

**Report of the
Task Force on Zoonoses Data Collection
on the Analysis of the baseline survey on the
prevalence of *Salmonella* in turkey flocks, in the
EU, 2006-2007¹**

Part A: *Salmonella* prevalence estimates

(Question N° EFSA-Q-2006-041A)

**Adopted by
The Task Force on 28 April 2008**

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Summary

Salmonella is an important cause of food-borne illnesses in humans. Farm animals and food of animal origin form an important source of human *Salmonella* infections. Therefore, in order to reduce the incidence of human salmonellosis in the European Union, the Community legislation foresees setting of *Salmonella* reduction targets for food-animal populations including turkey flocks. To underpin such a target, a European Union-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 survey was the third of several baseline surveys to be conducted in the Community.

The sampling of turkey flocks took place between October 2006 and September 2007. Five environmental faeces samples were taken from breeding turkey flocks within nine weeks of slaughter and from fattening turkey flocks within three weeks of slaughter. 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.

In each Member State, 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 population size. The geographical distribution of breeding turkeys in the European Union was highly heterogeneous. In fact, France accounted for 56.0% of the breeding population, followed by Italy (11.9%) and The United Kingdom (10.1%). None of the remaining Member States reached 5% of the total breeding population. The distribution of fattening turkeys was less heterogeneous. Still, five Member States 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%).

Six of the 14 Member States isolated *Salmonella* spp. in their breeding flocks, which resulted in a Community observed prevalence of *Salmonella*-positive breeding flocks of 13.6%. This means that in the European Union around one in seven breeding turkey flocks raised over the one year period of the baseline survey was *Salmonella*-positive. The *Salmonella* prevalence in these flocks varied widely amongst the Member States, from 0% to 82.9%. Three of those six Member States isolated *Salmonella* Enteritidis and/or *Salmonella* Typhimurium, the two most common serovars found in *Salmonella* infection cases in humans. This resulted in an estimated Community observed prevalence of 1.7% for these two serovars, varying from 0% to 8.3% within the Member States.

The Community observed prevalence of *Salmonella*-positive fattening flocks was 30.7%, 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 Member States, from 0% to 78.5%. Thirteen of the 22 Member States with fattening turkey flocks reported to have isolated *S. Enteritidis* and/or *S. Typhimurium* resulting in a Community observed prevalence of 3.8% in the fattening turkey flocks. The Member State-specific observed flock prevalence of *S. Enteritidis* and/or *S. Typhimurium* varied from 0% to 18.4% in fattening turkeys.

In breeding flocks no single *Salmonella* serovar was isolated in more than three of the 14 reporting Member States. The five most frequently isolated *Salmonella* serovars from fattening turkey flocks in the European Union, in decreasing order, were: *S. Bredeney*, *S. Hadar*, *S. Derby*, *S. Saintpaul* and *S. Kottbus*. Out of these, only *S. Hadar* and *S. Derby* are frequent causes of *Salmonella* infections in humans within the European Union. The serovar distribution varied amongst the Member States, with serovars tending towards specific distribution patterns of their own.

The number of positive samples in a *Salmonella* positive breeding or fattening flock ranged between one and five. Almost all Member States had a major part of their *Salmonella*-infected flocks of fattening turkeys with all five samples positive. Reducing the number of samples taken per flock would have led to a substantially lower prevalence estimate of *S. Enteritidis* and/or *S. Typhimurium* in fattening turkey flocks.

Salmonella positive turkey flocks contribute to a consequent contamination of turkey meat. The risk for human health arises from accidental under-cooking of the meat or cross-contamination to other foods. Thorough cooking and strict kitchen hygiene will prevent or reduce the risk posed by *Salmonella* contaminated turkey meat.

While Community reduction target will most likely be set for a transitional period only for *S. Enteritidis* and *S. Typhimurium*, Member States may wish to consider addressing in their national *Salmonella* control programmes also other serovars when these serovars are of public health importance in their country.

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1. Introduction

The following report describes the results of a baseline survey carried out in the European Union (EU) to estimate the prevalence of *Salmonella* spp. in commercial flocks of breeding and fattening turkeys. This study was the third in a series of baseline surveys of *Salmonella* carried out within the EU. The objective of the surveys has been to obtain comparable data for all Member States (MSs) through harmonised sampling schemes. According to Regulation (EC) No 2160/2003 on the control of *Salmonella* spp. and other zoonotic agents¹, which aims to reduce the incidence of food-borne diseases in the EU, results of such a survey will inform the setting of the Community target for reduction of the prevalence of the infection in turkey flocks.

The survey was carried out over a one year period, starting 1 October 2006. Tested flocks were selected in holdings with at least 250 birds for breeding turkeys and with at least 500 birds for fattening turkeys. Such holdings were considered as representative of approximately 80% of the EU commercial turkey production that constituted the study's target population. Twenty-two EU MSs participated to the study. Norway participated on a voluntary basis.

The objectives, the sampling frame, the diagnostic testing methods, as well as the collection and reporting of data, and the timelines of this baseline survey were specified in the Commission Decisions 2006/662/EC and 2007/208/EC^{2,3}.

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

² Commission Decision 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.

³ Commission Decision of 30 March 2007 concerning a financial contribution from the Community towards a baseline survey on the prevalence of *Salmonella* in turkeys to be carried out in Bulgaria and Romania. OJ L 92, 3.4.2007, p. 18.

2. Objectives

The aim of the survey was to estimate the prevalence of *Salmonella*-positive flocks amongst commercial holdings (i.e. holdings containing at least 250 birds) of breeding turkeys and amongst commercial holdings (i.e. holdings containing at least 500 birds) of fattening turkeys, at the European Community level as well as for each MS.

The specific respective objectives for flocks with breeding turkeys, and for flocks with fattening turkeys, were;

- to estimate the flock prevalence of *Salmonella* in commercial holdings at the EU level and for each MS individually,
- to estimate the flock prevalence of the two serovars, *S. Enteritidis* and *S. Typhimurium* which pursuant to article 4 of the Regulation EC No 2160/2003, will be the serovars subject to specific reduction targets in the first instance,
- to investigate the serovar distribution and determine the most frequently occurring serovars in turkey flocks across the EU,
- to investigate the effect of potential risk factors, such as number of birds per holding, and time of sampling, which may be associated with the occurrence of *Salmonella*,
- to evaluate the sampling design especially with regard to the precision and accuracy of the prevalence estimates.

MSs were also invited to submit additional information on *S. Enteritidis* and *S. Typhimurium* phage types and antimicrobial susceptibility of *Salmonella* isolates, but this testing was not a compulsory requirement of the survey.

This part A report includes the analyses of the prevalence of *Salmonella*, the most frequent serovars and the sampling design. The analyses of potential risk factors as well as more in depth analyses of serovar and phage type distribution will be provided in the part B report. The analyses of the antimicrobial susceptibility of *Salmonella* isolates will be specifically addressed with in a separate report to be published by the European Food Safety Authority (EFSA).

3. Materials and methods

A detailed description of the design of the baseline survey, the sample design and size and the bacteriological testing is found in the document of European Commission, Directorate General for Health and Consumer Affairs (DG SANCO): Baseline survey on the prevalence of *Salmonella* in flocks of turkeys in the EU: Technical specifications. SANCO/2083/2006¹.

Environmental faecal samples were taken from flocks with breeding turkeys and from flocks with fattening turkeys. Breeding flocks on holdings with at least 250 birds were sampled 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. In the fattening turkey sub-survey, the sampling frame covered primarily holdings representing at least 80% of the total population of turkey meat finishing flocks, which was to be achieved by including holdings with at least 500 birds. 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 under its supervision and were tested by the National Reference Laboratory (or an authorised laboratory) using the ISO 6579 Annex D method.

¹ European Commission Directorate General for Health and Consumer Affairs (DG SANCO). Baseline survey on the prevalence of *Salmonella* in flocks of turkeys in the European Union: Technical specifications. SANCO/2083/2006. Working document, 18 July 2006. Presented at the meeting of the Standing Committee on the Food Chain and Animal Health on 19 July 2005. (http://ec.europa.eu/food/food/biosafety/salmonella/tech_spec_sanco-2083-2006_rev1_en.pdf)

3.1. Data description

3.1.1. Data validation and cleaning

The European Food Safety Authority (EFSA) received the final dataset of the survey from the European Commission (COM) on 29 January 2008. This dataset contained data from 4,406 turkey flocks in 22 MSs and in Norway. Estonia, Latvia and Luxembourg reported not having commercial turkey flocks, but only backyard flocks. No data were received from Malta and Romania.

A set of data exclusion criteria (Annex III) was used to identify non-valid and non-plausible information in the dataset. This resulted in a cleaned, validated dataset comprising 4,308 turkey flocks from 22 MSs and Norway (final dataset), which formed the basis for all subsequent analyses. An overview of the number of excluded flocks per MS is given in Table 1. Altogether, 2.2% of the flocks (95 out of 4,329) were excluded from the final EU dataset. The reasons for exclusion of samples or flocks in accordance with the exclusion criteria are summarized in Annex III. The criterion that caused the highest number of flocks to be excluded was a within-flock sample size that differed from five. The second most common cause of excluding samples was delay in start of bacteriological test of more than seven days after the day of sampling.

3.2. Statistical analysis

3.2.1. Estimate of prevalence of infection

Data from breeding and fattening turkey flocks were separately analysed and the following three outcomes were considered:

- Positivity for *Salmonella* spp.,
- Positivity for *S. Enteritidis* and/or *S. Typhimurium*
- Positivity for serovars other than *S. Enteritidis* or *S. Typhimurium*.

