmonella* organisms in the sample. The performance of the sampling and testing programme should be subject to ongoing auditing in each MS to detect inefficiency or deception and the development of a reliable and economic test to identify specific antimicrobials in birds or samples should be prioritised.

5.2. Monitoring of *Salmonella* in turkey meat

5.2.1. Monitoring systems in the EU

Monitoring of *Salmonella* in different types of turkey meat and meat products in the EU is mainly carried out in the context of ensuring compliance with microbiological criteria (both food safety criteria for products and process hygiene criteria for poultry carcasses, including turkeys). Earlier Scientific Opinions of the EFSA Panel on Biological Hazards have addressed and considered in detail microbiological criteria issues for poultry meat in the EU (EFSA, 2007; EFSA Panel on Biological Hazards, 2010c). The latest of these Opinions, on the link between *Salmonella* criteria at different stages of the poultry production chain replied to a request from the European Commission in the frame of the possible establishment of a food safety criteria for *Salmonella* in fresh poultry meat.

The reporting of *Salmonella* in turkey meat and meat products in the EU presents several limitations when comparing and interpreting the results of monitoring between different MSs (EFSA and ECDC, 2011, 2012; EFSA Panel on Biological Hazards, 2010c), namely:

- Differences in test and analytical sensitivity from the different monitoring in the EU MSs;
- Monitoring of *Salmonella* in turkey meat is not fully harmonised between MSs. Sampling composition and size and sampling frequency varies between MSs. Also, the stage at which samples are taken during production may vary; and
- The level of detail of reporting provided by the MSs differs; in 2010, 22 MS and one non MS reported data on *Salmonella* in turkey meat.

The two standardised methods applied in MSs for the detection of *Salmonella* from meat are the ISO 6579:2002[27] and the NMKL[28] procedures; the ISO method prescribes the use of two selective enrichment media, whereas in the NMKL protocol only one medium is used.

According to Commission Regulation No 1086/2011[29], new microbiological criteria are set out in fresh poultry meat, and broiler and turkey carcasses. In fresh poultry meat, the absence of *S.* Enteritidis and *S.* Typhimurium, including its monophasic 1,4,[5],12:i:- variant, is required in five samples of 25 grams. According to the prescriptions of Commission Regulation No 2073/2005[30], any *Salmonella* spp. found in broiler or turkey carcasses, shall be further serotyped in order to exclude the presence of

[27] ISO 6579:2002. Microbiology of food and animal feeding stuffs – Horizontal method for the detection of *Salmonella* spp. – Amendment 1: Annex D: Detection of *Salmonella* spp. in animal faeces and in environmental samples from the primary production stage. International Organization for Standardization.

[28] NMKL 71. *Salmonella*. Detection in Food. Nordic Committee on Food Analysis.

[29] Commission Regulation (EU) No 1086/2011 of 27 October 2011 amending Annex II to Regulation (EC) No 2160/2003 of the European Parliament and of the Council and Annex I to Commission Regulation (EC) No 2073/2005 as regards *salmonella* in fresh poultry meat. OJ L 281, 28.10.2001, p. 7-11.

[30] Commission Regulation (EC) No 2073/2005 of 15 November 2005 on microbiological criteria for foodstuffs. OJ L 338, 22.12.2005, p. 1-29.

S. Enteritidis or *S.* Typhimurium. It is important that antigenic formulae of emerging *Salmonella* strains, e.g. monophasic variants of *S.* Typhimurium, are reported so that trends can be accurately monitored (EFSA Panel on Biological Hazards, 2010b).

5.2.2. Results of monitoring

In 2010, 22 MSs and one non MS reported data concerning *Salmonella* in fresh turkey meat and 9.0 % of the tested samples were positive for *Salmonella* in the EU, ranging from 3.3 % up to 29.6 % in single samples from Italy. No contamination in RTE products from turkey meat was detected by the four MSs that provided data.

Seventeen MSs reported *Salmonella* findings in non-RTE turkey meat products (meat products, meat preparations and minced meat), and eight of these MSs reported data with more than 25 samples. The proportion of *Salmonella*-positive samples varied between 2.0 % and 16.9 % with an average of 6.4 % at EU level. Data without indication of RTE or non-RTE have been assumed to originate from non-RTE materials.

6. Epidemiology of *Salmonella* in turkeys

6.1. The importance of vertical transmission

The sources of *Salmonella* infection in turkeys are numerous and similar to that of chickens. Poultry are often carriers, latently or subclinically infected or, rarely, clinically ill. They may excrete *Salmonella* in their faeces and form a large reservoir and source of contamination for other animals, humans and the environment (Poppe, 2000). There are numerous publications reporting true- and/or pseudo-vertical transmission of *Salmonella* in chickens, while for turkeys only a small number are available, but in general the transmission pathway seems to be similar.

In general, the most important source of *Salmonella* infection appears to be the true-vertical transmission from parents to progeny via internally contaminated eggs, due to colonisation of the reproductive organs (ovary or oviduct) or due to penetration into the forming egg, within the body of the turkey breeder (Cherrington et al., 1937) or by contact of follicles with infected peritoneum or air sacs. The pseudo-vertical transmission occurs from parents to progeny via externally contaminated eggs or in the hatchery when *Salmonella* from a very small number of internally contaminated eggs (via ovarian or trans-shell contamination) spreads within hatcher cabinets and via ventilation ducting or poorly cleaned equipment. Eggshells can be contaminated by faecal material from environments with subsequent penetration into the eggs (Cherrington et al., 1937; Pomeroy and Fensternmacher, 1941; Stokes et al., 1956; Williams et al., 1968). Williams and Dillard (1969) found that unpigmented turkey eggs were more frequently penetrated by *S.* Typhimurium than normally pigmented eggs. Such unpigmented eggs have thinner shells and larger pores.

In addition to the above mentioned routes of pseudo-vertical transmission, all other sources, which contaminate hatching eggs after laying through contaminated nests or during the hatch, as well as infection of hatched poults in the hatchery or during the transport to the fattening farm, should be considered as vertical transmission or hatchery-acquired salmonellae (Hafez and Jodas, 2000).

6.1.1. *Salmonella* serovar differences in their tendency for vertical transmission

True-vertical transmission through infected turkey eggs laid by infected carriers is documented for serovars such as *S.* Arizona, *S.* Senftenberg (Kumar et al., 1971), *S.* Typhimurium (Lee et al., 1936), *S.* Hadar (Mayer et al., 1984), *S.* Gallinarum (including biovar Pullorum) (Snoeyenbos, 1991) and *S.* Enteritidis (Jodas and Hafez, 2002). Although some serovars of *Salmonella* are generally considered to be invasive, there is significant variation between strains within serovars (Saeed et al., 2006).

In a two-year investigation of parent turkey flocks and a hatchery, different *Salmonella* serovars (*S.* Montevideo, *S.* Mbandaka, *S.* Braenderup and *S.* Hadar) were isolated from hatching eggs delivered to the hatchery from four out of six examined parent flocks. Bacteriological examinations of

485 samples collected from the hatchery (dead-in-shell, hatchery debris, meconium, 1-day old chicks, transport cartons) on 18 different hatching days failed to isolate *Salmonella*. The possibility of hatching eggshell contamination with isolated *Salmonella* serovars and vertical transmission to hatched poults could not be demonstrated, since all hatching eggs were sanitized by fumigation on the farm and pressure-differential dipping (PDD), using enrofloxacin, at the hatchery (Hafez et al., 1997).

On the other hand Jodas and Hafez (2002) reported on the isolation of *S.* Enteritidis PT4 in a turkey hatchery in seven out of 231 examined meconium samples. In addition, *S.* Enteritidis was detected in 10 out of 112 tested fluff samples, two out of 70 investigated eggs and in six day old poults out of 306 tested. From 146 environmental swabs collected at the hatchery *S.* Enteritidis could not be isolated. Immediately after the first *S.* Enteritidis isolation in the hatchery all parent flocks, which belonged to the hatchery owner, were intensively bacteriologically examined in aim to determine the source of the infection. From two out of three examined laying parent flocks (52-53 weeks of age) and from one breeding flock (6 weeks old) *S.* Enteritidis was isolated.

Hoover et al. (1997) examined poult-box liners and poults at day-0 on the arrival to the commercial farm and revealed positive *Salmonella* results. They concluded that is an indication that *Salmonella* contamination acquired from the breeder flocks or the hatchery. Crespo et al. (2004) investigated the possible relationships between *S. arizonae* isolated from breeder flocks, hatching eggs, and meat bird flocks belonging to a single turkey integrator. In all the meat bird cases selected for this study, arizonosis was the primary diagnosis. The presence of common pulsed-field patterns in breeder flocks, eggs, and meat bird flocks suggested that *S. arizonae* was being transmitted vertically from the breeder flock.

Recently, Iaffaldano et al. (2010) reported about the possibility of transmission of *Salmonella* spp. to breeder flocks by using of contaminated cryopreserved semen artificially contaminated with *S.* Liverpool, *S.* Montevideo, and *S.* Braenderup.

6.1.2. Hatcheries and horizontal transmission

In general hatcheries are one of the major sources of horizontal transmission after the hatch and *Salmonella* can survive for long periods in eggshells, meconium, dust and biofilms, which is the same in any type of poultry or game bird hatchery, although broiler chicken hatcheries have been most frequently studied (Cason et al., 1994; Poppe, 2000). According to Friend and Franson (1999), *Salmonella* spp. can persist for many years within the hatchery. This is normally by means of contamination of ventilation ducting, belt slots or door seals within hatchers, but may also result from infection and contamination that continuously recycles between hatchers, hatched birds, dust and crate washing equipment (Davies and Bedford, 2001; Davies and Wray, 1994).

Salmonella can also spread by air throughout the hatchery, resulting in rapid transmission (Hoover et al., 1997). Hatched birds may become infected by aerosols containing *Salmonella* (Agabou, 2009; Baskerville et al., 1992).

Rodents and litter beetles (Skov et al., 2004; Wales et al., 2010b) play an important role in the epidemiology of *Salmonella* infection in poultry farms (Henzler and Opitz, 1992). Mice can be a persistent reservoir of *Salmonella* infection between flocks and may even contaminate the hatchery equipment or eggs in small hatcheries (Kumar et al., 1971; McCapes et al., 1991).

In order to prevent contamination spread, hatcheries should be designed to permit only a one-way flow of traffic from the egg entry room through egg trays, incubation, hatching and holding rooms to the van-loading area. The ventilation system must prevent recirculation of contaminated air. Trays used in the hatchery should be thoroughly cleaned and disinfected before eggs are placed on them and ideally disposable delivery boxes should be used to avoid introducing *Salmonella* into hatchery tray wash systems by means of contaminated delivery baskets that are returned for washing and re-use (Hafez and Jodas, 2000).

6.1.3. Impact of *Salmonella* prevalence in flocks of breeding turkeys on *Salmonella* prevalence in flocks of fattening turkeys

The baseline survey of 2006/7 (EFSA, 2008b) was the first reliable source of prevalence and serovar distribution in breeding and fattening turkeys in the EU. *S.* Saintpaul was the most frequently isolated serovar in breeding turkey flocks in the EU but was only found in one MS. *S.* Kottbus was the second most frequent serovar but was still only found in three MSs. *S.* Typhimurium, *S.* Heidelberg and *S.* Derby were found in two MS each, and other less frequently occurring serovars were each only found in one MS. The limited distribution of predominant serovars at breeding flock level suggests that there is likely to be little association currently with international distribution of replacement parent breeding birds within the EU, but is difficult to assess the potential impact of importation of genetic lines originating from the USA and Canada (Liebana et al., 2004; Pedersen et al., 2002). It is also likely that *Salmonella* serovars and strains that originated from breeding flocks in earlier years may persist on commercial farms where standards of biosecurity, pest control and terminal hygiene are lower and there is little incentive to fully control non-regulated serovars in many countries (Danguy Des Deserts et al., 2010; Mueller-Doblies et al., 2010; Pires et al., 2008). The baseline survey may also have under-estimated associations between breeding flocks and fattening flocks because of the long fattening period, which may have lead to infected progeny being not eligible for testing during the survey period and removal of hatching eggs from infected flocks from hatcheries. Eventually, it is important to mention that the number of turkey breeding farms is rather small and limited to a few MSs, so the significance of results referred to breeding farms can be hampered by the scarcity of data available (in the baseline survey 532 breeding farms were sampled in 14 MSs, but just three MSs had a number of farms sampled >30). The same consideration is also valid for data arising from the 2010 monitoring.

A larger number of fattening flocks were sampled, higher prevalences were found together with a wider range of serovars, many of which were also found in breeding flocks and in multiple MSs (EFSA, 2008b). Correlation between the estimated prevalence of *Salmonella* in breeding and fattening turkeys in each MS was studied formally using the Spearman rank correlation coefficient, ρ, a nonparametric rank correlation procedure which can be used when few data pairs (15) are available. There was a statistically significant correlation between the estimated prevalence of *Salmonella* in breeding flocks and fattening flocks for *Salmonella* spp. and for *S.* Enteritidis and *S.* Typhimurium and a borderline significant finding for serovars other than *S.* Enteritidis and *S.* Typhimurium. This would suggest that if a MS has a higher prevalence of *Salmonella* in breeding flocks, it would be likely to result in a higher prevalence in fattening flocks. It should be noted that these significant correlation results are based on calculations taking into account countries where the infection was absent from both fattening and breeding turkeys (EFSA, 2008b).

The weighted prevalence of *S.* Enteritidis and *S.* Typhimurium and of other serovars in breeding and fattening turkey flocks, as resulted from the baseline survey, is reported in Figure 3, whereas Figure 4 represents similar data, but arising from the 2010 harmonised monitoring data. In both cases a statistically significant relationship between the prevalence or occurrence of *Salmonella* in breeders and in fattening flocks is not evident.

Figures 1 and 2 in Appendix E show the distribution of *Salmonella* serovars in breeding and fattening flocks, as resulted respectively from the baseline survey and from the 2010 harmonised monitoring.

For some MSs in the baseline survey, the serovar distribution in breeding and fattening flocks appear to be similar with regards to the most frequently isolated serovars (Figure 1, Appendix E). Nine of the twelve serovars that were isolated in breeding flocks (EFSA, 2008c) were amongst the most frequently isolated serovars in fattening flocks. The exceptions were *S.* Thompson, *S.* Bradford and *S.* Corvallis that were only isolated from single breeding flocks. This slight lack of concordance is not unexpected as the timescale for sampling breeding and fattening flocks in the baseline survey meant that the direct progeny of sampled breeding flocks would be unlikely to be sampled, larger numbers of holdings but only a proportion of fattening flocks were sampled in each MS and some *Salmonella* serovars are unlikely to transmit via egg or hatchery contamination. Analysing results from the 2010 monitoring

and the baseline survey (Figure 2, Appendix E and Table 8), it appears that five serovars were found both in breeders and in fattening flocks, one was present only in breeders, whereas 16 were found in fattening flocks but not in breeders. In the baseline survey, nine serovars were isolated both in breeders and in fattening flocks, 3 only in breeders, 11 only in fattening flocks.

