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.

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[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.

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[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.

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[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]
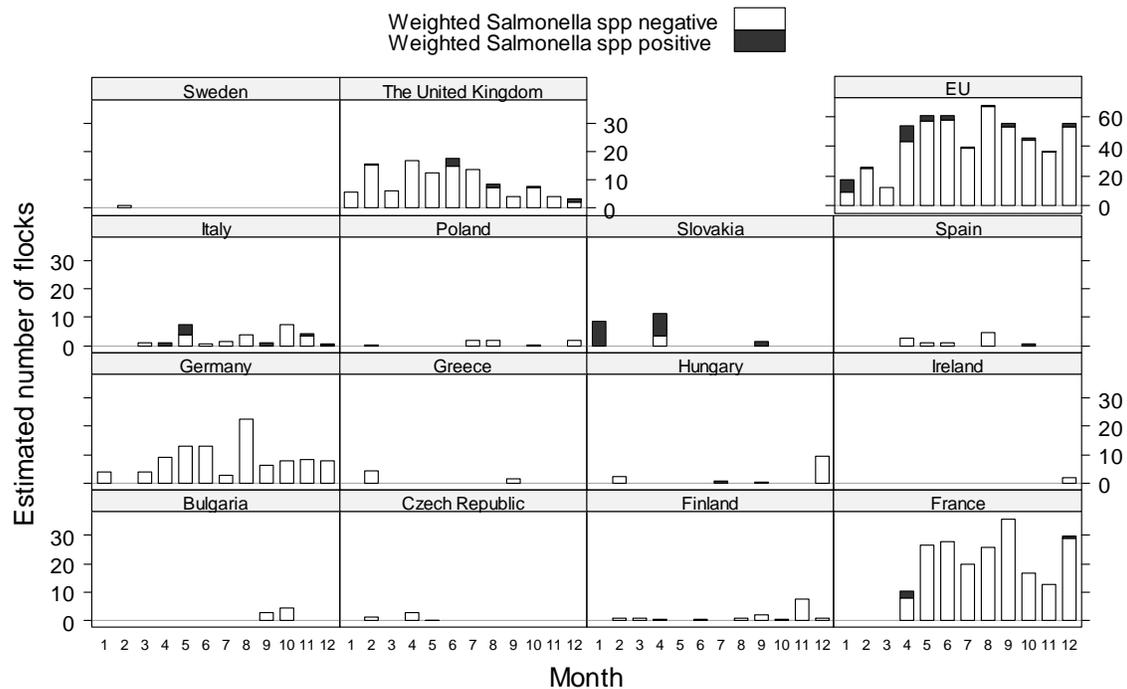
Variables associated with breeding holding size

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).

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[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.
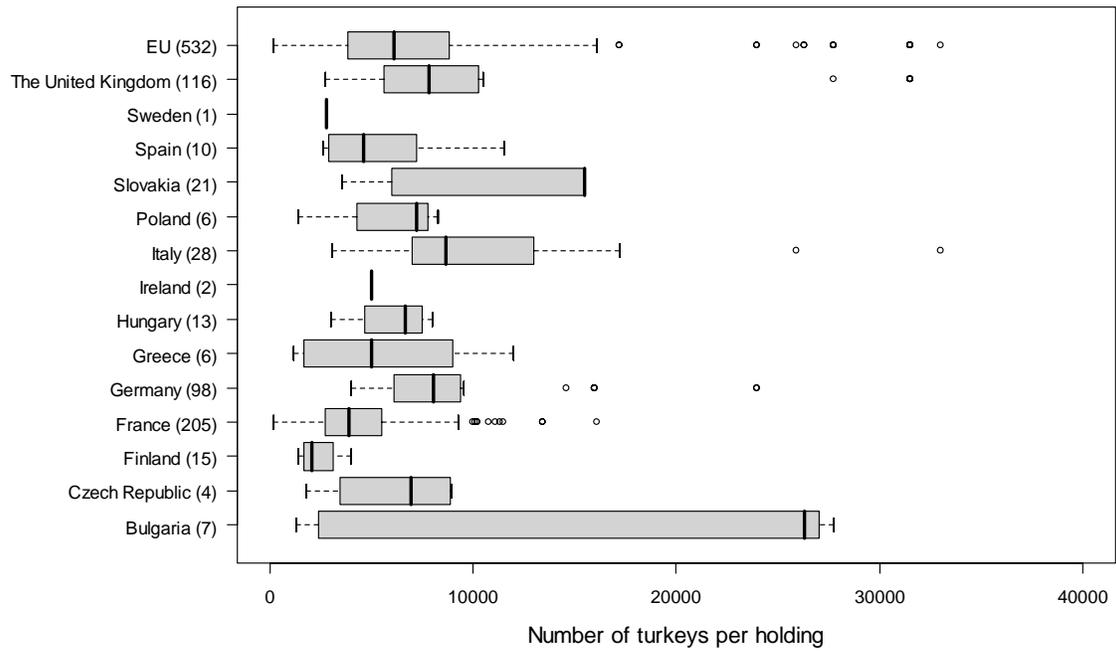
Figure 3. Box plot of the number of turkeys in a holding at the time of sampling, for *Salmonella* positive and negative breeding turkey flocks, in the EU.[8]
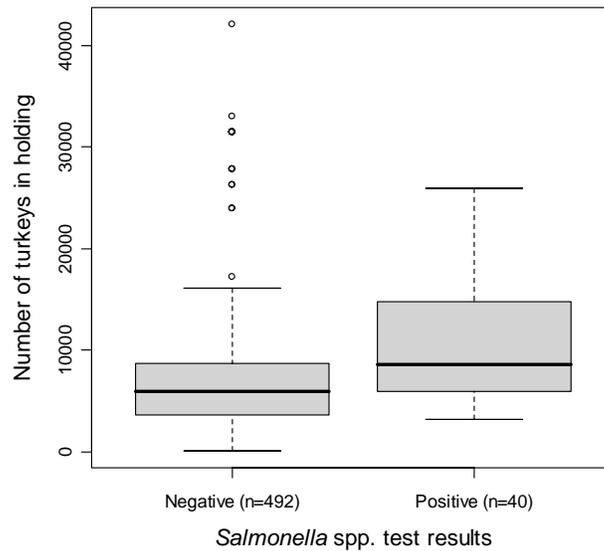
The median (Q1; Q3) number of flocks per holding at full capacity (Figure 1.I, Annex I), at EU level was 3.5 (2.0; 6.0) in the sampled holdings. The greatest number of flocks (17) was recorded in the United Kingdom, whereas medians were greatest in Slovakia (12) and Bulgaria (11).

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

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[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.
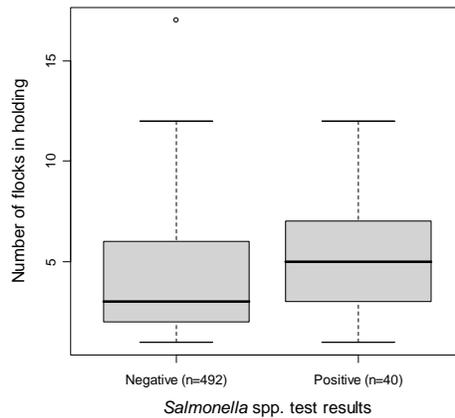
Flock size

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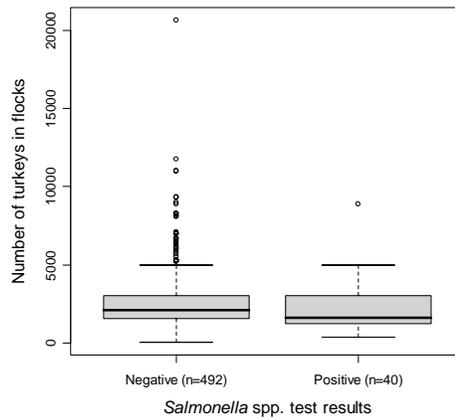
Figure 6. **Box plot of the age of turkeys at the time of sampling in *Salmonella* negative and positive breeding turkey flocks.**
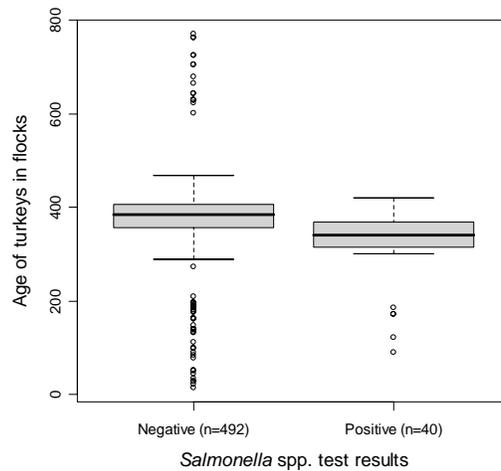
Variables associated with holding characteristics

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]

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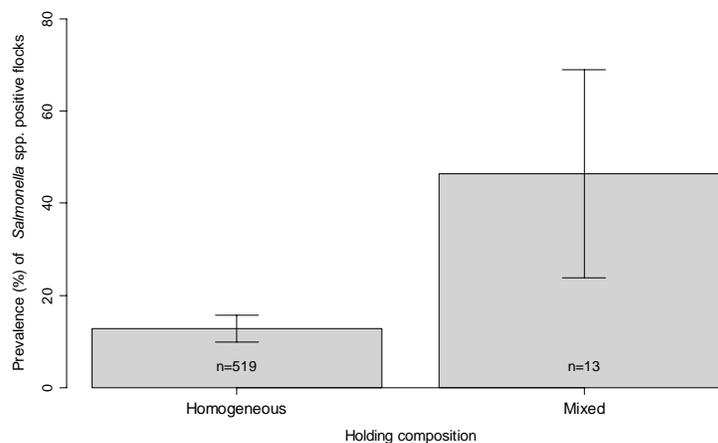
[9] - n indicates the number of sampled flocks
 - homogeneous: holding containing breeding turkey flocks only
 - mixed: holding containing flocks with breeding and fattening turkeys

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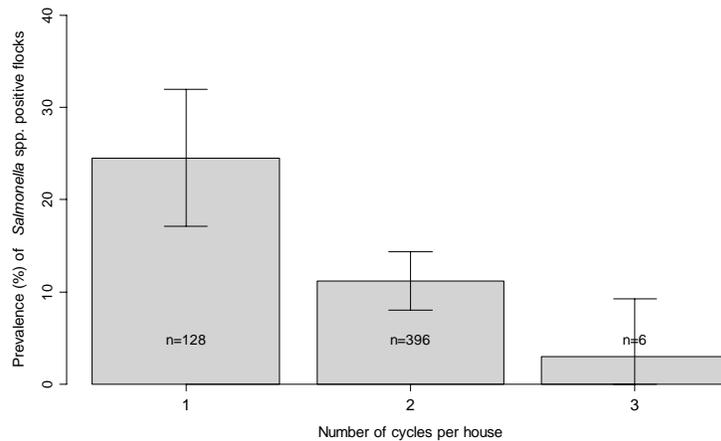
Variables associated with breeding flock characteristics

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.

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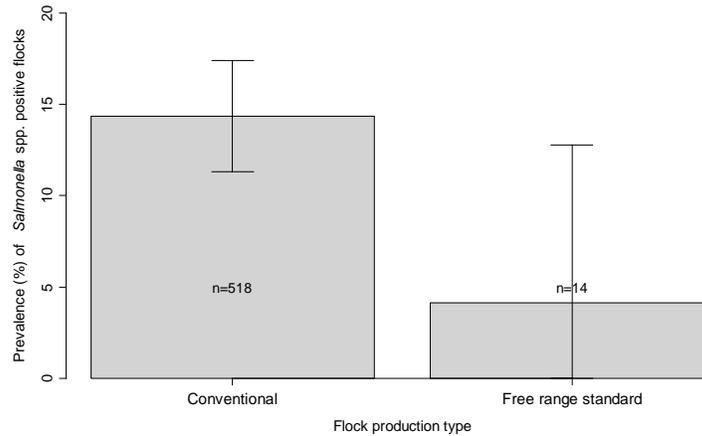
Figure 10. Frequency distribution of vaccination in breeding turkey flocks, by MS and for the EU, and by *Salmonella* status.

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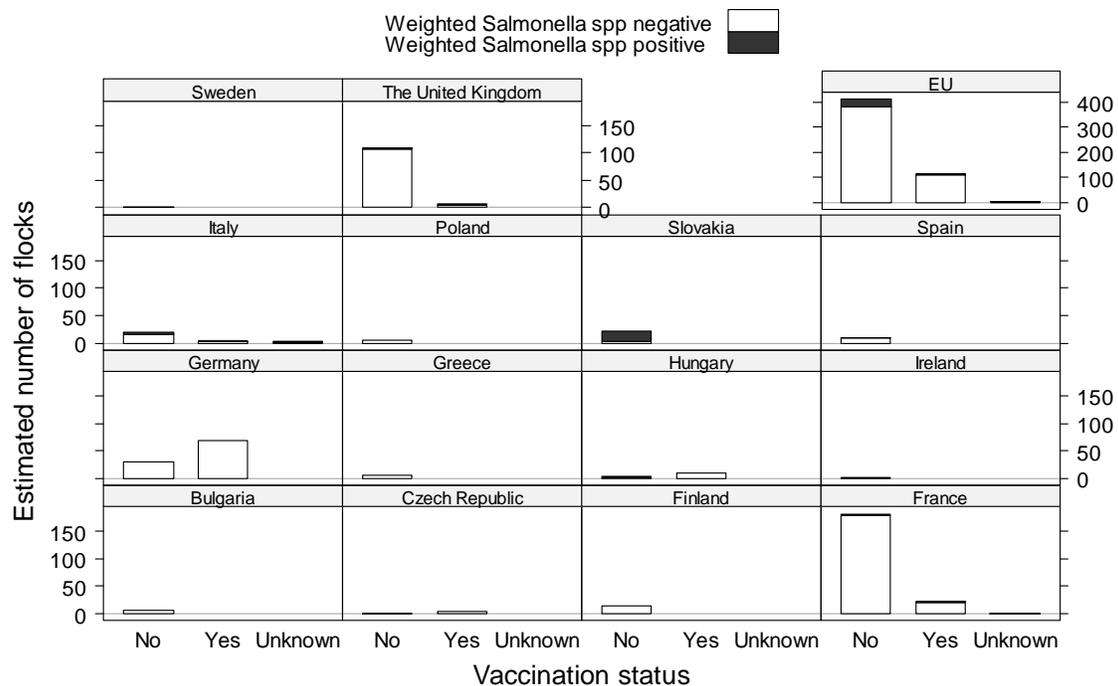
[11] n indicates the number of sampled flocks

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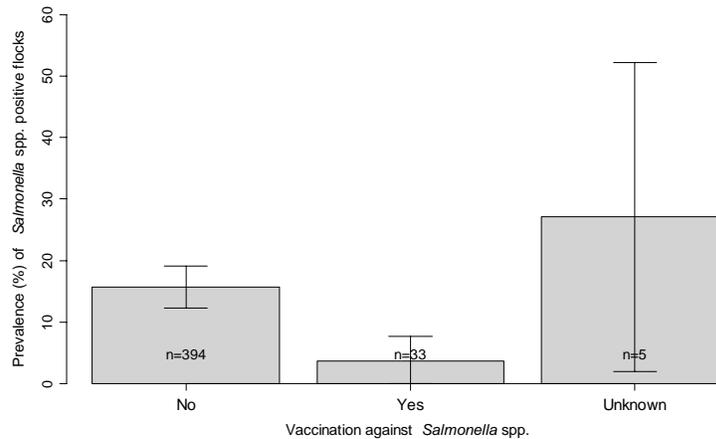
Medication with antimicrobials

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).

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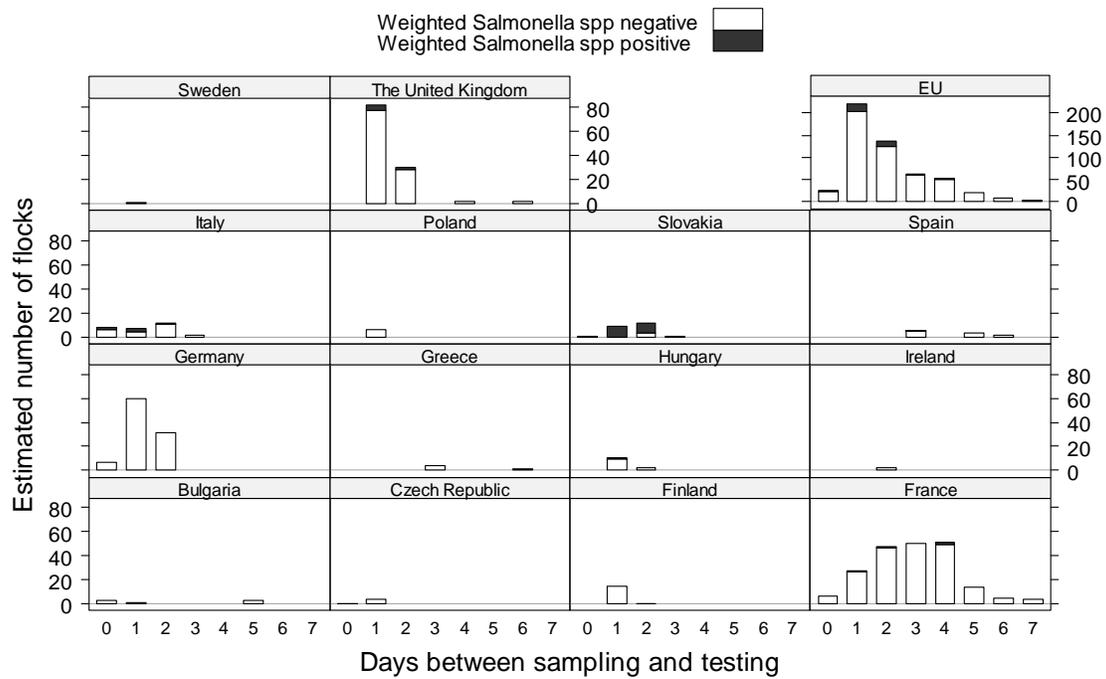
Figure 13. Weighted *Salmonella* prevalence by number of days between sampling and testing of breeding flock samples in the EU.[13]

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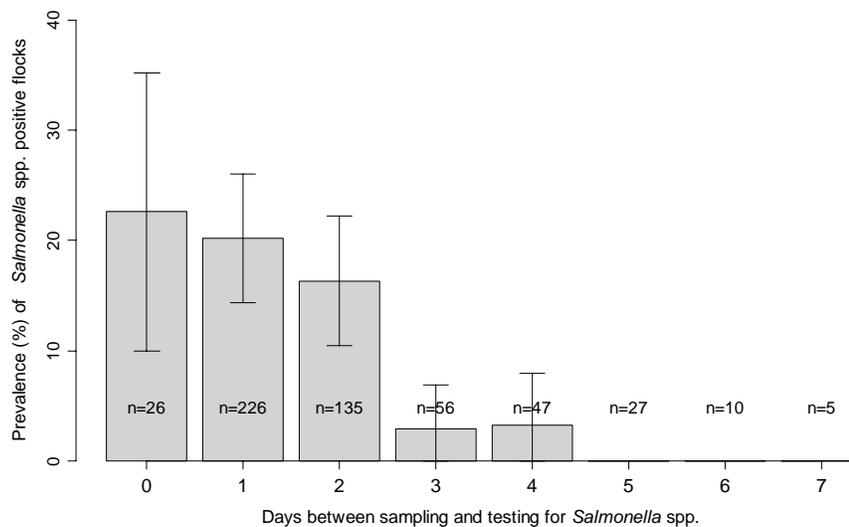
[13] n indicates the number of sampled flocks

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).
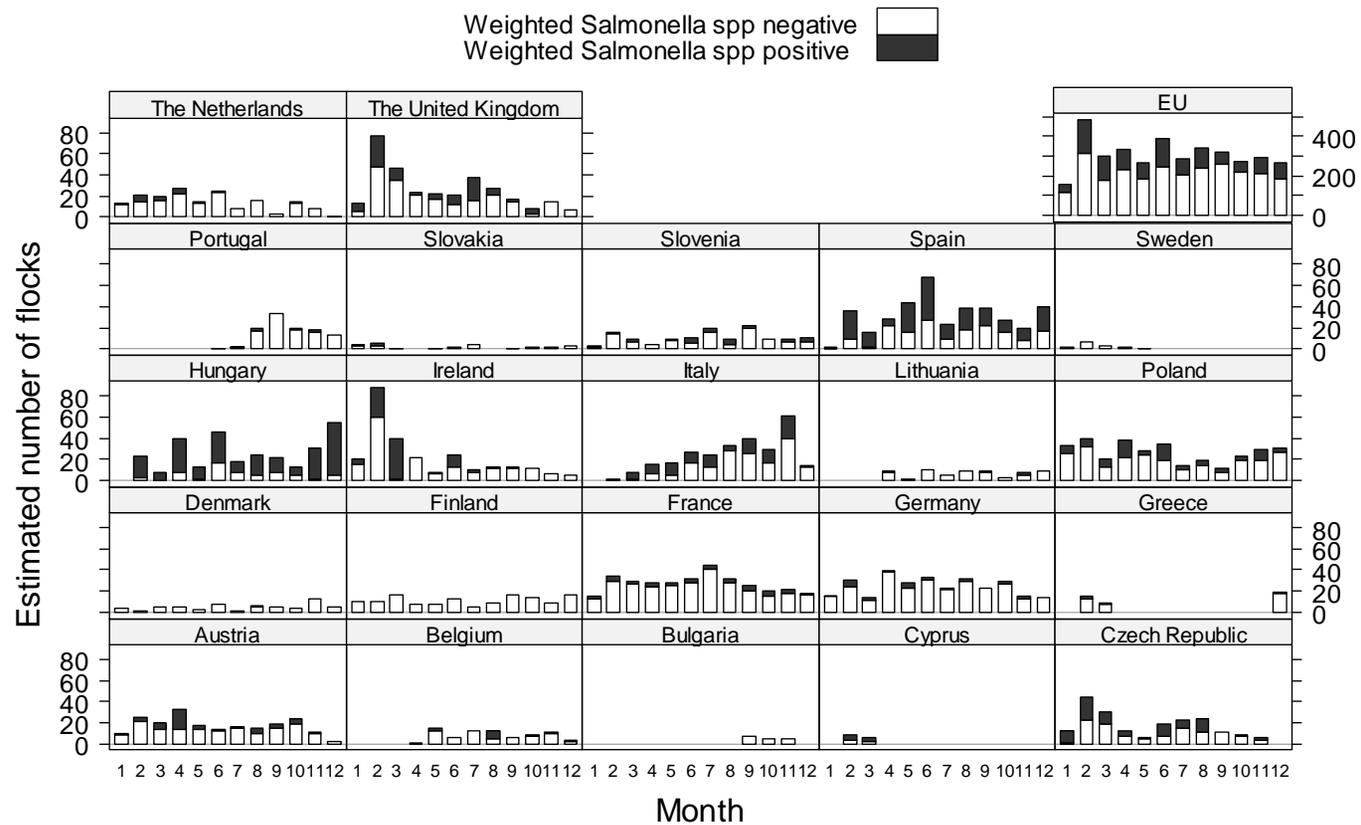
Variables associated with holding size

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]

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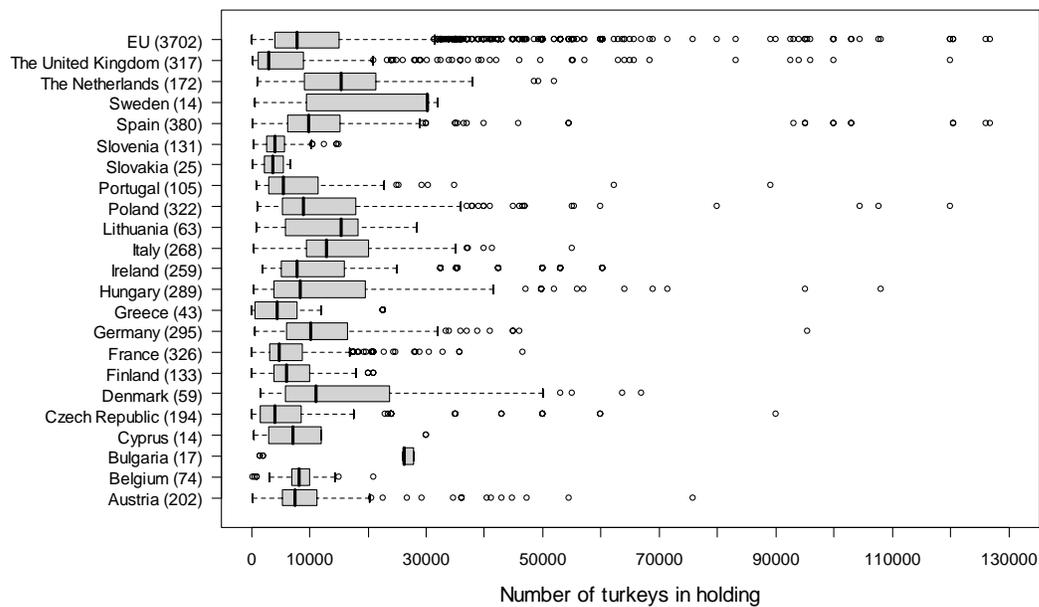
[14] A fattening flock in a holding in the United Kingdom with 419,815 turkeys at the time of sampling was excluded from the graph. Total number of sampled flocks between brackets.

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.
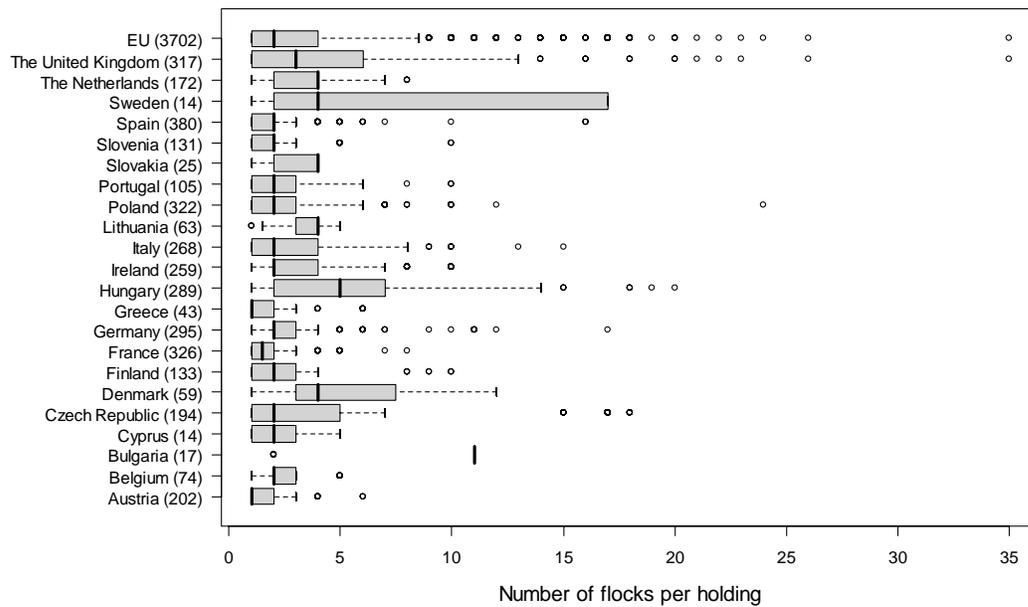
Flock size

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.
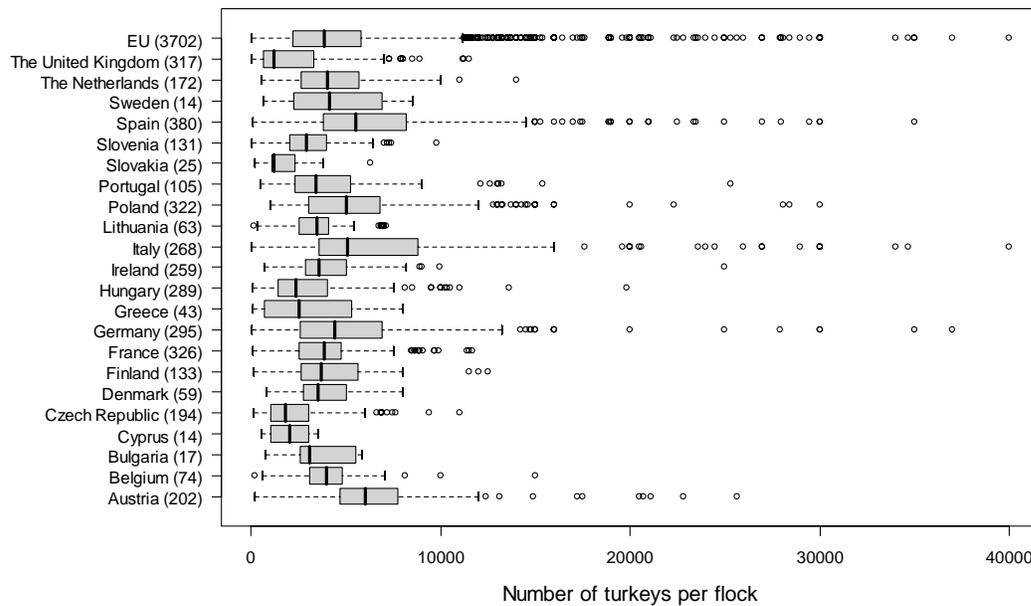
Age of fattening turkeys

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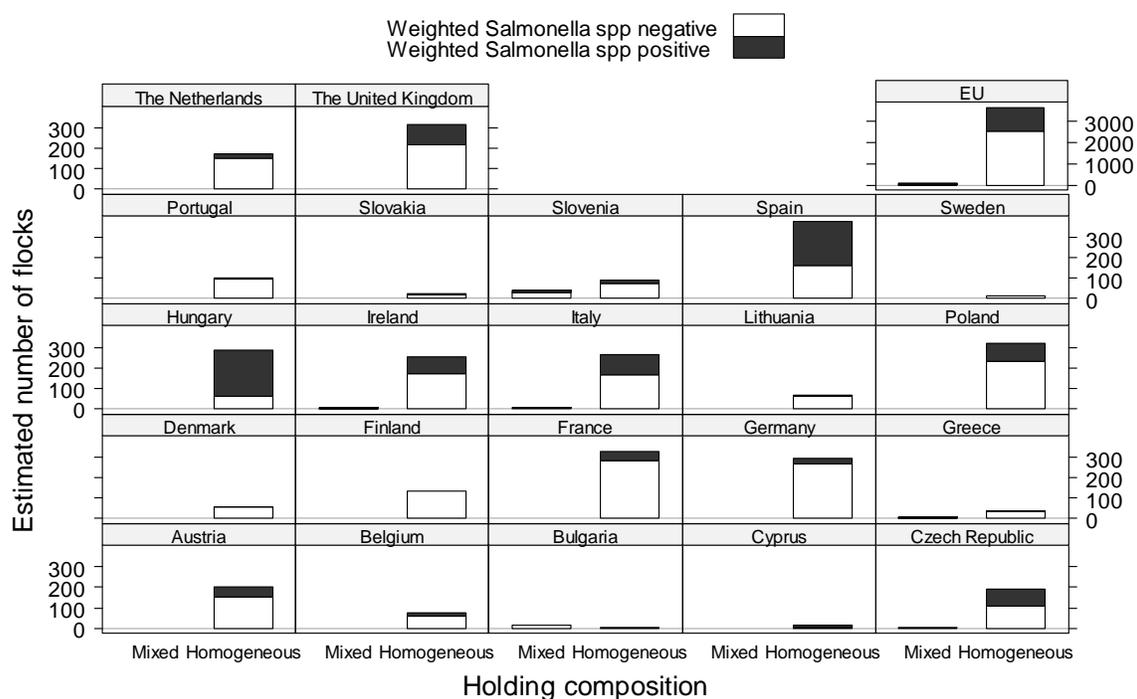
The number of flocks that were raised per house per year (number of cycles) mostly varied between two and three, in the MS (Figure 8.I, Annex I).

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

<u>Variables associated with flock characteristics</u>

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.
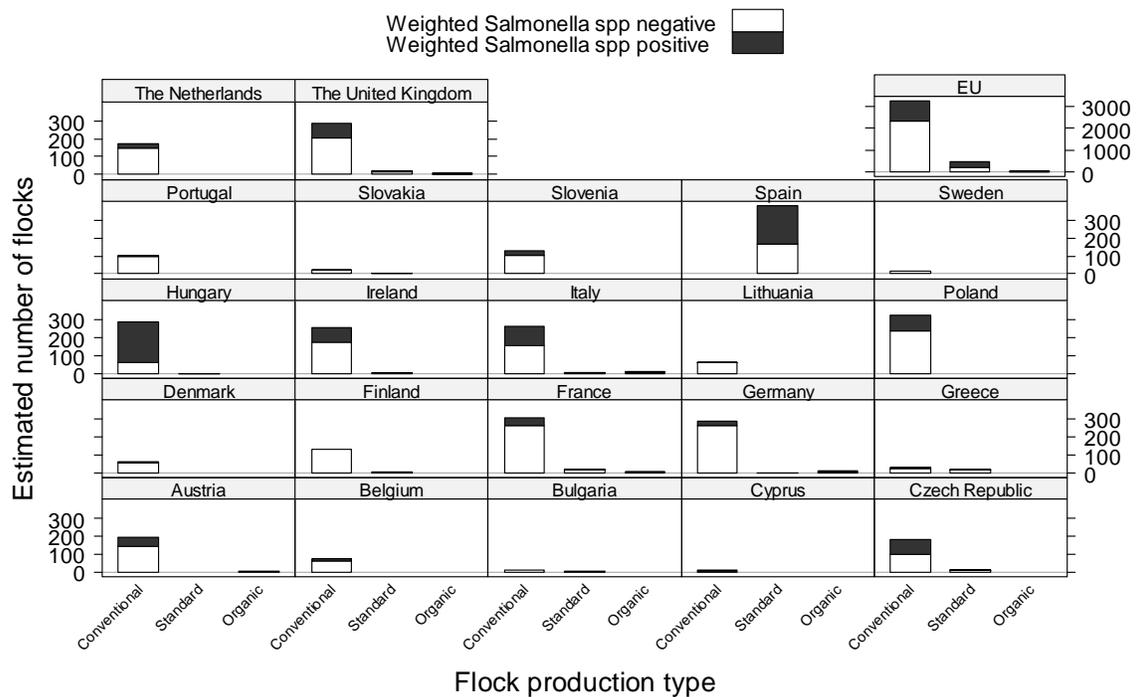
Vaccination against *Salmonella*

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.
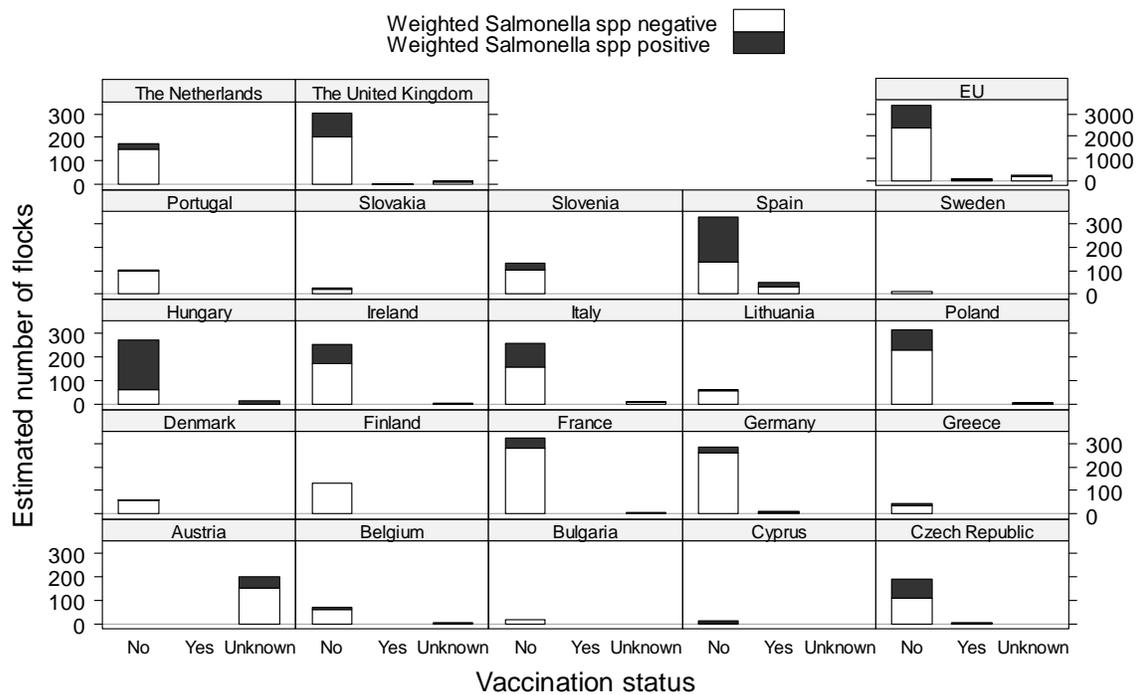
Medication with antimicrobials

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.
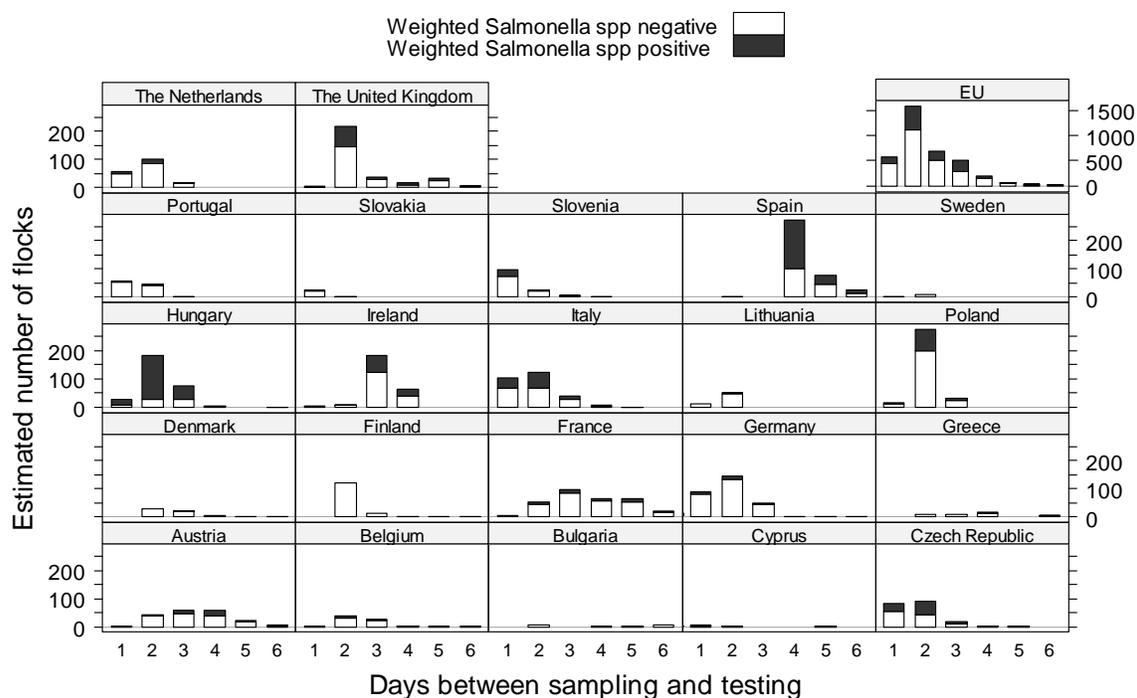
4.1.2.2 Analysis of multicollinearity among risk factors

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

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[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.

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[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

#	Country	No. of turkeys in holding	No. of flocks at full capacity	No. of flocks at sampling	No. of turkeys in flock at sampling	Quarter 1 vs 4	Quarter 2 vs 4	Quarter 3 vs 4	Age	Age at slaughter or depopulation	No. of cycles per house per year	Medication with antimicrobials 0 vs 1	Time between sampling and testing	Vaccination 1 vs 0	Vaccination 2 vs 0	Vaccination 1 vs 2	Holding composition 2 vs 3	Flock production type 1 vs 2	No. of flocks
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

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[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].
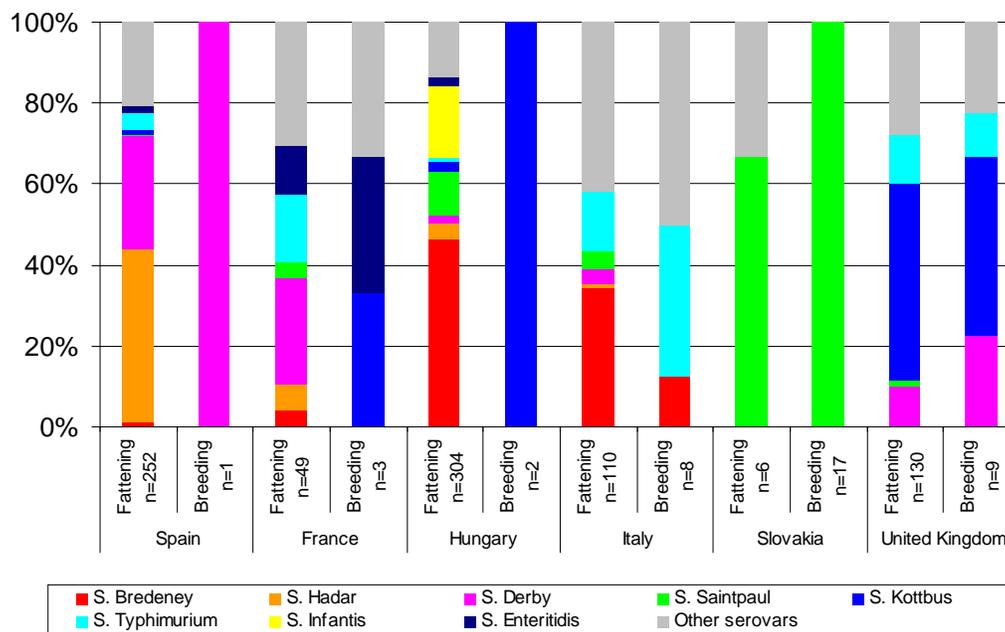
[20] n indicates the number of isolates.

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	HU	3.4	0.001
	Secondary	ES	2.0	0.001
S. Bredeney	Most Likely	HU,CY, IT	68.4	0.001
	Secondary	-	-	-
S. Hadar	Most Likely	ES	21.5	0.001
	Secondary	-	-	-
S. Derby	Most Likely	ES	7.6	0.001
	Secondary	UK	3.0	0.001
S. Saintpaul	Most Likely	CZ, AT, SI, SK, PL, HU	12.3	0.001
	Secondary	-	-	-
S. Kottbus	Most Likely	UK, IE, BE	10.8	0.001
	Secondary	GR, HU	2.3	0.001
S. Typhimurium	Most Likely	IT	2.8	0.001
	Secondary	UK	1.8	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).

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[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.
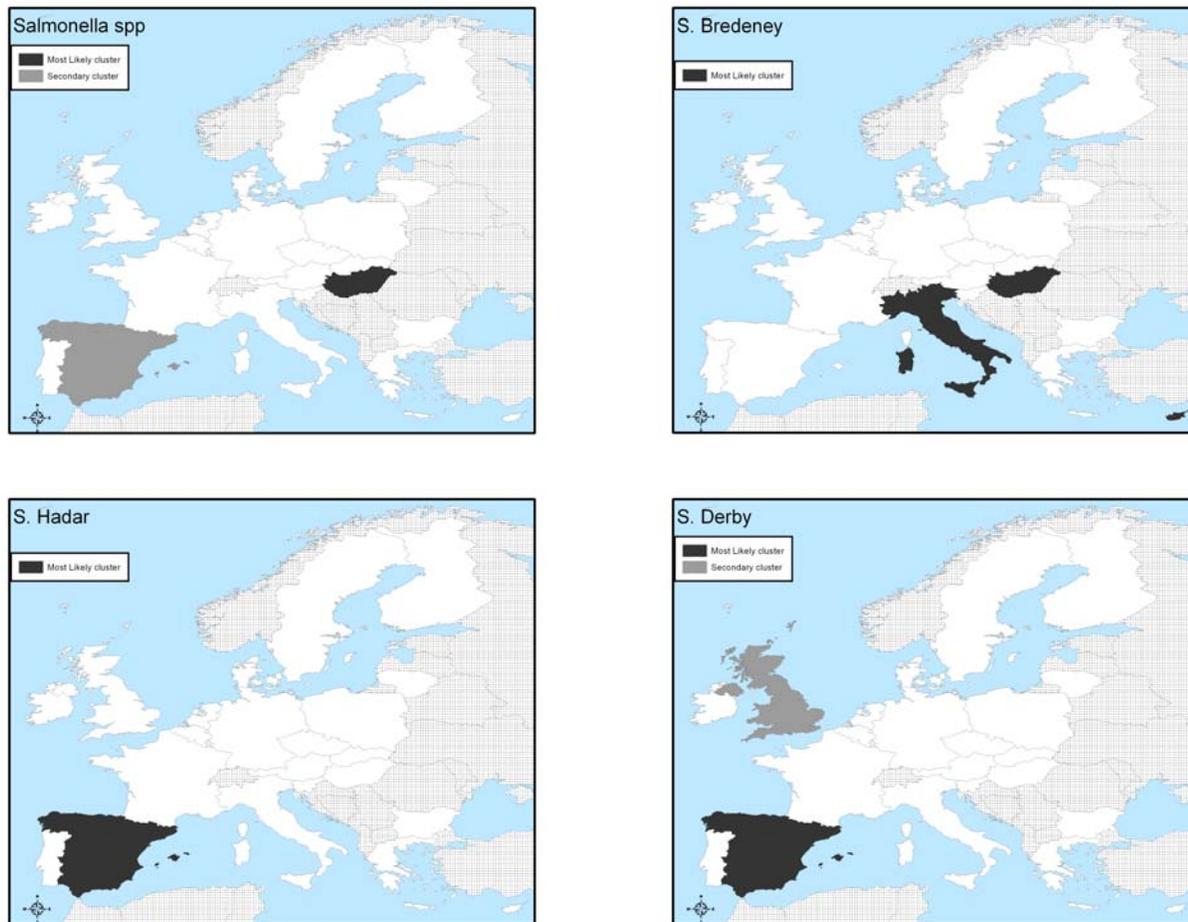
Figure 23 (continued)
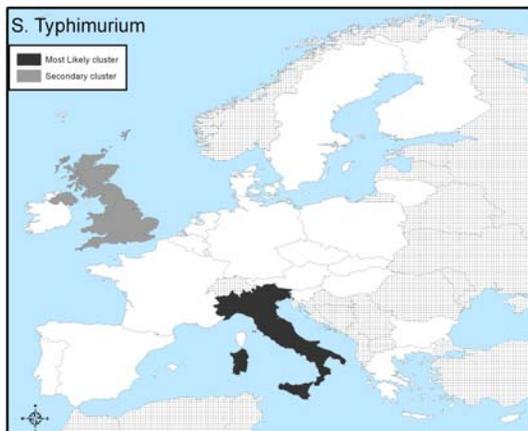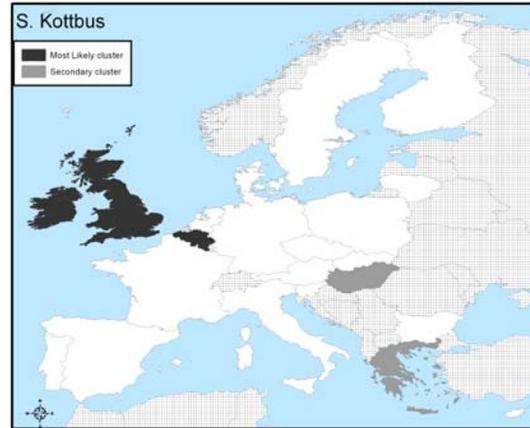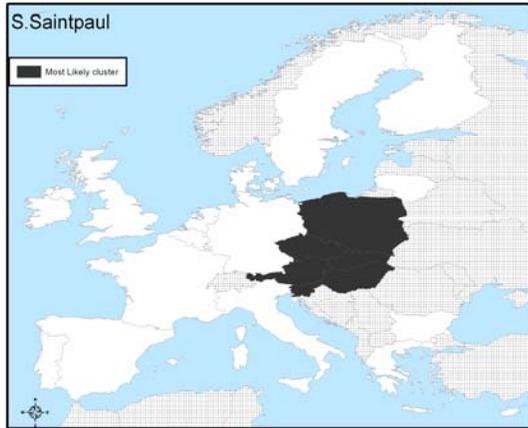
4.2.3   Comparison between EU serovar distributions in fattening turkeys, feed and human salmonellosis cases

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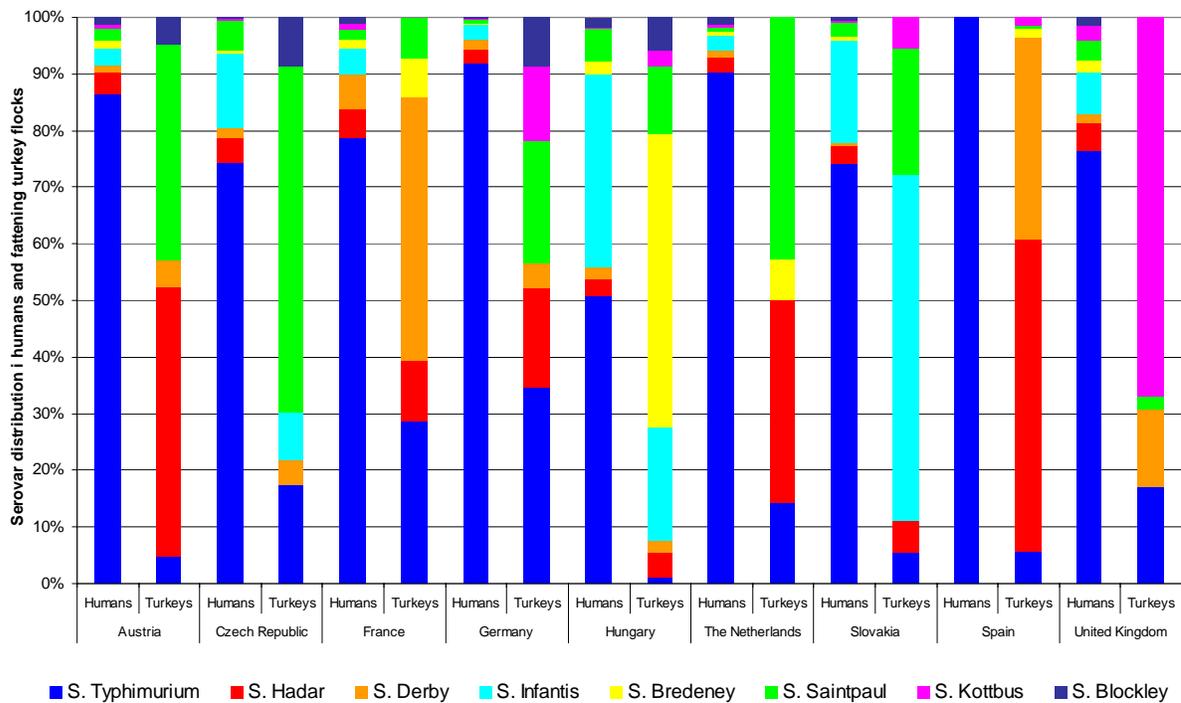
Frequencies of serovar isolation from fattening turkey flocks, feed, broiler chicken flocks and laying hen flocks are presented in Table 5. Most serovars were found in all of these sectors. However, in flocks with *Gallus gallus* (broilers and laying hens), *S*. Enteritidis was dominant, whereas in fattening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

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[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

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[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.

TASK FORCE ON ZOONOSES DATA COLLECTION MEMBERS

ACKNOWLEDGEMENTS

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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ANNEX I.   **ADDITIONAL FIGURES**

ANNEX II.   **TECHNICAL REPORT**

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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]

Annex I: Additional figures

Report of the Task Force on Zoonoses Data Collection

(Question N° EFSA-Q-2006-041B)

Adopted on 10 October 2008

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[1] For citation purposes: Report of the Task Force on Zoonoses Data Collection on the Analysis of the baseline survey on the prevalence of *Salmonella* in turkey flocks, Part B, *The EFSA Journal* (2008) 198, 1-224.

LIST OF FIGURES

Figure 1.1.   Box plot of the number of flocks of breeding turkeys per holding at full capacity, in the EU and per MS[2].