A flock was considered positive if *Salmonella* was detected in at least one of the five samples collected. Only the observed prevalence was investigated and no correction was made for test sensitivity or specificity. Only flock-level prevalence over the one year period (the proportion of tested flocks that were positive at any stage over the one year period of the survey) was investigated since it was considered as more relevant than the holding-level prevalence, from an epidemiological, as well as from a risk management perspective.

Table 1. Overview of the data validation at flock-level, *Salmonella* in turkey flocks baseline survey in the EU¹, 2006-2007.

Member States	Number of turkey flocks structurally validated by COM and sent to EFSA, full dataset	Number of turkey flocks validated by EFSA final dataset	Number of turkey flocks excluded by EFSA	Percent (%) of flocks excluded by EFSA
Austria	202	202	0	0.0
Belgium	75	74	1	1.3
Bulgaria	32	24	8	25.0
Cyprus	14	14	0	0.0
Czech Republic	200	198	2	1.0
Denmark	66	59	7	10.6
Finland	151	148	3	2.0
France	537	531	6	1.1
Germany	393	393	0	0.0
Greece	52	49	3	5.8
Hungary	304	302	2	0.7
Ireland	268	261	7	2.6
Italy	297	296	1	0.3
Lithuania	65	63	2	3.1
Poland	364	328	36	9.9
Portugal	114	105	9	7.9
Slovakia	47	46	1	2.1
Slovenia	134	131	3	2.2
Spain	390	390	0	0.0
Sweden	16	15	1	6.3
The Netherlands	175	172	3	1.7
The United Kingdom	433	433	0	0.0
EU Total	4,329	4,234	95	2.2
Norway	77	74	3	3.9
Total	4,406	4,308	98	2.2

1. Five MSs did not contribute to this data; Estonia, Latvia and Luxembourg that did not have commercial turkey flocks and Malta and Romania that did not participate to the survey.

Prevalence was estimated for each MS and at the EU-level, by Generalized Estimating Equations (GEE) taking into account that outcomes (presence or absence of infection) in flocks from the same holdings are expected to be more alike than in flocks from different holdings (PROC GENMOD, SAS, 1999). Weights, more specifically standardised year-aggregated weights (WY), were included in the GEE models to account for a disproportionate stratified sampling design. In fact, MSs and holdings were considered as strata, and the proportion of sampled holdings was not constant across MSs. Similarly, the proportion of sampled flocks was not constant across holdings. The reciprocal of the sampling proportion for holdings (the number of holdings in a MS divided by the number of sampled holdings in the same MS) was used as the MS-level weight (WY1), whereas the reciprocal of the sampling proportion for flocks (the estimated number of flocks produced in a holding during a year, divided by the number of sampled flocks in the same holding) was used as the holding-level weight (WY2). Only WY2 was used to estimate individual MS' prevalence, whereas the product between WY1 and WY2 was used to estimate the EU-level prevalence. To avoid artificial inflation of the sample size, weights were standardised so that their sum was equal to the original sample size, and this was done both at the MS (WY2) and at the EU level (WY1 by WY2). More details on statistical models and weighting are given in Annex I, section III-2.

3.2.2. Sensitivity analysis: expected results if fewer samples had been taken per flock

The number of samples per flock was expected to affect the probability of finding at least one positive result. Therefore, an in-silico simulation exercise was set up, based on the received data, separately for flocks with breeding turkeys and for flocks with fattening turkeys, to examine the effect of reducing the number of samples per flock on that probability of detection infection in a flock, focusing on the flock prevalence estimation of *S. Enteritidis* or *S. Typhimurium* in the EU and for each MS and Norway separately.

A bootstrap statistical technique was used to assess what would have been the estimated *S. Enteritidis* and/or *S. Typhimurium* EU flock observed prevalence in the baseline survey if only one, two, three or four samples per flock had been collected. More specifically, for each case investigated, 1000 replicates of the baseline survey were simulated by randomly selecting one to four samples. For each of these 1000 simulated studies, the fitting exercise previously described was performed, and the mean observed prevalence derived, with 95% simulated bootstrap confidence interval (accounting for data randomness). This allowed plotting the curve of EU flock prevalence estimates versus number of samples per flock. A SAS macro was developed for each sample size investigated, using SAS version 9.1.3.

3.2.3. Correlation between the *Salmonella* flock prevalence in flocks with breeding turkeys and in flocks with fattening turkeys

Correlation between the estimated prevalence of *Salmonella* in breeding and fattening turkeys in each MS and Norway was studied graphically via scatterplots and in a more formal way using the Spearman rank correlation coefficient.

4. Results

4.1. Features of the Community turkey population

A summary of the European Community turkey population is presented in Annex II. For breeding turkeys, the number of holdings in each MS was approximately equal to the number of sampled holdings. For fattening turkeys, a sample of holdings was selected for the survey.

4.1.1. Flocks with breeding turkeys

Of the 22 MSs that participated to the survey, 14 reported data on flocks with breeding turkeys, plus Norway. Breeding turkeys were concentrated in a limited number of MSs, and the greatest population was in France, which accounted for 52% of holdings and 56% of birds in the EU. Conversely, several countries had very small breeding turkey populations (Annex II).

4.1.2. Flocks with fattening turkeys

France, Germany, Italy, Spain, and Poland accounted for 79.3% of the total EU population of fattening turkeys, and the annual production in each of these MSs exceeded 10 million birds (Annex II).

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4.2. Observed flock prevalence of *Salmonella*

A total of 2.2% of the sampled flocks were excluded from the final EU dataset in the data validation and cleaning process. No flock was excluded from Austria, Cyprus, Germany, Spain, and The United Kingdom, whereas 25% of flocks from Bulgaria were excluded.

The numbers of *Salmonella*-positive, excluded flocks by country are reported in Annex IV. *Salmonella*-positive flocks were excluded in nine MSs. Poland was the only MS where *S. Enteritidis* and/or *S. Typhimurium*-positive flocks were excluded. The criterion that caused the highest number of positive flocks to be excluded (16 out of the total of 17) was a within-flock sample size that differed from five. The second most common cause of excluding positive flocks was delay in start of bacteriological test of more than seven days after the day of sampling.

4.2.1. Flocks with breeding turkeys

The weighted *Salmonella* prevalences in flocks with breeding turkeys in each MS and at EU level as well as for Norway are presented in Table 2. Although in some MS 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 flock was found infected. The raw, unweighted prevalence estimates are reported in Annex I, section IV-1.

Salmonella spp. was found in six out of 14 MSs providing data on flocks of breeding turkey (Figure 1). No positive flock was 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. The weighted EU-level prevalence was 1.7%, whereas the raw, unweighted prevalence was 0.9%. At the MS-level, prevalence was highest in Italy and it was low in France and the United Kingdom (Figure 2).

Salmonella serovars other than *S. Enteritidis* or *S. Typhimurium* were found in the breeding flocks from six MSs (Figure 3).

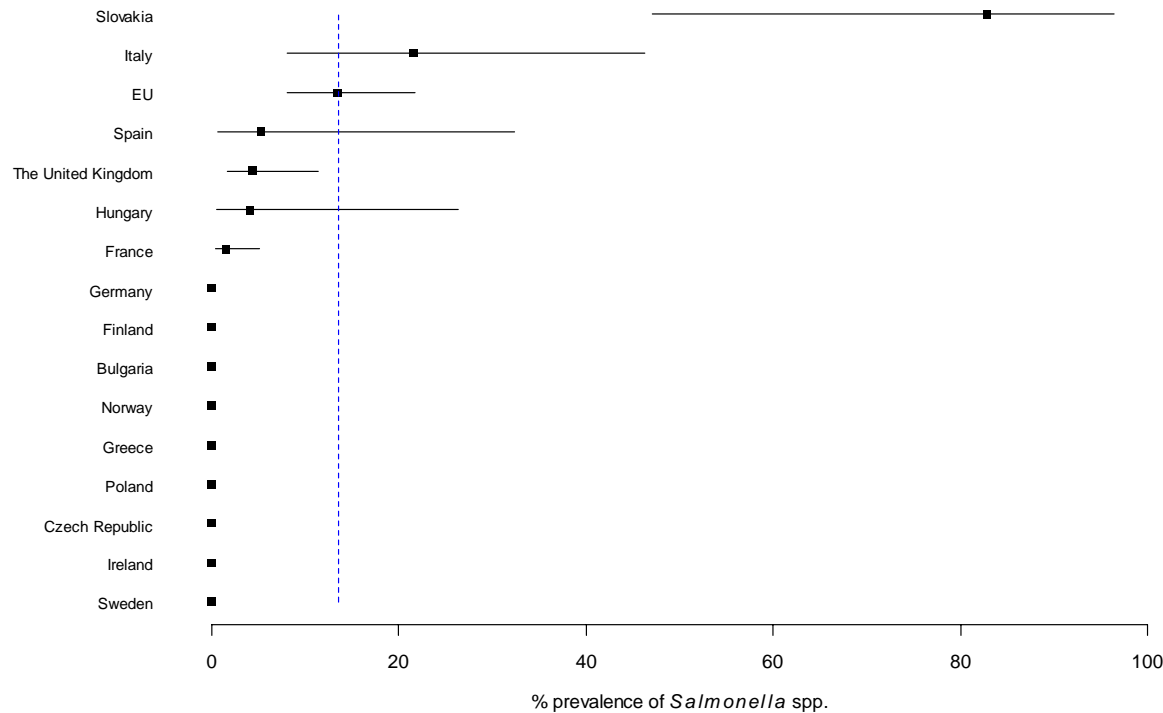
Table 2. Weighted prevalence of *Salmonella*¹ in breeding turkey flocks in the EU and Norway, 2006-2007.