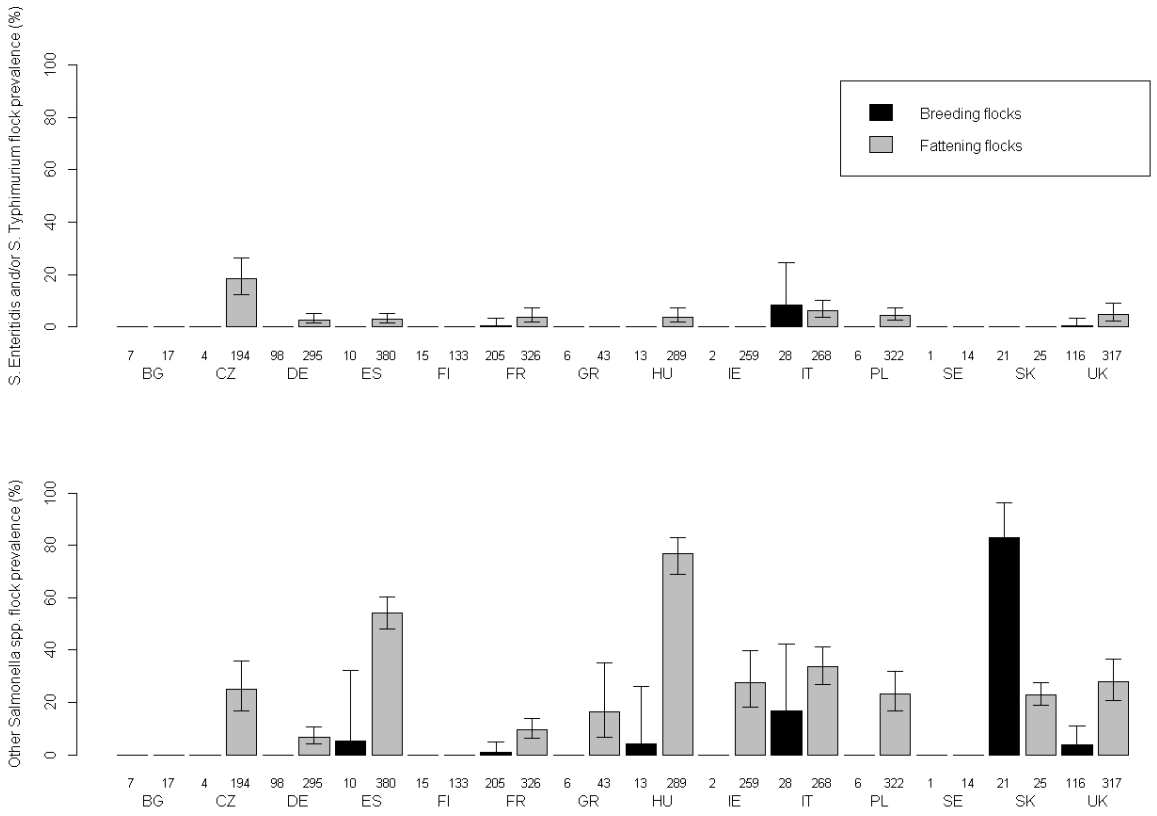


Figure 3: Weighted prevalence (%) of *S.* Enteritidis and/or *S.* Typhimurium (top) and other serovars (bottom) in breeding and fattening turkey flocks in the EU (Source: baseline survey in turkey fattening flocks carried out between 2006 and 2007). B = breeding flocks, F = fattening flocks. Horizontal bars represent 95 % confidence intervals.

In the UK evidence of transmission of *S.* Derby and *S.* Kottbus from positive breeding flocks to progeny was obtained by independent investigation of linked holdings (Danguy Des Deserts et al., 2010; Featherstone et al., 2010) but not all serovars that occur in breeding flocks can be found in the hatchery and contaminated feed is also an important source (Hafez et al., 1997). The vertically transmitted turkey *S.* Arizonae strains (Crespo et al., 2004) were not found in the survey but many serovars were the same as those previously related to world trade in turkey breeders (Beli et al., 2001; El-Agroudi, 1964; Hadad, 1996; Hird et al., 1993; Irwin et al., 1994; Koncicki et al., 2000; Osman et al., 2010; Papadopoulou et al., 2009; Pedersen et al., 2002) although detailed molecular epidemiology would be needed to confirm transmission routes as well as sources of human cases (Anderson et al., 2010). Some serovars such as *S.* Senftenberg readily colonise feed mills and hatcheries and can be found at a low prevalence in turkeys (Edwards, 1937; Lecuyer et al., 1996; Pedersen et al., 2008).

In France, while 15.6 % of the fattening turkey flocks were infected by *Salmonella* spp. at the end of the rearing period 1.5 % (3/205) of breeding flocks were found positive (Aury et al., 2010). *S.* Enteritidis was the only serovar found simultaneously in breeding and fattening turkey flocks. The other two serovars, *S.* Kottbus and Bradford detected in breeding flocks were not found in fattening flocks. Genotyping of *S.* Enteritidis isolates from breeding and fattening turkey flocks showed that

isolates were not similar. While *S.* Derby (25 %) dominated among positive flocks, *S.* Indiana (51 %) was the prevalent one on turkey products at the retail level, followed by *S.* Derby (15 %), *S.* Typhimurium (9 %) and *S.* Anatum (9 %) (Anonymous, 2011). The majority of positive meat samples (92 %) presented very low amounts of *Salmonella* (<1.6 cfu/g).

The relevance of *Salmonella* spp. infection in breeding turkeys is mainly related to the potential for vertical transmission to fattening flocks, although there may also be a direct risk as breeding birds are also slaughtered for human consumption. The significant correlation between prevalences of *Salmonella* spp. in breeding and fattening flocks was consistent with the hypothesis of an epidemiological association between these two flock types within the same MS. As there is intensive international trade in hatching eggs and day-old chicks, correlations between the prevalence in breeding flocks and fattening flocks at MS level are not very informative on the risk of vertical transmission. The finding of a prevalence in breeding flocks at about half that of fattening flocks may be explained by clearing of infection by the older breeding birds, and/or the intensified approach to biosecurity for the breeding stock. Furthermore, fattening flocks may also become colonised by *Salmonella* from other sources, i.e. feed and the environment. The relative importance of colonised breeder flocks will depend on the force of infection from these other sources although experience from field investigations suggests that most serovars that are found in breeding flocks of turkeys are likely to transmit to progeny flocks by true- or pseudo-vertical transmission (Danguy Des Deserts et al., 2010; Davies and Bedford, 2001).

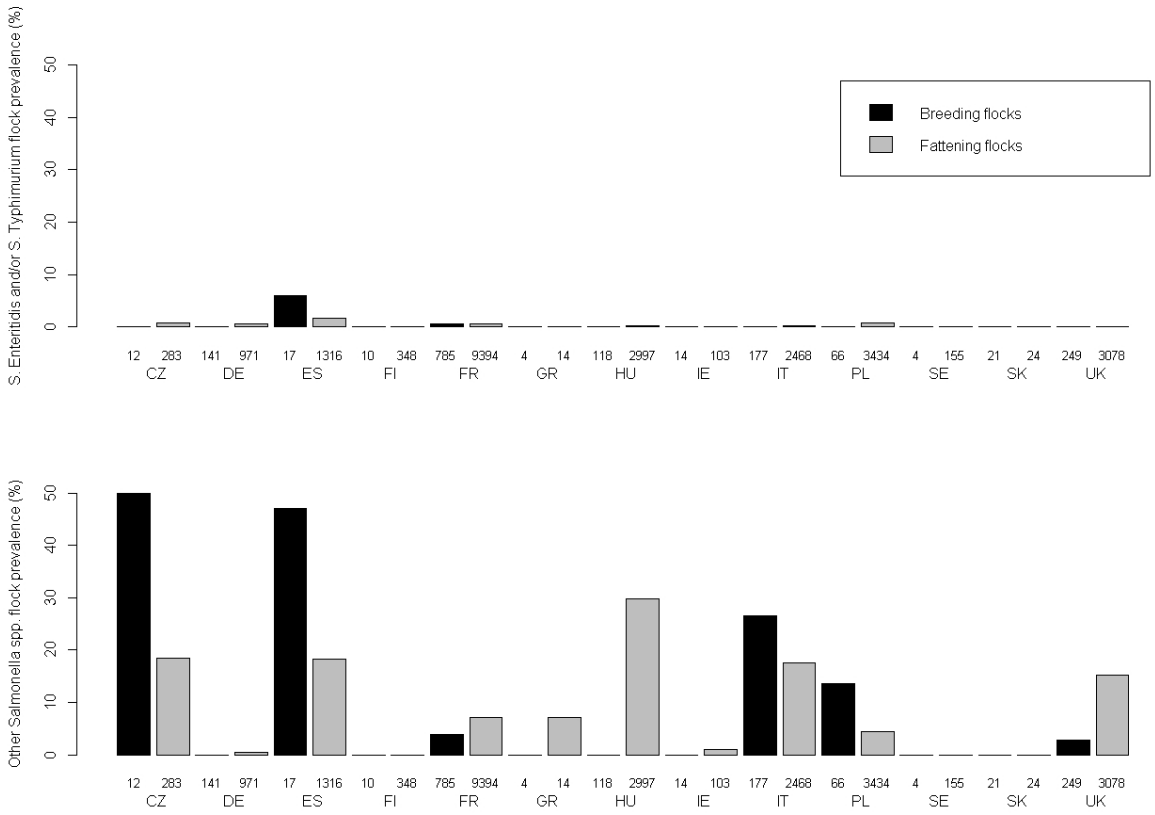


Figure 4: Proportion of positive flocks (%) of *S.* Enteritidis and/or *S.* Typhimurium (top) and other serovars (bottom) in breeding and fattening turkey flocks in the EU (Source: EU harmonised monitoring) (EFSA and ECDC, 2012). B = breeding flocks, F = fattening flocks.

Table 8: Distribution of serovars in turkey production in 2010 (EU harmonised monitoring) (EFSA and ECDC, 2012) and in 2006/07 (EU baseline survey) (EFSA, 2008b)

Presence	2010 Monitoring		BSL flocks 2006-2007	
	No. of serovars	Serovars	No. of serovars	Serovars
Both in breeding and fattening flocks of turkeys	5	*S.* Kentucky *S.* Newport *S.* Typhimurium *S.* Virchow *S.* 1,4, [5],12:i:-,	9	S. Blockley[a] S. Bredeney[a] *S.* Derby S. Enteritidis[a] *S.* Heidelberg *S.* Kottbus S. Saintpaul[a] *S.* Senftenberg[a] *S.* Typhimurium
In breeding flocks but not in fattening flocks of turkeys	1	*S.* Agama[a]	3	*S.* Bradford[a] *S.* Corvallis[a] *S.* Thompson[a]
In fattening flocks but not in breeding flocks of turkeys	16	*S.* Agona S. Bredeney S. Blockley *S.* Derby S. Enteritidis *S.* Hadar *S.* Heidelberg *S.* Indiana *S.* Infantis *S.* Kottbus *S.* Lille *S.* Montevideo *S.* Paratyphi B var. Java S. Saintpaul *S.* Senftenberg *S.* 1,4,[5],12:-,1,2	11	*S.* Agona *S.* Hadar *S.* Indiana *S.* Infantis *S.* Kedougou *S.* London[b] *S.* Montevideo *S.* Newport *S.* Orion *S.* Virchow *S.* Zanzibar

[a] For breeding turkey flocks, isolated in one country only.
[b] For fattening turkey flocks, isolated in one country only.

6.1.4. Concluding remarks on the relative importance of vertical and horizontal transmission

In conclusion true-vertical transmission of *Salmonella* as well as hatchery acquired *Salmonella* infection are important sources for *Salmonella* infection in turkeys. Controlling the infection in breeding turkey flocks as well as in rearing and in fattening flocks is necessary to minimise contamination of turkeys at slaughter. Eradicating *Salmonella* spp. in the production chain from the top down in order to prevent the vertical transmission of *Salmonella*, is a vital component of any strategy for the control of *Salmonella* in poultry.

6.2. Sources and risk factors for *Salmonella* infection of fattening turkeys

Most studies of risk factors for *Salmonella* contamination have been conducted on broiler and laying hen flocks. The main risk factors for *Salmonella* contamination of turkey flocks found in the literature were (i) flocks with more than two people taking care of the birds and with visitors entering the poultry house during rearing and (ii) the hatchery of origin (Arsenault et al., 2007b). Poor on-farm biosecurity, resulting in the transmission of infection between houses and between the inside of houses and the environment has been described (Danguy Des Deserts et al., 2010) and seems to play a role in some farms that have remained positive for *Salmonella*. Moreover, thorough cleaning and the choice of a suitable disinfectant are crucial for *Salmonella* elimination from turkey houses (Mueller-Doblies et al., 2010). Slaughtering practices and cross-contamination during transportation to slaughter by

feathers or feet contaminated during rearing can promote *Salmonella* contamination of turkey carcasses when a contaminated flock is processed on the slaughter line (Arsenault et al., 2007a).

Salmonella infection needs to be controlled at every stage of the production chain in order to reduce contamination of the end product. Several risk factors for *Salmonell*a contamination have been published for broilers and could be extrapolated to turkeys: season, hatchery of origin, feed mills, presence of rodents, inadequate level of hygiene in the house, *Salmonella* infection of the previous flock, number of houses on the farm (Angen et al., 1996; Cardinale et al., 2004; Rose et al., 1999). The study conducted by Aury et al. (2010) showed that the risk of *Salmonella* contamination in fattening turkey flocks was decreased when floors were disinfected during decontamination procedures (OR=0.4), when *Salmonella* detection was carried out during rearing (OR=0.4) and when there was a metering pump in the house (OR=0.4). However, in this study, the risk was increased when the farmer used a footbath at the turkey house entrance (OR=2.3). A footbath that does not contain enough disinfectant and/or is not changed regularly can quickly become a breeding ground for pathogens and allow their transmission into the poultry house via shoes.

7. *Salmonella* serovars of public health significance

The majority of the relatively small number of *Salmonella* serovars that are regularly reported from human illness, out of the total of more than 2 600 currently recognised serovars, belong to *Salmonella enterica* subspecies *enterica*. Almost all serovars are considered to be potentially pathogenic for humans but only ten serovars are responsible for around 85 % of human cases, and only three serovars (*S.* Enteritidis; *S.* Typhimurium; *S.* Infantis) individually contribute more than 1 % of human non-typhoidal *Salmonella* infections (EFSA Panel on Biological Hazards, 2010b).

Salmonella serovars can be functionally divided into host-specific serovars (e.g. *S.* Typhi in humans, *S.* Gallinarum in poultry), host-associated serovars that primarily affect specific hosts but which can occasionally infect other species, including humans, often causing serious disease (e.g. *S.* Dublin in cattle, *S.* Choleraesuis in pigs) and non-host adapted serovars (e.g. *S.* Enteritidis, *S.* Typhimurium) which are responsible for the majority of human zoonotic infections (Molbak et al., 2006) via food or environmental contamination with faecal material from infected carrier animals. Even within the largely zoonotic serovars there are variants which appear to be host-adapted to wildlife and do not commonly infect food animals or humans. Examples of these are *S.* Typhimurium definitive phage type (DT)2, which is associated with pigeons, and *S.* Enteritidis phage type (PT)11, which is associated with hedgehogs (Helm et al., 2004; Nauerby et al., 2000).

From a regulatory point of view and as per the guidance provided in the Terms of Reference of the request made by the Commission, criteria for *Salmonella* monitoring have been laid down in Regulation (EC) No. 2160/2003[31]. Annex II of this Regulation lists minimum requirements that food business operators have to respect in relation to having samples taken and analysed for the control of *Salmonella* in different animal species and categories. As far as flocks of *Gallus gallus*, turkeys and pigs are concerned, the Regulation requires all *Salmonella* serovars 'with public health significance' to be monitored at various production stages. Annex III of this Regulation defines the specific criteria to be adopted to determine *Salmonella* serovars with public health significance to which community targets will apply:

- the most frequent *Salmonella* serovars associated with human salmonellosis on this basis of data collected through EC monitoring systems;
- the route of infection (i.e. the presence of the serovar in relevant animal populations and feed);
- whether any serovar shows a rapid and recent ability to spread and cause disease in humans and/or animals; and
- whether any serovar shows increased virulence for instance, as regards invasiveness or resistance to relevant therapies for human infections.

[31] 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.

Since *Salmonella* is widespread in various types of animals, including wild and companion animals and most infections are caused by a limited range of serovars it is most efficient to focus targets and control measures on those zoonotic serovars which are of major importance within a food animal sector and in humans, especially in the early stages of control programmes. In breeding poultry and laying hens the ability to cause persistent infection in the ovary and oviduct and thereby to contaminate the interior of hatching eggs or table eggs is of major importance. In commercial meat birds the occurrence of the target serovars in human populations is the most important factor and control of these priority serovars in an effective way would be expected to produce more rapid public health benefits in most countries than an approach involving all serovars. The serovar-targeted approach allows vaccination, culling and segregation to be used to help rapidly eliminate major serovars whilst working on the more difficult task of reducing *Salmonella* from all sources.

