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Report of the Task Force on Zoonoses Data Collection on the Analysis of the baseline survey on the prevalence of *Salmonella* in broiler flocks of *Gallus gallus*, in the EU, 2005-2006[1]

Part A: *Salmonella* prevalence estimates

(Question N° EFSA-Q-2006-040)

Adopted by
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Summary

Salmonella is an important cause of food-borne illnesses in humans. Farm animals and food of animal origin form an important source of human *Salmonella* infections. Therefore European Community legislation foresees setting of *Salmonella* reduction targets for animal population including broiler flocks. A European Union-wide baseline survey was carried out to determine the prevalence of *Salmonella* in commercial flocks of broilers with at least 5,000 birds. This survey provides information for the *Salmonella* target setting. The survey was the second of several baseline surveys to be conducted in the Community.

The sampling of the broiler flocks took place between October 2005 and September 2006. Five faeces samples were taken from the flocks within 3 weeks before leaving for slaughter. A total of 6,325 holdings corresponding to 7,440 flocks with validated results were included in the survey analyses.

The Community observed prevalence of *Salmonella*-positive flocks was 23.7%. This means that in the European Union one in four broiler flocks raised over the one year period of the baseline survey was *Salmonella*-positive. The *Salmonella* prevalence varied widely amongst the Member States, from 0% to 68.2%.

A total of 11.0% of the broiler flocks was estimated to be positive for *Salmonella* Enteritidis and/or *Salmonella* Typhimurium, the two most common serovars found in *Salmonella* infection cases in humans. The Member State-specific observed flock prevalence of *S.* Enteritidis and/or *S.* Typhimurium varied also greatly, from 0% to 39.3%.

The number of positive samples in a *Salmonella* positive flock ranged between one and five but at European Union level 42% of the positive flocks was found positive for all the five samples taken.

The five most frequently isolated *Salmonella* serovars from broiler flocks in the European Union were respectively in decreasing order *S.* Enteritidis, *S.* Infantis, S. Mbandaka, *S.* Typhimurium and *S.* Hadar. All these serovars, with the exception of *S.* Mbandaka, are frequent causes of *Salmonella* infections in humans within the European Union. *S.* Enteritidis was the most common serovar and it was detected in 37% of the *Salmonella* positive flocks. S. Infantis accounted also for an important proportion of positive flocks (20%). The serovar distribution varied amongst the Member States, many of them having a specific distribution pattern of their own.

Reducing the number of samples taken from a flock was estimated to have a stronger impact on the *S.* Enteritidis and/or *S.* Typhimurium flock prevalence than on the overall *Salmonella* flock prevalence. Reducing the number of samples taken to 2 samples per flock would lead to significantly lower prevalence estimate of *S.* Enteritidis and/or *S.* Typhimurium.

Salmonella positive broiler flocks contribute in a consequent contamination of broiler meat. Broiler meat is an important source of human *Salmonella* infections in EU. The risk for human health arises from accidental under-cooking of the meat or cross-contamination to other foods. Thorough cooking and strict kitchen hygiene will prevent or reduce the risk posed by *Salmonella* contaminated broiler meat.

While the Community reduction target will most likely be set for a transitional period only for *S.* Enteritidis and *S.* Typhimurium, it is recommended that Member States would address in their national *Salmonella* control programmes also other serovars when these serovars are of public health importance in their country.

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1. Introduction

In order to provide the scientific basis for setting of the Community target for reduction of the prevalence of *Salmonella* in broiler flocks of *Gallus gallus*, a European Union-wide *Salmonella* baseline survey was carried out. The objective of the survey was to determine the prevalence of *Salmonella* on a randomised selection of commercial broiler holdings with at least 5,000 broilers on the holding[1]. This survey was the second of several baseline surveys organised at the European Community level.

The study was carried out between 1 October 2005 and 30 September 2006 in accordance with the Community legislation on zoonoses aiming at reducing the incidence of food-borne diseases in the European Union (EU). Regulation (EC) No 2160/2003 on the control of *Salmonella* and other specified zoonotic agents[2] foresees the setting of the Community target. This baseline survey provides comparable information on the prevalence of *Salmonella* in broiler flocks in the EU Member States (MSs). Norway also participated in the study on a voluntary basis.

The objectives, the sampling frame and the diagnostic testing methods, as well as the collection of data, evaluation, reporting and timelines of this baseline study are specified in Commission Decision 2005/636/EC concerning a baseline survey on the prevalence of *Salmonella* in broiler flocks of *Gallus gallus*[1].

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[1] Commission Decision of 1 September 2005 concerning a baseline survey on the prevalence of *Salmonella* spp. in broiler flocks of *Gallus gallus*. 2005/636/EC. *Official Journal of the European Union* 2004; L228/14: 3.9.2005.

[2] Regulation (EC) No 2160/2003 of the European Parliament and of the Council of 17 November 2003 on the control of *salmonella* and other specified food-borne zoonotic agents. *Official Journal of the European Union* 2003; L 325/1: 12.12.2003.

2. Objectives

The aim of the survey was to estimate the prevalence of *Salmonella*-positive flocks amongst commercial holdings (i.e. holdings containing at least 5,000 birds) of broilers, at the whole EU level as well as for each MS.

The specific objectives were:

- to estimate the holding and the flock prevalence of *Salmonella* in commercial holdings of broilers at the EU level and each MS specifically,
- to estimate the holding and the flock prevalence of the two serovars, *Salmonella* Enteritidis and *Salmonella* Typhimurium for, pursuant to article 4 of the Regulation EC No 2160/2003, the *Salmonella* reduction target should cover for a provisional period at least these two serovars,
- to investigate the serovar distribution and determine the most frequently occurring serovars in broiler holdings and flocks across the EU,
- to investigate the effect of potential risk factors, such as number of birds per holding, and time of sampling, which may be associated with the occurrence of *Salmonella*,
- to evaluate the sampling design especially with regard to the precision and accuracy of the prevalence estimates.

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

This part A report includes the analyses of the prevalence of *Salmonella*, the most frequent serovars and the sampling design. The analyses of potential risk factors as well as more in depth analyses of serovar distribution, phage types and antimicrobial susceptibility of *Salmonella* isolates will be provided in the part B report.

3. Materials and methods

A detailed description of the design of the baseline survey, the sample design and size and the bacteriological testing is found in the document European Commission DG SANCO: Baseline survey on the prevalence of *Salmonella* in broiler flocks of *Gallus gallus* in the EU: Technical specifications. SANCO/1688/2005 Rev1[1].