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[2]   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 2.1.   Box plot of the number of breeding turkeys in the sampled flocks, in the EU and per MS.
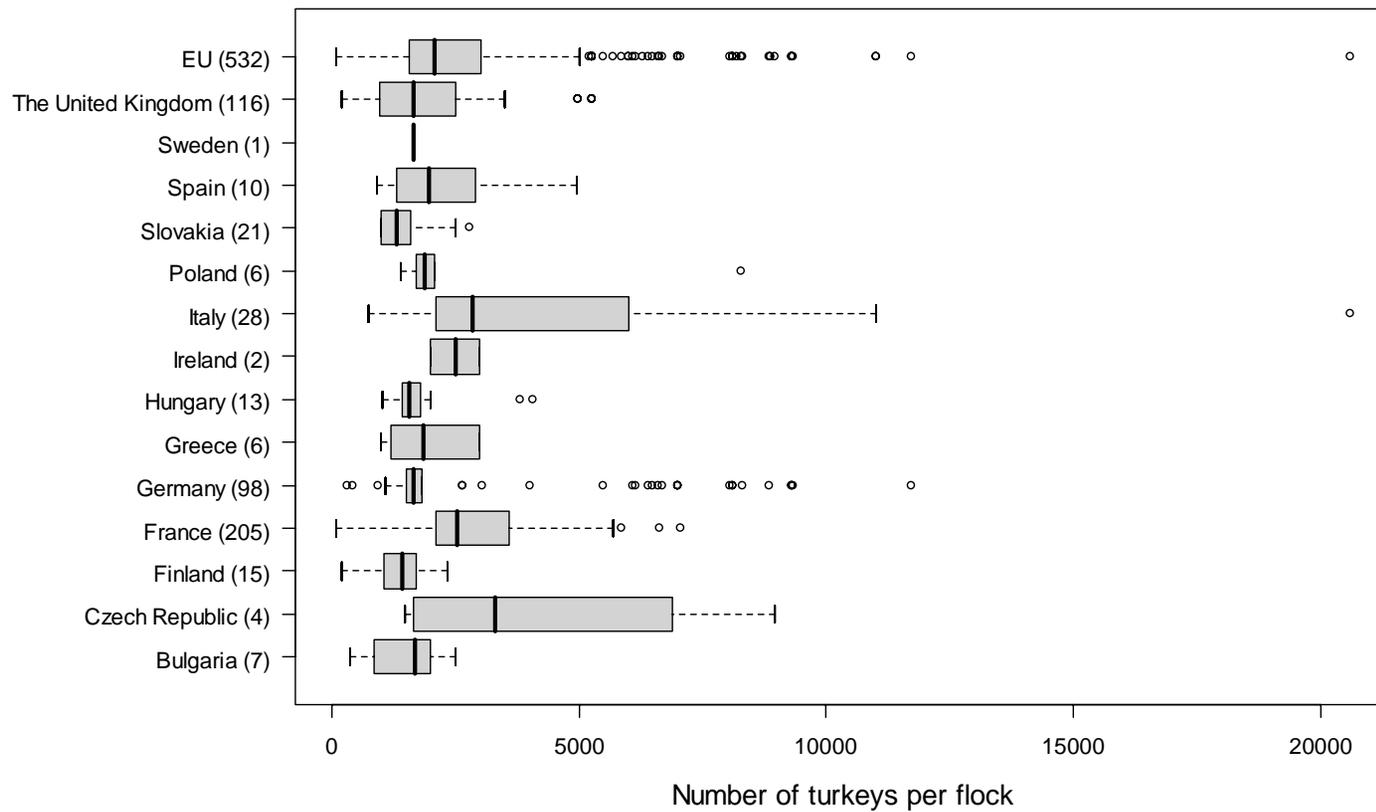
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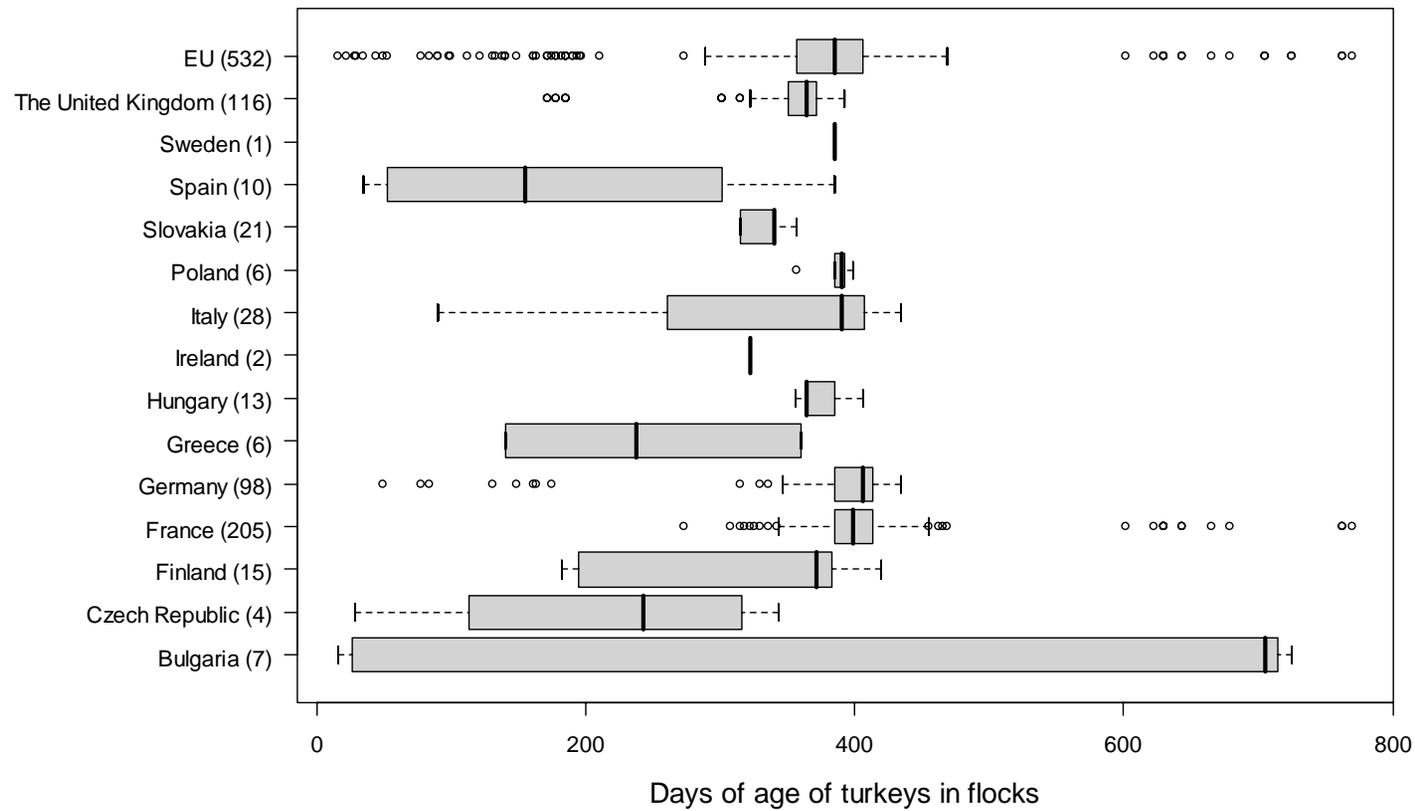
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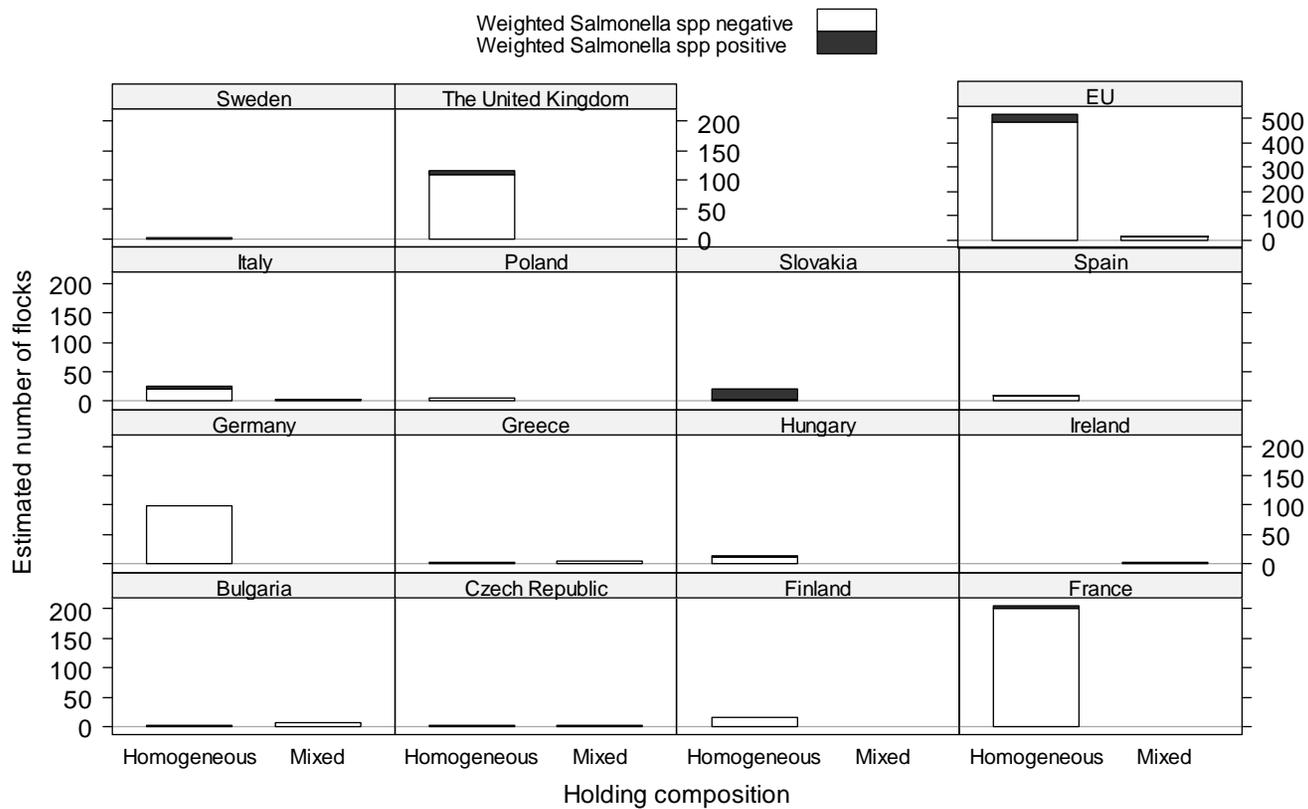
Figure 5.1. Frequency distribution of *Salmonella* negative and positive breeding turkey flocks, by number of cycles in the house, by MS and for the EU.
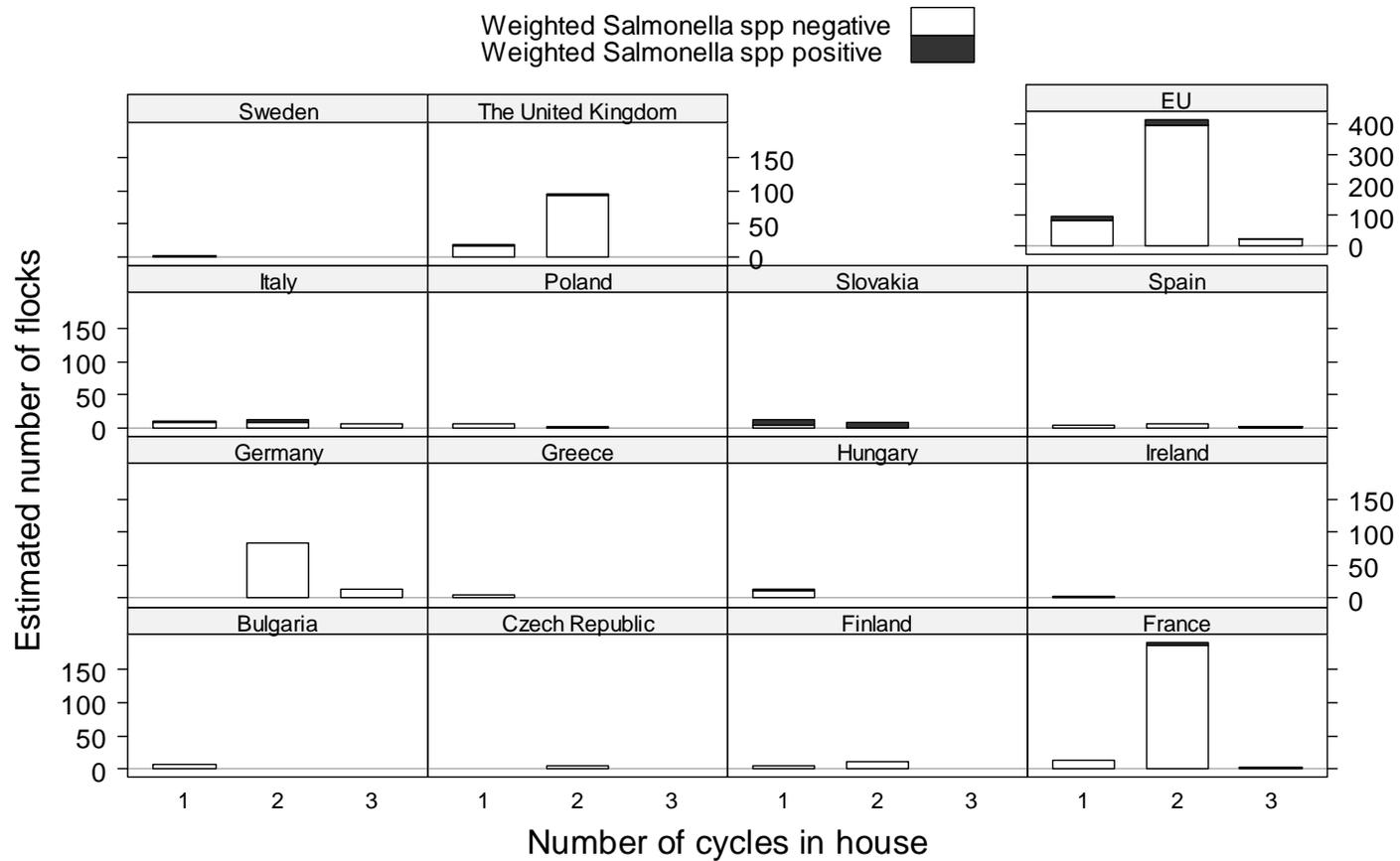
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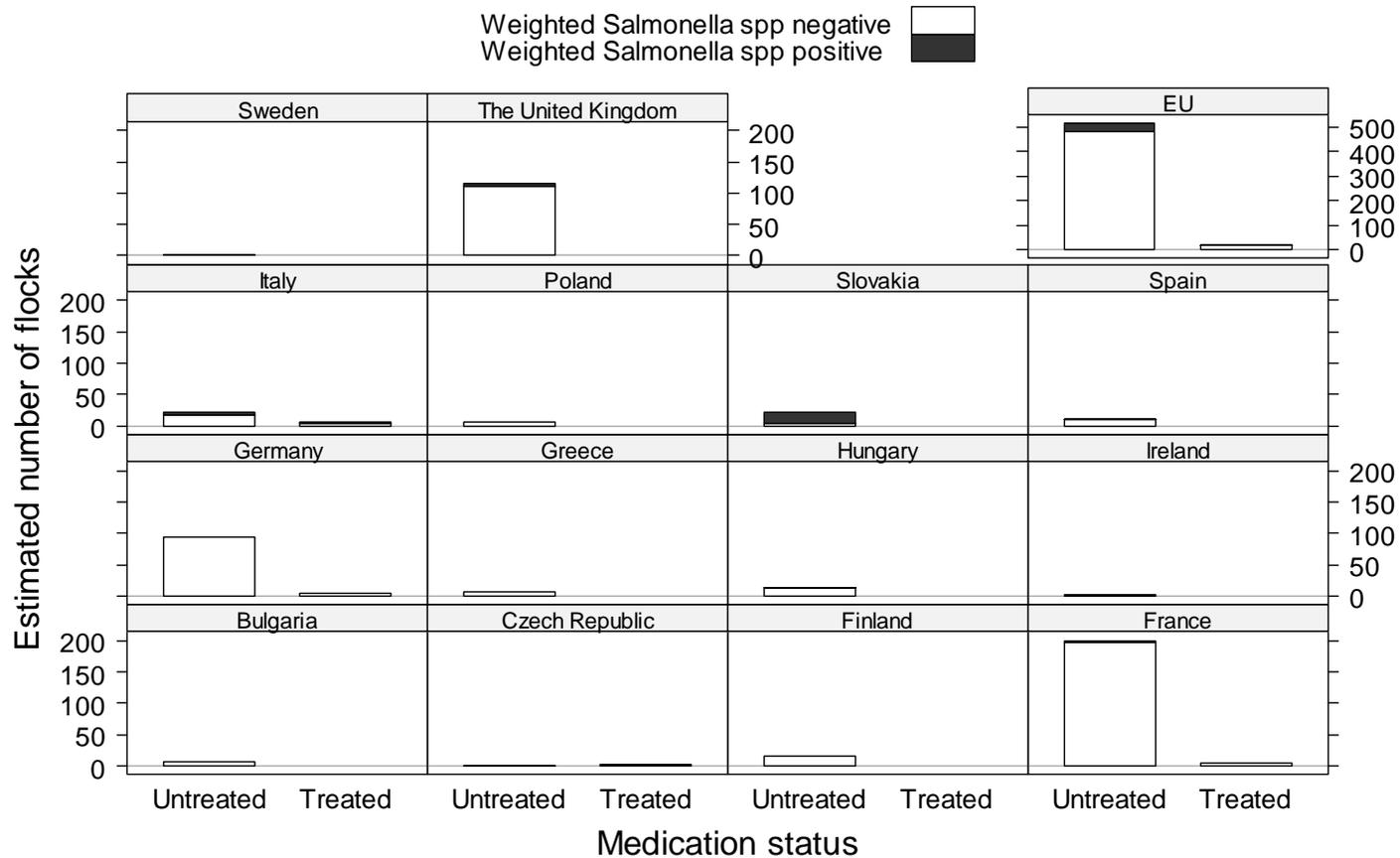
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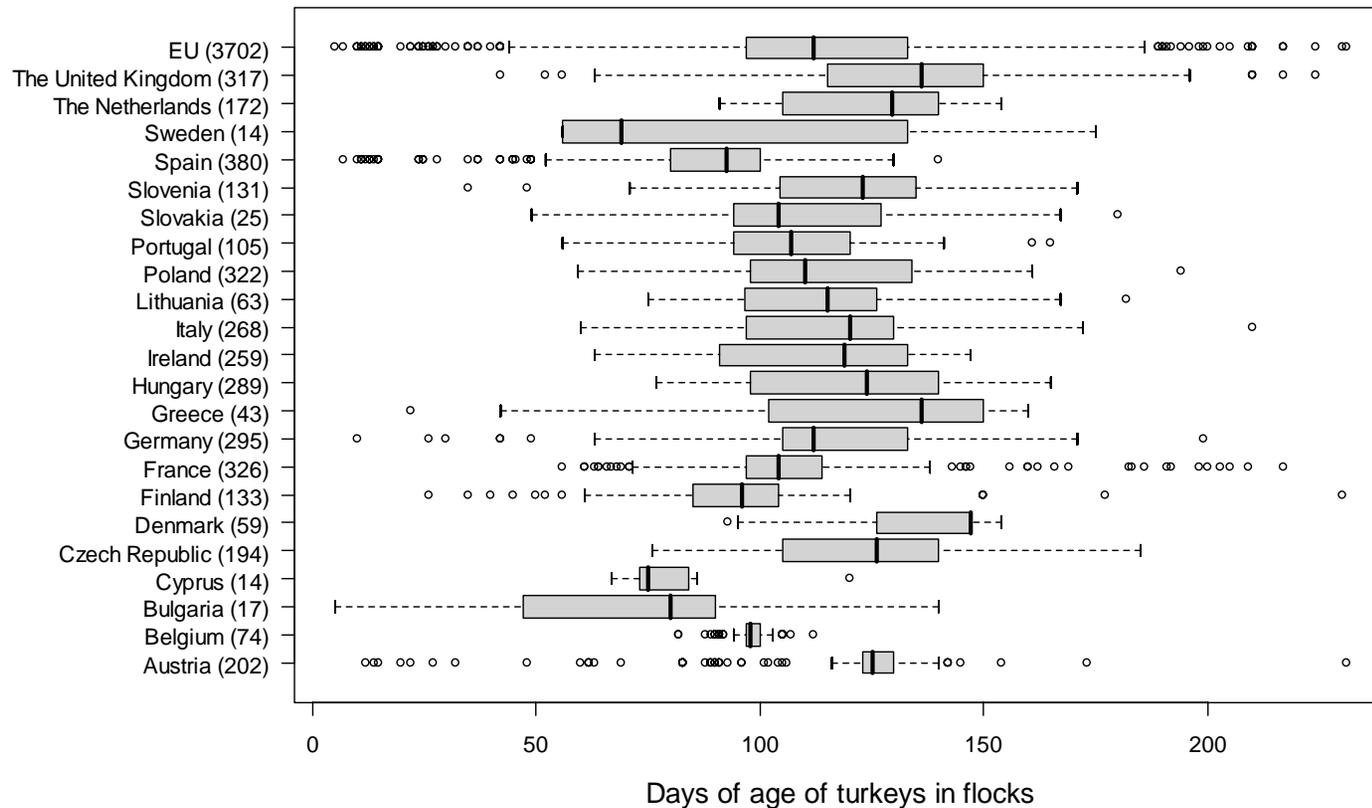
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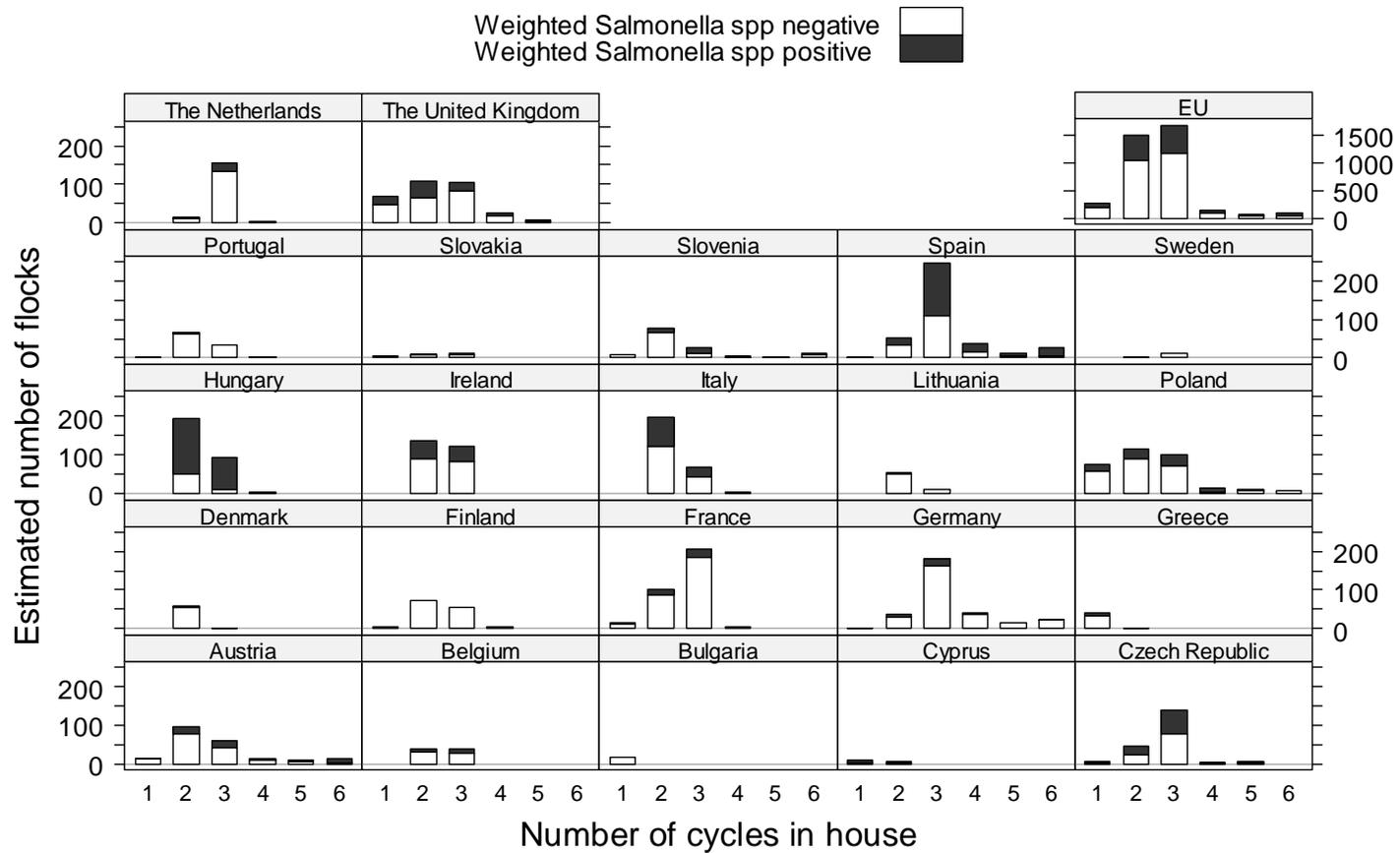
Figure 9.1.   Frequency distribution of treatment with antimicrobials of fattening turkey flocks, and by *Salmonella* status.
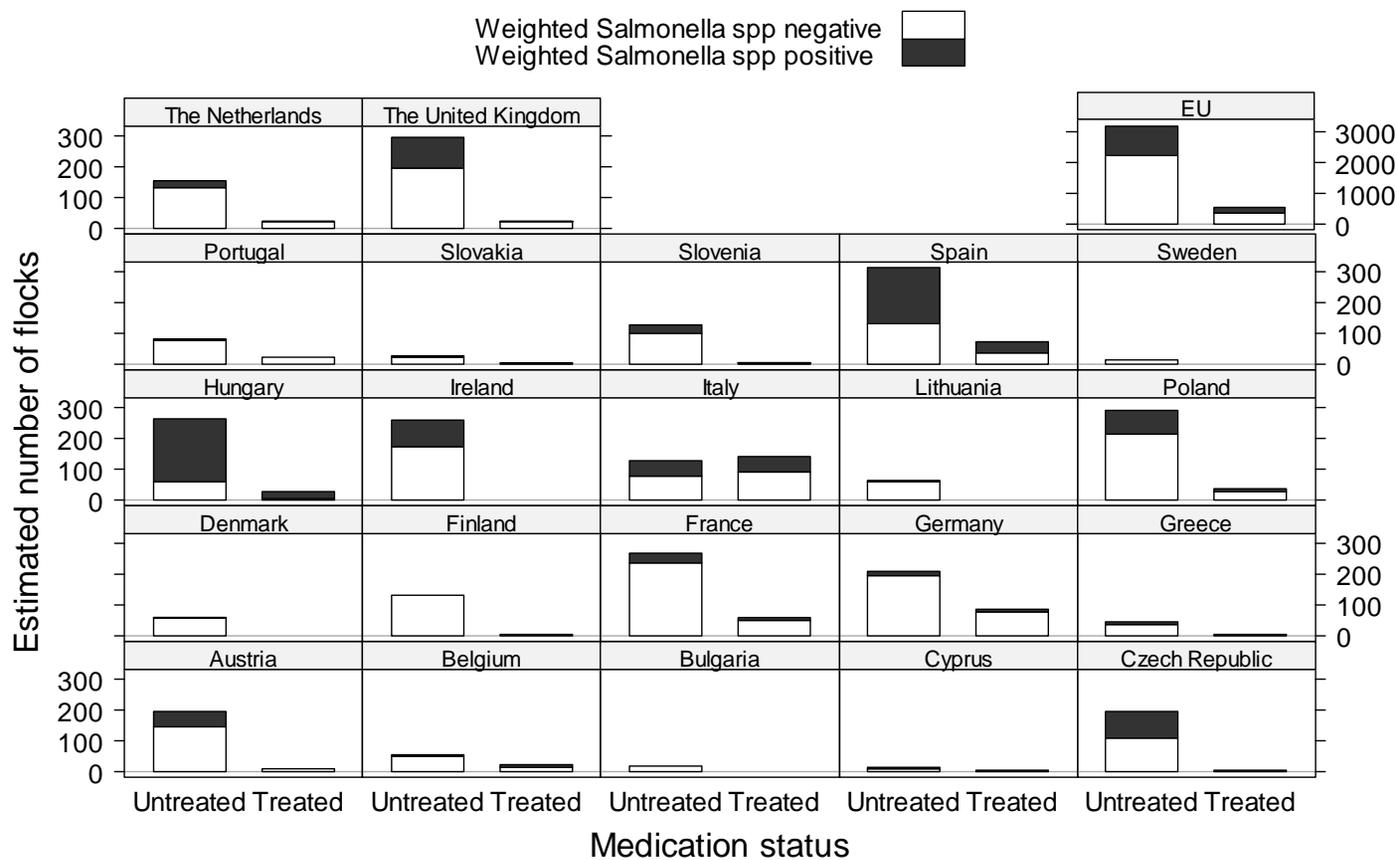
Figure 10.1. **Thematic maps of the estimated prevalence[3] of *Salmonella* spp., S. Bredeney, S. Hadar, S. Derby, S. Saintpaul, S. Kottbus and S. Typhimurium, in fattening turkey flocks, in the EU baseline survey in turkey flocks, 2006-2007.**

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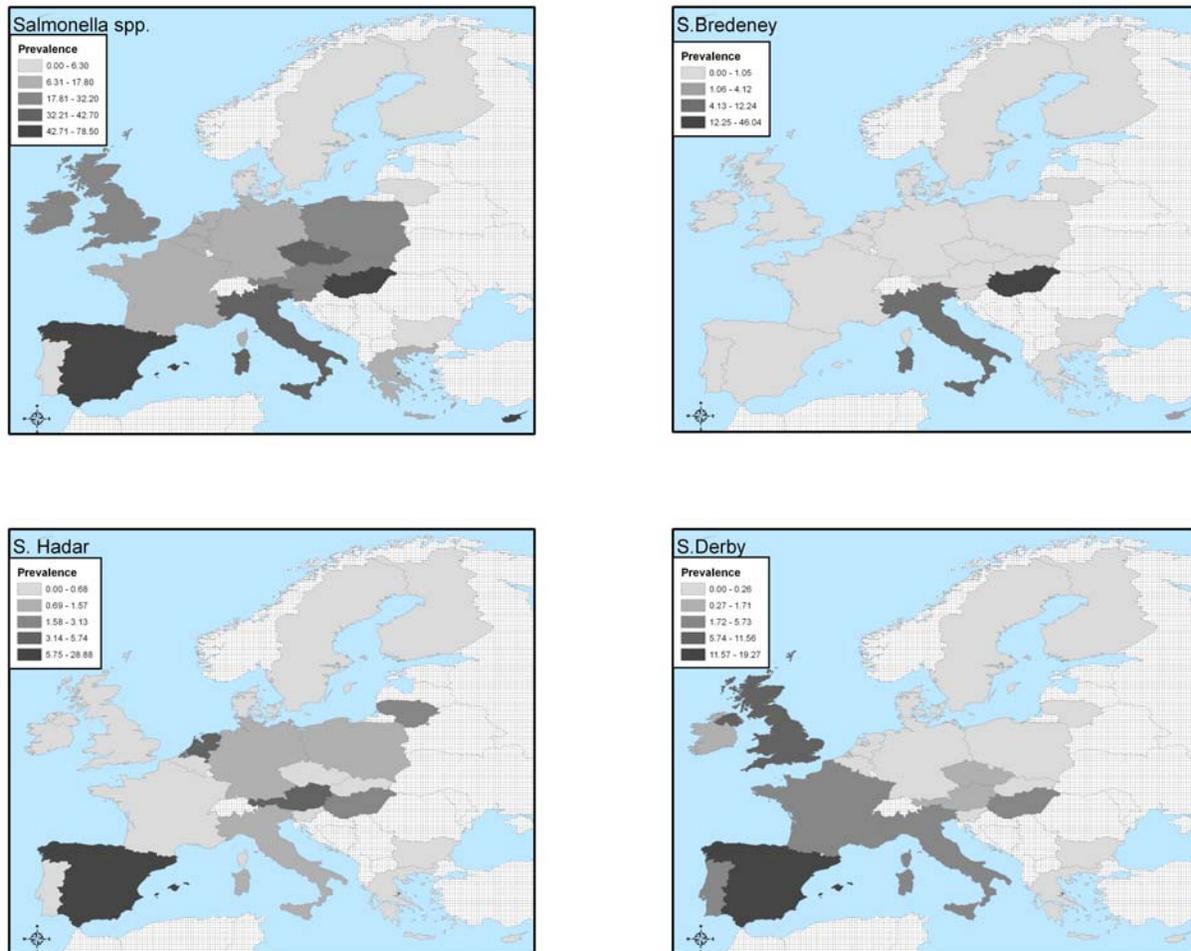
[3] Jenk´s optimized natural breaks were used to obtain prevalence classes for thematic mapping.

Figure 10.1 (continued)
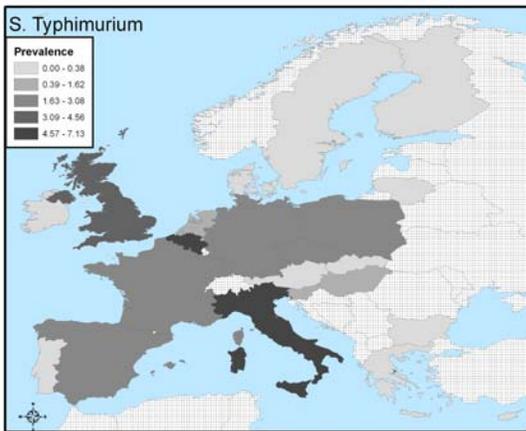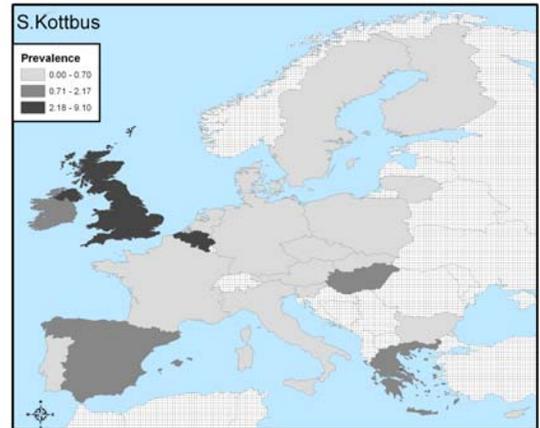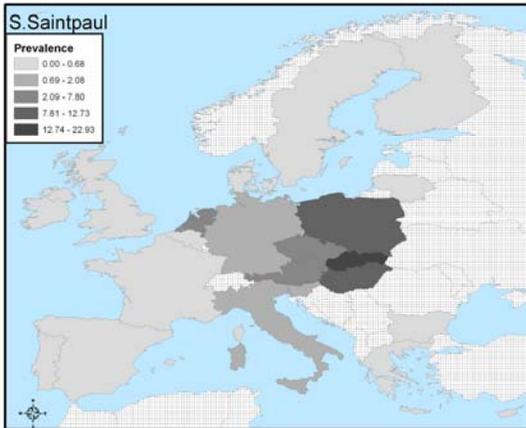
SCIENTIFIC REPORT

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]

Annex II: Technical report

Report of the Task Force on Zoonoses Data Collection

(Question N° EFSA-Q-2006-041B)

Adopted on 10 October 2008

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[1] For citation purposes: Report of the Task Force on Zoonoses Data Collection on the Analysis of the baseline survey on the prevalence of *Salmonella* in turkey flocks*, Part B, *The EFSA Journal* (2008) 198, 1-224

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1. Introduction

This technical Annex includes details on the statistical analysis of potential risk factors for *Salmonella* infection in flocks with turkeys in the EU and at individual Member State (MS) level. Moreover, results of the analysis of the bivariate association between individual, potential risk factors and *Salmonella* infection in fattening turkey flocks are presented here. It is to be noted that bivariate analysis does not allow for the adjustment of the potential confounding effect of several factors. For this reason, only results of multiple logistic regression are presented in the main Part B report for fattening turkey flocks. The analysis of the effects of optionally reported factors on *Salmonella* infection is also presented in this Annex.

2. Objectives

The overall objective of this report is to analyse and report on the baseline surveys conducted on the presence of *Salmonella* in turkey flocks. Whereas in Part A Report focussed on obtaining valid estimates of the prevalence of *Salmonella* serovars in turkey flocks, it is now of interest to obtain valid estimates of risk factors effects for a positive test result for *Salmonella* in turkey flocks, for all participating countries in the European Community.

'Positivity for *Salmonella*', is the main outcome variable to be analysed separately for fattening turkey flocks, and for breeding turkey flocks. Statistical analyses include:

- a descriptive analysis of all potential risk factors using frequency tables and measures of central tendency and dispersion, both in fattening and breeding turkey flocks.

- selection of risk factors in a model-building exercise for fattening turkey flocks. Effects of risk factors will be estimated through statistical modelling covered by the total of the dataset, i.e., in all Member States (MSs) and through a "matrix approach" for each individual MS.

3. Material and Methods

3.1 Data import and management

All data management and statistical analysis in this report were performed using the SAS System (SAS, 1999), whereas figures were constructed using R (http://cran.r-project.org).

The data contain information on the samples taken within flocks. However, since flock level prevalence of *Salmonella* needs to be estimated, some data manipulation was required. First, an additional variable was created, indicating whether each sample within a flock was found positive for *Salmonella*: variable Spp

A flock is defined positive for the outcome of interest when at least one sample is positive. This results in a new data set with information on flock level, containing the new outcome variable:

- *SalmSpp,* which equals 1 when the flock is found positive for *Salmonella*.

3.2 **Methodology and tools for descriptive analysis**

The descriptive section presents a thorough description of the sample of turkey holdings and flocks for every country, by all independent variables. This descriptive analysis is based on boxplots, frequency tables, simple chi-squared or trend tests and simple weighted logistic regression models. Note that these results should be interpreted only within the context of an exploratory analysis. Further analysis using appropriate modelling techniques should be used to validate these results in their proper context.

To study association between *Salmonella* prevalence and continuous risk factors, logistic regression will be considered including each covariate separately (Agresti, 2002; SAS Help documentation).

Multi-collinearity analysis among risk factors

A formal method to detect multi-collinearity is given by the variance inflation factor or VIF. This measures how much the variances of the estimated regression coefficients are inflated as compared to when the predictor variables are not linearly related. Essentially, each risk factor X_k is regressed on the other X risk factors in the model. The corresponding coefficient of multiple determination R_k^2 is then used to calculate the VIF:

$$VIF_k = (1 - R_k^2)^{-1}$$

Note that the VIF is equal to 1 when $R_k^2 = 0$, i.e., when X_k is not linearly related to the other risk factors. When $R_k^2 \neq 0$, then the VIF will be greater than 1, indicating an inflated variance for the estimated regression coefficients due to correlations among risk factors. A maximum VIF exceeding 10 is frequently interpreted as an indication of multi-collinearity.

For categorical covariates, the VIF can be calculated in a similar way using:

$$R^2 = 1 - \exp\{2[\log L(M) - \log L(0)]/n\},$$

with $\log L(M)$ and $\log L(0)$ representing the maximized log-likelihoods for the fitted model and the "null" model, containing only the intercept, and n referring to the sample size.

(Neter et al., 1996; Agresti, 1996).

3.3   Methodology and tools for the regression analysis

The hierarchical structure in the data can essentially be expressed as follows: samples within a flock, flocks within a holding, and holdings within a country. Interest is in flock level prevalence. Details on regression models, including underlying distribution and assumption, can be found in Annex I Part A report (An. 2008).

In order to take into account the possibility of samples from the same holding being more alike than those from different holdings (non-independence of observations) random effect logistic regression models were applied. In random-effects models, the intracluster correlation is assumed to arise from natural heterogeneity in the parameters across clusters (holdings).

There are two routes to introduce randomness into the model parameters. The first approach introduces random effects on the probability scale, such as the beta-binomial model (Skellam, 1948). The second approach introduces random effects in the linear predictor, yielding the classical mixed-effects models (Stiratelli et al., 1984). A random effects logistic regression model is an example of the second approach, where it is assumed that the number of positive flocks y_{ij} in holding j in country i follow a binomial distribution:

$$y_{ij} \sim Bin(n_{ij}, \pi_{ij}),\tag{1}$$

with mean modelled through a linear predictor containing fixed regression parameters β_i and holding specific parameters u_{ij}:

$$\text{Logit}(p_{ij}) = \beta_i + u_{ij}.$$

It is assumed that holding-specific effects are normally distributed with mean zero and some variance σ_i^2, i.e., $u_{ij} \sim N(0, \sigma_i^2)$. The above model can be interpreted as a logistic regression model for each holding, where some of the regression parameters are specific (random effects), while others are not (fixed effects). The random effects u_{ij} express how unit-specific trends deviate from the population-averaged trends. In case of repeated samples, the above model can be generalised by inclusion of a general time trend (fixed effect) and holding-specific time trends (random effect). This is often called a random-slopes model.

Unlike for correlated Gaussian outcomes, the parameters of the cluster-specific and population-averaged models for correlated binary data describe different types of effects of the covariates on response probabilities (Neuhaus 1992). The choice between population-averaged (i.e. marginal models) and cluster-specific (i.e. mixed models) strategies may heavily depend on scientific goals. Population-averaged models evaluate the overall risk as a function of covariates. With the cluster-specific approach, the response rates are modelled as a function of covariates and parameters, specific to a holding. In such models, the interpretation of fixed-effect parameters is conditional on a constant level of the holding-specific parameter (e.g. random effect). Diggle, Liang and Zeger (1994) and Diggle et. al. (2002) recommended the random-effect model for inferences on individual responses and the marginal model for inferences on margins, that is, the objectives (or the types of inferences) in a study should determine which suitable statistical model to use. For more details, see e.g. Aerts et al. 2002 and Molenberghs and Verbeke, 2005.

Weighting

Most statistical procedures analyse the data as if they were collected as a simple random sample. As a result, these procedures may underestimate the variability present in the data, when the data actually arise from complex surveys. Assigning weights to observations is one possible approach to correct differences between the complex survey design and simple random sampling. In general, by using weights, we try to 'reconstruct the total population', in order to avoid that certain strata or subpopulations are over- or under-represented. Details on the weighting procedure adopted in the analysis can be found in Annex I Part A report (EFSA, 2008).

4. Results

4.1 Results of the descriptive analysis: risk factors

In this section, a descriptive analysis of the independent variables is provided which may be of interest for risk analysis, starting with a group of variables associated with holding characteristics.

Group of variables associated with holding size

Figure 4.1-1 and Table 4.1-1 illustrate the distribution of the holdings by the number of turkey places, a variable with 6 categories:

- Cat 1. less than 500 birds,

- Cat 2. between 500 and 4,999 birds,

- Cat 3. between 5,000 and 9,999 birds,

- Cat 4. between 10,000 and 49,999 birds,

- Cat 5. between 50,000 and 99,999 birds,

- Cat 6. more than 100,000 birds.

Fattening turkeys are sampled mainly from relatively large holdings (between 5000 and 50000 bird places). Some countries also sampled from holdings with less than 500 bird places. Perhaps this was done to reach the targeted sample size. However, no breeding flocks were sampled from these small holdings. From it can be seen that most breeding flocks were sampled from middle-sized holdings (from 500 to 10,000 turkey places). Four out of the seven sampled flocks in Bulgaria were sampled from holdings with more than 100,000 turkey places. Note that now, the association between *Salmonella* prevalence and the size of a holding can be studied via a trend test. The results of this test are presented in Table 4.1-6. There seems to be a positive association between the prevalence of *Salmonella* in fattening turkeys and the size of the holding. As can also be seen from Figure 4.1-2, fattening turkey flocks in smaller holdings seem to be less affected by *Salmonella*. Although a significant upward trend can also be observed for breeding turkeys, it is less clearly visible in Figure 4.1-2.

The distribution of the number of turkeys in a holding at the time of sampling for each MS is displayed in Figure 4.1-5 by means of bar plots, and through central tendency statistics in Table 4.1-2 on average 7,060 birds were present at the time of sampling in holdings where breeding flocks were sampled and 11,854 birds in holdings where fattening flocks were sampled.

Observe that countries like Denmark, Germany, Italy, Poland, Sweden and Bulgaria considerably exceed these averages. In Figure 4.1-6 we have displayed the distribution of the number of turkeys in a holding at the time of sampling by their infection status. To increase the readability of the graph, we have also displayed this result on the log10 scale. Further, in Table 4.1-4 we have displayed the odds ratio estimates and corresponding 95% confidence intervals obtained from a weighted logistic regression, estimating the effect of the number of turkeys in a holding at the time of sampling. From this table and Figure 4.1-6 a positive association can be observed between the risk factor of interest and the probability of observing a positive flock, in both breeding and fattening turkeys. Increasing the holding size seems to result in increased odds of observing a positive flock.

Further, from Figure 4.1-7 and Table 4.1-5 it can be seen that, on average, 3.8 breeding flocks and 3.1 fattening flocks exist in one EU holding. Observe that Bulgaria considerably exceeds these averages. This can probably be explained by the fact that the flocks in Bulgaria were sampled from holdings with over 100,000 turkey places (see also Table 4.1-1). Furthermore, in this case, the size of the holding, now in terms of flocks at full capacity, also has a positive effect on *Salmonella* prevalence (see Figure 4.1-8 and Table 4.1-6).

Finally, observe that these bird counts translate into 3.6 (2.7) flocks of breeding (fattening) flocks which are on average available in the EU at the time of sampling (see Figure 4.1-11 and Table 4.1-7). Once more, a positive association of *Salmonella* presence can be observed with the number of flocks at the time of sampling. An increase in this factor results in an increase of the probability of observing a positive flock in both breeding and fattening turkeys (see Figure 4.1-12 and Table 4.1-8).

Figure 4.1-1 - Estimated number of fattening and breeding turkey flocks by number of turkey places and (weighted) *Salmonella* **outcome.**
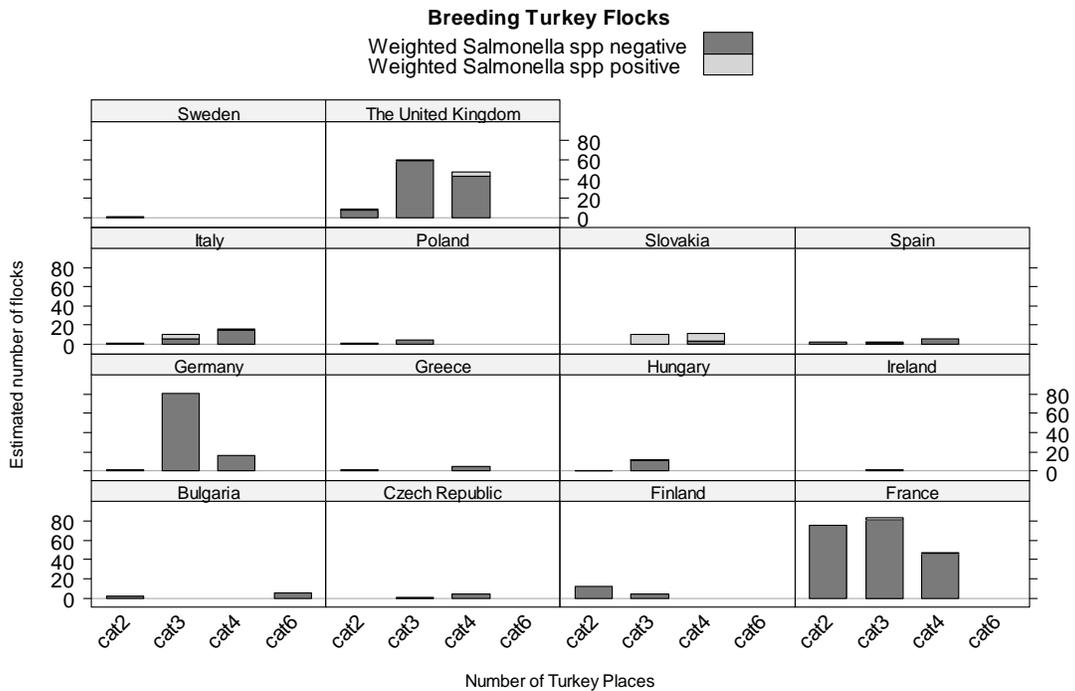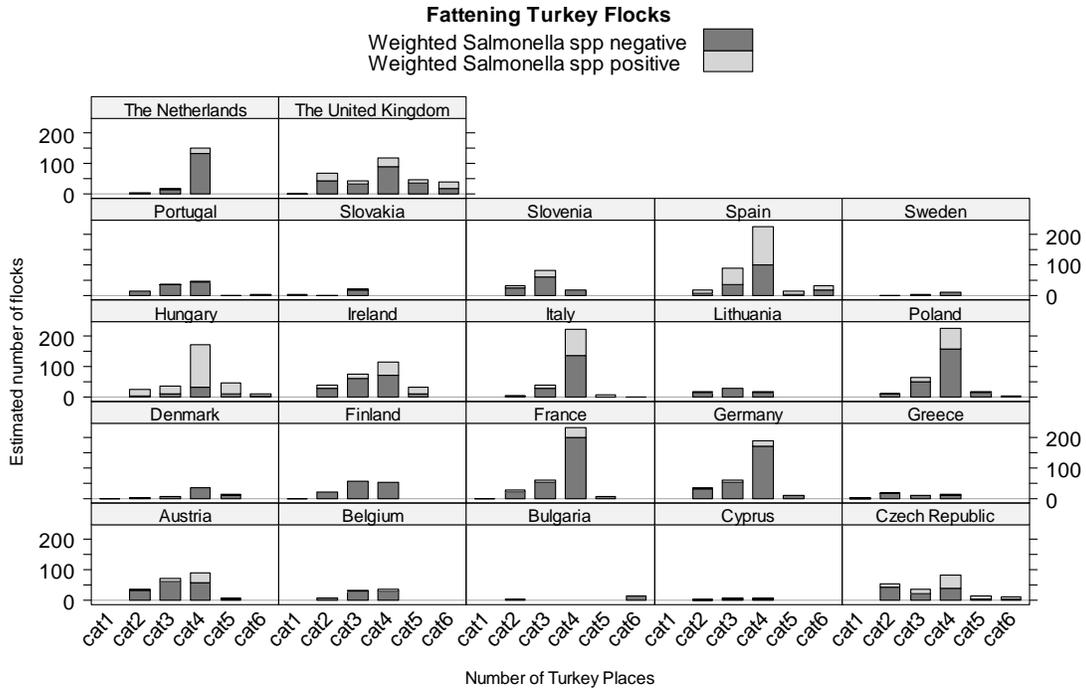
Table 4.1-1 - Distribution of the number of flocks by number of turkey places, per Member State and in EU.