7.1. *Salmonella* serovars in human salmonellosis

The ranking of the serovars most frequently isolated from reported cases of human salmonellosis cases in European countries for 2007-2010, is presented in Table 9. The reported human data represent aggregated data and in some cases serovars reported individually in one year may be reported in the group 'Other' in previous years.

It should be noted monophasic 1,4,[5],12:i:- variants of *S.* Typhimurium-like strains appear to be of increasing importance in many EU MSs (EFSA Panel on Biological Hazards, 2010b). In this Scientific Opinion, it was concluded that the public health risk posed by the emerging monophasic 1,4,[5],12:i:- variant of *S.* Typhimurium is considered comparable to that of other *S.* Typhimurium strains which have caused widespread epidemics of infection over the past four decades.

7.2. *Salmonella* serovars in the turkey meat production chain

The *Salmonella* serovars found in the EU baseline survey of fattening turkey flocks showed little similarity with those from humans (EFSA, 2008b, 2008d). *S.* Enteritidis, which was predominant (64.5 %) in human salmonellosis cases in 2007 only ranked 9th (5.1 % of positive flocks) amongst *Salmonella* from fattening turkey flocks in 2006/7, and this was concentrated in eight countries. It is recognised that hen's eggs are the predominant source of *S.* Enteritidis for humans (Pires et al., 2010). *S.* Enteritidis has been reported from turkeys in several countries, but the incidence has decreased as control measures in chicken flocks have improved (Dutta et al., 2010; Hafez, 1997; Turkyilmaz et al., 2009). *S.* Typhimurium ranked 6th in fattening turkey flocks in 2006/7, whereas *S.* Bredeney was the most common serovar in turkeys (17.2 % positive flocks) albeit in only six countries, but *S.* Bredeney is not a common isolate from human cases. It has been identified only rarely in human outbreaks but is predominantly associated with chicken meat (Baker et al., 1998; Moore et al., 2003). *S.* Hadar was found in 14.0 % of fattening flocks in ten countries. This serovar was previously amongst the top five serovars in humans but has declined in recent years (EFSA and ECDC, 2010, 2011, 2012). The reasons for this decline, as well as the origin of human infections with this serovar in many countries is unclear. Improvements in control in breeding chicken flocks following the introduction of EU MS targets in 2007 may be involved, resulting in reduced contamination of chicken meat which has been an important source of infection (Di Giannatale et al., 2008; Lenglet, 2005).

Salmonella Derby was the third most common serovar (11.3 % of positive flocks; 11 countries in 2006/7). This is also a serovar that has been associated with turkey breeding flocks in previous years (Papadopoulou et al., 2009), but is primarily known for its close association with pigs (EFSA, 2008a, 2009a). A comparison study between isolates from human, swine and turkey productions showed high similarities between human and swine isolates and also between turkey and human isolates (Kerouanton et al., 2010). The serovars appears to lack several 'virulence' genes, so, although it does appear to be able to contaminate eggs to a limited extent, human cases are likely to be both uncommon and mild (Betancor et al., 2010; Litrup et al., 2010) and primarily associated with a porcine source (Boyen et al., 2008; Valdezate et al., 2005).

Table 9: Distribution of confirmed salmonellosis cases in humans in the EU[a] by serovar (ten most frequent serovars). TESSy data, 2007-2010. Based on EFSA and ECDC (2010, 2011, 2012).

2010			2009			2008			2007		
Serovar	**N**	**%**	**Serovar**	**N**	**%**	**Serovar**	**N**	**%**	**Serovar**	**N**	**%**
Enteritidis	43 563	45.0	Enteritidis	53 382	52.3	Enteritidis	70 091	58.0	Enteritidis	81 472	64.5
Typhimurium	21 671	22.4	Typhimurium	23 759	23.3	Typhimurium	26 423	21.9	Typhimurium	20 781	16.5
Infantis	1 776	1.8	Infantis	1 616	1.6	Infantis	1 317	1.1	Infantis	1 310	1.0
Typhimurium, monophasic 1,4,[5],12:i:-	1 407	1.5	Newport	760	0.7	Virchow	860	0.7	Virchow	1 068	0.8
Newport	831	0.9	Virchow	736	0.7	Newport	787	0.7	Newport	733	0.6
Kentucky	780	0.8	Derby	671	0.7	Agona	636	0.5	Stanley	589	0.5
Virchow	685	0.7	Hadar	507	0.5	Derby	624	0.5	Hadar	479	0.4
Derby	665	0.7	Kentucky	460	0.5	Stanley	529	0.4	Derby	469	0.4
Mbandaka	470	0.5	Saintpaul	452	0.4	Bovismorbificans	501	0.4	Kentucky	431	0.3
Agona	444	0.5	Bovismorbificans	433	0.4	Kentucky	497	0.4	Agona	387	0.3
Other	24 453	25.3	Other	19 225	18.8	Other	18 495	15.3	Other	18 562	14.7
Total	96 745	100	Total	102 001	100	Total	120 760	100	Total	126 281	100
Unknown	nr[b]		Unknown	nr[b]		Unknown	6 636		Unknown	9 814	

[a] Source 26 MSs: Austria, Belgium, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden, the Netherlands, and the United Kingdom.

[b] nr = not reported.

Salmonella Saintpaul was the fourth most common serovar (10.3 % of positive flocks; 12 countries in 2006/7) found in fattening turkey flocks. Multiple antimicrobial resistant strains of this serovar have been circulating in turkeys in Germany since the 1990s (Beutlich et al., 2010; Beyer et al., 1998). *S.* Saintpaul have also been reported in Danish turkeys and humans but the strains involved were different in terms of their pulsed field profiles (Baggesen et al., 1996), suggesting a different source, and many outbreak investigations have identified contaminated fruit and vegetable products as important sources (Jain et al., 2009; Taylor et al., 2010).

The fifth most common serovar was *S.* Kottbus (8.3 % of positive flocks; 9 countries in 2006/7). This is an unusual serovar amongst human infections, and can also be found in free-living wildlife species (Handeland et al., 2008). Human outbreaks are rare and tend to involve vehicles such as contaminated water and sprouted seeds (Palmera-Suarez et al., 2007; Winthrop et al., 2003).

Turkey meat from infected flocks has been found to be contaminated, especially where slaughter hygiene is poor (Iseri and Erol, 2010; Jordan et al., 2006; Khaitsa et al., 2007; Rose et al., 2002; Trampel et al., 2000; Uyttendaele et al., 1998). International trade in frozen turkey meat may also be a hazard (Mondini and Gasparini, 1964) and in 1996 an outbreak of *S.* Agona linked with pre-cooked turkey meat was reported (Synnott et al., 1998). Closely related *S.* Heidelberg strains have been found in turkeys and in human cases (Hird et al., 1993; Kaldhone et al., 2008) but similar strains have also been identified in egg production, which may be a more likely source (Zhao et al., 2008). *S.* Agona linked with turkeys has also been reported (Doublet et al., 2004), but this is a widespread serovar which has also been linked to contaminated soya bean meal so could have multiple origins.

It is clear from the studies reported above that turkeys are likely to make a relatively minor contribution to human infection (EFSA Panel on Biological Hazards, 2011a). Nevertheless it is desirable that progress is made to reduce reservoirs of infection that might ultimately affect members of the public, particularly those with compromised immune systems (Larsen et al., 2011) resulting in chronic sequelae (Jess et al., 2011).

7.3. Changes in the ability of different *Salmonella* serovars to spread and cause disease in human and animals

As discussed above, *S.* Enteritidis and *S.* Typhimurium have been predominant in humans for decades (EFSA and ECDC, 2010). *S.* Hadar has been replaced in the top five human serovars by *S.* Newport, which can occasionally be found in turkeys but is more likely to occur in cattle and pigs. In the USA and Canada, *S.* Newport with resistance to extended-spectrum cephalosporins mediated by a $bla_{\text{CMY-2}}$ resistance gene has emerged in cattle after routine ceftiofur use and subsequently spread to other species, including turkeys and humans (Poppe et al., 1995). The multidrug-resistance plasmid involved has spread to other serovars and is also widespread in *E. coli*. *S.* Bredeney with the same $bla_{\text{CMY-2}}$ resistance gene was exported from Canada to the UK via live turkeys, but was subsequently eliminated (Frye and Fedorka-Cray, 2007; Liebana et al., 2004). *Salmonella* Kentucky with resistance to multiple antimicrobials including ciprofloxacin is the latest clone to show rapid international dissemination (Le Hello et al., 2011). The group of strains that has been infecting international travellers has originated from poultry in the Middle East, Africa and Turkey. A strain with similar characteristics has recently been identified in turkeys from Poland (Wasyl and Hoszowski, in press), and it is possible that the multiply-antibiotic resistant epidemic stain of *S.* Kentucky is now causing infections in food animals in the EU. Strains of *Salmonella* with ciprofloxacin resistance and ESBL genes such as $bla_{\text{CTX-M}}$ genes are also important but do not so far appear to have caused large numbers of human infections in most European countries. The most common example in Europe involves certain strains of *S.* Paratyphi B var. Java, found in broilers in the Netherlands, Belgium and Germany (EFSA Panel on Biological Hazards, 2011b).

No monophasic *S.* 1,4,[5],12:i:- variants of *S.* Typhimurium were isolated in the turkey baseline surveys but such strains have increased dramatically in pigs in recent years (Hauser et al., 2010) and have also spread to some extent to cattle, companion animals and chickens (EFSA Panel on Biological Hazards, 2010b). In turkey meat in Germany, for years the serovars *S.* Saintpaul and *S.* 1,4,[5],12:i:-,

were dominant followed of *S.* Newport (Hartung and Käsbohrer, 2011). EU legislation has been redrafted to include these variant strains in targets and control actions, which should avoid this potentially epidemic organism becoming established in chicken and turkey breeding and limit its occurrence in commercial flocks.

Although various serovars appear to be relatively widespread in turkeys they do not normally cause any clinical disease, unlike the turkey-specific *S.* Arizonae strains which appear to be largely or completely eradicated from most EU countries, as well as being more effectively controlled in the USA. The lack of harmonised monitoring makes it difficult to assess whether there has been a recent emergence of serovars with a particular ability to spread within the turkey population and in many cases the common occurrence of certain serovars, e.g. *S.* Kottbus, was only identified by the baseline survey which included samples from smaller companies. It is clear that serovars such as Derby, Kottbus, Newport, Kedougou and Indiana are able to become resident within turkey companies (Papadopoulou et al., 2009) but are of limited public health importance. Contaminated feed is also an important source of *Salmonella* for turkeys (Davies, 2009; Davies and Wales, 2010). Thus the potential for the emergence of new strains, such as the multidrug-resistant *S.* Infantis which has arisen in Hungary, Israel and some other countries (Gal-Mor et al., 2010; Nogrady et al., 2008) is theoretically always present in a situation where mobile virulence and antimicrobial resistance genes and phage incursions may lead to the emergence of new strains with either reduced or enhanced epidemiological fitness (Litrup et al., 2010).

7.4. Increased virulence or resistance to relevant therapies for human salmonellosis

Some serovars of *Salmonella* have been associated with excess mortality and serious clinical disease in humans. These include *S.* Enteritidis, *S.* Typhimurium, *S.* Choleraesuis, *S.* Dublin, *S.* Virchow and *S.* Heidelberg (Helms et al., 2003; Wollin, 2007). When the epidemic strains of *S.* Enteritidis PT4 and *S.* Typhimurium DT104 first emerged in animals and humans, cases appeared to be more severe than previous strains in turkeys, broiler chickens and laying hens, causing significant mortality in some flocks (Davies, 2001) and what appeared to be more severe illness in people (Helms et al., 2003). Such strains became less common with time for a variety of reasons, some of which remain unknown and many strains of *S.* Enteritidis and *S.* Typhimurium now appear to be relatively avirulent or host-adapted (Rabsch et al., 2002).

For many years there has been concern about the regular use of preventive or therapeutic antimicrobial treatments in large scale poultry production (Singer and Hofacre, 2006). It has been postulated that antimicrobial resistance might be partly responsible for the emergence of certain strains with enhanced virulence but antimicrobial resistance is more common in turkey-associated *Salmonella* than in chicken-associated organisms (Nde and Logue, 2008; Nde et al., 2006). One factor which may be involved in this is the common occurrence of ideopathic turkey enteritis, a multifactorial condition that used to be partially controlled by the use of antimicrobial growth promoters which are now banned in the EU (Higgins et al., 2005; Jindal et al., 2009; Parks et al., 2001). Increased use of preventive therapeutic antimicrobials (e.g. chlortetracycline, spectinomycin, amoxycillin and enrofloxacin) that are similar to classes of antimicrobials used in human therapies, may have contributed to selection of resistant strains of *Salmonella* or mobilization of plasmids from other resistant intestinal organisms (Chander et al., 2008). Use of antimicrobials can also result in perturbation of protective intestinal flora thereby enhancing the colonization and persistence of *Salmonella* (Bauer-Garland et al., 2006; Sekirov et al., 2008). Eradication programmes for mycoplasma or *S.* Arizonae infection in breeding flocks have often involved treatment of flocks or eggs with antimicrobials such as fluoroquinolones or gentamicin are also likely to have assisted the dissemination of resistance genes and resistant *Salmonella* through the turkey industry (Ekperigin et al., 1983; Garmyn et al., 2009; Marien et al., 2007; Saif, 1972). Unfortunately the protective methods such as competitive exclusion have met with little favour (Primm et al., 1997). The response of different serovars to antimicrobial exposure is quite variable, with some serovars remaining sensitive whilst others from the same treated flocks are resistant (Davies et al., 1999; Jones et al., 2002). Stable resistance patterns can therefore be useful

markers for epidemiological tracking and source attribution (Nayak and Kenney, 2002; Santos et al., 2007).

Two of the most important antimicrobial classes for treatment of human salmonellosis are fluoroquinolones, such as ciprofloxacin and extended spectrum cephalosporins such as ceftriaxone. The dramatic emergence of isolates with reduced susceptibility to fluoroquinolones in turkeys occurred rapidly during the 1990s in several countries, and predominantly involved *S.* Typhimurium DT104 (Allen and Poppe, 2002a, 2002b; Davies et al., 1999; Malorny et al., 2003; Piddock et al., 1998). The occurrence of such resistance may have been underestimated because of the high test cut off values used to define resistance in some countries (Aarestrup et al., 2010).

Resistance to extended spectrum cephalosporins in *Salmonella* has emerged more recently, predominantly in the USA and Canada initially (Gray et al., 2004; Poppe et al., 2006; Poppe et al., 2005; Salmon and Watts, 2000; Sjolund-Karlsson et al., 2010; Taylor et al., 2008). These strains typically possess the $bla_{\text{CMY-2}}$ resistance gene on a transferable multidrug resistance plasmid that can move between different *Salmonella* serovars and *E. coli* or other commensal flora (Allen and Poppe, 2002a). $bla_{\text{CTX-M}}$ and other enzymatic resistance mechanisms can also occasionally be found in *Salmonella* from poultry (Leverstein-van Hall et al., 2011; Weill et al., 2004). The origin of these strains uncertain, but the practice of injecting ceftiofur into hatching eggs to prevent bacterial contamination of eggs that have been vaccinated using in-ovo viral vaccines or to protect parent breeding chicks, layer chicks and broiler chicks against infections of hatchery origin has been associated with emergence of resistant *S.* Heidelberg and *E. coli* in broiler chickens and humans in Canada (Dutil et al., 2010). Similar isolates have been observed after the routine hatchery treatment of chicks by injection or spray in the Netherlands, France and the Far East (Cloeckaert et al., 2010; Dierikx et al., 2010; Ho et al., 2011) and a low prevalence has also been identified in the UK, despite lack of evidence of use of cephalosporins in turkeys (Randall et al., 2011). Recently there has been a very large outbreak of *S.* Heidelberg in the USA that involved a highly multiple resistant strain and was associated with ground turkey meat[32] and monophasic *S.* 1,4,[5],12:i:- variants of *S.* Typhimurium have been increasingly reported from German turkey flocks and people (EFSA and ECDC, 2012).

