SCIENTIFIC REPORT

Analysis of the baseline survey on the prevalence of *Salmonella* in turkey flocks, in the EU, 2006-2007

Part B: factors related to *Salmonella* flock prevalence and distribution of *Salmonella* serovars[1]

Report of the Task Force on Zoonoses Data Collection

(Question N° EFSA-Q-2006-041B)

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SUMMARY

A European Union-wide baseline survey was carried out to determine the prevalence of *Salmonella* in breeding turkey flocks and fattening turkey flocks in order to provide the scientific basis for setting a Community reduction target for *Salmonella* in turkey flocks. The sampling of turkey flocks took place between October 2006 and September 2007. Five pairs of bootswab samples were taken from the housing environment of breeding turkey flocks in the nine weeks preceding slaughter and from fattening turkey flocks in the three weeks preceding slaughter. A total of 532 breeding turkey flocks and 3,702 fattening turkey flocks with validated results from the European Union were included in the survey analyses. The analysis of *Salmonella* prevalence was carried out earlier and was published by the European Food Safety Authority on 30 April 2008 in the Part A report (EFSA 2008). The Community prevalence of *Salmonella*-positive breeding flocks was 13.6%, whereas prevalence of *Salmonella*-positive fattening flocks was 30.7%. The Member State-specific observed flock prevalence varied greatly.

In breeding turkey flocks, *Salmonella* infection was detected in six out of 14 Member States providing data. Visual inspection of the association between potential risk factors and *Salmonella* by means of graphs indicated that *Salmonella* positive flocks tended to be associated with holdings with relatively large numbers of birds distributed across flocks of relatively small size. The age of turkeys was lower in positive than in negative breeding flocks. Moreover, the prevalence of infection was greater in unvaccinated than in vaccinated breeding turkey flocks. In general, factors descriptively associated with *Salmonella* in breeding turkey flocks reflected the characteristics of the turkey production industry in the small number of Member States in which positive breeding flocks were concentrated. In fact, it was not possible to carry out formal statistical analysis of the effects of risk factors for *Salmonella* in breeding turkey flocks.

The effects of risk factors for *Salmonella* in fattening turkey flocks was analysed by multiple logistic regression. The risk of *Salmonella* infection increased as the number of turkeys in the holding increased. However, in holdings with the same number of turkeys, the risk of *Salmonella* infection decreased if birds were sub-divided into a relatively large number of flocks. The risk of *Salmonella* in fattening turkey flocks was greater in the periods October 2006-December 2007 and January-March 2007 than in July-September 2007. The presence of breeding turkey flocks in the same holding increased the risk of infection for fattening turkey flocks. Vaccinated flocks were at lower risk of infection than unvaccinated flocks. Finally, the risk of *Salmonella* was greater for free-range flocks (standard and organic) than for flocks raised conventionally.

The regression analyses also revealed that there is considerable variation between the significant risk factors for *Salmonella* infections of fattening turkeys among Member States.

The distribution of *Salmonella* serovars in fattening turkey flocks in different Member States was very heterogeneous. This suggests that the transmission of most *Salmonella* serovars mainly occurs among flocks within the same Member State. Only *S*. Saintpaul was detected in a cluster of neighbouring Member States, and this might suggest transmission and/or a common source of the serovar across these Member States.

The apparently poor correlation between *Salmonella* serovars present in turkeys with serovars isolated from salmonellosis cases in humans would suggest that the role of turkeys as a source of *Salmonella* infections in humans is lower than the role of some other animal species, such as *Gallus gallus* (broilers and laying hens). However, serovars such as *S*. Typhimurium, *S*. Hadar and *S.* Derby were found in turkeys and are often implicated in human disease. Therefore, the potential role of turkey meat as a source of *Salmonella* for people should not be overlooked.

Analysis of serovar and phage type distribution suggested that, while feed and other animal species could act as sources of *Salmonella* for turkey flocks, their role in this aspect remains to be clarified.

It is recommended that Member States consider the factors found to be associated with *Salmonella* infection in turkeys in this survey when they are designing their *Salmonella* control programmes for turkey flocks. In particular, Member States are encouraged to guarantee *Salmonella* controls in breeding flocks in order to prevent the subsequent infection of fattening flocks. Vaccination might be considered as a tool for control in Member States where *Salmonella* is present. Specific bio-security measures may also be devised for free-range farming. Member States are also invited to carry out further studies at national level to identify specifically national risk factors for *Salmonella* infections in turkeys.

Key words: *Salmonella*, turkeys, baseline surveys, risk factors.

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1 INTRODUCTION

This report describes the results of a baseline survey carried out in the European Union (EU) to estimate the prevalence of *Salmonella* spp. in commercial breeding turkey flocks and in fattening turkey flocks. This study was the third in a series of baseline surveys of *Salmonella* carried out within the EU. The objective of the surveys was 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 agents, which aims to reduce the incidence of food-borne diseases in the EU[2], results of the survey will enable the setting of Community targets for the reduction of the prevalence of infection in food animals including turkey flocks.

A report from the Task Force on Zoonoses Data Collection on the "Analysis of the baseline survey on the prevalence of *Salmonella* in turkeys flocks in the EU, 2006-2007, part A *Salmonella* prevalence estimates" *(*Part A report) was issued on 30 April 2008 (EFSA, 2008). That report included the analysis of the prevalence of *Salmonella* in turkey flocks, the most frequent *Salmonella* serovars reported, and sampling design.

The present Part B report contains analyses of the effects of potential risk factors for *Salmonella* infection. Further analyses of the distribution of serovars and phage types of *Salmonella* isolates are also included. Objectives, sampling frame, diagnostic testing methods, as well as data collection and evaluation, reporting and timelines of the baseline survey are specified in Commission Decision 2006/662/EC and 2007/208/EC concerning a baseline survey on the prevalence of *Salmonella* in turkey flocks.

[2] OJ L 325, 12.12.2003, p. 1.

2 OBJECTIVES

The objectives of the baseline survey on the prevalence of *Salmonella* in turkey flocks in the EU are described in detail in the Part A report.

The specific objectives related to this Part B report are:

- to investigate the effect of potential risk factors, which may be associated with the *Salmonella* flock prevalence,
- to investigate *Salmonella* serovar distribution in turkey flocks across the EU,
- to analyse the information submitted by MSs regarding *S.* Enteritidis and *S.* Typhimurium phage types.

The analyses of antimicrobial susceptibility of *Salmonella* isolates from the survey will be specifically addressed in a separate report on antimicrobial resistance to be published by the European Food Safety Authority (EFSA).

3 MATERIALS AND METHODS

Detailed descriptions of the design of the baseline survey, of sample design and size, and of bacteriological testing are given in the Part A report and the document of the 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/2083/2006).

3.1 Data description

A detailed description of the validation and cleaning of the dataset from the surveys that were carried out is provided in the Part A report[3]. The final EU dataset contained data from 333 holdings and 532 breeding turkey flocks (from 14 MSs), and from 2,811 holdings and 3,702 fattening turkey flocks (from 22 MSs), resulting in 21,170 samples and 3,969 *Salmonella* isolates all together.

3.2 Analysis of factors associated with the EU *salmonella* flock prevalence

The general assumptions and framework of the statistical analysis carried out are reported in detail in the Part A report. The observed flock prevalence[4] was defined as the proportion of positive turkey flocks raised over the one-year period of the baseline survey in MSs.

The effect of potential risk factors was analysed at flock level, using the same model-based approach as used and described in the Part A report. A flock was considered positive if the presence of *Salmonella* spp. was detected in at least one of the five samples taken, otherwise it was considered negative.

3.2.1 Definition of outcome variables

For the risk factor analysis, data from breeding and fattening turkey flocks were analysed separately, and positivity for *Salmonella* spp. was the only considered outcome. In the Part A report, prevalence of *S*. Enteritidis and/or *S*. Typhimurium, and of *Salmonella* of serovars other than *S*. Enteritidis and/or *S*. Typhimurium were presented. However, *S*. Enteritidis and *S*. Typhimurium were relatively infrequent in the EU turkey population and their presence was limited to certain MSs. Therefore, the analysis of risk factors for the specific outcome of *S*. Enteritidis and/or *S*. Typhimurium positivity was not carried out.

[3] Data from Norway were not included in this Part B report.

[4] In this report the observed prevalence means the prevalence estimate that accounts for the aspects of clustering and of weighting but not for imperfect test sensitivity or specificity.

3.2.2 Choice of factors to be investigated

Information on potential risk factors of the turkey flock being *Salmonella* positive was collected through a questionnaire which was distributed to farmers at the time of sample collection. Potential risk factors or other factors affecting *Salmonella* positivity could be classified in the following categories:

1. month of sampling,
2. variables associated with holding size and characteristics,
3. variables associated with flock size and characteristics,
4. age of turkeys,
5. vaccination against *Salmonella*,
6. medication with antimicrobials,
7. time between the date of sampling and testing in the laboratory.

3.2.3 Exploratory analysis of potential risk factors

Categorical variables were analysed through frequency tables and bar graphs. Multiple bar graphs, by MS and for EU global data, were produced by lattice packages in the R software. Quantitative variables were described through measures of central tendency and dispersion such as mean and standard deviation as well as median and first and third quartiles. Box plots were used for graphical visualisation.

The association between each potential risk factor and the outcome variable was visually explored by:

a) multiple bar graphs of estimated (weighted) frequency counts of *Salmonella* positive and negative flocks, by MS and different levels of categorical variables;
b) bar graphs of prevalence and 95% confidence intervals, by different levels of categorical variables;
c) box plots of quantitative variables for *Salmonella* positive and negative flocks.

3.2.4 Analysis of multicollinearity among risk factors

The Variance Inflation Factor (VIF) was used as a formal method to detect correlation among risk factors (multicollinearity, explained in the section on regression analysis). Essentially, each potential risk factor is used as the outcome in a regression analysis (described in detail in Annex II). A VIF value that equals 1 indicates that there is no correlation among risk factors, whereas VIF values greater than 1 indicate a correlation. VIF values exceeding 10 are interpreted as an indication of strong multicollinearity.

3.2.5 Identification of possible factors associated with EU *Salmonella* flock prevalence

Multiple regression analysis was applied to obtain estimates of the association between each factor, adjusted for the effect of other factors (potential for confounding)[5]. Multiple regression analysis was carried out at EU level and separately by MS.

Type of statistical model used

Given the use of a binary outcome variable (*Salmonella* positive or negative flock status) taking only two, mutually exclusive values (which were coded as 1 when the diagnostic test was positive and 0 otherwise) logistic regression was the model of choice. However, as previously done in the prevalence estimation (Part A report) certain characteristics of the data needed to be taken into account in the analysis.

1. Certain flocks, the epidemiological unit of the analysis, belonged to the same holding and were, therefore, exposed to the same conditions, including certain risk factors of *Salmonella* infection, on which no information was available in the current survey (i.e. origin of birds and feed, bio-security measures). Moreover, transmission of *Salmonella* is more likely among flocks in the same holding than among flocks belonging to different holdings. It was, therefore, reasonable to believe that observations from flocks belonging to the same holding could not be considered as independent in statistical analyses. Consequently, correlation among outcomes in flocks from the same holding was taken into account in the multiple logistic regression analysis of the effects of potential risk factors. A detailed explanation of common methods for analysis of non-independent data is presented in Annex II, section 3.3. The effect of holding was included in risk factor analysis as random, resulting in a random intercept logistic regression. The assumption underlying this type of statistical model is that each holding, and consequently each flock belonging to the holding, was characterised by a certain baseline level of risk of infection, regardless of the exposure to risk factors considered in the survey. Compared with alternative approaches, including generalised estimating equations (GEE) which were used in the Part A report to estimate prevalence, random intercept models, which are used for this Part B report, are considered as more efficient (statistically powerful) in risk factor analysis.

[5] In bivariate analysis, a potential risk factor might appear to be associated with *Salmonella* infection just because of its association with another risk factor for the infection. If, for example, turkey flocks from MSs with high prevalence were mostly sampled in summer months, summer could result as strongly associated with *Salmonella* when analysing the data at EU level. In this case, conclusions on a strong seasonality of the infection could be drawn, although it was just the effect of unbalanced sampling. In fact, in this example, season may not have any real effect on *Salmonella* infection. Confounding is, therefore, the over- or under- estimation of the effect of a potential risk factor due to its association with other risk factors. In the example, the effect of season was overestimated due to the confounding effect of MS. In order to eliminate confounding, and to obtain valid estimates of the effect of season, an adjustment for MS is necessary, which can be achieved by multiple regression analysis. In certain cases, however, two or more potential risk factors may be so strongly associated that separate estimates of their respective effects cannot be obtained. In this case, we use the term collinearity or multicollinearity.

2. The pre-established sampling design of this survey can be defined as stratified and disproportionate. In fact, flocks were sampled from holdings that, in turn, were sampled from MSs. Holding and MS can, therefore, be considered as strata. The number of flocks sampled in a holding was not proportionate to the number of flocks reared in the same holding and in many circumstances only one flock was sampled regardless of holding size. In analogous fashion, the number of holdings that were tested in each MS was not proportionate to the number of holdings in the MS. As previously carried out when calculating prevalence (Part A report), weights were applied in the statistical analysis of the effects of risk factors of *Salmonella* for turkeys flocks. The weight to account for disproportionate sampling of flocks within a holding was calculated as the ratio between the number of flocks produced in a holding during a year divided by the number of flocks sampled in the same holding. The weight to account for disproportionate sampling of holdings within a MS was calculated as the ratio between the number of holdings in the MS divided by the number of holdings sampled in the same MS.

Model building for fattening turkey flocks at EU level

Multiple regression analysis of the effects of risk factors was carried out for fattening turkey flocks only. No statistical modelling was carried out for breeding flocks since *Salmonella* spp. was only detected in six out of the 14 MSs providing breeding flock data and most of the positive flocks (85%) originated from three MSs.

For fattening turkey flocks, the investigation of the association between risk factors and the presence of *Salmonella* spp. in the EU was done using several steps. First, logistic regression was implemented using a backward selection procedure to reduce the number of risk factors. The starting model contained the country and the mandatory risk factors of interest as fixed effects. Data from countries without infected flocks were included in the exploratory analysis of potential risk factors but were not considered in the EU level regression analysis. In the selection procedure, risk factors with p-values over 0.35 were systematically removed from the model. In a second step, a random intercept for holding was included in the resulting, final model by using the GLIMMIX procedure in the SAS® System. The model was further reduced by removing stepwise non-significant risk factors until only covariates with p-values less than or equal to 0.05 remained in the model.

Model building for fattening turkeys at MS level

A similar model building exercise was performed at MS level, and a separate model was determined for each MS. The model for each country was reduced so that covariates with p-values below or equal to 0.25 remained. Further, for those countries for which only one flock per holding was sampled, no random effect was included in logistic regression.

The results of the MS level regression analysis were presented in a matrix, where rows correspond to MS and columns to potential risk factors. Each cell in the matrix contained the odds ratio (OR) measuring the effect of the risk factor in the corresponding column, in the MS in the corresponding row. The aim of this type of data presentation is to identify effect and direction (positive or negative) effects of risk factors across MSs.

Model building including optional variables

The effects of the optional variables, which did not need to be reported mandatorily by MSs, were evaluated by adding these covariates to the final EU model obtained for mandatory variables and described in the previous section. The final model containing optional variables was obtained using 1,135 sampled flocks. A backwards stepwise selection procedure was adopted, excluding the non-significant covariates until all remaining risk factors were significant with p-values below or equal to 0.05. For each of the covariates in the final model, as well as for each of the remaining optional variables, multicollinearity was evaluated by VIF (see Annex II, Table 4.3.7).