Samples were taken from flocks of broilers of *Gallus gallus* sampled within three weeks of leaving the selected holding for slaughter.

On each selected holding, one flock with broilers of the appropriate age was to be sampled. However, in MSs where the calculated number of flocks to be sampled was higher than the number of available holdings with at least 5,000 birds, up to four flocks were allowed to be sampled on the same holding in order to achieve the calculated number of flocks. Where possible the additional flocks from a single holding were to originate from different broiler houses and samples taken in different seasons. If the number of flocks to be sampled was still not sufficient, progressively smaller holdings were to be selected until at least 154 flocks, where possible, was attained. If the number of flocks to be sampled was still not sufficient, more than four flocks were allowed to be sampled on the same holding, focusing on larger holdings.

For MSs where fewer than 80 % of the birds were kept on holdings with more than 5,000 broiler chickens, progressively smaller holdings were initially to be selected.

Five pooled faeces samples were taken in any selected flock. Each pooled sample comprised faecal material fixed to a pair of boot swabs (or sock samples which are considered equivalent). This sampling procedure will theoretically provide 95% confidence of detection of 1% within flock prevalence assuming the test is 100% sensitive.

For all production types the same sampling approach was applied. For free range flocks, samples were to be collected in the area inside the house.

The number of flocks to be sampled was stratified according to the flock size, meaning that a certain number of flocks in different size categories of flocks had to be sampled.

Samples were taken by agents of the Competent Authority in each MS and were tested by the National Reference Laboratory (or a laboratory authorised by it) using the new ISO 6579 Annex D method.

3.1. Data description

3.1.1. Data validation and cleaning

The European Food Safety Authority (EFSA) received the final dataset from the European Commission on 29 November 2006. This dataset contained data from 6,183 broiler holdings and 7,347 broiler flocks in 24 MSs. It also included data from 320 holdings (and flocks) in Norway whereas there were no data from Luxembourg and Malta.

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[1] European Commission DG SANCO. Baseline survey on the prevalence of *Salmonella* in broiler flocks of *Gallus gallus* in the European Union: Technical specifications. SANCO/1688/2005 Rev1. Working document, 15 July 2005. Presented at the meeting of the Standing Committee on the Food Chain and Animal Health on 19 July 2005. (http://ec.europa.eu/food/food/biosafety/salmonella/tech_spec_sanco-1688-2005_rev1_en.pdf)

A set of data exclusion criteria (Annex I) was used to identify non-valid and non-plausible information in the dataset. This resulted in a cleaned, validated dataset comprising 6,325 broiler holdings and 7,440 broiler flocks (final dataset), which formed the basis for all subsequent analyses. An overview of the total number of holdings and flocks as well as of the number of sampled holdings and flocks per MS included in the validated final dataset is given in Annex II and in Annex III, respectively.

An overview of the number of excluded holdings and flocks per MS is given in Table 1 and Table 2, respectively. All together 2.9% of the holdings (178 out of 6,183) and 3.1% of the flocks (227 out of 7,347) were excluded from the final EU dataset. The reasons for exclusion of samples or holdings in accordance with the exclusion criteria are summarized in Annex IV. The criterion that caused the highest number of records to be excluded was 'days to start of bacteriological test above 7 days'. Some records had more than one non-plausible data characteristic.

Table 1. Overview of the data validation at holding-level, *Salmonella* in broiler flocks baseline survey in the EU, 2005-2006

Member States	Number of broiler holdings structurally validated by COM and sent to EFSA	Number of broiler holdings validated by EFSA	Number of holdings excluded by EFSA
	Full dataset	**Final dataset**	**Difference**
Austria	359	359	0
Belgium	376	373	3
Cyprus	92	91	1
Czech Republic	349	333	16
Denmark	239	228	11
Estonia	4	4	0
Finland	196	196	0
France	383	381	2
Germany	378	377	1
Greece	304	245	59
Hungary	337	336	1
Ireland	267	263	4
Italy	330	313	17
Latvia	3	3	0
Lithuania	20	20	0
Poland	383	357	26
Portugal	378	366	12
Slovakia	192	187	5
Slovenia	330	323	7
Spain	388	388	0
Sweden	123	121	2
The Netherlands	369	359	10
The United Kingdom	383	382	1
EU	6,183	6,005	178
Norway	320	320	0
total	6,503	6,325	178

Table 2. Overview of the data validation at flock-level, *Salmonella* in broiler flocks baseline survey in the EU, 2005-2006

Member States	Number of flocks structurally validated by COM and sent to EFSA	Number of flocks validated on contents by EFSA	Number of flocks excluded by EFSA
	Full dataset	**Final dataset**	**Difference**
Austria	365	365	0
Belgium	376	373	3
Cyprus	257	248	9
Czech Republic	350	334	16
Denmark	319	295	24
Estonia	150	139	11
Finland	360	360	0
France	383	381	2
Germany	378	377	1
Greece	309	245	64
Hungary	360	359	1
Ireland	358	351	7
Italy	330	313	17
Latvia	121	121	0
Lithuania	156	156	0
Poland	383	357	26
Portugal	382	367	15
Slovakia	238	230	8
Slovenia	333	326	7
Spain	388	388	0
Sweden	296	291	5
The Netherlands	372	362	10
The United Kingdom	383	382	1
EU	7,347	7,120	227
Norway	320	320	0
total	7,667	7,440	227

3.2. Analysis of data

3.2.1. General assumptions and framework of statistical analysis

The criterion for further analysis of the prevalence of *Salmonella* serovars or groups of *Salmonella* serovars was based on the frequency of isolation of those serovars, rather than based on the serovars which are most commonly found in human infection. Independent analysis was conducted for the five most frequently reported *Salmonella* serovars at the EU-level as well as for specific groups of *Salmonella* serovars, as follows:

- *Salmonella* spp., i.e. all *Salmonella* serovars,
- *S.* Enteritidis
- *S.* Typhimurium
- *S.* Infantis
- *S.* Mbandaka
- *S.* Hadar
- *S.* Enteritidis and/or *S.* Typhimurium
- Serovars other than *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Mbandaka and *S.* Hadar

Both the holding and the flock-level prevalence were investigated. The holding prevalence parameter was the obvious choice while taking account of the study design. The flock prevalence was more relevant from an epidemiological as well as from a risk management perspective. To this end model-based estimation of the flock prevalence was carried out.