	Country	Fattening turkey flocks: number of turkey places											
		<500		500-4,999		5,000-9,999		10,000-49,999		50,000-99,999		≥10,0000		Total
1	Austria			37	18%	92	46%	67	33%	6	3%			202
2	Belgium			8	19%	34	46%	32	43%					74
3	Cyprus			3	21%	5	36%	6	43%					14
4	Czech Republic			74	38%	44	23%	53	27%	20	10%	3	2%	194
5	Denmark	1	2%	4	7%	6	10%	33	56%	15	25%			59
7	Finland	2	2%	24	18%	58	44%	49	37%					133
8	France	1	0%	65	20%	94	29%	164	50%	2	1%			326
9	Germany			48	16%	71	24%	173	59%	3	1%			295
10	Greece	2	5%	18	42%	11	26%	12	28%					43
11	Hungary			51	18%	50	17%	146	51%	34	12%	8	3%	289
12	Ireland			57	22%	99	38%	83	32%	20	8%			259
13	Italy			8	3%	55	21%	201	75%	3	1%	1	0%	268
15	Lithuania			15	24%	31	49%	17	27%					63
18	Poland			22	7%	106	33%	180	56%	10	3%	4	1%	322
19	Portugal			19	18%	40	38%	43	41%	1	1%	2	2%	105
20	Slovakia	2	8%	1	4%	22	88%							25
21	Slovenia			33	25%	81	62%	17	13%					131
22	Spain			28	7%	124	33%	211	56%	9	2%	8	2%	380
23	Sweden			2	14%	2	14%	10	71%					14
24	The Netherlands			6	3%	26	15%	140	81%					172
25	The United Kingdom	4	1%	161	51%	46	15%	76	24%	21	7%	9	3%	317
27	Bulgaria			4	24%							13	76%	17
	European Union	12	0%	688	19%	1,097	30%	1,713	46%	144	4%	48	1%	3,702

	Country	Breeding turkey flocks: number of turkey places											
		<500		500-4,999		5,000-9,999		10,000-49,999		50,000-99,999		≥100,000		Total
4	Czech Republic					2	50%	2	50%					4
7	Finland			14	93%	1	7%							15
8	France			115	56%	67	33%	23	11%					205
9	Germany			1	1%	91	93%	6	6%					98
10	Greece			3	50%			3	50%					6
11	Hungary			1	8%	12	92%							13
12	Ireland					2	100%							2
13	Italy			2	7%	16	57%	10	36%					28
18	Poland			1	17%	5	83%							6
20	Slovakia					10	48%	11	52%					21
22	Spain			5	50%	3	30%	2	20%					10
23	Sweden			1	100%									1
25	The United Kingdom			10	9%	61	53%	45	39%					116
27	Bulgaria			3	43%							4	57%	7
	European Union			156	29%	270	51%	102	19%			4	1%	532

Figure 4.1-2 Weighted *Salmonella* prevalence by number of turkey places in the EU (number of sampled flocks represented inside each bar).
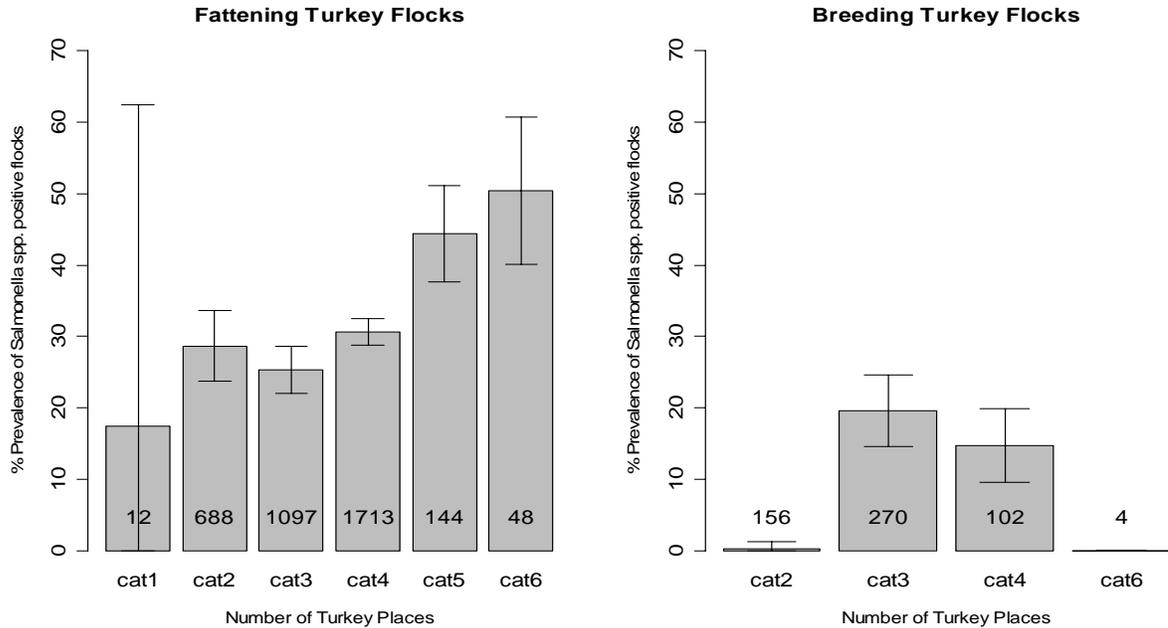
Note that the sample sizes by category represented in Table 4.1-1 differ slightly from the sample sizes displayed in Table 4.1-2. The first represent observed sample sizes, whereas the latter reflects an estimated sample size. Indeed, if a positive flock has weight 2, then in Table 4.1-3 it will be considered two positive flocks. The displayed proportion of positive flocks in each category is therefore an estimated proportion of positive flocks taking into account the weight of each observation. The chi-square statistics are also based on these weighted results. Further, observe that that these test results are not corrected for other risk factors which could be considered in the model building exercise. These and the following similar tables should therefore be interpreted with caution in the context of an exploratory data analysis.

Table 4.1-2 - Weighted *Salmonella* prevalence by Number of Turkey Places, by Flock Production Type in the EU

Fattening turkeys							*Salmonella*
Frequency *Row Pct* Col Pct	Number of Turkey Places						
	< 500	500-4,999	5,000-9,999	10,000-49,999	50,000-99,999	≥100,000	Total
Negative	2 *0%* 83%	234 *9%* 71%	512 *20%* 75%	1,653 *64%* 69%	118 *5%* 56%	44 *2%* 50%	2,564 *100%*
Positive	0 *0%* 17%	94 *8%* 29%	174 *15%* 25%	731 *64%* 31%	94 *8%* 44%	45 *4%* 50%	1,138 *100%*
Total	3 100%	328 100%	686 100%	2,383 100%	212 100%	90 100%	3,702

Breeding turkeys					*Salmonella*
Frequency *Row Pct* Col Pct	Number of Turkey Places				
	500-4999	5000-9999	10000-49999	≥100000	Total
Negative	104 *23%* 100%	194 *42%* 80%	156 *34%* 85%	3 *1%* 100%	458 *100%*
Positive	0 *0%* 0%	47 *63%* 20%	27 *36%* 15%	0 *0%* 0%	74 *100%*
Total	105 100%	241 100%	183 100%	3 100%	532

Trend statistic (one-sided p-value) [2]	Fattening	Breeding
Salmonella	5.19 (<0.001)	2.40 (0.016)

---

[2] Positive outcome trend.

Figure 4.1-3 Central tendency and distribution of number of turkeys in a holding at the time of sampling by Member State3 (number of sampled flocks between brackets).

Fattening Turkeys Flocks

Breeding Turkey Flocks

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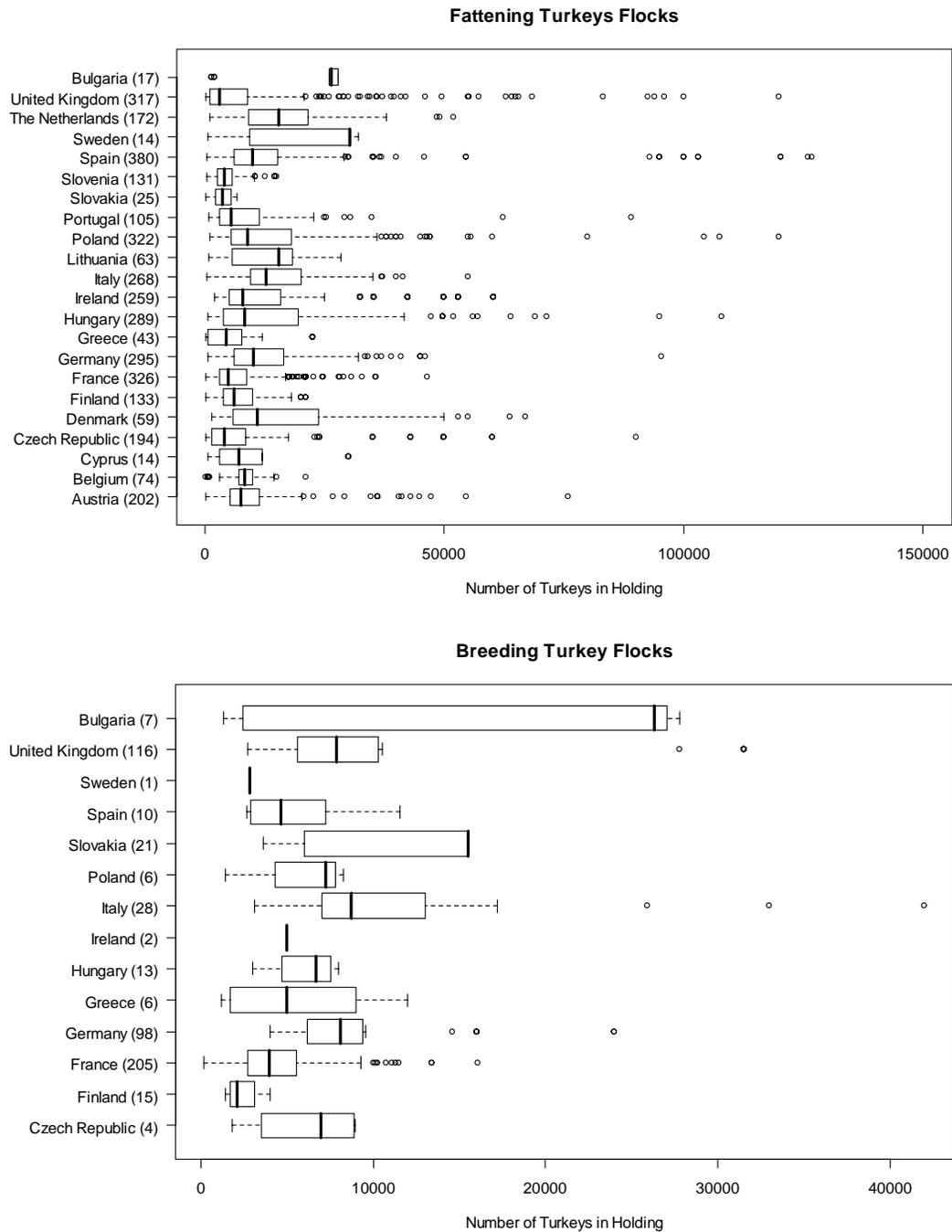
[3] One outlying data point left out for readability of graph: a fattening flock in a holding in the UK with 419815 turkeys at the time of sampling. The flock was tested positive for *Salmonella*

Table 4.1-3 Central tendency (mean, median) and dispersion measures (standard deviation and quantiles) of number of turkeys in a holding at the time of sampling.[4]

	Country	Number of turkeys in holding: fattening turkey flocks				
		Q1	Median	Q2	Mean	StD
1	Austria	5,300	7,475	11,290	10,084	9,868
2	Belgium	7,000	8,234	10,000	8,504	3,721
3	Cyprus	3,000	7,100	12,000	10,614	11,147
4	Czech Republic	1,500	4,000	8,550	8,280	12,791
5	Denmark	5,800	11,000	24,300	16,899	15,764
7	Finland	3,813	6,000	9,983	6,885	4,448
8	France	3,100	4,836	8,780	6,978	6,464
9	Germany	6,000	10,100	16,500	12,527	9,962
10	Greece	670	4,400	8,000	6,511	7,366
11	Hungary	3,780	8,345	19,500	13,858	15,233
12	Ireland	5,135	7,920	16,000	14,134	14,503
13	Italy	9,500	12,850	20,000	15,108	8,407
15	Lithuania	4,500	15,400	19,100	13,269	7,880
18	Poland	5,380	9,000	18,000	13,939	14,813
19	Portugal	3,000	5,500	11,400	9,271	11,771
20	Slovakia	2,200	3,700	5,400	3,620	2,120
21	Slovenia	2,520	4,000	5,790	4,479	2,774
22	Spain	6,125	9,900	15,289	14,262	18,039
23	Sweden	9,400	30,200	30,350	23,332	12,111
24	The Netherlands	9,160	15,400	21,420	16,553	9,751
25	The United Kingdom	1,100	3,000	9,000	11,549	30,169
27	Bulgaria	26,051	26,300	27,774	20,913	10,980
	European Union	4,001	7,805	15,000	11,854	14,886

	Country	Number of Turkeys in Holding				
		Q1	Median	Q2	Mean	StD
4	Czech Republic	3,478	6,975	8,880	6,179	3,406
7	Finland	1,650	2,100	3,647	2,419	,920
8	France	2,731	3,928	5,531	4,682	2,599
9	Germany	6,142	8,065	9,374	8,357	3,146
10	Greece	1,700	5,000	9,000	5,650	4,377
11	Hungary	4,700	6,670	7,530	6,210	1,607
12	Ireland	5,000	5,000	5,000	5,000	
13	Italy	7,000	8,695	13,000	11,804	8,763
18	Poland	4,310	7,232	7,792	6,037	2,669
20	Slovakia	6,000	15,500	15,500	10,700	5,200
22	Spain	2,900	4,625	7,250	5,660	3,242
23	Sweden	2,800	2,800	2,800	2,800	
25	The United Kingdom	5,600	7,834	10,300	8,847	6,056
27	Bulgaria	2,300	26,300	27,774	16,321	13,384
	European Union	3,842	6,142	8,861	7,060	5,162

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[4] Q1: 25% quantile, Q3: 75% quantile, StD: standard deviation

Figure 4.1-4 Number of turkeys in a holding at the time of sampling, on natural and on log10 scale, observed *Salmonella* prevalence in the EU (number of sampled flocks between brackets). [5]
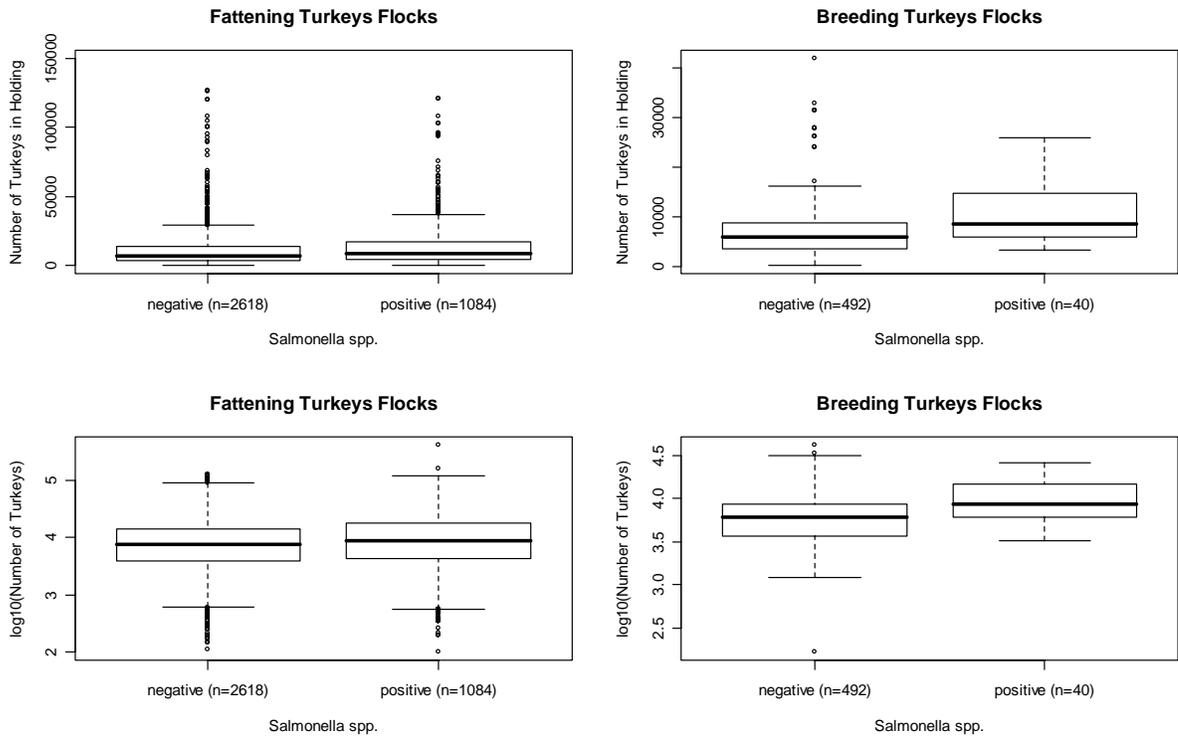
Table 4.1-4 Odds ratio estimates and corresponding 95% confidence intervals obtained from a logistic regression, modelling the weighted probability of observing a positive flock using an intercept and the number of turkeys in a holding at the time of sampling, by flock production type

Turkeys in holding[6]	Outcome of interest	Estimate	LB	UB
Fattening turkeys	*Salmonella*	1.130	1.089	1.173
Breeding turkeys	*Salmonella*	1.645	1.227	2.204

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[5] In the first figure, one outlying data point has been left out for readability of graph: a fattening flock in a holding in the UK with 419815 turkeys at the time of sampling. The flock was tested positive for *Salmonella*

[6] Results obtained for V007_TurkeyinH/10000.

Figure 4.1-5 Central tendency and distribution of the number of flocks in a holding at full capacity by Member State (number of sampled flocks between brackets).

Fattening Turkeys Flocks

Breeding Turkey Flocks
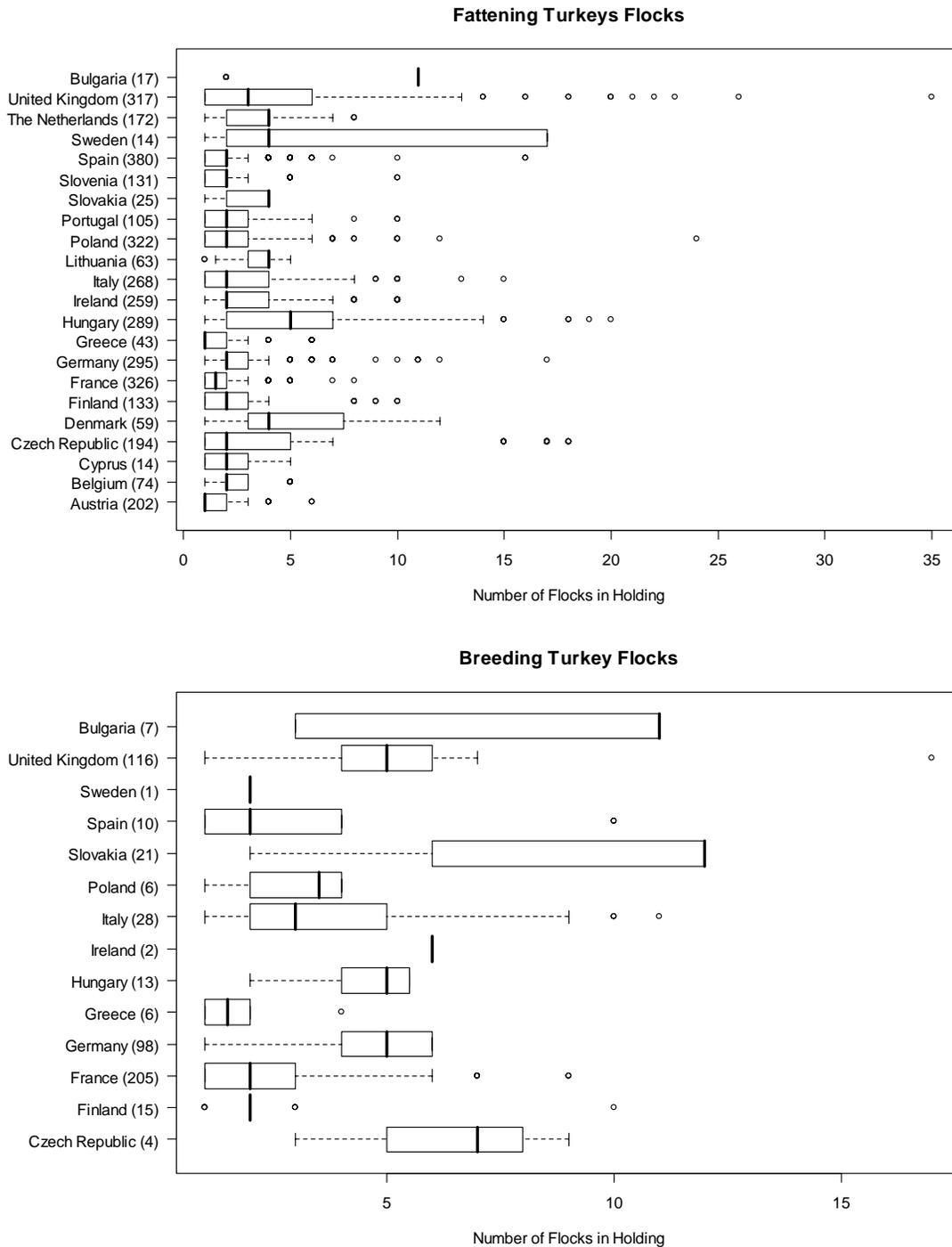
Table 4.1-5 Central tendency (mean, median) and dispersion measures (standard deviation and quantiles) of the number of flocks in a holding at full capacity.

	Country	Number of flocks in holding: fattening turkey flocks				
		Q1	Median	Q2	Mean	StD
1	Austria	1	1	2	1.6	0.9
2	Belgium	2	2	3	2.4	1.2
3	Cyprus	1	2	3	2.1	1.1
4	Czech Republic	1	2	5	4.5	5.4
5	Denmark	3	4	8	4.9	2.4
7	Finland	1	2	3	2.4	1.8
8	France	1	1.5	2	1.9	1.1
9	Germany	2	2	3	2.7	2.0
10	Greece	1	1	2	2.1	1.8
11	Hungary	2	5	7	5.3	3.7
12	Ireland	2	2	4	3.3	2.4
13	Italy	1	2	4	3.0	2.2
15	Lithuania	3	4	4	3.7	0.9
18	Poland	1	2	3	2.5	2.2
19	Portugal	1	2	3	2.3	1.7
20	Slovakia	2	4	4	3.2	1.1
21	Slovenia	1	2	2	1.9	1.4
22	Spain	1	2	2	2.0	1.5
23	Sweden	2	4	17	7.9	7.1
24	The Netherlands	2	4	4	3.6	1.5
25	The United Kingdom	1	3	6	4.5	4.5
27	Bulgaria	11	11	11	8.9	3.9
	European Union	1	2	4	3.1	2.9

	Country	Number of flocks in holding: breeding turkey flocks				
		Q1	Median	Q2	Mean	StD
4	Czech Republic	5	7	8	6.5	2.5
7	Finland	2	2	2	2.5	2.2
8	France	1	2	3	2.1	1.5
9	Germany	4	5	6	4.5	1.7
10	Greece	1	1.5	2	1.8	1.2
11	Hungary	4	5	5.5	4.4	1.4
12	Ireland	6	6	6	6.0	
13	Italy	2	3	5	4.2	3.1
18	Poland	2	3.5	4	3.0	1.3
20	Slovakia	6	12	12	8.4	4.1
22	Spain	1	2	4	3.6	3.5
23	Sweden	2	2	2	2.0	
25	The United Kingdom	4	5	6	5.0	1.8
27	Bulgaria	3	11	11	7.6	4.3
	European Union	2	3.5	6	3.8	2.6

Figure 4.1-6 Number of flocks in a holding at full capacity, in the EU by observed *Salmonella* prevalence (number of sampled flocks between brackets).
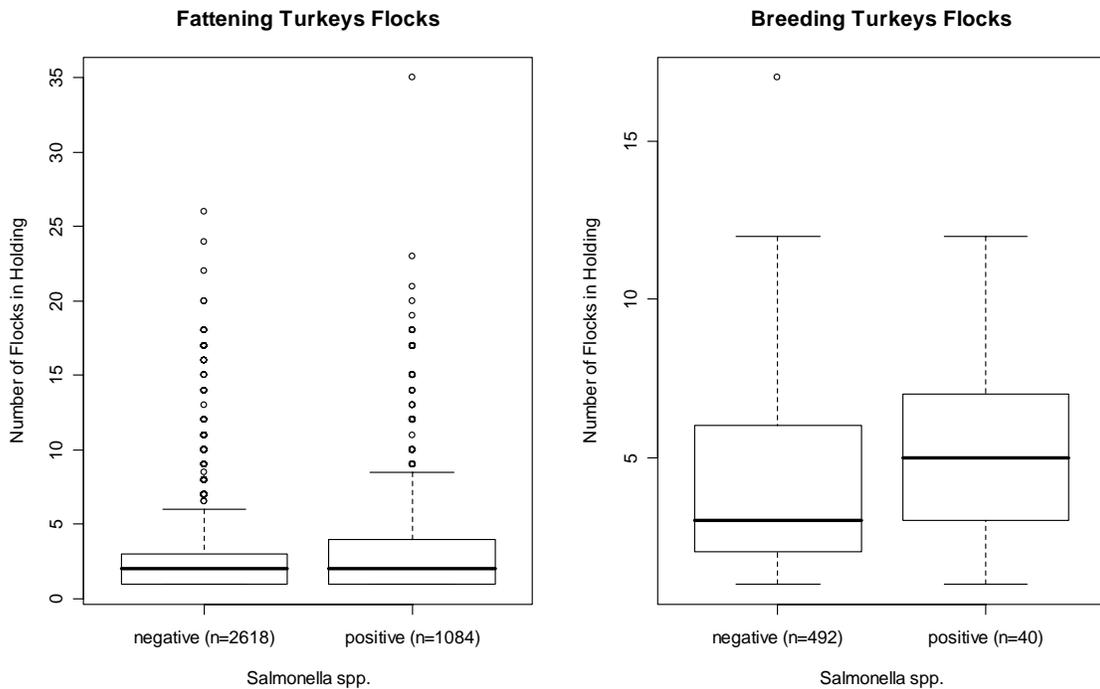
Table 4.1-6 Odds ratio estimates and corresponding 95% confidence intervals obtained from a logistic regression, modelling the weighted probability of observing a positive flock using an intercept and the number of flocks in a holding at full capacity, by flock production type.

Flocks in holding	Outcome of interest	Estimate	LB	UB
Fattening turkeys	*Salmonella*	1.084	1.065	1.103
Breeding turkeys	*Salmonella*	1.178	1.101	1.260

Figure 4.1-7 Central tendency and distribution of the number of flocks in a holding at the time of sampling, by Member State (number of sampled flocks between brackets).

Fattening Turkeys Flocks

Breeding Turkey Flocks
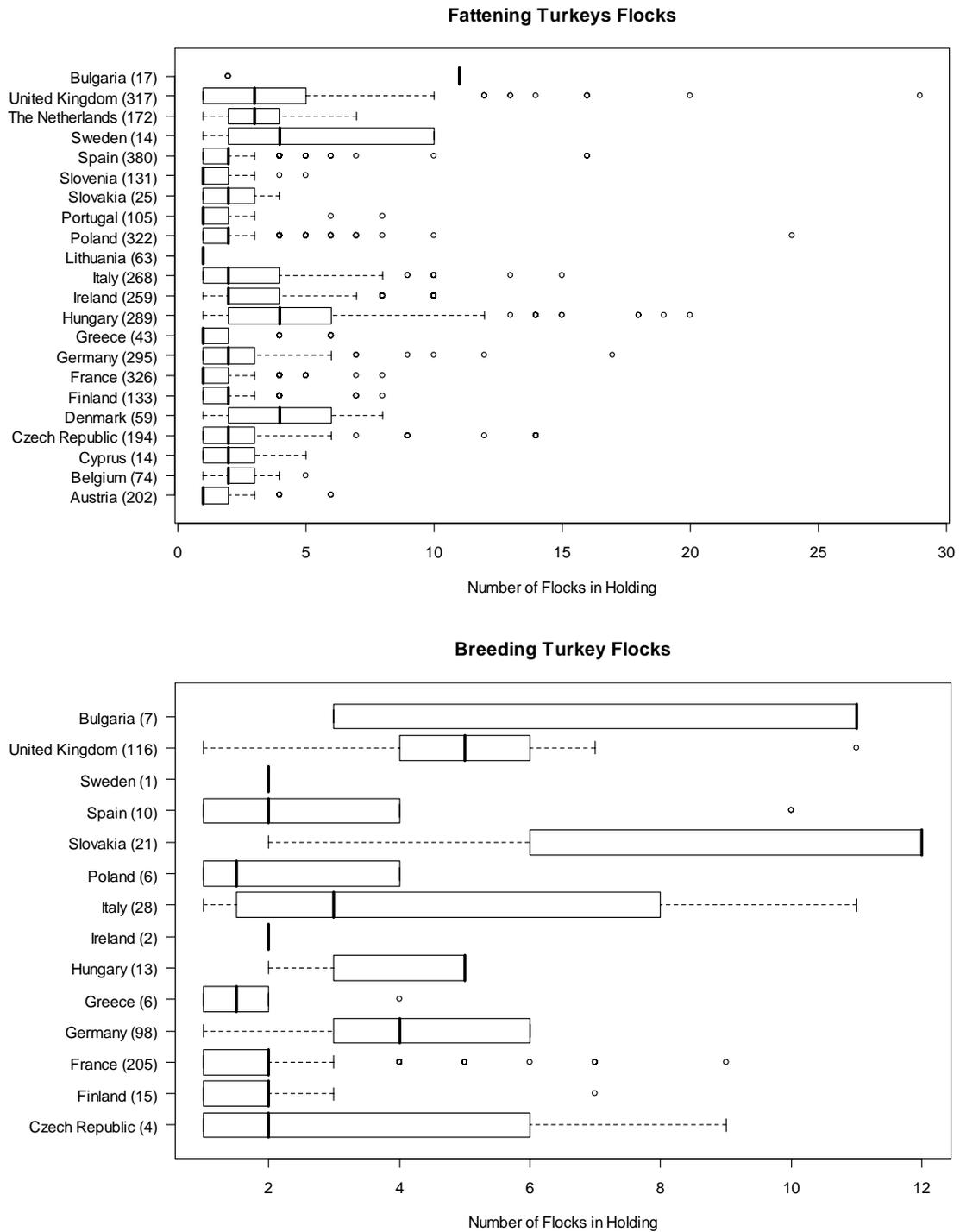
Table 4.1-7 Central tendency (mean, median) and dispersion measures (standard deviation and quantiles) of the number of flocks in a holding at the time of sampling

	Country	Number of turkeys in holding: fattening turkey flocks				
		Q1	Median	Q2	Mean	StD
1	Austria	1	1	2	1.6	0.9
2	Belgium	2	2	3	2.3	1.0
3	Cyprus	1	2	3	2.1	1.1
4	Czech Republic	1	2	3	3.0	3.5
5	Denmark	2	4	6	3.9	2.3
7	Finland	1	2	2	2.0	1.3
8	France	1	1	2	1.7	1.1
9	Germany	1	2	3	2.3	1.7
10	Greece	1	1	2	2.0	1.8
11	Hungary	2	4	6	4.8	3.7
12	Ireland	2	2	4	3.3	2.4
13	Italy	1	2	4	2.8	2.1
15	Lithuania	1	1	1	1.0	0.0
18	Poland	1	2	2	2.1	1.8
19	Portugal	1	1	2	1.6	0.9
20	Slovakia	1	2	3	2.2	1.0
21	Slovenia	1	1	2	1.5	0.7
22	Spain	1	2	2	2.0	1.5
23	Sweden	2	4	10	5.4	3.7
24	The Netherlands	2	3	4	3.4	1.5
25	The United Kingdom	1	3	5	3.7	3.4
27	Bulgaria	11	11	11	8.9	3.9
	European Union	1	2	3	2.7	2.4

	Country	Number of turkeys in holding: breeding turkey flocks				
		Q1	Median	Q2	Mean	StD
4	Czech Republic	1	2	6	3.5	3.8
7	Finland	1	2	2	2.1	1.5
8	France	1	2	2	2.0	1.4
9	Germany	3	4	6	4.2	1.9
10	Greece	1	1.5	2	1.8	1.2
11	Hungary	3	5	5	4.1	1.3
12	Ireland	2	2	2	2.0	
13	Italy	1.5	3	8	4.4	3.3
18	Poland	1	1.5	4	2.2	1.5
20	Slovakia	6	12	12	8.4	4.1
22	Spain	1	2	4	3.6	3.5
23	Sweden	2	2	2	2.0	
25	The United Kingdom	4	5	6	4.9	1.5
27	Bulgaria	3	11	11	7.6	4.3
	European Union	1	3	6	3.6	2.5

Figure 4.1-8 Number of flocks in a holding at the time of sampling, by observed *Salmonella* prevalence in the EU (number of sampled flocks between brackets).
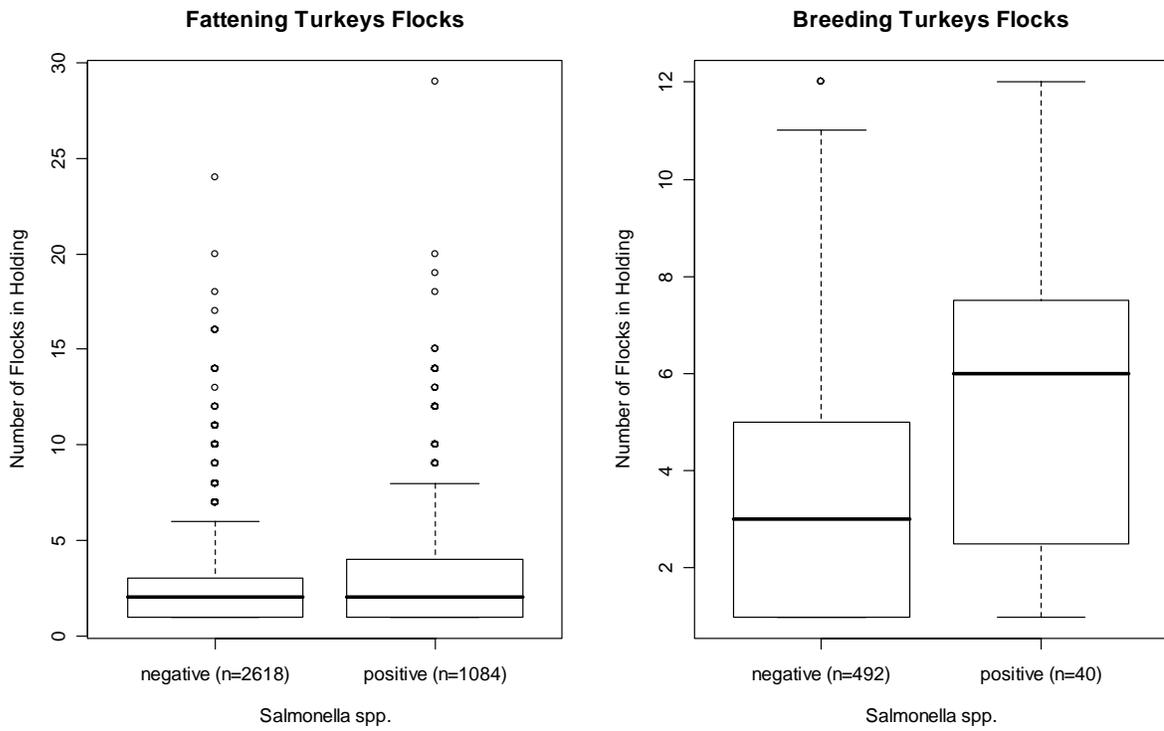
Table 4.1-8 Odds ratio estimates and corresponding 95% confidence intervals obtained from a logistic regression, modelling the weighted probability of observing a positive flock using an intercept and the number of flocks in a holding at the time of sampling, by flock production type.

Fattening turkeys

Flocks in holding	Outcome of interest	Estimate	LB	UB
Fattening turkeys	*Salmonella*	1.102	1.081	1.123
Breeding turkeys	*Salmonella*	1.254	1.166	1.348

Flock characteristics

In this section we describe some independent variables associated with flock characteristics. In Figure 4.1-9 and Table 4.1-9 we have displayed the distribution of the number of turkeys available in a flock at the time of sampling. On average, 2,571 birds are available in breeding flocks in the EU, whereas 4,613 turkeys are present in fattening flocks in the EU. In general, fattening turkey flocks appear to be bigger than breeding turkey flocks. The box plots in Figure 4.1-10 and the odds ratio estimates in Table 4.1-10 do not indicate any association between the number of turkeys in a flock at the time of sampling and the presence of *Salmonella* in fattening turkeys. A negative association is observed for breeding turkeys. This suggests that the odds of observing an infection decreases as the flock size increases.

From Figure 4.1-11 and Table 4.1-11 it can be seen that flock production types are mainly conventional. However, in fattening turkeys a considerable amount of flocks have free-range birds. Further for fattening turkeys, there seems to be some association between the prevalence of *Salmonella* and flock production type (see Figure 4.1-12 and Table 4.1-12). Note again that in many MSs most information is contained only in the conventional category. As a result, it will not be possible to obtain for these MSs an estimate of the impact of this effect.

Finally, most of the breeding (fattening) turkeys are sampled in holdings which consist solely of breeding (fattening) turkeys (see Figure 4.1-13 and Table 4.1-13). However, some holdings in Bulgaria, Czech Republic, Greece, Ireland, Italy and Slovenia produce both types of turkeys. Further, there appears to be some association between this holding composition and the prevalence of *Salmonella* (see Figure 4.1-14 and Table 4.1-14). Flocks in mixed holdings seem more infected than flocks in homogeneous production holdings. Nevertheless, it should be stressed again that only a few countries sampled flocks from mixed production holdings so that it may not be possible to obtain meaningful results for this variable in both an MS-specific and a EU-level model.

Figure 4.1-9 Central tendency and distribution of number of turkeys available in the flock at the time of sampling, by Member State (number of sampled flocks between brackets).

Fattening Turkeys Flocks

Breeding Turkey Flocks
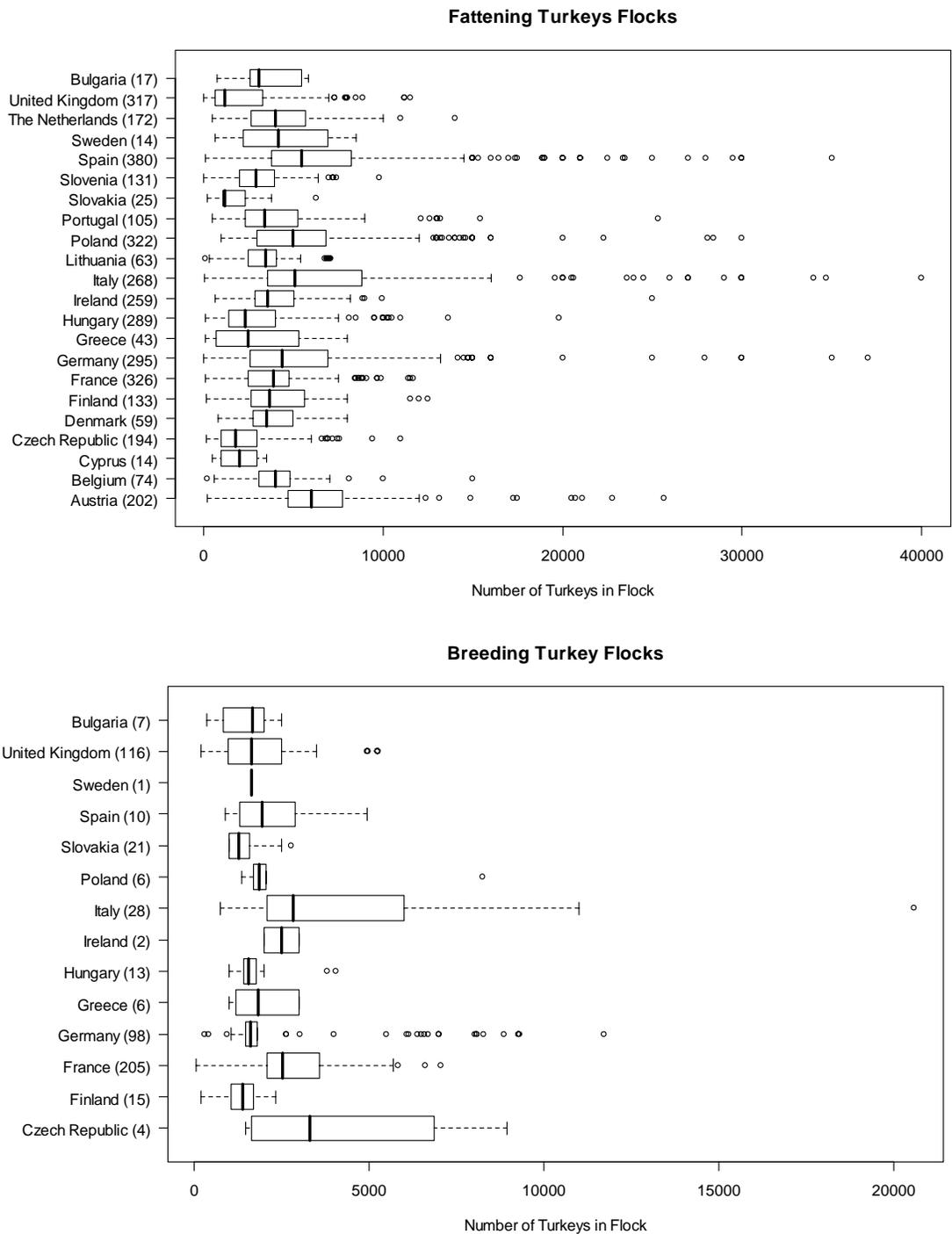
Table 4.1-9 Central tendency (mean, median) and dispersion measures (standard deviation and quantiles) of the number of turkeys available in the flock at the time of sampling, by flock production group, per Member State and in EU.[7]

	Country	Fattening turkeys					Breeding turkeys				
		Q1	Median	Q3	Mean	StD	Q1	Median	Q3	Mean	StD
1	Austria	4,700	6,000	7,750	6,550.0	3,742.0					
2	Belgium	3,067	3,991	4,792	4,096.0	2,159.0					
3	Cyprus	1,000	2,000	3,000	1,935.7	9,86.5					
4	Czech Republic	1,000	1,800	3,000	2,309.3	1,786.0	1,644	3,305	6,882	4,262.8	3,470.4
5	Denmark	2,750	3,500	5,000	3,933.9	1,861.8					
7	Finland	2,650	3,700	5,640	3,953.5	2,208.9	900	1,408	1,773	1,388.4	633.3
8	France	2,499	3,880	4,755	3,921.1	1,999.6	2,108	2,535	3,596	2,868.9	1,050.5
9	Germany	2,600	4,400	7,000	5,635.0	5,011.1	1,497	1,637	1,820	2,776.9	2,540.6
10	Greece	670	2,500	5,600	3,060.0	2,443.9	1,200	1,850	3,000	1,983.3	863.5
11	Hungary	1,400	2,350	4,000	2,979.5	2,404.4	1,432	1,567	1,800	1,910.8	940.2
12	Ireland	2,870	3,573	5,047	4,051.0	2,180.7	2,000	2,500	3,000	2,500.0	707.1
13	Italy	3,575	5,065	8,800	7,396.6	6,361.8	2,100	2,840	6,000	4,590.9	4,253.9
15	Lithuania	2,500	3,468	4,062	3,586.3	1,902.6					
18	Poland	3,000	5,000	6,800	5,853.3	4,101.7	1,710	1,862	2,075	2,861.0	2,660.5
19	Portugal	2,300	3,400	5,240	4,372.3	3,601.4					
20	Slovakia	1,100	1,200	2,300	1,716.4	1,309.9	1,000	1,300	1,600	1,433.3	485.1
21	Slovenia	2,000	2,900	3,950	3,083.0	1,694.3					
22	Spain	3,800	5,490	8,200	6,954.4	5,275.3	1,315	1,950	2,900	2,245.0	1,185.9
23	Sweden	2,220	4,150	6,900	4,442.1	2,752.3	1,655	1,655	1,655	1,655.0	
24	The Netherlands	2,650	4,000	5,700	4,412.5	2,363.0					
25	The United Kingdom	650	1,200	3,300	2,253.2	2,240.2	975	1,656	2,500	1,877.0	1,255.1
27	Bulgaria	2,593	3,104	5,490	3,514.9	1,919.9	378	1,689	2,300	1,464.0	843.2
	European Union	2,200	3,851	5,800	4,613.3	3,970.4	1,558	2,085	3,003	2,571	1,894

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[7] Q1: 25% quantile, Q3: 75% quantile, StD: standard deviation

Figure 4.1-10 Number of turkeys in flock at the time of sampling, on natural and log10 scale, by observed *Salmonella* prevalence in the EU (number of sampled flocks between brackets).
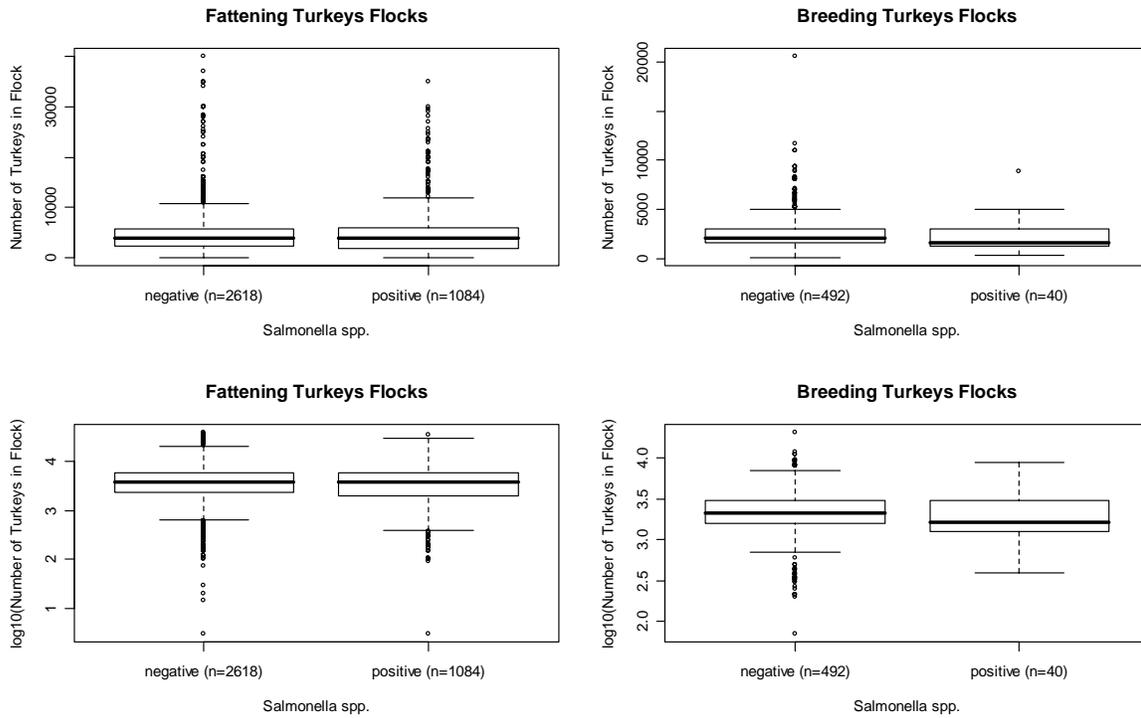

Table 4.1-10 Odds ratio estimates and corresponding 95% confidence intervals obtained from a logistic regression, modelling the weighted probability of observing a positive flock using an intercept and the number of turkeys in a flock at the time of sampling, by flock production type.

Fattening turkeys

Turkeys in flock[8]	Outcome of interest	Estimate	LB	UB
Fattening turkeys	*Salmonella*	1.014	0.996	1.033
Breeding turkeys	*Salmonella*	0.615	0.477	0.794

[8] Results obtained for V012_TurkeysInFlock/1000.

Figure 4.1-11 Estimated number of fattening and breeding turkey flocks by flock production type and (weighted) *Salmonella* **outcome.**
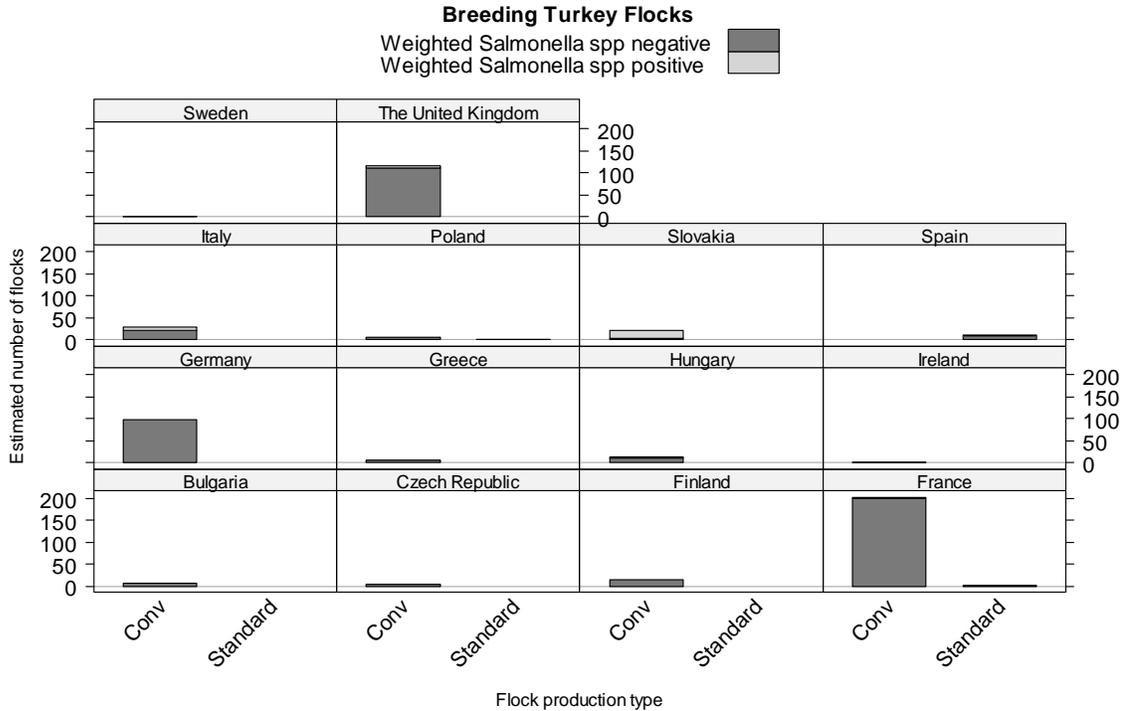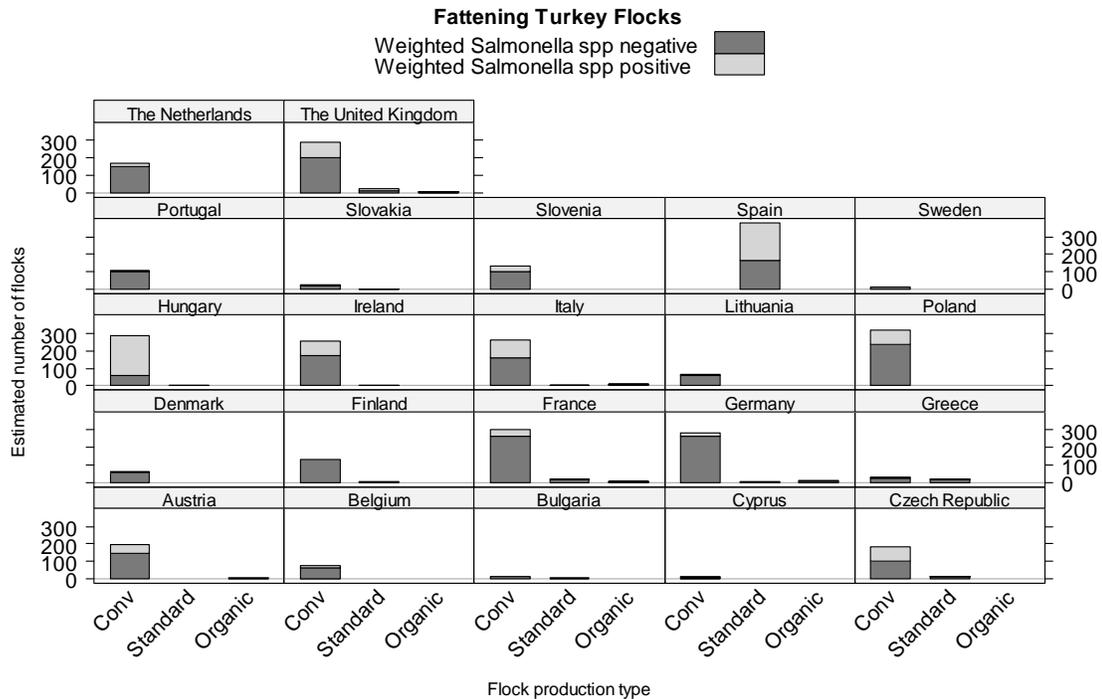
Table 4.1-11 Distribution of the number of flocks by flock production type, per Member State and in EU.