3.3 Analysis of serovars and phage type distribution

3.3.1 Spatial distribution of reported *Salmonella* serovars

As the location (geographic coordinates) of the individual flocks enrolled in the survey was not known, analysis of the serovar distribution was carried out at country level. The spatial scan statistic developed by Kulldorff (SaTScan software) was applied to detect spatial clusters of EU MSs where each of the selected serovars was detected. The detection of clusters would allow generating hypotheses on transmission, or on common sources of *Salmonella* serovars in turkey flocks of neighbouring MSs. Moreover, SaTScan allowed the detection of individual MSs characterised by a risk of *Salmonella* infection in turkey flocks significantly higher than the EU average.

SaTScan uses a circular window of different sizes to scan the study area until a certain percentage of the total population is included. The most probable cluster is selected corresponding to the least likely circle to be observed by chance alone. SaTScan also accounts for multiple testing through the calculation of the greatest likelihood of occurrence for all possible cluster locations and sizes. The Poisson model was chosen, which requires information about the number of estimated positive flocks in each EU MS and population data. The estimated number of positive cases for each serovar was calculated from the estimated prevalence. All estimated positive flocks were geocoded to the centroid of its respective country. The maximum window size was defined here as 50% of the cases and 999 replications were performed. Cluster analysis was performed only for the fattening flocks. It was set to look for clusters of *Salmonella* spp., *S.* Bredeney, *S*. Hadar, *S*. Derby, *S*. Saintpaul, *S*. Kottbus and *S.* Typhimurium. Only the most likely cluster and non-overlapping significant secondary clusters are displayed in this analysis. For the analysis, the SaTScan output was imported into Arc GIS 9 to create cluster maps to visually examine and compare the identified clusters. Prevalence maps were produced for the same serovars which were analysed using SaTScan.

3.3.2 Comparison between *Salmonella* serovar and phage type distributions in turkeys, feed and human cases

The serovar distribution found in flocks with turkeys was compared with the serovar distribution by MS, in animal feed and in human salmonellosis cases, as reported in the Community Summary Report on Zoonoses in 2006 (EFSA, 2007a). Phage type distribution

was analysed for *S.* Enteritidis and *S.* Typhimurium in breeding turkey flocks and in fattening turkey flocks. The descriptive analysis of serovar and phage type data was performed in Microsoft Excel.

4 RESULTS

4.1 Analysis of factors associated with EU *Salmonella* flock prevalence

For breeding turkey flocks, the results of the univariate description of potential risk factors and the bivariate association between potential risk factors and *Salmonella* spp. infection are presented below. No formal statistical analysis or multiple regression was conducted for breeding flocks due to the few MSs reporting positive flocks.

For fattening turkey flocks, the univariate description of potential risk factors and the results of the multiple regression analysis are presented both at EU level and separately at individual MS level. Bivariate analysis for fattening flocks is presented in Annex II.

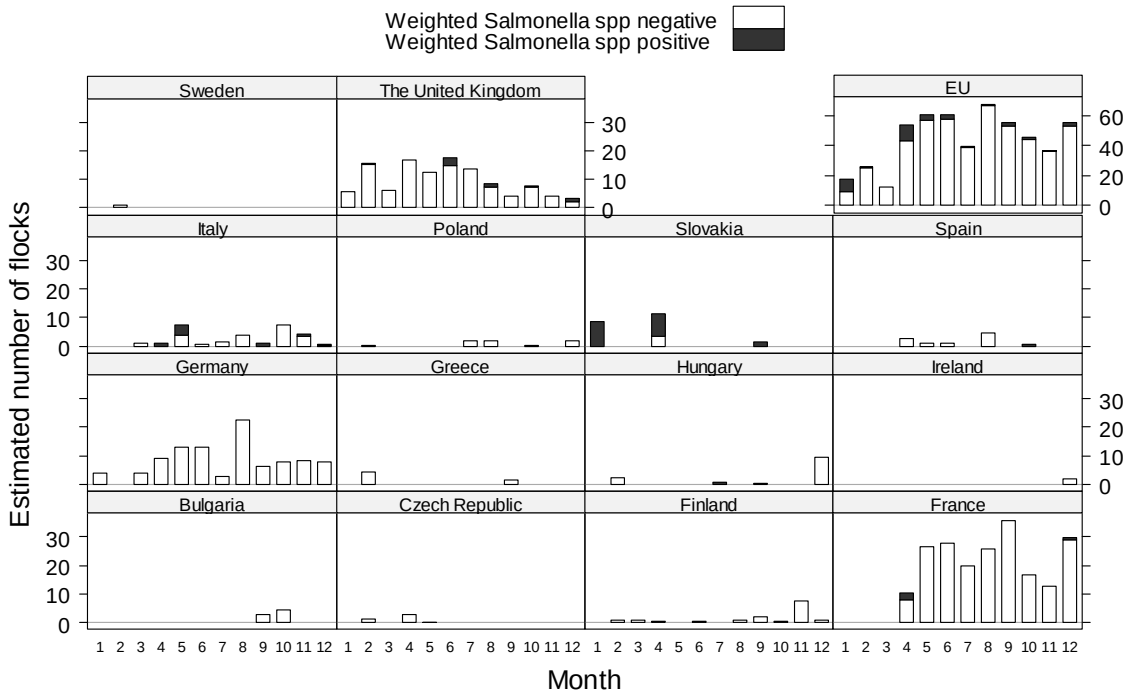
4.1.1 Breeding turkey flocks

Month of sampling

A graphical display of the numbers of breeding turkey flocks sampled and their *Salmonella* status at MS-specific and at EU level in each month during the survey is presented in Figure 1.

The number of sampled breeding turkey flocks at EU level was relatively low during the first three months of the survey (October - December 2006) and peaked in May 2007 when 67 flocks were sampled. Most positive flocks were found in those months when sampling was carried out in MSs with higher prevalence (October 2006, January and February 2007). There were, in fact, differences in the time of sampling at MS level. In France, the MS with the greatest population of breeding turkeys in the EU, sampling was carried out starting January 2007. Conversely, in the United Kingdom, sampling was initiated earlier and 17 flocks were sampled in November 2006.

Figure 1. Bar plot of the number of sampled breeding turkey flocks, by month and MS, and for the EU, and by *Salmonella* status.[6]



Variables associated with breeding holding size

The number of turkeys in the holding at the time of sampling is shown in Figure 2[7]. The EU level median was 6,142 birds, for the first quartile (Q1) 3,842, and for the third quartile (Q3) 8,861. The greatest median (Q1; Q3) was recorded in Bulgaria: 26,300 birds in a holding (2,300; 27,774).

The median number of turkeys present in the holding at the time of sampling was greater in holdings with *Salmonella* positive flocks than in holdings with negative flocks (Figure 3).

[6] Months are ordered from October 2006 (1) to September 2007 (12)

[7] In the horizontal box plots, the left of the box represents the first quartile of the distribution and the right the third quartile, whereas the bar inside the box represents the median. Small circular symbols indicate extreme values, differing from the box > 1.5 times the difference between the third and the first quartile (interquartile range).

Figure 2. Box plot of the number of breeding turkeys per holding at the time of sampling, in the EU and per MS.

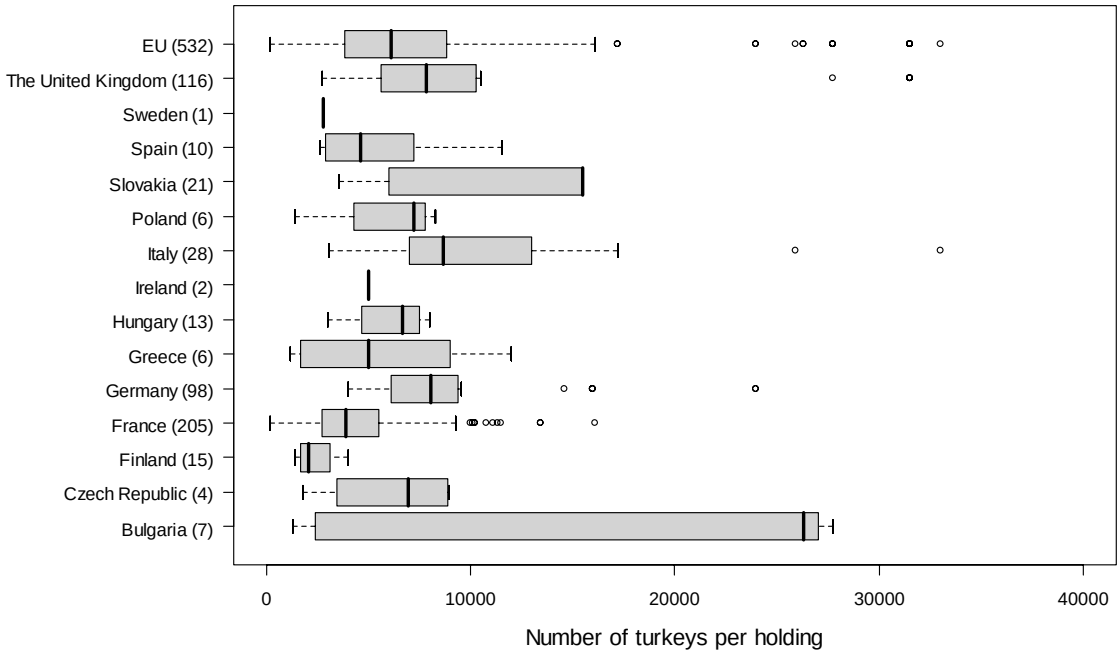
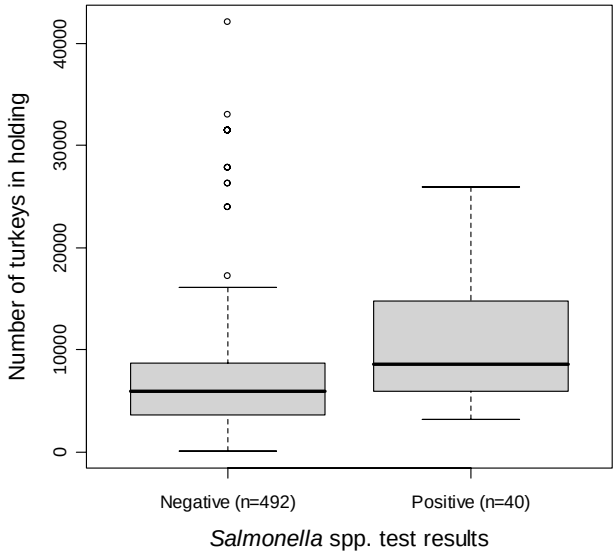


Figure 3. Box plot of the number of turkeys in a holding at the time of sampling, for *Salmonella* positive and negative breeding turkey flocks, in the EU.[8]

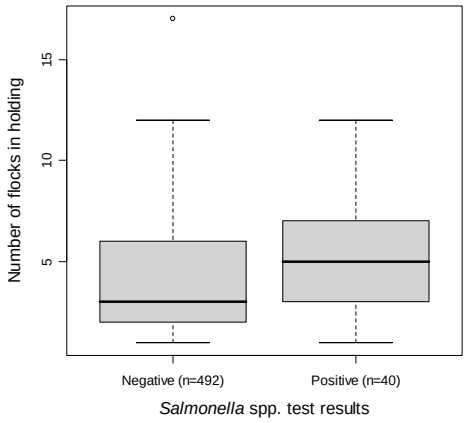


The median (Q1; Q3) number of flocks per holding at full capacity (Figure 1.I, Annex I), at EU level was 3.5 (2.0; 6.0) in the sampled holdings. The greatest number of flocks (17) was recorded in the United Kingdom, whereas medians were greatest in Slovakia (12) and Bulgaria (11).

The median number of flocks per holding at full capacity was greater for *Salmonella* positive than for negative breeding turkey flocks (Figure 4).

[8] - number of sampled flocks between brackets

Figure 4. Box plot of the number of breeding flocks per holding at full capacity, by *Salmonella* status.



Flock size

The median (Q1; Q3) number of breeding turkeys in the sampled flocks at EU level was 2,085 birds (1,558; 2,003) (Figure 2.I, Annex I). Among MSs, the greatest median number of turkeys per flock was recorded in the Czech Republic: 3,305 birds (1,644; 6,882). The smallest median was found in Slovakia: 1,300 (1,000; 1,600) which, on the other hand, had the greatest number of flocks per holding (Figure 1.I, Annex I). The median number of birds per flock was slightly greater for *Salmonella* negative flocks than for positive flocks (Figure 5).

Age of breeding turkeys

At EU level the median (Q1; Q3) age of breeding turkeys at sampling in this survey was 385 days (357; 406) but it varied greatly among MSs (Figure 3.I, Annex I). The greatest median age was recorded in Bulgaria: 705 days (22; 725). In Bulgaria, Czech Republic, Spain, and Germany, flocks with young birds were also sampled.

The median age of turkeys in *Salmonella* negative flocks was greater than the median age of turkeys in positive flocks (Figure 6). Thus, *Salmonella* positive flocks tended to have younger birds.

Figure 5. Box plot of the number of birds per flock at the time of sampling in *Salmonella* negative and positive breeding turkey flocks, in the EU.

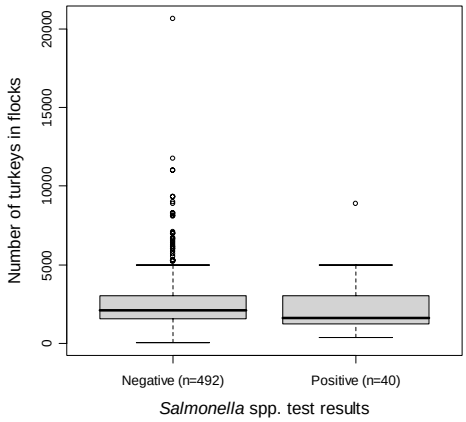
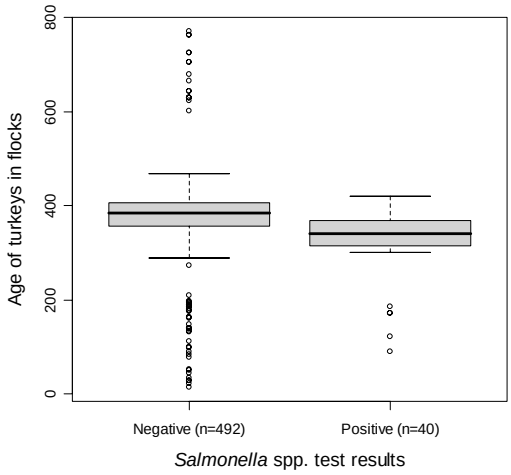


Figure 6. Box plot of the age of turkeys at the time of sampling in *Salmonella* negative and positive breeding turkey flocks.

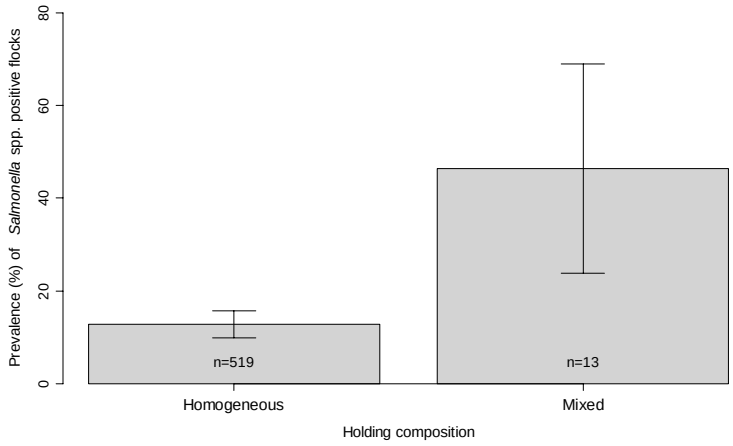


Variables associated with holding characteristics

Most breeding turkey flocks belonged to homogeneous holdings (containing breeding turkey flocks only), whereas small numbers of flocks from mixed holdings (containing both flocks with breeding and fattening turkeys) were sampled in some MSs (Figure 4.I, Annex I). Prevalence of *Salmonella* positive breeding flocks was greater in mixed holdings (Figure 7).