A flock was considered positive if the presence of *Salmonella* or the specific serovar was detected in at least one of the five samples taken. A holding was defined to be positive when its flock (or at least one of its flocks) was positive. Only the observed prevalence was investigated. In statistical words, this translates into the assumption that no case of false negative flock would occur in the survey.

At the EU-level, the study design was interpreted as a stratified cluster sampling design with unequal sampling probabilities in each stratum. Each MS represents one stratum.

To estimate the EU observed prevalence, weighting was implemented to take into account the population size (total numbers) of holdings and flocks in each MS. The population size of flocks (in holdings with more than 5,000 birds) was defined as the total number of broiler flocks raised over the one year period of the baseline survey in the MS. This sum was obtained by using the following equation for each holding [number *of broiler houses per holding * number of broiler flocks (cycles) raised per house per year*]. For each holding and flock prevalence estimate a 95%-confidence interval was derived.

3.2.2. Estimation of the observed Salmonella holding prevalence

The observed holding *Salmonella* prevalence was estimated at the EU-level and for each Member States independently. At the EU-level MSs were grouped into two categories according to whether only one flock per holding was sampled or if more than one flock per holding were included in the sampling. Data were fitted to a logistic model using proc LOGISTIC in SAS version 9.1.3.

3.2.3. Estimation of the observed Salmonella flock prevalence

A meaningful estimation of the observed *Salmonella* flock prevalence, at EU and MS-level was not possible when considering the one-flock-per-holding sampling design. Proper estimation of the observed *Salmonella* flock prevalence was possible using a model-based approach that allowed using strength across holdings and across MSs. The information on the within-holding *Salmonella* flock prevalence deriving from the MSs that had sampled more than one flock per holding was used to estimate the within-holding *Salmonella* flock prevalence in countries that had sampled strictly one flock per holding. To this end a statistical model was fitted to the global EU dataset and an accurate description of this model is given in the technical appendix (Annex V).

Basically, the statistical model relies on the assumptions that:
- within a given holding, within a given country, at a given period of the year, flocks have a similar observed prevalence,
- the between-holding variability of observed flock prevalence is comparable across countries, meaning that it is either the same variability or it increases proportionally to the level of infection (i.e. for countries with high prevalence, such a between-holding variability will be larger than for countries with low prevalence).

In statistical terms, this translates into:

- the use of a logistic regression with a random effect on the holding-level,
- the fact that a flock is defined as a sampling unit in space and time, i.e. a flock within a given holding within a given cycle of production,
- the flock sampling within each holding is described by a binomial model (conditionally to the holding),
- the variance of the random effect (assumed to be Gaussian in the probit scale) is either the same for every country or increasing linearly with its mean (country-specific). The choice between the 2 structures was driven by the data observed (see technical appendix). Note that in 2 cases ("*S.* Hadar" and "*Salmonella* serovars other than the 5 most frequent ones"), the data did not allow this approach. Therefore, the variance was fixed to the average value observed in other groups of serovars (standard deviation = 0.6). This additional assumption makes the results less robust for these two outcome variables.

In order to account for the finite and fixed population sizes and the fact that all holdings do not have the same number of flocks (this was highly variable, even within one country), the derived observed prevalence was calculated as follow:

- a flock level prevalence estimate (with standard deviation) was derived per holding,
- the flock level prevalence estimate per country was derived by weighting according to number of flocks per holding.

The model was fitted using SAS proc NLMIXED version 9.1.3. It allows a natural way to handle covariate analysis for future work (risk factor analysis). In order to allow for the convergence of the algorithms, MSs without any isolate for considered *Salmonella* serovars were excluded from the modelling exercise and their corresponding prevalence estimates and confidence intervals were set to 0.

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

A simulation exercise was set up to address the sensitivity of the EU flock prevalence results with respect to the number of samples per flocks. The purpose was to evaluate what the observed *S.* Enteritidis and/or *S.* Typhimurium flock observed prevalence estimate would have been if MSs had asked to collect less than 5 samples per flock.

First, a bootstrapping-like Monte Carlo technique was used to assess what would have been the estimated *S.* Enteritidis and/or *S.* Typhimurium EU flock observed prevalence in the past baseline survey if only 1, 2, 3 or 4 samples per flock had been collected. More specifically, for each case investigated, 1000 replicates of the baseline study were simulated by randomly censoring 1 to 4 samples. For each of these 1000 simulated studies, the fitting exercise previously described was performed, and the mean observed prevalence derived, with a 95%-confidence interval (accounting for data randomness). This allowed plotting the curve of EU flock prevalence estimates versus number of samples per flock. A SAS macro was developed for each sample size investigated, using SAS version 9.1.3.

Secondly, it was evaluated what would have been the observed EU *S.* Enteritidis and/or *S.* Typhimurium flock observed prevalence estimate if the design had accounted for the flock size, by taking fewer samples for smaller flocks. For this purpose, the flocks were classified into 4 size categories (based on the 4 quartiles):

- Category 1: flocks with less than 11,000 broilers
- Category 2: flocks with number of broilers between 11,000 and 17,999
- Category 3: flocks with number of broilers between 18,000 and 26,869
- Category 4: flocks with more than 26,870 broilers

Since the definition of categories is based on the quartile values, they all have the same number of flocks. Two sampling design were investigated

- design 1: taking 1 sample in flocks of category 1; 2 samples in flocks of category 2; 3 samples in flocks of category 3 and 4 samples in flocks of category 4, and
- design 2: taking 2 samples in flocks of category 1; 3 samples in flocks of category 2; 4 samples in flocks of category 3 and 5 samples in flocks of category 4.

At the EU level, the average number of samples per flock was consequently 2.5 for design 1 and 3.5 for design 2. This average number of samples per flock was of course different for each country. Again, based on Monte-Carlo simulations, the observed EU *S.* Enteritidis and/or *S.* Typhimurium flock observed prevalence estimates were derived and compared with the global curve (flock prevalence estimates versus number of samples per flock) previously plotted.

The sensitivity analysis was performed at the EU level and for every MS specifically.

4. Results

4.1. Features of the European broiler population

A short overview of the features of the European broilers population is given in Annex VI. France has the highest number of broiler holdings and flocks as well as broilers, whereas Latvia and Estonia have the lowest numbers. The density of broiler population was highest in Cyprus and The Netherlands.