Multiple antimicrobial resistant *Salmonella* can be found in retail turkey meat more commonly than in broiler meat (Little et al., 2008; Logue et al., 2003; Miranda et al., 2008) so it is important to adequately monitor resistance trends across the EU and to intervene appropriately (EFSA, 2008d).

8. Estimating the public health impact of *Salmonella* in turkey production

8.1. Source attribution methods

A variety of methods to estimate the relative contribution of food-animal sources to human foodborne disease has been developed, including the microbial subtyping approach, comparative exposure assessment, epidemiological analyses of sporadic cases, analysis of data from outbreak investigations, and expert elicitations (EFSA, 2008e; Pires et al., 2009). Each of these general methods presents advantages and limitations, and the usefulness of each depends on the public health questions being addressed. Additionally, methods have different data requirements and attribute human illness at different points of the farm-to-consumption chain (production or exposure), and therefore their utility will vary depending on the hazard and/or the country or region in question.

Several of the approaches have been applied for *Salmonella* source attribution and published in a variety of European countries. Examples include application of the subtyping approach (Hald et al., 2004; Pires and Hald, 2010; Pires et al., 2008; Valkenburgh et al., 2007; Wahlstrom et al., 2010); analyses of data from outbreak investigations in Europe (Pires et al., 2011; Pires and Hald, 2010); a global meta-analysis of case-control studies of sporadic infections (Domingues et al., in press); and an expert elicitation study (Havelaar et al., 2008). The different models attributed human salmonellosis to different food categories or animal sources, depending among other on data availability.

[32] CDC (2011) www.cdc.gov/salmonella/heidelberg/081111/index.html - accessed 2.10.11.

8.1.1. Source attribution using microbial subtyping

The microbial subtyping approach is routinely applied in Denmark to estimate the relative contribution of domestic and imported food-animal sources for human salmonellosis. The proportion of cases acquired abroad is also estimated, as is the proportion of disease that cannot be attributed to any of the sources for which data are available. Results from 2010 showed that domestically produced pork was the most important source of disease in the country (15 %, including outbreak-related cases), followed by imported pork (5 %), imported beef (2 %) and table eggs (2 %) (Table 10). Nearly half of the reported *Salmonella* infections (47 %) were estimated to be acquired during international travel. Denmark has no commercial production of turkey meat meaning that all turkey meat is imported. In 2010, the attribution estimate for imported turkey meat was 1 % (DTU Food, 2011).

A similar model was applied to *Salmonella* data from Sweden, results revealing that over 80 % of the *Salmonella* cases were acquired abroad and that domestic food-producing animals were responsible for less than 1 % of the reported infections (Table 10) (Wahlstrom et al., 2010).

Recently, the microbial subtyping approach was adapted to accommodate *Salmonella* surveillance data from the EU in a model that utilized data provided by the European Center for Disease Control (ECDC) and EFSA (Pires et al., 2011). This model referred to before as EU-SSA was applied to data from 24 MSs and attributed human sporadic salmonellosis to four animal reservoirs: pigs, broilers, layers and turkeys. The model also considered trade of food between the MSs. The attribution estimates presented below for each country and region includes both domestically produced and imported (from other EU MSs) food. Results showed that the relative contribution of food-animal sources varied between regions and countries (Table 10). The laying hen reservoir was estimated to be the most important source in the EU, contributing with 43.8 % (95 % Credibility Interval (CI) 43.2-44.4 %) of cases, followed by pigs (26.9 %, 95 % CI 26.3-27.6 %). Turkeys (4.0 %, 95 % CI 3.8-4.3 %) and broilers (3.4 %, 95 % CI 3.1-3.7 %) were estimated to be less important sources of *Salmonella*. Around 9 % of all salmonellosis cases were reported as being travel-related. However, travel information was unknown or incomplete in many MSs. 3.6 % of cases were reported as being part of outbreaks with unknown source. Nine percent of cases could not be attributed to any source included in the model.

The microbial subtyping approach was also used to provide a quantitative estimate of the public health impact of setting a new target for the reduction of *Salmonella* in broilers. In this case, the model, referred to as BT-SAM (EFSA Panel on Biological Hazards, 2011a; Vose et al., 2011), used data from 22 MSs and 23 *Salmonella* serovars. This BT-SAM model estimated that 65 % (95 % CI 63-67 %), 28 % (95 % CI 27-30 %), 4.5 % (95 % CI 4-5 %) and 2.4 % (95% CI 1.8-3.4 %), of the human salmonellosis cases are attributable to laying hens (eggs), pigs, turkeys and broilers, respectively.

Table 10: Proportion of disease (%) attributable to animal-food sources, travel and outbreaks in Denmark, Sweden and the EU estimated by a microbial subtyping approach (Pires et al., 2011).

	Denmark[a]	**Sweden**[b]	**EU**[c]	**Eastern EU**[c]	**Northern EU**[c]	**Southern EU**[c]	**Western EU**[c]
Pigs	15.1	0.08	29.6	22.7	10.6	34.1	43.6
Cattle	0.8	0.1	-[d]	-[d]	-[d]	-[d]	-[d]
Layers	1.8	0.16	48.1	59.4	30	41.8	28.4
Broilers	0.5	0.09	3.7	7.0	1.2	2.1	3.1
Ducks	0.1	-[d]	-[d]	-[d]	-[d]	-[d]	-[d]
Turkeys	1.0[e]	-[d]	4.4	2.2	7.4	4.1	7.6
Imported pork	5.4	-[d]	-[d]	-[d]	-[d]	-[d]	-[d]
Imported beef	1.9	-[d]	-[d]	-[d]	-[d]	-[d]	-[d]
Wildlife	-[d]	0.6	-[d]	-[d]	-[d]	-[d]	-[d]
Travel	46.9	82	10.2	0.8	34.5	4.8	0.7
Outbreaks, source unknown	5.1	2.9	3.9	5.4	4.0	2.2	4.2
Unknown	19.7	7.7	9.0	2.5	12.4	10.9	12.5

[a] Data from 2010.
[b] Data from 2004-2006.
[c] Data from 2007-2009. EU regions as defined by the United Nations. Eastern Europe: Czech Republic, Hungary, Poland and Slovakia. Northern Europe: Denmark, Estonia, Finland, Ireland, Latvia, Lithuania, Sweden and the United Kingdom. Southern Europe: Cyprus, Greece, Italy, Portugal, Slovenia, Spain. Western Europe: Austria, Belgium, France, Germany, Luxembourg and the Netherlands.
[d] -: Source not included in the model.
[e] Imported turkey meat only.

The relative importance of sources varied between countries (Figure 5) and EU region (Table 10), probably reflecting true differences in the epidemiology of *Salmonella*, in the occurrence of *Salmonella* in the food-animal sources, in food consumption patterns, and potentially differences in the efficiency of surveillance systems and data availability. For the regional analysis, the laying hen reservoir was the most important source in Northern, Eastern and Southern Europe, with between 30 % and 59 % of the *Salmonella* reported cases attributed to this source, whereas pigs were the major source of salmonellosis in Western Europe, contributing 44 % of the human cases. Turkeys and broilers contributed with varying but lower proportions of reported cases. A large proportion of the reported *Salmonella* infections in Northern European countries were ascribed to travel abroad.

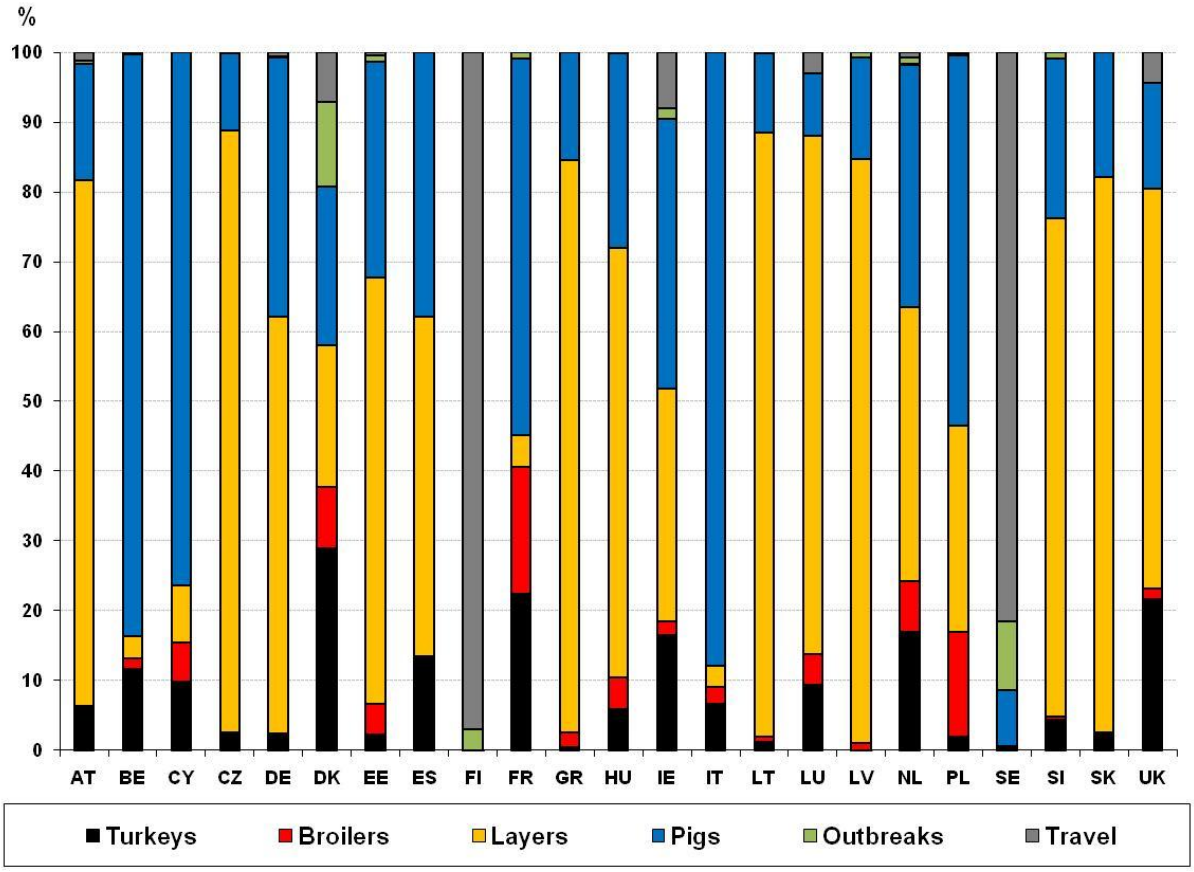


Figure 5: Proportion of *Salmonella* human cases attributed to food animal reservoirs, travel and outbreaks in 24 EU MSs, 2007-2009 (median %) (Pires et al., 2011).

The contribution of turkeys represented around 1 % of the total reported *Salmonella* cases in Denmark and 4.4 % in EU countries in general (Table 10). The analysis by EU region indicated that the proportion of disease attributed to turkeys was higher in Northern and Western Europe (around 7.5 %).

8.1.2. Source attribution using outbreak data

An analysis of data from outbreak investigations included data from 27 MSs, Norway and Switzerland and attributed salmonellosis to 19 food sources and water in the period between 2007 and 2009 (Pires et al., 2011). Eggs were estimated to be the most important source of disease in the study period, followed by pork, chicken, the broader categories 'meat' and 'poultry', and dairy products. An analysis by year showed that the contribution of eggs decreased in 2009, and the proportion of disease attributed to remaining sources varied over the years and between regions. In the overall study period, eggs were estimated to be the most important source of salmonellosis in all regions, source attribution estimates being higher in Eastern Europe (76 %) and Southern Europe (60 %). Pork followed in importance in Western Europe (10 %), whereas vegetables were estimated to be a major contributor for salmonellosis in Northern Europe (9 %). Chicken and dairy products revealed to be of importance in all regions. The proportion of *Salmonella* outbreaks attributed to an unknown source varied substantially between regions (Table 11).

Table 11: Proportion (%) of *Salmonella* outbreaks attributed to food sources in the EU by region, 2007-2009 (median value) (Pires et al., 2011)

	Eastern EU	Northern EU	Southern EU	Western EU
Eggs	76.18	19.7	59.86	35.6
Dairy	2.4	3.46	1.15	2.27
Goat milk	0	0	0	0
Meat	1.55	1.49	1.66	2.47
Poultry	0	0	11.08	0.19
Chicken	3.65	5.78	1.66	2.28
Ducks	0	0	0	0
Turkey	**0.27**	**0.75**	**0**	**0.39**
Beef	0.63	0.1	0.28	0.84
Pork	2.18	6.92	0	9.54
Lamb	0.02	0	0	0.19
Mutton	0	0	0	0
Game	0	0	0	0
Fruits and nuts	0.002	0.75	0	0.25
Vegetables	0.47	9.1	1.08	1.19
Grains and beans	1.21	0.49	0.35	0.41
Oils and sugar	1.53	0.13	0.1	0.38
Seafood	0.25	0.58	3.11	1.28
Water	0	0	0.83	0
Unknown	9.63	50.75	18.84	42.72

The estimated relative contribution of turkey for salmonellosis was below 1 %, but in Southern EU potential turkey associated outbreaks may have been reported as poultry related.

A comparison of the results of the microbial subtyping approach and the analysis of outbreak data conducted for EU regions in the same time period (from 2007 and 2009) revealed discrepancies in the contribution of the sources common to both models in each region (Figure 6). Differences varied between regions, being less relevant in Northern EU and particularly evident in Southern EU. The contribution of layers/eggs for salmonellosis, the most important source in all regions, was in agreement in all regions, whereas discrepancies were more substantial for other sources, particularly pigs/pork.

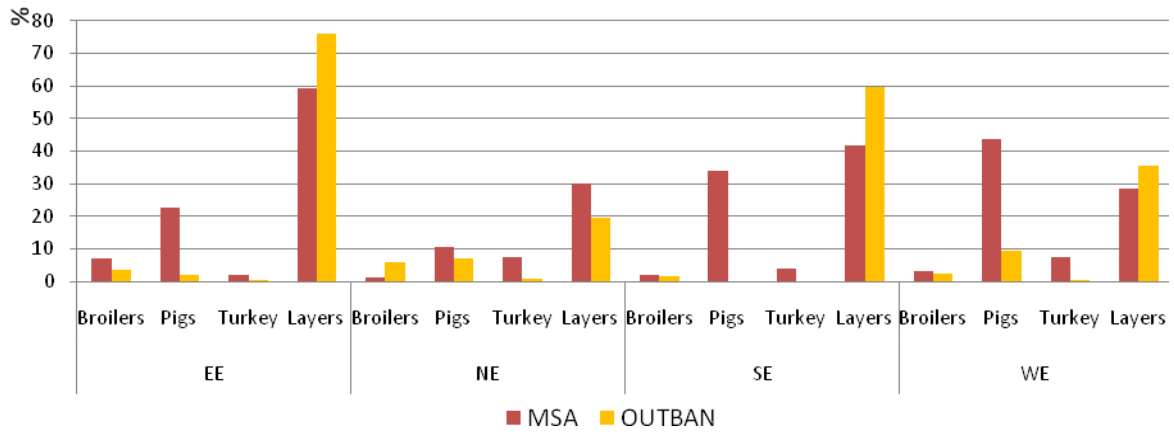


Figure 6: Comparison of *Salmonella* source attribution estimates in EU regions obtained by the microbial subtyping approach (MSA) and the analysis of outbreak data (OUTBAN), 2007-2009 (Pires et al., 2011).

It is emphasized that the two approaches have different data requirements and attribute human cases at different points of the farm-to-consumption chain. The microbial subtyping approach requires *Salmonella* prevalence data from the production level (i.e. farm or slaughter), and thus attribute human cases to the reservoir level, while an analysis of data from outbreak investigation uses data from the exposure level (i.e. the foods, at the point of consumption, that caused the reported outbreaks), and thus estimate the relative importance of food categories for human salmonellosis. In addition, the same methods applied in different countries often includes a different set of food-animal sources, depending on data availability, and utilizes data with varied degrees of representativeness or quality. As a consequence, comparisons of methods and results should be made with care.