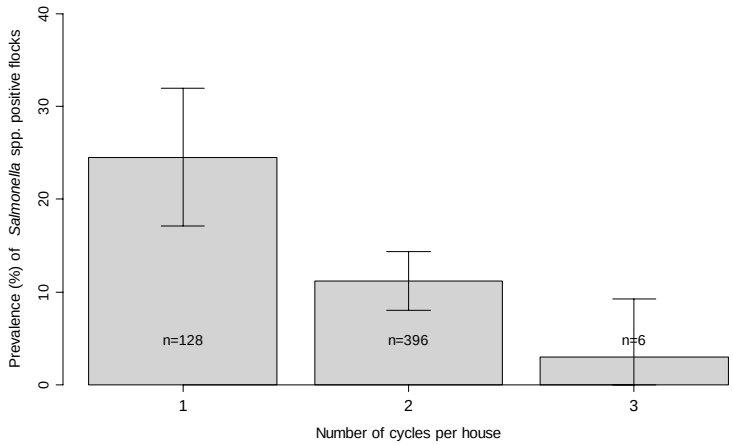
Two breeding turkey flocks were raised in the majority of houses, corresponding to two cycles per year (Figure 5.I, Annex I). Prevalence of *Salmonella* positive breeding flocks was greater in holdings where one cycle per house was carried out (Figure 8). Very few houses with three cycles were sampled.

Figure 7. Weighted *Salmonella* prevalence in breeding turkey flocks, by holding composition with 95% confidence intervals.[9]



[9] - n indicates the number of sampled flocks
- homogeneous: holding containing breeding turkey flocks only
- mixed: holding containing flocks with breeding and fattening turkeys

Figure 8. Weighted *Salmonella* prevalence in breeding turkey flocks by number of cycles per house per year, with 95% confidence intervals.[10]



Variables associated with breeding flock characteristics

The weighted prevalence of *Salmonella* spp. was higher in flocks of conventional production type compared to free-range standard production type for breeding turkeys (Figure 9). However, only 14 flocks of the free-range standard production type were sampled.

Vaccination against *Salmonella*

Vaccination against *Salmonella* in breeding turkey flocks was carried out in some MSs only (Figure 10), including Germany where the number of vaccinated flocks was greater than the number of unvaccinated flocks. Prevalence of *Salmonella* was higher in unvaccinated than in vaccinated flocks (Figure 11). In addition, there were five flocks of unknown vaccination status with a relatively high weighted *Salmonella* prevalence estimate.

[10] - n indicates the number of sampled flocks

Figure 9. Weighted *Salmonella* prevalence by breeding flock production type (conventional and free-range standard), with 95% confidence intervals (indicated by vertical bars).[11]

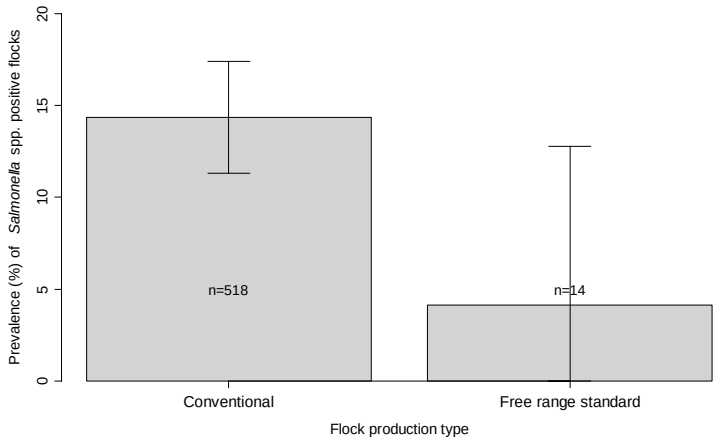
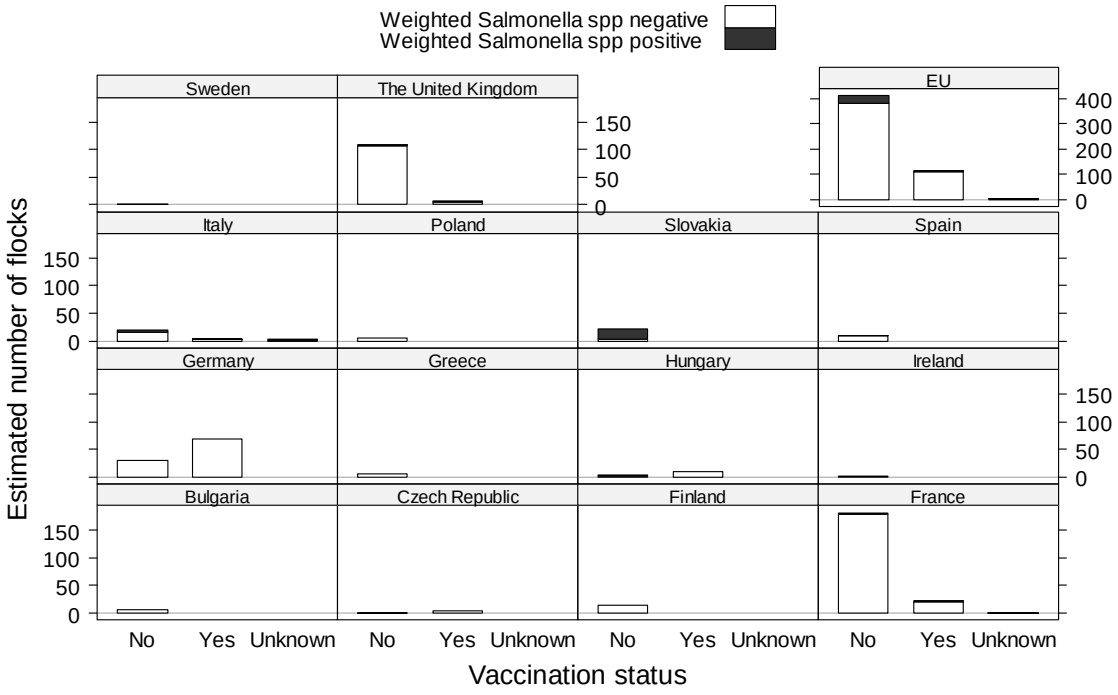
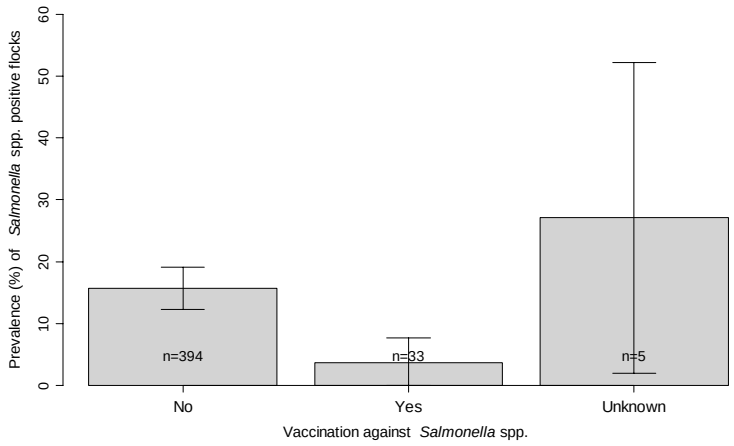


Figure 10. Frequency distribution of vaccination in breeding turkey flocks, by MS and for the EU, and by *Salmonella* status.



[11] n indicates the number of sampled flocks

Figure 11. Weighted *Salmonella* prevalence, and 95% confidence intervals, by flock vaccination status in the EU for breeding turkey flocks.[12]



Medication with antimicrobials

Antimicrobial treatment within two weeks prior to sampling was reported in 11 breeding turkey flocks and prevalence of *Salmonella* was similar in treated and untreated flocks (Figure 6.I, Annex I).

Time between sampling and testing

The time between the date of sampling and testing in the laboratory varied among MSs (Figure 12). In Slovakia, where most of *Salmonella* positive breeding flocks were found, this time period was mostly one or two days. In general, there was a decrease in *Salmonella* prevalence associated with the increased number of days between sampling and testing (Figure 13).

[12] - n indicates the number of sampled flocks

Figure 12. Frequency distribution of the time (days) between sampling and testing, for breeding turkey flocks, by MS and for the EU, and by *Salmonella* status.

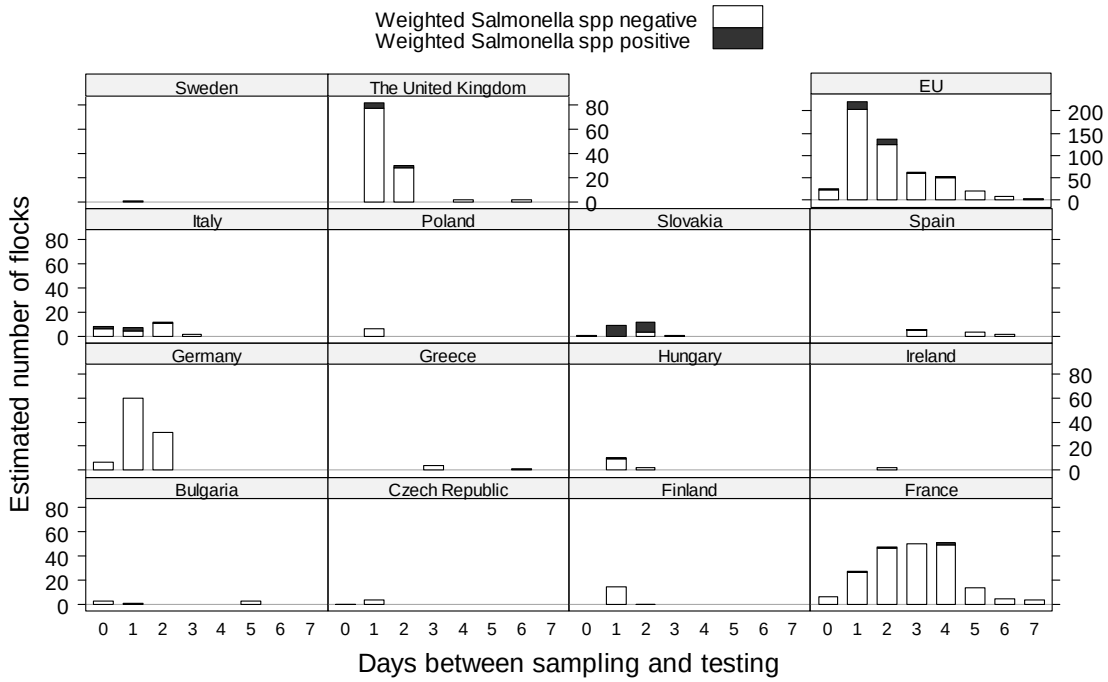
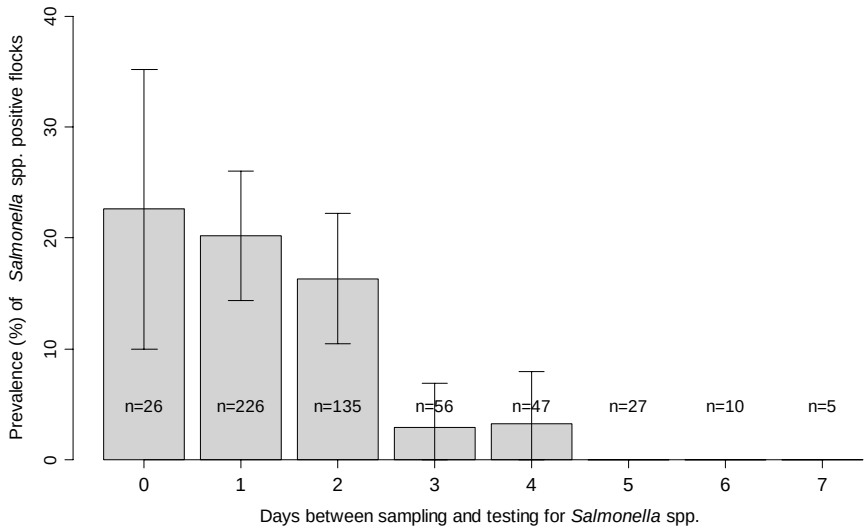


Figure 13. Weighted *Salmonella* prevalence by number of days between sampling and testing of breeding flock samples in the EU.[13]



[13] n indicates the number of sampled flocks

Overview of findings in breeding flocks of turkeys

Factors that were associated with *Salmonella* spp. infection in breeding turkey flocks reflected the characteristics of the turkey industry in certain MSs, particularly Slovakia, where 18 out of the total of 40 positive flocks were concentrated. Although associations were not tested by formal statistical analysis, graphical representation suggests a tendency of *Salmonella* spp. positive flocks belonging to holdings with relatively large numbers of birds distributed into many flocks of relatively small size. Turkey age tended to be lower in positive than in negative flocks. *Salmonella* prevalence was higher in the relatively small number of breeding flocks raised in mixed holdings, containing also fattening flocks, and in holdings where one cycle per house per year was carried out. Moreover, prevalence of infection was greater in unvaccinated than in vaccinated flocks, whereas no association was found with medication. *Salmonella* prevalence decreased with an increasing delay between sampling and testing.