4.2. Observed prevalence of *Salmonella*

4.2.1. Observed *Salmonella* holding prevalence

The results of the observed *Salmonella* holding prevalence are presented in Annex VIII. The MS-specific holding prevalence estimates equals the proportion of sampled holdings that were positive. Moreover also the weighted prevalence is provided for the two categories of MSs according to whether only one flock per holding was sampled or whether more than one flock per holding was included in the sampling. Since in Estonia, Latvia and Lithuania all holdings were sampled no confidence intervals for these MSs were calculated assuming that there was no statistical sample variation.

4.2.2. Observed *Salmonella* flock prevalence

In total 3.1% of the flocks were excluded from the final EU dataset in the data validation and cleaning. This proportion of excluded data was considered to be very small and unlikely to have a significant impact on the results; therefore, the results are reported based on the final dataset only.

The observed *Salmonella* prevalence in flocks of broilers in each MS and at EU level as well as for Norway is presented in Table 3. The observed EU prevalence is weighted by the number of broiler flocks in each MS. Analogous tables that also include the reported proportions of positive sampled broiler flocks in the MSs are in Annex VII.

***Salmonella* spp. flock observed prevalence**

The presence of *Salmonella* spp. was detected in 20.3% of the flocks sampled in the EU (1,448 out of 7,120 in the sample). This resulted in a Community weighted observed *Salmonella* spp. flock prevalence of 23.7% (95% CI=23.0%-24.5%). The observed *Salmonella* spp. flock prevalence in the EU ranged from a minimum of 0% (Sweden) to a maximum of 68.2% (Hungary). High *Salmonella* spp. prevalence was also observed for Poland (58.2%), Portugal (43.5%) and Spain (41.2%). A graphical display showing the 95% CIs of the observed prevalence of *Salmonella* spp.-positive flocks for each MS, at Community level, and for Norway is presented in Figure 1.

Salmonella Enteritidis and/or *Salmonella* Typhimurium flock observed prevalence

The presence of *S.* Enteritidis and/or *S.* Typhimurium was detected in 13.0% of the flocks sampled in the EU (927 out of 7,120 in the sample). This resulted in a Community weighted *S.* Enteritidis and/or *S.* Typhimurium observed flock prevalence of 11.0% (95% CI=10.2%-11.9%) with a range from 0% (Finland, Ireland, and Sweden) to 39.3% (Portugal). High *S.* Enteritidis and/or *S.* Typhimurium prevalence was also observed for Poland (32.4%) and Spain (28.2%). A graphical display showing the 95% CIs of the observed prevalence of *S.* Enteritidis and/or *S.* Typhimurium-positive flocks for each MS, at Community level, and for Norway, is presented in Figure 2.

Observed flock prevalence for *Salmonella* Enteritidis, for *Salmonella* Typhimurium, for *Salmonella* Infantis, for *Salmonella* Mbandaka, for *Salmonella* Hadar, and for serovars other than *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Mbandaka and *S.* Hadar

The observed prevalences for every MS, at EU level, and for Norway, of flocks positive for the 5 most frequently reported S*almonella* serovars: *S.* Enteritidis, *S.* Typhimurium, S. Infantis, *S.* Mbandaka *S.* Hadar and for serovars other than these five are presented in Table 3 and Annex VIII.

The Community weighted observed flock prevalence were

- *S.* Enteritidis 10.9% (95% CI= 10.2%-11.6%);
- *S.* Typhimurium 0.5% (95% CI= 0.4%-0.5%);
- *S.* Infantis 2.2% (95% CI= 2.0%-2.4%);
- *S.* Mbandaka 0.4% (95% CI= 0.3%-0.5%);
- *S.* Hadar 1.1% (95% CI= 1.0%-1.3%);
- and for serovars other than *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Mbandaka and *S.* Hadar 6.5% (95% CI= 6.2%-6.9%).

The latter serovar group contained also the non-typeable serovars. Graphical displays of the 95% CIs of these prevalences for every MS, at EU level, and for Norway, are shown in Figures 3 to 8, respectively.

The highest *S.* Enteritidis prevalence was observed in Portugal (37.8%), Poland (31.8%), Spain (29.5%), and the Czech Republic (11.3%); these figures were significantly higher when compared to other MSs.

S. Typhimurium prevalence was generally much lower in the MSs, and the highest prevalence was recorded for Poland (2.3%) as well as for Hungary and Belgium (both 1.9%).

Hungary accounted by far for the highest *S.* Infantis prevalence (64%) followed by Poland with 8% prevalence. *S.* Mbandaka prevalence was clearly the highest in Ireland (14.5%) and *S.* Hadar prevalence in Poland (4.2%) and Spain (3.0%).

The prevalence of serovars other than the five most frequent ones was the highest in Italy (20.7%) and Greece (17.7%).

It is worthwhile to mention that the independent model-based estimation of the flock prevalence occasionally resulted in small fluctuations and sometimes deviations from common sense which remain within the confidence interval, and are therefore meaningless. An example can be given for Cyprus. For this MS the estimated *S.* Enteritidis and/or *S.* Typhimurium flock prevalence was 1.7 whereas the *S.* Enteritidis flock prevalence was 1.9, which is not plausible but meaningless because the CIs are overlapping.

Table 3. Observed *Salmonella* broiler flock prevalence (with 95% confidence intervals) in the EU, 2005-2006