8.2. Methodological approaches

8.2.1. Model choice

In order to answer the questions put forward by the Commission in the Terms of References, the chosen modelling approach would have to be able to:

- estimate the relative (or absolute) contribution of the turkey reservoir to the burden of human salmonellosis in EU, and
- distinguish between the recognised, but uncertain, differences between the various serovars in their ability to cause human disease.

In addition, the modelling approach needed to include the prevalence observed during monitoring in the MSs as an explanatory variable. The human health impact as a consequence of a change in this value should be the main outcome of the model.

The principles, advantages and limitations of both the 'traditional' farm-to-consumption risk assessment modelling and the Bayesian microbial subtyping approach have been discussed thoroughly before (EFSA Panel on Biological Hazards, 2011a). The advantages of the Bayesian microbial subtyping approach to answer such Terms of References when compared to the farm-to-consumption modelling approach are described in EFSA Panel on Biological Hazards (2011a) and Vose et al. (2011).

As described in the introduction of this Scientific Opinion, EFSA launched a negotiated procedure for the provision of source-attribution modelling work in order to support the estimation of the quantitative aspects inherent to the request made by the European Commission. Out of this negotiated procedure and following EFSA outsourcing procedures, a contractor who met the technical and

administrative criteria of the call was selected. The report of the contractor (Hald et al., 2012) must be read together with this Scientific Opinion.

The model is based on the Bayesian approach using microbial subtyping data described above, but with MSs added to the model as a third dimension. The contractor adapted the modelling approach of the Broiler Target *Salmonella* Attribution Model or BT-SAM (used for the Opinion on *Salmonella* in broilers (EFSA Panel on Biological Hazards, 2011a)) and the EU-*Salmonella* Source Attribution or EU-SSA, in order to provide updated results concerning turkeys. As mentioned before, the model is referred to as Turkey Target *Salmonella* Attribution Model or TT-SAM.

8.2.2. Data choice

The following are the key types of data employed for building the TT-SAM model:

- Reported cases of human salmonellosis in the EU by MSs and the related serovar distribution for both sporadic cases and outbreak data (TESSy[33] data supplied by ECDC[34] and outbreak[35] data from the EU Summary Reports supplied by the EFSA Unit on Biological Monitoring) in 2010. The total number of reported cases includes sporadic, travel and outbreak-related infections. To estimate the number of sporadic cases, the number of outbreak-related cases per serovar and country were substracted from the total number of domestically acquired cases. The true number of cases was calculated using underreporting factors estimated for 2009 (EFSA Panel on Biological Hazards, 2011a).
- Data from EUROSTAT on production, import and export data of different animal-related foodstuffs were used to calculate an approximation for the consumption of the different types of food with different origin for each MS in 2010. The amount available for consumption was calculated by [production-export+import] for each MS. The amount available for consumption produced in a MS was calculated by [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. 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.
- Occurrence of *Salmonella* in food-producing animal populations. For fattening turkey flocks, broiler flocks, and laying hen flocks, this information was obtained as reported through the European Union Community Summary Report and kindly supplied by the EFSA Unit on Biological Monitoring (EFSA and ECDC, 2012). For slaughter pigs, this information was obtained through the EU baseline survey (EFSA, 2008a). For the serovar distributions, the selection criteria are shown in Table 12.

Only sparse data on *Salmonella* occurrence including distributions of serovars in cattle herds, beef products or dairy products are available from MSs according to the Community Summary Reports. For this reason, data from the cattle reservoir were not included in the model. The consequence of the omission of the cattle reservoir may have on the model results is discussed later. *Salmonella* spp. has been isolated in other animal species throughout the EU under different sampling schemes. These animal species include both food production animals (e.g. poultry species other than chickens and turkeys, sheep, goats and solipeds) and pets (e.g. cats, dogs, reptiles). However, only sparse data is available from MSs on their occurrence and on the serovars encountered.

[33] 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.

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

[35] EFSA, Release 1 on 11/10/2011 and updated on 18/01/2012. Validation of data based on draft Tables of 30/01/2012 to be included in draft EU SR.

Table 12: Selection criteria for serovar distribution data

	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.

The above datasets chosen for the model are assessed as currently being those providing the best comparability between MSs due to harmonised baseline surveys as well as monitoring programme thereby ensuring the most accurate and robust model. The model included data from 25 MSs, four animal-food sources (broilers, laying hens, pigs and turkeys) and 23 individual serovars as listed in Table 15. The 23 serovars were selected based on their presence and importance in humans and in each of the four animal-food sources. 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:- in *S.* Typhimurium based on the conclusions from a recent Scientific Opinion (EFSA Panel on Biological Hazards, 2010b) and based on the fact that some countries report the monophasic variants as *S.* Typhimurium making a clear distinction impossible.

The results of the TT-SAM model are then compared with the results of the model ran under different scenarios as described in the following section.

9. Risk assessment results

In order to provide source-attribution estimates that would serve for underlining the answer to the ToRs made by the Commission, the results of the baseline TT-SAM model were compared with results under following scenarios:

- **Baseline.** The actual prevalence of all *Salmonella* serovars as reported by the MSs in 2010 (see Table 6). 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 12 for turkey flocks);
- **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 serovars in humans in 2010 (i.e. *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Newport, S. Kentucky) = 1 % or less;
- **Scenario 6.** The prevalence of the top-6 serovars in turkeys that contribute most to human cases (i.e. *S.* Enteritidis, S. Kentucky, *S.* Typhimurium, *S.* Newport, *S.* Virchow, *S.* Saintpaul) (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.* Hadar, *S.* Infantis and *S.* Virchow) = 1 % or less.

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 % in any MS.

9.1. Estimates of the public health impact of different *Salmonella* flock prevalence values in turkey production

9.1.1. Results Employing the 'Turkey-Target *Salmonella* Attribution Model' (TT-SAM)

The model included the following 25 MSs: Austria, Belgium, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden, the Netherlands and the United Kingdom. Two MSs were excluded from the analysis because of lack of sufficient data: Bulgaria and Malta. The estimated changes to human incidence rates therefore only apply to the MSs included in the model.

Key results of the TT-SAM model are presented in Tables 13, 14 and 15. Further detailed results can be found in the report by the contractor (Hald et al., 2012).

Table 13: Estimated number and percent (%) of human salmonellosis cases in EU attributable to the four main animal reservoirs included in the baseline model (Hald et al., 2012)

	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.

Table 14: Relative risk of human salmonellosis in EU per kg meat/eggs eaten attributable to the four main animal reservoirs included in the baseline model (Hald et al., 2012)

	Pigs	**Broilers**	**Laying hens/ shell eggs**	**Turkeys**
Available for consumption (× 1 000 tonnes)	24 505	10 508	6 968	2 061
Cases per tonne	0.127	0.053	0.133	0.066
Risk relative to turkey meat[a]	1.93	0.81	2.03	1.00

[a] The risk ratios can be interpreted as the risk of salmonellosis for the individual consumer when consuming e.g. 100 grams of eggs is 2 times higher than when eating 100 grams of turkey meat.

Table 15: Estimated number of human salmonellosis cases by the serovars included in the model and originating from the turkey reservoir (baseline model) (Hald et al., 2012)

Serovar	mean	median	2.5 %	97.5 %	% of total
S. Enteritidis	29 770	25 010	10 240	77 140	22.0 %
S. Kentucky	22 970	20 640	10 290	49 500	17.0 %
S. Typhimurium	20 010	16 060	6 180	57 880	14.8 %
S. Newport	10 030	8 823	4 319	22 900	7.4 %
S. Virchow	9 110	7 380	3 038	25 640	6.7 %
S. Saintpaul	8 439	7 700	4 028	17 390	6.2 %
S. Infantis	7 274	6 263	2 875	17 660	5.4 %
S. Hadar	6 820	6 090	2 915	14 980	5.0 %
S. Bredeney	4 924	4 444	2 142	10 520	3.6 %
S. Agona	2 923	2 262	777	9 109	2.2 %
S. Kottbus	2 907	2 367	993	8 090	2.2 %
S. Derby	2 445	1 992	769	6 839	1.8 %
S. Mbandaka	2 046	1 512	399	6 896	1.5 %
S. Senftenberg	1 437	1 053	271	4 914	1.1 %
S. Bovismorbificans	1 157	992	407	2 899	0.9 %
S. Heidelberg	1 095	980	458	2 399	0.8 %
S. Montevideo	850	634	187	2 829	0.6 %
S. London	317	238	64	1 024	0.2 %
S. Livingstone	307	223	52	1 062	0.2 %
S. Anatum	143	108	32	457	0.1 %
S. Brandenburg	112	82	19	388	0.1 %
S. Rissen	39	29	7	135	0.0 %
S. Braenderup	0	0	0	0	0.0 %
Total	135 100				100 %

The results indicate that:

- The estimated number of all human salmonellosis cases (i.e. estimated true number of cases when accounting for underreporting) in the EU in 2010 was 5.4 million (95 % CI: 3.0-9.5), a 13 % decrease compared to 2009.
- 2.6 % (95 % CI: 1.2-5.2) of all human salmonellosis cases in the EU were attributed to turkeys. This is estimated to correspond to around 135 100 (95 % CI: 60 790-293 600) human cases in 2010.
- Approximately 63.2 % 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 causing human infections from turkeys.
- *Salmonella* Enteritidis, *S.* Kentucky and *S.* Typhimurium constituted 22.0 %, 17.0 % and 14.8 % of all turkey-associated cases respectively. *Salmonella* Newport, *S.* Virchow and *S.* Saintpaul constituted individually between 6 % and 8 % of all turkey-associated cases. Other serovars constituted less than 6 % on an individual basis.

- Four serovars (*S.* Kentucky, *S.* Saintpaul, *S.* Senftenberg and *S.* Kottbus) had turkeys as the most important reservoir for human infections, although the occurrence of these serovars in turkeys was limited to a minor number of MSs (4-10 MSs).

- For the other *Salmonella* sources included, the model estimated that 17.0 % (95 % CI: 11.3-24.0), 56.8 % (95 % CI: 48.2-65.8) and 10.6 % (95 % CI: 5.1-18.3) of human salmonellosis cases could be attributed to laying hens (eggs), pigs and broilers, respectively. Around 13 % of human cases could not be attributed to any of the included source. A proportion of these were reported as known travel-related.

- The model estimated that per tonne of food available for consumption, table eggs were associated with the highest risk (0.13 cases per tonne) closely followed by the risk associated with pig meat whereas the risks associated with broiler and turkey meat were similar and were approximately two-fold lower (0.05 and 0.07 cases per tonne, respectively).

- According to the results of the model, the majority of the *S.* Typhimurium human cases were attributed to the pig reservoir. Pigs appeared to be the most important reservoir of *S.* Enteritidis cases, but the laying hen/shell eggs and broiler reservoirs contributed significantly.

- These conclusions are based on analysis of retrospective data, and as the *Salmonella* situation in the EU is dynamic- the foodstuff associated risks and which serovars are important. Therefore, it is important to review the model and its conclusions as new information emerge. An example of this is the diminished importance of poultry meat and eggs as a source of *Salmonella* and the apparent emergence of pork as a *Salmonella* source.

9.1.2. Results of the scenario analyses

Tables 16 and 17 provide the overall summary statistics for each output and scenario. The mean represents the average, or 'centre of gravity', of the uncertainty distribution. The percentiles (2.5 and 97.5) represent the low and high values across the range estimated by the model.

Table 16: Estimated number and percentage (%) of human salmonellosis cases in EU originating from the turkey reservoir under the different scenarios (Hald et al., 2012)

	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 17: Estimated reduction in the number and percentage (%) of human salmonellosis cases in EU originating from the turkey reservoir when compared to the baseline model under the different scenarios (Hald et al., 2012)

	Number of cases[a] from turkey reservoir				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.

The following key scenarios addressing the terms of reference requested by the Commission address that:

- The scenario (scenario 1) where the achievement of the current transitional target of the EU control programme of *Salmonella* in fattening turkey 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 per the 2010 reporting in turkey flocks) results in an estimated reduction in the number of turkey-associated human salmonellosis cases of 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) out of the 5.4 million human salmonellosis true cases.

- The scenario (scenario 2) where the prevalence of *S.* Enteritidis being 1 % or less and the prevalence of *S.* Typhimurium equals 0 (and keeping the prevalence for the other 21 serovars as per the 2010 reporting in turkey flocks) results in an estimated reduction in the number of turkey-associated human salmonellosis cases of 14.0 % (95 % CI: 7.5-21.8) compared to the situation in 2010. In absolute numbers, this corresponds to an estimated reduction of 20 010 (95 % CI: 6 180-57 880) out of the 5.4 million human salmonellosis true cases.

- The scenario (scenario 3) where the prevalence of *S.* Enteritidis equals 0 and the prevalence of *S.* Typhimurium being 1 % or less (and keeping the prevalence for the other 21 serovars as per the 2010 reporting in turkey flocks) results in an estimated reduction in the number of turkey-associated human salmonellosis cases of 21.6 % (95 % CI: 13.6-28.4) compared to the situation in 2010. In absolute numbers, this corresponds to an estimated reduction of 30 360 (95 % CI: 10 530-78 410) out of the 5.4 million human salmonellosis true cases.

- The scenario (scenario 4) where an EU-wide target is of maximum of 1 % of fattening turkey flocks remaining positive for all the *Salmonella* serovars considered in the model would be met results in an estimated reduction in the number of turkey-associated human salmonellosis cases of 83.2 % (95 % CI: 79.0-87.4) equivalent to 2.0 % of all human cases compared to the situation in 2010. In absolute numbers, this corresponds to an estimated reduction of around 112 300 (95 % CI: 50 410-243 400) out of the 5.4 million human salmonellosis true cases.

- The scenario (scenario 5) where an EU-wide target is of maximum of 1 % of fattening turkey flocks remaining positive for the top-5 *Salmonella* serovars in humans in 2010 (*S.* Enteritidis,

S. Typhimurium, *S.* Infantis, *S.* Newport, S. Kentucky) would be met results in an estimated reduction in the number of turkey-associated human salmonellosis cases of 29.6 % (95 % CI: 13.0-44.8) compared to the situation in 2010. In absolute numbers, this corresponds to an estimated reduction of around 37 870 (95 % CI: 17 570-78 780) out of the 5.4 million human salmonellosis true cases.

- The scenario (scenario 6) where an EU-wide target is of maximum of 1 % of fattening turkey flocks remaining positive for the top-6 *Salmonella* serovars in turkeys that contribute most to human cases (*S.* Enteritidis, S. Kentucky, *S.* Typhimurium, *S.* Newport, *S.* Virchow, *S.* Saintpaul) would be met results in an estimated reduction in the number of turkey-associated human salmonellosis cases of 37.2 % (95 % CI: 19.2-54.0) compared to the situation in 2010. In absolute numbers, this corresponds to an estimated reduction of around 48 110 (95 % CI: 22 580-100 500) out of the 5.4 million human salmonellosis true cases.

- The scenario (scenario 7) where an EU-wide target is of maximum of 1 % of fattening turkey flocks remaining positive for the *Gallus gallus* breeder flocks regulated serovars (*S.* Enteritidis, *S.* Typhimurium, *S.* Hadar, *S.* Infantis and *S.* Virchow) would be met results in an estimated reduction in the number of turkey-associated human salmonellosis cases of 18.1 % (95 % CI: 9.4-28.4) compared to the situation in 2010. In absolute numbers, this corresponds to an estimated reduction of around 23 740 (95 % CI: 10 070-52 980) out of the 5.4 million human salmonellosis true cases.

It should be noted that the individual Member States' contributions to the estimated reductions vary greatly.

To conclude, the scenario analyses suggest that Scenario 4, i.e. reducing the prevalence of all serovars to 1 % or less, would result in the largest reduction in human salmonellosis cases. Scenario 1, i.e. achieving the transitional target in all MSs, would result in the smallest reduction in human cases as in 2010 all MSs except one had already met this target. Scenario 5, i.e. reducing the prevalence of the top-5 serovars in humans to 1 % or less is in between these groups and is somewhat lower compared to scenario 6, i.e. reducing the prevalence of the top-6 serovars in turkeys that contribute most to human cases to 1 % or less. Scenario 7, i.e. reducing the prevalence of the *Gallus gallus* breeding hen regulated serovars to 1 % or less would lead to a reduction of turkey-associated human salmonellosis cases in between that of Scenario 1 and Scenario 6.