	Country	Fattening turkeys							Breeding turkeys				
		Conventional		Standard free-range		Organic free range		Total	Conventional		Standard free-range		Total
1	Austria	198	98%			4	2%	202					
2	Belgium	74	100%					74					
3	Cyprus	14	100%					14					
4	Czech Republic	177	91%	17	9%			194	4	100%			4
5	Denmark	59	100%					59					
7	Finland	132	99%	1	1%			133	15	100%			15
8	France	268	82%	49	15%	9	3%	326	202	99%	3	1%	205
9	Germany	284	96%	1	0%	10	3%	295	98	100%			98
10	Greece	26	60%	17	40%			43	6	100%			6
11	Hungary	288	100%	1	0%			289	13	100%			13
12	Ireland	258	100%	1	0%			259	2	100%			2
13	Italy	260	97%	3	1%	5	2%	268	28	100%			28
15	Lithuania	63	100%					63					
18	Poland	322	100%					322	5	83%	1	17%	6
19	Portugal	105	100%					105					
20	Slovakia	24	96%	1	4%			25	21	100%			21
21	Slovenia	131	100%					131					
22	Spain			380	100%			380			10	100%	10
23	Sweden	14	100%					14	1	100%			1
24	The Netherlands	172	100%					172					
25	The United Kingdom	259	82%	49	15%	9	3%	317	116	100%			116
27	Bulgaria	13	76%	4	24%			17	7	100%			7
	European Union	3,141	85%	524	14%	37	1%	3702	518	97%	14	3%	532

Figure 4.1-12 Weighted *Salmonella* **prevalence by flock production type in the EU (number of sampled flocks represented inside each bar).**

Table 4.1-12 Weighted *Salmonella* prevalence by Flock Production Type in the EU.

Fattening turkeys			*Salmonella*	
Frequency *Row Pct* Col Pct	Holding production type			
	Conventional	Standard free-range	Organic free-range	Total
Negative	2,337 *91%* 71%	194 *8%* 51%	33 *1%* 75%	2,564 *100%*
Positive	944 *83%* 29%	183 *16%* 49%	11 *1%* 25%	1,138 *100%*
Total	3,281 100%	377 100%	44 100%	3,702

Breeding turkeys		*Salmonella*	
Frequency *Row Pct* Col Pct	Holding production type		
	Conventional	Standard free-range	Total
Negative	438 *96%* 86%	19 *4%* 96%	458 *100%*
Positive	74 *99%* 14%	1 *0%* 4%	74 *99%*
Total	512 100%	20 100%	532

	Fisher's exact test: p-value	
Salmonella	Fattening	Breeding
	<0.001	0.336

Figure 4.1-13 Estimated number of fattening and breeding turkey flocks by holding composition[9] and (weighted) *Salmonella* **outcome.**

Fattening Turkey Flocks
Weighted Salmonella spp negative
Weighted Salmonella spp positive

Breeding Turkey Flocks
Weighted Salmonella spp negative
Weighted Salmonella spp positive

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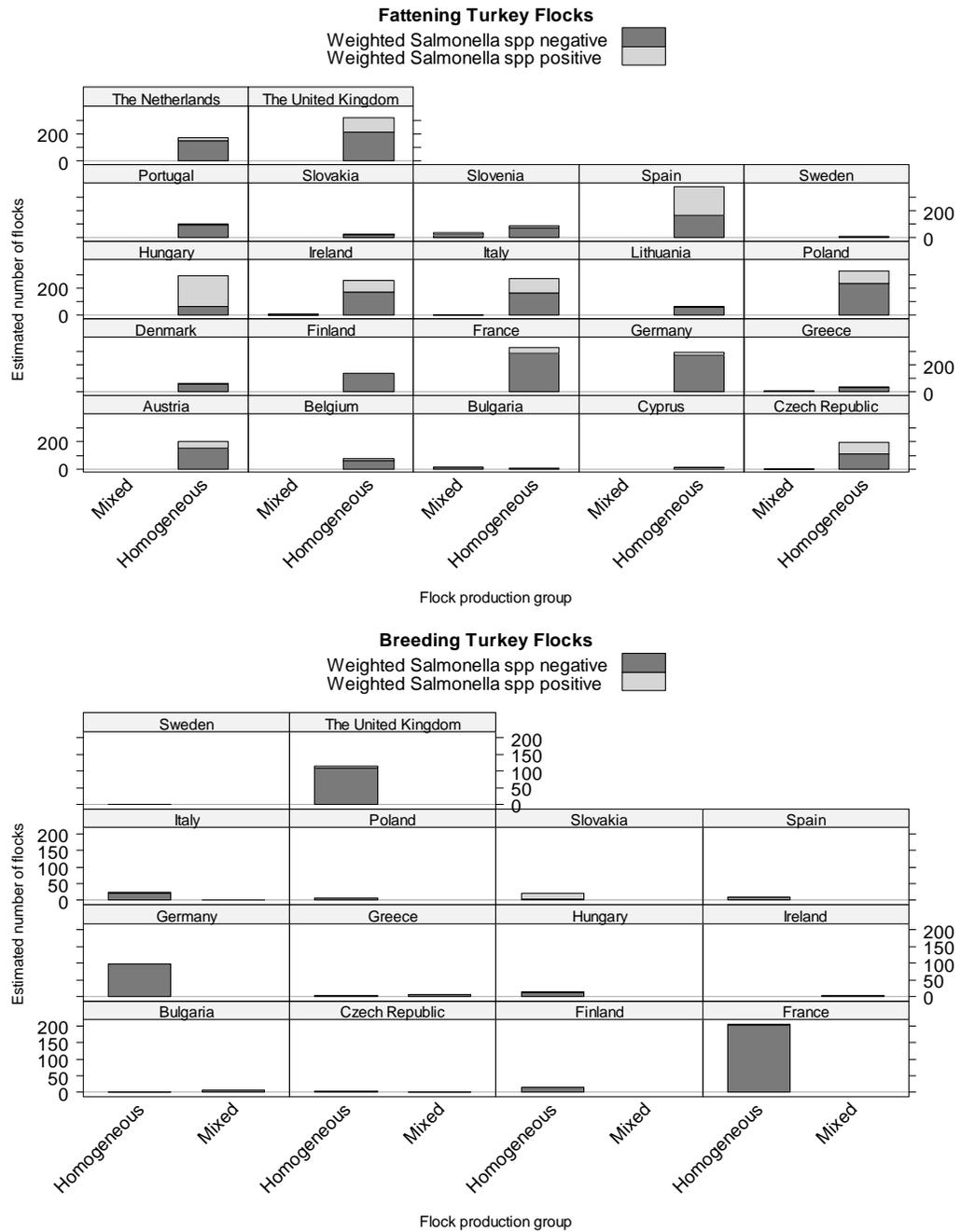
[9] Newly created variable V014_FTypeWH indicating whether the flock was sampled from a homogeneous composition holding or a mixed composition holding

Table 4.1-13 Distribution of the number of flocks by holding composition, per Member State and in the EU.

	Country	Fattening turkeys					Breeding turkeys				
		Mixed production		Homogeneous fattening		Total	Homogenous breeding		Mixed production		Total
1	Austria			202	100%	202					
2	Belgium			74	100%	74					
3	Cyprus			14	100%	14					
4	Czech Republic	1	1%	193	99%	194	1	25%	3	75%	4
5	Denmark			59	100%	59					
7	Finland			133	100%	133	15	100%			15
8	France			326	100%	326	205	100%			205
9	Germany			295	100%	295	98	100%			98
10	Greece	5	12%	38	88%	43	3	50%	3	50%	6
11	Hungary			289	100%	289	13	100%			13
12	Ireland	6	2%	253	98%	259		0%	2	100%	2
13	Italy	1	0%	267	100%	268	27	96%	1	4%	28
15	Lithuania			63	100%	63					
18	Poland			322	100%	322	6	100%			6
19	Portugal			105	100%	105					
20	Slovakia			25	100%	25	21	100%			21
21	Slovenia	49	37%	82	63%	131					
22	Spain			380	100%	380	10	100%			10
23	Sweden			14	100%	14	1	100%			1
24	The Netherlands			172	100%	172					
25	The United Kingdom			317	100%	317	116	100%			116
27	Bulgaria	13	76%	4	24%	17	3	43%	4	57%	7
	European Union	75	2%	3,627	98%	3,702	519	98%	13	2%	532

Figure 4.1-14 Weighted *Salmonella* prevalence by holding composition in the EU (number of sampled flocks represented inside each bar).
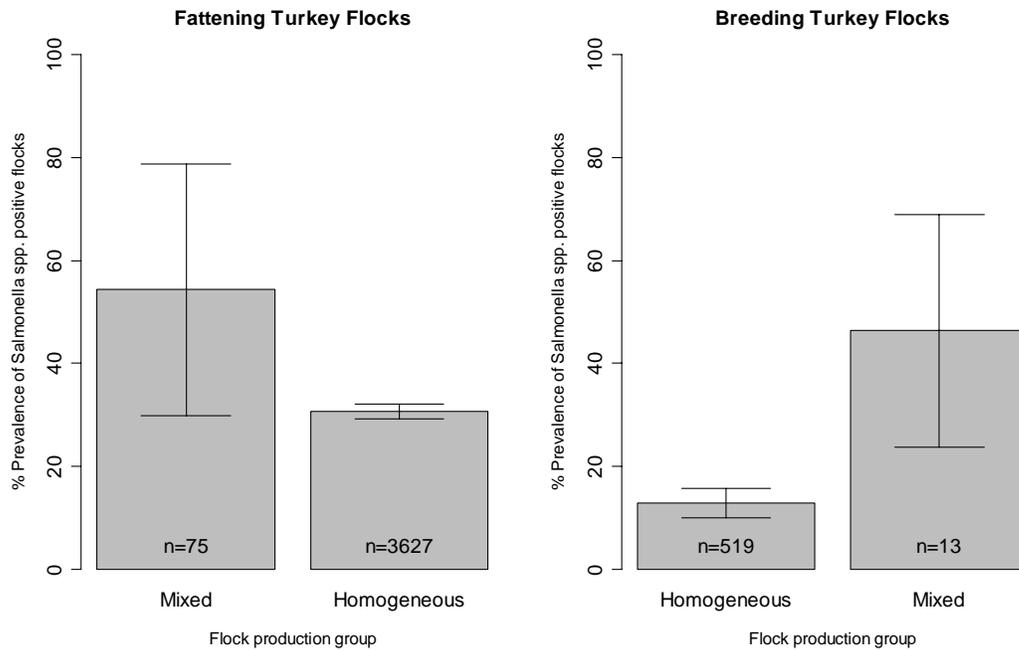
Table 4.1-14 Weighted *Salmonella* prevalence by holding composition in the EU.

Fattening turkeys		*Salmonella*	
Frequency	Flock production type		
Row Pct Col Pct	Mixed production	Homogeneous fattening	Total
Negative	7 *0%* 46%	2,556 *100%* 69%	2,564 *100%*
Positive	9 *1%* 54%	1,130 *99%* 31%	1,138 *100%*
Total	16 100%	3,686 100%	3,702

Breeding turkeys		*Salmonella*	
Frequency	Flock production type		
Row Pct Col Pct	Mixed production	Homogeneous fattening	Total
Negative	448 *98%* 87%	10 *2%* 54%	458 *100%*
Positive	66 *88%* 13%	9 *12%* 46%	74 *100%*
Total	513 100%	19 100%	532

Salmonella	Fisher's exact test: p-value	
	Fattening	Breeding
	0.052	<0.001

Sampling month

In the following illustrations, we study the impact of sampling month on *Salmonella* prevalence estimates. In Figure 4.1-15 and Table 4.1-15 and Table 4.1-16 we have displayed the distribution of the sampling of fattening and breeding turkeys over the different months in the study. From the first table it can be seen that Cyprus, Greece, Portugal, Sweden and Bulgaria sampled fattening turkey flocks within the time frame of one quarter up to half a year. The sampling of breeding flocks, displayed in Table 4.1-16, was evenly spread by most of the participating countries to cover the different quarters of the year.

Further, Figure 4.1-16 and Table 4.1-17 suggest an association between the sampling month and the prevalence of *Salmonella* The months between April and July, and October seem to be less affected in fattening turkeys. In breeding turkeys some peaks appear in October (based on a sample with only 10 flocks), January to February and in June.

Figure 4.1-15 Estimated number of fattening and breeding turkey flocks by sampling month and (weighted) *Salmonella* **outcome.**
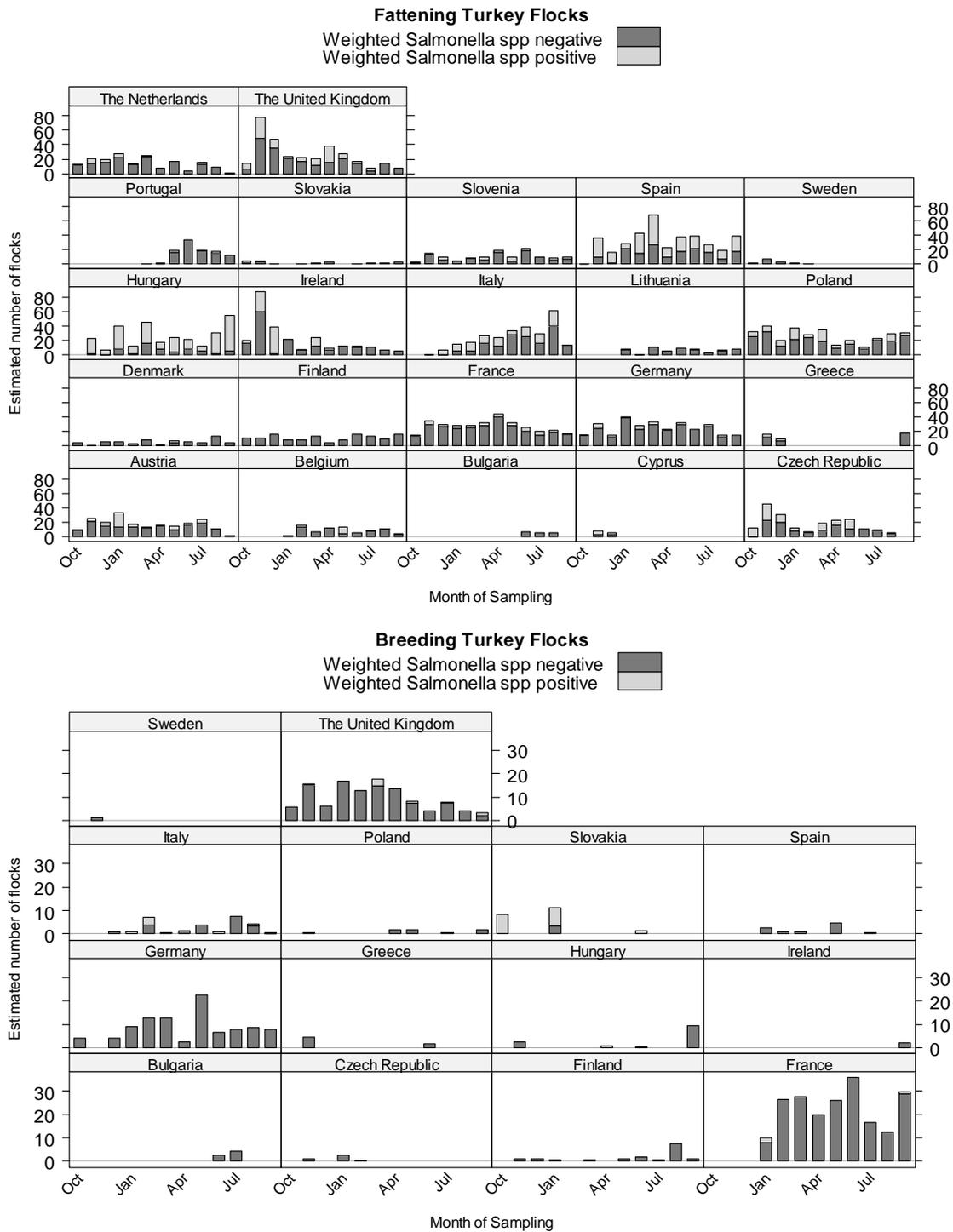
Table 4.1-15 Distribution of the number of fattening flocks by sampling month, per Member State and in the EU.

|	Country	Oct/06	Nov/06	Dec/06	Jan/07	Feb/07	Mar/07	Apr/07	May/07	Jun/07	Jul/07	Aug/07	Sep/07	Total
1	Austria	10	23	17	25	19	16	15	16	20	23	15	3	202
		5%	11%	8%	12%	9%	8%	7%	8%	10%	11%	7%	1%	100%
2	Belgium				1	14	8	8	11	8	11	9	4	74
					1%	19%	11%	11%	15%	11%	15%	12%	5%	100%
3	Cyprus		7	7										14
			50%	50%										100%
4	Czech Republic	8	51	34	13	8	18	19	20	9	12	2		194
		4%	26%	18%	7%	4%	9%	10%	10%	5%	6%	1%		100%
5	Denmark	4	1	4	4	4	8	2	5	3	5	16	3	59
		7%	2%	7%	7%	7%	14%	3%	8%	5%	8%	27%	5%	100%
7	Finland	13	9	19	8	7	10	5	11	15	14	8	14	133
		10%	7%	14%	6%	5%	8%	4%	8%	11%	11%	6%	11%	100%
8	France	15	33	39	26	34	34	35	24	26	20	19	21	326
		5%	10%	12%	8%	10%	10%	11%	7%	8%	6%	6%	6%	100%
9	Germany	11	28	16	41	28	34	24	34	22	26	16	15	295
		4%	9%	5%	14%	9%	12%	8%	12%	7%	9%	5%	5%	100%
10	Greece		14	9									20	43
			33%	21%									47%	100%
11	Hungary		19	10	39	12	38	15	23	23	16	43	51	289
			7%	3%	13%	4%	13%	5%	8%	8%	6%	15%	18%	100%
12	Ireland	34	56	30	19	12	33	13	14	12	15	12	9	259
		13%	22%	12%	7%	5%	13%	5%	5%	5%	6%	5%	3%	100%
13	Italy		1	6	12	18	30	25	32	41	31	58	14	268
			0%	2%	4%	7%	11%	9%	12%	15%	12%	22%	5%	100%
15	Lithuania				9	1	11	6	9	8	3	8	8	63
					14%	2%	17%	10%	14%	13%	5%	13%	13%	100%
18	Poland	20	33	16	28	24	32	24	36	20	27	31	31	322
		6%	10%	5%	9%	7%	10%	7%	11%	6%	8%	10%	10%	100%
19	Portugal						1	3	21	32	17	15	16	105
							1%	3%	20%	30%	16%	14%	15%	100%
20	Slovakia	5	4	1		1	2	3		1	2	2	4	25
		20%	16%	4%		4%	8%	12%		4%	8%	8%	16%	100%
21	Slovenia	4	17	10	5	11	11	19	8	15	9	9	13	131
		3%	13%	8%	4%	8%	8%	15%	6%	11%	7%	7%	10%	100%
22	Spain	2	38	13	26	38	59	25	39	50	25	23	42	380
		1%	10%	3%	7%	10%	16%	7%	10%	13%	7%	6%	11%	100%
23	Sweden	2	6	3	2	1								14
		14%	43%	21%	14%	7%								100%
24	The Netherlands	15	20	18	25	15	22	10	16	4	16	10	1	172
		9%	12%	10%	15%	9%	13%	6%	9%	2%	9%	6%	1%	100%
25	The United Kingdom	7	107	88	20	13	12	18	19	16	4	7	6	317
		2%	34%	28%	6%	4%	4%	6%	6%	5%	1%	2%	2%	100%
27	Bulgaria									7	5	5		17
										41%	29%	29%		100%
	European Union	150	467	340	303	260	379	269	338	332	281	308	275	3702
		4%	13%	9%	8%	7%	10%	7%	9%	9%	8%	8%	7%	100%

Table 4.1-16 Distribution of the number of breeding flocks by sampling month, per Member State and in the EU

	Country	Oct/06	Nov/06	Dec/06	Jan/07	Feb/07	Mar/07	Apr/07	May/07	Jun/07	Jul/07	Aug/07	Sep/07	Total
4	Czech Republic		2 50%		1 25%	1 25%								4 100%
7	Finland		2 13%	1 7%	1 7%		1 7%		1 7%	2 13%	1 7%	4 27%	2 13%	15 100%
8	France				12 6%	26 13%	23 11%	20 10%	28 14%	37 18%	20 10%	12 6%	27 13%	205 100%
9	Germany	3 3%		5 5%	10 10%	12 12%	15 15%	4 4%	23 23%	2 2%	6 6%	7 7%	11 11%	98 100%
10	Greece		3 50%							3 50%				6 100%
11	Hungary		3 23%					2 15%		1 8%			7 54%	13 100%
12	Ireland												2 100%	2 100%
13	Italy			2 7%	1 4%	4 14%	2 7%	1 4%	2 7%	1 4%	6 21%	7 25%	2 7%	28 100%
18	Poland		1 17%					2 33%	1 17%		1 17%		1 17%	6 100%
20	Slovakia	6 29%			11 52%					4 19%				21 100%
22	Spain				3 30%	3 30%	1 10%		2 20%		1 10%			10 100%
23	Sweden		1 100%											1 100%
25	United Kingdom	1 1%	17 15%	6 5%	18 16%	12 10%	17 15%	10 9%	10 9%	4 3%	11 9%	4 3%	6 5%	116 100%
27	Bulgaria									2 29%	5 71%			7 100%
	European Union	10 2%	29 5%	14 3%	57 11%	58 11%	59 11%	39 7%	67 13%	56 11%	51 10%	34 6%	58 11%	532 100%

Figure 4.1-16 Weighted *Salmonella* prevalence by sampling month in the EU (number of sampled flocks represented inside each bar).
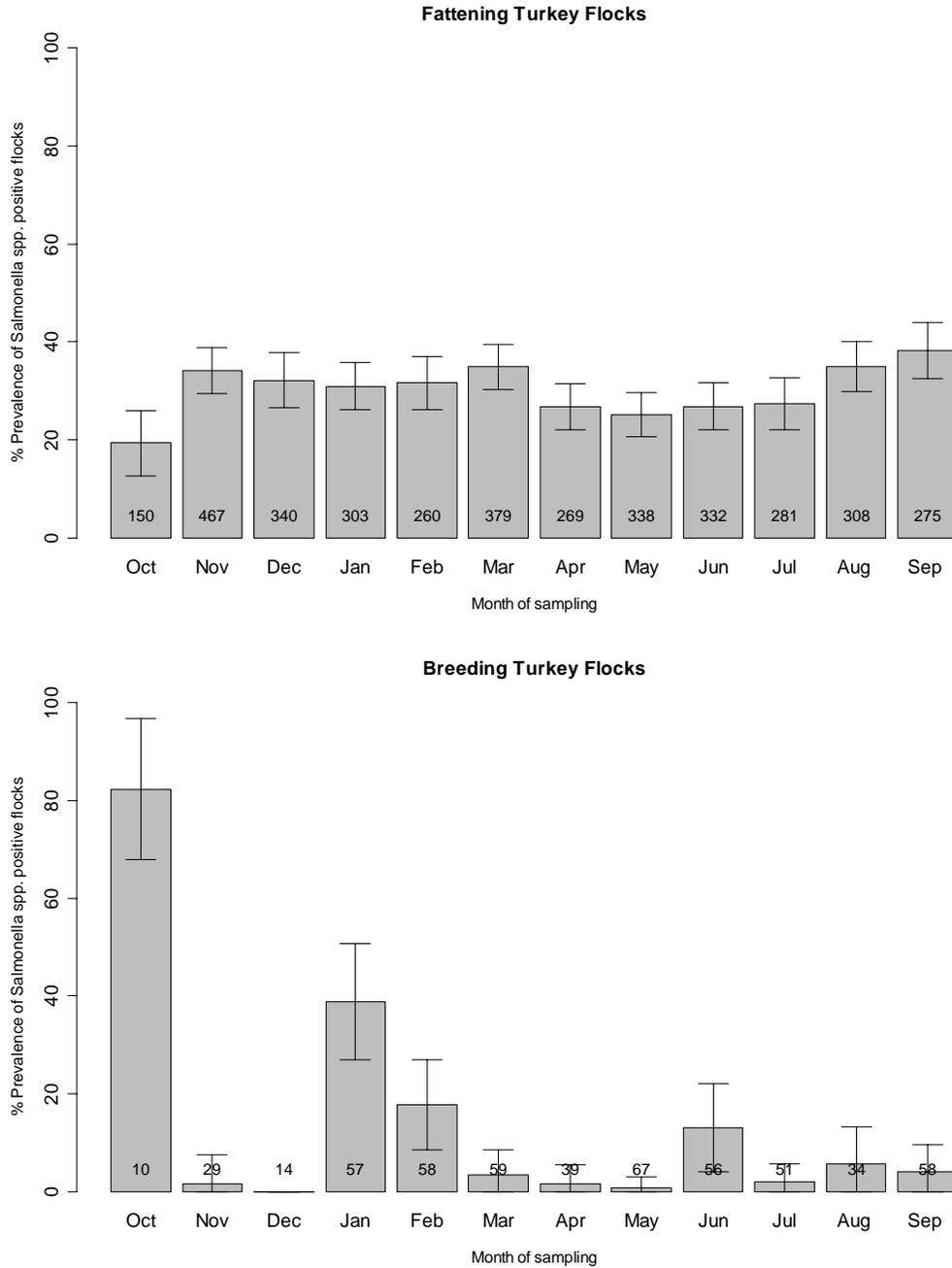
Table 4.1-17 Weighted *Salmonella* prevalence by sampling month in the EU.

Fattening turkeys	*Salmonella*												
Frequency *Row Pct* Col Pct	Sampling month												
	Oct/06	Nov/06	Dec/06	Jan/07	Feb/07	Mar/07	Apr/07	May07	Jun/07	Jul/07	Aug/07	Sep/07	Total
Negative	108	257	175	241	193	264	246	267	234	194	217	169	2564
	4%	10%	7%	9%	8%	10%	10%	10%	9%	8%	8%	7%	100%
	81%	66%	68%	69%	68%	65%	73%	75%	73%	73%	65%	62%	838%
Positive	26	133	83	108	89	141	90	90	86	73	116	104	1138
	2%	12%	7%	9%	8%	12%	8%	8%	8%	6%	10%	9%	100%
	19%	34%	32%	31%	32%	35%	27%	25%	27%	27%	35%	38%	362%
Total	134	390	258	348	282	405	336	357	319	266	333	273	3702
	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	

Breeding turkeys	*Salmonella*												
Frequency *Row Pct* Col Pct	Sampling month												
	Oct/06	Nov/06	Dec/06	Jan/07	Feb/07	Mar/07	Apr/07	May/07	Jun/07	Jul/07	Aug/07	Sep/07	Total
Negative	5	17	9	40	55	47	37	65	46	54	36	47	458
	1%	4%	2%	9%	12%	10%	8%	14%	10%	12%	8%	10%	100%
	18%	98%	100%	61%	82%	97%	99%	99%	87%	98%	94%	96%	86%
Positive	22	0	0	25	12	2	1	1	7	1	2	2	74
	29%	0%	0%	34%	16%	2%	1%	1%	9%	1%	3%	3%	100%
	82%	2%	0%	39%	18%	3%	1%	1%	13%	2%	6%	4%	14%
Total	27	17	9	65	67	48	37	65	53	55	38	49	532
	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	

Salmonella	Chi-square statistic (p-value)	
	Fattening	Breeding
	32.0 (<0.001)	172.8 (<0.001)

Variables associated with age of turkeys

In this section a closer look at variables will be taken, which are associated with the age of the breeding and fattening turkeys. This information is provided in the format of different variables. If the age of all the turkeys in the flock is equal, then this information was collected in the variable V016_AgeofTurkeys. If not, then the age of the youngest (oldest) bird at the time of sampling was saved in the variable V017_AgeYoungest (V018_AgeOldest). To study turkey age, we have created a new age variable, labelled "Age" which is equal either to V016, or to the average of V017 and V018. Descriptions of this new variable for fattening and breeding turkeys can be found in Figure 4.1-17 and Table 4.1-18. The birds in breeding flocks are considerably older than in fattening flocks: an average age of 373 days compared to 108 days in fattening turkeys.

Further, the odds ratios displayed in Table 4.1-19 for breeding turkey flocks only seem to indicate a negative association between *Salmonella* and turkey age at the time of sampling. The probability of an infection slightly decreases in older birds. Note that countries like France or Bulgaria, with flocks older than average flocks in the EU, could be driving this result as these older sampled flocks were not infected by *Salmonella*. For instance, in France, the oldest infected flock contained birds of 413 days, whereas the oldest flocks contained birds of almost 800 days of age (see Figure 4.1-18 for breeding turkeys).

Figure 4.1-17 Central tendency and distribution of turkey flock age, by Member State (number of sampled flocks between brackets).

Fattening turkey flocks

Days of age of turkeys in flocks

Breeding Turkey Flocks

Age of Turkeys in Flock
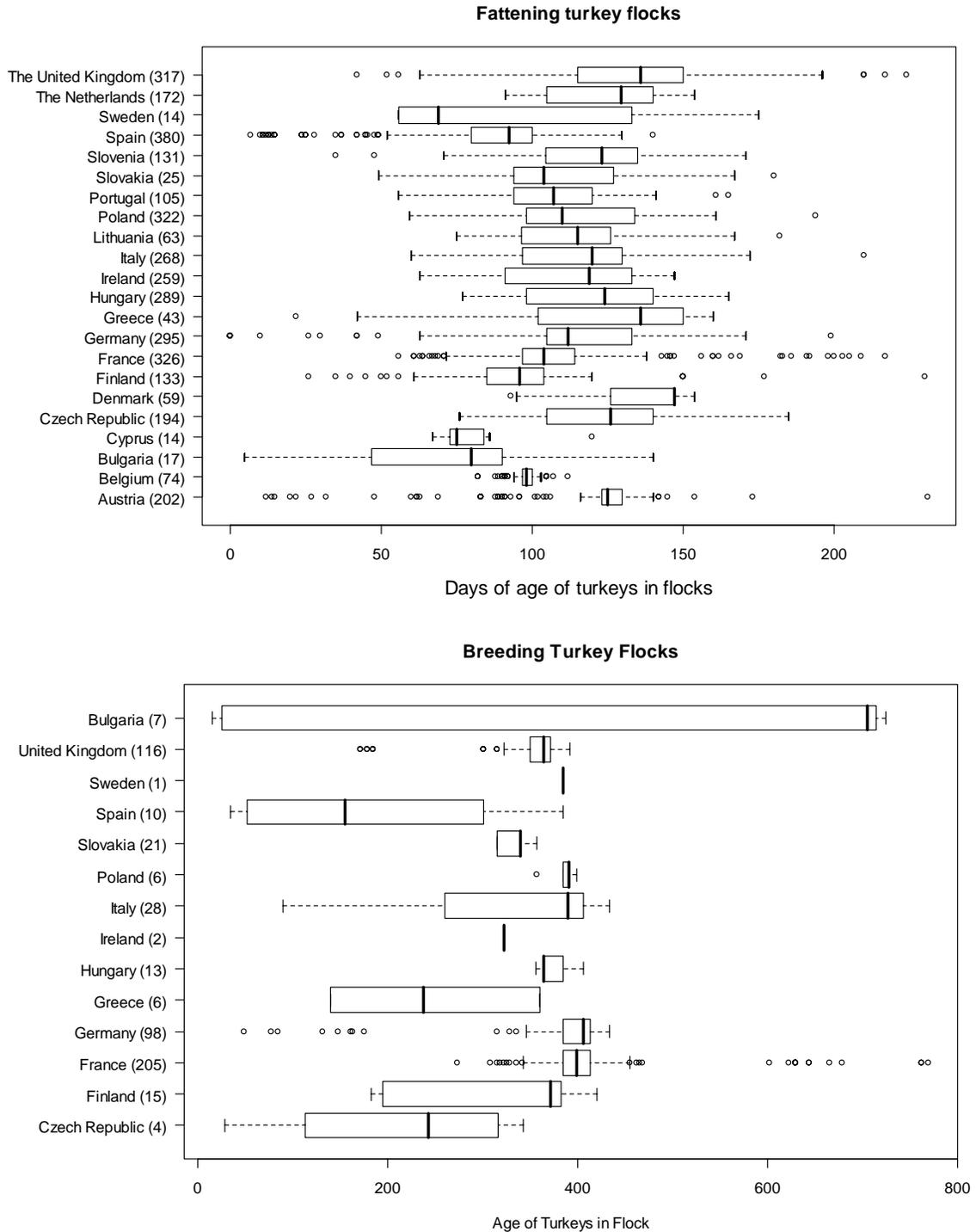
Table 4.1-18 Central tendency (mean, median) and dispersion measures (standard deviation and quantiles) of turkey flock age, by flock production group, per Member State and in the EU.[10]

	Country	Fattening turkeys					Breeding turkeys				
		Q1	Median	Q3	Mean	StD	Q1	Median	Q3	Mean	StD
1	Austria	123	125	130	119.2	26.0					
2	Belgium	97	98	100	98.1	5.2					
3	Cyprus	73	75	84	79.1	13.2					
4	Czech Republic	105	126	140	123.7	22.6	113	243	316	214.3	138.0
5	Denmark	126	147	147	136.5	17.8					
7	Finland	85	96	104	95.3	23.6	193	371	385	319.2	96.2
8	France	97	104	114	107.5	24.1	385	399	413	411.7	73.7
9	Germany	105	112	133	113.4	27.8	385	406	413	377.4	80.7
10	Greece	84	136	150	120.0	39.7	140	238	360	245.8	116.3
11	Hungary	98	124	140	120.4	22.9	364	364	385	373.8	16.4
12	Ireland	91	119	133	111.7	25.4	322	322	322	322.0	0.0
13	Italy	97	120	130	114.9	21.3	261	390	407	327.8	123.3
15	Lithuania	95	115	126	113.3	23.7					
18	Poland	98	110	134	114.2	22.1	385	391	392	385.7	14.8
19	Portugal	94	107	120	107.3	19.0					
20	Slovakia	94	104	127	108.6	31.8	315	340	340	334.7	13.7
21	Slovenia	104	123	135	118.0	23.7					
22	Spain	80	92.5	100	87.1	22.6	52	155	301	185.9	137.4
23	Sweden	56	69	133	94.9	43.2	385	385	385	385.0	
24	The Netherlands	15	18.5	20	17.4	2.5					
25	The United Kingdom	115	136	150	132.9	29.3	350	364	371	350.3	48.0
27	Bulgaria	47	80	90	73.8	37.4	22	705	725	418.0	370.5
	European Union	92	109	131	107.9	33.5	357	385	406	372.8	94.5

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[10] Q1: 25% quantile, Q3: 75% quantile, StD: standard deviation

Figure 4.1-18 Turkey flock age by observed *Salmonella* prevalence in the EU.
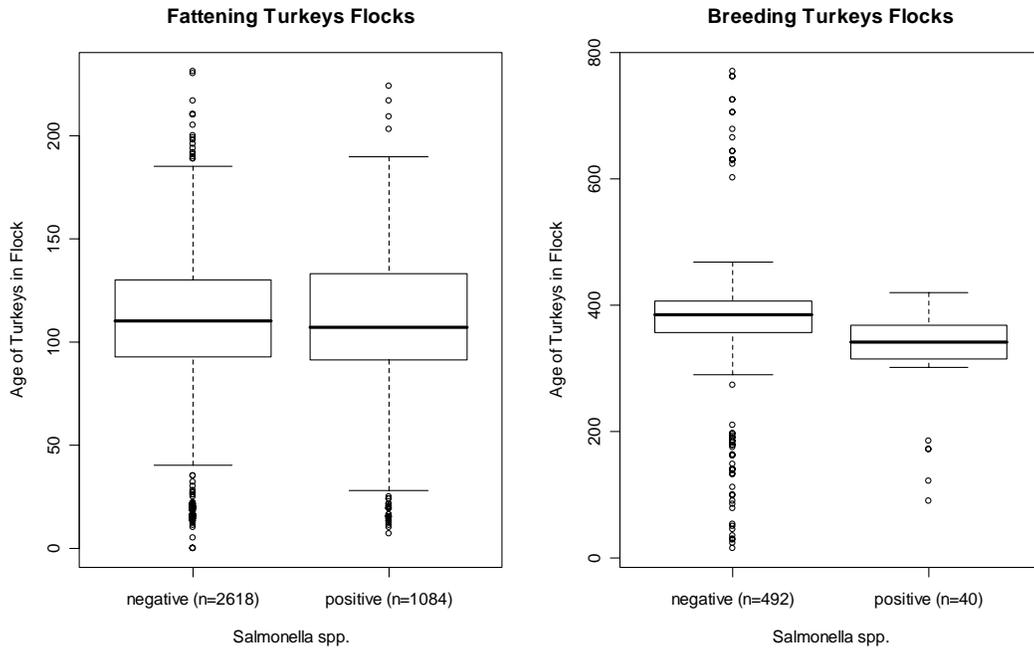
Table 4.1-19 Odds ratio estimates and corresponding 95% confidence intervals obtained from a logistic regression, modelling the probability of observing a positive flock using an intercept and (separately) the age of turkeys at the time of sampling, by flock production type.

Fattening turkeys

Age of turkeys[11]	Outcome of interest	Estimate	LB	UB
Fattening turkeys	*Salmonella*	1.212	0.944	1.556
Breeding turkeys	*Salmonella*	0.794	0.633	0.995

Further, Figure 4.1-19 and Table 4.1-20 show the distribution of the expected age of turkeys at the time of slaughter or depopulation. A big difference is once more observed between fattening and breeding turkeys. Breeding turkeys are slaughtered or depopulated at the average age of 404 days (in the EU), whereas fattening turkeys are removed around the average age of 128 days. Figure 4.1-20 and the corresponding odds ratios displayed in Table 4.1-21 do not suggest a strong association between *Salmonella* and turkey age at the time of depopulation of slaughter.

Another variable of interest is the number of cycles in the house where the turkeys are residing. The distribution of this variable is summarised in Figure 4.1-21 and Table 4.1-22. In holdings with breeding turkeys, most houses have around 1-2 cycles of turkey flocks per year, whereas holdings with fattening turkeys have around 1-3 cycles. The association between the number of cycles and the prevalence of *Salmonella* is studied in Figure 4.1-22 and Table 4.1-23. From these tables, for fattening turkeys, a positive association can be observed between the prevalence of *Salmonella* and the number of cycles. On the other hand, in breeding turkeys a clearly significant negative association was observed with the prevalence of *Salmonella*   The more cycles there are in a house, the lower the prevalence.

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[11] Results obtained for Age/100.

Figure 4.1-19 Central tendency and distribution of expected turkey age at slaughter or depopulation, by Member State (number of sampled flocks between brackets).

Fattening Turkeys Flocks

Age of Turkeys at Slaughter or Depopulation

Breeding Turkey Flocks

Age of Turkeys at Slaughter or Depopulation
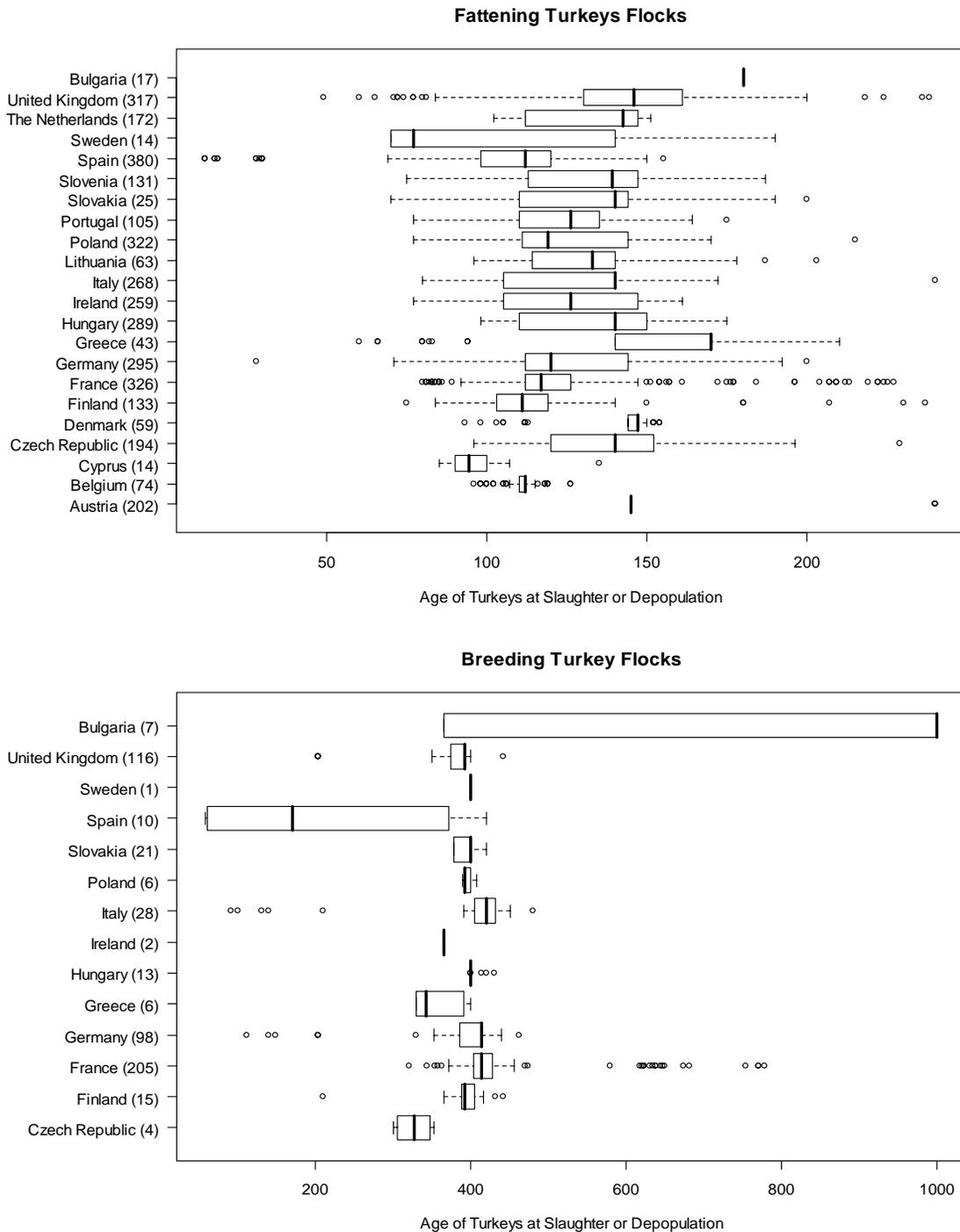
Table 4.1-20 Central tendency (mean, median) and dispersion measures (standard deviation and quantiles) of expected turkey age at the time of slaughter or depopulation, by flock production group, per Member State and in the EU.[12]

	Country	Fattening turkeys					Breeding turkeys				
		Q1	Median	Q3	Mean	StD	Q1	Median	Q3	Mean	StD
1	Austria	145	145	145	146.9	13.3					
2	Belgium	110	112	112	110.9	5.9					
3	Cyprus	90	95	100	96.9	12.4					
4	Czech Republic	120	140	152	138.0	22.4	305	327	348	326.3	25.1
5	Denmark	144	147	147	138.6	16.9					
7	Finland	103	111	119	113.4	22.1	386	392	406	386.1	52.6
8	France	112	117	126	122.6	24.7	403	413	427	434.3	77.6
9	Germany	112	120	144	127.5	19.8	385	413	415	389.2	65.0
10	Greece	140	170	170	147.0	39.7	330	343	390	355.8	32.0
11	Hungary	110	140	150	132.2	21.2	400	400	400	404.8	10.0
12	Ireland	105	126	147	125.5	24.5	365	365	365	365.0	0.0
13	Italy	105	140	140	127.7	20.3	405	420	432	372.8	115.9
15	Lithuania	114	133	140	130.1	23.8					
18	Poland	111	119	144	125.1	19.4	392	392	399	395.2	6.7
19	Portugal	110	126	135	122.6	17.4					
20	Slovakia	110	140	144	132.4	35.5	378	400	400	396.1	13.1
21	Slovenia	112	139	147	129.4	22.3					
22	Spain	98	112	120	105.9	21.0	60	171	371	215.5	154.0
23	Sweden	70	77	140	105.3	42.2	400	400	400	400.0	
24	The Netherlands	112	143	147	130.9	17.0					
25	The United Kingdom	130	146	161	144.0	28.8	375	392	392	376.1	45.9
27	Bulgaria	180	180	180	180.0		365	1000	1000	727.9	339.4
	European Union	112	126	145	127.7	24.9	389	400	417	403.8	93.7

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[12] Q1: 25% quantile, Q3: 75% quantile, StD: standard deviation

Figure 4.1-20 Expected turkey age at the time of slaughter or depopulation, by observed *Salmonella* prevalence in the EU.
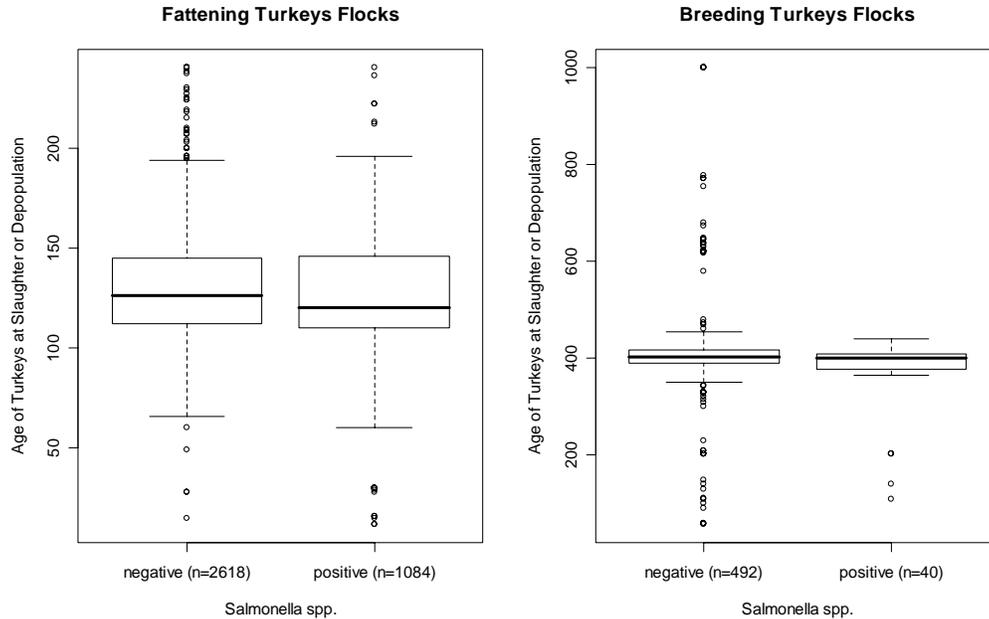
Table 4.1-21 Odds ratio estimates and corresponding 95% confidence intervals obtained from a logistic regression, modelling the probability of observing a positive flock using an intercept and (separately) the expected age at slaughter or depopulation, by flock production type.

Fattening turkeys

Age at slaughter or depopulation[13]	Outcome of interest	Estimate	LB	UB
Fattening turkeys	*Salmonella .*	0.857	0.628	1.168
Breeding turkeys	*Salmonella .*	0.816	0.639	1.042

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[13] Result obtained for V020_DepAge/100.

Figure 4.1-21 Estimated number of fattening and breeding turkey flocks by number of house cycles and (weighted) *Salmonella* **prevalence.**
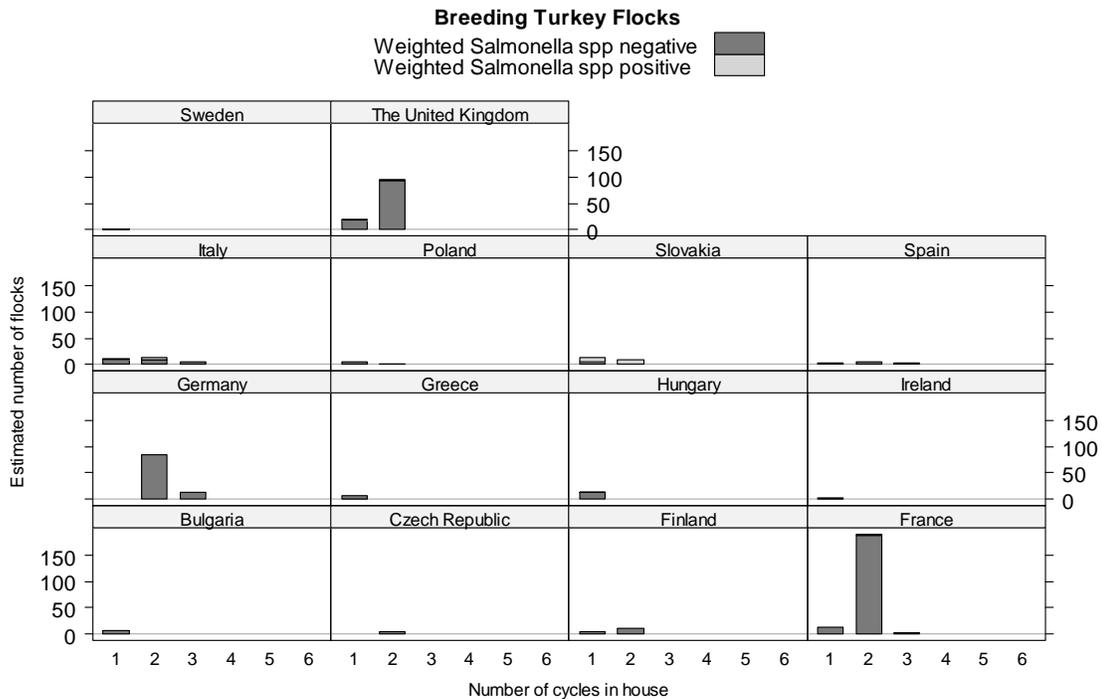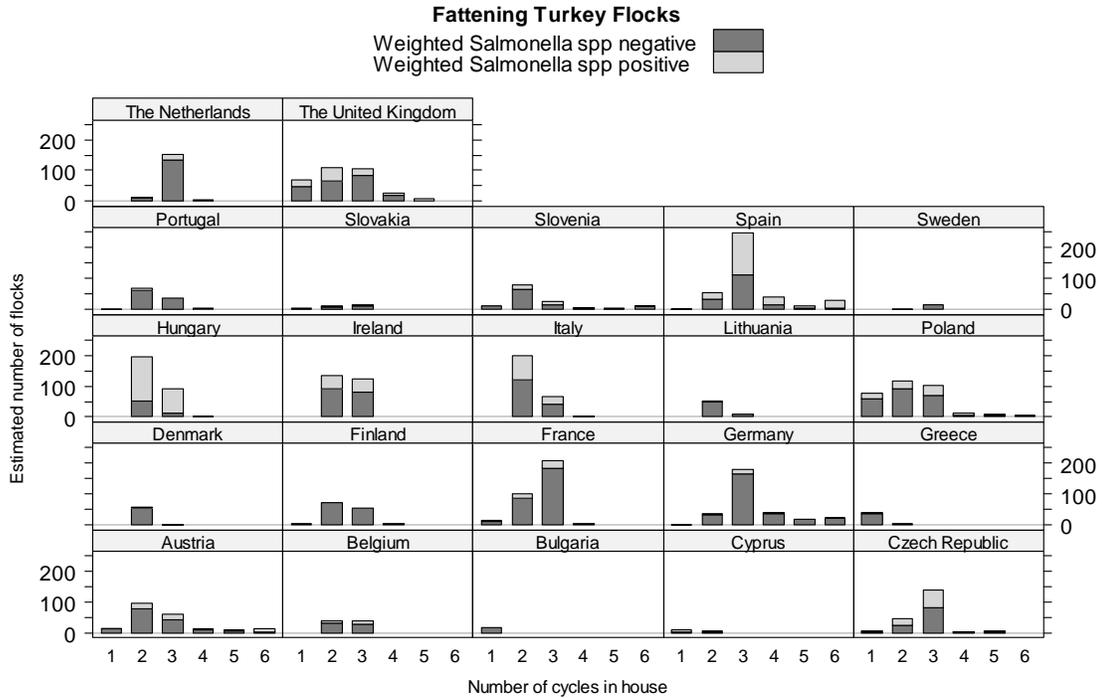
Table 4.1-22 Distribution of the number of cycles per house, per Member State and in the EU.