		***Salmonella* spp.**		***S.* Enteritidis**		***S.* Typhimurium**		***S.* Enteritidis and/or S. Typhimurium**	
Member State	**N**	**prev est***	**CI 95%**	**prev est**	**CI 95%**	**prev est**	**CI 95%**	**prev est**	**CI 95%**
Austria	365	5.4	4.6 - 6.2	0.9	0.7 - 1.1	0.2	0.1 - 0.2	1.3	1 - 1.5
Belgium	373	12.4	11.2 - 13.7	0.0	0 - 0	1.9	1.6 - 2.3	2.0	1.7 - 2.3
Cyprus	248	9.1	7 - 11.3	1.9	1.2 - 2.5	0.0	0 - 0	1.7	1.1 - 2.4
Czech Republic	334	19.3	17.2 - 21.5	11.3	9.8 - 12.8	0.2	0.1 - 0.2	9.6	7.8 - 11.5
Denmark	295	1.6	1.2 - 2	0.0	0 - 0	0.1	0 - 0.1	0.3	0.2 - 0.3
Estonia	139	2.0	0 - 4	1.9	0 - 3.9	0.0	0 - 0	1.7	0 - 3.7
Finland	360	0.1	0 - 0.1	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
France	381	6.2	5.2 - 7.2	0.2	0.2 - 0.3	0.1	0 - 0.1	0.5	0.4 - 0.6
Germany	377	15.0	12.9 - 17.1	0.5	0.4 - 0.7	0.7	0.4 - 1.1	1.6	1.1 - 2
Greece	245	24.0	21.2 - 26.9	2.3	1.8 - 2.8	0.9	0.6 - 1.2	3.2	2.4 - 4
Hungary	359	68.2	65.4 - 71	3.3	2.7 - 3.8	1.9	1.4 - 2.3	5.1	4 - 6.2
Ireland	351	27.6	24.5 - 30.6	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
Italy	313	28.3	25.8 - 30.9	2.4	2 - 2.8	0.1	0 - 0.1	2.3	1.8 - 2.8
Latvia	121	6.2	2.7 - 9.7	5.2	1.9 - 8.5	0.0	0 - 0	5.1	1.8 - 8.3
Lithuania	156	2.9	1.3 - 4.6	3.2	1.5 - 5	0.0	0 - 0	3.3	1.4 - 5.2
Poland	357	58.2	54.1 - 62.3	31.8	27.8 - 35.9	2.3	1.7 - 3	32.4	26.9 - 37.8
Portugal	367	43.5	40.2 - 46.8	37.8	34 - 41.5	0.1	0 - 0.1	39.3	34.1 - 44.5
Slovakia	230	5.7	4.5 - 6.9	3.7	2.9 - 4.5	0.1	0.1 - 0.2	3.3	2.4 - 4.3
Slovenia	326	1.6	1.3 - 1.9	1.6	1.3 - 1.9	0.0	0 - 0	1.6	1.3 - 1.9
Spain	388	41.2	38.3 - 44.1	29.5	26.6 - 32.3	0.3	0.2 - 0.4	28.2	24.4 - 31.9
Sweden	291	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
The Netherlands	362	7.5	6.6 - 8.3	0.7	0.6 - 0.9	0.1	0 - 0.1	1.0	0.8 - 1.1
The United Kingdom	382	8.2	7.1 - 9.4	0.0	0 - 0	0.1	0 - 0.1	0.2	0.2 - 0.3
EU	**7,120**	**23.7**	**23 - 24.5**	**10.9**	**10.2 - 11.6**	**0.5**	**0.4 - 0.5**	**11.0**	**10.2 - 11.9**
Norway	320	0.1	0 - 0.1	0.0	0 - 0	0.1	0 - 0.1	0.2	0.2 - 0.3

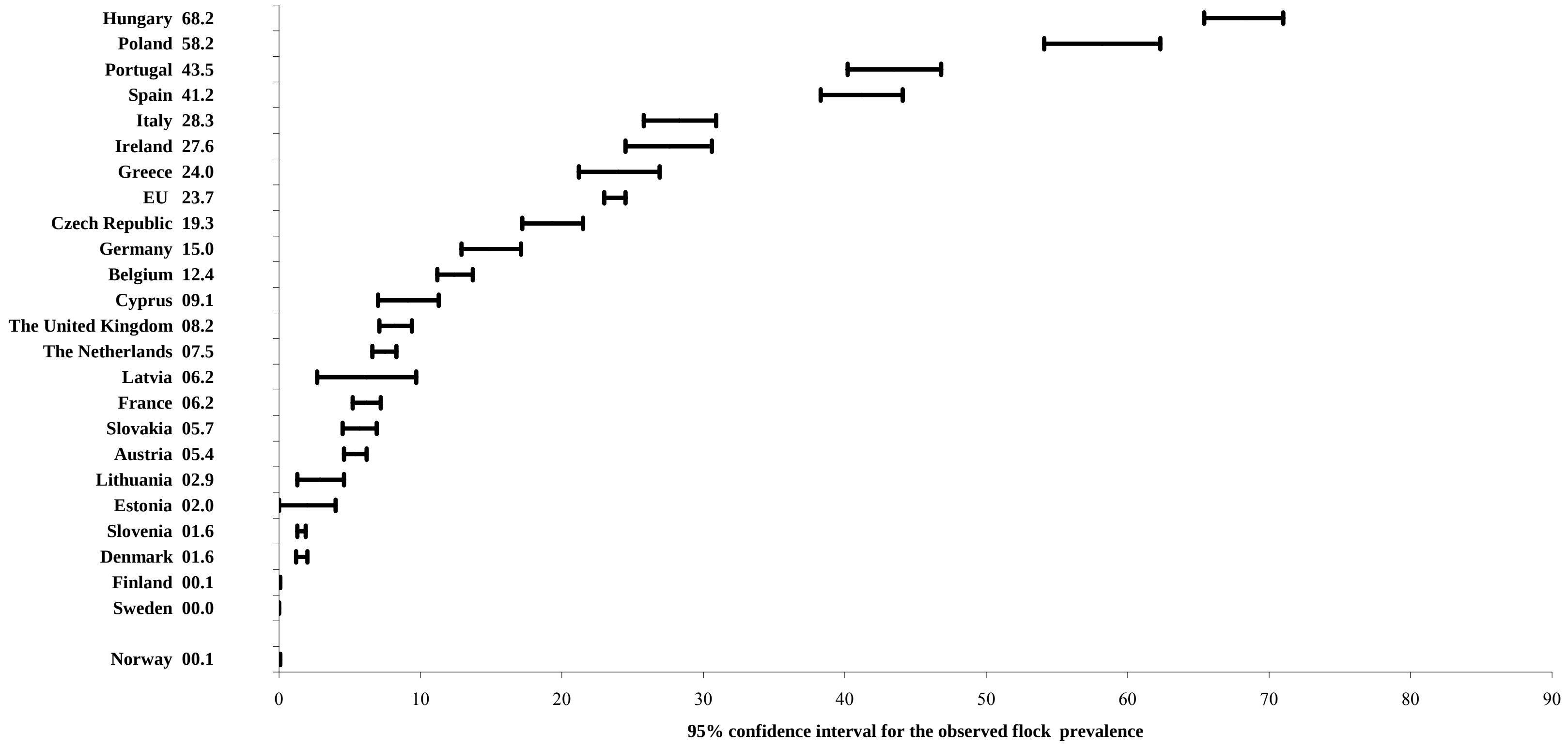
*: Broiler flock prevalence estimate (proportion of the total number of broiler flocks over the one year period that are positive)

Table 3. (continued). Observed *Salmonella* broiler flock prevalence (with 95% confidence intervals) in the EU, 2005-2006