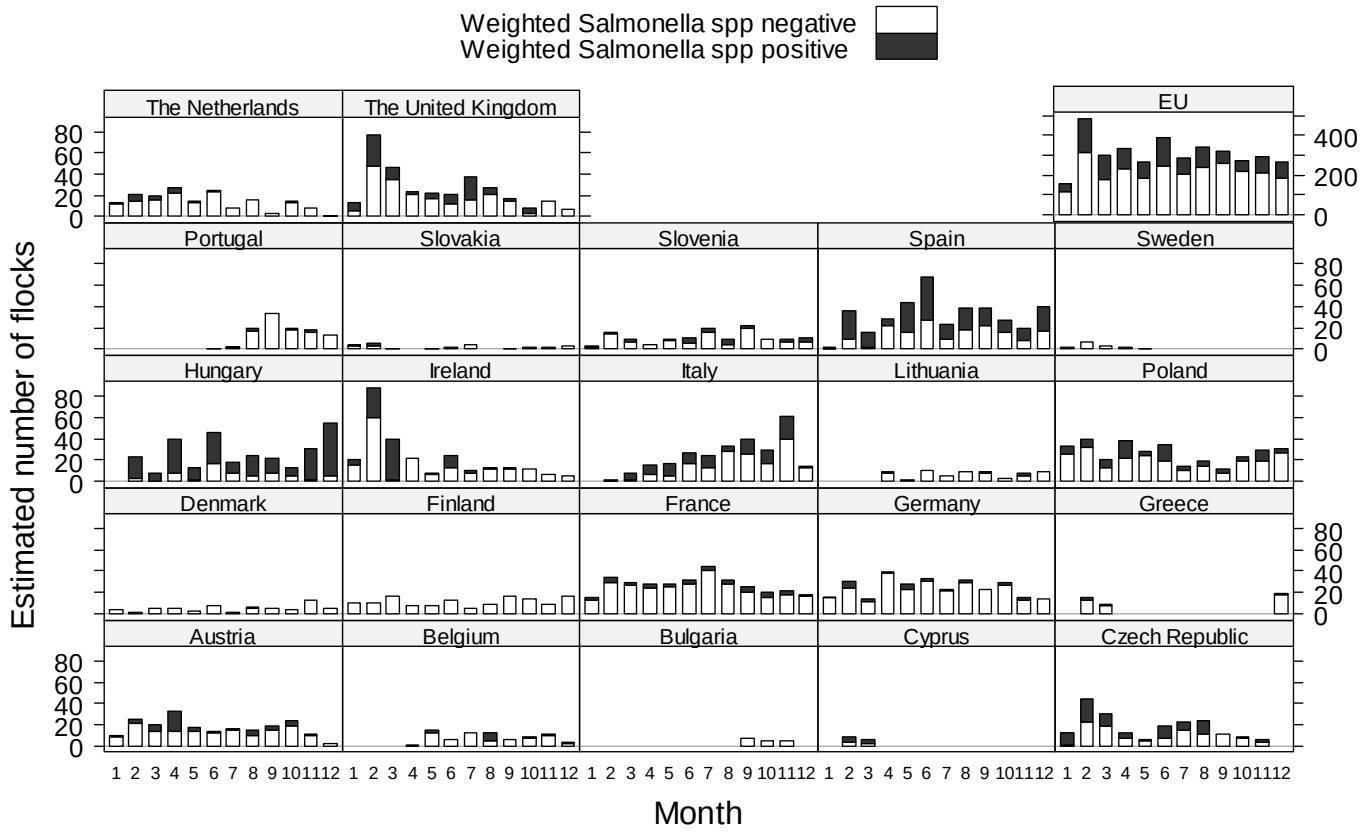
4.1.2 Fattening turkey flocks

4.1.2.1 Descriptive analysis of potential factors associated with *Salmonella* prevalence in fattening turkey flocks.

Month of sampling

A graphical display of the numbers of fattening turkey flocks sampled and their *Salmonella* status at MS-specific and at EU level in each month during the survey is presented in Figure 14. The number of sampled fattening turkey flocks was more evenly distributed throughout the year in certain MSs than in other MSs where sampling was characterised by seasonal peaks. The number of sampled flocks at EU level peaked in November 2006 (467) largely due to the contributions of Ireland and the United Kingdom, where most flocks were sampled in that month. A similar pattern of sampling in autumn to winter 2006 was observed in the Czech Republic. Conversely, in Italy, sampling was the most intense in summer 2007. Although no strong seasonal pattern was detected, the relative frequency of *Salmonella* positive flocks seems to be reduced in the last four months of sampling (June - September 2007).

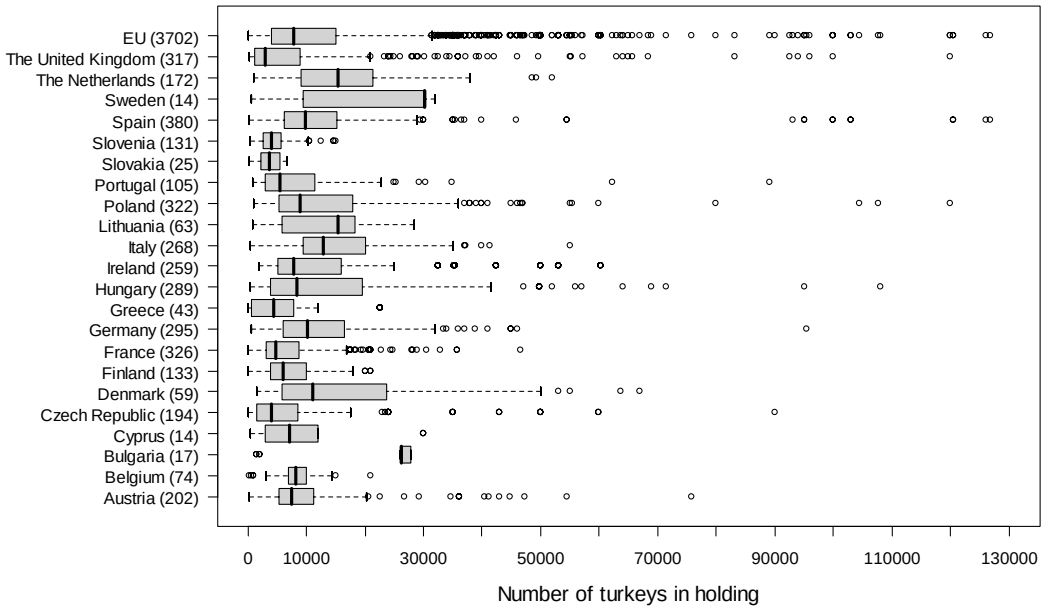
Figure 14. Frequency distribution of the number of tested fattening turkey flocks, by month, MS, and by *Salmonella* status. Months are ordered from October 2006 (1) to September 2007 (12).



Variables associated with holding size

The number of turkeys per holding at the time of sampling was very variable among MSs (Figure 15). The EU level median (Q1; Q3) was 7,805 birds (4,001; 15,000). The greatest median (Q1; Q3) was found in Sweden: 30,200 (14,600; 30,350), whereas the holding with the highest number of turkeys (419,815) was in the United Kingdom.

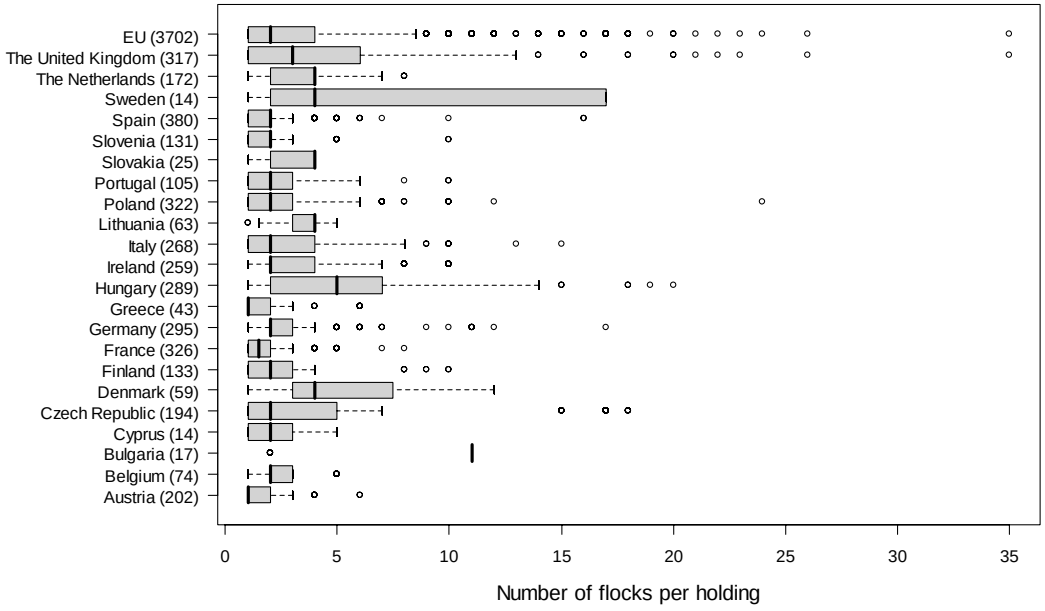
Figure 15. Box plot of the number of turkeys per holding at the time of sampling, in the EU and per MS.[14]



[14] A fattening flock in a holding in the United Kingdom with 419,815 turkeys at the time of sampling was excluded from the graph. Total number of sampled flocks between brackets.

The number of flocks per holding at full capacity, at EU level and by MS was also characterised by great heterogeneity (Figure 16). At EU level, the median (Q1; Q3) was 2.0 (1.0; 4.0), but in a holding in the United Kingdom the number was 35. The greatest median, Q1; Q3 (5.0, 2.0; 7.0) was recorded in Hungary.

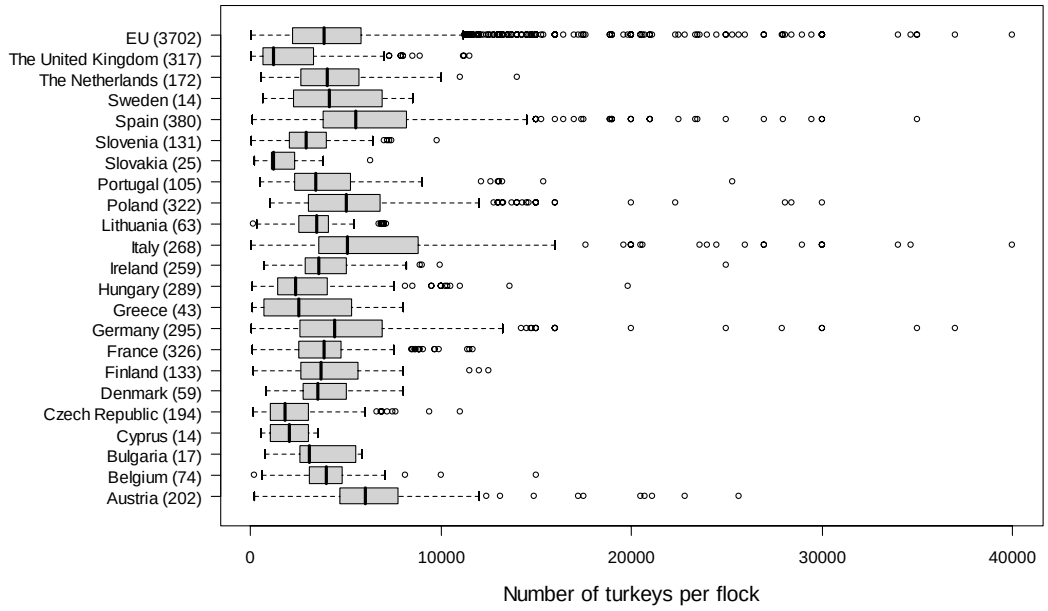
Figure 16. Box plot of the number of flocks per holding at full capacity, in the EU and per MS.



Flock size

The number of fattening turkeys in MSs and EU in the sampled flocks is represented in Figure 17. At EU level, the median (Q1; Q3) number of turkeys per sampled flocks was 3,851 (2,200; 5,800). The median value was greatest in Austria: 6,000 (4,718; 7,744). The smallest median was observed in the United Kingdom: 1,200 (650; 3,300).

Figure 17. Box plot of the number of fattening turkeys per flock, in the EU and per MS.



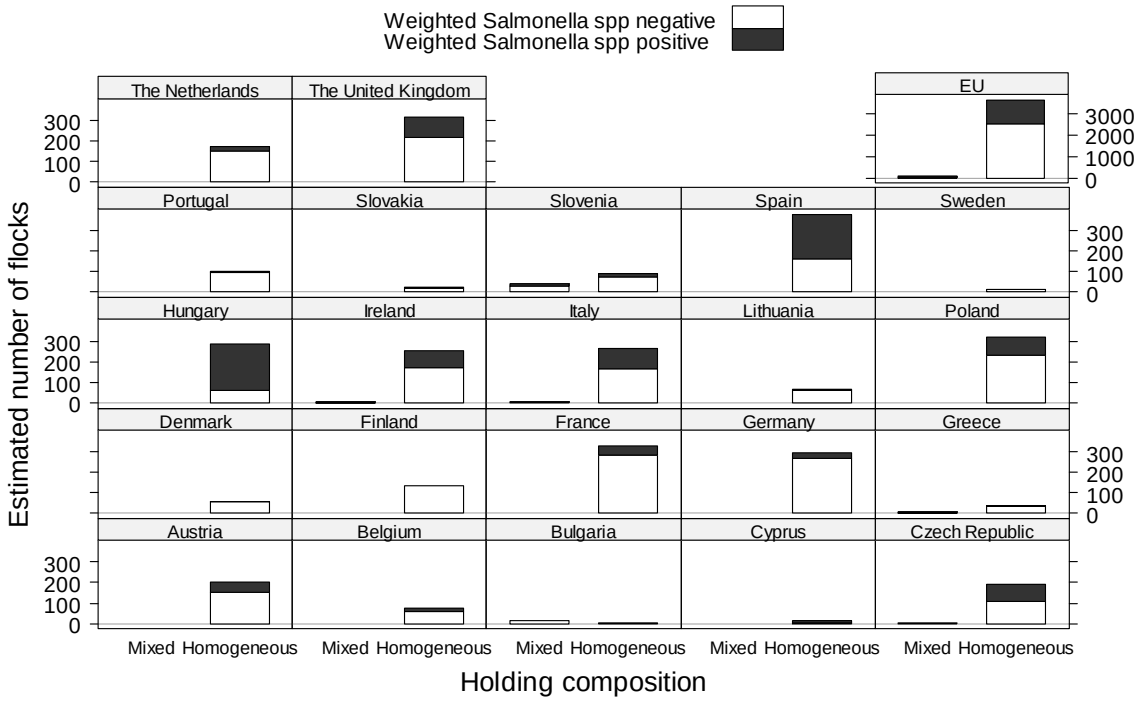
Age of fattening turkeys

The median age of fattening turkeys at the time of sampling in this survey was 109 days (92; 131) at EU level (Figure 7.I, Annex I). Denmark had the greatest median: 147 days (126; 147).

Variables associated with holding characteristics

Most fattening turkey flocks (98.3%) belonged to homogeneous holdings (containing fattening turkey flocks only). Relatively small numbers of flocks (1.7%) from mixed holdings (containing both flocks with breeding and fattening turkeys) were sampled in five MSs (Figure 18).

Figure 18. Frequency distribution of holding composition for fattening turkey flocks, by MS and for the EU, and by *Salmonella* status.[15]



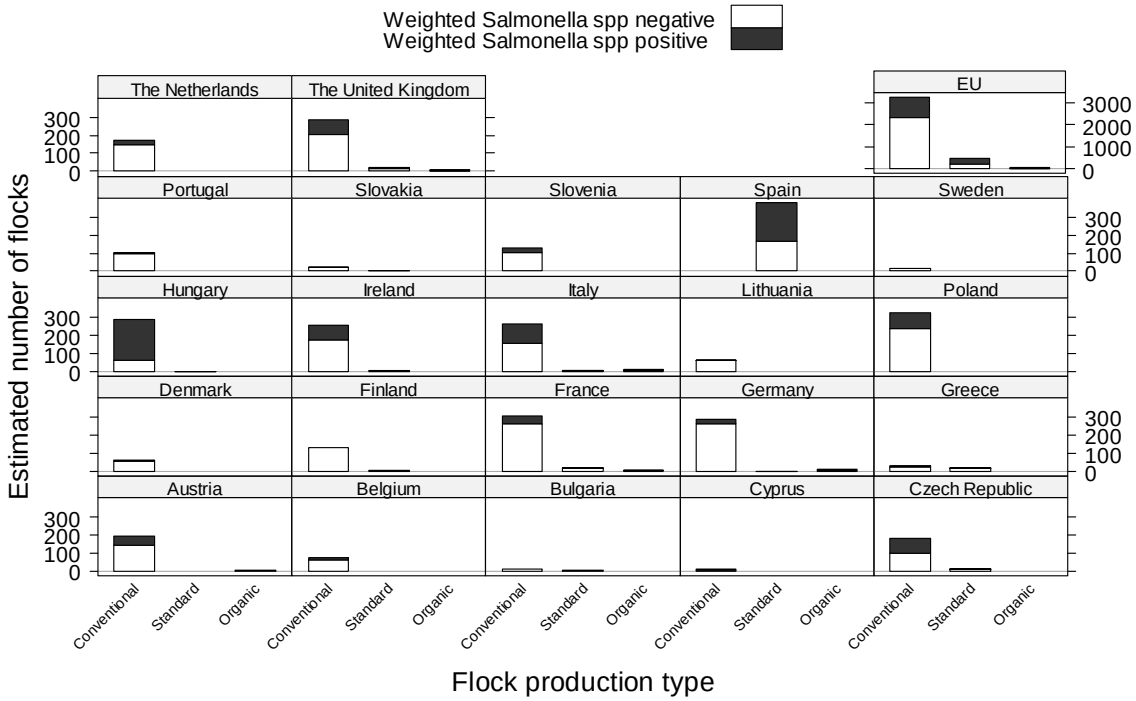
The number of flocks that were raised per house per year (number of cycles) mostly varied between two and three, in the MS (Figure 8.I, Annex I).