9.2. Model validation, assumptions and data uncertainty

The TT-SAM model used to attribute human salmonellosis cases to food-animal reservoirs in the EU implies a number of assumptions, which are fully documented in relation to data availability and data quality in the contractor's report (Hald et al., 2012). In particular, the results of the model should be interpreted with the following aspects in mind:

- The model only included turkeys, pigs, laying hens and broilers as putative reservoirs. Some *Salmonella* reservoirs (e.g. cattle, other poultry, companion animals, reptiles) were not included in the model due to lack of data. It is therefore likely that the contribution of the human salmonellosis cases allocated to the animal reservoirs included in the model have been overestimated. In particular, *S.* Typhimurium has mainly been attributed to the pig reservoir whereas most likely, a considerable number of cases is actually related to the cattle reservoir.

- The model includes prevalence and serovar distribution data for turkeys, broilers and laying hens from EU harmonised monitoring data in 2010. For pigs, such data were not available and data from the baseline survey (dating back to 2006/7) were used instead. As the epidemiology of *Salmonella* in food animals is rapidly evolving, this may have resulted in inaccuracies in the attribution to the pig reservoir.

- Data on travel-and outbreak-related cases were available to a variable degree in EU MSs and this may have resulted in increased attribution of particular serovars (such as *S.* Enteritidis) to indigenous food-animal sources.

- A previously developed approach to correct for variable rates of under-ascertainment and underreporting of human salmonellosis cases was employed in the TT-SAM. This approach assumes that the incidence rates among Swedish travellers returning from a particular country are predictive of the incidence rate of the local residents.

- Subtyping data (in particular phage typing data for the common serovars *S.* Enteritidis and *S.* Typhimurium) were available to a variable extent. This may have resulted in inaccurate attribution of human cases to food-animal reservoirs.

- Trade data were not available from one single source and at the same step in the food chain. This may have led to inaccurate attribution results, e.g. overestimation of the contribution of the pig reservoir.

The model was validated by comparing the estimated number of human cases of salmonellosis by MS with the observed number of human cases. For most MSs, the goodness of fit was acceptable. However, for two countries with poor data availability or quality, a poor fit was observed. Running the baseline model without these two countries, the results were similar to those of the baseline model.

Compared to other attribution studies at EU-level (BT-SAM (Vose et al., 2011) and EU-SSA (Pires et al., 2011)), the TT-SAM model attributed a relatively high proportion of human salmonellosis cases to the pig reservoir. Partly, this can be explained by the data quality issues described above. Furthermore, the total number of human salmonellosis cases in the EU has continuously decreased from 2006 onwards with a particular decrease in *S.* Enteritidis cases (EFSA and ECDC, 2012). This is explained by risk management interventions in the breeding and laying hen and broiler populations. As a consequence, the relative importance of other serovars and their reservoirs becomes more important. Nevertheless, an increase in the absolute number of *S.* Typhimurium (typically attributed to the pig and cattle reservoirs) cases is also observed, and is partly related to the emergence of monophasic variants (1,4,[5],12:i:-).

CONCLUSIONS AND RECOMMENDATIONS

CONCLUSIONS

General Conclusions

- In the EU, the overall reported incidence of human salmonellosis decreased from 2006 to 2010 in particular because of a downward trend in *Salmonella* Enteritidis infections presumably due to improved monitoring and control in breeding and laying hens in many MSs.

- In contrast, the absolute reported incidence of human *Salmonella* Typhimurium infections (including the monophasic variant 1,4,[5],12:i:-) has increased indicating that one or more sources of these infections are increasing in importance.

- It is estimated that in 2010 there were approximately 5.4 (95 % CI: 3.0-9.5) million true cases of human salmonellosis in the EU27, a 13 % decrease compared to 2009.

- Turkey production in the EU is concentrated in a few MSs. In 2009, five countries (Germany, France, Italy, the UK and Hungary) produced 84.6 % of all EU turkey meat. Only a small number of companies in a limited number of MSs are involved in the turkey primary breeding sector (in 2006/7 only 6 MSs had more than 10 flocks of breeding turkeys. Also the consumption of turkey meat varies strongly between MSs, with the percentage of consumers ranging from 0.2 % to 47.9 %.

- With few exceptions, higher prevalences of *Salmonella* spp. and *S.* Enteritidis and/or *S.* Typhimurium were observed in the baseline survey than through the statutory monitoring, both in breeding and in fattening turkeys. This is attributable to the application of control measures in the period between the two sampling schemes, as well as to the different sensitivity of sampling and testing schemes applied.

- Monitoring of turkey breeding flocks in the EU specifies minimum requirements which allow various sampling options, mostly with undefined detection sensitivity and specificity. This complicates the calculation of prevalence.

Answers to the terms of Reference

TOR 1: To indicate and rank the *Salmonella* serotypes with public health significance according to Annex III of Regulation (EC) No 2160/2003

- In the EU, *S.* Enteritidis and *S.* Typhimurium (including the monophasic variant 1,4,[5],12:i:-) were the two most commonly reported serovars in cases of human infection in 2010, representing 69 %, of the cases where the isolate was serotyped. Other serovars constituted less than 2 % on an individual basis.

- The *Salmonella* serovars found in the EU baseline survey in fattening turkey flocks in 2006/7 showed little similarity with those from humans -the 'top 5' in turkey flocks being *S.* Bredeney, *S.* Hadar, *S.* Saintpaul, *S.* Derby and *S.* Kottbus, none of which were among the 'top 5' in humans in the period 2007-2010.

- There was a similar minimal concordance between the predominant *Salmonella* serovars in humans in 2010 and those reported from harmonised monitoring programmes in turkey flocks in 2010.

- Of the two serovars in the transitional target (*S.* Enteritidis and *S.* Typhimurium), only *S.* Typhimurium was found in five breeding flocks of turkeys in two MSs in the harmonised monitoring of 2010.

- In turkeys data about the dissemination of the monophasic variant 1,4,[5],12:i:- of *S.* Typhimurium are still sparse since it is not yet formally included in specific legislation in primary production, but in the 2010 monitoring it was isolated both in breeding and in fattening turkey flocks.

- *Salmonella* Kentucky strains with resistance to multiple antimicrobials, including ciprofloxacin and third generation cephalosporins, are becoming more important in humans and has been found in turkeys in some EU countries.

TOR 2: 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

- The most frequently isolated serovars from breeding and fattening turkey flocks in the baseline survey appear to be similar for some MSs. Nine of the twelve serovars isolated in breeding flocks were amongst the most frequently isolated in fattening flocks. Analysing results from the 2010 monitoring, it appears that five serovars were found both in breeders and in fattening flocks, one was present only in breeders, whereas 16 were found in fattening flocks but not in breeding flocks of turkeys.

- Although no quantification is currently possible, vertical transmission and hatchery acquired infection appear as most important sources for *Salmonella* infection in fattening turkeys. Controlling the infection in breeders is necessary, but not sufficient to control *Salmonella* in flocks of fattening turkeys.

- *Salmonella* detection in breeding flocks of turkeys may be difficult due to low within-flock prevalence, intermittent excretion and clustering of infection resulting from distribution of birds in multiple small pens.

- When hatchery monitoring is carried out it is not always possible to intervene in a timely way in order to stop distribution of infected poults. It may also be difficult to attribute positive samples to individual breeding flocks (or to the hatchery resident flora) without additional confirmatory sampling at the holding, which is not compulsory in the case of non-regulated serovars.

TOR 3: To assess the relative public health impact if a new target for reduction of *Salmonella* is set in turkeys being 1 % or less of flocks remaining positive for all *Salmonella* serotypes with public health significance

- It is estimated that 2.6 % (95 % CI: 1.2-5.2) of all human salmonellosis cases in the EU in 2010 were attributed to turkeys. For the other *Salmonella* food-animal reservoirs, it is estimated that 17.0 % (95 % CI: 11.3-24.0), 56.8 % (95 % CI: 48.2-65.8) and 10.6 % (95 % CI: 5.1-18.3) of the estimated number of human salmonellosis cases could be attributed to laying hens (eggs), pigs and broilers, respectively.

- The top-6 serovars of fattening turkeys that contribute most to human cases are *S.* Enteritidis, *S.* Kentucky, *S.* Typhimurium, *S.* Newport, *S.* Virchow and *S.* Saintpaul.

- The relatively high attribution of human salmonellosis cases to the pig reservoir may partly be explained by data availability and quality issues, in particular a lack of harmonised data on the cattle reservoir and lack of phage typing data on *S.* Enteritidis and *S.* Typhimurium. Nevertheless, there are indications that the importance of the pig reservoir has increased in recent years, both in a relative and in an absolute sense.

- Per tonne of food available for consumption, table eggs were associated with the highest risk (0.13 cases per tonne) closely followed by the risk associated with pig meat whereas the risks

associated with broiler and turkey meat were similar and approximately two-fold lower (0.05 and 0.07 cases per tonne, respectively).

- If the current transitional target of the EU control programme of *Salmonella* in fattening turkey flocks (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 per the 2010 reporting in turkey flocks) would be met in all EU MSs, the number of turkey-associated human salmonellosis cases is estimated to be reduced by 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) out of the 5.4 million true cases of human salmonellosis. In 2010 all MSs except one had already met the transitional target.

- An EU-wide target for a maximum of 1 % of fattening turkey flocks remaining positive for all 23 *Salmonella* serovars considered in the model would result in an estimated reduction in the number of turkey-associated human salmonellosis cases of 83.2 % (95 % CI: 79.0-87.4) compared to the situation in 2010. This corresponds to around 112 300 (95 % CI: 50 410-243 400) out of the 5.4 million true cases of human salmonellosis, a 2.2 % reduction in overall human cases.

- An EU-wide target for a maximum of 1 % of fattening turkey flocks remaining positive for the top-5 *Salmonella* serovars in humans in 2010 (*S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Newport, S. Kentucky) would result in an estimated reduction in the number of turkey-associated human salmonellosis cases of 29.6 % (95 % CI: 13.0-44.8) compared to the situation in 2010. This corresponds to around 37 870 (95 % CI: 17 570-78 780) out of the 5.4 million true cases of human salmonellosis.

- An EU-wide target for a maximum of 1 % of fattening turkey flocks remaining positive for the top-6 *Salmonella* serovars in turkeys that contribute most to human cases (*S.* Enteritidis, S. Kentucky, *S.* Typhimurium, *S.* Newport, *S.* Virchow, *S.* Saintpaul) would result in an estimated reduction in the number of turkey-associated human salmonellosis cases of 37.2 % (95 % CI: 19.2-54.0) compared to the situation in 2010. This corresponds to around 48 110 (95 % CI: 22 580-100 500) out of the 5.4 million true cases of human salmonellosis.

- An EU-wide target for a maximum of 1 % of fattening turkey flocks remaining positive for the *Gallus gallus* breeder flocks regulated serovars (*S.* Enteritidis, *S.* Typhimurium, *S.* Hadar, *S.* Infantis and *S.* Virchow) would result in an estimated reduction in the number of turkey-associated human salmonellosis cases of 18.1 % (95 % CI: 9.4-28.4) compared to the situation in 2010. This corresponds to around 23 740 (95 % CI: 10 070-52 980) out of the 5.4 million true cases of human salmonellosis.

RECOMMENDATIONS

- The establishment of active surveillance of human salmonellosis in all MSs, including harmonised typing of human *Salmonella* isolates and efforts to quantify the level of under-ascertainment and underreporting, would improve the estimation of the human health effects of interventions in primary animal production and would better inform cost/benefit analysis.

- Sample types, sampling options and their detection capability for poultry, especially for breeding flocks, should be further examined.

- Full serotyping should be carried out on at least one isolate per positive turkey flock, and results reported within statutory monitoring, to assist with epidemiological investigations and attribution studies. Representative isolates of *S.* Enteritidis and *S.* Typhimurium of all animal reservoirs should be subtyped through a harmonised method.

- The antigenic formulae of emerging *Salmonella* strains, e.g. monophasic variants of *S*. Typhimurium, should be reported so that trends can be accurately monitored.

- Targeted control of *Salmonella* serovars other than *S.* Enteritidis and *S.* Typhimurium in turkey flocks should be guided by the level of their occurrence and public health impact in individual EU MSs.

- If sufficient information becomes available to reliably identify particular clones of public health significance, the inclusion of such clones as part of the EU-wide targets should be considered. This will require that MSs are able to apply harmonised and standardised methods of identification and typing in order to identify these clones unambiguously and report their emergence at an early stage.

- Development of a reliable and economic multiplex test to identify antimicrobial residues in birds or samples that are involved in *Salmonella* control programmes should be prioritised.

- An EU-wide baseline survey of *Salmonella* in cattle or beef could be considered to investigate the role of the cattle reservoir as a source of human infections via beef, dairy products or environmental contamination by cattle. This would allow the inclusion of this source in *Salmonella* attribution models.

DOCUMENTATION PROVIDED TO EFSA

1. Letter (Ref. SANCO/E2/KK/rz D(2010) 520170 dated 2 June 2010) from the European Commission for a request for an opinion on an estimation of the public health impact of setting a new target for the reduction of *Salmonella* in turkeys.

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APPENDICES

A. AN ESTIMATION OF THE UNDERREPORTING FACTOR FOR HUMAN SALMONELLOSIS IN THE EU BASED FROM SWEDISH TRAVELLERS

Table 1 shows the estimated risk to Swedish travellers, the true incidence of human salmonellosis in the EU27 and the estimated underreporting factor.

Table 1: An estimation of the underreporting factor of human salmonellosis in the different EU MSs based on the estimation of the true incidence of human salmonellosis. For detailed explanations on data used, methodology and limitations see (EFSA Panel on Biological Hazards, 2011a).

	Swedish travellers		True incidence		Underreporting	
	Risk		Cases	Incidence rate	Factor	% reported
Country	(per 100 000)	(relative to NL)	(× 1 000)	(per 100 000)		
Austria	2.92	1.90	30.5	364	11.0	9.10 %
Belgium	0.81	0.52	10.8	101	3.5	29.0 %
Bulgaria	94.3	61.3	896	11 800	719	0.14 %
Cyprus	23.3	15.2	23.2	2 910	173	0.58 %
Czech Republic	23.1	15.1	303	2 890	28.9	3.46 %
Denmark	1.35	0.88	9.3	169	4.4	22.9 %
Estonia	2.64	1.72	4.4	330	17.0	5.90 %
Finland	0.13	0.08	0.9	16.3	0.4	268 %
France	2.39	1.55	192	299	26.9	3.72 %
Germany	2.99	1.95	307	374	9.8	10.2 %
Greece	35.2	22.9	496	4 390	1230	0.08 %
Hungary	31.3	20.4	392	3 910	66.7	1.50 %
Ireland	0.32	0.21	1.8	40.4	5.4	18.6 %
Italy	3.97	2.58	298	497	71.8	1.39 %
Latvia	12.5	8.11	35.2	1 560	44.3	2.26 %
Lithuania	29.1	18.9	122	3 640	59.1	1.69 %
Luxembourg	1.18	0.77	0.7	147	4.5	22.2 %
Malta	53.4	34.7	27.6	6 680	223	0.45 %
Poland	20.4	13.3	973	2 550	114	0.88 %
Portugal	34.5	22.4	458	4 310	2080	0.05 %
Romania	14.4	9.36	386	1 800	350	0.29 %
Slovakia	32.9	21.4	222	4 110	53.2	1.88 %
Slovenia	9.78	6.4	24.8	1 220	40.3	2.48 %
Spain	16.1	10.5	922	2 010	214	0.47 %
Sweden	NA	0.08	1.5	16.3	0.5	202 %
The Netherlands	1.54	1.00	*31.6*	*192*	*26.3*	3.80 %
United Kingdom	1.00	0.65	76.5	125	7.3	13.7 %
EU-27	**8.44**	**5.49**	**6 250**	**1 260**	**57.5**	**1.74 %**
Norway	0.24	0.159	1.5	30.5	1.2	84.4 %
Switzerland	0.98	0.639	9.4	122	7.1	14.0 %

Estimated results have to be considered understanding the different assumptions and limitations behind the model and the data employed. These include:

- The case data are extracted from the Swedish infectious disease surveillance system (SmiNet) and rely on laboratories and physicians reporting diagnosed cases to SMI. Clearly, only a fraction of all cases of illness will be reported. For this model, mainly the potential of differential reporting per country should be considered.