		S. Infantis		*S.* Mbandaka		*S.* Hadar		Other serovars than *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Mbandaka and *S.* Hadar	
Member State	**N**	**prev est***	**CI 95%**	**prev est**	**CI 95%**	**prev est**	**CI 95%**	**prev est**	**CI 95%**
Austria	365	0.5	0.5 - 0.6	0.0	0 - 0	0.0	0 - 0	3.0	2.5 - 3.5
Belgium	373	0.1	0 - 0.2	0.2	0.1 - 0.3	0.1	0 - 0.1	8.9	7.9 - 9.9
Cyprus	248	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	6.2	4.5 - 7.8
Czech Republic	334	2.5	2.2 - 2.8	0.0	0 - 0	0.1	0 - 0.1	2.4	1.9 - 2.9
Denmark	295	0.7	0.6 - 0.8	0.0	0 - 0	0.0	0 - 0	0.9	0.7 - 1.1
Estonia	139	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
Finland	360	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.1	0 - 0.1
France	381	0.5	0.4 - 0.6	0.0	0 - 0.1	0.3	0.2 - 0.3	4.1	3.4 - 4.9
Germany	377	1.5	1.4 - 1.6	0.2	0.1 - 0.3	0.0	0 - 0	10.4	8.8 - 12
Greece	245	0.0	0 - 0	0.1	0 - 0.2	0.3	0.2 - 0.4	17.7	15.3 - 20.1
Hungary	359	64.0	60.1 - 67.9	1.3	0.5 - 2	0.0	0 - 0	4.0	3.2 - 4.8
Ireland	351	0.0	0 - 0	14.5	11.1 - 17.8	0.0	0 - 0	9.4	7.9 - 11
Italy	313	0.2	0.1 - 0.3	1.2	0.7 - 1.6	1.2	0.9 - 1.5	20.7	18.5 - 22.9
Latvia	121	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	1.1	0 - 2.7
Lithuania	156	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
Poland	357	8.0	6.2 - 9.8	1.1	0.6 - 1.5	4.2	3.2 - 5.3	3.9	3 - 4.9
Portugal	367	2.5	2.2 - 2.8	0.0	0 - 0.1	0.0	0 - 0	2.9	2.3 - 3.5
Slovakia	230	0.4	0.2 - 0.5	0.0	0 - 0	0.1	0.1 - 0.2	1.0	0.7 - 1.4
Slovenia	326	0.2	0.1 - 0.3	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
Spain	388	0.8	0.7 - 0.8	0.2	0 - 0.5	3.0	2.5 - 3.6	4.0	3.3 - 4.7
Sweden	291	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
The Netherlands	362	2.0	1.8 - 2.1	0.1	0 - 0.1	0.0	0 - 0	4.0	3.5 - 4.6
The United Kingdom	382	0.0	0 - 0	0.1	0 - 0.2	0.0	0 - 0	7.2	6.1 - 8.2
EU	**7,120**	**2.2**	**2 - 2.4**	**0.4**	**0.3 - 0.5**	**1.1**	**1 - 1.3**	**6.5**	**6.2 - 6.9**
Norway	320	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0

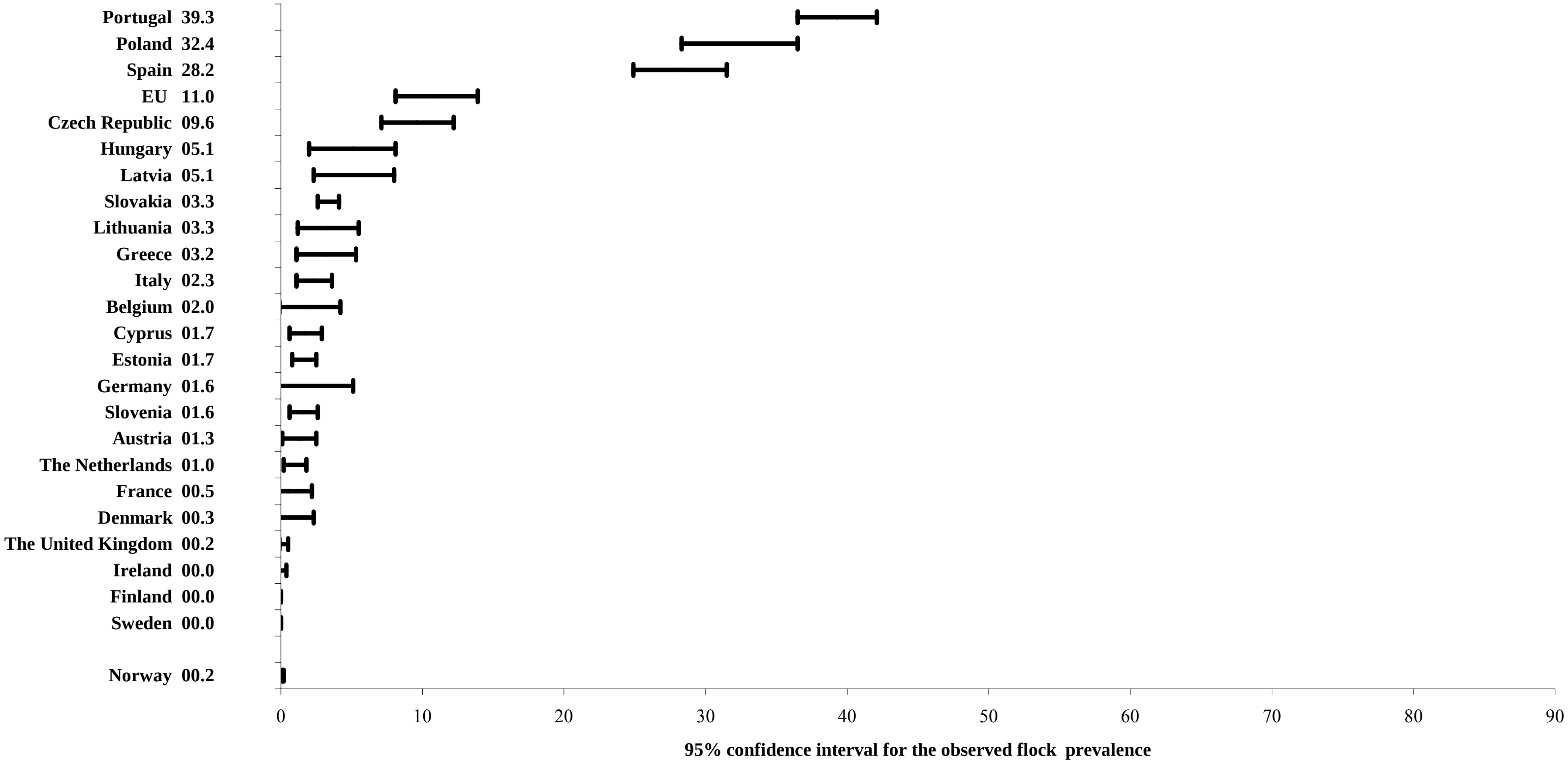
*: Broiler flock prevalence estimate (proportion of the total number of broiler flocks over the one year period that are positive)