	Country	Number of house cycles of sampled flock of fattening turkeys	
		\multicolumn{2}{c}{1}	\multicolumn{2}{c}{2}	\multicolumn{2}{c}{3}	\multicolumn{2}{c}{4}	\multicolumn{2}{c}{5}	\multicolumn{2}{c}{6}	Total
1	Austria	19	9%	115	57%	52	26%	8	4%	3	1%	5	2%	202
2	Belgium			45	61%	29	39%							74
3	Cyprus	10	71%	4	29%									14
4	Czech Republic	13	7%	57	29%	120	62%	2		2	1%			194
5	Denmark			58	98%	1	2%							59
7	Finland	6	5%	86	65%	39	29%	2	2%					133
8	France	47	14%	125	38%	153	47%	1	0%					326
9	Germany	1	0%	55	19%	190	64%	27	9%	7	2%	15	5%	295
10	Greece	42	98%	1	2%									43
11	Hungary			198	69%	90	31%	1	0%					289
12	Ireland			176	68%	83	32%							259
13	Italy			205	76%	62	23%	1	0%					268
15	Lithuania			53	84%	10	16%							63
18	Poland	146	45%	118	37%	49	15%	4	1%	4	1%	1	0%	322
19	Portugal	1	1%	71	68%	31	30%	2	2%					105
20	Slovakia	4	16%	8	32%	13	52%							25
21	Slovenia	13	10%	86	66%	23	18%	3	2%	2	2%	4	3%	131
22	Spain	4	1%	71	19%	258	68%	29	8%	7	2%	11	3%	380
23	Sweden			1	7%	13	93%							14
24	The Netherlands			20	12%	148	86%	4	2%					172
25	The United Kingdom	160	50%	68	21%	67	21%	19	6%	3	1%			317
27	Bulgaria	17	100%										0%	17
	European Union	483	13%	1621	44%	1431	39%	103	3%	28	1%	36	1%	3702

	Country	Number of house cycles of sampled flock of breeding turkeys	
		\multicolumn{2}{c}{1}	\multicolumn{2}{c}{2}	\multicolumn{2}{c}{3}	Total
4	Czech Republic			4	100%			4
7	Finland	4	27%	11	73%			15
8	France	24	12%	180	88%	1	0%	205
9	Germany			95	97%	3	3%	98
10	Greece	6	100%					6
11	Hungary	13	100%					13
12	Ireland	2	100%					2
13	Italy	18	64%	8	29%	2	7%	28
18	Poland	5	83%	1	17%			6
20	Slovakia	15	71%	6	29%			21
22	Spain	5	50%	3	30%	2	20%	10
23	Sweden	1	100%					1
25	The United Kingdom	28	24%	88	76%			116
27	Bulgaria	7	100%					7
	European Union	128	24%	396	74%	8	2%	532

Figure 4.1-22 Weighted *Salmonella* prevalence by number of house cycles of sampled flock, in the EU (number of sampled flocks represented inside each bar).
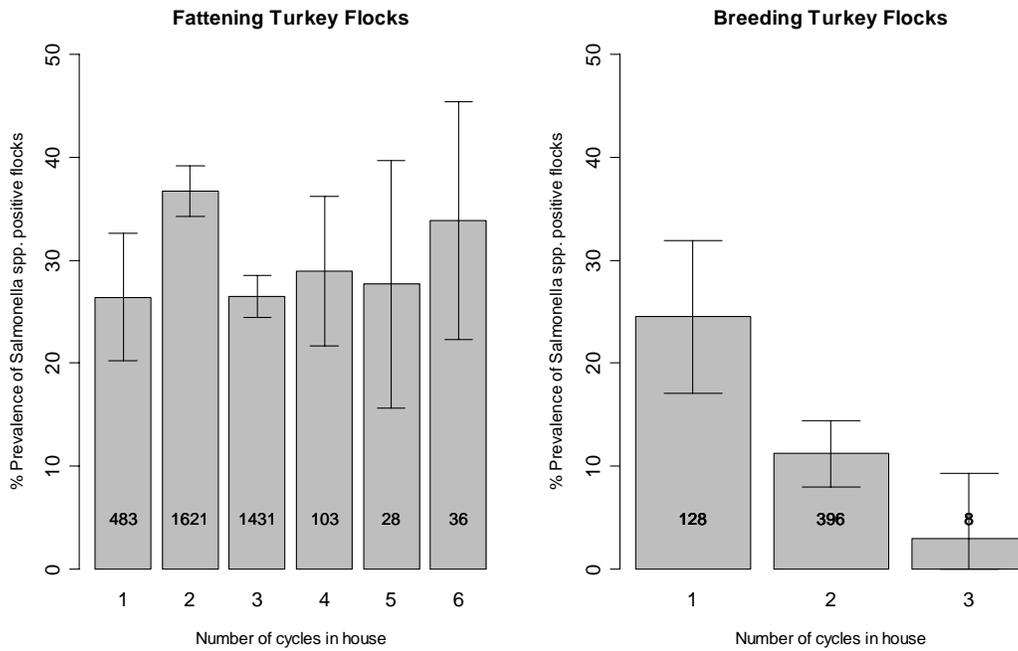
Table 4.1-23 Weighted *Salmonella* prevalence by the number of cycles per house (flock level).

Fattening turkeys				*Salmonella*			
Frequency *Row Pct* Col Pct	Number of cycles in house of sampled flock						
	1	2	3	4	5	6	Total
Negative	144 *6%* 74%	925 *36%* 63%	1307 *51%* 74%	106 *4%* 71%	38 *1%* 72%	43 *2%* 66%	2564 *100%*
Positive	52 *5%* 26%	537 *47%* 37%	470 *41%* 26%	43 *4%* 29%	15 *1%* 28%	22 *2%* 34%	1138 *100%*
Total	196 100%	1462 100%	1777 100%	149 100%	53 100%	64 100%	3702

Breeding turkeys		*Salmonella*		
Frequency *Row Pct* Col Pct	Number of cycles in house of sampled flock			
	1	2	3	Total
Negative	97 *21%* 75%	333 *73%* 89%	27 *6%* 97%	458 *100%*
Positive	32 *43%* 25%	42 *56%* 11%	1 *1%* 3%	74 *100%*
Total	129 100%	375 100%	28 100%	532

	Trend statistic (one-sided p-value)[14]	
Salmonella	Fattening	Breeding
	2.97 (0.003)	-4.09 (<0.001)

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[14] Positive outcome trend.

Variables associated with vaccination

Figure 4.1-23 and Table 4.1-24 summarise the number of flocks in the study by their vaccination (against *Salmonella*) status. Only 25% of breeding turkeys and 2% of fattening turkeys in the EU are known to have received a vaccine. These were mostly inactivated vaccines or a combination between a live and an inactivated vaccine.

The barplot in Figure 4.1-24 would suggest an association between vaccination and *Salmonella* infection. On the other hand, the chi-squared test represented in Table 4.1-25 indicates a borderline association of *Salmonella* infection with vaccination status in fattening turkeys and a significant association in breeding turkeys. In fattening turkeys, vaccinated birds and birds with unknown vaccination status seem to be more infected. In breeding turkeys, the unvaccinated birds have a greater risk of infection.

Figure 4.1-23 Estimated number of fattening and breeding turkey flocks by vaccination status and (weighted) *Salmonella* prevalence.
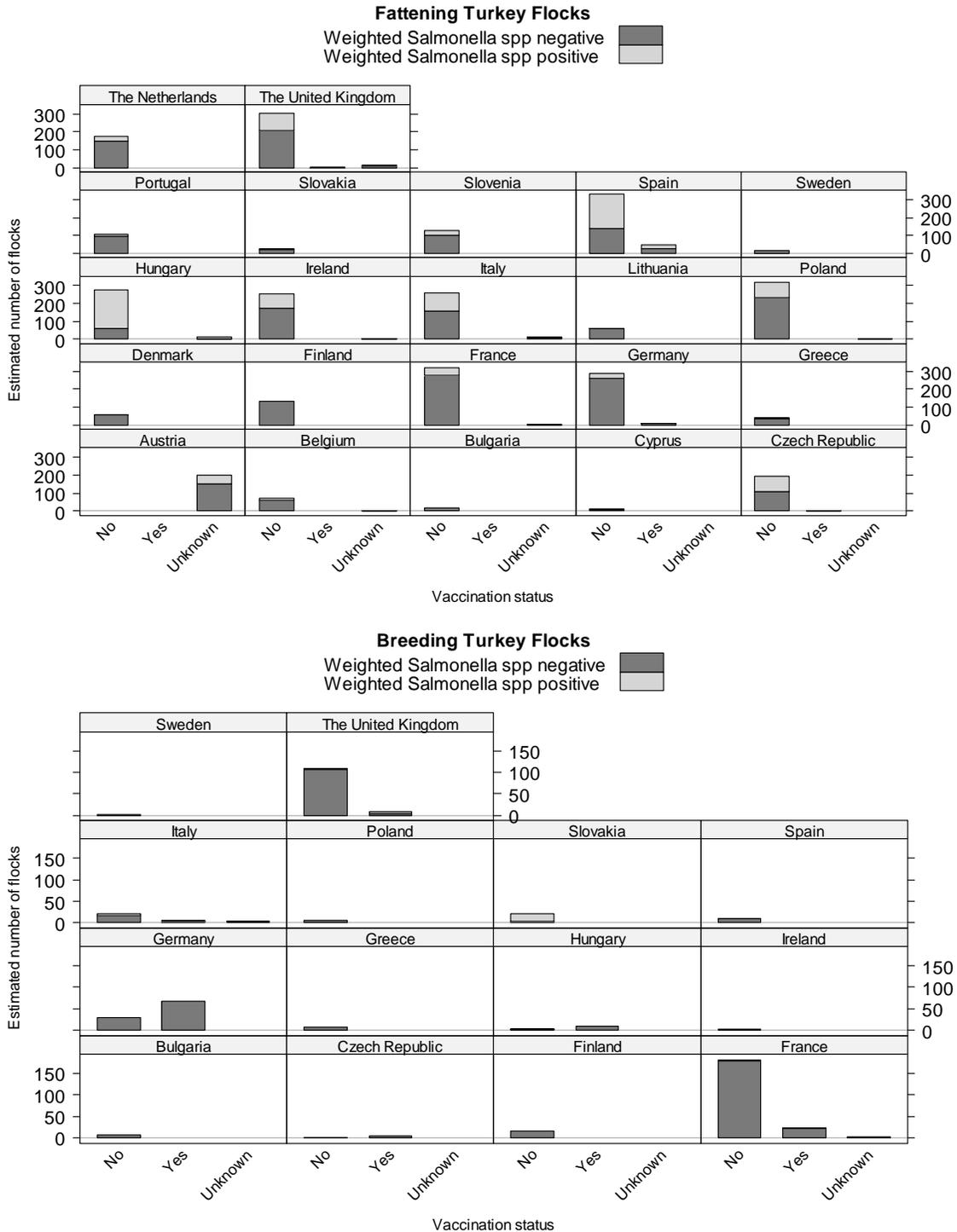
Table 4.1-24 Distribution of the number of flocks by their vaccination status, per Member State and in the EU.[15]

|	Country	Fattening turkeys							Breeding turkeys							
		No		Yes		Unknown		Total	No		Yes		Unknown		Total
1	Austria					202	100%	202							
2	Belgium	72	97%			2	3%	74							
3	Cyprus	14	100%					14							
4	Czech Republic	192	99%	2[**]	1%			194	1	25%	3[**]	75%			4
5	Denmark	59	100%					59							
7	Finland	133	100%					133	15	100%					15
8	France	322	99%			4	1%	326	176	86%	28[**]	14%	1	0%	205
9	Germany	287	97%	8[+]	3%			295	18	18%	80[**,+]	82%			98
10	Greece	43	100%					43	6	100%					6
11	Hungary	270	93%			19	7%	289	4	31%	9[**,***]	69%			13
12	Ireland	256	99%			3	1%	259	2	100%					2
13	Italy	255	95%			13	5%	268	18	64%	6[**]	21%	4	14%	28
15	Lithuania	63	100%					63							
18	Poland	319	99%			3	1%	322	6	100%					6
19	Portugal	105	100%					105							
20	Slovakia	25	100%					25	21	100%					21
21	Slovenia	131	100%					131							
22	Spain	328	86%	52[*,**,+]	14%			380	10	100%					10
23	Sweden	14	100%					14	1	100%					1
24	The Netherlands	172	100%					172							
25	The United Kingdom	300	95%	2	1%	15	5%	317	109	94%	7[+]	6%			116
27	Bulgaria	17	100%					17	7	100%					7
	European Union	3,377	91%	64	2%	261	7%	3,702	394	74%	133	25%	5	1%	532

[15] [*] live vaccine
 [**] inactivated vaccine
 [***] live and inactivated vaccines
 [+] missing information

Figure 4.1-24 Weighted *Salmonella* prevalence by flock vaccination status in the EU (number of sampled flocks represented inside each bar).
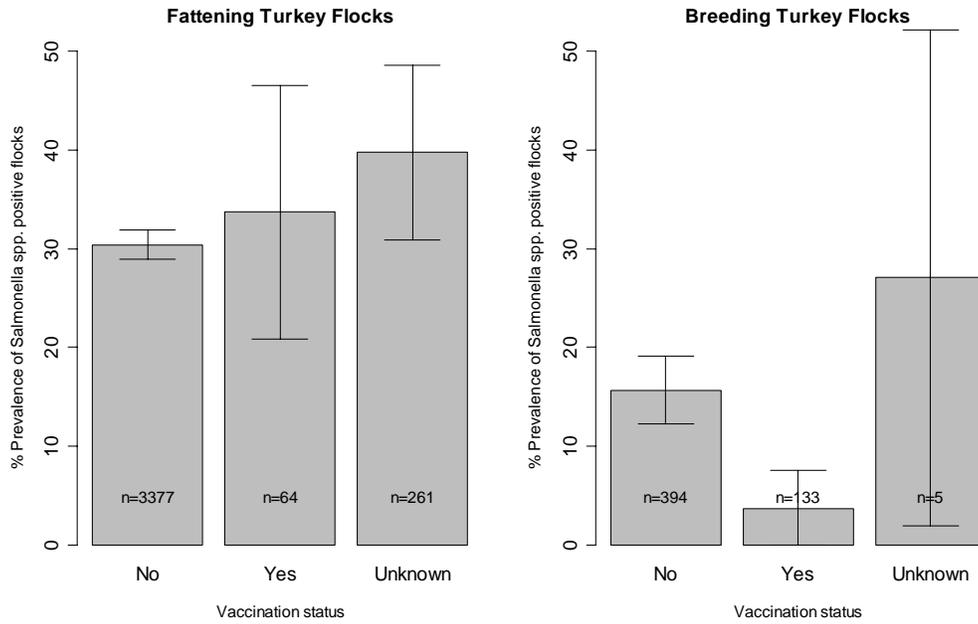
Table 4.1-25 Weighted *Salmonella* prevalence by flock vaccination status.

Fattening turkeys			*Salmonella*	
Frequency *Row Pct* Col Pct	Vaccination status			
	No	Yes	Unknown	Total
Negative	2,459 *96%* 70%	35 *1%* 66%	70 *3%* 60%	2,564 *100%*
Positive	1075 *94%* 30%	18 *2%* 34%	46 *4%* 40%	1,138 *100%*
Total	3,534 100%	52 100%	116 100%	3,702

Breeding turkeys			*Salmonella*	
Frequency *Row Pct* Col Pct	Vaccination status			
	No	Yes	Unknown	Total
Negative	367 *80%* 84%	82 *18%* 96%	9 *2%* 73%	458 *100%*
Positive	68 *91%* 16%	3 *4%* 4%	3 *4%* 27%	74 *100%*
Total	435 100%	85 100%	12 100%	532

Salmonella	Chi-square statistic (p-value)	
	Fattening	Breeding
	4.81 (0.090)	10.3 (0.006)

Variables associated with medication

In Figure 4.1-25 and Table 4.1-26 the distribution of flocks by medication status has been presented. From this table it appears that fattening turkeys are more frequently medicated than breeding turkeys. Nevertheless, the majority of turkeys were not medicated during the two weeks prior to sampling. Medication status does not appear to be associated with the prevalence of *Salmonella* (see Figure 4.1-26 and Table 4.1-27).

Figure 4.1-25 Estimated number of fattening and breeding turkey flocks by medication status and (weighted) *Salmonella* **prevalence.**

Fattening Turkey Flocks

Breeding Turkey Flocks
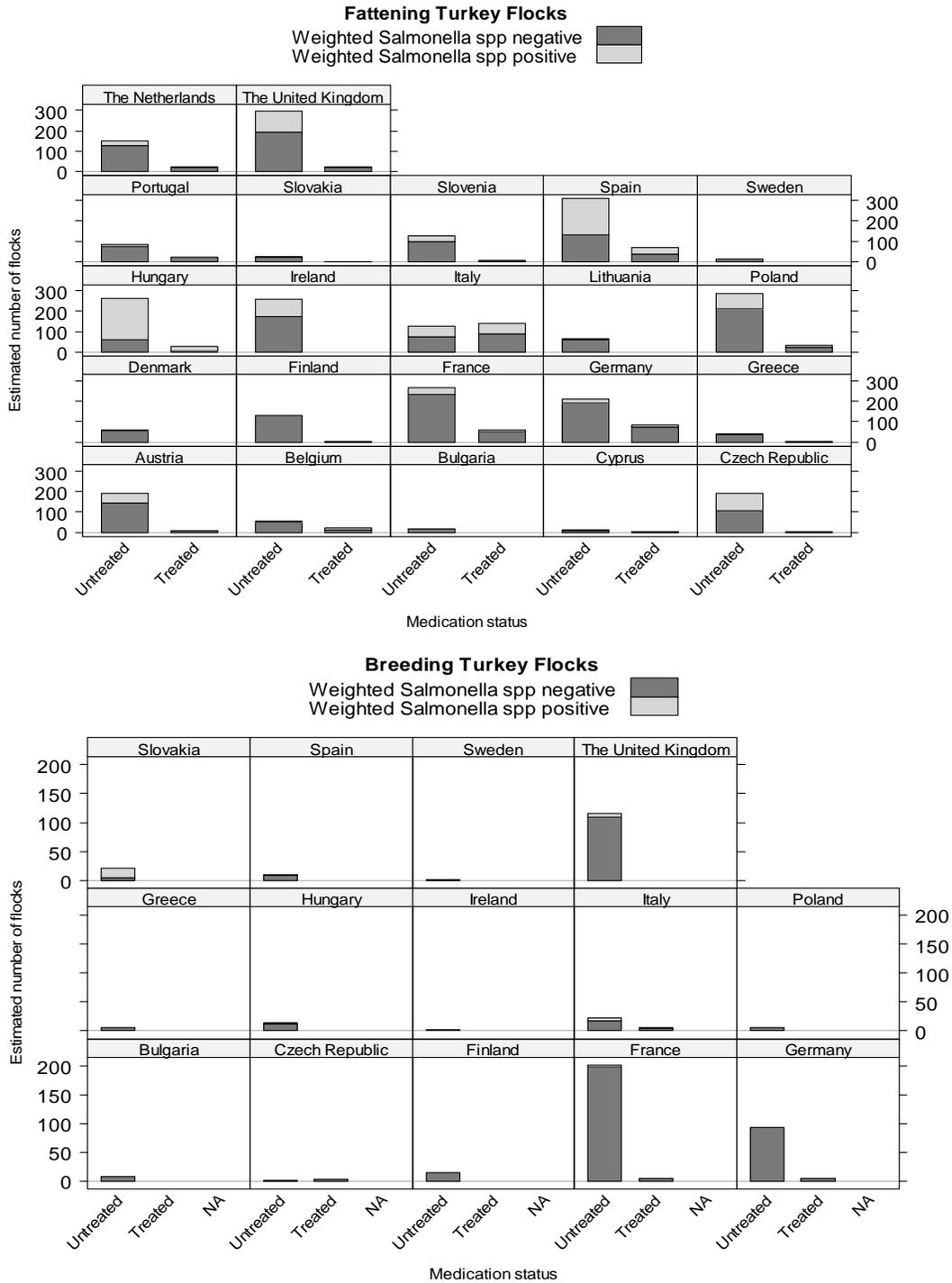
Table 4.1-26 Distribution of the number of flocks by flock medication status, per Member State and in the EU.

	Country	Fattening turkeys					Breeding turkeys				
		No		Yes		Total	No		Yes		Total
1	Austria	191		11	5%	202					
2	Belgium	55	74%	19	26%	74					
3	Cyprus	13	93%	1	7%	14					
4	Czech Republic	193	99%	1	1%	194	3	75%	1	25%	4
5	Denmark	59	100%			59					
7	Finland	132	99%	1	1%	133	15	100%			15
8	France	278	85%	48	15%	326	201	98%	4	2%	205
9	Germany	217	74%	78	26%	295	96	98%	2	2%	98
10	Greece	42	98%	1	2%	43	6	100%			6
11	Hungary	259	90%	30	10%	289	13	100%			13
12	Ireland	259	100%			259	2	100%			2
13	Italy	132	49%	136	51%	268	24	86%	4	14%	28
15	Lithuania	63	100%			63					
18	Poland	298	93%	24	7%	322	6	100%			6
19	Portugal	85	81%	20	19%	105					
20	Slovakia	24	96%	1	4%	25	21	100%			21
21	Slovenia	126	96%	5	4%	131					
22	Spain	312	82%	68	18%	380	10	100%			10
23	Sweden	14	100%			14	1	100%			1
24	The Netherlands	149	87%	23	13%	172					
25	The United Kingdom	298	94%	19	6%	317	116	100%			116
27	Bulgaria	17	100%			17	7	100%			7
	European Union	3,216	87%	486	13%	3,702	521	98%	11	2%	532

Figure 4.1-26 Weighted *Salmonella* prevalence by flock medication status in the EU (number of sampled flocks represented inside each bar).
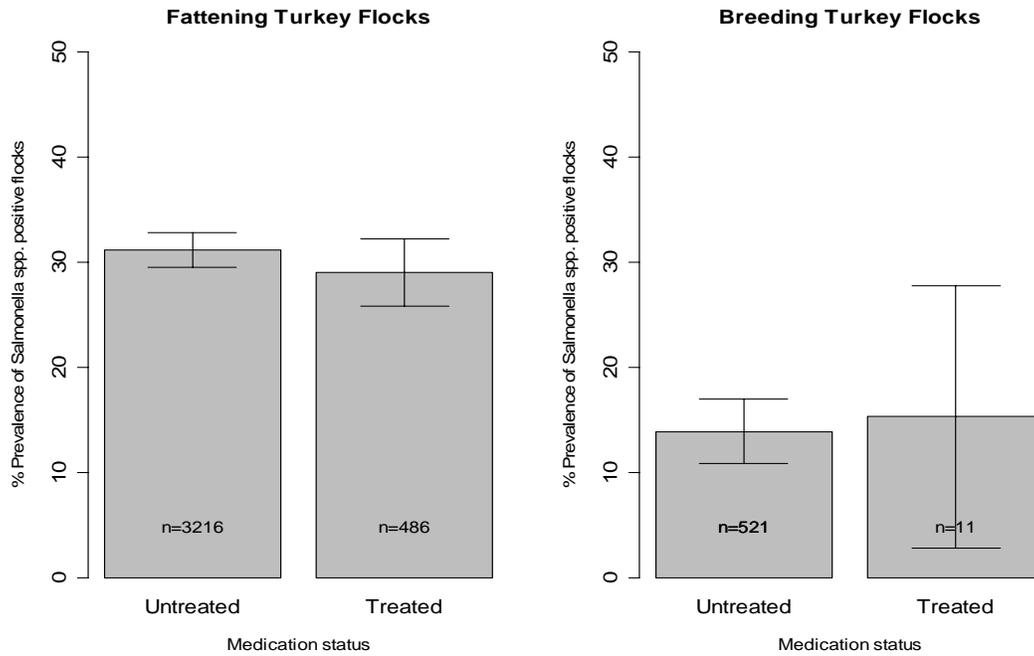
Table 4.1-27 Weighted *Salmonella* prevalence by medication status in the EU.

Fattening turkeys	*Salmonella*		
Frequency *Row Pct* Col Pct	Vaccination status		
	No	Yes	Total
Negative	2,029 *79%* 69%	535 *21%* 71%	2,564 *100%*
Positive	920 *81%* 31%	219 *19%* 29%	1138 *100%*
Total	2,949 100%	753 100%	3,702

Breeding turkeys	***Salmonella***		
Frequency *Row Pct* Col Pct	Vaccination status		
	No	Yes	Total
Negative	431 *94%* 86%	27 *6%* 85%	458 *100%*
Positive	70 *93%* 14%	5 *7%* 15%	74 *100%*
Total	500 100%	32 100%	532

Salmonella	Fisher's exact test: p-value	
	Fattening	Breeding
	0.25	0.79

Time between sampling and testing

The time between sampling and testing is studied in detail by means of frequency graphs in Figure 4.1-27 and some descriptive statistics summarised in Table 4.1-28. The time between sampling and testing is at most 1 week, for both fattening and breeding turkeys. On average, the time between sampling and testing seems to be around two days. Table 4.1-29 shows a significant negative association between the prevalence of *Salmonella* in fattening and breeding turkeys. The odds of observing a positive flock seems to decrease as the time between sampling and testing increases (Figure 4.1-27).

Figure 4.1-27 Estimated number of fattening and breeding turkey flocks by number of days between sampling and testing and (weighted) *Salmonella* prevalence.
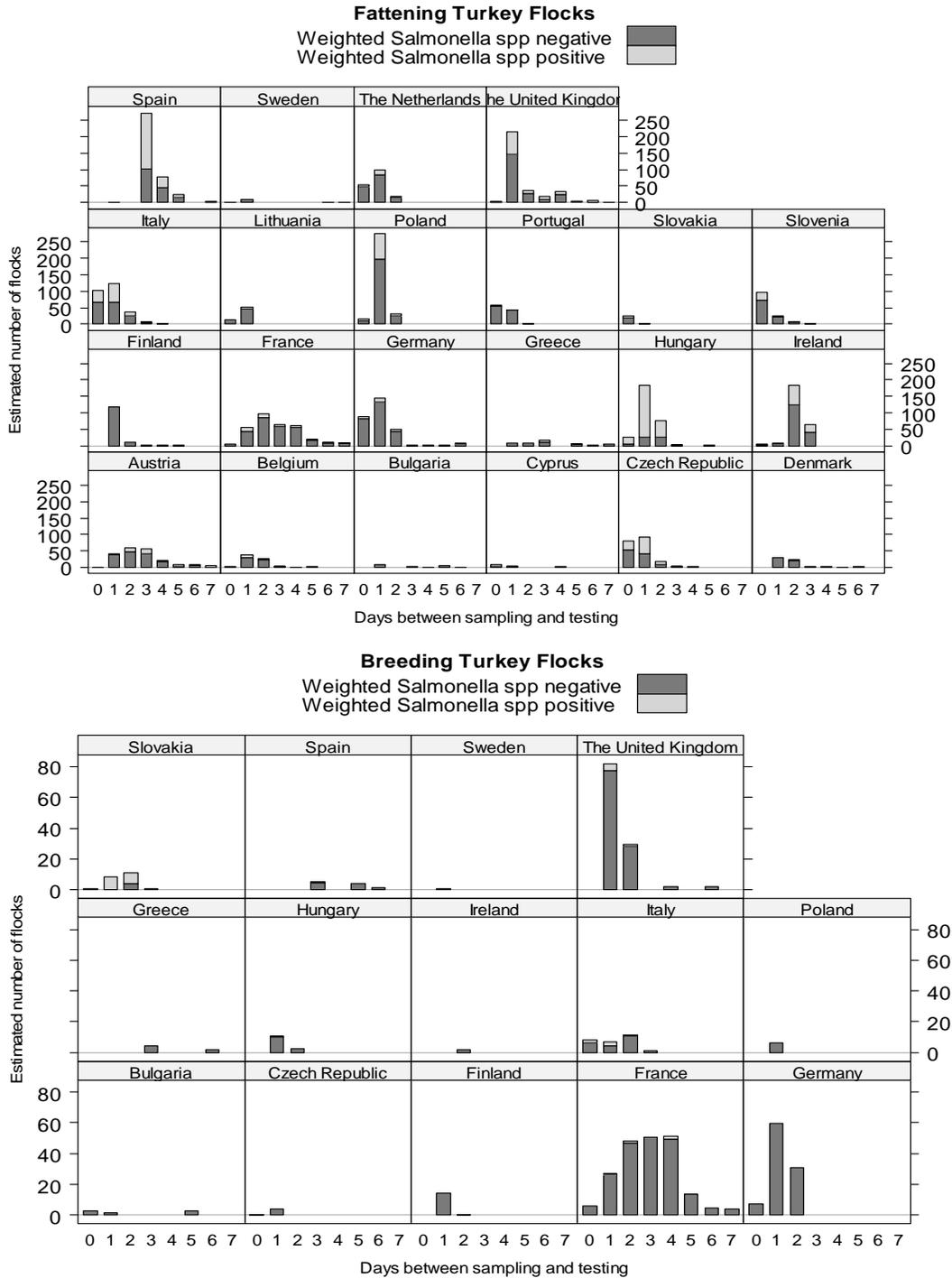
Table 4.1-28 Central tendency (mean, median) and dispersion measures (standard deviation and quantiles) of the number of days between sampling and testing, by flock production group, per Member State and in the EU.[16]

	Country	Fattening turkeys					Breeding turkeys				
		Q1	Median	Q3	Mean	StD	Q1	Median	Q3	Mean	StD
1	Austria	2	2	3	2.6	1.4					
2	Belgium	1	1	2	1.5	1.0					
3	Cyprus	0	0	1	0.5	1.1					
4	Czech Republic	0	1	1	0.7	0.8	0.5	1	1	0.8	0.5
5	Denmark	1	2	2	1.9	1.2					
7	Finland	1	1	1	1.2	0.6	1	1	1	1.1	0.3
8	France	2	3	4	2.9	1.5	2	3	4	2.9	1.5
9	Germany	0	1	1	1.0	1.0	1	1	2	1.3	0.5
10	Greece	2	3	5	3.2	1.8	3	4.5	6	4.5	1.6
11	Hungary	1	1	2	1.2	0.6	1	1	1	1.2	0.4
12	Ireland	2	2	2	2.1	0.5	2	2	2	2.0	
13	Italy	0	1	1	0.8	0.8	0	1	2	1.2	0.9
15	Lithuania	1	1	1	0.8	0.4					
18	Poland	1	1	1	1.0	0.4	1	1	1	1.0	
19	Portugal	0	0	1	0.5	0.6					
20	Slovakia	0	0	0	0.0	0.2	1	2	2	1.6	0.8
21	Slovenia	0	0	0	0.3	0.6					
22	Spain	3	3	4	3.4	0.7	3	5	5	4.3	1.2
23	Sweden	1	1	1	2.1	2.5	1	1	1	1.0	
24	The Netherlands	0	1	1	0.8	0.6					
25	The United Kingdom	1	1	2	1.7	1.2	1	1	2	1.4	0.8
27	Bulgaria	1	3	5	2.9	2.0	0	0	5	1.6	2.4
	European Union	1	1	2	1.6	1.3	1	2	3	2.0	1.4

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[16] Q1: 25% quantile, Q3: 75% quantile, StD: standard deviation

Figure 4.1-28 Weighted *Salmonella* prevalence by number of days between sampling and testing in the EU.
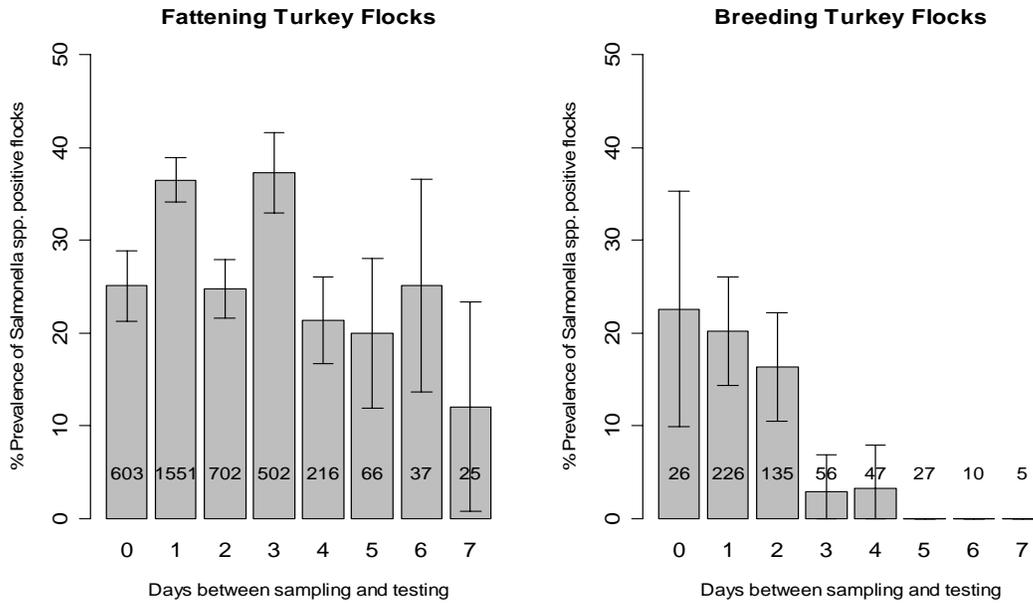

Table 4.1-29 Odds ratio estimates and corresponding 95% confidence intervals obtained from a logistic regression, modelling the weighted probability of observing a positive flock using an intercept and the time between sampling and testing, by flock production type.

Time between sampling and testing	Outcome of interest	Estimate	LB	UB
Fattening turkeys	*Salmonella*	0.921	0.876	0.969
Breeding turkeys	*Salmonella*	0.557	0.435	0.712

Variables on sample level

The last variable we will discuss in the context of a description of the mandatory independent variables is the type of sample which was taken to study whether a flock has been infected by *Salmonella*. A summary of this variable is given in Table 4.1-30. Observe that most of the samples were taken using a boot or sock swab. Therefore an extensive description of this covariate, or a risk factor analysis including this variable will not be very informative.

Table 4.1-30 Distribution of the flocks by type of sample taken, by flock production group, per member state and in the EU.

|	Country	Fattening turkeys							Breeding turkeys		
		Boot or sock swab		Hand swab		Other		Total	Boot or sock swab		Total
1	Austria	202	100%					202			
2	Belgium	74	100%					74			
3	Cyprus	14	100%					14			
4	Czech Republic	194	100%					194	4	100%	4
5	Denmark	59	100%					59			0
7	Finland	133	100%					133	15	100%	15
8	France	326	100%					326	205	100%	205
9	Germany	295	100%					295	98	100%	98
10	Greece	43	100%					43	6	100%	6
11	Hungary	289	100%					289	13	100%	13
12	Ireland	259	100%					259	2	100%	2
13	Italy	265	99%	2	1%			268	28	100%	28
15	Lithuania	63	100%					63			0
18	Poland	322	100%					322	6	100%	6
19	Portugal	105	100%					105			0
20	Slovakia	25	100%					25	21	100%	21
21	Slovenia	131	100%					131			0
22	Spain	380	100%					380	10	100%	10
23	Sweden	14	100%					14	1	100%	1
24	The Netherlands	171	99%			1	1%	172			0
25	The United Kingdom	317	100%					317	116	100%	116
27	Bulgaria	17	100%					17	7	100%	7
	European Union	3,698	100%	2	0%	1	0%	3,702	532	100%	532

To conclude this section, we have constructed a scatter plot matrix to study the correlation between the different continuous variables for breeding and fattening turkeys. These are displayed in Figure 4.1-29 and Figure 4.1-30. Note that these plots are for illustrative purposes only within the context of an exploratory analysis. The p-values displayed in these graphs simply give an indication of whether or not significant correlation is observed between the variables.

Figure 4.1-29 Scatterplot matrix for the continuous independent variables observed for fattening turkeys in the EU. The upper triangular part displays the estimated correlation coefficient together with p-values for H0: r = 0.
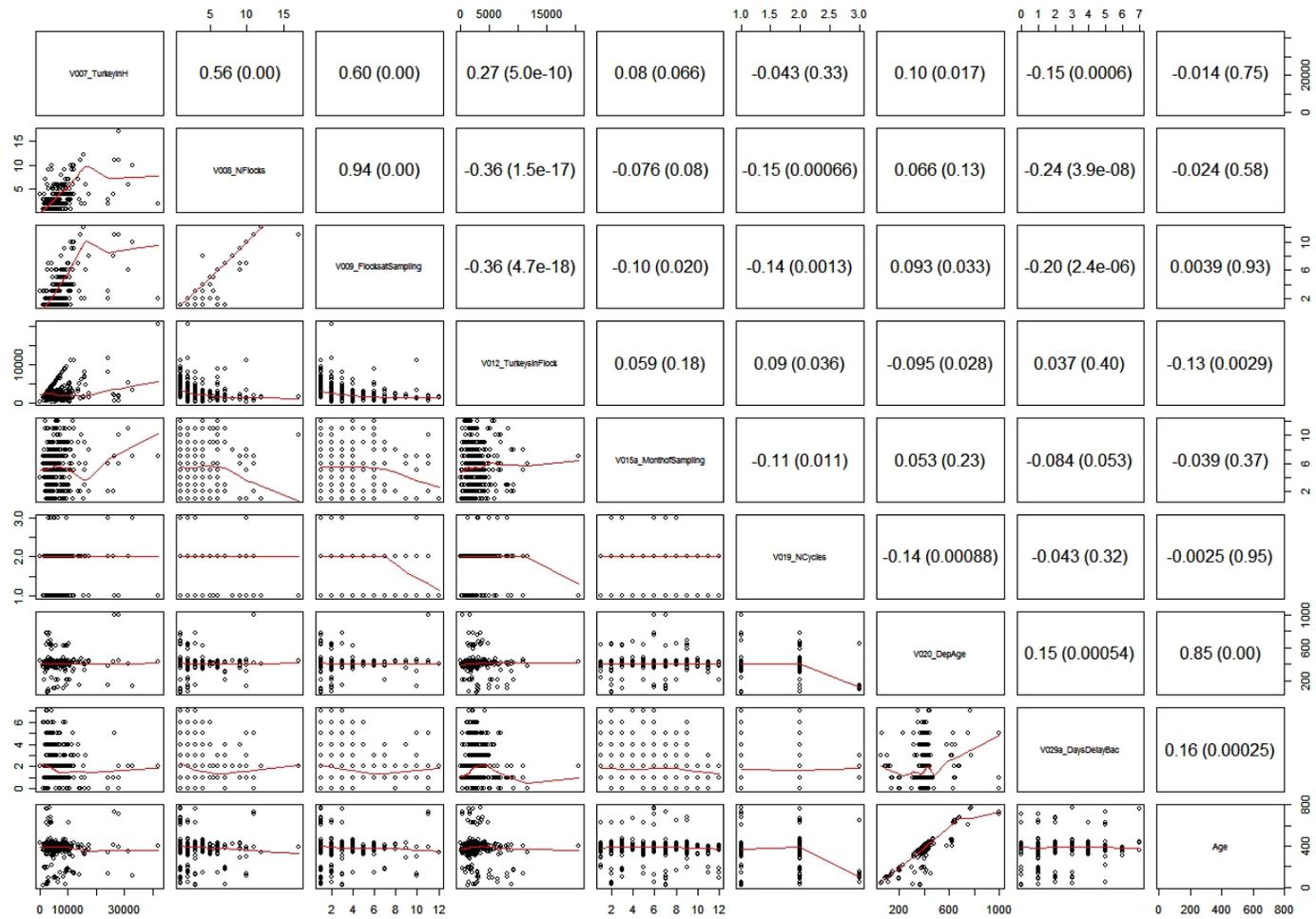
Figure 4.1-30 Scatterplot matrix for the continuous independent variables observed for breeding turkeys in the EU. The upper triangular part displays the estimated correlation coefficient together with p-values for H0: r = 0.
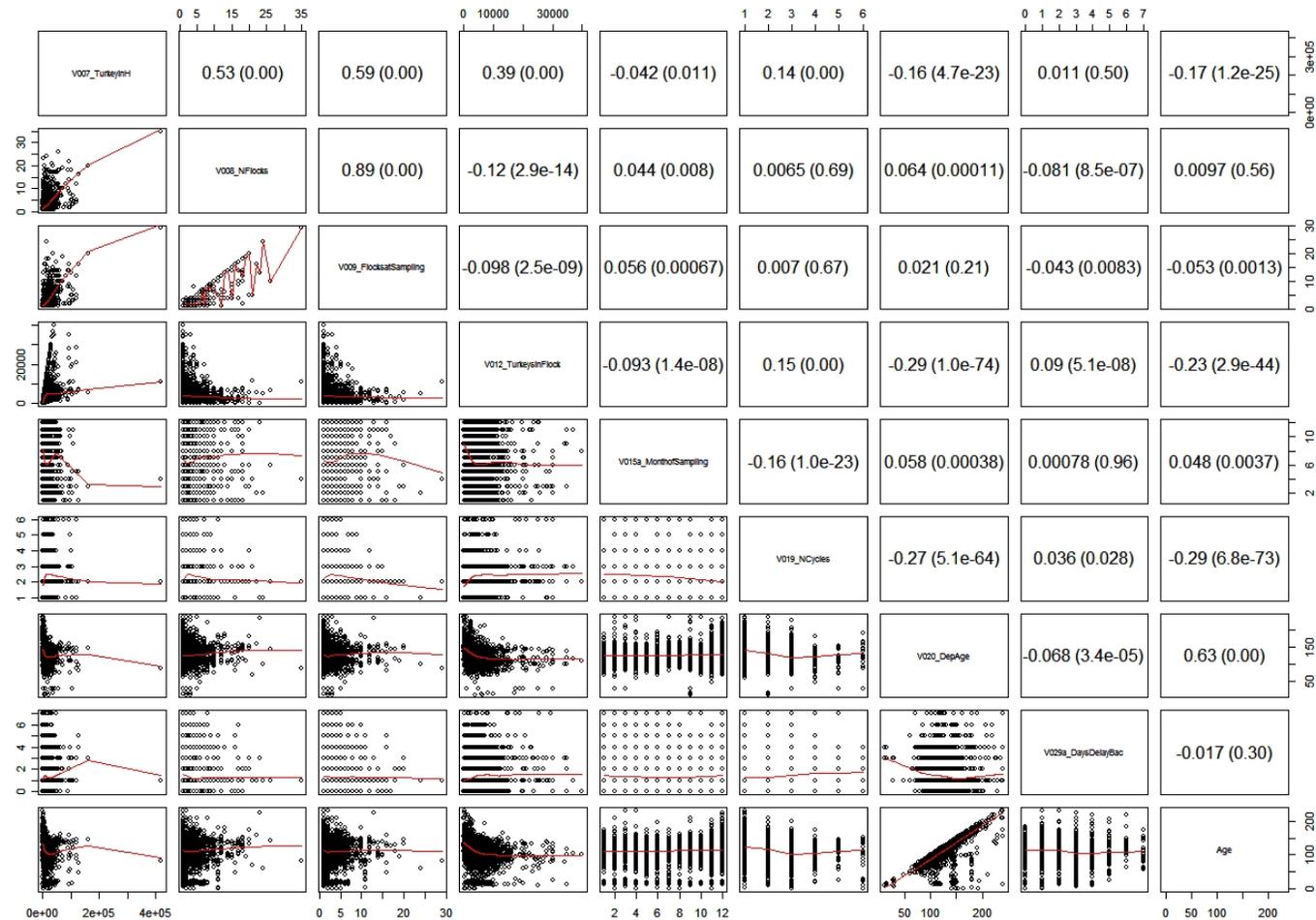
4.2 Results of the descriptive analysis: optional risk factors

In this section we will take a closer look at some of the optional variables, recorded from at least 50% of the samples by each country.

In Figure 4.2-1 and Table 4.2-1 the distribution of the number of flocks has been displayed by the parent flock holding. In fattening turkey flocks, only 1% of the flocks have parents which belong to the same holding, whereas in breeding turkey flocks 23% of the flocks had parents belonging to the same integration. For a high percentage of flocks the holding of the parents was unknown. However, these results are mainly driven by information from France. From Figure 4.2-2 and Table 4.2-2 a significant association can be observed between the parent holding and *Salmonella* presence, both in fattening and breeding turkey flocks. The flocks appear more infected when the parents of the flock were taken from the same integration, from another MS or a third country.

Similar results are obtained for the origin of the hatchery (see Figure 4.2-3 and Table 4.2-3). For only 2% of the fattening turkey flocks, the hatchery belonged to the same holding compared to 23% for breeding turkey flocks. This information is again unknown for France which drives the EU level distribution into the unknown category. In addition, in this case, a significant impact of the hatchery holding was observed (Figure 4.2-4 and Table 4.2-4). For fattening turkey flocks, *Salmonella* prevalence was higher when the hatchery holding belonged to the same integration. In breeding turkey flocks, prevalence was higher when the hatchery belonged to the same integration or to a different MS.

The distribution of rearing holdings is slightly different from the previous two variables (see Figure 4.2-5 and Table 4.2-5). In this case, 45% of the rearing of fattening turkey flocks is carried out on the same holding. Nevertheless, it has also been observed that due to the results from France, for 20% of fattening flocks the rearing holding is unknown in comparison to 59% for breeding turkey flocks. A significant association between the rearing holding and *Salmonella* is observed (see Figure 4.2-6 and Table 4.2-6). When the rearing holding belongs to a different MS or to the same integration (mainly for fattening flocks), the prevalence of *Salmonella* is greater.

The distribution of feed origin is shown in Figure 4.2-7 and Table 4.2-7. 58% of fattening turkey flocks are fed with feed from an unrelated holding, whereas 56% of breeding turkey flocks receive their feed from the same holding. For fattening turkey flocks, *Salmonella* prevalence seems to be highest when feed origin is from the same integration (see Figure 4.2-8 and Table 4.2-8).

Note that there was no information on feed supplements.

In Figure 4.2-9 and Table 4.2-9 the distribution of antimicrobial treatment (used at any stage of production within the flock) has been presented for each of the participating MS. In fattening turkey flocks, only 38% of flocks received treatment, compared to 61% of breeding turkey flocks. This treatment is given mainly in countries such as France and Germany. The association between antimicrobial treatment and the prevalence of *Salmonella* is significant (see Figure 4.2-10 and Table 4.2-10): flocks without antimicrobial treatment are more infected.

The distribution of thinnings number is described by means of boxplots in Figure 4.2-11 and by means of some central tendency statistics and dispersion measures in Table 4.2-11. On (EU) average there is one thinning in fattening flocks and 0.4 thinnings in breeding flocks. Czech Republic exceeds these averages considerably: fattening turkey flocks have on average 3.3 thinnings and the two breeding turkey flocks have 3 thinnings. Further, a significant association between thinnings number and *Salmonella* prevalence is observed for fattening flocks (see Figure 4.2-12 and Table 4.2-12). The odds of observing a positive flock increase as the number of thinnings increase. In Figure 4.2-13 and Table 4.2-13 the number of days to first thinning has been presented. On average there are 33 days between the first thinning and sampling in fattening turkey flocks, and 99 days in breeding turkey flocks. However, there does not appear to be any association between the number of days to first thinning and the presence of *Salmonella* in fattening turkey flocks. In breeding turkey flocks, the odds of observing a positive flock seems to increase as the number of days to first thinning (in absolute value) increase (see Figure 4.2-14 and Table 4.2-14).

Further, in Figure 4.2-15 and Table 4.2-15 we can see the distribution of the variable all in/all out flock. The all in/all out flock principle was applied to 62 % of fattening turkey flocks compared to 87% of breeding turkey flocks. Flocks have a lower probability of being infected with *Salmonella* (see Figure 4.2-16 and Table 4.2-16). In addition, the all in/all out holding principle was applied to 54% of fattening turkey flocks and 84% of breeding turkey flocks (see Figure 4.2-17 and Table 4.2-17). In this case it can also be seen that the flocks to which this principle was applied have a smaller probability of being infected (Figure 4.2-18 and Table IV-2-18).

For 81% of fattening flocks and 97% of breeding flocks the time between flocks was recorded to be over 14 days (see Figure 4.2-19 and Table 4.2-19). A significant positive association was also observed between the time between flocks and *Salmonella* prevalence in fattening turkey flocks: the longer the time between two flocks the higher the probability of observing a positive flock (see Figure 4.2-20 and Table 4.2-20).

In 85% of fattening flocks and 95% of breeding turkey flocks *Salmonella* was not detected during the preceding 6 months (see Figure 4.2-21 and Table 4.2-21). Therefore, the probability of observing a positive flock is much higher when *Salmonella* was detected during the preceding 6 months (Figure 4.2-22). This is supported by the significant association observed in Table 4.2-22.

Further, in Table 4.2-23 and Figure 4.2-23 we have displayed the distribution of other livestock, consisting of no other livestock, other poultry, pigs, cattle, small ruminants and other livestock. From these illustrations it follows that 61% of fattening flocks and 80% of breeding flocks were sampled from holdings with turkey flocks only. A significant association with *Salmonella* prevalence was only found for fattening turkey flocks: flocks with other poultry, and flocks with cattle appear to be less infected (see Figure 4.2-24 and Table 4.2-24).

The distribution of rodent presence and control is displayed in Figure 4.2-25 and Table 4.2-25. For 87% of fattening flocks and 98% of breeding flocks rodent control measures were taken, whether or not rodents had been detected. A significant association between rodent control and *Salmonella* prevalence in fattening turkey flocks can be observed in Figure 4.2-26 and Table 4.2-26. The probability of observing a positive flock is highest when rodents have been detected but not controlled.

Finally, the distribution of houses age is shown in Figure 4.2-27 and Table 4.2-27: 78% of fattening flocks were sampled from houses over 10 years old, compared to 81% for breeding flocks. In fattening turkey flocks, the probability of observing a positive flock increases as the house age increases (see Figure 4.2-28 and Table 4.2-28). No association was observed for breeding turkey flocks.

Figure 4.2-1 Estimated number of fattening and breeding turkey flocks by parent holding and (weighted) *Salmonella* **outcome.**
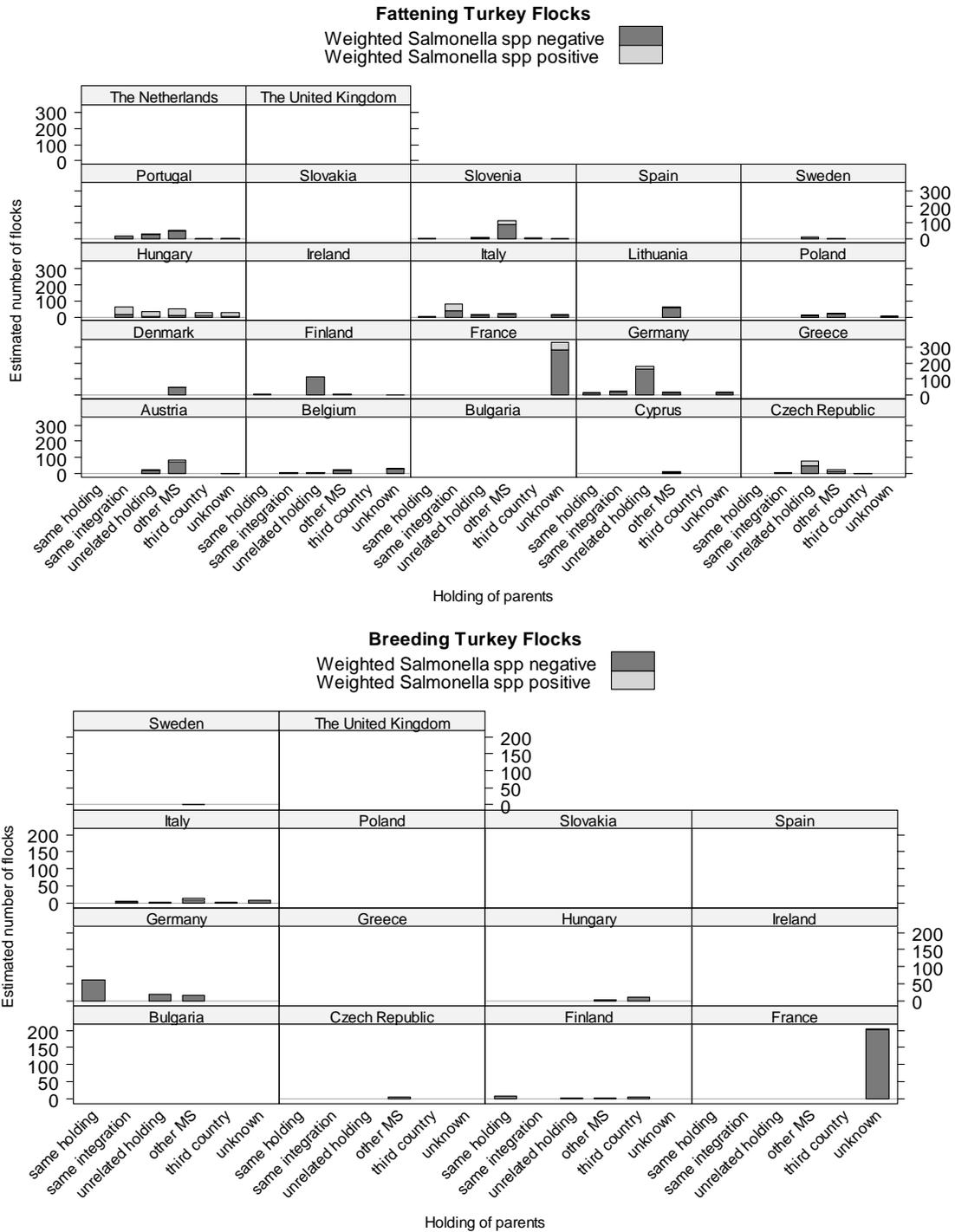
Table 4.2-1 Distribution of holding flock number by parent holding, per Member State and in the EU.