Member State	N	<i>Salmonella</i> spp.		<i>S. Enteritidis</i> and/or <i>S. Typhimurium</i>		Serovars other than <i>S. Enteritidis</i> and/or <i>S. Typhimurium</i>	
		% prevalence	CI	% prevalence	CI	% prevalence	CI
Bulgaria	7	0		0		0	
Czech Republic	4	0		0		0	
Finland	15	0		0		0	
France	205	1.6	0.5 - 5.2	0.5	0.1 - 3.3	1.1	0.2 - 5
Germany	98	0		0		0	
Greece	6	0		0		0	
Hungary	13	4.1	0.5 - 26.3	0		4.1	0.5 - 26.3
Ireland	2	0		0		0	
Italy	28	21.5	8 - 46.3	8.3	2.5 - 24.4	16.6	5.1 - 42.4
Poland	6	0		0		0	
Slovakia	21	82.9	47.1 - 96.3	0		82.9	47.1 - 96.3
Spain	10	5.3	0.6 - 32.4	0		5.3	0.6 - 32.4
Sweden	1	0		0		0	
The United Kingdom	116	4.4	1.6 - 11.4	0.5	0.1 - 3.2	3.9	1.3 - 10.9
EU	532	13.6	8.1-21.8	1.7	0.6 - 4.9	12.3	7.0 - 20.6
Norway	7	0		0		0	

N = number of tested flocks; % prevalence = weighted prevalence estimate; CI = 95% confidence interval

¹ For some MSs, the sum of the weighted prevalence for *Salmonella* Enteritidis and / or *S. Typhimurium* plus the weighted prevalence for *Salmonella* belonging to other serovars is not equal to the weighted prevalence for *Salmonella* spp. Such apparent discrepancies can be attributed to the combined effects of co-infection of multiple serovar groups in the same flock, the attribution of weights based upon holding size, and rounding error in the model – based estimates.

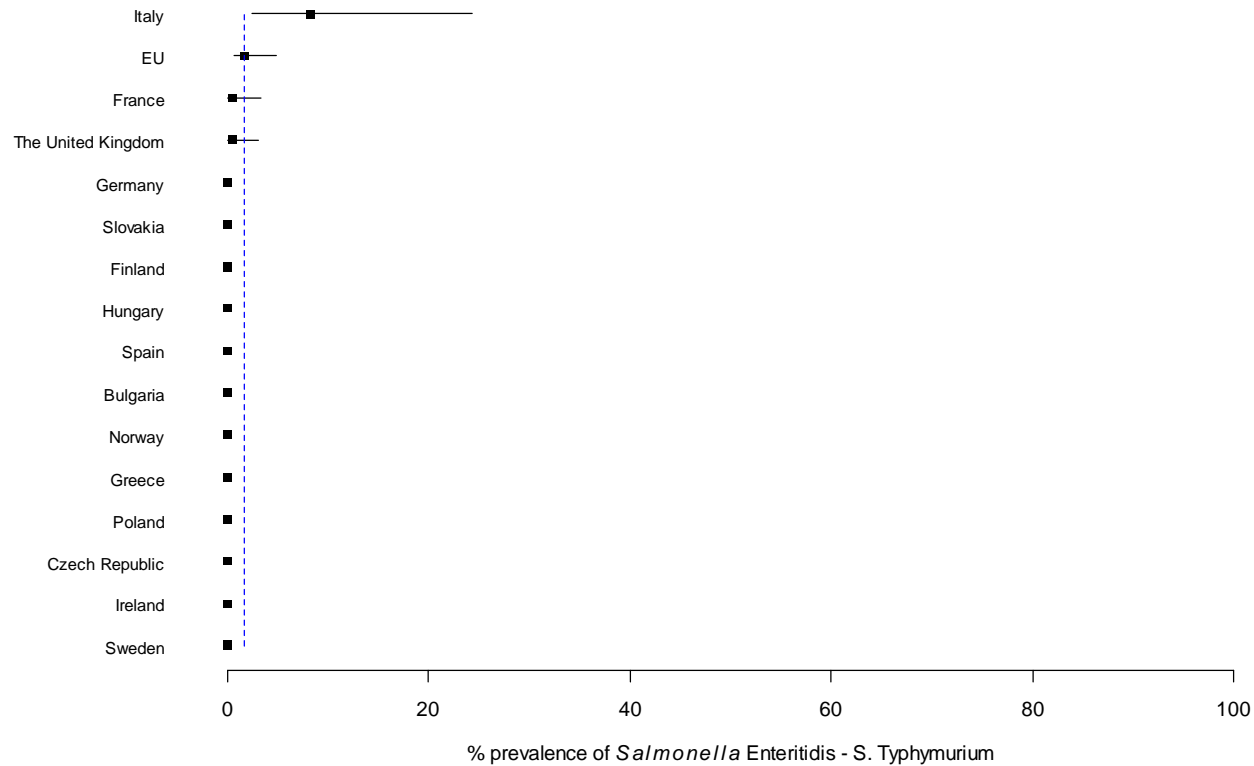
Figure 1. Weighted prevalence* of *Salmonella* spp. in breeding turkey flocks in the EU and Norway, 2006-2007. Horizontal bars represent 95% confidence intervals.**



* Breeding turkeys flock prevalence estimate (proportion of the total number of breeding turkey flocks over the one year period that were positive).

** Confidence intervals are not represented for MSs where no flock was found positive (prevalence = 0); these negative MSs are ordered, from top to bottom, by decreasing number of tested flocks.

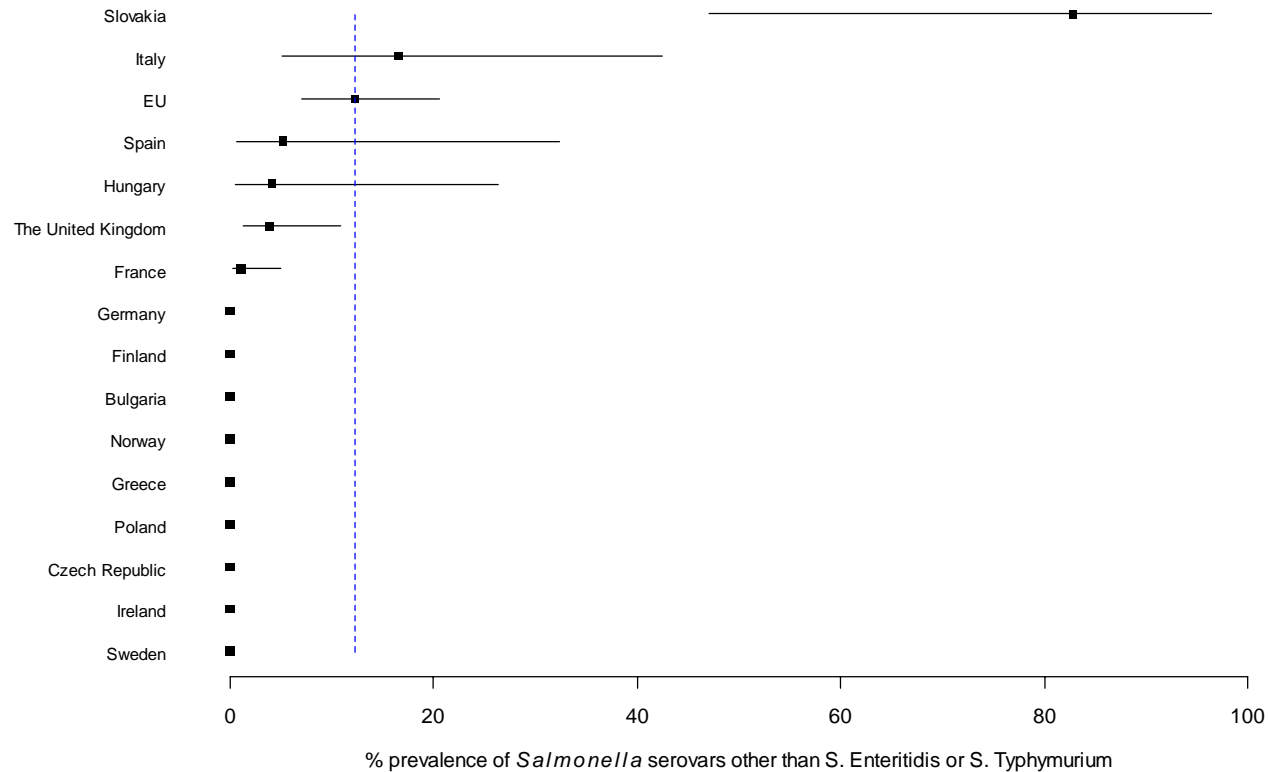
Figure 2. Weighted prevalence* of *Salmonella* Enteritidis and/or *S. Typhimurium* in breeding turkey flocks in the EU and Norway, 2006-2007. Horizontal bars represent 95% confidence intervals.**



* Breeding turkeys flock prevalence estimate (proportion of the total number of breeding turkey flocks over the one year period that were positive).

** Confidence intervals are not represented for MSs where no flock was found positive (prevalence = 0); these negative MSs are ordered, from top to bottom, by decreasing number of tested flocks.

Figure 3. Weighted prevalence* of serovars other than *Salmonella* Enteritidis or *S. Typhimurium* in breeding turkey flocks in the EU and Norway, 2006-2007. Horizontal bars represent 95% confidence intervals.**



* Breeding turkeys flock prevalence estimate (proportion of the total number of breeding turkey flocks over the one year period that were positive).