[15] - homogeneous: holding containing fattening turkey flocks only;
- mixed: holding containing flocks with fattening and breeding turkeys.

Variables associated with flock characteristics

The large majority of fattening turkey flocks belonged to the conventional flock production type (Figure 19). Standard free-range or organic free-range production types were recorded in 12 MSs.

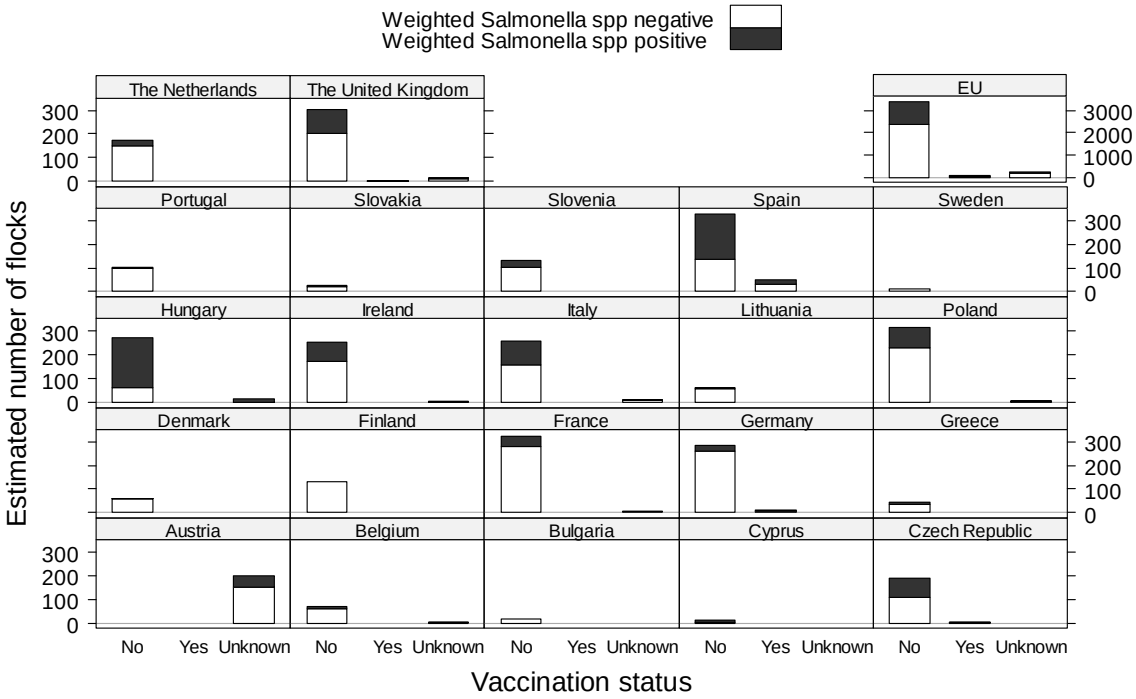
Figure 19. Frequency distribution of flock production type for fattening turkey flocks, at EU level, MS and by *Salmonella* status.



Vaccination against *Salmonella*

Vaccination against *Salmonella* was infrequent in fattening turkey flocks (Figure 20). In fact, only 2.0% of flocks were vaccinated and this took place in Spain, Germany, the United Kingdom, and the Czech Republic.

Figure 20. Frequency distribution of the vaccination status of fattening turkey flocks by EU level, MS and by *Salmonella* status.



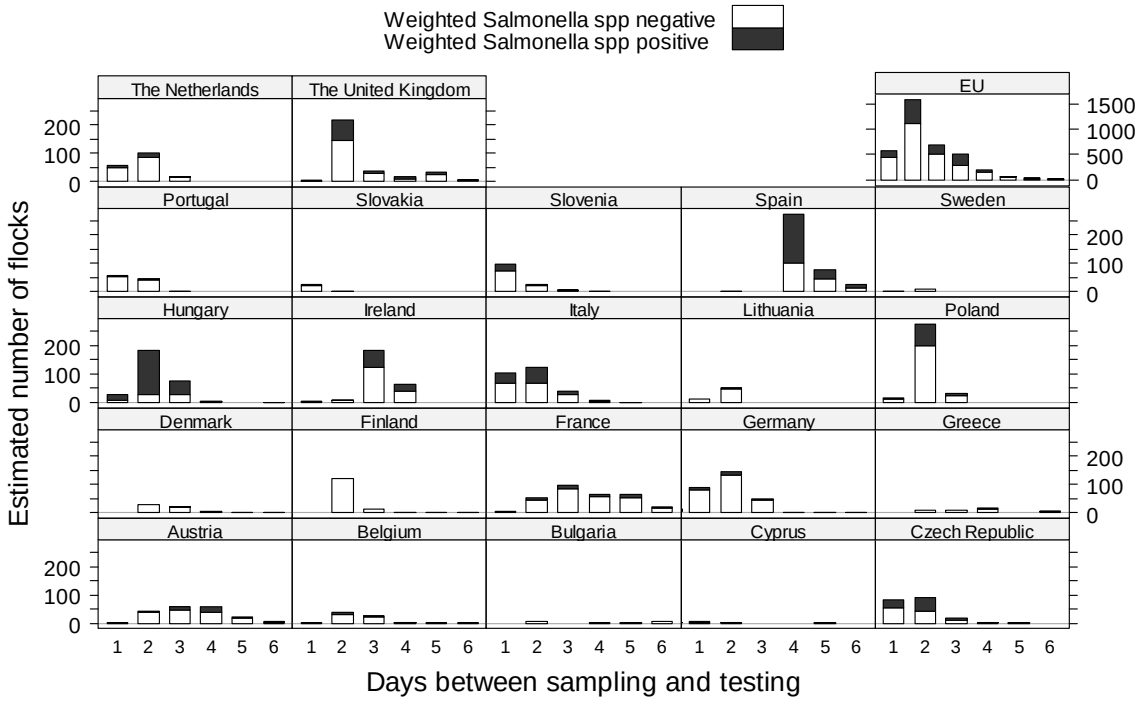
Medication with antimicrobials

Antimicrobial treatment during the two weeks prior to sampling was reported in fattening turkey flocks in 17 out of 22 MSs, although the proportion of medicated flocks was generally low. Italy was the only MS where the number of medicated flocks exceeded the number of untreated flocks (Figure 9.I. Annex I).

Time between sampling and testing

For the majority of fattening turkey flocks, testing in the laboratory was carried out less than four days after sampling (Figure 21).

Figure 21. Frequency distribution of the time (days) between sampling and testing, for fattening turkey flocks, by MS and for the EU, and by *Salmonella* status.



4.1.2.2 Analysis of multicollinearity among risk factors

Results at the EU-level of the analysis of multicollinearity among the risk factors in fattening turkeys are shown in Annex II, Table 4.3.1. Further, the exercise was repeated focussing on each MS separately and those results are displayed Annex II, Table 4.3.2. In countries with small sample sizes, like Cyprus (14 sampled flocks), Greece (43 sampled flocks) and Slovakia (25 sampled flocks), it was very difficult to obtain a good model fit because many parameters were to be estimated with small sample sizes. This resulted in extremely large variance inflation factor (VIF) values for some of the covariates in these countries. Very inflated VIF values can also be observed in Ireland.

4.1.2.3 Multiple regression analysis of risk factors for *Salmonella* infection in fattening turkey flocks

The following potential risk factors for *Salmonella* prevalence in fattening turkey flocks were retained in the final logistic regression model:

- number of turkeys in holding at the time of sampling;
- number of flocks in holding at the time of sampling;
- month of sampling (quarter);
- holding composition (presence or absence of breeding turkey flocks);
- vaccination against *Salmonella*;
- flock production type (standard and organic free-range *vs* conventional).

The OR estimates for the risk factors in the final model at EU level are presented in Table 1. Results of the preliminary bivariate analysis for fattening turkey flocks are reported in Annex II, section 4-1.

Table 1. Results of a multiple logistic regression analysis of the effects of risk factors on the risk of *Salmonella* spp. infection in fattening turkey flocks in the EU[16].

Risk factor	Comparison			Odds ratio	95% confidence interval	
					Lower limit	Upper limit
Number of turkeys in holding				1.15	1.10	1.25
Number of flocks at sampling				0.93	0.87	1.0
Month of sampling (quarter)	October - December	*vs*	July - September	2.2	1.5	3.1
	January - March	*vs*	July - September	1.4	1.0	2.0
	April - June	*vs*	July - September	1.10	0.75	1.5
Holding composition	Presence of breeding turkey flocks	*vs*	Fattening turkey flocks only	6.6	1.9	22.3
Vaccination against *Salmonella* spp.	Vaccinated	*vs*	Unvaccinated	0.39	0.20	0.76
	Unknown status	*vs*	Unvaccinated	1.10	0.52	2.3
Flock production type	Free-range (standard and organic)	*vs*	Conventional	1.9	1.2	3.2

[16] A random intercept was included to account for the correlation among outcomes from flocks belonging to the same holdings.

In Table 1, an OR > 1 indicates that exposure to the risk factor increases the risk of *Salmonella* infection, whereas an OR < 1 indicates a negative association between the factor and the infection. An OR equal to 1 indicates no effect of the risk factor on *Salmonella* infection. Consequently, if the 95% confidence interval of the OR does not comprise 1, meaning that both the lower and the upper limits are either greater, or less than 1, it can be concluded that the association with a potential risk factor and *Salmonella* is statistically significant ($P < 0.05$). The model included MS-specific effects (not shown) and ORs are, therefore, adjusted for MSs.

According to the analyses, the risk of *Salmonella* infection increases as the number of turkeys in the holding increases. In fact, an observed OR = 1.15 (Table 1) suggests that the risk of infection for fattening turkey flocks increased approximately by 15% for every 10,000 increase in the number of turkeys in the holding. However, in holdings with the same number of turkeys, the risk of *Salmonella* decreases if birds are distributed among a relatively great number of flocks, as shown by an adjusted OR for numbers of flocks at the time of sampling, significantly smaller than 1.

In order to test the effect of the month of sampling on the risk of *Salmonella*, a new variable: Quarter, was created. Compared to the period July - September (Quarter 4), the risk of *Salmonella* infection was higher in the period October - December (Quarter 1) and January - March (Quarter 2). On the other hand there does appear to be a significant difference between the risk of infection in April - June (Quarter 3) compared to July - September.

The risk of *Salmonella* infection in fattening turkey flocks in holdings with a mixed production (breeding turkey flocks and fattening turkey flocks in the same holding) was more than six times higher than the risk of infection in holdings with a homogenous fattening production (OR = 6.6, Table 1).

Vaccinated flocks were characterised by a lower risk of *Salmonella* infection compared to unvaccinated flocks. In fact, at EU level, the risk of *Salmonella* in vaccinated fattening turkey flocks was approximately 39% of the risk in unvaccinated flocks (OR=0.39, Table 1). On the other hand, there was no difference between unvaccinated flocks and flocks with unknown vaccination status.

Finally, the risk of infection in standard and organic free-range flocks (pooled data) was almost twice than in conventional flocks (OR=1.9, Table 1).

The results of the analysis by MS are displayed in Table 2. The different levels of significance are indicated by different shades of grey.

The empty cells in the table imply that the effect of the potential risk factor was not significant in that particular country to be maintained in the final model. Further, for some factors, not all categories were available in all countries. For instance, in the Czech Republic only conventional (1) and standard free-range (2) flocks were sampled. Therefore, in this country it was only possible to compare these two levels to obtain an OR estimate. OR estimates which are displayed in italic were obtained with confidence limits close to extremes (either 0 or ∞ or both).

Finland, Sweden and Bulgaria did not have any infected flocks, and it is, therefore, not possible to investigate the impact of risk factors on *Salmonella* prevalence. The contributions for these countries in Table 2 have therefore been left blank[17].

The effects of risk factors varied among MSs (Table 2). Some factors even had contrasting effects depending on the country. For instance, the risk of *Salmonella* infection was highest for flocks which had received antimicrobials during the last two weeks prior to sampling in countries such as Belgium and Slovenia (OR = 0.02 and 0.1, indicating the negative effect of not receiving medication). On the contrary, the risk was highest when the flock had not received medication in countries such as the United Kingdom and the Netherlands (OR >> 1). It should be noted that when these effects are studied at EU level these results may average out so that no significant effect is observed in the EU model.

[17] No *Salmonella* infected flock was found in Norway (see the Part A report), but data from this country were not included in this Part B report.

Table 2. Results of a multiple logistic regression analysis of the effects of risk factors on the risk of *Salmonella* infection in fattening turkey flocks in the EU. Odds ratio estimates are presented for risk factors at different significance levels.[18]

P value: <0.01; 0.01-0.05; 0.05-0.10; 0.10-0.25; not available		No. of turkeys in holding	No. of flocks at full capacity	No. of flocks at sampling	No. of turkeys in flock at sampling	Quarter			Age	Age at slaughter or depopulation	No. of cycles per house per year	Medication with antimicrobials	Time between sampling and testing	Vaccination against *Salmonella*			Holding composition	Flock production type	No. of flocks
						1 vs 4	2 vs 4	3 vs 4				0 vs 1		1 vs 0	2 vs 0	1 vs 2	2 vs 3	1 vs 2	
1	Austria		0.4	3.9	1.2	0.8	2.3	0.7			1.4		1.3						202
2	Belgium		0.2	*15*					1.2		0.1	*0.02*			*54*				74
3	Cyprus		3.9						0.9										14
4	Czech Republic		1.1		1.2	4.3	4.6	1.4										5.5	194
5	Denmark																		59
7	Finland	zero-prevalence																	133
8	France	0.3		1.7	1.2						0.7								326
9	Germany		0.8			3.1	1.3	0.7					1.4						295
10	Greece	*478*	0.03					*253*	1.1										43
11	Hungary	1.4		0.9		1.5	0.6	0.4	1.0	1.0	2.8	0.4	0.6						289
12	Ireland	1.9							1.1	0.9					*23*				259
13	Italy	1.3	0.7	1.6		47	2.7	1.0				1.7							268
15	Lithuania	0.2	2.2																63
18	Poland				0.9														322
19	Portugal	0.6							1.0										105
20	Slovakia		2.0	2.2	2.0				1.1										25
21	Slovenia		0.1	*11*	0.6	8.4	6.6	2.3	1.0		2.4	0.1	0.6				2.9		131
22	Spain		0.9			3.2	0.9	1.0	1.0		1.7	1.6	0.8	0.4					380
23	Sweden	zero-prevalence																	14
24	The Netherlands	0.4		1.4	0.8					1.0		4.4							172
25	The United Kingdom	1.3		0.9		4.2	1.8	2.2	1.0	1.0		8.0	1.1					0.3	317
27	Bulgaria	zero-prevalence																	17

[18] A random intercept was included to account for the correlation among outcomes from flocks belonging to the same holdings.