- Both cases and travels are counted as such, without consideration of the duration of the stay abroad, or the purpose of the visit (business or leisure). Day travels were excluded from the dataset. There are, for example, a very high number of travels to Denmark, Finland and Norway, which may be mainly for business purposes and of short duration (Ekdahl and Giesecke, 2004). For these trips, the duration of exposure may be shorter but on the other hand travellers who fall ill will most likely have returned to their home country and will be reported in the Swedish public health system when seeking health care. On the other hand, trips to the Mediterranean area may be mainly for leisure purpose and last one or more weeks. Travellers may be exposed for longer time periods, but when ill may have recovered before returning home. It is difficult to predict in which direction biases may occur.

- The estimated underreporting factor for Finland is less than 1, implying that there are fewer cases than actually reported, which is highly unlikely. This might indicate that for –presumably– short-term visits, the risks to travellers may be underestimated.

- Further biases may be introduced by seasonal travel patterns. It is likely that most travels to the Mediterranean take place in summer, when the prevalence of *Salmonella* in animals and food is highest.

- Health-seeking behaviour of travellers or medical decisions about stool cultures may be affected by the country of destination.

- Another important assumption is that relative risks to Swedish travellers are predictive of risks for the local population. This assumption ignores any potential effects of acquired immunity, differences in eating habits and local residents, differences between strains circulating in different parts of Europe.

It is currently not possible to conclude on the magnitude or even the direction of these biases. A detailed discussion of potential biases in the data is provided by Ekdahl and Giesecke (2004).

B. TURKEY MEAT PRODUCTION IN THE EU, TRADE AND CONSUMPTION

Table 1: Turkey meat production in the EU and Norway in tonnes (FAOSTAT, accessed 30 September 2011)

Country	Year					
	2004	**2005**	**2006**	**2007**	**2008**	**2009**
Austria	30 947	29 872	29 573	28 105	27 603	25 000
Belgium	8 065[a]	7 410[a]	6 600[b]	5 400[b]	5 350[b]	5 100[b]
Bulgaria	1 700	1 301	1 425	1 700[b]	1 682[a]	1 801[a]
Cyprus	1 210[c]	1 210[c]	1 210[c]	1 210[c]	1 210[c]	1 210[c]
Czech Republic	20 751	16 323	10 382	4 836	4 314	3 296
Denmark	1 000	474	92	144[b]	125[b]	120[a]
Finland	4 433[c]	5 200[c]	6 383[c]	2 925[c]	3 081[c]	3 192[c]
France	624 400	546 100	505 400	455 200	427 300	397 000
Germany	390 741	384 765	375 996	374 880	440 000	438 005
Greece	2 100[c]	2 100[c]	2 100[c]	1 474[c]	2 100[c]	2 184[c]
Hungary	127 332	98 198	102 304	103 176	101 905	94 130
Ireland	33 500[d]	33 500[d]	29 400[d]	26 400[d]	27 000[b]	27 000[b]
Italy	279 355	299 844	273 816	279 504	310 604	305 100
Lithuania	3 588	3 585	3 925	4 568	4 646	4 323
Malta	147[c]	147[c]	168[c]	147[c]	168[c]	168[c]
The Netherlands	57 477[a]	58 692[a]	58 038[a]	52 000[b]	52 684[a]	58 060[a]
Norway	6 795	6 387	6 911	7 117	8 792	11 830
Poland	55 000[b]	60 000[b]	62 106[a]	67 609[a]	54 955[a]	49 725[a]
Portugal	34 440	36 899	37 417	39 713	37 871	35 793
Slovakia	185	178	804	683	1 650	158
Slovenia	9 570	9 306	5 482	6 664	6 664	6 264
Spain	20 585	20 154	21 304	24 320	25 457	26 000[b]
Sweden	3 400[b]	3 280	2 840	2 490	2 730	2 760
United Kingdom	227 939	206 031	183 835	151 339	135 439	156 744
EU (Total)	**1 937 865**	**1 824 569**	**1 720 600**	**1 634 487**	**1 674 538**	**1 644 133**

[a] FAO data based on imputation methodology.
[b] FAO estimate.
[c] Calculated data.
[d] Unofficial figure.

Table 2: World market and trade with turkey meat (in tonnes Ready to Cook Equivalent) (USDA, 2010)[a]

	Year					
	2006	**2007**	**2008**	**2009**	**2010**	**2011**
Production						
EU-27	1 858	1 790	1 830	1 795	1 946	1 940
Brazil	353	458	465	466	485	505
Canada	163	170	180	167	159	160
Russia	19	25	37	40	70	90
Mexico	14	15	15	11	11	10
South Africa	5	7	7	8	8	8
China	4	5	5	5	6	6
Others	4	4	nr[b]	nr[b]	nr[b]	nr[b]
Total Foreign	**2 420**	**2 474**	**2 539**	**2 492**	**2 685**	**2 719**
United States	**2 543**	**2 664**	**2 796**	**2 535**	**2 526**	**2 593**
Total	**4 963**	**5 138**	**5 335**	**5 027**	**5 211**	**5 312**
Total Domestic Consumption						
EU-27	1 841	1 769	1 835	1 801	1 880	1 880
Brazil	197	281	261	302	365	365
Mexico	197	211	212	155	169	169
Canada	144	150	163	151	145	145
Russia	110	100	102	84	123	123
South Africa	39	47	38	34	41	41
China	21	35	50	32	37	37
Others	23	23	nr[b]	nr[b]	nr[b]	nr[b]
Total Foreign	**2 572**	**2 616**	**2 661**	**2 559**	**2 760**	**2 760**
United States	**2 295**	**2 401**	**2 431**	**2 360**	**2 297**	**2 297**
Total	**4 867**	**5 017**	**5 092**	**4 919**	**5 057**	**5 057**

[a] From 2008, Taiwan is excluded.
[b] nr = no data.

Table 3: Turkey meat import in the EU (in tonnes) (AVEC, 2011)

Product definition	Year				
	2000	**2005**	**2008**	**2009**	**2010**
Meat and edible offal, of the poultry of heading 0105, fresh, chilled or frozen					
Frozen boneless cuts of turkey	7 981	16 846	13 054	11 088	12 814
Meat, salted, in brine, dried or smoked					
Prepared/preserved meat of turkeys	30 092	94 561	106 522	97 643	83 787
Preparations containing exclusively uncooked turkey meat (excl. sausages and similar products)	28 940	92 790	102 874	94 553	78 940

Table 4: Import of fresh and frozen turkey meat (in 1 000 tonnes)[36]

	Year							
	2000	**2001**	**2002**	**2003**	**2004**	**2005**	**2006**	**2007**
Europe	**433.7**	**537.6**	**541.0**	**503.0**	**517.4**	**535.1**	**499.7**	**485.8**
of which								
Austria	15.3	16.6	17.5	18.5	18.4	31.4	27.7	33.4
Belgium	41.4	40.0	36.1	36.7	40.1	48.6	39.4	34.0
France	5.0	10.2	14.2	12.9	13.5	16.3	18.5	19.2
Germany	92.4	112.2	87.1	94.1	83.1	80.1	74.2	86.5
The Netherlands	26.2	23.5	25.4	26.3	21.8	22.5	20.3	44.9
Russian Federation	105.2	162.3	164.8	113.0	94.8	103.9	89.4	72.9
Spain	35.6	35.5	31.1	31.4	33.0	33.9	29.3	31.0
United Kingdom	17.8	17.6	23.8	28.6	28.6	25.9	44.8	26.9

[1] Less than 50 tonne, no figure is given.

Table 5: Per capita consumption of turkeys in selected EU and 3rd countries (in kilos) (AVEC, 2011)

Country	Year					
	2005	**2006**	**2007**	**2008**	**2009**	**2010**
Austria	6.9	6.0	6.5	6.2	6.4	6.4
France	5.8	5.7	5.5	5.2	5.0	4.9
Germany	6.2	5.9	5.7	6.2	6.2	6.0
Italy	5.0	4.5	5.0	5.0	4.9	4.9
The Netherlands	1.9	1.6	1.5	1.2	1.1	1.0
United Kingdom	4.0	4.5	4.0	3.9	4.0	3.9
EU 27	**3.8**	**3.7**	**3.6**	**3.5**	**3.4**	**3.3**
3rd countries						
Brazil	1.1	1.0	1.5	1.4	1.6	1.6
Canada	4.4	4.4	4.6	4.9	4.5	4.4
Mexico	1.9	1.9	2.0	2.0	1.4	1.4
Russian Federation	0.9	0.8	0.7	0.7	0.6	0.5
USA	7.6	7.6	8.0	7.9	7.7	7.4

[36] from http://www.fas.usda.gov/psdonline/circulars/livestock_poultry.pdf

Table 6: Average and 95th percentile consumption of turkey and broiler meat (in grams/day) in the EU for total population and consumers only for adults (EFSA, 2011b)

Country	Survey	No of subjects	Turkey meat			Chicken meat		
			Average consumption for total population (g/day)	Percentage of consumers	Average consumption for consumers only (g/day)	Average consumption for total population (g/day)	Percentage of consumers	Average consumption for consumers only (g/day)
Austria	ASNS	2 123	0.3	0.2	117.2			
Belgium	Diet_national_2004	1 356	3.1	5.2	59.2	18.3	28.7	63.8
Bulgaria	NSFIN	691				21.4	23.2	92.6
Czech Republic	SISP04	1 666	1.3	1.5	85.9	33.6	39.8	84.5
Denmark	Danish_Dietary_Survey	2 822	7.4	47.9	15.5	16.7	84.6	19.7
Estonia	NDS_1997	1 866	0.7	0.3	261.8	15.6	8.6	182.1
Finland	FINDIET_2007	1 575	4.5	14.3	31.5	25.8	35.7	72.2
France	INCA2	2 276	7.2	35.7	20.1	18.3	62.5	29.3
Germany	National_Nutrition_Survey_II	10 419	5.1	8.5	60.9	7.5	11.1	67.5
Hungary	National_Repr_Surv	1 074	4.9	9.4	51.7	35.6	62.2	57.3
Ireland	NSIFCS	958	5.3	26.7	19.7	36.0	85.1	42.3
Italy	INRAN_SCAI_2005_06	2 313	3.6	9.6	37.5	16.5	34.7	47.7
Latvia	EFSA_TEST	1 384	0.3	0.4	60.0	22.1	24.5	90.2
Poland	IZZ_FAO_2000	2 527	3.6	2.1	174.0	57.3	23.5	243.2
Slovenia	CRP_2008	407	8.2	4.4	185.5	29.9	17.9	166.9
Slovakia	SK_MON_2008	2 761	2.9	2.1	140.0	30.2	22.6	133.5
Spain	AESAN	418	1.7	3.6	46.8	31.4	40.2	78.2
Spain	AESAN_FIAB	982	1.3	4.5	30.0	39.4	57.4	68.6
Sweden	Riksmaten_1997_98	1 210	0.2	1.4	11.7	6.5	30.8	21.2
The Netherlands	DNFCS_2003	750	0.8	1.2	63.7	23.2	32.1	72.2
The United Kingdom	NDNS	1 724	3.9	21.6	17.9	31.5	83.2	37.9

Table 7: Average and 95th percentile consumption of turkey ham and preserved poultry meat (in grams/day) in the EU for total population and consumers only for adults (EFSA, 2011b)

Country	Survey	No of subjects	Turkey ham			Preserved poultry meat		
			Average consumption for total population (g/day)	Percentage of consumers	Average consumption for consumers only (g/day)	Average consumption for total population (g/day)	Percentage of consumers	Average consumption for consumers only (g/day)
Austria	ASNS	2 123	0.6	1.2	52.0			
Belgium	Diet_national_2004	1 356	1.4	6.3	22.4			
Czech Republic	SISP04	1 666				0.9	2.0	43.8
Hungary	National_Repr_Surv	1 074	1.6	6.6	24.5			
Slovakia	SK_MON_2008	2 761	0.8	0.7	115.8	2.4	3.1	75.5
Spain	AESAN	418	3.1	7.2	43.5			
Spain	AESAN_FIAB	982	0.1	0.4	23.3			
Poland	IZZ_FAO_2000	2 527	1.7	3.2	51.2	0.3	0.5	59.8
The Netherlands	DNFCS_2003	750	0.1	0.7	13.5	0.9	5.6	15.8

C. MAIN POTENTIAL CONTAMINATION ROUTES IN TURKEY BREEDING AND PRODUCTION

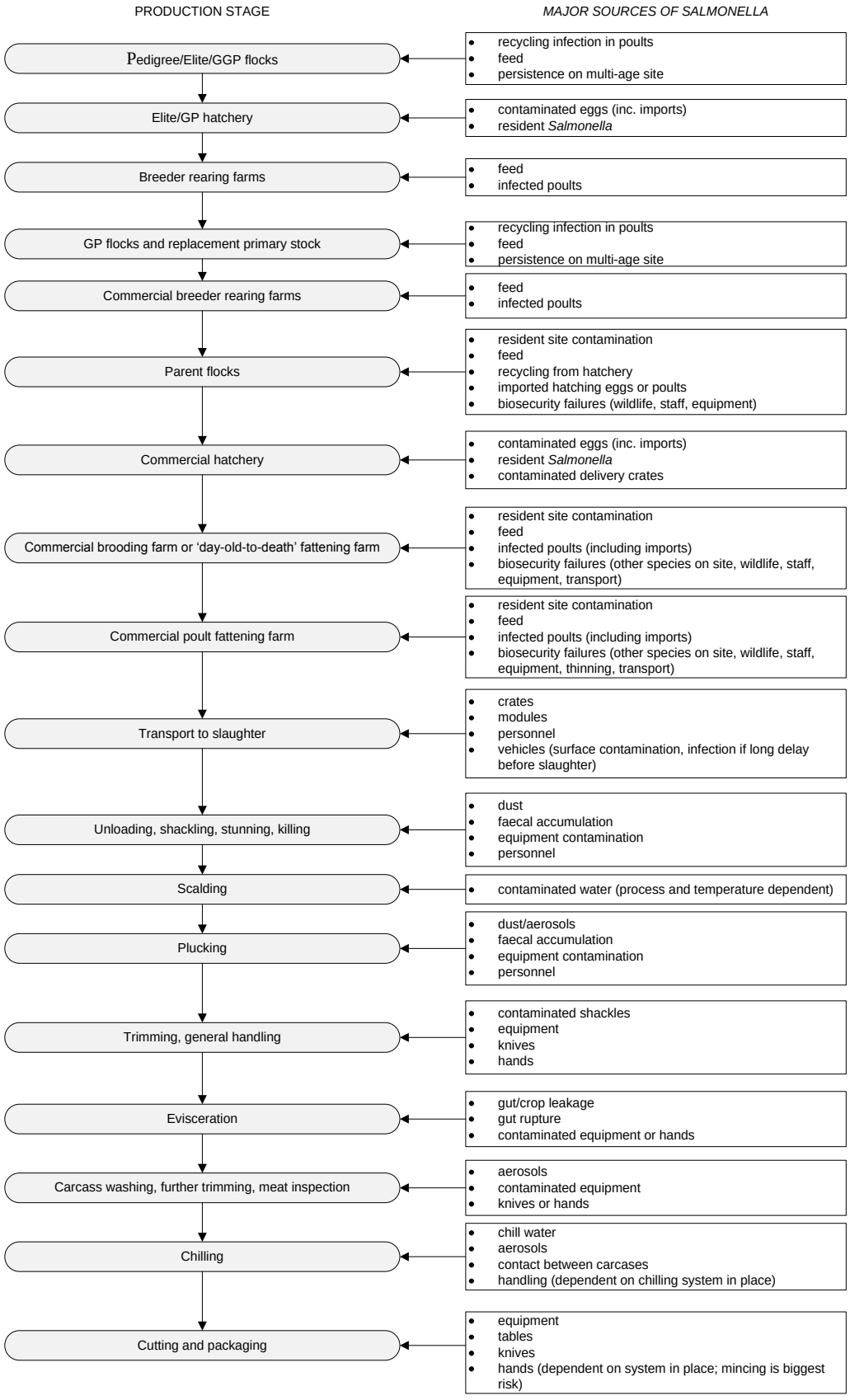

Figure 1: Diagram of main potential contamination routes in turkey breeding and production

D. *SALMONELLA* MONITORING PROGRAMMES IN TURKEY FLOCKS AND ACTIONS TAKEN FOLLOWING IDENTIFICATION OF A POSITIVE FLOCK

The following tables are sourced from EFSA and ECDC (2012).