** Confidence intervals are not represented for MSs where no flock was found positive (prevalence = 0); these negative MSs are ordered, from top to bottom, by decreasing number of tested flocks.

4.2.2. Flocks with fattening turkeys

The weighted *Salmonella* prevalences in flocks with fattening turkeys in each MS and at EU level as well as for Norway are presented in Table 3. The raw, unweighted prevalence estimates are reported in Annex I, section IV-1.

Salmonella spp. was found in 19 out of 22 MSs providing data on fattening turkey flocks (Figure 4). 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%). 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. The EU-level, weighted prevalence estimate (3.8%) was almost equal to the unweighted prevalence (3.9%). MS-level prevalence peaked in the Czech Republic followed by Belgium and Italy (Figure 5).

Salmonella serovars other than *S. Enteritidis* and/or *S. Typhimurium* was found in 19 MSs and prevalence values were similar to those observed for *Salmonella* spp. (Figure 6).

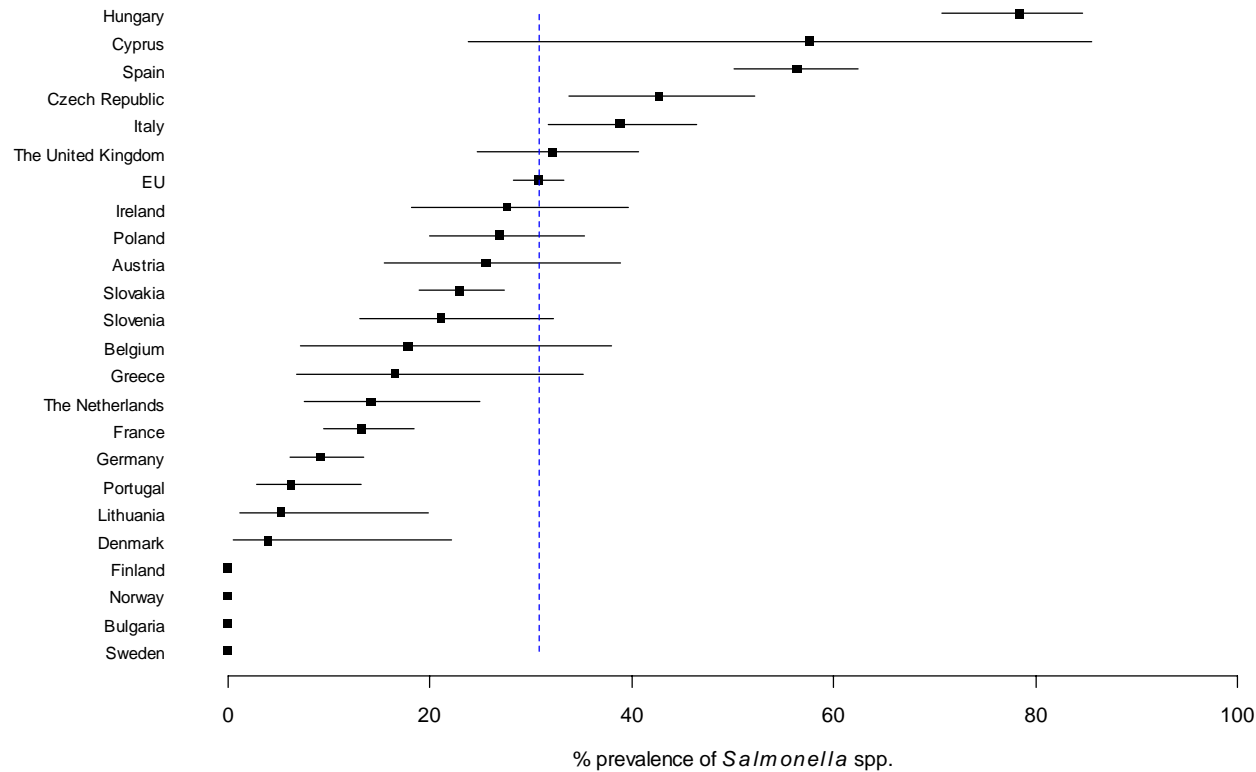
Table 3. Weighted prevalence of *Salmonella*¹ in fattening turkey flocks in the EU and Norway, 2006-2007.

Member State	N	<i>Salmonella</i> spp.		<i>S. Enteritidis</i> and/or <i>S. Typhimurium</i>		Serovars other than <i>S. Enteritidis</i> and/or <i>S. Typhimurium</i>	
		% prevalence	CI	% prevalence	CI	% prevalence	CI
Austria	202	25.5	15.5 - 38.9	0.4	0.1 - 2.7	25.1	15.1 - 38.7
Belgium	74	17.8	7.1 - 38	7.1	1 - 36.3	10	4.9 - 19.4
Bulgaria	17	0		0		0	
Cyprus	14	57.6	23.9 - 85.5	0	0 - 0	57.6	23.9 - 85.5
Czech Republic	194	42.7	33.8 - 52.1	18.4	12.4 - 26.4	25.2	16.9 - 35.8
Denmark	59	4.0	0.6 - 22.2	0	0 - 0	4	0.6 - 22.2
Finland	133	0		0		0	
France	326	13.3	9.4 - 18.4	3.8	1.9 - 7.4	9.5	6.4 - 14
Germany	295	9.2	6.2 - 13.4	2.6	1.3 - 5.2	6.8	4.3 - 10.8
Greece	43	16.5	6.7 - 35.1	0	0 - 0	16.5	6.7 - 35.1
Hungary	289	78.5	70.7 - 84.6	3.6	1.7 - 7.3	76.7	69 - 83
Ireland	259	27.6	18.1 - 39.7	0	0 - 0	27.6	18.1 - 39.7
Italy	268	38.8	31.8 - 46.4	6.1	3.5 - 10.2	33.6	26.8 - 41.2
Lithuania	63	5.3	1.2 - 19.9	1.5	0.2 - 9.1	4.4	1.2 - 14.8
Poland	322	26.9	19.9 - 35.4	4.2	2.4 - 7.2	23.4	16.6 - 31.9
Portugal	105	6.3	2.9 - 13.2	0	0 - 0	6.3	2.9 - 13.2
Slovakia	25	22.9	19 - 27.4	0	0 - 0	22.9	19 - 27.4
Slovenia	131	21.1	13.1 - 32.2	4.7	1.7 - 12.1	14.5	8.3 - 24.1
Spain	380	56.3	50.1 - 62.4	2.8	1.5 - 4.9	54.3	48.1 - 60.4
Sweden	14	0		0		0	
The Netherlands	172	14.1	7.5 - 24.9	1.5	0.3 - 6.9	12.2	6.1 - 23
The United Kingdom	317	32.2	24.7 - 40.6	4.6	2.2 - 9	28	20.9 - 36.5
EU	3,702	30.7	28.2 - 33.2	3.8	3.0 - 5.0	27.3	25.0 - 29.8
Norway	67	0		0		0	

N = number of tested flocks; % prevalence = weighted prevalence estimate; CI = 95% confidence interval

¹ For some MSs, the sum of the weighted prevalence for *Salmonella* Enteritidis and / or *S. Typhimurium* plus the weighted prevalence for *Salmonella* belonging to other serovars is not equal to the weighted prevalence for *Salmonella* spp. Such apparent discrepancies can be attributed to the combined effects of co-infection of multiple serovar groups in the same flock, the attribution of weights based upon holding size, and rounding error in the model – based estimates.

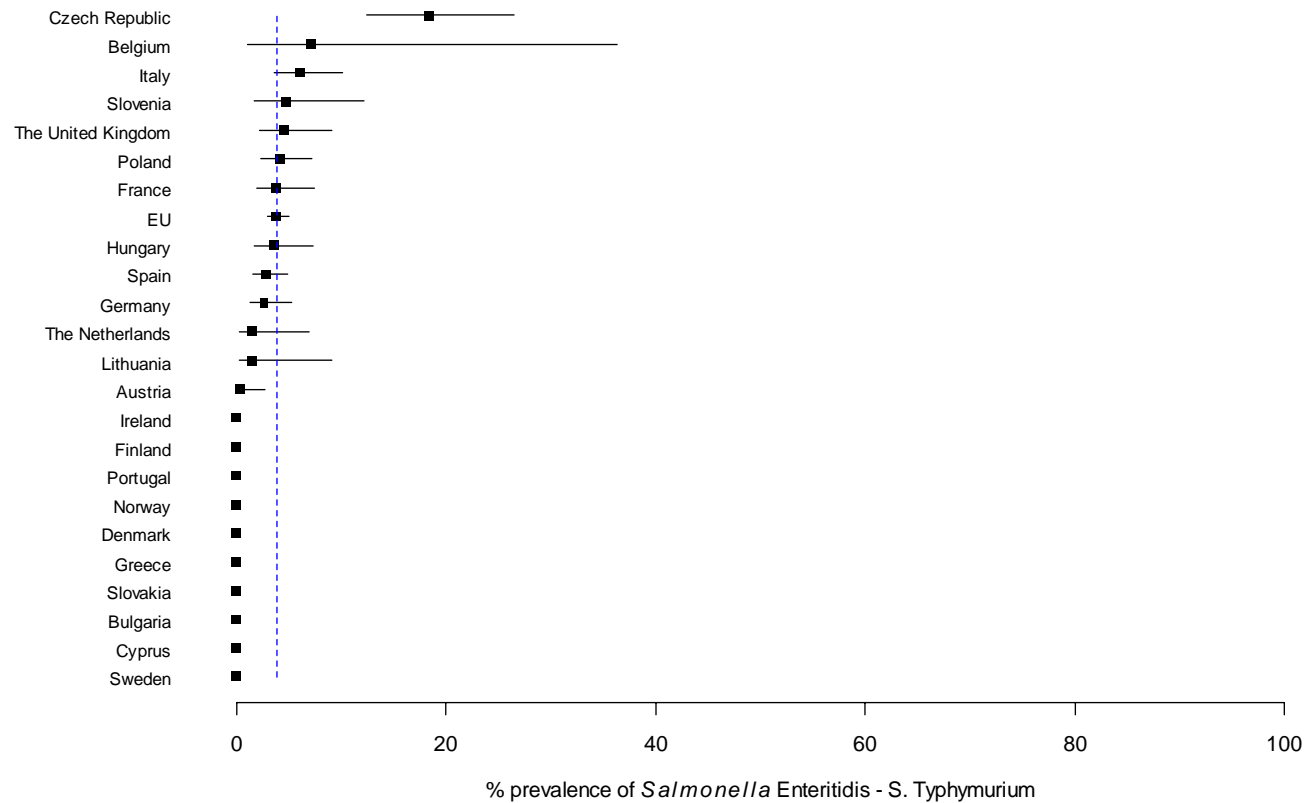
Figure 4. Weighted prevalence* of *Salmonella* spp. in fattening turkey flocks in the EU and Norway, 2006-2007. Horizontal bars represent 95% confidence intervals.**