Figure 1. Observed prevalence* of *Salmonella* - positive broiler flocks, with 95% confidence intervals, in the EU, 2005-2006



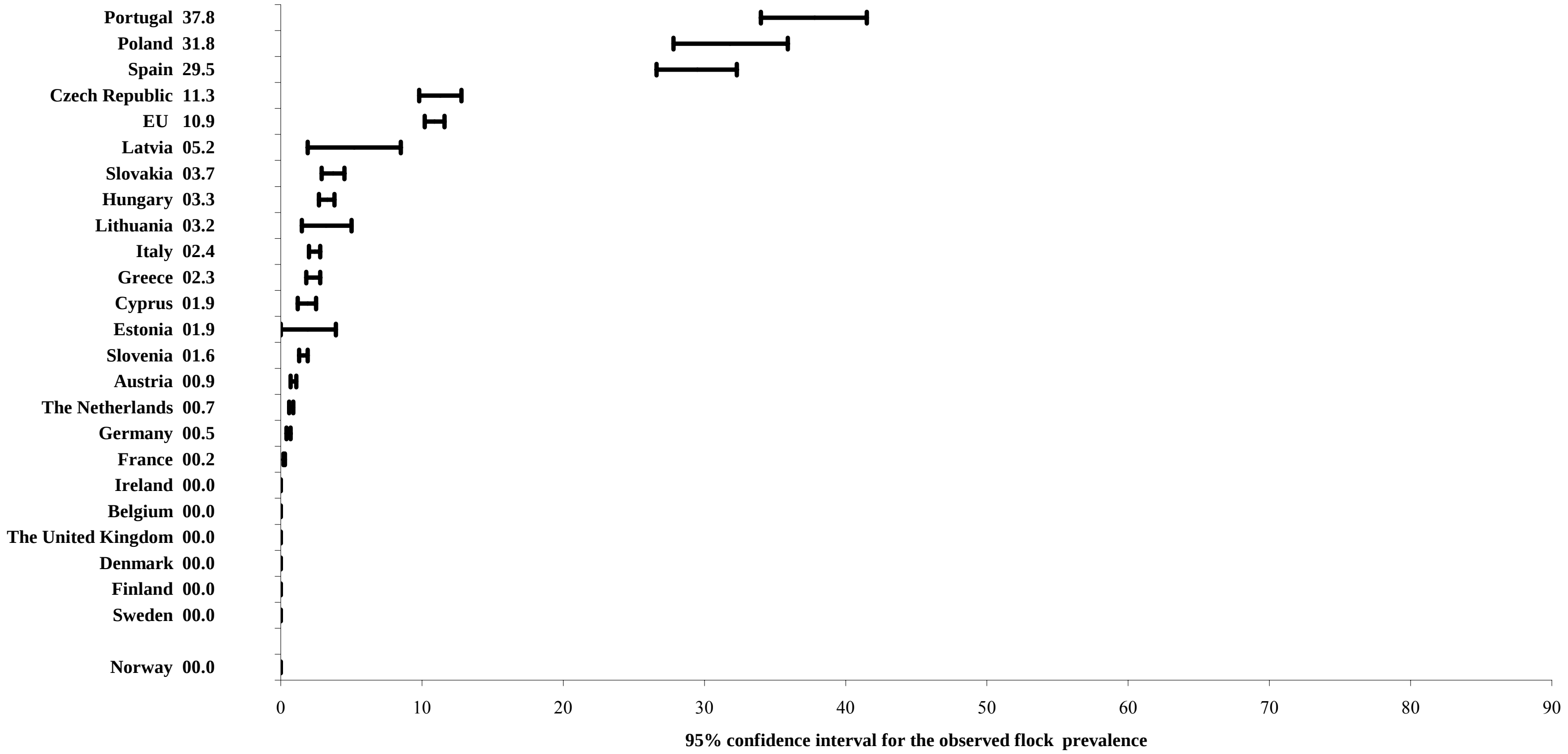
*: Broiler flock prevalence estimate (proportion of the total number of broiler flocks over the one year period that are positive)

Figure 2. Observed prevalence* of *S.* Enteritidis and/or *S.* Typhimurium - positive broiler flocks, with 95% confidence intervals, in the EU, 2005-2006