	Country	Fattening turkeys													
		Same holding		Same integration		Unrelated holding		Other MS		Third country		Unknown		Total	Missing
1	Austria					27	23%	88	75%			2	2%	117	85
2	Belgium			3	4%	7	10%	19	28%			40	58%	69	5
3	Cyprus							14	100%					14	
4	Czech Republic			12	11%	79	74%	15	14%	1	1%			107	87
5	Denmark							47	100%					47	12
7	Finland	4	3%			113	87%	12	9%			1	1%	130	3
8	France											326	100%	326	
9	Germany	14	6%	23	9%	176	71%	20	8%			15	6%	248	47
10	Greece														43
11	Hungary			49	24%	48	24%	58	29%	18	9%	29	14%	202	87
12	Ireland														259
13	Italy	2	1%	90	63%	14	10%	19	13%			17	12%	142	126
15	Lithuania							63	100%					63	
18	Poland					12	35%	19	56%			3	9%	34	288
19	Portugal			15	14%	34	32%	50	48%	4	4%	2	2%	105	
20	Slovakia														25
21	Slovenia	2	2%			6	5%	115	88%	6	5%	2	2%	131	
22	Spain														380
23	Sweden					13	93%	1	7%					14	
24	The Netherlands														172
25	The United Kingdom														317
27	Bulgaria														17
	European Union	22	1%	192	11%	529	30%	540	31%	29	2%	437	25%	1,749	1,953

	Country	Breeding turkeys													
		Same holding		Same integration		Unrelated holding		Other MS		Third country		Unknown		Total	Missing
4	Czech Republic							2	100%					2	2
7	Finland	2	13%			1	7%	4	27%	8	53%			15	
8	France											205	100%	205	
9	Germany	77	81%			7	7%	11	12%					95	3
10	Greece														6
11	Hungary							4	40%	6	60%			10	3
12	Ireland														2
13	Italy			6	27%	1	5%	11	50%	2	9%	2	9%	22	6
18	Poland														6
20	Slovakia														21
22	Spain														10
23	Sweden							1	100%					1	
25	The United Kingdom														116
27	Bulgaria														7
	European Union	79	23%	6	2%	9	3%	33	9%	16	5%	207	59%	350	182

Figure 4.2-2 Weighted *Salmonella* prevalence by parent holding in the EU (number of sampled flocks represented inside each bar).
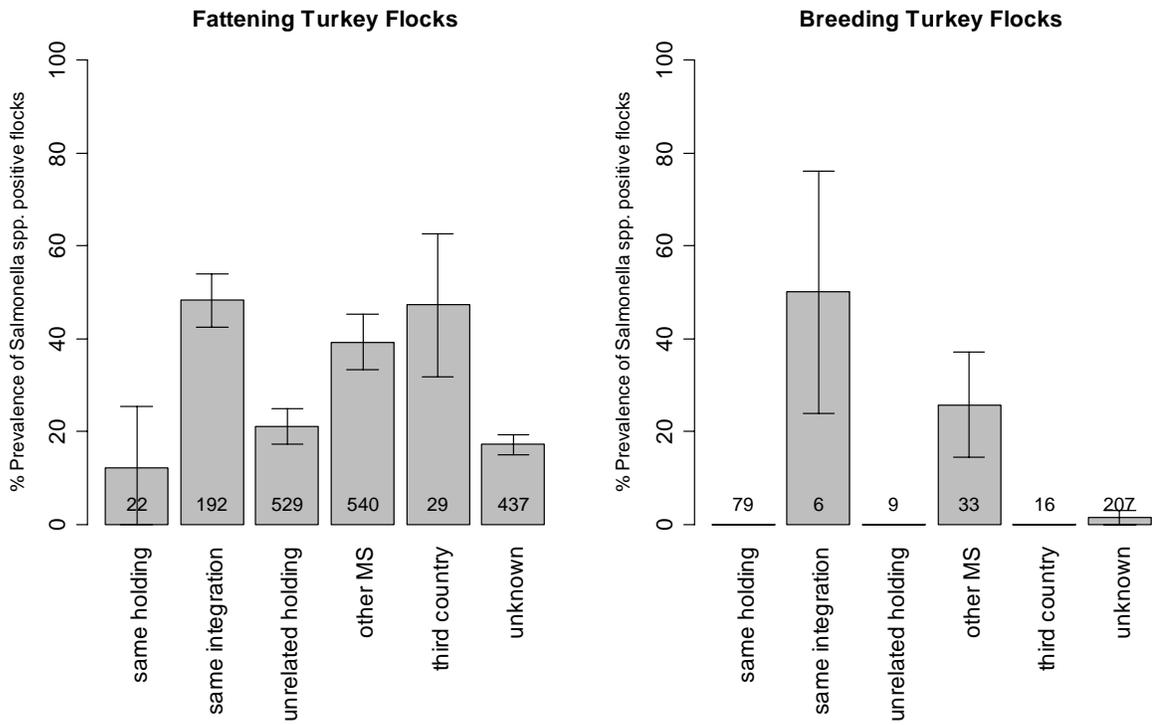
Table 4.2-2 Weighted *Salmonella* prevalence by parent holding and by flock production type in the EU.

Fattening turkeys			*Salmonella*				
Frequency	Holding of parents						
Row Pct Col Pct	Same holding	Same integration	Unrelated holding	Other MS	Third country	Unknown	Total
Negative	21 *1%* 88%	151 *9%* 52%	355 *22%* 79%	161 *10%* 61%	21 *1%* 53%	939 *57%* 83%	1648 *100%*
Positive	3 *1%* 12%	141 *25%* 48%	95 *17%* 21%	104 *19%* 39%	19 *3%* 47%	195 *35%* 17%	557 *100%*
Total	24 100%	292 100%	450 100%	265 100%	41 100%	1134 100%	2205

Breeding turkeys			*Salmonella*				
Frequency	Holding of parents						
Row Pct Col Pct	Same holding	Same integration	Unrelated holding	Other MS	Third country	Unknown	Total
Negative	29 *9%* 100%	7 *2%* 50%	9 *3%* 100%	42 *13%* 74%	13 *4%* 100%	230 *70%* 99%	331 *100%*
Positive	0 *0%* 0%	7 *28%* 50%	0 *0%* 0%	15 *59%* 26%	0 *0%* 0%	3 *13%* 1%	25 *100%*
Total	29 100%	14 100%	9 100%	57 100%	13 100%	233 100%	356

Figure 4.2-3 Estimated number of fattening and breeding turkey flocks by hatchery holding and (weighted) *Salmonella* **outcome.**
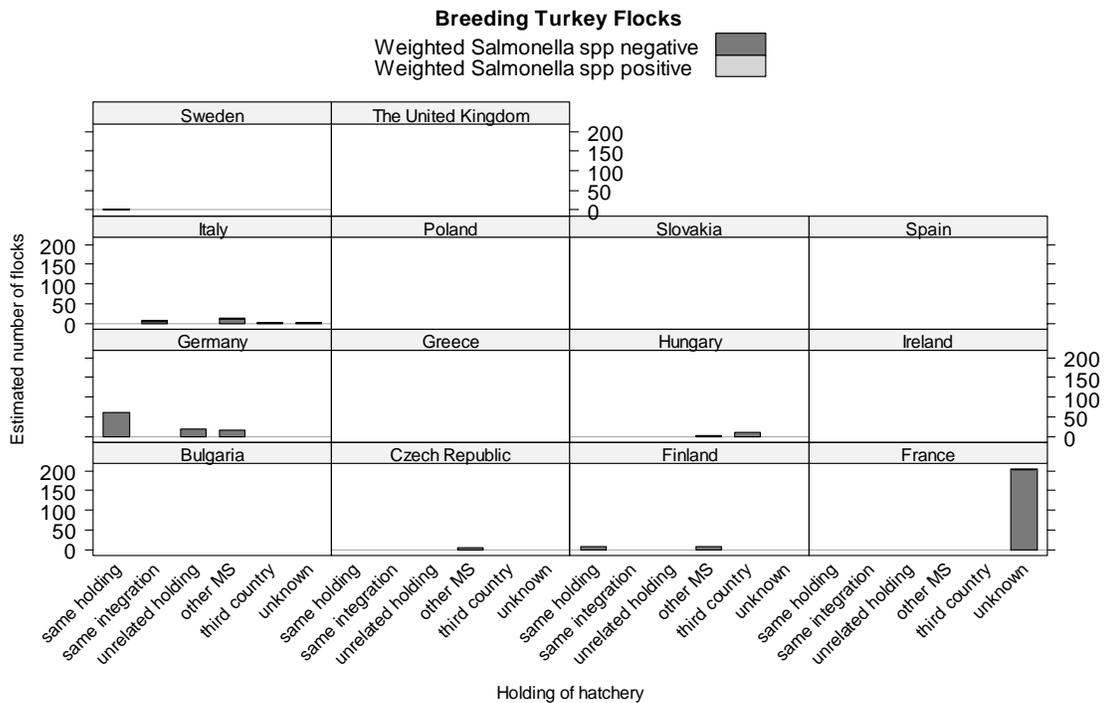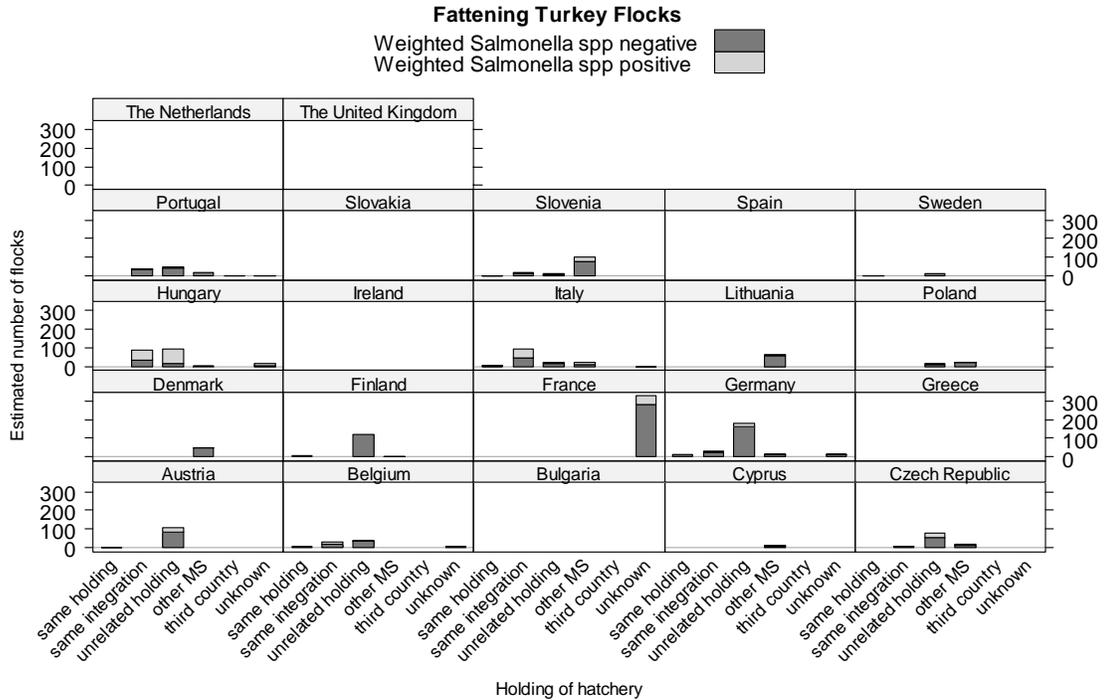
Table 4.2-3 Distribution of the holding flock numbers by hatchery holding, per Member State and in the EU.

	Country	Fattening turkeys												
		Same holding		Same integration		Unrelated holding		Other MS		Third country		Unknown		Total	Missing
1	Austria	1	1%			117	99%							118	84
2	Belgium	2	3%	22	31%	40	57%					6	9%	70	4
3	Cyprus							14	100%					14	
4	Czech Republic			13	12%	83	78%	11	10%					107	87
5	Denmark							47	100%					47	12
7	Finland	4	3%			122	95%	3	2%					129	4
8	France											326	100%	326	
9	Germany	12	5%	28	11%	180	73%	17	7%			11	4%	248	47
10	Greece													0	43
11	Hungary			75	37%	109	54%	5	2%			13	6%	202	87
12	Ireland													0	259
13	Italy	7	5%	105	71%	18	12%	17	11%			1	1%	148	120
15	Lithuania							63	100%					63	
18	Poland					15	44%	19	56%					34	288
19	Portugal			33	31%	53	50%	17	16%	1	1%	1	1%	105	
20	Slovakia													0	25
21	Slovenia	2	2%	8	6%	8	6%	113	86%					131	
22	Spain													0	380
23	Sweden	1	7%			13	93%							14	
24	The Netherlands													0	172
25	The United Kingdom													0	317
27	Bulgaria													0	17
	European Union	29	2%	284	16%	758	43%	326	19%	1	0%	358	20%	1,756	1,946

	Country	Breeding turkeys												
		Same holding		Same integration		Unrelated holding		Other MS		Third country		Unknown		Total	Missing
4	Czech Republic							2	100%					2	2
7	Finland	2	13%					13	87%					15	
8	France											205	100%	205	
9	Germany	77	81%			7	7%	11	12%					95	3
10	Greece														6
11	Hungary							4	40%	6	60%			10	3
12	Ireland														2
13	Italy			5	23%			14	64%	2	9%	1	5%	22	6
18	Poland														6
20	Slovakia														21
22	Spain														10
23	Sweden	1	100%											1	
25	The United Kingdom														116
27	Bulgaria														7
	European Union	80	23%	5	1%	7	2%	44	13%	8	2%	206	59%	350	182

Figure 4.2-4 Weighted *Salmonella* **prevalence by hatchery holding in the EU (number of sampled flocks represented inside each bar).**
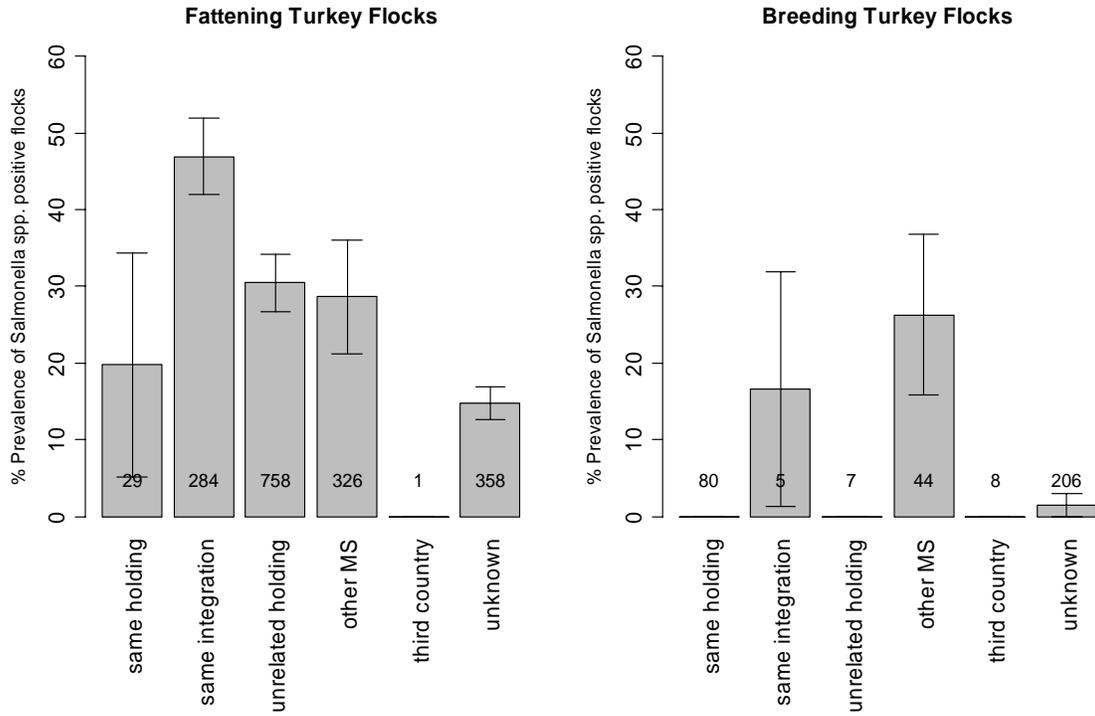
Table 4.2-4 Weighted *Salmonella* prevalence by hatchery holding and by flock production type in the EU.

Fattening turkeys				*Salmonella*			
	Holding of hatchery						
Frequency *Row Pct* Col Pct	Same holding	Same integration	Unrelated holding	Other MS	Third country	Unknown	Total
Negative	23 *1%* 80%	203 *12%* 53%	408 *25%* 70%	101 *6%* 71%	0 *0%* 100%	913 *55%* 85%	1648 *100%*
Positive	6 *1%* 20%	180 *32%* 47%	179 *32%* 30%	40 *7%* 29%	0 *0%* 0%	159 *28%* 15%	563 *100%*
Total	29 100%	384 100%	587 100%	141 100%	0 100%	1071 100%	2211

Breeding turkeys				*Salmonella*			
	Holding of hatchery						
Frequency *Row Pct* Col Pct	Same holding	Same integration	Unrelated holding	Other MS	Third country	Unknown	Total
Negative	30 *9%* 100%	19 *6%* 83%	8 *2%* 100%	50 *15%* 74%	10 *3%* 100%	214 *65%* 99%	331 *100%*
Positive	0 *0%* 0%	4 *15%* 17%	0 *0%* 0%	18 *72%* 26%	0 *0%* 0%	3 *13%* 1%	25 *100%*
Total	30 100%	23 100%	8 100%	68 100%	10 100%	217 100%	356

Figure 4.2-5 Estimated number of fattening and breeding turkey flocks by rearing holding and (weighted) *Salmonella* **outcome.**


Fattening Turkey Flocks

Weighted Salmonella spp negative
Weighted Salmonella spp positive

Breeding Turkey Flocks

Weighted Salmonella spp negative
Weighted Salmonella spp positive
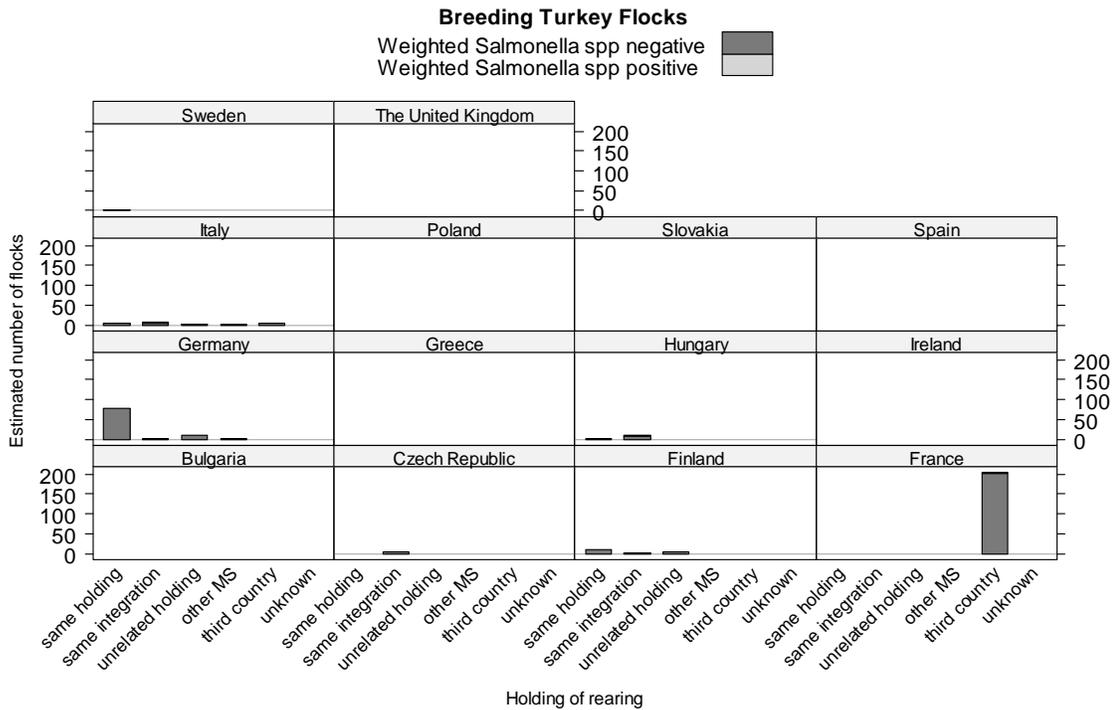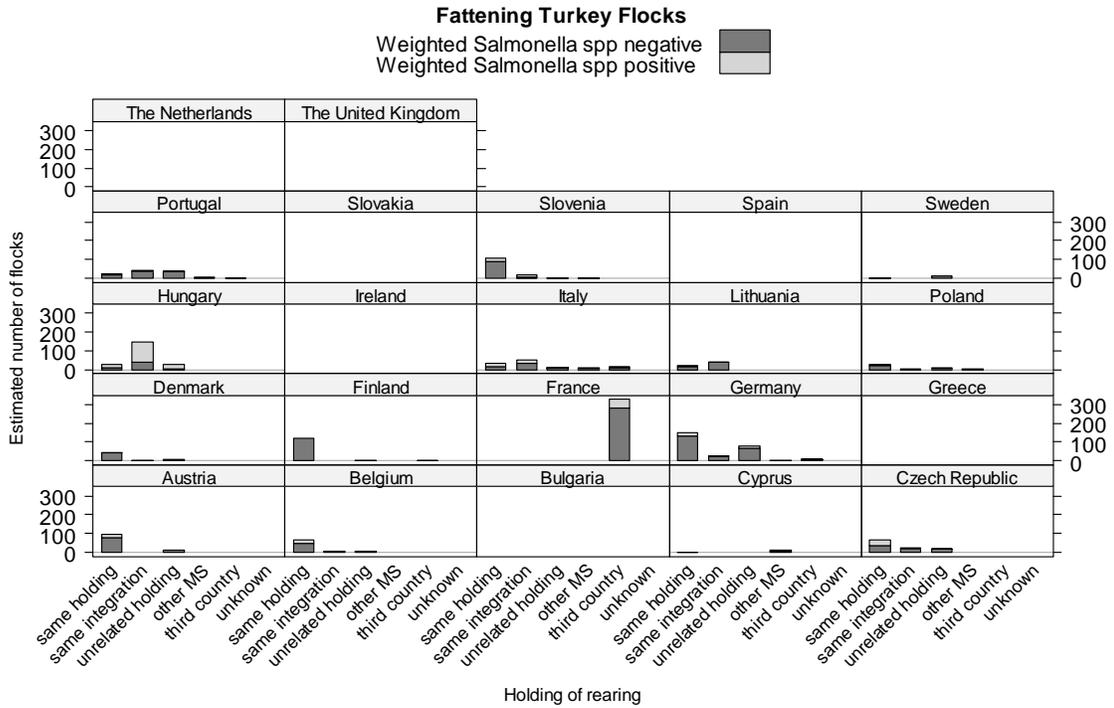
Table 4.2-5 Distribution of holding flock numbers by rearing holding, per Member State and in the EU.

	Country	Fattening turkeys											
		Same holding		Same integration		Unrelated holding		Other MS		Unknown		Total	Missing
1	Austria	110	92%			9	8%					119	83
2	Belgium	65	93%	3	4%	2	3%					70	4
3	Cyprus	1	7%					13	93%			14	
4	Czech Republic	49	46%	29	27%	29	27%					107	87
5	Denmark	41	87%	1	2%	5	11%					47	12
7	Finland	120	94%			5	4%			2	2%	127	6
8	France									326	100%	326	
9	Germany	142	56%	27	11%	79	31%	1	0%	6	2%	255	40
10	Greece												43
11	Hungary	34	17%	134	66%	34	17%					202	87
12	Ireland												259
13	Italy	36	29%	58	46%	10	8%	3	2%	18	14%	125	143
15	Lithuania	21	33%	42	67%							63	
18	Poland	23	68%	3	9%	5	15%	3	9%			34	288
19	Portugal	27	26%	35	33%	37	35%	5	5%	1	1%	105	
20	Slovakia												25
21	Slovenia	108	83%	18	14%	2	2%	2	2%			130	1
22	Spain												380
23	Sweden	1	7%			13	93%					14	
24	The Netherlands												172
25	The United Kingdom												317
27	Bulgaria												17
	European Union	778	45%	350	20%	230	13%	27	2%	353	20%	1,738	1,964

	Country	Breeding turkeys											
		Same holding		Same integration		Unrelated holding		Other MS		Unknown		Total	Missing
4	Czech Republic			2	100%							2	2
7	Finland	8	53%	1	7%	6	40%					15	
8	France									205	100%	205	
9	Germany	86	91%	3	3%	4	4%	1	1%			94	4
10	Greece												6
11	Hungary	1	10%	9	90%							10	3
12	Ireland												2
13	Italy	6	27%	11	50%	3	14%	1	5%	1	5%	22	6
18	Poland												6
20	Slovakia												21
22	Spain												10
23	Sweden	1	100%									1	
25	The United Kingdom												116
27	Bulgaria												7
	European Union	102	29%	26	7%	13	4%	2	1%	206	59%	349	183

Figure 4.2-6 Weighted *Salmonella* prevalence by rearing holding in the EU (number of sampled flocks represented inside each bar).
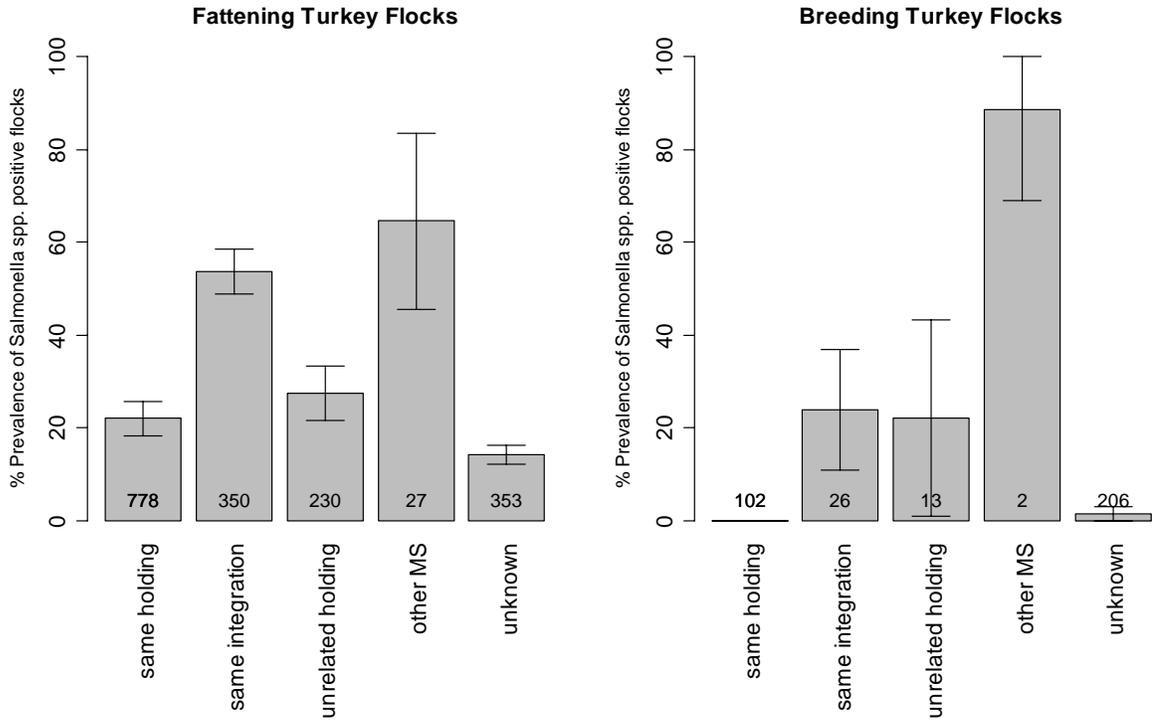
**Table 4.2-6 Weighted *Salmonella* prevalence by rearing holding and by flock production type in the EU.**

Fattening turkeys				*Salmonella*		
Frequency *Row Pct* Col Pct	Holding of rearing					
	Same holding	Same integration	Unrelated holding	Other MS	Unknown	Total
Negative	368 *22%* 78%	186 *11%* 46%	163 *10%* 73%	9 *1%* 35%	920 *56%* 86%	1,647 *100%*
Positive	104 *19%* 22%	215 *39%* 54%	62 *11%* 27%	16 *3%* 65%	153 *28%* 14%	550 *100%*
Total	472 100%	402 100%	225 100%	24 100%	1,073 100%	2,197

Breeding turkeys				*Salmonella*		
Frequency *Row Pct* Col Pct	Holding of rearing					
	Same holding	Same integration	Unrelated holding	Other MS	Unknown	Total
Negative	61 *18%* 100%	31 *9%* 76%	12 *3%* 78%	1 *0%* 11%	226 *68%* 99%	330 *100%*
Positive	0 *0%* 0%	10 *39%* 24%	3 *13%* 22%	9 *35%* 89%	3 *13%* 1%	25 *100%*
Total	61 100%	41 100%	15 100%	10 100%	229 100%	355

Figure 4.2-7 Estimated number of fattening and breeding turkey flocks by feed origin and (weighted) *Salmonella* **outcome.**
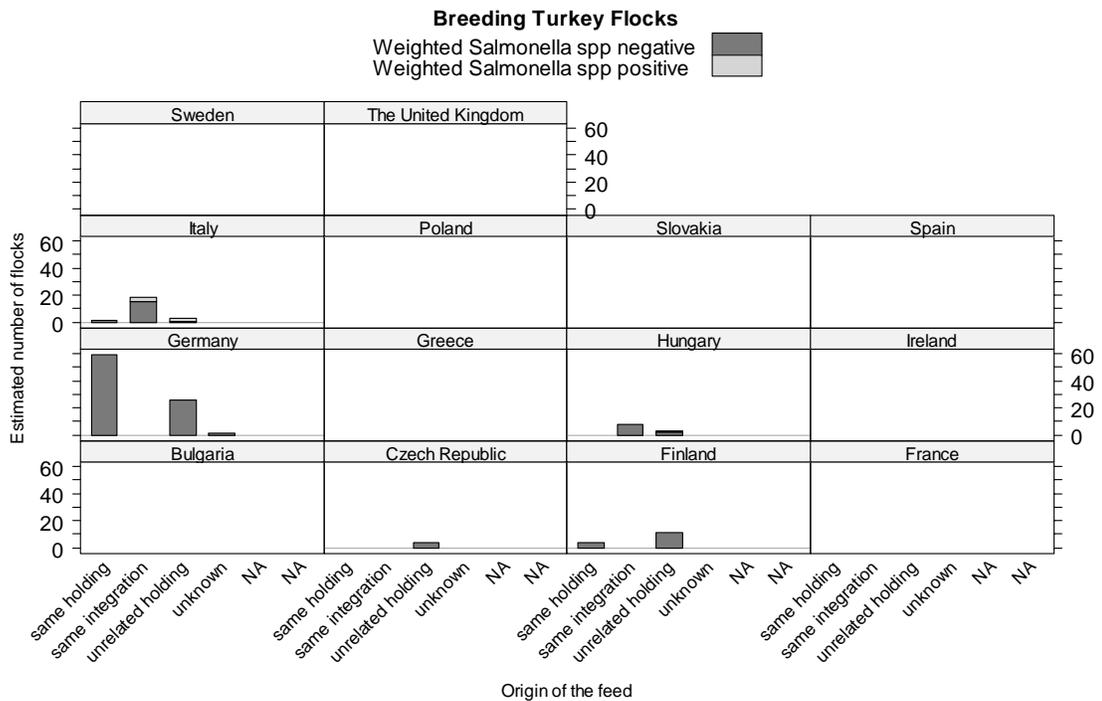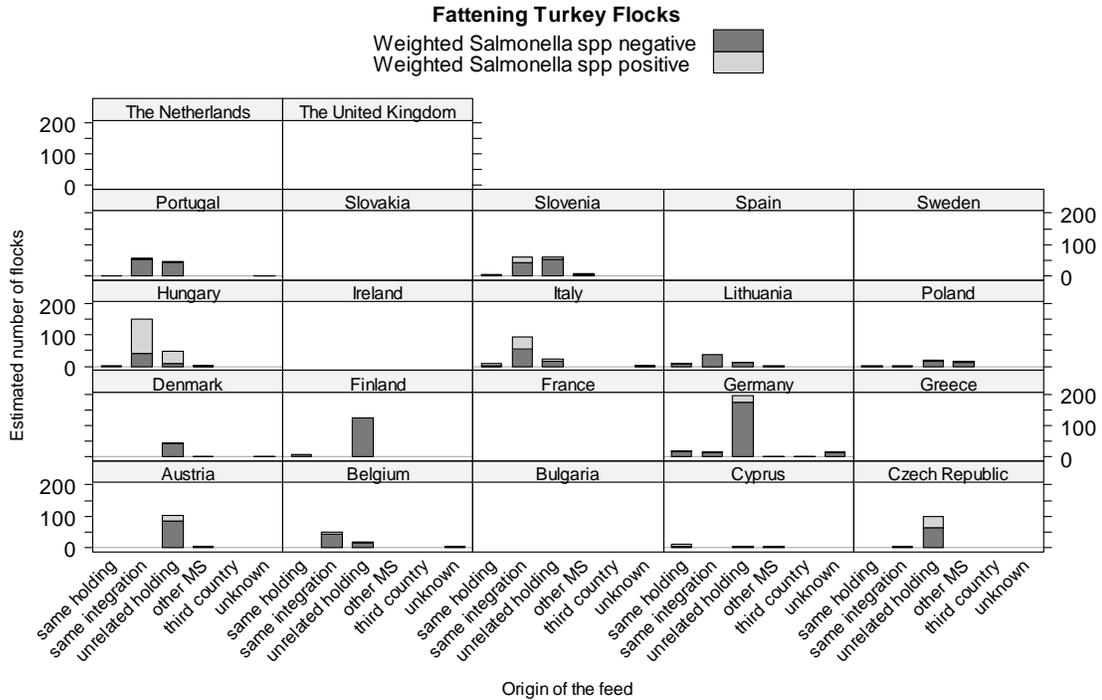
Table 4.2-7 Distribution of the holding flock number by feed origin, per Member State and in the EU.

Country		Fattening turkeys												
		Same holding		Same integration		Unrelated holding		Other MS		Third country		Unknown		Total	Missing
1	Austria					114	97%	4	3%					118	84
2	Belgium			43	61%	21	30%					6	9%	70	4
3	Cyprus	11	79%			2	14%	1	7%					14	
4	Czech Republic			2	2%	105	98%							107	87
5	Denmark					42	95%	1	2%			1	2%	44	15
7	Finland	5	4%			125	96%							130	3
8	France														326
9	Germany	18	7%	22	9%	187	76%	1	0%	1		16	7%	245	50
10	Greece														43
11	Hungary	3	1%	143	71%	52	26%	4	2%					202	87
12	Ireland														259
13	Italy	10	7%	109	75%	24	16%					3	2%	146	122
15	Lithuania	8	13%	36	57%	15	24%	4	6%					63	
18	Poland	3	9%	1	3%	17	50%	13	38%					34	288
19	Portugal	1	1%	58	55%	45	43%					1	1%	105	
20	Slovakia														25
21	Slovenia	5	4%	57	44%	63	48%	6	5%					131	
22	Spain														380
23	Sweden														14
24	The Netherlands														172
25	The United Kingdom														317
27	Bulgaria														17
	European Union	64	5%	471	33%	812	58%	34	2%	1	0%	27	2%	1,409	2,293

Country		Breeding turkeys									
		Same holding		Same integration		Unrelated holding		Unknown		Total	Missing
4	Czech Republic					2	100%			2	2
7	Finland	1	7%			14	93%			15	
8	France										205
9	Germany	76	84%			13	14%	1	1%	90	8
10	Greece										6
11	Hungary			7	70%	3	30%			10	3
12	Ireland										2
13	Italy	1	5%	19	86%	2	9%			22	6
18	Poland										6
20	Slovakia										21
22	Spain										10
23	Sweden										1
25	The United Kingdom										116
27	Bulgaria										7
	European Union	78	56%	26	19%	34	24%	1	1%	139	393

Figure 4.2-8 Weighted *Salmonella* **prevalence by feed origin in the EU (number of sampled flocks represented inside each bar).**
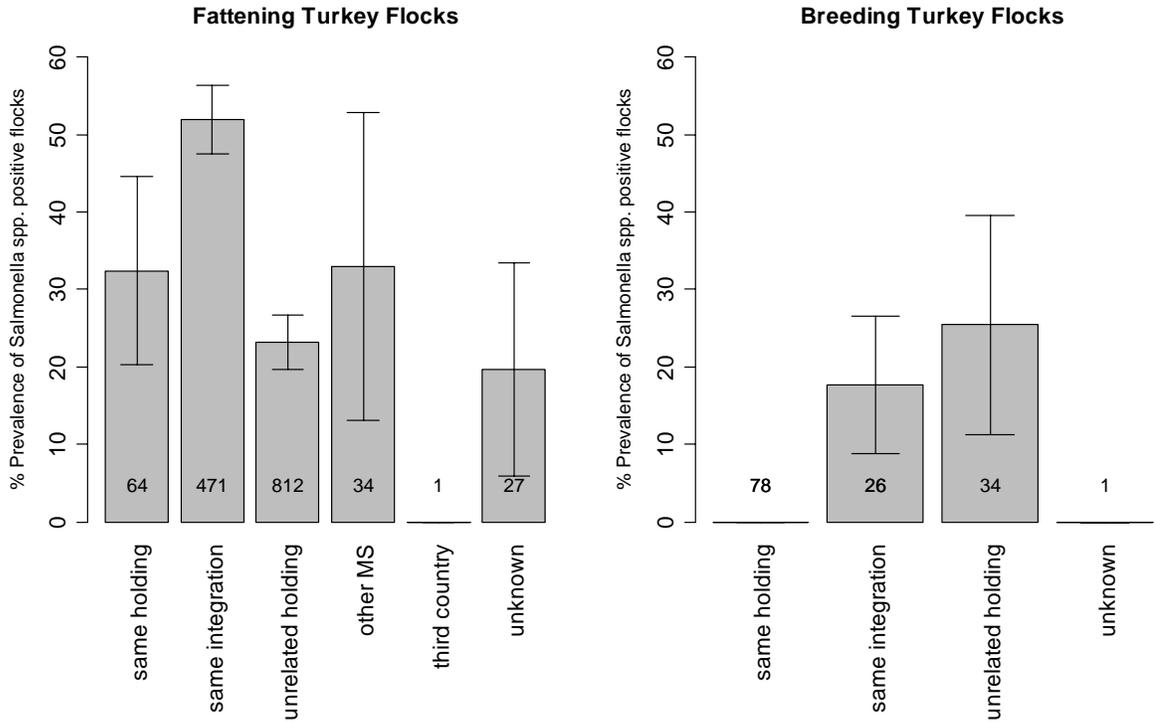
Table 4.2-8 Weighted *Salmonella* prevalence by feed origin and by flock production type in the EU.

Fattening turkeys				*Salmonella*			
	Origin of the feed						
Frequency *Row Pct* Col Pct	Same holding	Same integration	Unrelated holding	Other MS	Third country	Unknown	Total
Negative	39 *5%* 68%	234 *31%* 48%	430 *58%* 77%	14 *2%* 67%	4 *1%* 100%	26 *3%* 80%	747 *100%*
Positive	19 *4%* 32%	252 *61%* 52%	130 *31%* 23%	7 *2%* 33%	0 *0%* 0%	6 *2%* 20%	414 *100%*
Total	57 100%	486 100%	560 100%	22 100%	4 100%	32 100%	1,161

Breeding turkeys			*Salmonella*		
	Origin of the feed				
Frequency *Row Pct* Col Pct	Same holding	Same integration	Unrelated holding	Unknown	Total
Negative	32 *27%* 100%	58 *50%* 82%	27 *23%* 75%	1 *0%* 100%	118 *100%*
Positive	0 *0%* 0%	12 *57%* 18%	9 *43%* 25%	0 *0%* 0%	22 *100%*
Total	32 100%	71 100%	36 100%	1 100%	139

Figure 4.2-9 Estimated number of fattening and breeding turkey flocks under antimicrobial treatment and (weighted) Salmonella outcome.
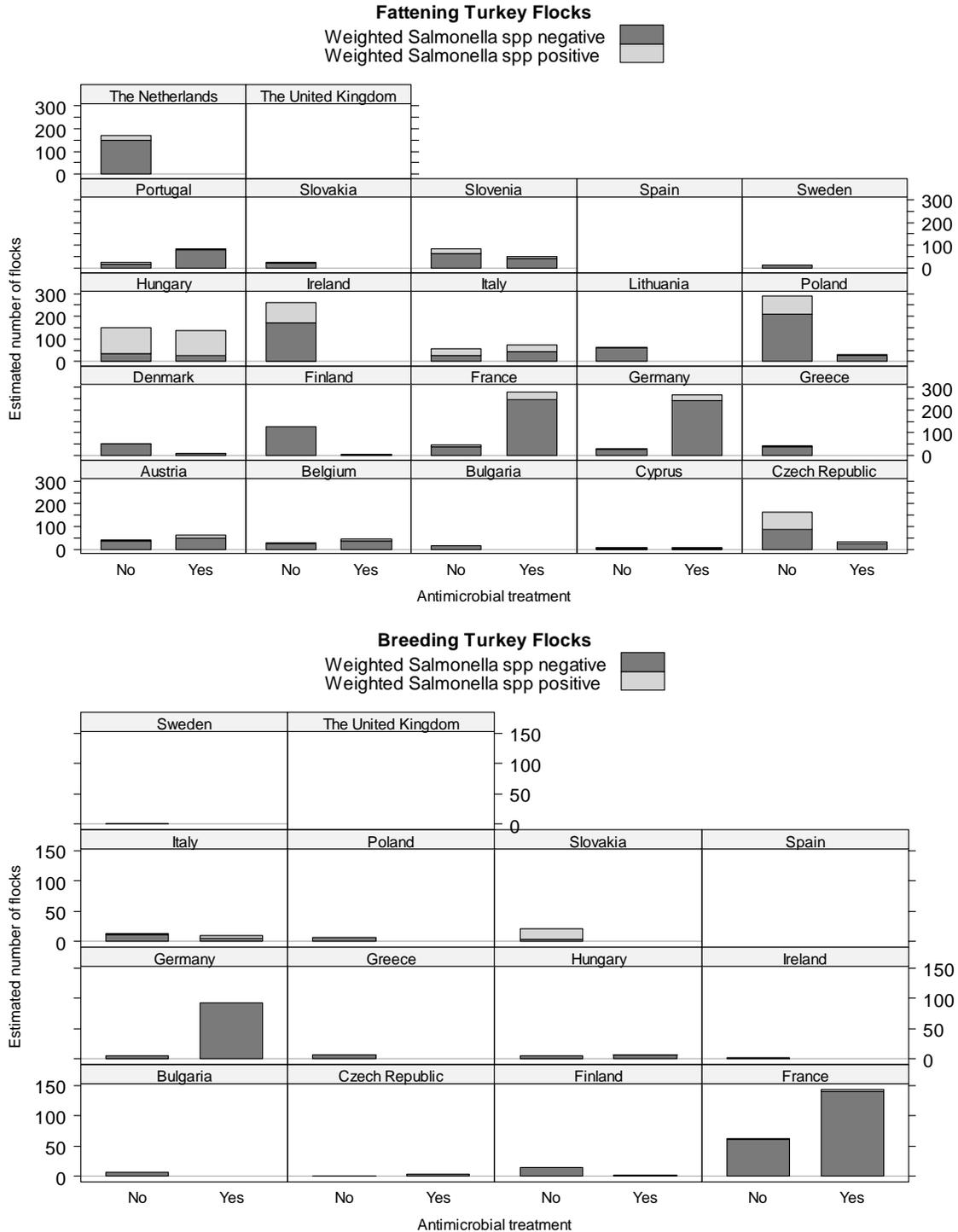
Table 4.2-9 Distribution of the number of flocks in holding under antimicrobial treatment, per Member State and in the EU.

	Country	Fattening turkeys No		Yes		Total	Missing	Breeding turkeys No		Yes		Total	Missing
1	Austria	44	38%	72	62%	116	86						
2	Belgium	23	31%	51	69%	74							
3	Cyprus	9	64%	5	36%	14							
4	Czech Republic	163	84%	31	16%	194		2	50%	2	50%	4	
5	Denmark	55	93%	4	7%	59							
7	Finland	127	95%	6	5%	133		14	93%	1	7%	15	
8	France	60	18%	266	82%	326		69	34%	136	66%	205	
9	Germany	25	8%	270	92%	295		5	5%	93	95%	98	
10	Greece	43	100%			43		6	100%			6	
11	Hungary	153	53%	136	47%	289		7	54%	6	46%	13	
12	Ireland	259	100%			259		2	100%			2	
13	Italy	51	38%	84	62%	135	133	16	76%	5	24%	21	7
15	Lithuania	63	100%			63							
18	Poland	296	92%	26	8%	322		6	100%			6	
19	Portugal	27	26%	78	74%	105							
20	Slovakia	25	100%			25		21	100%			21	
21	Slovenia	88	67%	43	33%	131							
22	Spain					0	380						10
23	Sweden	14	100%			14		1	100%			1	
24	The Netherlands	172	100%			172							
25	The United Kingdom					0	317						116
27	Bulgaria	17	100%			17		7	100%			7	
	European Union	1,714	62%	1,072	38%	2,786	916	156	39%	243	61%	399	133

Figure 4.2-10 Weighted *Salmonella* prevalence under antimicrobial treatment in the EU (number of sampled flocks represented inside each bar).
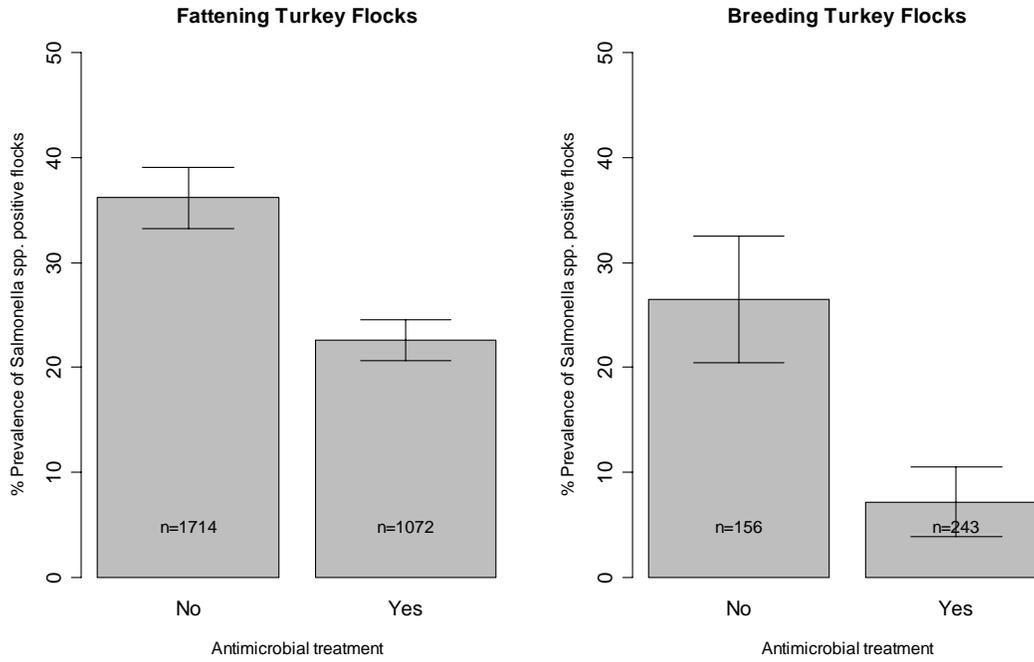
Table 4.2-10 Weighted *Salmonella* prevalence under antimicrobial treatment, by flock production type in the EU.

Fattening turkeys	*Salmonella*		
Frequency *Row Pct* Col Pct	Antimicrobial treatment		
	No	Yes	Total
Negative	682 *33%* 64%	1,362 *67%* 77%	2,044 *100%*
Positive	387 *49%* 36%	397 *51%* 23%	783 *100%*
Total	1,069 100%	1,758 100%	2,827

Breeding turkeys	*Salmonella*		
Frequency *Row Pct* Col Pct	Antimicrobial treatment		
	No	Yes	Total
Negative	149 *41%* 74%	217 *59%* 93%	366 *100%*
Positive	54 *76%* 26%	17 *24%* 7%	70 *100%*
Total	202 100%	234 100%	436

	Chi-square statistic (p-value)	
Salmonella	Fattening	Breeding
	61.4 (<0.001)	29.9 (<0.001)

Figure 4.2-11 Central tendency and distribution of thinnings number, by Member State (number of sampled flocks between brackets).

Fattening Turkeys Flocks

Breeding Turkey Flocks
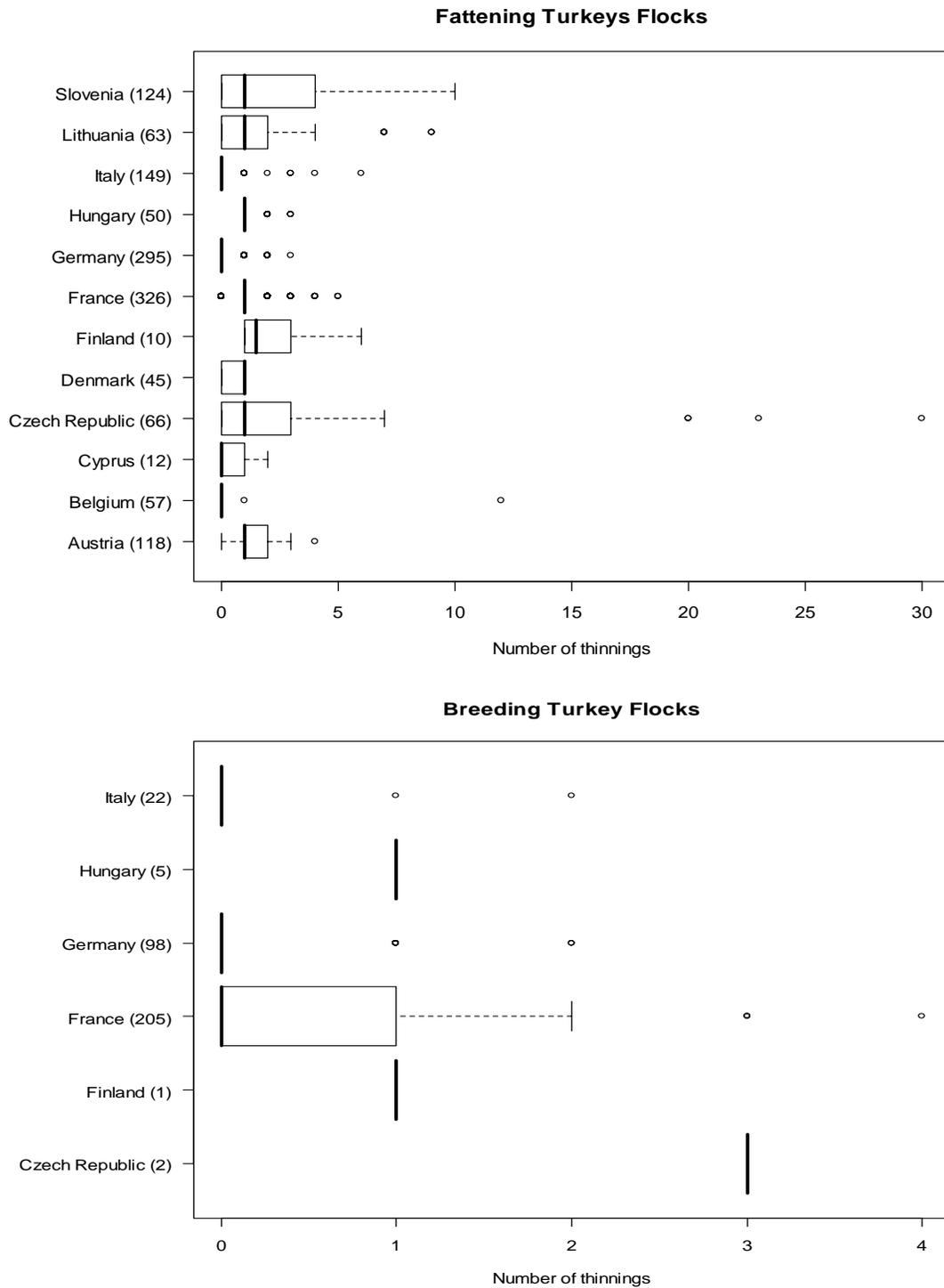
Table 4.2-11 Central tendency (mean, median) and dispersion measures (standard deviation and quantiles) thinnings number.