*: Fattening turkeys flock prevalence estimate (proportion of the total number of fattening turkey flocks over the one year period that are positive).

** Confidence intervals are not represented for MSs where no flock was found positive (prevalence = 0); these negative MSs are ordered, from top to bottom, by decreasing number of tested flocks.

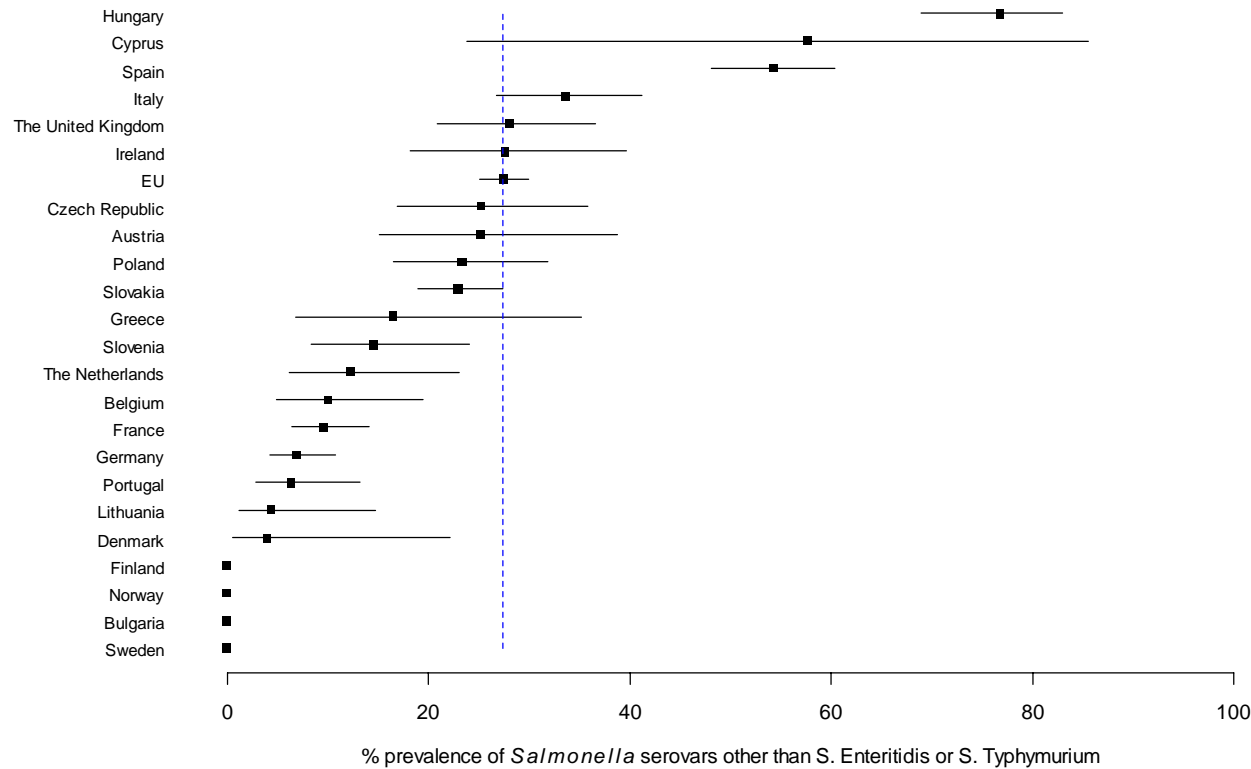
Figure 5. Weighted prevalence* of *Salmonella* Enteritidis and/or *S. Typhimurium* in fattening turkey flocks in the EU and Norway, 2006-2007. Horizontal bars represent 95% confidence intervals.**



* Fattening turkeys flock prevalence estimate (proportion of the total number of fattening turkey flocks over the one year period that are positive).

** Confidence intervals are not represented for MSs where no flock was found positive (prevalence = 0); these negative MSs are ordered, from top to bottom, by decreasing number of tested flocks.

Figure 6. Weighted prevalence* of serovars other than *Salmonella* Enteritidis or *S. Typhimurium* in fattening turkey flocks in the EU and Norway, 2006-2007. Horizontal bars represent 95% confidence intervals.**



* Fattening turkeys flock prevalence estimate (proportion of the total number of Fattening turkey flocks over the one year period that are positive).

** Confidence intervals are not represented for MSs where no flock was found positive (prevalence = 0); these negative MSs are ordered, from top to bottom, by decreasing number of tested flocks.

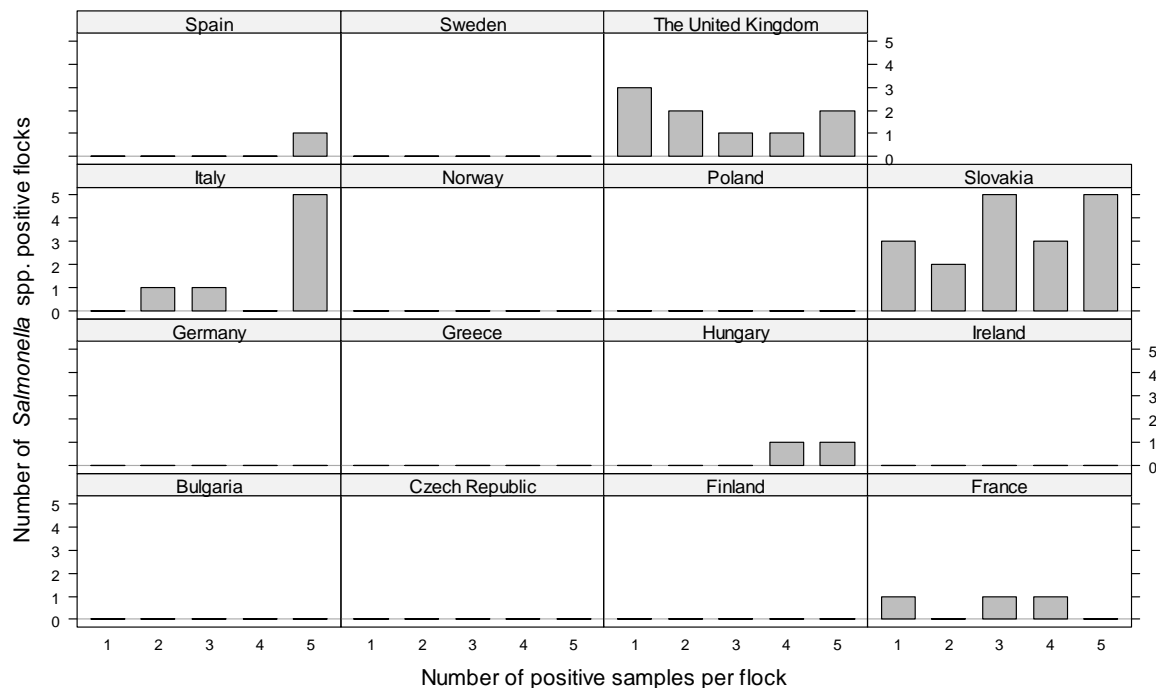
4.3. Number of *Salmonella* spp. positive samples per flock

A total of five samples were taken from each flock sampled and, in positive flocks, one to five samples were positive.

4.3.1. Flocks with breeding turkeys

The overall proportions of *Salmonella* spp. positive breeding flocks found positive on the basis of one, two, three, four and five positive samples was not evenly distributed but was 17.5%; 12.5%; 20.0%; 15.0% and 35.0%, respectively. The MS-specific distribution of the within-flock number of *Salmonella*-positive samples in the positive breeding turkey flocks varied between countries and is shown in Figure 7.