Table 1: *Salmonella* monitoring programmes in turkey breeders, 2010 (EFSA and ECDC, 2012)

Day old chicks		Rearing period			Production period		
Sampling scheme following the provisions of Directive 1992/117/EC							
Samples from the inside of the delivery boxes (internal lining/paper/crate material)	FI, NO, PL, SK, LT	At age of 4 weeks and 2 weeks before moving	Faecal samples	FI, NO, PL, SK, LT	Official sampling every 8 weeks	Meconium samples at the hatchery	PL, SK
Meconium	SE	At age of 4 weeks and 2 weeks before moving	2 pairs of sock samples	FI, SE	At hatchery: every 2 weeks; At holding: every 2 weeks	Samples from the underlying papers of hatching baskets. One pair of sock sample and one dust sample.	FI
Dead chickens/destroyed chickens	PL, SK, LT				Every 2 weeks	Faecal samples	LT
					Every 2 weeks	5 pair of sock samples	NO, SE
					Official sampling 3 times during production period	5 pair of sock samples	NO, SE
					Every 2 weeks	Dead chickens	PL, SK
Other sampling schemes							
Internal lining papers of delivery boxes	FR		Swabs/faeces	FR, NL		Swabs/faeces	FR, NL
Sample scheme approved by EU (Decision 96/389/EC)	IE	Every 4 weeks	Chicks, dust swab	FR	Every 4 weeks	On farm: chicks, dust swab	FR
Samples from the lorry and 1 week after arrival: Wooswool samples	NL	Sample scheme approved by EU (Decision 96/389/EC)		IE	Sample scheme approved by EU (Decision 96/389/EC)		IE
					Hatchery, every hatch, every machine	Fluff samples	NL
					Every 4 weeks	At hatchery: Environmental swab	FR
					Hatchery	Samples of imported eggs	AT
Diagnostic methods used							
ISO 6579:2002		CZ, NO, PL, SE					
ISO 6579:2002 / Amendment 1:2007		FI					
Countries not providing detailed information about monitoring programmes							
No information available		CY, FR, DE, GR, HU, IE, LT, LU, MT, PT, ES					
No official surveillance programme		BG, CZ, IT, NL, UK[1]					
No turkey breeder flocks present		AT, BE, DK, EE, LV, SI					

[1] In the United Kingdom monitoring programmes are voluntary. Farmers producing breeders are encouraged to monitor in the same way as for *Gallus gallus* under Regulation (EC) No 2160/2003. All isolations of *Salmonella* must be reported.

Table 2: *Salmonella* monitoring programmes in turkeys, turkey meat and meat products, 2010 (EFSA and ECDC, 2012)

Day old chicks		**Rearing period and before slaughter**		**At slaughter and at cutting plants**		**Processing plants**		**Turkey meat and meat products at retail**	
Type of sample									
Dust samples	IE	Faecal samples/boot swabs	AT, DK, FI, FR, NO, NL, RO, SE, SK, SI	Fresh meat	AT, SI	Crushed meat	SE[1]	Fresh meat, meat preparations, meat products, minced meat	
Chicks	NL	Dust samples	FR			Fresh meat, minced meat, final products	AT, IE, LV, LT	Fresh meat, final products	EE, LV, LT
Sampling based on the directive	PL	Sampling based on the directive	PL	Neck skin samples	AT[1], LT, SE[1]			Final product	CZ, DE, IE
				Dependent on survey	UK	Final product	IE, DE[3]	Depend on survey	DK, SE, UK
				Carcasses	AT	Depend on survey	DK, UK	Fresh meat, meat preparations	DE[4]
				Cloacal swabs and caecum	IT				
				Crushed meat	FI[1, 2]				
Frequency of sampling									
Every two months	IE	1 – 3 weeks before slaughter	AT, DK, FI, NO, PL, SK, SI	Every batch	SE	Twice yearly	IE	Surveys	DK
		Max 4 weeks before slaughter	NL	Random and continuous	FI	Surveys	DK, UK	Random and continuous	CZ, EE, SI
		2 weeks before slaughter	SE	Continuous	AT	Continuous	AT, IE, LV, SE	Continuous	IE, LV
				Monthly	SI	Random or routine, depend on programme	LT	Monitoring	DE, UK, LT
				Every flock	LT				

Day old chicks	Rearing period and before slaughter	At slaughter and at cutting plants	Processing plants	Turkey meat and meat products at retail
Diagnostic methods used				
ISO 6579:2002	CZ, EE, FI, FR, IT, LT, LV, NO, PL, SE (faecal samples), SI, UK			
NMKL No 71:1999	FI, SE (meat samples)			
Modified ISO 6579:2002	AT, DE, IT			
ISO 6579:2002/Amendment 1:2007	FI (flocks), RO			
Depend on the laboratory and/or survey	DK			
Bacteriological culture	IE			
Countries not providing detailed information about monitoring programmes				
No information available	AT, CY, DE, GR, HU, LT, LU, MT, PT, SK, ES			
No official surveillance programme	BE, BG, CZ, IT, UK[5]			
No turkey production flocks present	EE, LV			

1. Sample size and frequency depend on slaughterhouse and cutting plant capacity.
2. Crushed fresh meat from cleaning tools, tables etc.; similar approach for ducks, geese and guinea fowl.
3. In Germany, the food surveillance covers all level of the food chain.
4. One year national monitoring programme.
5. Monitoring programme in the United Kingdom is voluntary. All isolations of *Salmonella* must be reported.

Table 3: Measures taken in turkey in case of *Salmonella* infections, 2010 (EFSA and ECDC, 2012)

Control measures	Countries
Serovars covered	
All Serovars	DK, FI, NO, SE
S. Enteritidis and *S.* Typhimurium	CZ, FR, PL, PT, RO, SI, UK
Restrictions on the flock	
Immediately following suspicion	CZ, FI, NO, PL, RO, SI
Consequence for the flock	
Slaughter	PL, RO, SK, UK
Slaughtered and heat treated	FI, FR[5], SI
Sanitary slaughter	BE, DK, FI
Destruction	SE, UK[7]
Slaughter or destruction	CZ, PL, SI
Other consequence	
Feedingstuffs are restricted (heat treatment or destruction)	FI, NO, PL[6]
Disposal of manure restricted	CZ, NO, PL, SK, SI
Cleaning and disinfection	
Obligatory	BE, CZ, DK, FI, FR, NO, PL, PT, RO, SK, SI, SE, UK
Negative bacteriological result required before restocking	BE, CZ, DK, FI, NO, SK, SI, SE, UK
Requirement of an empty period	NO
Further investigations	
Epidemiological investigation is always started	CZ[2], FI, NO, PL, SE, UK
Feed suppliers are always included in the investigation	FI, NO
Contact herds are included in the investigation	FI, NO
Breeding flock that contributed to the hatch will be traced	NO
Vaccination	
Permitted	CZ[1], ES, FR[3], SI, UK
Vaccine not registered	
Prohibited	DK, FI, FR[4], NO

1. In the Czech Republic, vaccination of breeding and fattening turkeys is mandatory.
2. In the Czech Republic, epidemiological investigation is performed in the case of positive official samples and positive confirmatory examination for *S.* Enteritidis and/or *S.* Tyhimurium.
3. In France, vaccination of parent flocks is authorised with inactivated vaccines only.
4. In France, vaccination of elite flocks is forbidden.
5. In France, carcasses are heat-treated if *Salmonella* is identified in muscle.
6. In Poland, in case of positive results in feed samples.
7. In the UK, eggs from positive flocks must be removed from hatchery and destroyed.

E. COMPARISON OF FREQUENCY DISTRIBUTION OF *SALMONELLA* SEROVARS IN BREEDING AND FATTENING TURKEY FLOCKS

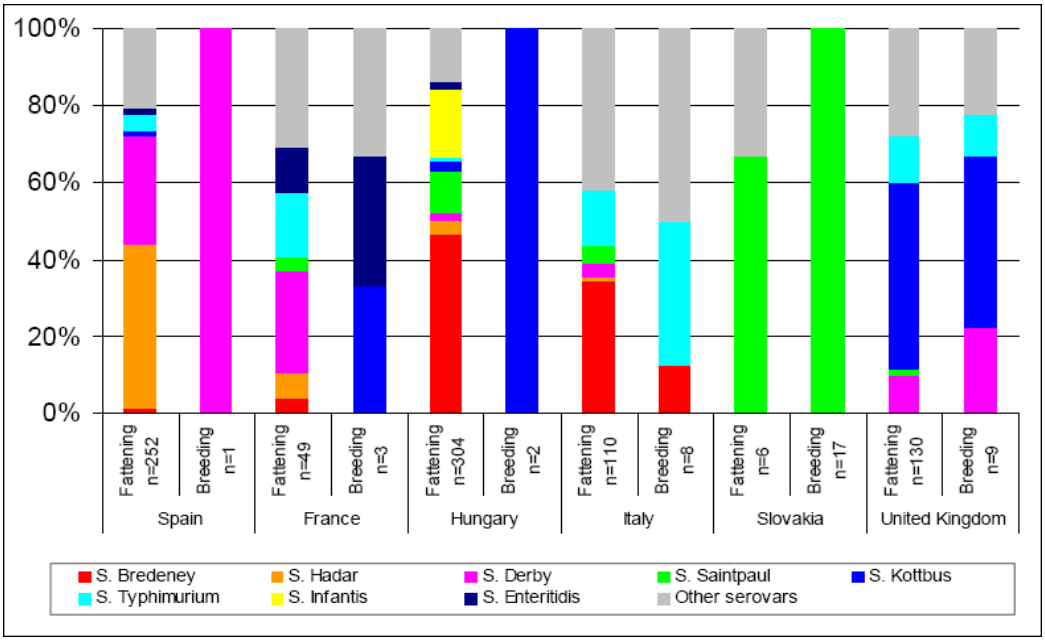

Figure 1: Relative frequency distribution (%) of *Salmonella* serovars in fattening turkey flocks and breeding turkey flocks in EU MSs where *Salmonella* positive breeding turkey flocks were identified. B = breeding flocks, F = fattening flocks. The number of positive turkey flocks is shown at the bottom of each bar. Note that the number of *Salmonella* isolates breeding flocks is generally very small (less than 10 and any interpretation concerning the serovar distribution should be made cautiously. This also applies to the number of fattening flocks in Slovakia. However, for some MSs, the serovar distributions in breeding and fattening flocks appear to be similar with regard to the most frequently isolated serovars (Source: baseline survey in turkey fattening flocks carried out between 2006 and 2007).

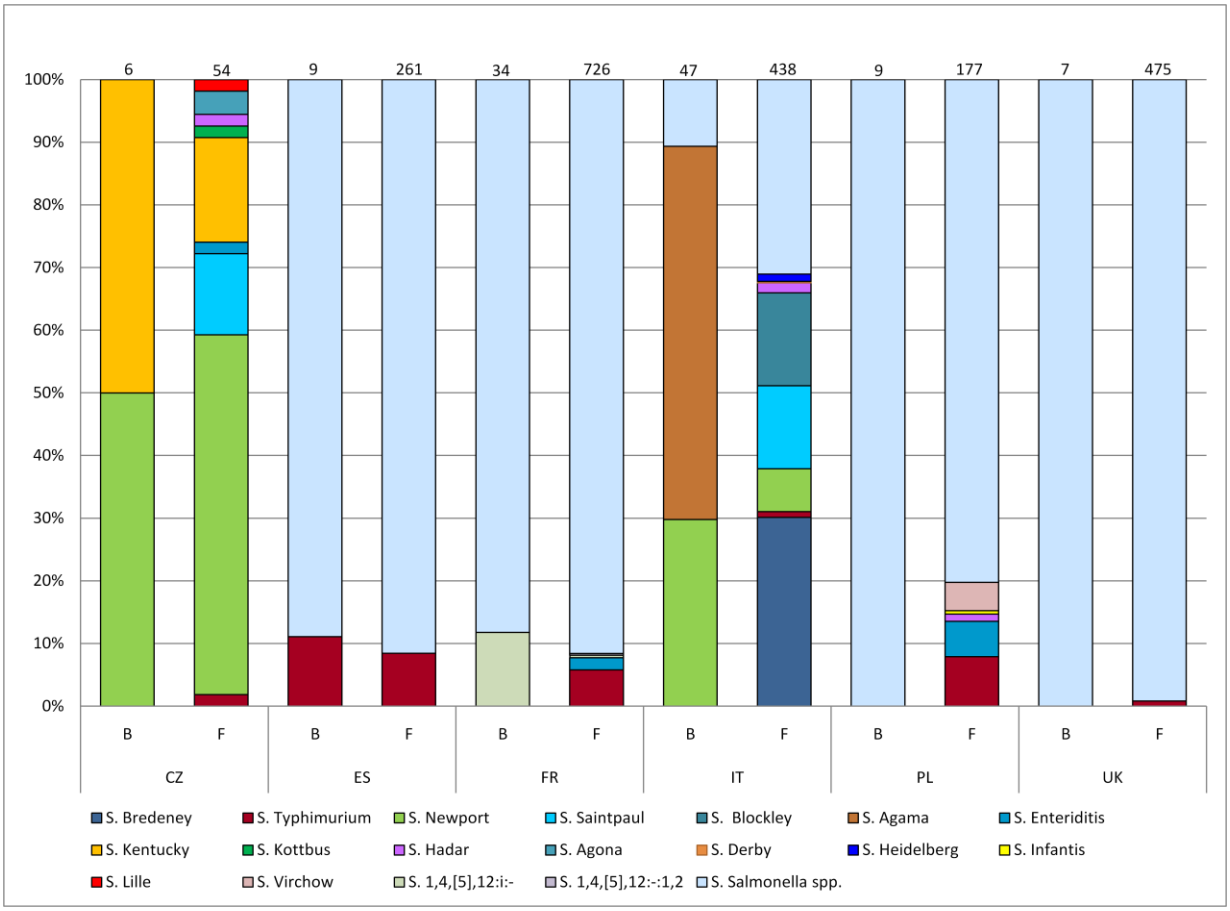

Figure 2: Relative frequency distribution (%) of the reported *Salmonella* serovars in fattening turkey flocks and breeding turkey flocks in six EU MSs where both *Salmonella* positive breeding and fattening turkey flocks were identified. The number of positive turkey flocks is shown at the top of each bar. Note that the number of *Salmonella* isolates breeding flocks is generally very small (less than 10 and any interpretation concerning the serovar distribution should be made cautiously. Czech Republic (CZ) reported more than one serotype found in the same flock. (Source: 2010 EU harmonised monitoring) (EFSA and ECDC, 2012). Figure provided by the EFSA Unit on Zoonoses data collection.

GLOSSARY AND ABBREVIATIONS

BT-SAM	Broiler-Target *Salmonella* Attribution Model
DALY	Disability-adjusted life years
EU-SSA	EU-*Salmonella* Source Attribution
GGP	Great grand parent
GP	Grand parent
MAP	Modified Atmosphere Packaging
MIC	Minimum Inhibitory Concentration
NCP	National Control Programme
NRL	National Reference Laboratory
OR	Odds ratio
PS	Parent stock
RTE	Ready-to-eat
TT-SAM	Turkey-Target *Salmonella* Attribution Model