	Country	Fattening turkeys						Breeding turkeys					
		Q1	Median	Q3	Mean	StD	No. of flocks available	Q1	Median	Q3	Mean	StD	No. of flocks available
1	Austria	1	1	2	1.4	0.8	118						
2	Belgium	0	0	0	0.2	1.6	57						
3	Cyprus	0	0	1	0.5	0.9	12						
4	Czech Republic	0	1	3	3.3	5.6	66	3	3	3	3.0	0.0	2
5	Denmark	0	1	1	0.6	0.5	45						
7	Finland	1	1.5	3	2.1	1.6	10	1	1	1	1.0	.	1
8	France	1	1	1	1.1	0.8	326	0	0	1	0.5	0.8	205
9	Germany	0	0	0	0.3	0.5	295	0	0	0	0.1	0.4	98
10	Greece	.	.	.	.	.		.	.	.	.	.	
11	Hungary	1	1	1	1.2	0.5	50	1	1	1	1.0	0.0	5
12	Ireland	.	.	.	.	.		.	.	.	.	.	
13	Italy	0	0	0	0.2	0.7	149	0	0	0	0.1	0.5	22
15	Lithuania	0	1	2	1.7	2.3	63						
18	Poland	.	.	.	.	.		.	.	.	.	.	
19	Portugal	.	.	.	.	.							
20	Slovakia	.	.	.	.	.		.	.	.	.	.	
21	Slovenia	0	1	4	2.0	2.6	124						
22	Spain	.	.	.	.	.		.	.	.	.	.	
23	Sweden	.	.	.	.	.		.	.	.	.	.	
24	The Netherlands	.	.	.	.	.							
25	The United Kingdom	.	.	.	.	.		.	.	.	.	.	
27	Bulgaria	.	.	.	.	.		.	.	.	.	.	
	European Union	0	1	1	1.0	1.9	1,315	0	0	1	0.4	0.7	333

Figure 4.2-12 Number of thinnings by observed *Salmonella* in the EU (number of sampled flocks between brackets).
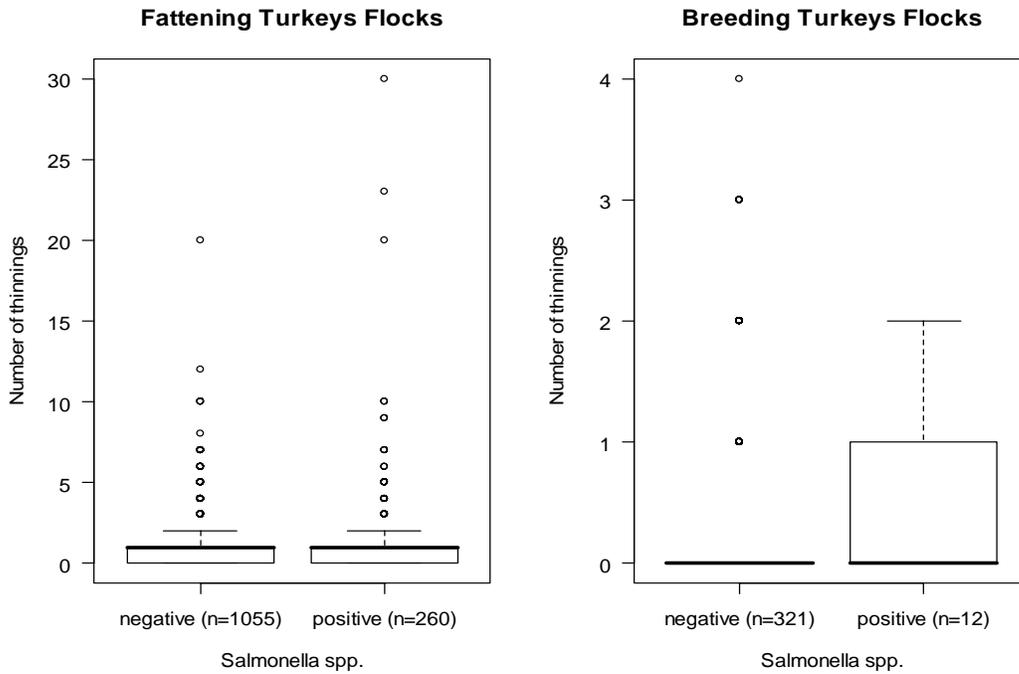
Table 4.2-12 Odds ratio estimates and corresponding 95% confidence intervals obtained from a logistic regression, modelling the weighted probability of observing a positive flock using an intercept and the number of thinnings, by flock production type.

Turkeys in holding	Outcome of interest	Estimate	LB	UB
Fattening turkeys	*Salmonella*	1.692	1.132	2.527
Breeding turkeys	*Salmonella*	0.985	0.881	1.101

Figure 4.2-13 Central tendency and distribution of the number of days to first thinning, by Member State (number of sampled flocks between brackets).

Fattening Turkeys Flocks

Number of days to first thinning

Breeding Turkey Flocks

Number of days to first thinning
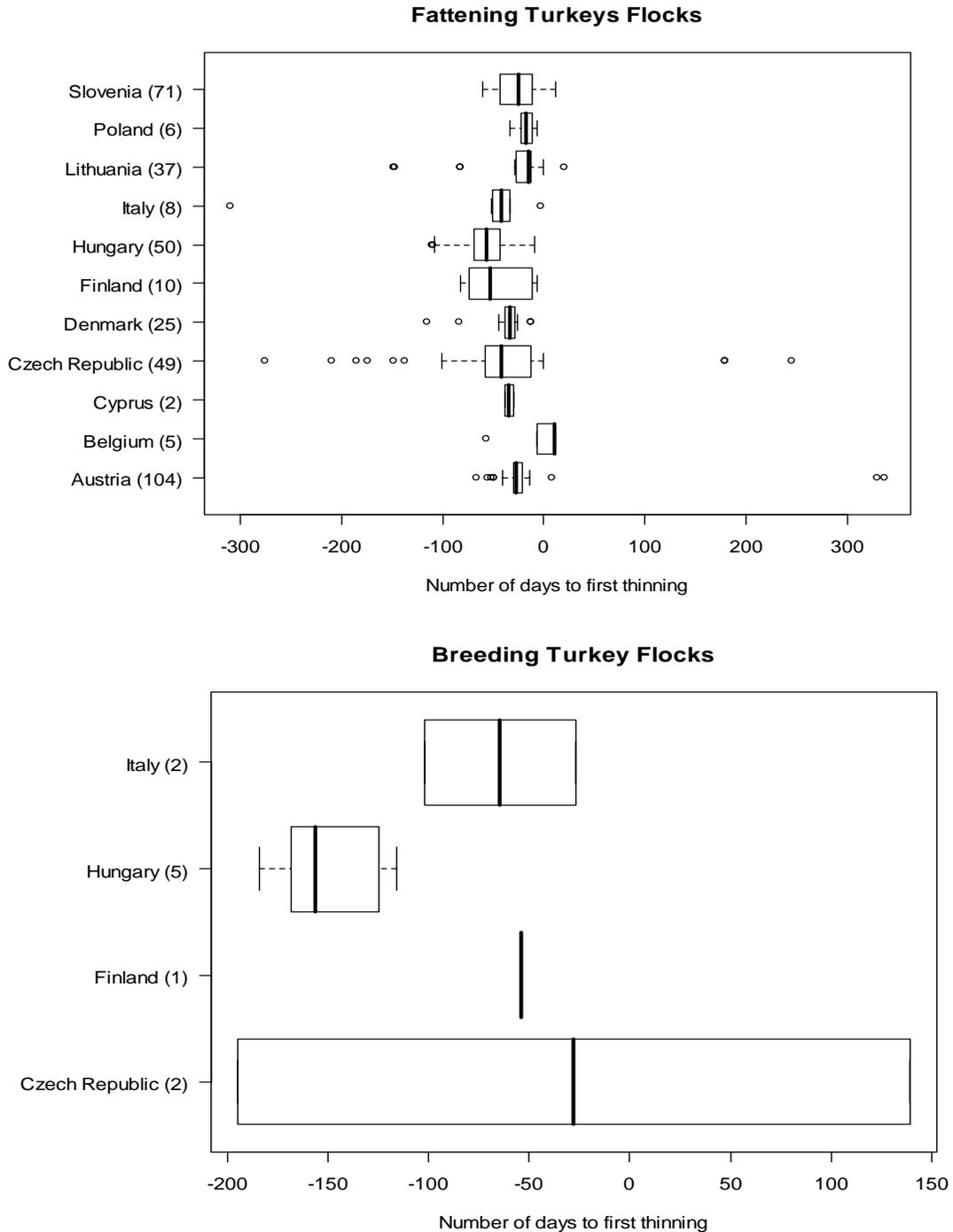
Table 4.2-13 Central tendency (mean, median) and dispersion measures (standard deviation and quantiles) of number of days to first thinning.

	Country	Fattening turkeys						Breeding turkeys					
		Q1	Median	Q3	Mean	StD	No. of flocks available	Q1	Median	Q3	Mean	StD	No. of flocks available
1	Austria	-30	-27	-21	-19.9	50.5	104						
2	Belgium	-7	10	12	-6.0	29.6	5						
3	Cyprus	-39	-35	-30	-34.5	6.4	2						
4	Czech Republic	-58	-42	-13	-40.2	85.2	49	-195	-28	139	-28.0	236.2	2
5	Denmark	-38	-34	-29	-37.6	20.6	25						
7	Finland	-74	-53	-12	-45.6	32.5	10	-54	-54	-54	-54.0	.	1
8	France	.	.	.	.	.		.	.	.	.	.	
9	Germany	.	.	.	.	.		.	.	.	.	.	
10	Greece	.	.	.	.	.		.	.	.	.	.	
11	Hungary	-69	-57	-43	-60.3	24.5	50	-168	-156	-125	-149.8	28.7	5
12	Ireland	.	.	.	.	.		.	.	.	.	.	
13	Italy	-51	-43	-34	-70.9	97.8	8	-102	-64.5	-27	-64.5	53.0	2
15	Lithuania	-27	-15	-13	-26.8	34.1	37						
18	Poland	-23	-18	-12	-18.5	9.4	6	.	.	.	.	.	
19	Portugal	.	.	.	.	.							
20	Slovakia	.	.	.	.	.		.	.	.	.	.	
21	Slovenia	-44	-25	-11	-26.1	18.3	71	.	.	.	.	.	
22	Spain	.	.	.	.	.		.	.	.	.	.	
23	Sweden	.	.	.	.	.							
24	The Netherlands	.	.	.	.	.		.	.	.	.	.	
25	The United Kingdom	.	.	.	.	.		.	.	.	.	.	
27	Bulgaria	.	.	.	.	.		.	.	.	.	.	
	European Union	-45	-28	-17	-32.9	49.0	367	-168	-120.5	-54	-98.8	99.6	10

Figure 4.2-14 Number of days to first thinning in *Salmonella* negative and positive flocks, in the EU (number of sampled flocks between brackets).

Fattening Turkeys Flocks

Breeding Turkeys Flocks
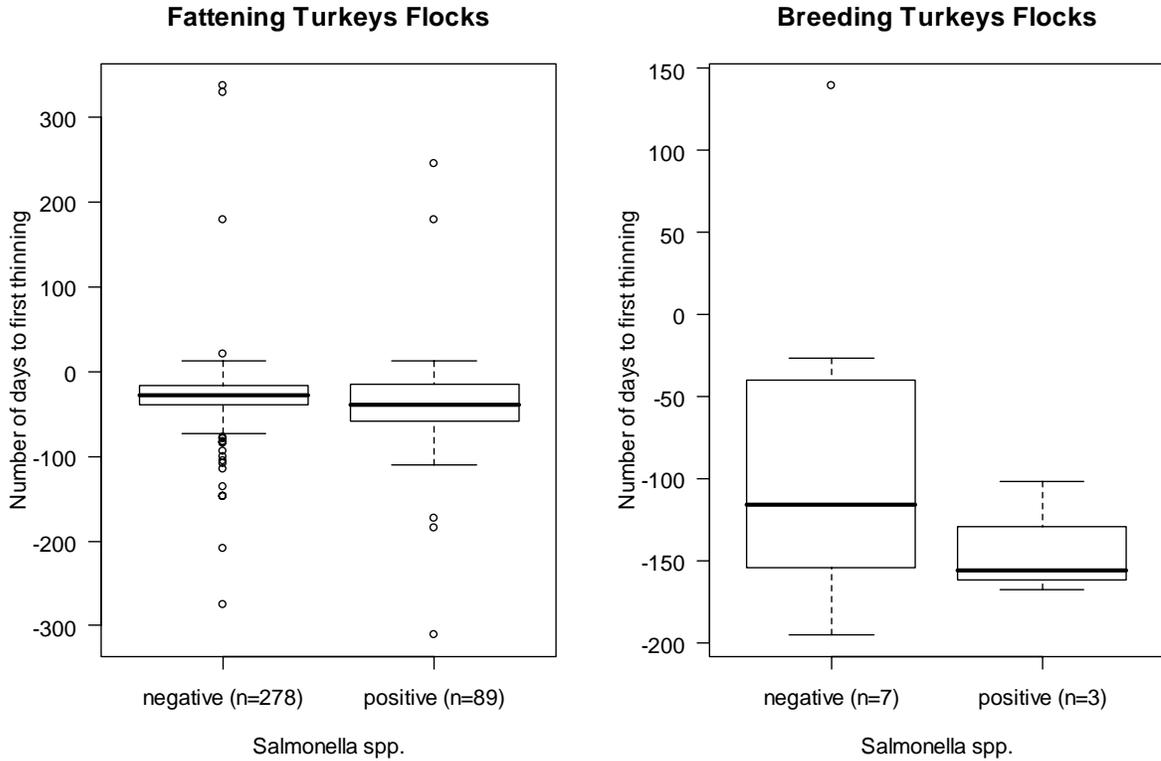
Table 4.2-14 Odds ratio estimates and corresponding 95% confidence intervals obtained from a logistic regression, modelling the weighted probability of observing a positive flock using an intercept and the number of days to first thinning, by flock production type.

Turkeys in holding	Outcome of interest	Estimate	LB	UB
Fattening turkeys	*Salmonella*	0.999	0.989	1.009
Breeding turkeys	*Salmonella*	0.987	0.987	0.997

Figure 4.2-15 Estimated number of fattening and breeding turkey flocks by all in/all out flock and (weighted) *Salmonella* **outcome.**
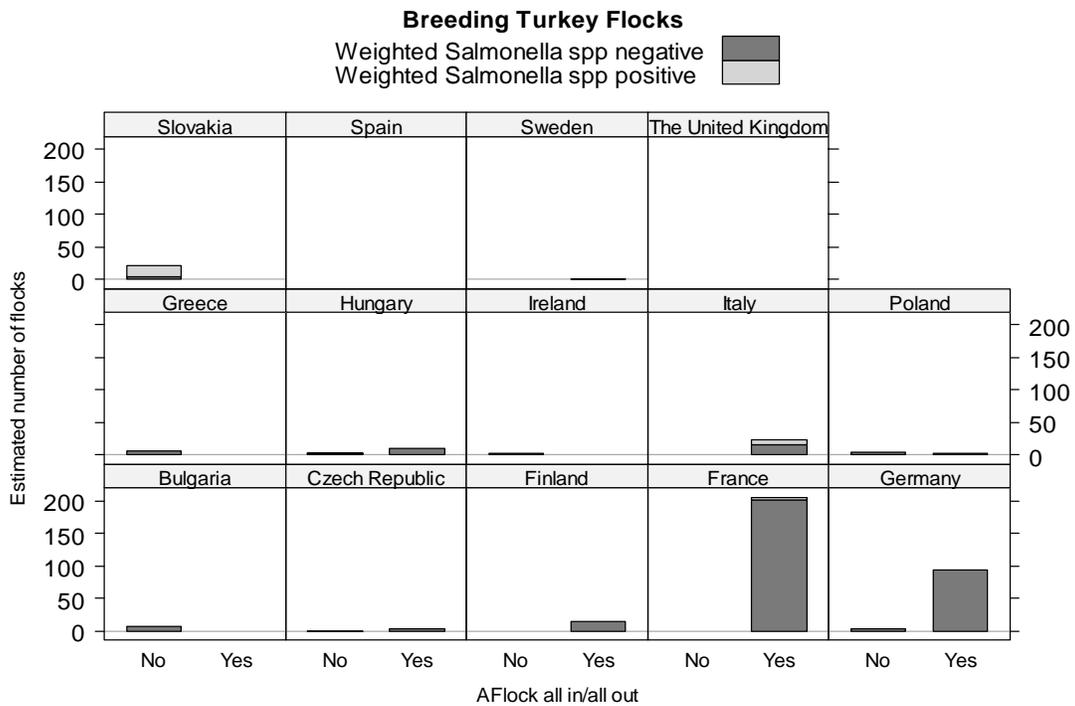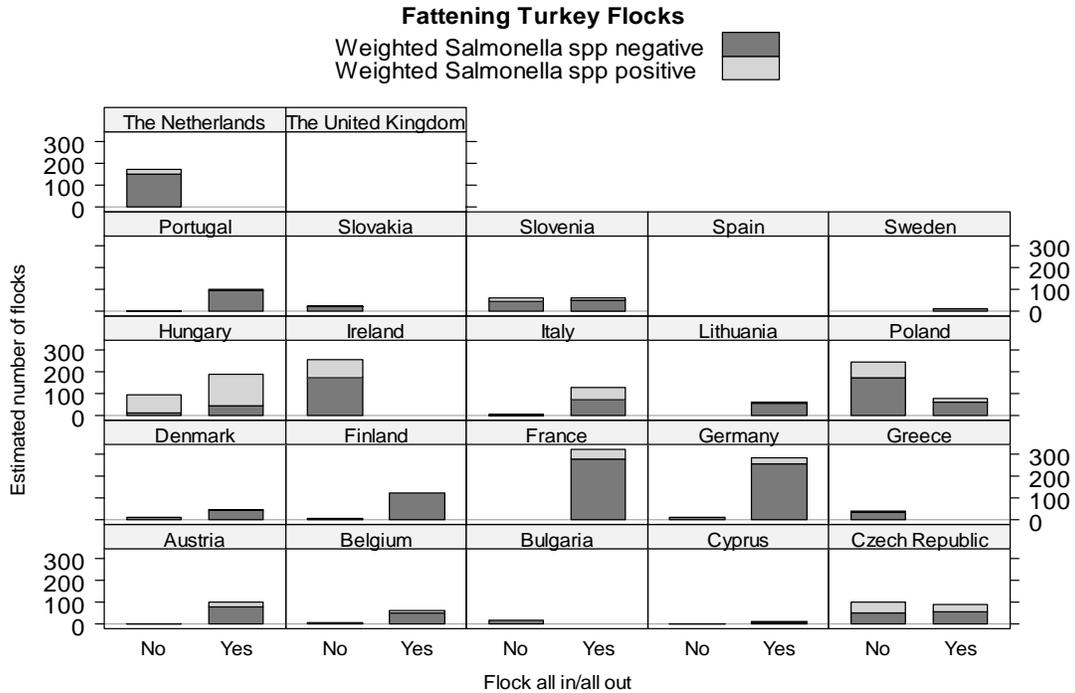
Table 4.2-15 Distribution of the number of flocks in holding by all in/all out flock, per Member State and in the EU.

	Country	Fattening turkeys						Breeding turkeys					
		No		Yes		Total	Missing	No		Yes		Total	Missing
1	Austria	2	2%	115	98%	117	85						
2	Belgium	8	11%	66	89%	74							
3	Cyprus	2	14%	12	86%	14							
4	Czech Republic	102	53%	92	47%	194		2	50%	2	50%	4	
5	Denmark	14	24%	45	76%	59							
7	Finland	10	8%	123	92%	133				15	100%	15	
8	France			326	100%	326				205	100%	205	
9	Germany	13	4%	282	96%	295		3	3%	95	97%	98	
10	Greece	43	100%			43		6	100%			6	
11	Hungary	96	33%	193	67%	289		5	38%	8	62%	13	
12	Ireland	259	100%			259		2	100%			2	
13	Italy	6	4%	140	96%	146	122			22	100%	22	6
15	Lithuania			63	100%	63							
18	Poland	242	75%	80	25%	322		4	67%	2	33%	6	
19	Portugal	1	1%	104	99%	105							
20	Slovakia	25	100%			25		21	100%			21	
21	Slovenia	59	45%	72	55%	131							
22	Spain					0	380					0	10
23	Sweden			14	100%	14		1	100%			1	
24	The Netherlands	172	100%			172							
25	The United Kingdom					0	317					0	116
27	Bulgaria	17	100%			17		7	100%			7	
	European Union	1,071	38%	1,727	62%	2,798	904	51	13%	349	87%	400	132

Figure 4.2-16 Weighted *Salmonella* prevalence by all in/all out flock in the EU (number of sampled flocks represented inside each bar).
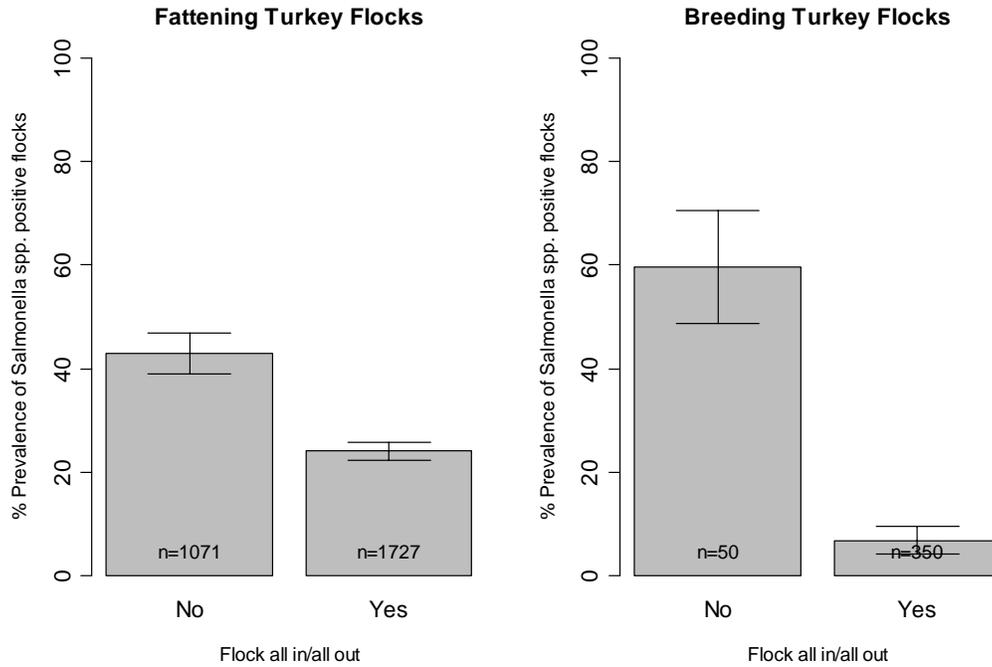
Table 4.2-16 Weighted *Salmonella* prevalence by all in/all out flock and by flock production type in the EU.

Fattening turkeys	*Salmonella*		
Frequency *Row Pct* Col Pct	Flock all in/all out		
	No	Yes	Total
Negative	337 *16%* 57%	1,709 *84%* 76%	2,046 *100%*
Positive	253 *32%* 43%	540 *68%* 24%	793 *100%*
Total	590 100%	2249 100%	2,839

Breeding turkeys	*Salmonella*		
Frequency *Row Pct* Col Pct	Flock all in/all out		
	No	Yes	Total
Negative	31 *8%* 40%	335 *92%* 93%	366 *100%*
Positive	46 *65%* 60%	24 *35%* 7%	70 *100%*
Total	77 100%	359 100%	436

	Chi-square statistic (p-value)	
Salmonella	Fattening	Breeding
	82.8 (<0.001)	131.0 (<0.001)

Figure 4.2-17 Estimated number of fattening and breeding turkey flocks by all in/all out holding and (weighted) *Salmonella* outcome.

Fattening Turkey Flocks

Breeding Turkey Flocks
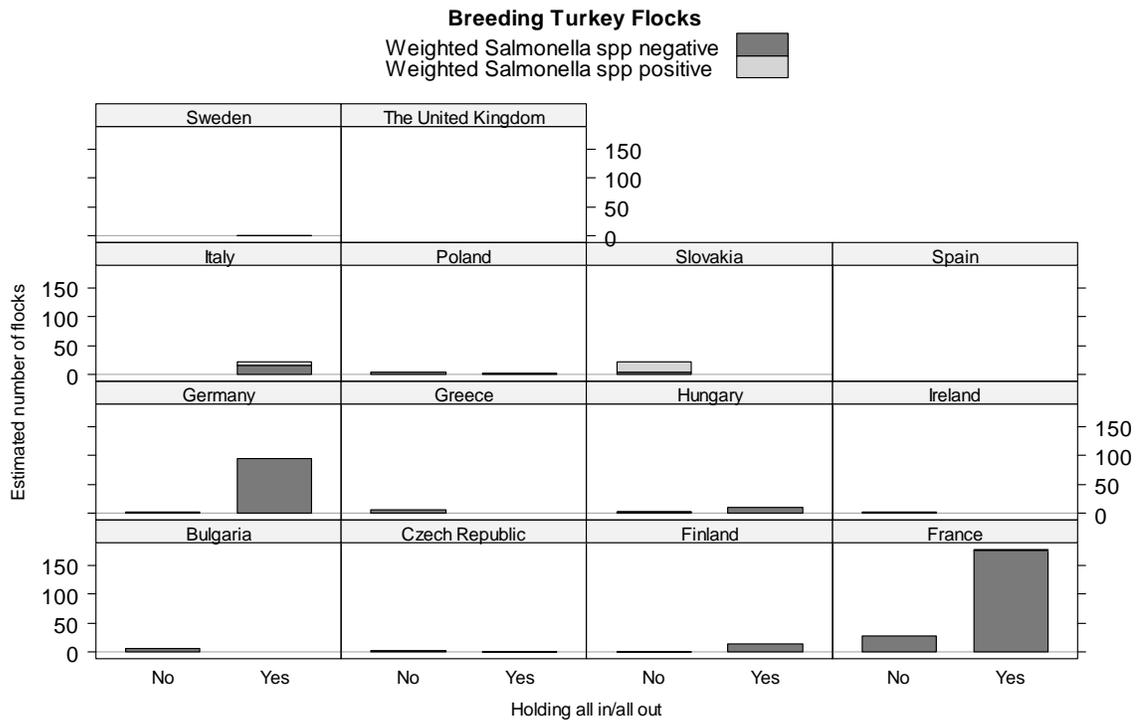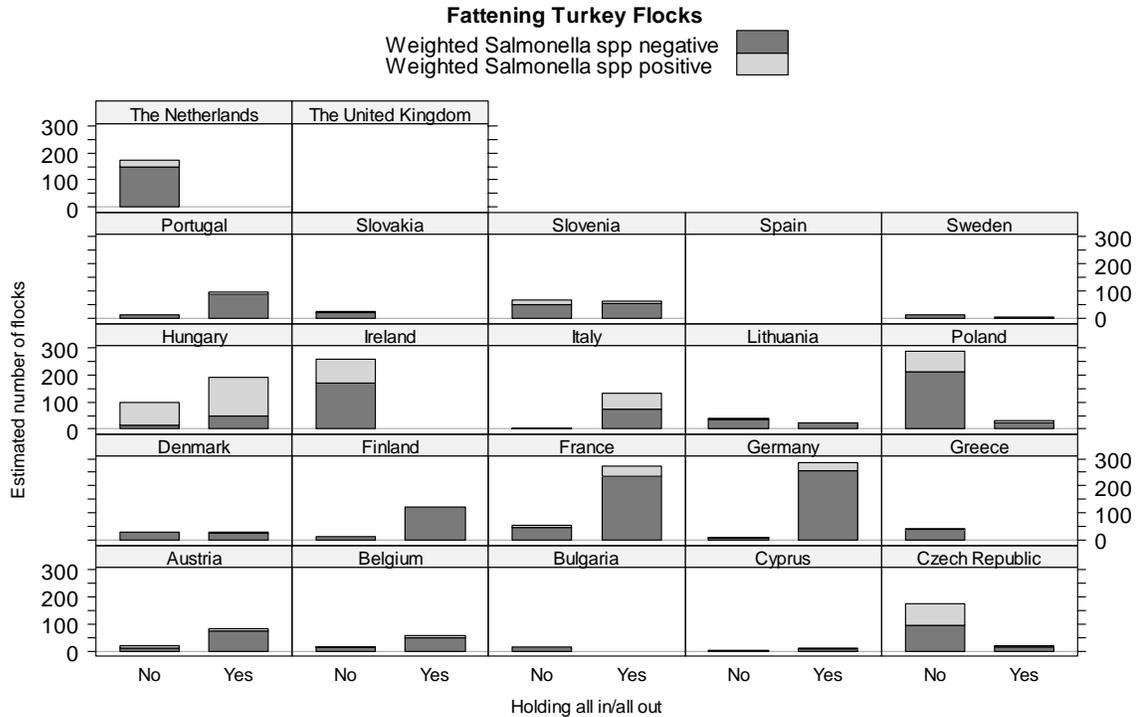
Table 4.2-17 Distribution of the holding flock numbers by all in/all out holding, per Member State and in the EU.

	Country	Fattening turkeys							Breeding turkeys						
		No		Yes		Total	Missing		No		Yes		Total	Missing	
1	Austria	16	14%	101	86%	117	85								
2	Belgium	14	19%	60	81%	74									
3	Cyprus	2	14%	12	86%	14									
4	Czech Republic	160	82%	34	18%	194			3	75%	1	25%	4		
5	Denmark	29	49%	30	51%	59									
7	Finland	15	11%	118	89%	133			2	13%	13	87%	15		
8	France	28	9%	298	91%	326			14	7%	191	93%	205		
9	Germany	15	5%	280	95%	295			2	2%	96	98%	98		
10	Greece	43	100%			43			6	100%			6		
11	Hungary	99	34%	190	66%	289			5	38%	8	62%	13		
12	Ireland	259	100%			259			2	100%			2		
13	Italy	4	3%	142	97%	146	122				22	100%	22	6	
15	Lithuania	40	63%	23	37%	63									
18	Poland	271	84%	51	16%	322			4	67%	2	33%	6		
19	Portugal	9	9%	96	91%	105									
20	Slovakia	25	100%			25			21	100%			21		
21	Slovenia	61	47%	70	53%	131									
22	Spain					0	380						0	10	
23	Sweden	11	79%	3	21%	14					1	100%	1		
24	The Netherlands	172	100%			172									
25	The United Kingdom					0	317						0	116	
27	Bulgaria	17	100%			17			7	100%			7		
	European Union	1,290	46%	1,508	54%	2,798	904		66	17%	334	84%	400	132	

Figure 4.2-18 Weighted *Salmonella* prevalence by all in/all out holding in the EU (number of sampled flocks represented inside each bar).
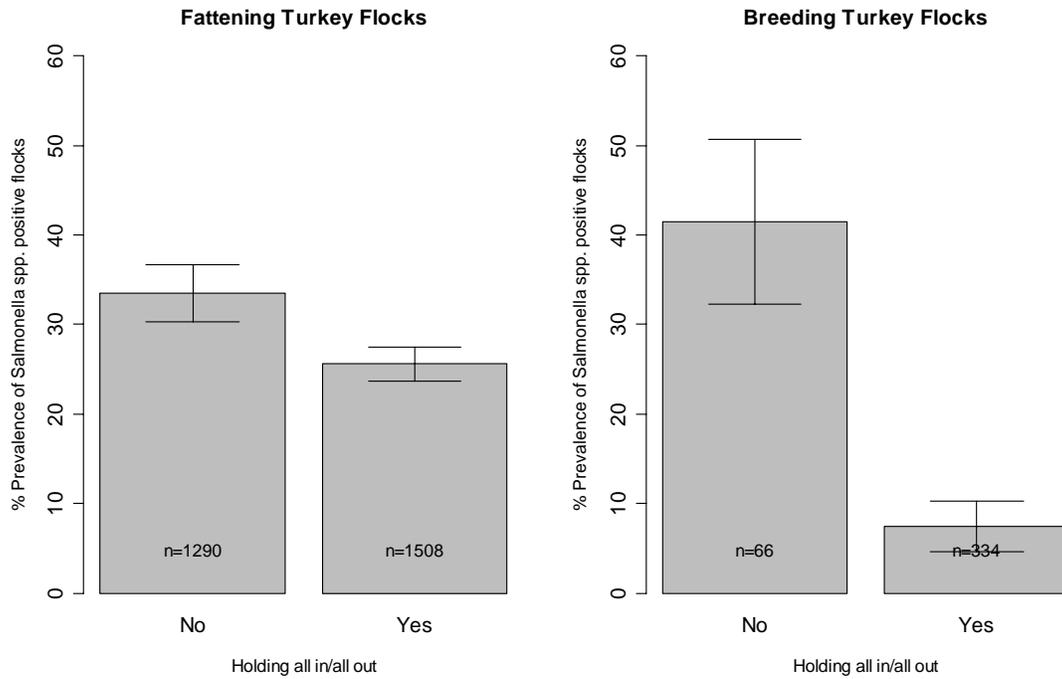
Table 4.2-18 Weighted *Salmonella* prevalence by all in/all out holding, by flock production type in the EU.

Fattening turkeys	*Salmonella*		
Frequency *Row Pct* Col Pct	Holding all in/all out		
	No	Yes	Total
Negative	551 *27%* 67%	1,496 *73%* 74%	2,047 *100%*
Positive	278 *35%* 33%	514 *65%* 26%	792 *100%*
Total	829 100%	2,010 100%	2,839

Breeding turkeys	*Salmonella*		
Frequency *Row Pct* Col Pct	Holding all in/all out		
	No	Yes	Total
Negative	65 *18%* 58%	301 *82%* 93%	366 *100%*
Positive	46 *65%* 42%	24 *35%* 7%	70 *100%*
Total	111 100%	326 100%	436

Salmonella	Chi-square statistic (p-value)	
	Fattening	Breeding
	18.2 (<0.001)	70.8 (<0.001)

Figure 4.2-19 Estimated number of fattening and breeding turkey flocks by time between flocks and (weighted) *Salmonella* outcome.
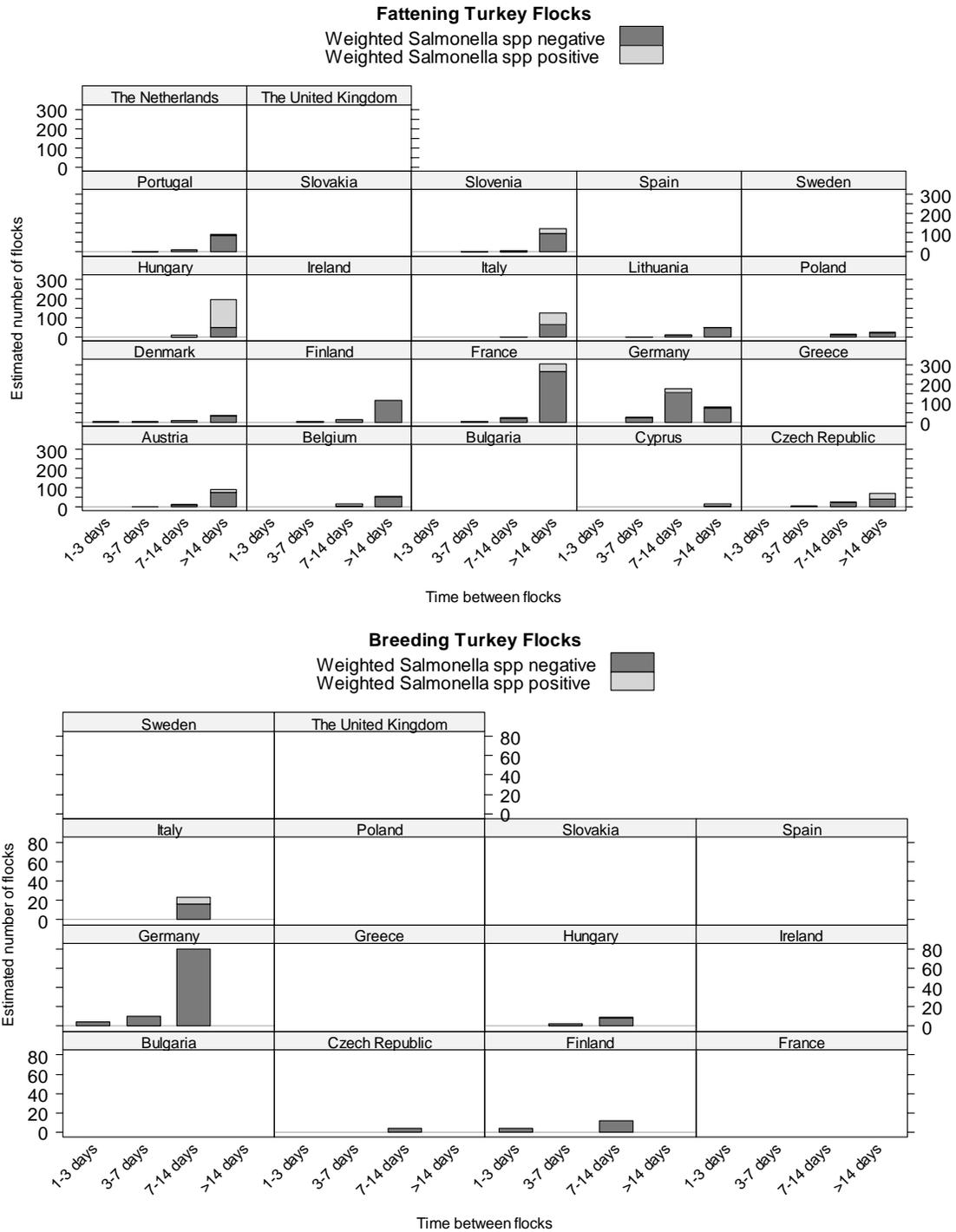
Table 4.2-19 Distribution of the holding flock numbers by time between flocks, per Member State and in the EU.

	Country	Fattening turkeys									
		1- 3 days		3 - 7 days		7 - 14 days		Over 14 days		Total	Missing
1	Austria			2	2%	14	12%	103	87%	119	83
2	Belgium					13	18%	58	82%	71	3
3	Cyprus							14	100%	14	
4	Czech Republic			4	4%	26	25%	73	71%	103	91
5	Denmark	4	9%	2	4%	8	18%	31	69%	45	14
7	Finland			2	2%	11	9%	111	90%	124	9
8	France			1	0%	19	6%	306	94%	326	
9	Germany			17	6%	167	61%	89	33%	273	22
10	Greece										43
11	Hungary					8	4%	194	96%	202	87
12	Ireland										259
13	Italy					1	1%	132	99%	133	135
15	Lithuania			1	2%	10	16%	52	83%	63	
18	Poland					9	26%	25	74%	34	288
19	Portugal			2	2%	8	8%	95	90%	105	
20	Slovakia										25
21	Slovenia			1	1%	6	5%	120	94%	127	4
22	Spain										380
23	Sweden										14
24	The Netherlands										172
25	The United Kingdom										317
27	Bulgaria										17
	European Union	4	0%	32	2%	300	17%	1,403	81%	1,739	1,963

Country	Breeding turkeys							
	3 - 7 days		7 - 14 days		Over 14 days		Total	Missing
4 Czech Republic					2	100%	2	2
7 Finland	1	7%			14	93%	15	
8 France								205
9 Germany	1	1%	2	2%	91	97%	94	4
10 Greece								6
11 Hungary			1	10%	9	90%	10	3
12 Ireland								2
13 Italy					22	100%	22	6
18 Poland								6
20 Slovakia								21
22 Spain								10
23 Sweden								1
25 The United Kingdom								116
27 Bulgaria								7
European Union	2	1%	3	2%	138	97%	143	389

Figure 4.2-20 Weighted *Salmonella* prevalence by time between flocks in the EU (number of sampled flocks represented inside each bar).
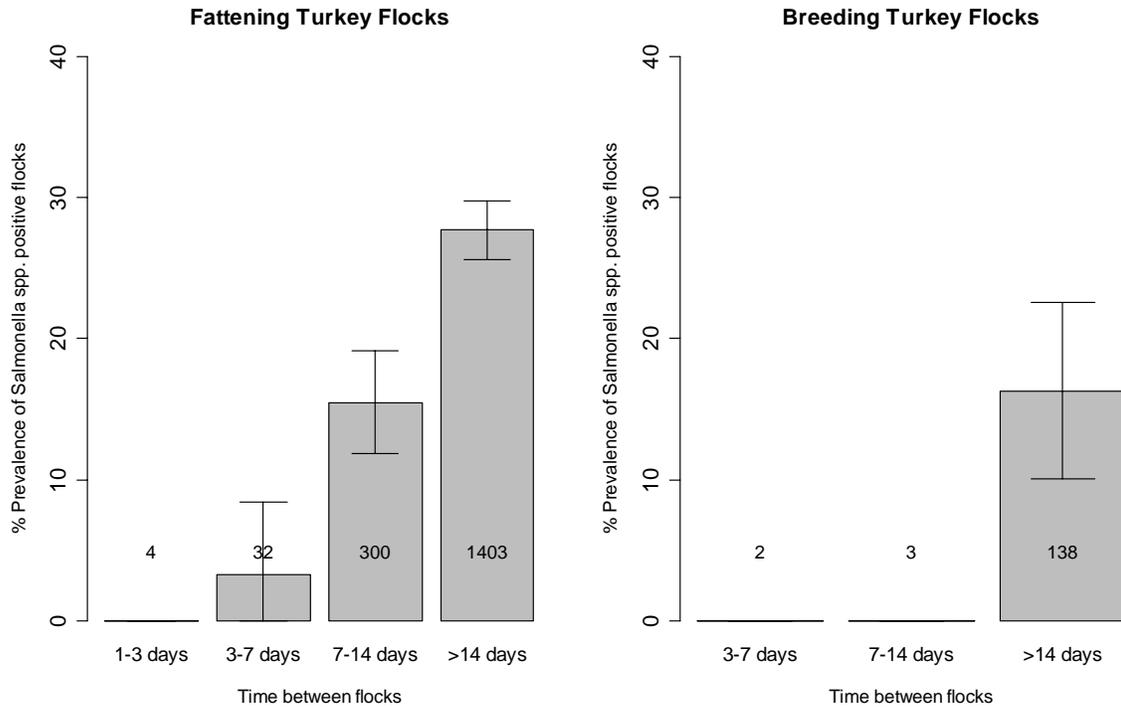
Table 4.2-20 Weighted *Salmonella* prevalence by time between flocks and by flock production type in the EU.

Fattening turkeys	*Salmonella*			
Frequency *Row Pct* Col Pct	Time between flocks			
	1-3 days	3-7 days	7-14 days	>14 days	Total
Negative	1 *0%* 100%	44 *3%* 97%	319 *19%* 85%	1291 *78%* 72%	1655 *100%*
Positive	0 *0%* 0%	2 *0%* 3%	58 *11%* 15%	495 *89%* 28%	555 *100%*
Total	1 100%	46 100%	377 100%	1786 100%	2209

Breeding turkeys	*Salmonella*		
Frequency *Row Pct* Col Pct	Time between flocks		
	3-7 days	7-14 days	>14 days	Total
Negative	4 *3%* 100%	6 *5%* 100%	111 *92%* 84%	121 *100%*
Positive	0 *0%* 0%	0 *0%* 0%	22 *100%* 16%	22 *100%*
Total	4 100%	6 100%	133 100%	142

Salmonella	Trend statistic (one-sided p-value)[17]	
	Fattening	Breeding
	6.08 (<0.001)	1.24 (0.213)

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[17] Positive outcome trend.

Figure 4.2-21 Estimated number of fattening and breeding turkey flocks by *Salmonella* detection during preceding 6 months and (weighted) *Salmonella* outcome.
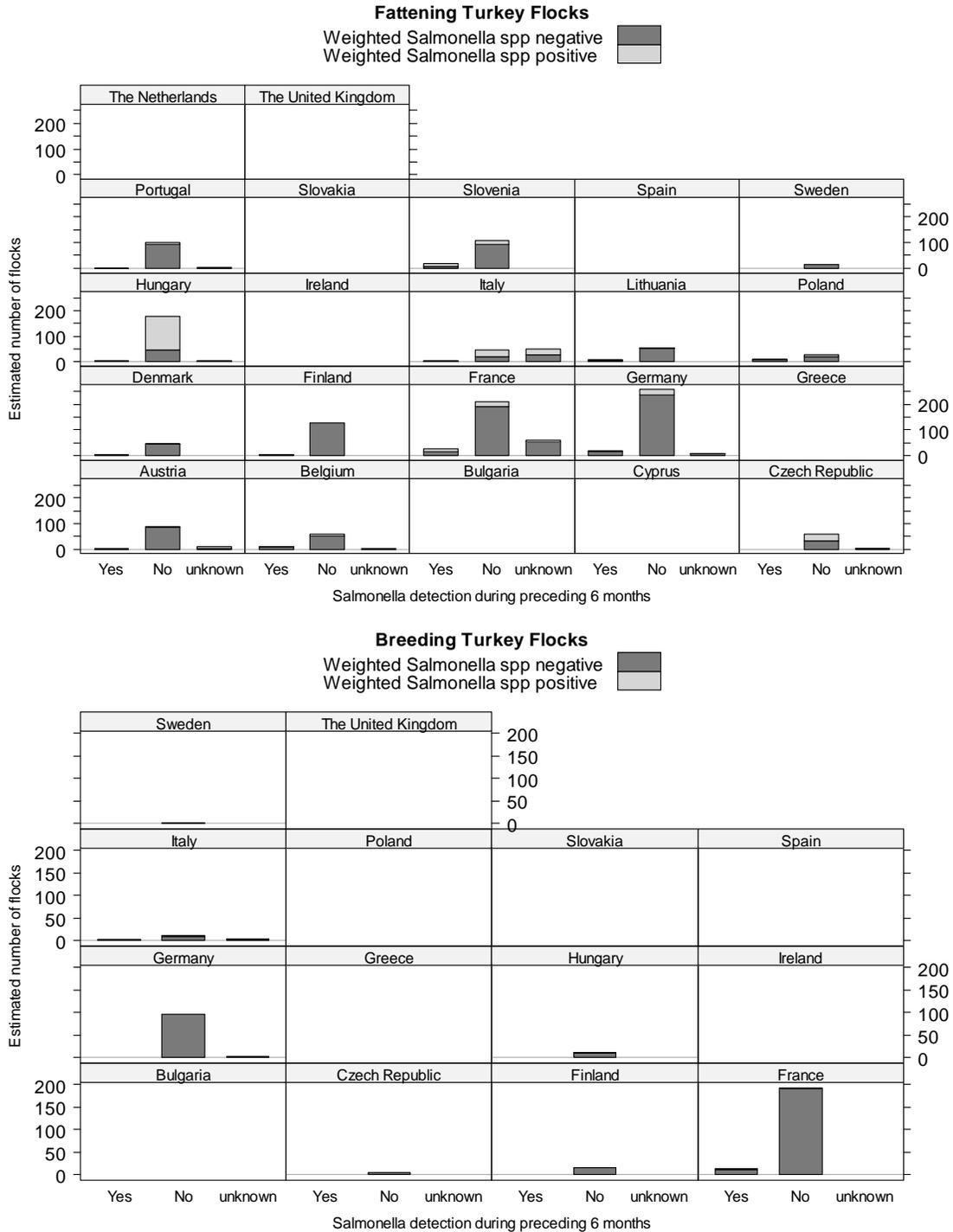
Table 4.2-21 Distribution of the holding flock numbers by *Salmonella* detection during preceding 6 months, per Member State and in the EU.

	Country	Fattening turkeys							
		Yes		No		Unknown		Total	Missing
1	Austria	1	1%	106	91%	9	8%	116	86
2	Belgium	14	20%	56	79%	1	1%	71	3
3	Cyprus								14
4	Czech Republic			57	95%	3	5%	60	134
5	Denmark	2	4%	45	96%			47	12
7	Finland	2	2%	125	98%			127	6
8	France	29	10%	201	70%	56	20%	286	40
9	Germany	19	7%	256	90%	10	4%	285	10
10	Greece								43
11	Hungary	7	4%	171	94%	4	2%	182	107
12	Ireland								259
13	Italy	3	3%	54	51%	48	46%	105	163
15	Lithuania	8	13%	55	87%			63	
18	Poland	4	12%	30	88%			34	288
19	Portugal	1	1%	100	95%	4	4%	105	
20	Slovakia								25
21	Slovenia	17	13%	111	87%			128	3
22	Spain							0	380
23	Sweden			14	100%			14	
24	The Netherlands								172
25	The United Kingdom								317
27	Bulgaria								17
	European Union	107	7%	1,381	85%	135	8%	1623	2,079

	Country	Breeding turkeys							
		Yes		No		Unknown		Total	Missing
4	Czech Republic			2	100%			2	2
7	Finland			15	100%			15	
8	France	13	6%	192	94%			205	
9	Germany			97	99%	1	1%	98	
10	Greece								6
11	Hungary			10	100%			10	3
12	Ireland								2
13	Italy	1	6%	12	75%	3	19%	16	12
18	Poland								6
20	Slovakia								21
22	Spain								10
23	Sweden			1	100%			1	
25	The United Kingdom								116
27	Bulgaria								7
	European Union	14	4%	329	95%	4	1%	347	185

Figure 4.2-22 Weighted *Salmonella* prevalence by *Salmonella* detection during preceding 6 months in the EU (number of sampled flocks represented inside each bar).

Table 4.2-22 Weighted *Salmonella* prevalence by time between flocks and by flock production type in the EU.