Quarter: 1 = October - December; 2 = January - March; 3 = April - June; 4 = July - September.

Holding composition: 2 = presence of breeding turkey flocks in the holding; 3 = fattening turkey flocks only.

Flock production type: 1 = conventional; 2 = standard free-range; 3 = organic free-range.

Vaccination status: 0 = unvaccinated; 1 = vaccinated; 2 = unknown status.

Medication status: 0 = untreated; 1 = treated.

4.1.2.4 Multiple regression analysis including optionally recorded risk factors for *Salmonella* infection in fattening turkey flocks

The survey questionnaire form also included some fields that could be completed on a voluntary basis. The results of the model building exercise of these variables are shown in Table 3. More details can be found in Annex II, section 4.2. The final model showed a significant overall effect of *Salmonella* detection in fattening flocks on the holding during the six months preceding sampling (information available for 1,623 flocks in 14 MSs), and of the presence of other livestock (information available for 1,471 flocks in 13 MSs) during the present study. The risk of *Salmonella* infection for flocks in holdings where *Salmonella* was detected during the six months preceding sampling was almost 13 times higher than the risk for flocks in holdings where the infection was not detected. The presence of small ruminants in a holding appeared to be associated with a reduced risk of *Salmonella* for fattening turkey flocks, whereas no association was found between the presence of other livestock species and the infection in turkeys (Table 3).

Table 3. Results of a logistic regression analysis of the effects of risk factors on the risk of *Salmonella* infection in fattening turkey flocks in the EU, including optional variables[19].

Risk factor	Comparison			Odds ratio	95% confidence interval	
					Lower limit	Upper limit
Salmonella detection during the 6 months preceding sampling	*Salmonella* detected	*vs*	not detected	12.9	4.5	36.7
	no information	*vs*	not detected	1.3	0.64	2.8
Other livestock	other poultry	*vs*	none	1.2	0.42	3.3
	pigs	*vs*	none	1.4	0.42	4.6
	cattle	*vs*	none	1.1	0.51	2.4
	small ruminants	*vs*	none	0.15	0.04	0.50
	other	*vs*	none	1.9	0.82	4.3

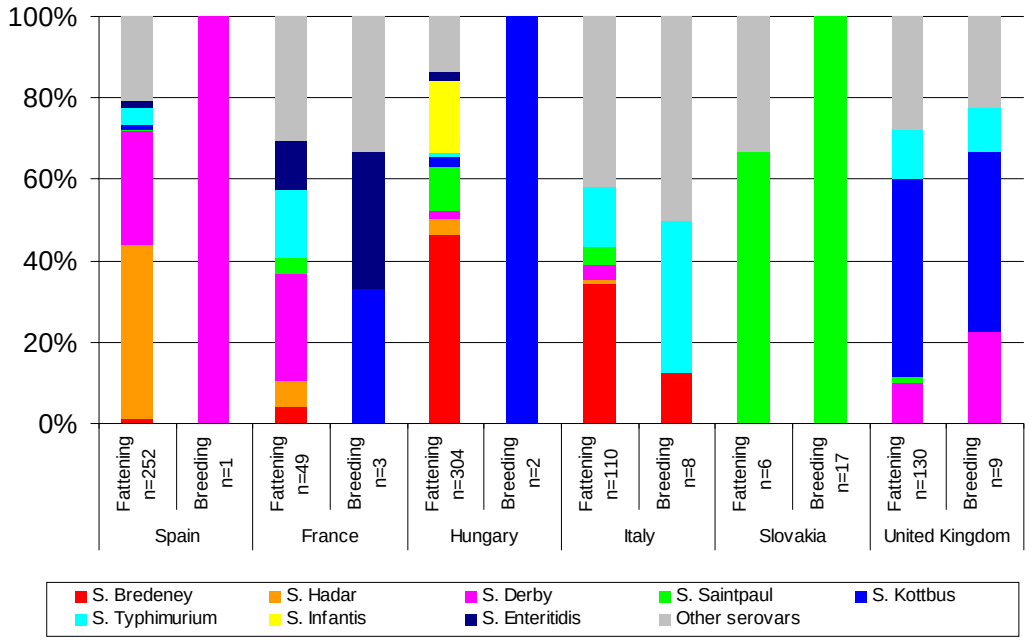
[19] A random intercept was included to account for the correlation among outcomes from flocks belonging to the same holdings.

4.2 Analysis of serovar and phage type distribution

4.2.1 Comparison between serovar distributions in breeding and fattening turkeys

Salmonella serovars isolated from the breeding and the fattening turkey flocks during this EU survey were previously reported in the Part A report. For some MSs, these serovar distributions in breeding and fattening flocks appear to be similar with regard to the most frequently isolated serovars (Figure 22). Nine of the 12 isolated serovars in breeding flocks were all among 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.

Figure 22. 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[20].



[20] n indicates the number of isolates.

4.2.2 Spatial distribution of *Salmonella* serovars in fattening turkey flocks

To investigate the spatial distribution of the most frequently reported serovars in fattening turkey flocks, a spatial analysis was performed by SatScan. Table 4 shows the most likely and secondary spatial clusters with their respective relative risk (RR) and level of significance (P-value), for fattening turkeys.

Table 4. Most likely clusters of *Salmonella*, *S.* Bredeney, *S.* Hadar, *S.* Derby, *S.* Saintpaul, *S.* Kottbus and *S.* Typhimurium, in fattening turkey flocks, in the EU baseline survey in turkey flocks, 2006-2007.

Serovar	Cluster type	Area included[21]	Relative Risk (RR)	P-Value
***Salmonella* spp.**	**Most Likely** **Secondary**	**HU** **ES**	**3.4** **2.0**	**0.001** **0.001**
***S.* Bredeney**	**Most Likely** **Secondary**	**HU,CY, IT** **-**	**68.4** **-**	**0.001** **-**
***S.* Hadar**	**Most Likely** **Secondary**	**ES** **-**	**21.5** **-**	**0.001** **-**
***S.* Derby**	**Most Likely** **Secondary**	**ES** **UK**	**7.6** **3.0**	**0.001** **0.001**
***S.* Saintpaul**	**Most Likely** **Secondary**	**CZ, AT, SI, SK, PL, HU** **-**	**12.3** **-**	**0.001** **-**
***S.* Kottbus**	**Most Likely** **Secondary**	**UK, IE, BE** **GR, HU**	**10.8** **2.3**	**0.001** **0.001**
***S.* Typhimurium**	**Most Likely** **Secondary**	**IT** **UK**	**2.8** **1.8**	**0.001** **0.001**

For several serovars, single, high-risk MSs were identified, rather than clusters of MSs. Among fattening flocks, spatial analysis yielded a RR of 3.4 for Hungary, suggesting that fattening flocks in this MS are three times more likely to become infected with *Salmonella* spp. than in other countries. Spain was detected as the secondary cluster for *Salmonella* spp. and as the most likely cluster for *S.* Hadar and *S.* Derby. *S.* Typhimurium clustered in Italy, with the United Kingdom as the secondary spatial cluster. The most likely spatial cluster for *S.* Saintpaul included neighbouring MSs: the Czech Republic, Austria, Slovenia, Slovakia, Poland and Hungary. *S.* Bredeney clustered in Hungary, Cyprus and Italy, with a high calculated RR for flocks from this area. Finally, *S.* Kottbus clustered spatially in the area covering the United Kingdom, Ireland and Belgium (RR=10.8). Greece and Hungary also presented a significant cluster of this serovar. Maps of most likely and secondary clusters presented in Table 4 can be seen in Figure 23. Prevalence maps of the same serovars are shown in Figure 10.I (Annex I).

[21] AT: Austria; BE: Belgium; CY: Cyprus; CZ: Czech Republic; ES: Spain; GR: Greece; HU: Hungary; IE: Ireland; IT: Italy; PL: Poland; SI: Slovenia; SK: Slovakia; UK: United Kingdom.

Figure 23. Most likely and secondary clusters of *Salmonella* spp., *S.* Bredeney, *S.* Hadar, *S.* Derby, *S.* Saintpaul, *S.* Kottbus, and *S.* Typhimurium, in fattening turkey flocks, in the EU baseline survey in turkey flocks, 2006-2007.

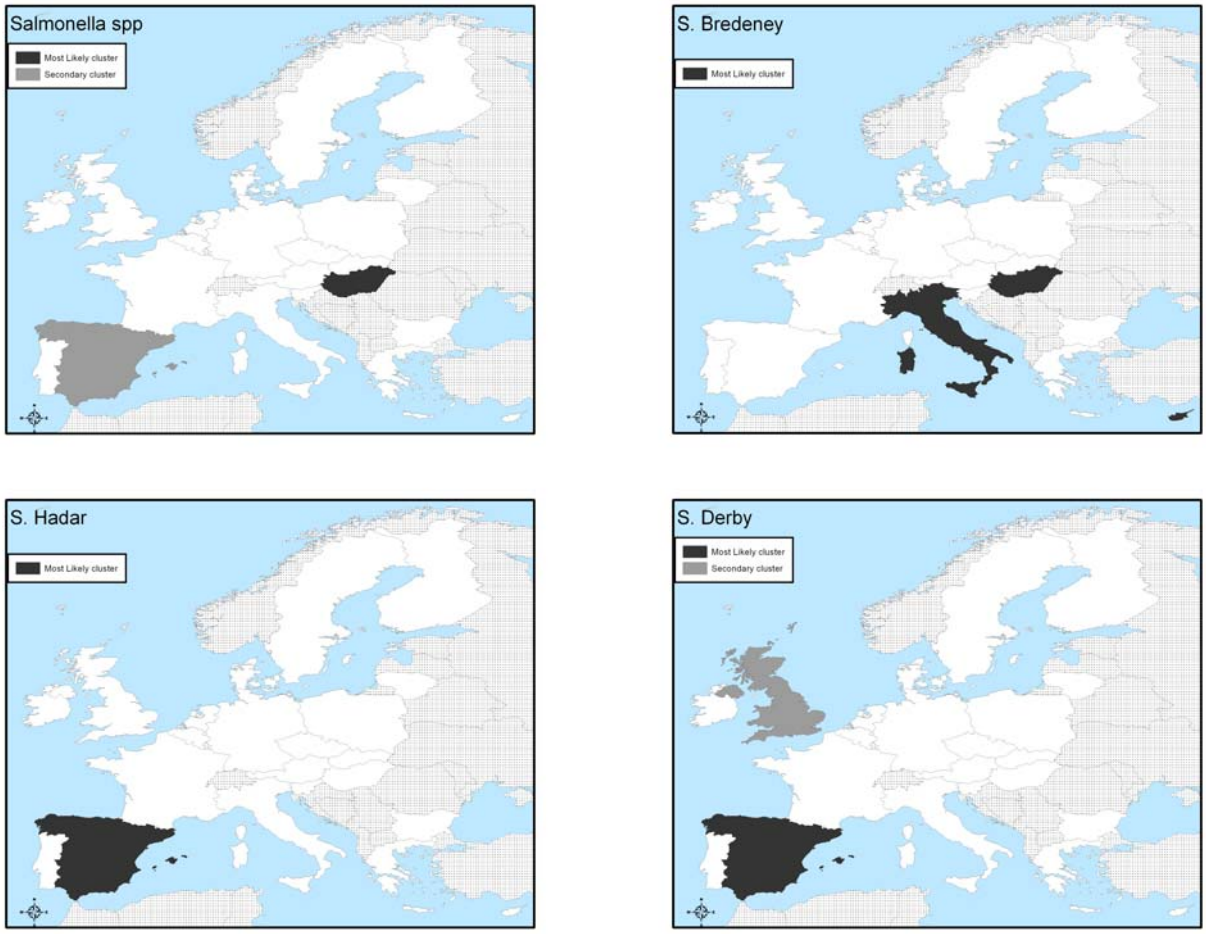
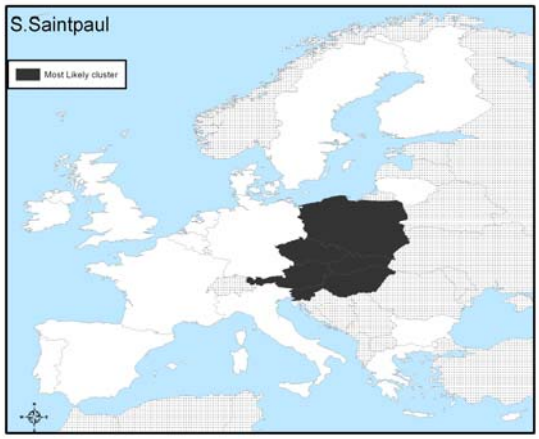
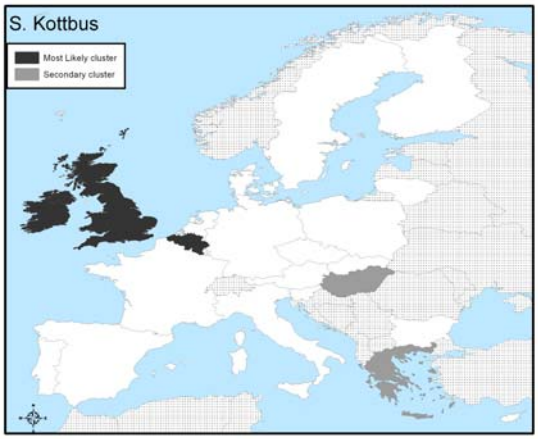
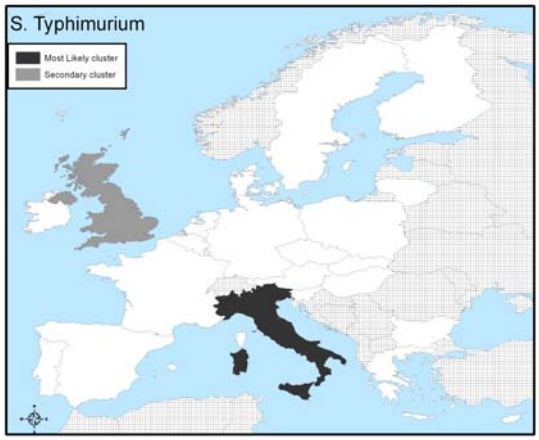


Figure 23 (continued)





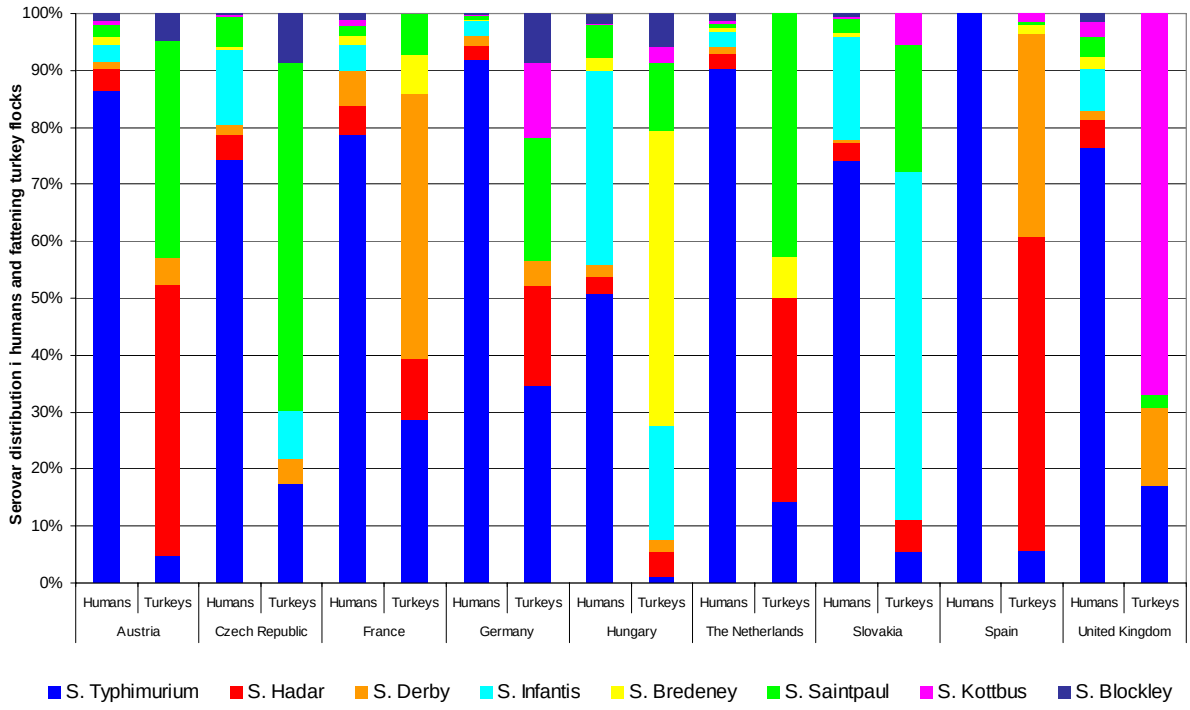


4.2.3 Comparison between EU serovar distributions in fattening turkeys, feed and human salmonellosis cases

Generally, relative serovar distribution in human salmonellosis cases differs from the serovar distributions found in fattening turkeys in MSs (Figure 24). In France, however, the serovar distribution in humans and turkeys appears more similar.