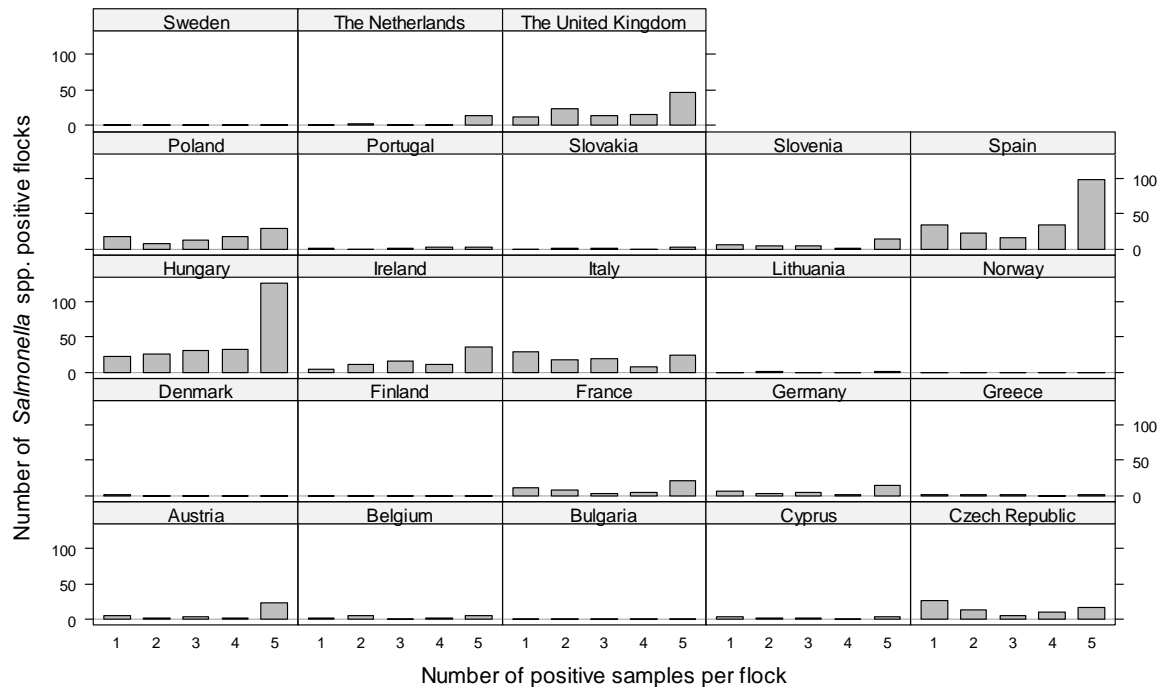
Figure 7. Distribution of the within-flock number of positive samples in *Salmonella* spp. positive flocks with breeding turkeys observed in the EU MSs, 2006-2007.



4.3.2. Flocks with fattening turkeys

The overall proportions of *Salmonella* positive fattening flocks found positive on the basis of one, two, three, four and five positive samples was not evenly distributed, but was 16.9%; 13.7%; 12.2%; 13.2% and 44.0%, respectively. The MS-specific distribution of the within-flock number of *Salmonella*-positive samples in the positive fattening turkey flocks varied among countries and is shown in Figure 8. However, almost all MSs had a major proportion of their *Salmonella* infected flocks with all five samples positive.

Figure 8. Distribution of the within-flock number of positive samples in *Salmonella* spp. positive flocks with fattening turkeys observed in the EU MSs, 2006-2007.



4.4. Sensitivity analysis of the effect of number of samples per flock on *S. Enteritidis* and/or *S. Typhimurium* EU prevalence

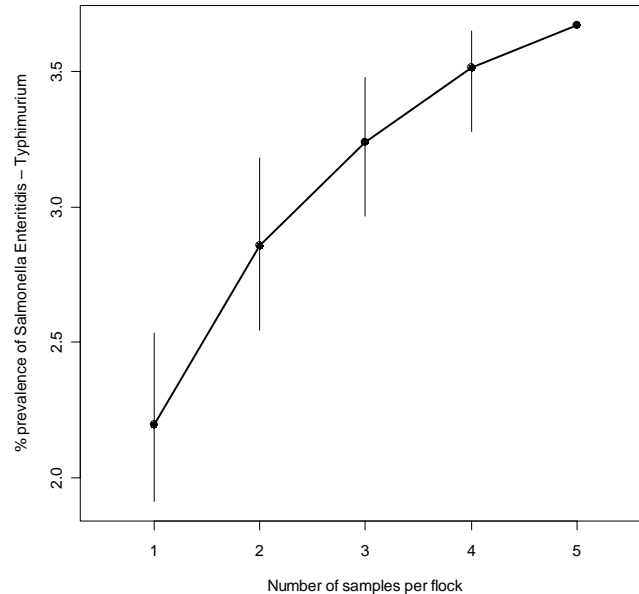
4.4.1. Flocks with breeding turkeys

S. Enteritidis and/or *S. Typhimurium* were found in breeding flocks in only three MSs. Moreover less than 1% of the sampled flocks were positive. Consequently, simulated prevalence estimates of *S. Enteritidis* and/or *S. Typhimurium*, which were obtained through the EU-level sensitivity analysis, were characterised by extreme uncertainty, as demonstrated by very wide confidence intervals. Therefore, the results of sensitivity analysis for breeding flocks were not considered as useful and are not presented in this report.

4.4.2. Flocks with fattening turkeys

Figure 9 represents the simulated effect of the number of samples per flock on the EU-level prevalence of *S. Enteritidis* and/or *S. Typhimurium* in fattening turkey flocks. The sensitivity of sampling and the EU-level prevalence decreased with decreasing sample size, i.e. collecting only two instead of five samples would have lead to a prevalence estimate of 2.8% (95% confidence interval: 2.5%, 3.2%), instead of 3.8%.

Figure 9. Simulated EU prevalence of *S. Enteritidis* and/or *S. Typhimurium* -positive flocks with fattening turkeys and 95% confidence intervals for sample sizes less than five per flock.



Similarly, results for each MS are reported in Annex I, section IV-3. At the MS' level, the general tendency follows a similar pattern as for the EU level. However, variability across MSs is large.

4.5. Frequency distribution of *Salmonella* serovars

The serotyping of *Salmonella* isolates was mandatory according to the technical specifications of the survey. At least one isolate from each positive sample was to be typed according to the Kaufmann-White Scheme. Results from any flock where the serovar information was not available for any isolate were excluded from the final dataset.

4.5.1. Flocks with breeding turkeys

In total there were 135 *Salmonella*-positive samples (5.0% of 2,695 samples) originating from 40 positive breeding turkey flocks. More than one *Salmonella* serovar was not isolated from any *Salmonella*-positive sample.

The frequency distribution of isolated *Salmonella* serovars in the EU is listed in Table 4. This table is ranked based on the percentages of specific *Salmonella* serovar-positive flocks, as flock was the epidemiological unit of interest. MS-specific overviews of the frequency distribution of serovars are shown in Annex V.

S. Saintpaul was the most frequently reported serovar from the breeding turkey flocks in EU, found in 42.5% of the *Salmonella* positive flocks. The two next most frequent serovars were *S.*

Kottbus and *S. Typhimurium* (17.5% and 10.0% of the *Salmonella* positive flock, 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 United Kingdom (four flocks positive). *S. Typhimurium* was the most frequently reported serovar for Italy (three flocks positive).

4.5.2. Flocks with fattening turkeys

There were a total of 3,814 *Salmonella*-positive samples (20.2% of 18,845 samples) originating from 1,084 positive fattening flocks. Two different *Salmonella* serovars were isolated from 20 *Salmonella*-positive samples.

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. MS-specific overviews of the frequency distribution of serovars are shown in Annex VI.

S. Bredeney was the most frequently reported serovar from the fattening turkey flocks in EU, representing 17.2% of the *Salmonella* positive flocks. The three next most frequent serovars were *S. Hadar*, *S. Derby* and *S. Saintpaul* (14.0%, 11.3% and 10.4% of the positive flocks, respectively). *S. Saintpaul* and *S. Typhimurium* were the serovars most commonly isolated in terms of the number of MSs, in total 12.

The distribution of the serovars varied widely amongst the MSs. *S. Bredeney* was the dominant serovar in only two MSs: Hungary and Italy. In fact, Hungary accounted for 75.8% (141 out of 186), while Italy accounted for 20.4% (38 out of 186) of the *S. Bredeney*-positive flocks. *S. Hadar* was the leading serovar in three MSs: Austria, Lithuania and Spain. Spain accounted for 71.1% (108 out of 152) of the *S. Hadar* -positive flocks. *S. Derby* was the leading serovar in two MSs: France and Portugal, *S. Saintpaul* in three MSs: Poland, Slovakia and The Netherlands, and *S. Typhimurium* in Germany.

From comparison of the MS-specific overviews of the frequency distribution of serovars in breeding and in fattening turkeys (Annexes V and VI) it can be generally noticed that the diversity of observed serovars in fattening turkeys was bigger compared to the one in breeding flocks. Also all isolated serovars in breeding flocks are almost always also isolated in the fattening flocks in the same MS, with the exception of one serovar, *S. Corvalis* in France.

Table 4. Frequency distribution of isolated *Salmonella* serovars in the breeding turkey flocks baseline survey in the EU and Norway, 2006-2007.

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

Table 5. Frequency distribution of isolated *Salmonella* serovars in the fattening turkey flocks baseline survey in the EU and Norway, 2006-2007.