Fattening turkeys	*Salmonella*			
Frequency *Row Pct* Col Pct	*Salmonella* detection			
	Yes	No	Unknown	Total
Negative	82 *5%* 55%	1,252 *80%* 77%	235 *15%* 76%	1,569 *100%*
Positive	67 *13%* 45%	366 *72%* 23%	75 *15%* 24%	508 *100%*
Total	149 100%	1,619 100%	310 100%	2,077

Breeding turkeys	*Salmonella*			
Frequency *Row Pct* Col Pct	*Salmonella* detection			
	Yes	No	Unknown	Total
Negative	11 *4%* 52%	289 *94%* 97%	7 *2%* 68%	308 *100%*
Positive	10 *45%* 48%	10 *41%* 3%	3 *14%* 32%	23 *100%*
Total	22 100%	299 100%	10 100%	331

	Fisher's exact test: p-value	
Salmonella	Fattening	Breeding
	<0.001	<0.001

Figure 4.2-23 Estimated number of fattening and breeding turkey flocks by other livestock and (weighted) *Salmonella* outcome.
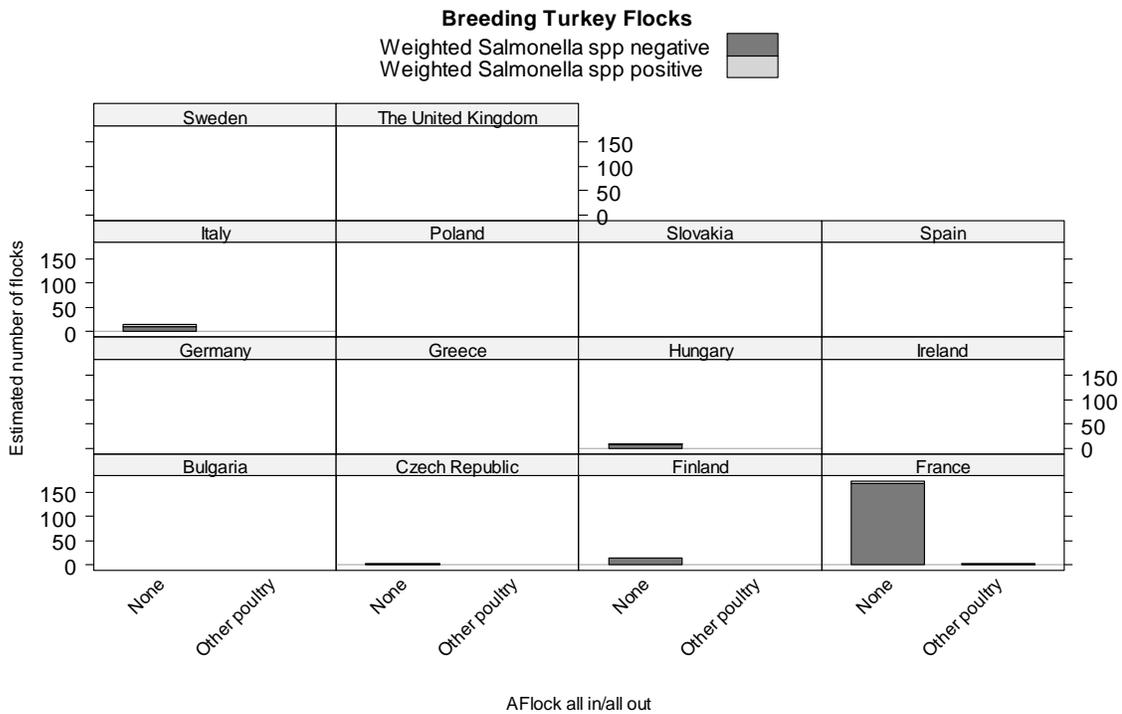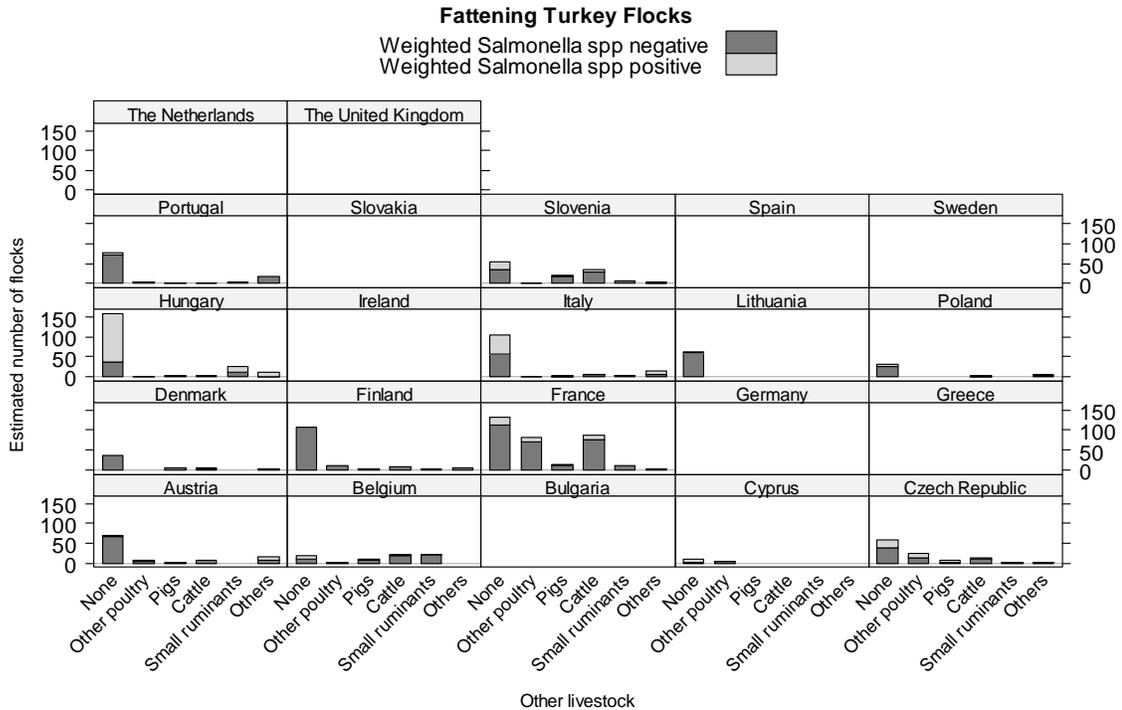
Table 4.2-23 Distribution of the number of flocks in holding by other livestock, per Member State and in the EU.

	Country	Fattening turkeys												
		None		Other poultry		Pigs		Cattle		Small ruminants		Others		Total	Missing
1	Austria	85	74%	9	8%	2	2%	6	5%			13	11%	115	87
2	Belgium	15	21%	1	1%	11	15%	23	32%	21	30%			71	3
3	Cyprus	10	71%	4	29%									14	
4	Czech Republic	60	56%	17	16%	6	6%	17	16%	2	2%	5	5%	107	87
5	Denmark	39	85%			2	4%	3	7%			2	4%	46	13
7	Finland	108	83%	9	7%	4	3%	4	3%	2	2%	3	2%	130	3
8	France	97	30%	105	32%	12	4%	98	30%	11	3%	3	1%	326	
9	Germany														295
10	Greece														43
11	Hungary	162	80%	2	1%	4	2%	2	1%	19	9%	13	6%	202	87
12	Ireland														259
13	Italy	112	79%	1	1%	2	1%	8	6%	2	1%	17	12%	142	126
15	Lithuania	63	100%											63	
18	Poland	25	74%					2	6%			7	21%	34	288
19	Portugal	77	73%	4	4%	3	3%	1	1%	3	3%	17	16%	105	
20	Slovakia														25
21	Slovenia	44	38%	1	1%	25	22%	39	34%	4	3%	3	3%	116	15
22	Spain														380
23	Sweden														14
24	The Netherlands														172
25	The United Kingdom														317
27	Bulgaria														17
	European Union	897	61%	153	10%	71	5%	203	14%	64	4%	83	6%	1,471	2,231

	Country	Breeding turkeys												
		None		Other poultry		Pigs		Cattle		Small ruminants		Others		Total	Missing
4	Czech Republic	2	100%											2	2
7	Finland	14	93%									1	7%	15	
8	France	160	78%	1	0%	2	1%	36	18%	4	2%	2	1%	205	
9	Germany														98
10	Greece														6
11	Hungary	9	90%									1	10%	10	3
12	Ireland														2
13	Italy	17	81%			1	5%			1	5%	2	10%	21	7
18	Poland														6
20	Slovakia														21
22	Spain														10
23	Sweden														1
25	The United Kingdom														116
27	Bulgaria														7
	European Union	202	80%	1	0%	3	1%	36	14%	5	2%	6	2%	253	279

Figure 4.2-24 Weighted *Salmonella* prevalence by other livestock in the EU (number of sampled flocks represented inside each bar).
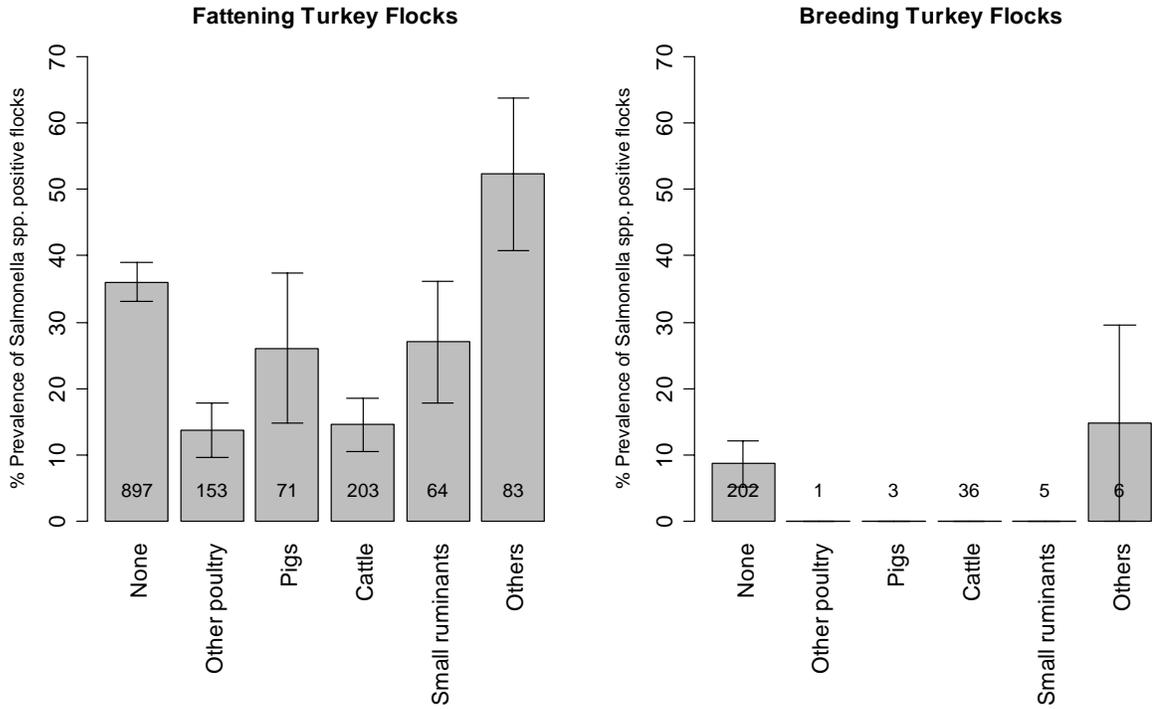
Table 4.2-24 Weighted *Salmonella* prevalence by other livestock and by flock production type in the EU.

Fattening turkeys	*Salmonella*					
Frequency *Row Pct* Col Pct	Other livestock					
	None	Other poultry	Pigs	Cattle	Small ruminants	Others	Total
Negative	644 *50%* 64%	233 *18%* 86%	43 *3%* 74%	258 *20%* 85%	66 *5%* 73%	34 *3%* 48%	1,278 *100%*
Positive	363 *70%* 36%	37 *7%* 14%	15 *3%* 26%	44 *8%* 15%	24 *5%* 27%	38 *7%* 52%	521 *100%*
Total	1,007 100%	270 100%	58 100%	301 100%	90 100%	72 100%	1,799

Breeding turkeys	*Salmonella*					
Frequency *Row Pct* Col Pct	Other livestock					
	None	Other poultry	Pigs	Cattle	Small ruminants	Others	Total
Negative	229 *79%* 91%	4 *1%* 100%	3 *1%* 100%	26 *9%* 100%	8 *3%* 100%	19 *7%* 85%	289 *100%*
Positive	22 *87%* 9%	0 *0%* 0%	0 *0%* 0%	0 *0%* 0%	0 *0%* 0%	3 *13%* 15%	25 *100%*
Total	251 100%	4 100%	3 100%	26 100%	8 100%	22 100%	314

Figure 4.2-25 Estimated number of fattening and breeding turkey flocks by rodent presence and control and (weighted) *Salmonella* **outcome.**
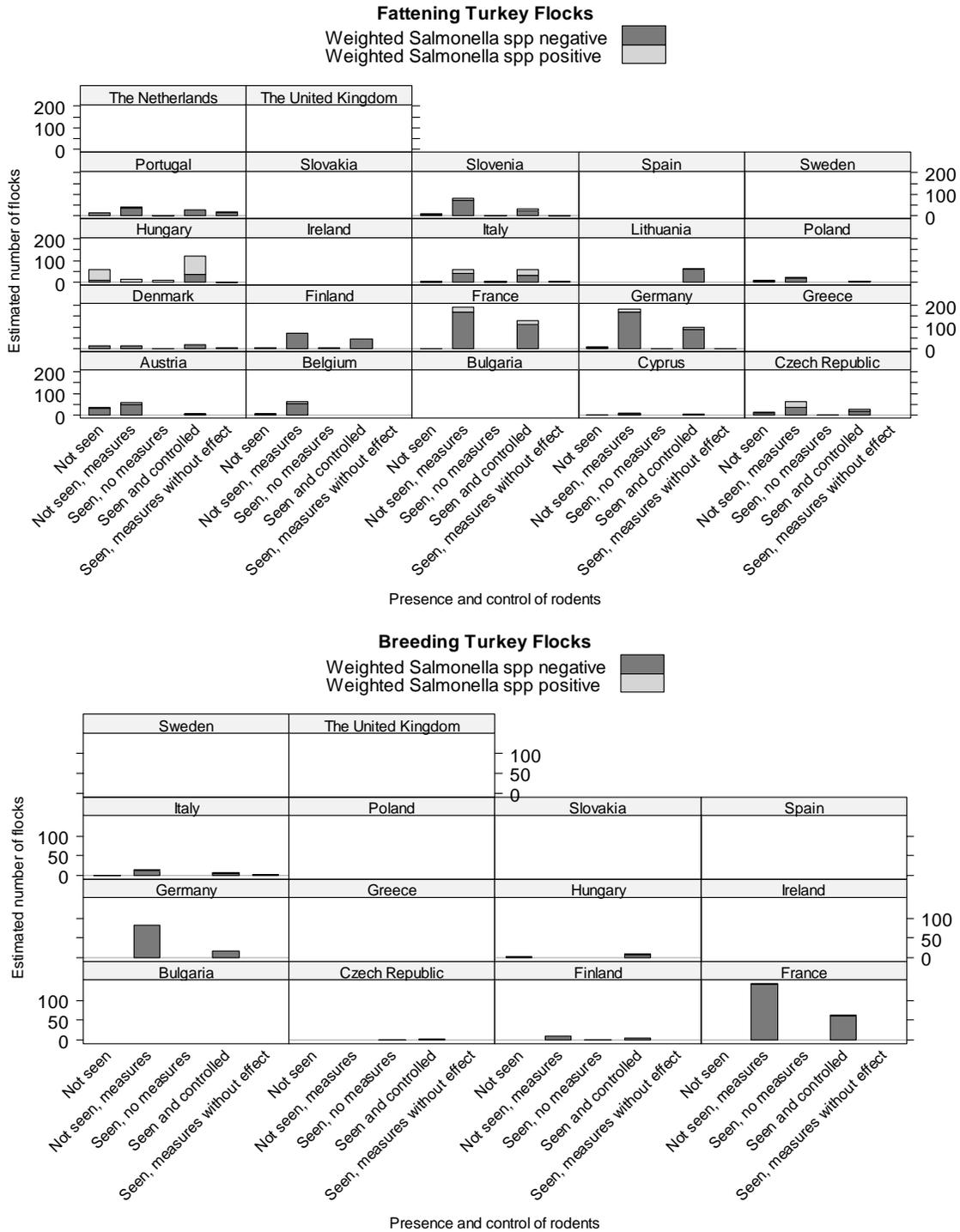
Table 4.2-25 Distribution of holding flock numbers by livestock presence and control, per Member State and in the EU.

Country	Fattening turkeys											
	Not detected		Not detected & control measures		Detected & no control measures		Detected & controlled		Detected & control measures without effect		Total	Missing
1 Austria	42	37%	65	57%			7	6%			114	88
2 Belgium	8	11%	62	89%							70	4
3 Cyprus	1	7%	7	50%			6	43%			14	
4 Czech Republic	11	10%	65	61%	1	1%	30	28%			107	87
5 Denmark	18	38%	8	17%	1	2%	16	34%	4	9%	47	12
7 Finland	11	9%	67	52%	7	5%	43	34%			128	5
8 France	1	0%	191	59%			134	41%			326	
9 Germany	13	4%	183	63%	1	0%	93	32%	1	0%	291	4
10 Greece												43
11 Hungary	59	29%	21	10%	8	4%	111	55%	3	1%	202	87
12 Ireland												259
13 Italy	7	5%	61	42%	4	3%	68	47%	5	3%	145	123
15 Lithuania							63	100%			63	
18 Poland	8	24%	22	65%			4	12%			34	288
19 Portugal	18	17%	46	44%	2	2%	20	19%	19	18%	105	
20 Slovakia												25
21 Slovenia	10	8%	83	63%	1	1%	34	26%	3	2%	131	
22 Spain												380
23 Sweden												14
24 The Netherlands												172
25 The United Kingdom												317
27 Bulgaria												17
European Union	207	12%	881	50%	25	1%	629	35%	35	2%	1,777	1,925

Country	Breeding turkeys											
	Not detected		Not detected & control measures		Detected & no control measures		Detected & controlled		Detected & control measures without effect		Total	Missing
4 Czech Republic					1	50%	1	50%			2	2
7 Finland			12	80%	1	7%	2	13%			15	
8 France			143	70%			62	30%			205	
9 Germany			87	90%			10	10%			97	1
10 Greece												6
11 Hungary	2	20%					8	80%			10	3
12 Ireland												2
13 Italy	1	5%	12	55%			8	36%	1	5%	22	6
18 Poland												6
20 Slovakia												21
22 Spain												10
23 Sweden												1
25 The United Kingdom												116
27 Bulgaria												7
European Union	3	1%	254	72%	2	1%	91	26%	1	0%	351	181

Figure 4.2-26 Weighted *Salmonella* prevalence by rodent presence and control in the EU (number of sampled flocks represented inside each bar).
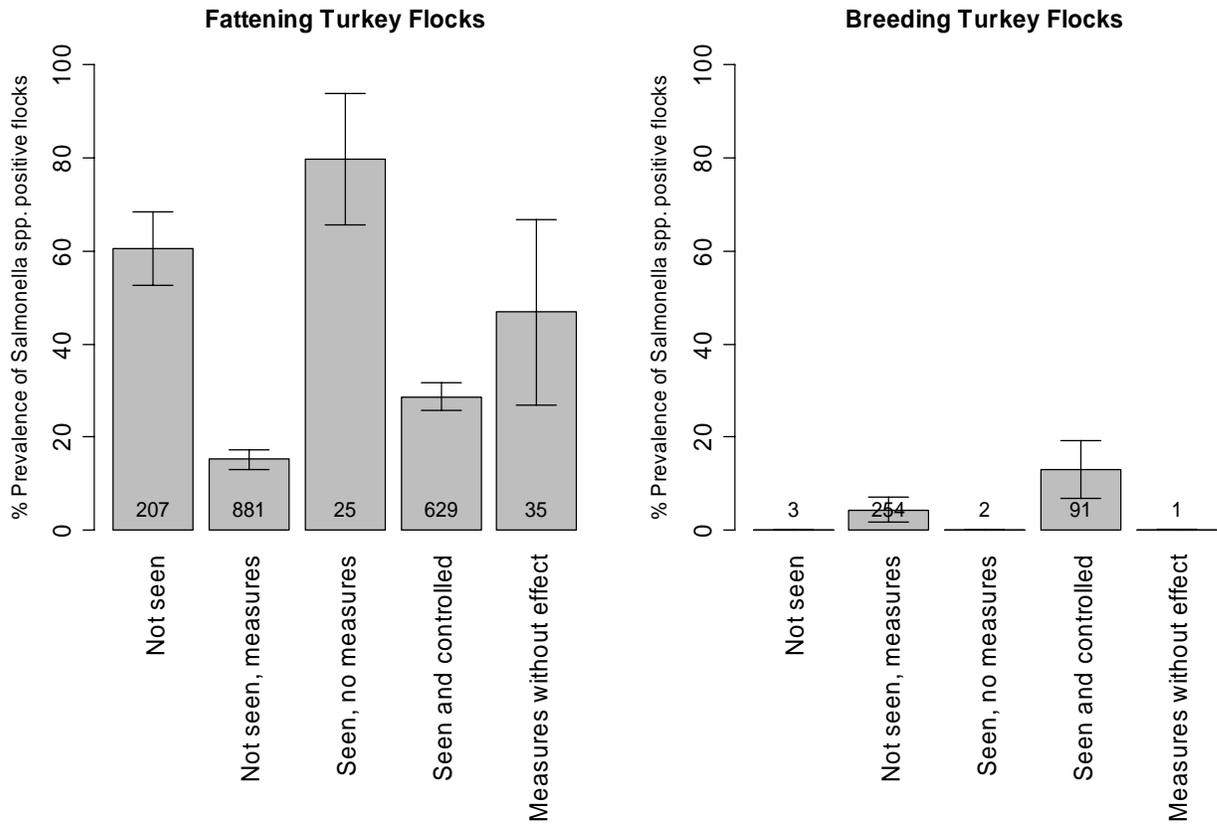
Table 4.2-26 Weighted *Salmonella* prevalence by rodent presence and control and by flock production type in the EU.

Fattening turkeys			*Salmonella*			
	Control and presence of rodents					
Frequency *Row Pct* Col Pct	Not detected	Not detected & control measures	Detected, & no control measures	Detected & controlled	Detected & control measures without effect	Total
Negative	59 *3%* 39%	965 *57%* 85%	6 *0%* 20%	655 *39%* 71%	13 *1%* 53%	1698 *100%*
Positive	91 *16%* 61%	174 *31%* 15%	24 *4%* 80%	264 *47%* 29%	11 *2%* 47%	565 *100%*
Total	149 100%	1139 100%	31 100%	919 100%	24 100%	2262

Breeding turkeys			*Salmonella*			
	Control and presence of rodents					
Frequency *Row Pct* Col Pct	Not detected	Not detected & control measures	Detected & no control measures	Detected & controlled	Detected & control measures without effect	Total
Negative	3 *1%* 100%	225 *68%* 96%	2 *1%* 100%	96 *29%* 87%	4 *1%* 100%	331 *100%*
Positive	0 *0%* 0%	10 *42%* 4%	0 *0%* 0%	14 *58%* 13%	0 *0%* 0%	25 *100%*
Total	3 100%	236 100%	2 100%	110 100%	4 100%	356

Figure 4.2-27 Estimated number of fattening and breeding turkey flocks by house age and (weighted) *Salmonella* outcome.
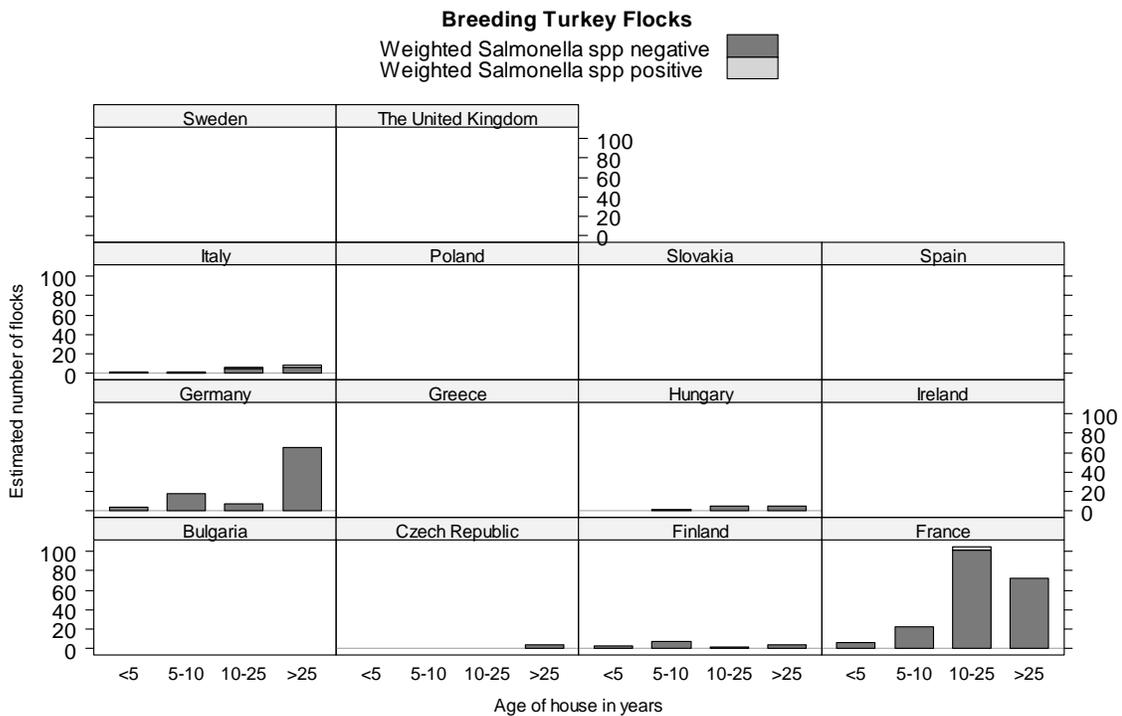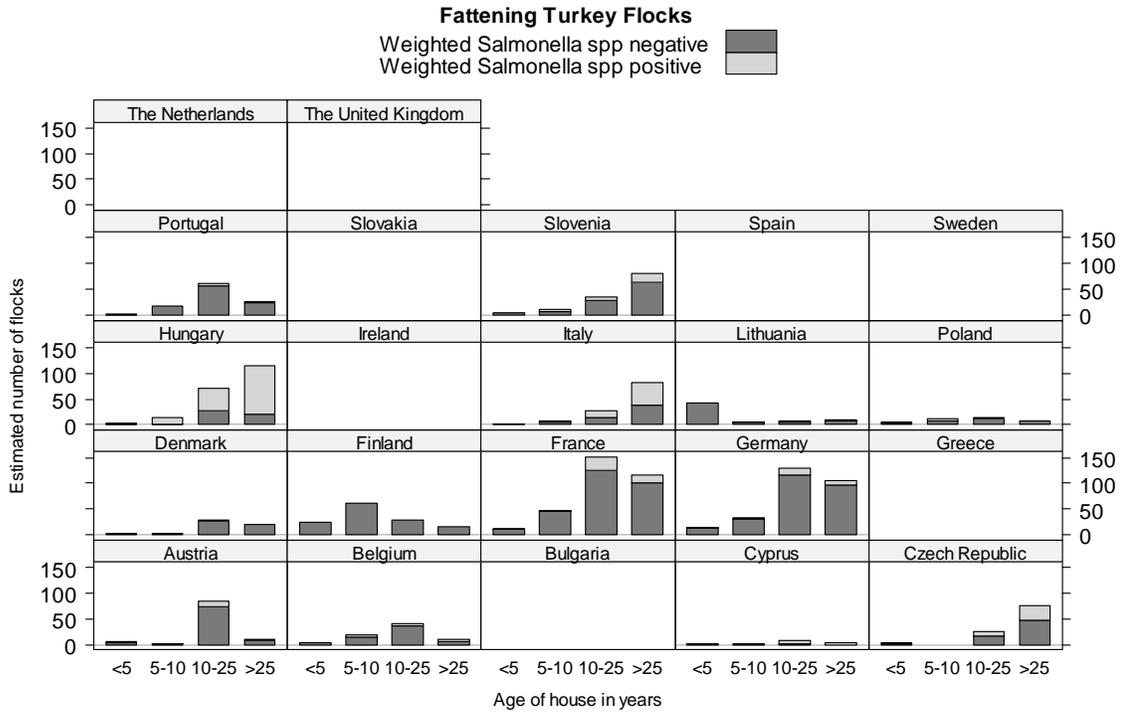
Table 4.2-27 Distribution of the holding flock number by house age, per Member State and in the EU.

	Country	Fattening turkeys											
		<5 years		5-10 years		10-25 years		>25 years		Total	Missing
1	Austria	9	8%	2	2%	97	84%	7	6%	115	87
2	Belgium	2	3%	19	26%	43	60%	8	11%	72	2
3	Cyprus	1	7%	1	7%	9	64%	3	21%	14	
4	Czech Republic	4	4%			22	21%	81	76%	107	87
5	Denmark	2	4%	1	2%	24	51%	20	43%	47	12
7	Finland	26	20%	63	49%	20	16%	19	15%	128	5
8	France	14	4%	55	17%	149	46%	108	33%	326	
9	Germany	17	6%	40	14%	137	49%	88	31%	282	13
10	Greece										43
11	Hungary	4	2%	17	8%	63	31%	118	58%	202	87
12	Ireland										259
13	Italy	1	1%	11	8%	41	31%	78	60%	131	137
15	Lithuania	44	70%	5	8%	5	8%	9	14%	63	
18	Poland	5	15%	7	21%	14	41%	8	24%	34	288
19	Portugal	3	3%	17	16%	58	55%	27	26%	105	
20	Slovakia										25
21	Slovenia	4	3%	11	9%	39	30%	75	58%	129	2
22	Spain										380
23	Sweden										14
24	The Netherlands										172
25	The United Kingdom										317
27	Bulgaria										17
	European Union	136	8%	249	14%	721	41%	649	37%	1,755	1,947

	Country	Breeding turkeys											
		<5 years		5-10 years		10-25 years		>25 years		Total	Missing
4	Czech Republic							2	100%	2	2
7	Finland	4	27%	6	40%	3	20%	2	13%	15	
8	France	8	4%	30	15%	109	53%	58	28%	205	
9	Germany	2	2%	8	9%	5	5%	79	84%	94	4
10	Greece										6
11	Hungary			2	20%	3	30%	5	50%	10	3
12	Ireland										2
13	Italy	1	6%	2	12%	8	47%	6	35%	17	11
18	Poland										6
20	Slovakia										21
22	Spain										10
23	Sweden										1
25	The United Kingdom										116
27	Bulgaria										7
	European Union	15	4%	48	14%	128	37%	152	44%	343	189

Figure 4.2-28 Weighted *Salmonella* prevalence by house age in the EU (number of sampled flocks represented inside each bar).
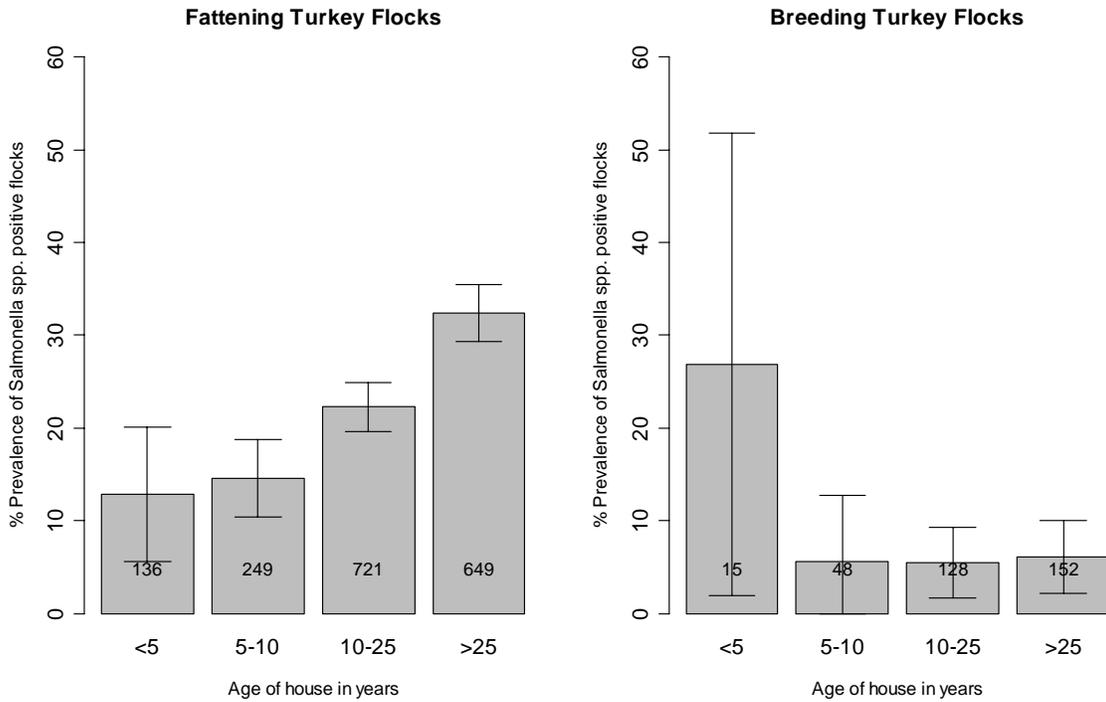
Table 4.2-28 Weighted *Salmonella* prevalence by house age and by flock production type in the EU.

Fattening turkeys					*Salmonella*
Frequency *Row Pct* Col Pct	House age				
	<5 years	5-10 years	10-25 years	>25 years	Total
Negative	71 *4%* 87%	234 *14%* 85%	727 *44%* 78%	625 *38%* 68%	1657 *100%*
Positive	10 *2%* 13%	40 *7%* 15%	208 *37%* 22%	300 *54%* 32%	558 *100%*
Total	82 100%	274 100%	935 100%	925 100%	2216

Breeding turkeys					*Salmonella*
Frequency *Row Pct* Col Pct	House age				
	<5 years	5-10 years	10-25 years	>25 years	Total
Negative	9 *3%* 73%	37 *12%* 94%	130 *42%* 95%	134 *43%* 94%	310 *100%*
Positive	3 *15%* 27%	2 *10%* 6%	8 *35%* 5%	9 *40%* 6%	22 *100%*
Total	12 100%	39 100%	138 100%	142 100%	331

Salmonella	Trend statistic (one-sided p-value)[18]	
	Fattening	Breeding
	7.08 (<0.001)	-1.44 (0.149)

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[18] Positive outcome trend.

4.3   **Results of the model-building**

Sampling month versus quarter

Considering sampling month as a continuous variable would imply a linear trend, however, one could expect a seasonal trend to occur. In some periods of the year flocks could be more affected by *Salmonella* than in others (see for instance Figure 4.3-1). Note, however, that this figure does not take into account the weighting scheme and is not correcting correlation between flocks within a holding. Therefore, to study the effect of sampling month on prevalence estimation more rigorously, we have estimated the prevalence of *Salmonella* within each flock using a simple random-effects model including only a fixed intercept and a random intercept for each holding. These prevalence estimates were then plotted by sampling month and a Loess smoothing technique was used to obtain a mean profile over time. This mean profile is displayed in Figure 4.3-1. When the information on all MSs are pooled there does not seem to be any specific trend observed by sampling month.

Figure 4.3-1 Fattening turkeys - Mean flock-level prevalence profile by sampling month. Loess smoother was used to obtain average over the flock level prevalence estimates.
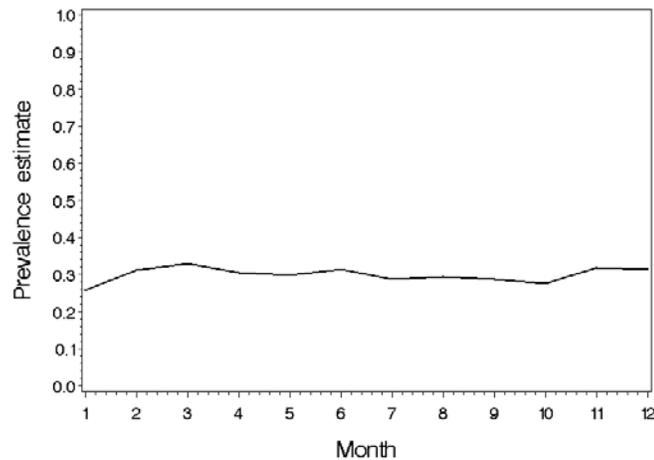
Nevertheless, to include sampling month in the model as a categorical variable results in many extra parameters and will complicate the model fit. Therefore, a new variable, labelled "quarter", has been created such that it equals 1 when the flock was sampled in the period October to December, 2 when sampled in the period January to March, 3 in the period April to June, and 4 in the period July to September.

Multi-collinearity analysis

The analysis studying multi-collinearity among risk factors in fattening turkeys in the EU has shown that the variable Number of turkey places (V006) cannot be included in the model-building due to quasi-complete separation issues. A quasi-complete separation problem implies that an almost deterministic relationship exists between the risk factor of interest and (a combination of) risk factor(s) in the predictor structure. The VIF values calculated for the remaining covariates are shown in Table 4.3-1.

Table 4.3-1 Variance Inflation Factors (EU-level)

Risk factor	VIF
Number of turkey places (V006)	10.42
Number of flocks at sampling (V009)	5.72
Number of flocks at full capacity (V008)	5.32
Vaccination status (V021)	5.30
Flock production type (V013)	4.83
Age of turkeys at slaughter or depopulation (V020)	3.54
Flock production group (V014a)	3.46
Age of turkeys	3.34
Number of turkeys in holding (V007)	3.02
Medication status (V024)	1.94
Number of turkeys in flock at sampling (V012)	1.82
Days delay between sampling and testing (V029a)	1.35
Number of cycles (V019)	1.18
Quarter	1.12

Note that these VIF are calculated without taking into account the association of the covariates with the country-specific effect. An analysis including this effect resulted in many quasi-complete separation warnings and unreliable model results. Still, a country-specific effect will be included in the linear predictor when a model is constructed for EU level data.

Further, the exercise focussing on each of the participating countries was repeated separately and the results have been presented in Table 4.3-2. Some elements in this matrix are left empty. This is the result of the fact that (i) the risk factor had (almost) all of its information contained in one level, (ii) quasi-complete separation issues occurred.

In countries with small sample sizes, like Cyprus (14 sampled flocks), Greece (43 sampled flocks) and Slovakia (25 sampled flocks), it is very difficult to obtain a good model fit (many parameters to be estimated with very little data). This has resulted in extremely large VIF values for some of the covariates in these countries. Also in Ireland, very inflated VIF values can be observed. In this country, model-building with risk factor quarter was very problematic, which most likely results in these elevated VIFs. Note that Finland, Sweden and Bulgaria do not have any infected flocks. It is therefore not possible to study the impact of the risk factors on *Salmonella* prevalence. The contributions for these countries in Table 4.3-2 have therefore been left blank.

Further, we observed some multi-collinearity issues with variables associated with the size of the holding (number of turkey places, number of turkeys in holding at the time of sampling, number of flocks at full capacity and number of flocks at the time of sampling). In this case one could opt for a principal component analysis to reduce the number of variables on the size of the holding or one variable could be selected which reflects the holding size and is most meaningful from an epidemiological point of view.

Table 4.3-2 Variance Inflation Factors (country level)

	Country	Number of Turkey Places (V006)	Nr of turkeys in holding (V007)	Nr of flocks at full capacity (V008)	Nr of flocks at sampling (V009)	Nr of turkeys in flock (V012)	Quarter	Age of turkeys	Age of turkeys at slaughter or depopulation (V020)	Number of cycles (V019)	Days delay between sampling and testing (V029a)	Medication status (V024)	Vaccination status (V021)	Number of flocks
1	Austria	8.1	6.3	10.8	11.5	3.0	1.2	1.1	1.2	1.9	1.1			202
2	Belgium	9.7	6.8	15.9	25.0	4.6	2.3	3.7	3.6	2.1	1.8			74
3	Cyprus		438.7			14.2		248.8	45.6	192.5	60.6			14
4	Czech Republic	4.4	13.3	6.6	9.9	2.1	2.3	6.9	6.8	1.5	1.3			194
5	Denmark	12.5	3.3	4.2	3.6	2.0		6.7	6.5	1.5	1.6			59
7	Finland													133
8	France	13.4	6.7	6.3	9.5	3.3		4.6	4.2	1.6	1.1	2.0	3.7	326
9	Germany	4.1	2.5	5.1	5.3	1.8	1.2	1.4	1.5	1.2	1.1	1.4		295
10	Greece		49.3	63.9	39.3	4.9		5.4	7.7	1.5	4.2			43
11	Hungary	5.1	6.3	12.1	14.5	2.9	1.5	14.0	15.3	1.8	1.1	2.3	2.7	289
12	Ireland	8.7	19.5	225.0	222.7	2.1	2.8	42.1	39.7	2.3	1.4			259
13	Italy	8.4	4.3	11.6	12.2	2.8		8.3	8.9	1.5	1.1	1.2	2.9	268
15	Lithuania		3.7	3.9	1.0	3.5		57.1	58.2	1.9	1.9			63
18	Poland	5.4	3.1	6.4	6.3	1.6	1.4	6.3	6.1	1.3	1.1	2.6	3.9	322
19	Portugal		8.2	3.0	6.6	2.2		7.7	7.4	1.3	1.2	2.0		105
20	Slovakia		138.5	33.0	88.6	3.1		12.5	11.3	18.7	1.7			25
21	Slovenia	2.4	3.5	2.5	2.2	2.6		3.8	4.0	1.8	1.2	3.2		131
22	Spain	6.1	12.8			3.9	1.4	3.7	3.3	1.2	1.2	1.8	2.0	380
23	Sweden													14
24	The Netherlands	6.3	2.5	10.8	12.7	1.8	1.6	6.9	6.8	1.1	1.1	2.0		172
25	The United Kingdom	12.9	3.6	5.2	5.7	2.9		14.3	14.8	2.2	1.1	2.7		317
27	Bulgaria													17

Turkey age also seems to suffer from multi-collinearity at the time of sampling and the expected age of the birds at depopulation or slaughter. In this case, one of the two covariates could be selected for further analysis.

Model-building for fattening turkeys

The study of the association between risk factors and the presence of *Salmonella* in the EU was carried out using several steps. First, logistic regression and a backward selection procedure were used to reduce the number of risk factors. The starting model contained a global intercept, a country-specific fixed effect and the mandatory risk factors of interest. Note that in countries without infected flocks there is no information to estimate country-specific effect. Therefore, countries without infected flocks are not considered in the EU-level analysis. In the selection procedure, risk factors with p-values greater than 0.35 were systematically removed from the model. The final model obtained using this selection procedure, was then completed with a random intercept for holding and fit using the GLIMMIX procedure in the SAS system. We further reduced the model by removing step-by-step the most non-significant risk factors until only covariates with p-values less than or equal to 0.05 remained in the model. The odds ratio estimates for the risk factors in the final model are shown in Table 4.3-3. The parameter estimates for country-specific intercepts are shown in Table 4.3-4.

Table 4.3-3 Fattening turkeys - *Salmonella* **Odds ratio estimates and corresponding 95% confidence intervals for final model including random intercept for holding and country-specific fixed intercept.**

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
Time 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 turkeys only	6. 6	1.9	22.3
Vaccination against *Salmonella*	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

Table 4.3-4 Fattening turkeys – *Salmonella* **Parameter estimates for fixed and country-specific intercept.**

Effect		Estimate	StdErr	p-value
Intercept		-0.62	0.64	0.337
Austria	1	-0.39	0.49	0.428
Belgium	2	-0.32	0.52	0.540
Cyprus	3	1.19	0.74	0.110
Czech Republic	4	0.58	0.26	0.026
Denmark	5	-2.16	0.94	0.021
France	8	-1.30	0.26	<.0001
Germany	9	-1.41	0.28	<.0001
Greece	10	-1.47	0.58	0.011
Hungary	11	3.05	0.27	<.0001
Ireland	12	0.02	0.31	0.961
Italy	13	0.62	0.26	0.017
Lithuania	15	-1.63	0.79	0.039
Poland	18	-0.14	0.26	0.576
Portugal	19	-1.40	0.47	0.003
Slovakia	20	-1.03	0.57	0.071
Slovenia	21	-0.83	0.50	0.096
Spain	22	0.81	0.34	0.016
The Netherlands	24	-1.06	0.38	0.005
The United Kingdom	25	0.00		

In Table 4.3-3, an odds ratio (OR) > 1 indicates that exposure to the risk factor increases the risk of *Salmonella* infection, whereas OR < 1 indicate a negative association between the factor and the infection. 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 including MS-specific effects and OR are, therefore, adjusted per MS.

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 4.3-3) suggests that the risk of infection for fattening turkey flocks approximately increased 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 large number of flocks, as shown by an adjusted OR for number of flocks at sampling, significantly smaller than 1.

In order to test the effect of sampling month on the risk of *Salmonella*, a new variable, quarter, was created. Compared to the period July to September (Quarter 4), the risk of *Salmonella* infection was higher in the period October to December (Quarter 1) and January to March (Quarter 2). However, there does not appear to be a significant difference between the risk of infection in April to June (Quarter 3) compared to July to 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 that six times higher than the risk of infection in holdings with a homogenous fattening production (OR=6.6, Table 4.3-3).

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 represented a risk of approximately 39% in unvaccinated flocks (OR=0.39, Table 4.3-3). Nonetheless, there was no difference between unvaccinated flocks and flocks of an unknown vaccination status.

Finally, the risk of infection in standard and organic free-range flocks (pooled data) was almost twice that of conventional flocks (OR=1.9, Table 4.3-3).

The results of the analysis by MS are displayed in Table 4.3-5. 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 Czech Republic only conventional (1) and standard free-range (2) flocks were sampled. Therefore, in this country it was only possible compare these two levels to obtain an OR estimate. Odds ratio estimates which are displayed in italic were obtained with confidence limits close to extremes (either 0 or ∞ or both).

Finland, Sweden and Bulgaria do 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 4.3-5 have therefore been left blank.

A similar model-building exercise was performed at country level: for each participating country a separate model was determined. As for the EU-model-building, covariates were selected through a backward selection procedure using independent logistic regression. Those covariates with a p-value less than or equal to 0.35 remained in the model. A holding-specific random intercept was then added to the model, which was fitted using GLIMMIX. The model for each country was then reduced further so that only covariates with p-values less than or equal to 0.25 remained. Further, for those countries for which only one flock per holding was available, ordinary logistic regression was used instead of a random-effects logistic regression analysis. The results of this analysis are displayed in Table 4.3-5. The different levels of significance are indicated by different shades of grey, darker meaning more significant.

First, note that empty cells imply that the effect of the covariate was not significant enough in that particular country to be maintained in the final model. Further, for some multi-level covariates not all categories were available in all countries. For instance, in Czech Republic only conventional (1) and standard free-range (2) flocks were sampled. Therefore, in this country we can only 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). This suggests that the model fit may have been problematic.

Clearly, a lot of variability between significant risk factors obtained for each country can be observed in Table 4.3-5. The effect of some factors even change direction depending on the country. For instance, the odds of observing a positive flock are (much) higher when the flock received medication in countries like Belgium and Italy. However the odds of observing a positive flock are lower when the flock received medication in countries such as the UK and the Netherlands. This could be the result of country-specific regulations on appropriate medication. Note that when these effects are studied at community level, these results may average out so that no significant effect is observed in the EU model.

Table 4.3-5. Fattening turkeys - Significant risk factors (at different levels) and odds ratio estimates obtained from model-building for each country separately. Frequency of occurrence of significant risk factors over all countries

P value
- <0.01
- 0.01-0.05
- 0.05-0.10
- 0.10-0.25
- not available

No.	Country	No. of turkeys in holding	No. of flocks at full capacity	No. of flocks at sampling	No. of turkeys in flock at sampling	Quarter 1 vs 4	Quarter 2 vs 4	Quarter 3 vs 4	Age	Age at slaughter or depopulation	No. of cycles per house per year	Medication with antimicrobials 0 vs 1	Time between sampling and testing	Vaccination against Salmonella 1 vs 0	Vaccination against Salmonella 2 vs 0	Vaccination against Salmonella 1 vs 2	Holding composition 2 vs 3	Flock production type 1 vs 2	No. of flocks
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	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

*results based on independent logistic regression
Quarter: 1 = October - December; 2 = January - March; 3 = April - June; 4 = July - September.
Medication status: 0 = untreated; 1 = treated.
Vaccination status: 0 = unvaccinated; 1 = vaccinated; 2 = unknown status.
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.

Model-building: including optional variables

In this section, we study the impact of the optional variables by adding these covariates to the final EU logistic regression model obtained in the previous section. The information available on these optional variables has been summarised in Table 4.3-6. To increase sample size for this risk factor analysis, the variables feed origin, thinnings number and number of days to first thinning were excluded from the model-building. Note that excluding feed origin allows us to include information from France in the analysis. Further, it should be noted that the final model containing optional variables was obtained using 1135 sampled flocks.

For each of the covariates in the final model as well as for each of the remaining optional variables, the VIF was calculated (see Table 4.3-7).

In the model-building, we started from the final model containing the risk factors obtained from the previous exercise and we added the additional optional variables. A backwards selection procedure was then adopted, excluding step-by-step the most non-significant covariates until all remaining risk factors were significant with p-values less than or equal to 0.05. The results of this model-building exercise are shown in Table 4.3-8. The final model now includes again a significant country-specific effect. Additionally, the analysis showed a significant overall effect of *Salmonella* detection during the preceding 6 months and of the other livestock. For the first effect, a significant positive effect was observed only when level 1 was compared to level 4. This means that the odds of observing a positive flock when *Salmonella* was detected during the preceding 6 months is almost 6 times the odds of observing a positive flock when this information was unknown. The confidence interval for the OR estimates for no *Salmonella* detection versus unknown detection contains 1, therefore, there is no evidence to conclude that there was a significant difference between these two outcomes. The presence of small ruminants in a holding is 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, by multiple logistic regression analysis.

Table 4.3-6 Available information on optional variables in fattening turkey flocks.

	Country	Parent holding	Hatchery holding	Rearing holding	Feed origin	Antimicrobial treatment	No. of thinnings	No. of days to first thinning	All in/all out flock	All in/all out holding	Time between flocks	S. during 6 preceding months	Other livestock	Rodents	Age of the house	Total no. of flocks
1	Austria	117	118	119	118	116	118	104	117	117	119	116	115	114	115	202
2	Belgium	69	70	70	70	74	57	5	74	74	71	71	71	70	72	74
3	Cyprus	14	14	14	14	14	12	2	14	14	14		14	14	14	14
4	Czech Republic	107	107	107	107	194	66	49	194	194	103	60	107	107	107	194
5	Denmark	47	47	47	44	59	45	25	59	59	45	47	46	47	47	59
7	Finland	130	129	127	130	133	10	10	133	133	124	127	130	128	128	133
8	France	326	326	326		326	326		326	326	326	286	326	326	326	326
9	Germany	248	248	255	245	295	295		295	295	273	285		291	282	295
10	Greece					43			43	43						43
11	Hungary	202	202	202	202	289	50	50	289	289	202	182	202	202	202	289
12	Ireland					259			259	259						259
13	Italy	142	148	125	146	135	149	8	146	146	133	105	142	145	131	268
15	Lithuania	63	63	63	63	63	63	37	63	63	63	63	63	63	63	63
18	Poland	34	34	34	34	322		6	322	322	34	34	34	34	34	322
19	Portugal	105	105	105	105	105			105	105	105	105	105	105	105	105
20	Slovakia					25			25	25						25
21	Slovenia	131	131	130	131	131	124	71	131	131	127	128	116	131	129	131
22	Spain															380
23	Sweden	14	14	14		14			14	14		14				14
24	The Netherlands					172			172	172						172
25	The United Kingdom															317
27	Bulgaria					17			17	17						17
	Total	1,749	1,756	1,738	1,409	2,786	1,315	367	2,798	2,798	1,739	1,623	1,471	1,777	1,755	3,702

Table 4.3-7 Variance Inflation Factor (optional variables model-building).

Risk factor	VIF
Hatchery holding (V043)	12.97
Parent holding (V042)	10.71
Flock production type (V013)	3.43
All in/all out flock(V050)	3.23
Rearing holding (V044)	2.84
Salmonella detection (V053)	2.67
House age (V056)	2.54
Rodent presence and control (V055)	2.08
Number of flocks at sampling (V009)	2.07
Quarter	2.04
Number of turkeys in holding (V007)	2.00
All in/all out holding (V051)	1.99
Other livestock (V054)	1.28
Time between flocks (V052)	1.08

Table 4.3-8 Fattening turkeys - *Salmonella* Odds ratio estimates and corresponding 95% confidence intervals for extended final model including random intercept for holding and country-specific fixed intercept.

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

5. Discussion and conclusions

Discussion and conclusions are included in the main, Part B report (pages 1- 67).

6. References

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7. List of Tables

8. List of Figures