Salmonella Enteritidis - the most frequent cause of human salmonellosis, was relatively rare in turkey flocks. Therefore, it is excluded from this visual analysis to allow an effective comparison of frequencies of other serovars.

Figure 24. Comparison of the serovar distribution in humans and fattening turkeys in MSs for which sufficient human and turkey data were available in 2006. Only the distribution of the most commonly reported human serovars is presented.



Frequencies of serovar isolation from fattening turkey flocks, feed, broiler chicken flocks and laying hen flocks are presented in Table 5. Most serovars were found in all of these sectors. However, in flocks with *Gallus gallus* (broilers and laying hens), *S.* Enteritidis was dominant, whereas in fattening turkey flocks, other serovars were most frequently found.

Table 5. Frequency of *Salmonella* serovars isolated from turkey flocks (baseline survey 2006-2007), feed (Community Summary Report, 2006), broiler flocks (baseline survey 2005-2006) and laying hen holdings (baseline survey 2004-2005).

***Salmonella* serovar**	Fattening turkey flocks	Detected in feed (unspecified poultry feed, or oil seed and fruit)	Flocks with broilers (in top 20 serovars)	Flocks with laying hens (in top 20 serovars)
***S.* Bredeney**	186	Yes	10	26
***S.* Hadar**	152		59	53
***S.* Derby**	123	Yes	13	14
***S.* Saintpaul**	113			
***S.* Kottbus**	90	Yes		
***S.* Typhimurium**	86	Yes	65	123
***S.* Infantis**	72	Yes	295	171
***S.* Orion**	66	Yes		
***S.* Enteritidis**	55	Yes	538	899
***S.* Blockley**	40		29	4
***S.* Newport**	33	Yes	8	11
***S.* Indiana**	32		19	11
***S.* Agona**	31	Yes	16	38
***S.* London**	31			
***S.* Heidelberg**	18		10	4
***S.* Senftenberg**	15	Yes	28	30
***S.* Montevideo**	13	Yes	31	27
***S.* Kedougou**	12	Yes		
***S.* Zanzibar**	11			
***S.* Virchow**	11	Yes	30	41
***S.* Mbandaka**	9	Yes	114	101

4.2.4 Phage type distribution

Salmonella Enteritidis phage types in turkey flocks

Data on *S.* Enteritidis phage types were only provided from fattening flocks by three countries (the Czech Republic, Hungary and Lithuania). Five MSs with *S.* Enteritidis isolates did not report phage typing information. The remaining MSs did not isolate *S.* Enteritidis from turkey flocks.

MSs providing information on *S.* Enteritidis phage types reported a total of 60 isolates in 31 flocks, out of which 44 isolates (73%) were phage typed. This represented 37% of the total 117 *S.* Enteritidis isolates from turkey flocks in the EU. Reported phage types are presented in Table 6, which also displays the number of MSs and flocks where *S.* Enteritidis phage types were detected. In this table the ranking is based on the percentage of specific *S.* Enteritidis phage type-positive flocks in the EU. MS-specific overviews of *S.* Enteritidis phage types are shown in Table 8.

Table 6. Distribution of the *S.* Enteritidis phage types in fattening turkey flocks in the EU, 2006-2007.

***S.* Enteritidis (N=44)**			**No. of MSs reporting phage type**	**Flocks with phage types (N=30)**	
Phage type	**n**	**%**		**n**	**%**
PT14b	24	54.5	2	20	66.7
PT13	13	29.5	1	4	13.3
PT8	2	4.5	1	2	6.7
PT6c	1	2.3	1	1	3.3
PT4	1	2.3	1	1	3.3
Non-typeable	3	6.8	2	2	6.7

In the EU baseline survey on *Salmonella* in laying hen holdings (EFSA, 2007b), PT4 was by far the most commonly reported S. Enteritidis phage type, followed by PT8. In the baseline survey on broiler flocks (EFSA, 2007c) PT8, PT4, PT21 and PT2 were the most frequently isolated phage types (in total 76.4% of the phage types).

Salmonella Typhimurium phage types in turkey flocks

Phage type information on breeding flocks was reported for three of four flocks from two MSs. Phage type DT12 was isolated from one positive flock in the United Kingdom, whereas from two of three positive Italian flocks DT104 (1 flock) and DT41, DT7 and RDNC (1 flock) were identified.

Data on *S.* Typhimurium phage types was provided from fattening flocks by five MSs (Austria, Czech Republic, Hungary, Italy, United Kingdom), whereas seven MSs with *S.* Typhimurium isolates did not provide any phage typing information.

The MSs that reported information regarding *S.* Typhimurium phage types had 125 isolates in 44 flocks out of which 104 (83%) were phage typed. This represented 37% of the total 282 *S.* Typhimurium isolates in the EU. Reported phage types are presented in Table 7, which also displays the number of MSs and flocks where *S.* Typhimurium phage types were detected. The ranking is based on the percentages of *S.* Typhimurium phage type positive flocks in the EU. MS-specific overviews of *S.* Typhimurium phage types are shown in Table 9.

In the EU baseline survey on *Salmonella* in laying hen holdings, DT104 was the most frequently reported *S.* Typhimurium phage type, followed by DT1. In the baseline survey in broiler flocks DT104b, DT104L and U302 were the most frequently isolated phage types (in total 31.8%). Phage types DT135 and DT41 were not isolated from laying hens or broilers.

Table 7. Distribution of the *S.* Typhimurium phage types in fattening turkey flocks, in the EU Baseline survey in turkey flocks, 2006-2007.

***S.* Typhimurium (N=104)**			**No. of MSs reporting the phage type**	**Holdings/Flocks with phage types (N=45)**	
Phage type	**n**	**%**		**n**	**%**
DT104	22	21.2	4	11	24.4
DT135	20	19.2	2	6	13.3
U302	9	8.7	1	4	8.9
DT41	8	7.7	1	2	4.4
DT104b	7	6.7	1	3	6.7
DT12	6	5.8	1	2	4.4
DT7	5	4.8	1	3	6.7
DT193	5	4.8	2	3	6.7
DT208	2	1.9	1	1	2.2
DT104L	1	1.0	1	1	2.2
RDNC	12	11.5	2	4	8.9
Non-typeable	7	6.7	2	5	11.1

4.2.5 Comparison between phage type distribution in turkeys and in *Salmonella* isolates from humans

In order to evaluate the role of turkey meat as a source of human *S.* Enteritidis and *S.* Typhimurium infections, the phage typing results from the turkey baseline survey and human isolates (Community Summary Report, 2006) were compared (Table 8 and 9). Phage typing distribution in humans is only available from a fraction of the MSs and also only a minor proportion of the MSs applied phage typing on the isolates found in the baseline survey. Interpretation should consequently be done very cautiously due to limited numbers and lack of representativeness.

Table 8. Comparison of *S.* Enteritidis phage types isolated from human salmonellosis cases and turkeys.

Phage type	*S.* Enteritidis phage types reported in humans in 2006[22]						Total	No. of turkey flocks as reported in the EU baseline survey, 2006-2007			
	AT[23]	CZ	HU	NL	PT	UK		CZ	HU	LT	No. of MSs
PT 4	1,125	3	398	315	-	2,069	3,910	1	-	-	1
PT 8	964	90	642	41	-	1,088	2,825	2	-	-	1
PT 1	212	4	22	47	-	1,492	1,777	-	-	-	-
PT 21	884	2	174	55	-	609	1,724	-	-	-	-
PT 6	371	1	246	69	-	246	933	-	-	-	-
PT 14b	67	-	20	9	23	538	657	19	1	-	2
PT 6a	201	-	-	17	-	218	436	-	-	-	-
PT1b	3	1	85	-	296	12	397	-	-	-	-
PT 13a	30	13	113	-	-	117	273	-	-	-	-
RDNC	91	-	89	-	-	46	226	-	-	-	-
PT 13	1	83	44	-	-	1	129	-	4	-	1
PT 56	-	-	-	-	-	93	93	-	-	-	-
PT 11	3	-	-	8	-	78	89	-	-	-	-
PT 4b	5	6	22	2	28	4	67	-	-	-	-
PT 3	38	-	-	10	-	14	62	-	-	-	-
PT 1c	56	-	-	-	-	2	58	-	-	-	-
PT 2	11	-	32	1	-	2	46	-	-	-	-
PT 23	10	4	20	2	-	-	36	-	-	-	-
PT 7	33	-	-	2	-	-	35	-	-	-	-
PT U	32	-	-	-	-	-	32	-	-	-	-
PT 19	27	-	-	-	-	-	27	-	-	-	-
PT 6c	-	-	24	-	-	-	24	-	1	-	1
Non-typeable	-	-	28	-	23	20	71	-	1	1	2
Other	79	6	59	15	47	1,089	1,295	-	-	-	-

For *S.* Enteritidis, phage types PT4 and PT8 were identified in both human cases and turkey flocks in the Czech Republic. However, in the same MS, phage type PT 14b was dominant in turkeys but was not found in humans (Table 8). For *S.* Typhimurium, phage type DT 104 was found in humans and turkey flocks in the Czech Republic and the United Kingdom (Table 9).

[22] Data received from the European Centre of Disease prevention and Control (ECDC) by EFSA's Zoonoses Collaborating Centre.

[23] AT: Austria; CZ: Czech Republic; HU: Hungary; LT: Lithuania; NL: Netherlands; PT: Portugal; UK: United Kingdom.

Table 9. Comparison of *S.* Typhimurium phage types isolated from human salmonellosis cases and turkeys.

Phage types	*S.* Typhimurium phage types reported in humans, in 2006 [24]				Total	No. of turkey flocks as reported in the EU baseline survey, 2006-2007					
	AT [25]	CZ	HU	UK		AT	CZ	HU	IT	UK	No. of MSs
DT 104	-	63	-	370	433	-	4	2	1	4	4
DT 46	267	-	-	-	267	-	-	-	-	-	-
FT 560	-	-	-	-	185	-	-	-	-	-	-
DT 193	14	-	62	108	184	-	-	-	2	1	2
DT 104l	79	-	103	-	182	1	-	-	-	-	1
RDNC	92	-	24	46	162	-	-	-	-	-	-
DT 104b	-	-	64	72	136	-	-	-	-	3	1
FT 507	-	-	-	-	116	-	-	-	-	-	-
DT 120	33	8	-	73	114	-	-	-	-	-	-
DT 8	4	-	-	93	97	-	-	-	-	-	-
DT 1	18	22	-	46	86	-	-	-	-	-	-
DT 41	68	3	-	9	80	-	-	-	2	-	1
FT 506	-	-	-	-	79	-	-	-	-	-	-
U 302	-	-	45	10	55	-	-	-	-	4	1
DT 56	-	-	-	50	50	-	-	-	-	-	-
DT 135	-	2	-	44	46	-	-	1	-	5	2
U 311	-	-	-	38	38	-	-	-	-	-	-
U 288	-	-	-	37	37	-	-	-	-	-	-
FT 510	-	-	-	-	27	-	-	-	-	-	-
DT U	18	5	-	-	23	-	-	-	-	-	-
FT 296	-	-	-	-	21	-	-	-	-	-	-
Non-typeable	-	-	33	13	46	-	-	-	3	2	2
Other	34	45	101	726	983	-	-	1	5	3	3

[24] Data received from the European Centre of Disease prevention and Control (ECDC) by EFSA's Zoonoses Collaborating Centre.
[25] AT: Austria; CZ: Czech Republic; HU: Hungary; IT: Italy; UK: United Kingdom.

5 DISCUSSION

5.1 Analysis of factors associated with *Salmonella* flock prevalence

The present report provides a further analysis of the dataset on *Salmonella* in turkey flocks in the EU which was previously described in the Part A report. Additional information gathered by MSs as part of the baseline survey on *Salmonella* in turkeys was analysed to identify factors associated with *Salmonella* infection of the flocks. The distribution of *Salmonella* serovars and phage types were also analysed.

As reported in the Part A report, the specific flock prevalence of the serovars *S.* Enteritidis and *S.* Typhimurium was relatively low in turkeys in the EU. Risk factor analyses for the small number of positive outcomes for these two serovars would not have been meaningful and was therefore not undertaken in the present report.

Salmonella positive breeding turkey flocks were clustered in certain MSs. Analysis of the factors associated with *Salmonella* prevalence in breeding flocks in the EU would therefore tend to identify factors present in those MSs. Therefore analysis of risk factors in breeding flocks was limited to exploratory analysis, whereas additional multiple regression analysis of risk factors for *Salmonella* spp. was carried out for fattening turkey flocks.

MSs have their own characteristics for production and husbandry of turkeys, with differences in, for example, housing style, feed materials used, water quality and the potential for cross contamination to other food production chains. While the baseline survey attempted to record relevant data, many potential factors of relevance to *Salmonella* infection such as specific sources of birds, feed and information on bio-security measures at holdings, were not part of the present survey.

5.1.1 Breeding turkey flocks

As described in the Part A report, *Salmonella* infection in breeding flocks was an issue for a small number of MSs, together 34 out of the total of 40 positive flocks originated from only three MSs. Therefore, the factors that emerged as being associated with *Salmonella* infection in breeding flocks are essentially descriptors of husbandry and or sampling in those particular MSs. Thus, while the highest *Salmonella* prevalence in breeding flocks was associated with holdings containing greater numbers of turkeys, and greater numbers of flocks per holding with smaller numbers of birds per flock; these were the types of holdings present in those few MSs with a high prevalence of *Salmonella* in breeding flocks.

Generally, there was a trend of greater *Salmonella* positivity in conventionally housed breeding flocks, compared to free-range standard flocks. However, this observation was based only on data from 14 sampled free-range breeding flocks and, therefore, it should be interpreted with caution. Presence of both breeding and fattening turkeys in the same holdings (mixed holding composition) seemed to be associated with an increased *Salmonella* risk, but again this observation was based on few observations, since only 13 breeding flocks were raised in holdings with mixed composition. Breeding flocks with younger turkeys, unvaccinated flocks, and flocks raised in holdings where only one cycle per house per year was produced tended to be more at risk of *Salmonella*, but this might, again, reflect the sampled populations in those few MSs with a higher *Salmonella* prevalence.