	Samples with serovars (N=3,834)		Holdings with serovars (N=934)		Flocks with serovars (N=1,084)		Countries with serovars
	N	%	N	%	N	%	N
<i>S. Bredeney</i>	633	16.5	157	16.8	186	17.2	6
<i>S. Hadar</i>	494	12.9	146	15.6	152	14.0	10
<i>S. Saintpaul</i>	417	10.9	105	11.2	112	10.3	12
<i>S. Derby</i>	377	9.8	122	13.1	123	11.3	11
<i>S. Kottbus</i>	286	7.5	88	9.4	90	8.3	9
<i>S. Typhimurium</i>	272	7.1	84	9.0	86	7.9	12
<i>S. Orion</i>	231	6.0	29	3.1	66	6.1	2
<i>S. Infantis</i>	204	5.3	55	5.9	72	6.6	4
<i>S. Enteritidis</i>	117	3.1	54	5.8	55	5.1	8
<i>S. Agona</i>	99	2.6	20	2.1	31	2.9	8
<i>S. Newport</i>	95	2.5	30	3.2	33	3.0	9
<i>S. Blockley</i>	86	2.2	39	4.2	40	3.7	7
<i>S. Indiana</i>	71	1.9	26	2.8	32	3.0	8
<i>S. London</i>	70	1.8	31	3.3	31	2.9	1
<i>S. Heidelberg</i>	46	1.2	17	1.8	18	1.7	3
<i>S. Kedougou</i>	44	1.1	12	1.3	12	1.1	2
<i>S. Senftenberg</i>	35	0.9	15	1.6	15	1.4	7
<i>S. Montevideo</i>	34	0.9	11	1.2	13	1.2	3
<i>S. Zanzibar</i>	25	0.7	11	1.2	12	1.1	2
<i>S. Virchow</i>	23	0.6	11	1.2	11	1.0	2
Others	191	5.0					
<i>Salmonella</i> untypeable	2	0.1	2	0.2	2	0.2	2
Total isolates	3,852						

4.6. Correlation between the *Salmonella* flock prevalence in flocks with breeding turkeys and in flocks with fattening turkeys

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 non-parametric rank correlation procedure which can be used when few data pairs (15) are available.

The estimated correlations are displayed in Table 6. This table also includes p-values from testing the null hypothesis of no association between the prevalence estimates in the two types of flocks. Significant correlation was observed for *Salmonella* spp. and for *S. Enteritidis* or Typhimurium ($p < 0.05$), whereas correlation for serovars other than *S. Enteritidis* or Typhimurium was near the threshold of statistical significance.

Table 6. Spearman correlation coefficients and corresponding p-values for the test of the correlation between the prevalence estimates of breeding and fattening turkeys equal to zero.

	ρ	p-value
<i>Salmonella</i> spp.	0.563	0.036
<i>S. Enteritidis</i> or <i>S. Typhimurium</i>	0.611	0.020
Serovars other than <i>S. Enteritidis</i> or <i>S. Typhimurium</i>	0.523	0.055

These significant results are based on calculations taking into account the results of MSs that reported no positive outcomes for both breeding and fattening turkeys.

4.7. Overview of the quality of the bacteriological testing

In the technical specifications of the baseline survey it was indicated that at least one isolate from each positive sample should be serotyped in the National Reference Laboratory (NRL) for *Salmonella*, following the Kaufmann-White scheme. For quality assurance of the serotyping, a maximum of 16 non-typable isolates of the one year survey had to be sent to the Community Reference Laboratory (CRL) for *Salmonella*.

The CRL-*Salmonella* reported on the quality of the serotyping of non-typable *Salmonella* isolates from the baseline survey in turkey flocks performed by the NRLs.

Seven NRLs-*Salmonella* (of the 23 participating countries) sent in some non-typable isolates to the CRL; 16 NRLs indicated that they had not found any non-typable isolates.

Only a very low number of non-typable *Salmonella* strains were found during this baseline survey by the NRLs-*Salmonella*. A total of 25 non-typable strains were received by the CRL-*Salmonella*. Of these strains, CRL-*Salmonella* was able to further identify 13 strains to serovar names. Although the CRL-*Salmonella* also followed the Kauffmann-White scheme for serotyping the strains, extra or alternative culture steps were used, which are in most cases not routinely used at

the NRLs-*Salmonella*, and were not required by the technical specifications of the survey. Because of this ‘special treatment’ the CRL-*Salmonella* was able to further identify the strains where the NRL was not able to do so. Still 11 isolates could only be identified to the level of subspecies and two isolates could only biochemically be identified as *Salmonella* while serotyping was not possible as the strains were rough.

5. Discussion

5.1. Survey design, and data analysis

The aim of this survey was to estimate the prevalence of *Salmonella* in turkey flocks in the EU. A flock is defined by Regulation (EC) No 2160/2003, as "a group of birds constituting a single epidemiological unit and, in the case of housed poultry, all birds sharing the same airspace".

Three issues were taken into consideration in the statistical analysis, in order to obtain valid prevalence estimates: 1) the potential correlation between outcomes (presence or absence of infection) for flocks belonging to the same holding; 2) sampling of different proportions of the total numbers of holdings present in the participating MSs; 3) sampling of different proportions of the numbers of flocks present in the sampled holdings. The statistical techniques that were implemented in the analysis (GEE) are specific for correlated observations (issue 1). Moreover, disproportionate sampling at the country (issue 2), and at the holding level (issue 3) were considered through weighting of the results. In this way, an effort was made to apply the most appropriate analysis to such a complex study design. The resulting, weighted prevalence estimates are therefore valid and representative indices of the presence of *Salmonella* spp. in EU turkey flocks. Therefore, such estimates are most suitable to be used in target setting for the control of *Salmonella* infection in the EU, and as references for further studies at the EU level and within MSs.

The boot-swab/sock method of obtaining pooled faecal samples from the environment of the flock is a reliable and sensitive method of detecting *Salmonella* spp. in a house of litter-bedded birds, and it was used in previous baseline surveys coordinated by the European Commission. Nevertheless, a sensitivity analysis of the sampling design suggests that, in fattening turkeys, the number of samples taken per flock might affect prevalence estimate for *Salmonella* Enteritidis and/or *Salmonella* Typhimurium. Accordingly, collecting less than five samples would have yielded lower prevalence values compared with those reported here. This result could be partially associated with the fact that each sample was taken from a different part of the house where a flock was reared. Because the distribution of *S. Enteritidis* and/or *S. Typhimurium* in the house may not be uniform, excluding one or more samples would reduce the probability of detecting the infection.

Turkey flocks are not uniformly distributed throughout the EU. This was particularly true for flocks of breeding turkeys which are concentrated in a small number of MSs. The very small numbers of breeding holdings in several MSs tended towards virtually complete coverage sampling (census) of breeder flocks.

The dataset analysed was not the complete dataset submitted by MSs, due to exclusion of some samples with implausible data values. In total, 2.2% of the flocks were excluded from the final EU dataset. This proportion of excluded data can be considered to be very small at EU-level. Therefore the exclusion is unlikely to have a significant impact on the results at the Community-level. On the other hand, in certain MSs, the proportion of excluded data was relatively high and reached 25% in Bulgaria (however, none of the excluded flocks from this MS was *Salmonella*

positive). Two MSs, Malta and Romania, did not submit any data. Since Romanian turkey population appears to be large (although entirely constituted by relatively small holdings), the impact of this MS to the EU prevalence of *Salmonella* could have been substantial, but it remains unknown.

5.2. Observed *Salmonella* turkey flock prevalence

5.2.1. Flocks with breeding turkeys

The EU-level, weighted prevalence of *Salmonella* spp. in breeding turkey flocks was 13.6%. This means that one in seven breeding flocks in the EU was expected to be infected with *Salmonella* spp. within nine weeks of slaughter. However the variation amongst MSs was considerable. *Salmonella* spp. was not detected in eight of the 14 MSs providing data on breeding flocks or in Norway, and prevalence was less than 6% in four out of six MSs where the infection was found. Prevalence in the remaining two MSs with *Salmonella*-positive breeding flocks, Italy and Slovakia, was in excess of 20% and 80% respectively. *S. Enteritidis* or *S. Typhimurium* were reported from the breeding flocks in three MSs, and the prevalence exceeded 1% only in Italy. In the MS with the highest prevalence of *Salmonella* spp. in breeding flocks, Slovakia, none of the isolates were *S. Enteritidis* or *S. Typhimurium*.

The relevance of *Salmonella* spp. infection in breeding turkeys is mainly related to the potential for vertical transmission to fattening flocks. 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. 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 stock¹. Overall, the findings of the present survey indicate localised *Salmonella* spp. problems in the breeding flocks of a small number of MSs with relatively high prevalence.

5.2.2. Flocks with fattening turkeys

The overall EU weighted prevalence of *Salmonella* spp. in fattening flocks was 30.7%. Variation existed amongst MSs, with three MSs reporting no detected *Salmonella* spp. Of the 19 MSs that reported *Salmonella* spp. in fattening flocks, six had prevalences in excess of the EU weighted prevalence, although for two of those MSs the prevalence seemed not markedly different from that EU weighted average. In analogy with the breeding turkeys, the contribution of *S. Enteritidis* or *S. Typhimurium* to this prevalence was much less than that of serovars other than *S. Enteritidis* or *S. Typhimurium*, 3.8% and 26.3% respectively. Of the 13 MS reporting *S. Enteritidis* or *S. Typhimurium*, only three MS reported an observed prevalence greater than 5%, one of which was 18.4%. In Hungary, where the highest prevalence of *Salmonella* spp. was observed, most of the isolates belonged to serovars other than *S. Enteritidis* or *S. Typhimurium*.

¹ Cox, N.A., N.J. Stern, S.E. Craven, M.E. Berrang, and M.T. Musgrove. 2000. Prevalence of *Campylobacter* and *Salmonella* in the cecal droppings of turkeys during production. J. Appl. Poultry Res. 9:542-545.

The reported EU prevalence of 30.7% means that almost one in three fattening flocks in the EU harbours *Salmonella* within three weeks prior to slaughter. Hygiene of slaughter and subsequent cutting and processing of meat may be optimised to minimise spread of *Salmonella* in the turkey food-chain. However, the presence of *Salmonella* in about one third of the flocks before the slaughtering reduces chances of producing turkey meat with low *Salmonella* contamination level.

5.3. Frequency of isolated *Salmonella* serovars

In breeding flocks of turkeys, no clearly dominant *Salmonella* serovar emerged in the present survey. The distribution of serovars was particularly heterogeneous, with no indication of EU-wide serovar of particular relevance. The most frequently-isolated serovar in the EU breeding flock population was *S. Saintpaul* accounting for 42.5% of the positive breeding flocks, but it was only present in Slovakia. *S. Kottbus* was the next most common serovar in breeding flocks at 17.5% of positive flocks; and the most widely distributed, being present in breeding flocks in three MSs. *S. Typhimurium* was the third most common serovar isolated in breeding flocks, present in two MSs, and the most frequent serovar in breeding flocks in one MS. Whilst human disease has been attributed to each of these serovars, only *S. Typhimurium* was amongst the ten most frequently isolated serovars in human salmonellosis cases in the EU in 2006 (Community Summary Report on Zoonoses in 2006¹).

In fattening turkey flocks, a dominant *Salmonella* serovar was equally unapparent as the serovar distribution greatly varied between the MSs. *S. Bredeney* was the serovar most frequently isolated from fattening flocks accounting for 17.2% of positive units. However, *S. Bredeney* demonstrated a relatively narrow geographic distribution; while being found in only six MSs, Hungary and Italy accounted together for more than 95% of the positive flocks. *S. Saintpaul* and *S. Typhimurium* were the two serovars most widely distributed in fattening turkey flocks, each reported by 12 MSs. In addition to these two serovars, *S. Hadar*, *S. Derby*, and *S. Kottbus* demonstrated frequent contributions to positive flocks, and wide distribution amongst MSs. Three of those six serovars, *S. Typhimurium*, *S. Hadar* and *S. Derby*, were amongst the ten most frequently isolated serovars in human salmonellosis cases in the EU in 2006 (Community Summary Report on Zoonoses in 2006).

Overall, this survey demonstrates a wide variation in the distribution of *Salmonella* serovars in turkeys and the absence of a dominant serovar in this poultry species. These results contrast with those found in *Gallus gallus* (fowl), where *S. Enteritidis* (uncommon in turkeys) predominates in both laying hens and broilers in many MSs. A risk factor analysis, as well as a more in depth analysis of the *Salmonella* serovars including the phage types will be presented in the Part B report.

5.4. Relevance of the findings to human health

This survey investigated the prevalence of *Salmonella* in the rearing environment of turkeys, and therefore, at the primary production phase of the food-chain. *Salmonella* serovars of potential

¹ The Community Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents, Antimicrobial Resistance and Foodborne Outbreaks in the European Union in 2006, *The EFSA Journal* (2006), 130.

public health significance were detected both in breeding and fattening flocks, in some MS-specific cases at relatively high prevalence. The translation of any risk from live birds to food may be modified, either adversely or positively, by subsequent food production processes such as transport, slaughter, cutting or processing. In particular, slaughter technology might facilitate horizontal transfer to carcasses from *Salmonella*-free flocks, while de-skinning operations such as filleting, and other processes such as freezing, might afford useful *Salmonella* reduction. At a consumer level, heat treatments, such as the thorough cooking normally received by turkeys, eliminates the risk arising from *Salmonella* contamination. However significant potential for cross contamination of the domestic environment including other foodstuffs, might arise from the manual manipulations common to turkey carcasses e.g. stuffing / washing, as well as the issues arising from physical size of turkey carcasses exceeding the domestic capacity for raw meat storage and handling. Such augmentation or amelioration of risk would not be reflected in a prevalence survey such as this.

Additionally, despite a relatively biosecure approach to primary production, *Salmonella* infection in turkeys represents a potential source of risk for other food producing animal species and zoonotic pathways, possibly through vectors such as wildlife. Thus these data provide a useful overall indication of the potential role of turkeys in the epidemiology of *Salmonella* species in the global ecosystem.

As the serovar distribution varied greatly amongst the MSs, the situations are likely to be MS specific. The most common serovar associated with human disease, *S. Enteritidis* was only rarely isolated from turkeys. The second most common serovar implicated in human disease, *S. Typhimurium* was one of the more frequently isolated from turkeys in this survey, and serovars of emerging human significance such as *S. Hadar* and *S. Derby* were also amongst the more frequent and more widely distributed turkey isolates. A more in depth analysis of serovar distribution, including animal source attribution for serovars provoking human cases of salmonellosis, will be the subject of a specific EFSA report.

5.5. The *Salmonella* reduction targets

A reduction target for *S. Enteritidis* or *S. Typhimurium*, as foreseen in Regulation (EC) No 2160/2003 and as justified from a public health perspective, may well be informed by the finding of this survey. With some MS-specific exceptions, the prevalences of these two serovars, particularly *S. Enteritidis*, is already quite low at an EU level, lower than those identified for broilers (*Gallus gallus*), which means that a target prevalence of 1% or less is likely to be achievable. MSs may be informed by the specific results, and investigate risk management approaches to address specific reduction targets for serovars such as *S. Saintpaul*, *S. Kottbus*, *S. Bredeney*, *S. Hadar*, *S. Infantis* or *S. Derby*, in case these serovars are of public health importance in their countries.

6. Conclusions

This baseline survey has established a baseline turkey flock observed *Salmonella* prevalence in EU, which should inform the EU *Salmonella* reduction target. The baseline prevalence figures may be used later to compare future trends and follow the impact of the control programmes. The other variables studied, such as the proportion of positive samples in flocks, impact of reducing number of samples and the serovar distribution, will also contribute to understanding and managing the *Salmonella* infections.

- The survey provides valuable data for risk managers on the prevalence and distribution of *Salmonella* in EU MSs, and results are suitable to be used for setting targets for the reduction of the frequency of the infection in the EU.
- In the EU about half of the MSs reported having holdings with breeding turkeys and France accounted for about half of the breeding flocks and breeding birds. With regard to fattening turkeys, almost all MSs have flocks and France accounted for about one sixth of the fattening flocks and fattening birds.
- An effort was made to achieve a harmonised sampling across MS to favour comparability of results. Moreover, statistical analysis was carried out in order to account for survey design. However, very small numbers of flocks were tested in certain MSs. Therefore, even if the sample comprised all available flocks during the sampling period, prevalence, as an estimate of the risk of infection in turkey production in those MS, was affected by a high degree of uncertainty.
- The observed flock prevalence of *Salmonella* spp. varied widely amongst MSs.
- The weighted prevalence of *Salmonella* spp. in breeding flocks within the EU was estimated to be 13.6% whereas the weighted flock prevalence of *S. Enteritidis* and/or *S. Typhimurium* was 1.7%.
- *S. Saintpaul* was the most frequently isolated serovar from breeding flocks (42.5% of positive flocks) but it was only found in Slovakia. Of the two next frequent serovars, *S. Kottbus* was found in three MSs, and *S. Typhimurium* in two MSs.
- For fattening turkey flocks the weighted EU prevalence of *Salmonella* spp. was estimated to be 30.7% whereas the weighted flock prevalence of *S. Enteritidis* and/or *S. Typhimurium* was 3.8%.
- The six most frequently isolated *Salmonella* serovars from the fattening flocks were *S. Bredeney* (17.2% of the positive flocks), *S. Hadar* (14.0%), *S. Derby* (11.3%), *S. Saintpaul* (10.4%), *S. Kottbus* (8.3%), *S. Typhimurium* (7.9%) and out of these, *S. Hadar*, *S. Derby*, and *S. Typhimurium* are amongst the 10 most commonly reported serovars in humans.
- The serovar distribution varied amongst the MSs, many of them having a specific distribution pattern of their own. Often, for a specific *Salmonella* serovar, a few MSs accounted for the majority of the positive flocks.
- Reducing the number of samples taken from a flock of fattening turkeys is likely to have a strong impact on *S. Enteritidis* and/or *S. Typhimurium* flock prevalence estimation.
- There was correlation between serovars found in breeding flocks and fattening flocks in many MSs.
- *Salmonella* infected turkey flocks contribute to consequent contamination of fresh turkey meat. *Salmonella* infection in humans may result from undercooking of the meat or cross-contamination to other foods. Thorough cooking of the turkey meat and strict kitchen

hygiene would prevent or reduce the risk posed by *Salmonella* contaminated turkey meat at the consumer level.

7. Recommendations

- It is recommended that MSs would address in their *Salmonella* control programmes also serovars other than *S. Enteritidis* and *S. Typhimurium*, when these other serovars are of public health importance in their country.
- The analysis of potential risk factors for *Salmonella* spp. at the flock-level, including season and flock size, as well as in depth serovar and phage type analyses, should be the subjects of the report part B, and will help to generate hypotheses on maintenance and transmission of the infection and the importance of findings to public health.
- Although the level of data exclusions was low overall it affected certain MS disproportionately because of low numbers of flocks sampled. It is recommended that MS pay close attention to the data dictionary and exclusion criteria in future surveys to avoid losing data resulting from valuable sampling visits.
- The one-in-three positivity of fattening flocks would warrant enhanced hygiene measures and related official controls in order to reduce the *Salmonella* contamination of turkey meat.

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Abbreviations

CI	Confidence Interval
CRL	Community Reference Laboratory
EEA	European Economic Area
EFSA	European Food Safety Authority
EU	European Union
MS(s)	Member State(s)
NRL	National Reference Laboratory

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