Nevertheless, the biological relevance of trends found is worth considering, for those MSs with a *Salmonella* problem in their turkey breeding flocks. Large holdings with many small flocks would not appear to be a prudent approach for the husbandry of breeding turkeys with regards *Salmonella*. The bio-security challenge of maintaining the barriers to *Salmonella* ingress into each of these smaller epidemiological units may be greater than for a smaller number of large flocks per holding. Once ingress has occurred, the potential for spread within the holding then becomes relevant. *Salmonella* positivity in younger flocks is consistent with the potential for older birds to acquire sufficient immunity to clear infections of some serovars with increasing age. Therefore, younger flocks on breeding holdings should be regarded as being those at highest risk and accorded the most stringent bio-security. While vaccination was an infrequently reported event in breeding flocks, the association of *Salmonella* positivity with non-vaccination of breeding flocks illustrates the potential role for such a tool, particularly in the prevention of *Salmonella* infection in those MSs with high prevalence.

Even though it was not possible to exclude the confounding effect of MSs in finding lower positivity in samples tested several days after sampling, such a finding could be explained by die-off or failure to recover *Salmonella*, with a likely significant role of competing growth of other organisms in the relatively dirty matrix of a boot-swab. Therefore, MSs may wish to consider these findings when designing national control programmes.

5.1.2 Fattening turkey flocks

As described in the Part A report, *Salmonella* was more prevalent and more widely distributed across MSs in fattening turkey flocks than in breeding turkey flocks. This allowed a formal analysis, by multiple logistic regression, of the potential factors associated with *Salmonella* infection in fattening turkey flocks, at EU level and for individual MSs. In this way, the estimated effect of each of the potential risk factors was adjusted for the confounding effect of other factors. Statistical significance was also tested to help rule out chance as a cause of observed associations.

EU level analysis resulted in a relatively small number of factors significantly associated with *Salmonella* infection after adjusting for MS effect. Substantial variation in the outcome of the regression analyses were observed between MSs, with trends contrary to EU means observed in some instances, and significant MS-specific trends balanced out to no effect at EU level. This could be explained by variations in husbandry systems and with different *Salmonella* serovars present in MSs. In fact, factors associated with salmonella transmission may vary for different serovars.

The EU analysis of holding size variables indicated a significantly higher risk of *Salmonella* infection in fattening turkey flocks for holdings with more turkeys. Moreover, when the number of turkeys in a holding was similar, the risk was lower for holdings with a greater number of flocks. The protective effect of a greater number flocks per holding is consistent with the containing effect of small epidemiological units, less potential for horizontal transfer, greater hygiene between batches and including fallow periods for certain houses. These results contrast with those obtained for breeding turkey flocks, where the greater number of flocks in a holding seemed to be associated with higher *Salmonella* prevalence. However, in breeding turkey flocks, it was not possible to separate the effect of the number of flocks from the number of turkeys in a holding.

In fattening turkey flocks at EU level, the risk of *Salmonella* appeared to be highest in the period from October to March. In many MSs, turkey fattening involves a relatively seasonal cycle with available housing and husbandry infrastructures and systems stretched to peak capacity in winter months, bringing commensurate pressure on bio-security controls. This might explain the observed temporal pattern in *Salmonella* prevalence. Winter temperature may slow the growth of competitive microorganisms in feed and water favouring *Salmonella* transfer. Moreover, the effect of low temperature may increase the likely encroachment of wildlife reservoirs to domestic feed production, e.g. due to poor availability of food. However, studies in excess of one year would be useful to confirm the observed impact of the season.

At EU level the presence of fattening turkey flocks and breeding turkey flocks on the same holding was associated with an increased risk of *Salmonella* infection in fattening turkey flocks. Such flocks from holdings with a mixed composition were over six times more likely to be *Salmonella* positive than flocks from holdings including fattening turkey flocks only. In the context of an overall higher prevalence of *Salmonella* spp. in fattening turkey flocks than in breeding turkey flocks, the apparent breeding turkey flocks contribution of *Salmonella* to fattening turkey flocks on the same holding is worthy of consideration. While bio-security benefits should accrue from not having to bring in extraneous birds for fattening, the longer length of production cycle of breeding turkey flocks is likely to inhibit practices such as all-in-all-out policies on particular holdings. The potential for longevity in breeding turkey flocks on mixed holdings to transcend production cycles of fattening turkey flocks creates a potential for reservoirs of *Salmonella* infection to persist on that holding including for personnel, surface water, or feed.

Vaccination of turkeys against *Salmonella* appeared to be generally protective against the infection. However, vaccination seems relatively infrequent and is only carried out in certain MSs. Some MSs do not permit vaccination in order to achieve seronegative status in the context of overall control programmes and trade access. At MS Level, vaccination against *Salmonella* was associated with mixed results and sometimes it appeared that vaccinated flocks or flocks of unknown status were more at risk. This might be explained by the fact that in fattening turkey flocks vaccination may be used reactively, when there has already been infection present on a holding, so vaccination status can often be viewed as an indirect indicator of risk. For certain MSs, the highest risk of *Salmonella* infection, in both fattening turkey flocks and breeding turkey flocks, was associated with flocks in which the vaccination status was unknown. This is likely to be associated with a lower level of knowledge among flock owners and a lesser degree of control over the sources of birds.

At EU level, the associated risk of *Salmonella* occurring in the free-range production of fattening turkey flocks was almost twice the risk of conventional production. This finding is consistent with *Salmonella* risks associated with outdoor access. Moreover, the use of potent disinfectant might be relatively limited in free-range production due to difficulties of application. Different sources of birds for free-range and for conventional flocks may also contribute to the difference of risk of *Salmonella* infection in the two production types. A valid comparison between standard free-range and organic free-range production was prevented by the low numbers of these minority production types in the survey.

Increasing delays between the sampling and testing of fattening turkey flocks at EU level appeared not to be significantly associated with a reduced chance of *Salmonella* identification.

Relatively few MSs provided data relating to additional voluntary risk factors in fattening turkey flocks. A limited analysis at EU level was carried out, including those MSs which provided suitable data. Analysis of voluntarily-submitted risk factors indicated that *Salmonella* detection within the past six months was strongly associated with current *Salmonella* infection. This serves to illustrate the potential for *Salmonella* persistence in the holding production environment, and the need for intensive hygienic efforts to manage risk of carry-over infection, e.g. disinfection procedures between flocks. Analysis of the data available did not result in any association between the presence of other animal species and *Salmonella* risk in turkey flocks, which is consistent with serovar-specific host adaptation and little uniformity at the *Salmonella* genus level. However, as an exception, the presence of ruminants seemed to be associated with a reduced prevalence of *Salmonella* infection in turkeys. However, the biological plausibility of this result is difficult to interpret.

5.2 Analysis of serovar and phage type distribution

5.2.1 Spatial distribution of *Salmonella* serovars

Spatial analysis confirmed the fattening turkey flocks findings described in the Part A report of a heterogeneous geographic distribution of specific *Salmonella* serovars among MSs and the absence of a dominant serovar. In fact, single MSs resulted high risk for specific serovars. This distribution is consistent with geographically confined shared sources of *Salmonella* infection for flocks in the same MS, such as contaminated feed sources or reservoir hosts; as well as lateral spread, e.g. through animal movement within specific MSs. Moreover, dominance of a single serovar in certain MSs, together with the high degree of similarity between *Salmonella* serovars found in breeding turkey flocks and fattening turkey flocks in many MSs, might be associated with breeding turkey flocks serving as major sources of infection for fattening turkey flocks in the country. MSs embarking on a control programme might recognise the necessity for curtailing spread within their country, while attempting to identify any specific ongoing source of relevance to that state.

The spatial distribution of *S.* Saintpaul in fattening turkey flocks was characterised by a significant cluster of neighbouring MSs (Figure 23). It is important to notice that, in breeding turkey flocks, *S.* Saintpaul was only found, and was the dominant serovar in one of these MSs. Consequently, acknowledging the fact that no information on trade patterns in live birds was included in this survey, a major role of breeding turkey flocks in the transmission of *S.* Saintpaul in neighbouring MSs, can be hypothesised.

5.2.2 Comparison of EU *Salmonella* serovar and phage type distribution in turkeys, in poultry species and feed.

The majority of *Salmonella* serovars isolated from fattening turkeys have also been isolated from broilers and laying hens, suggesting the existence of common sources of *Salmonella* infection for poultry production. Feed is a plausible source of a part of these infections, and many of those serovars in turkeys have also been detected in poultry feed, feed mills or feed raw materials. The absence of a dominant serovar in turkeys contrast with the situation previously found in *Gallus gallus* (broilers and laying hens) where *S.* Enteritidis (that is relatively uncommon in turkeys) predominates in many MSs. The overall prevalence of *S.* Typhimurium in turkey flocks in the EU was relatively low, suggesting relatively good current control in most MSs of this major zoonotic serovar, which has previously been frequently associated with turkeys (SANCO/927/2002).

Further characterisation of the phage types of *S.* Enteritidis isolated from fattening turkey flocks was voluntarily performed and submitted only by three MSs, resulting in such information for 37% of the *S.* Enteritidis isolates. Phage type 14b was the dominant *S.* Enteritidis present, although it was only detected in two MSs. This phage type has previously been implicated in human disease and associated with egg food chains. Based on the few reported phage results, it was not possible to evaluate if a correlation existed, at EU level, between the phage types isolated in turkeys and those isolated from laying hens and broilers in the previous EU-wide baseline surveys.

In the case of *S.* Typhimurium further characterisation of phage types was performed and submitted by five MSs. Based on scant reported phage typing data, DT104 was the most frequently reported *S.* Typhimurium phage type in both turkey flocks and laying hen holdings. In addition several other *S.* Typhimurium phage types associated with laying hens and broilers were also isolated from turkeys. This may suggest the existence of common sources of infection. However, some of the phage types of *S.* Typhimurium found in turkeys might more commonly be associated with other farm animals, particularly pigs. Furthermore, DT41, which is mostly associated with wild birds, was found on two turkey holdings in one MS.

It appears that the role of feed and other animal species as a source of *Salmonella* infection in turkeys need to be clarified further, even though there is some indication of a common source.

5.2.3 Comparison of the EU *Salmonella* serovar and phage type distribution in turkeys and in human salmonellosis cases.

The *Salmonella* serovars present in turkeys show relatively poor correlation with the serovars causing human disease in MSs. This poor correlation would suggest a relatively low attribution to human salmonellosis disease originating from turkeys. This may partly be explained by the low per capita consumption of turkey meat in EU MSs (4.5 kg per year in 2003) compared to, for instance, broiler meat consumption (15.4 kg per year in 2003) (Windhorst, 2006). In France, however, the serovar distribution in humans and turkeys appeared more similar than in other MSs. Acknowledging that France is the largest producer of turkey meat in the EU, this could be due to a higher consumption of turkey meat in this country.

However, some prevalent serovars in turkeys, such as *S.* Typhimurium and *S.* Hadar and *S.* Derby, have been and continue to be implicated in human disease. The actual contribution of the turkey food-chain to their epidemiology remains poorly understood without a more specific source attribution study and further molecular characterisation of *Salmonella* isolated from all sources.

6 CONCLUSIONS

- In breeding turkey flocks, *Salmonella* was found in only six MSs, and the observed trends of association with *Salmonella* infection reflected farming characteristics in MSs where most of the positive flocks were aggregated. However, biologically plausible risk factors, such as holding size and husbandry type, were identified, therefore providing ground for further MS-specific studies.
- In fattening turkey flocks, where *Salmonella* was more prevalent, a formal multiple regression analysis showed that the risk of infection increased with increasing numbers of turkeys in the holding. Moreover, the presence of breeding turkey flocks in the same holding was associated with an increased *Salmonella* risk for fattening turkey flocks on the holding. The risk of *Salmonella* in vaccinated fattening turkey flocks was lower than the risk in unvaccinated flocks; this result was, however, based on data from a small number of vaccinated flocks. The sampling period of October 2006 to March 2007 was associated with higher *Salmonella* prevalence. Also free-range production of fattening turkey flocks was associated with a greater risk of *Salmonella* compared to conventional production.
- There was evidence of considerable variation between significant risk factors for *Salmonella* in fattening turkey flocks obtained for each MS as compared to EU level, and among MSs.
- More detailed information on several factors associated with bio-security, at holding and flock levels, as well as information on the trade of animals and feed were not investigated in the survey. Therefore, it was not possible to estimate the association of these factors with *Salmonella* and their potential confounding role on the effect of factors on which data were available. However, results of this analysis are useful starting points for more specifically aimed studies in the EU and in individual MSs.
- There was a high degree of similarity between *Salmonella* serovars found in breeding turkey flocks and fattening turkey flocks in many MSs, suggesting an important role for amplification and dissemination of infection from breeding turkey flocks to fattening turkey flocks.
- The heterogeneous geographical distribution of *Salmonella* serovars in turkeys in the EU suggests that *Salmonella* transmission is more likely to occur within each MS rather than among MSs. However, the spatial clustering of MSs where *S*. Saintpaul was found suggests transmission of this serovar among neighbouring MSs.
- Analysis of serovar and phage type distribution suggested that, while feed and other animal species could act as sources of *Salmonella* for turkey flocks, their role in this aspect remains to be clarified.
- In general, *Salmonella* serovar and phage type distribution in fattening turkey flocks differs from the corresponding distribution in salmonellosis cases in humans. These results suggest that the role of turkeys as a source of *Salmonella* infections for people is lower than the role of many other animal species, such as *Gallus gallus* (broilers and laying hens). However, the proven pathogenicity of some *Salmonella* serovars that are most frequent in turkeys, suggest that such a role should not be overlooked.

7 RECOMMENDATIONS

- As the *Salmonella* infection in breeding turkey flocks and fattening turkey flocks seems to be associated, MSs are encouraged to guarantee effective *Salmonella* control in breeding turkey flocks, in order to reduce and prevent the subsequent contamination of fattening turkey flocks.
- MSs are also invited to consider other risk factors found to be significantly associated with *Salmonella* infections in flocks at EU level in this survey, when designing the national *Salmonella* control programmes for turkey flocks. Vaccination might be considered as a tool for control in MSs where *Salmonella* is present. Specific bio-security measures may also be devised for free-range farming.
- Only a few potential risk factors were demonstrated as being associated with *Salmonella* prevalence in turkey flocks at EU level. Moreover, considerable variation existed among MSs in the significant risk factors for fattening turkey flocks. Therefore, MSs are invited to carry out further national studies to identify the factors that put turkey flocks at risk of becoming infected with *Salmonella* taking into account their *Salmonella* prevalence and serovar distribution.
- It is further recommended that MSs serotype all *Salmonella* isolates originating from turkey flocks to enable the evaluation of the risk to public health.
- The potential for risk factor analysis in this survey was restricted by the limited set of mandatory potential risk factors to be coded and submitted by MSs. It is therefore recommended that if risk factor analysis is planned for future baseline surveys more factors investigating major risk corners should be compulsory.
- More phage typing of isolated *Salmonella* serovars from both turkeys (and other food-producing animal species) and humans would allow more precise analyses on source attribution and would provide a comprehensive picture of the situation in the EU.

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ABBREVIATIONS

CI	Confidence Interval
CRL	Community Reference Laboratory
EFSA	European Food Safety Authority
EU	European Union
MS(s)	Member State(s)
NRL	National Reference Laboratory
OR	Odds Ratio
RR	Relative Risk
VIF	Variance Inflation Factor

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