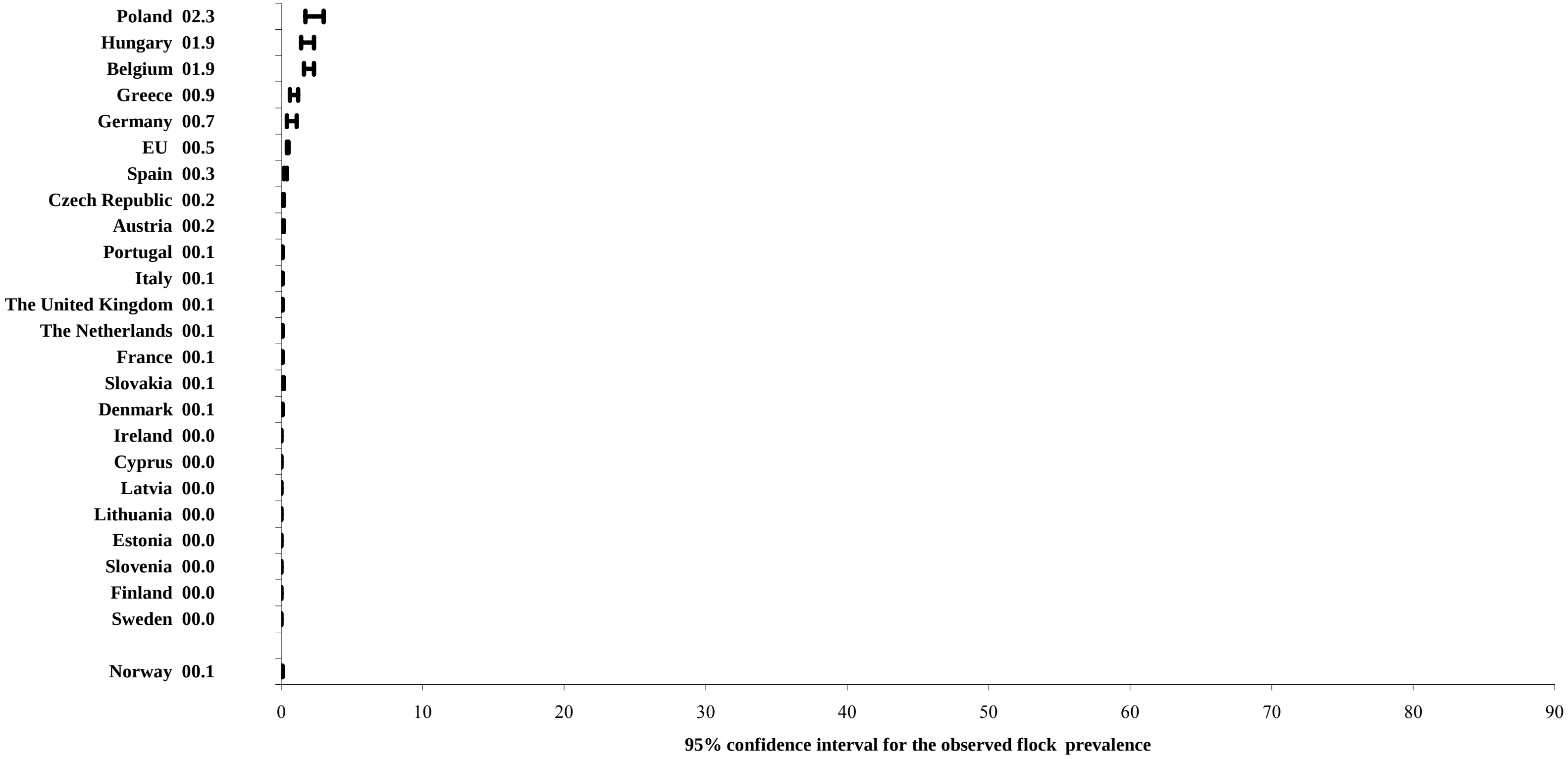
*: Broiler flock prevalence estimate (proportion of the total number of broiler flocks over the one year period that are positive)

Figure 3. Observed prevalence* of *S.* Enteritidis - positive broiler flocks, with 95% confidence intervals, in the EU, 2005-2006



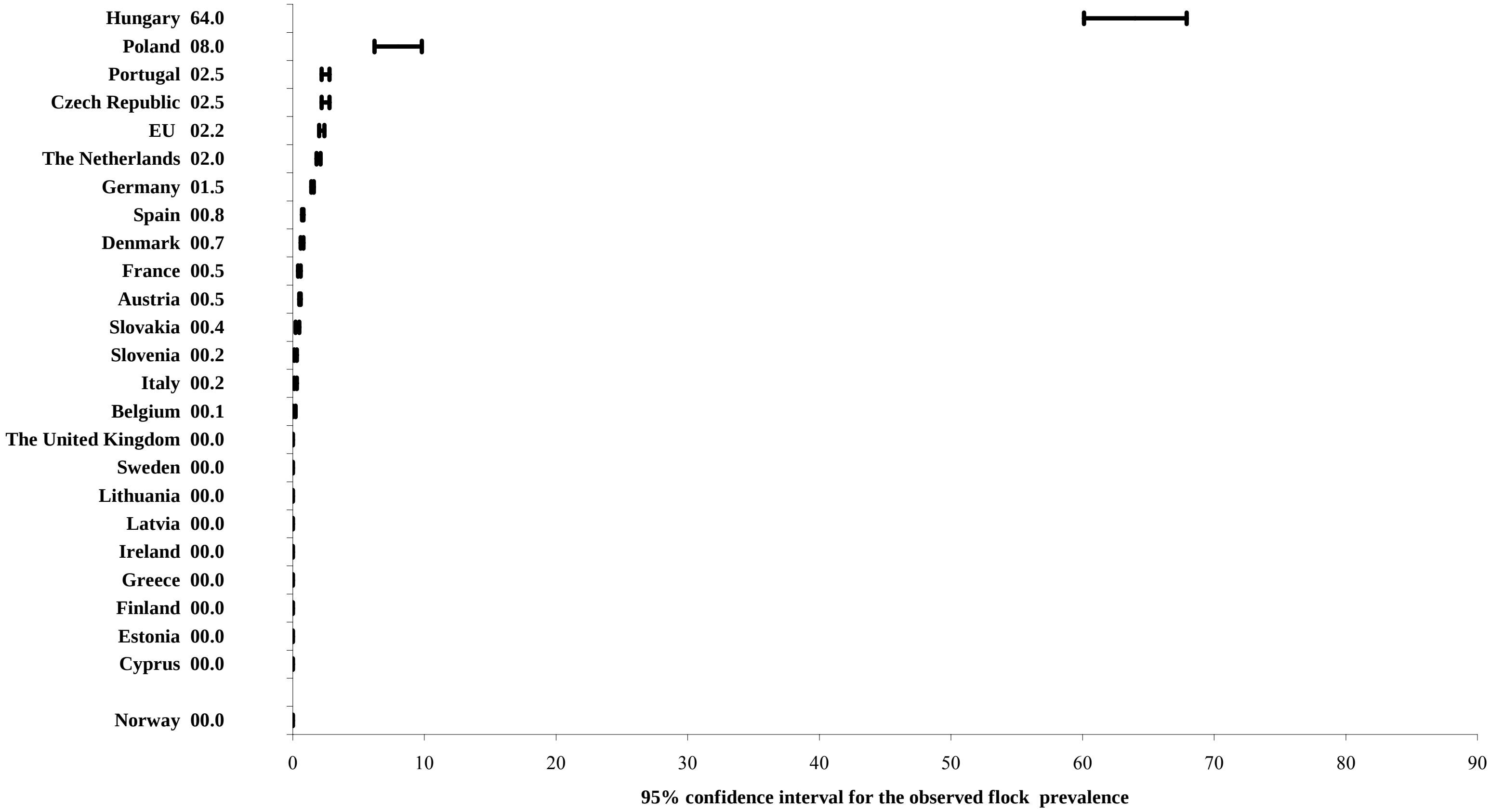
*: Broiler flock prevalence estimate (proportion of the total number of broiler flocks over the one year period that are positive)

Figure 4. Observed prevalence* of *S.* Typhimurium - positive broiler flocks, with 95% confidence intervals, in the EU, 2005-2006



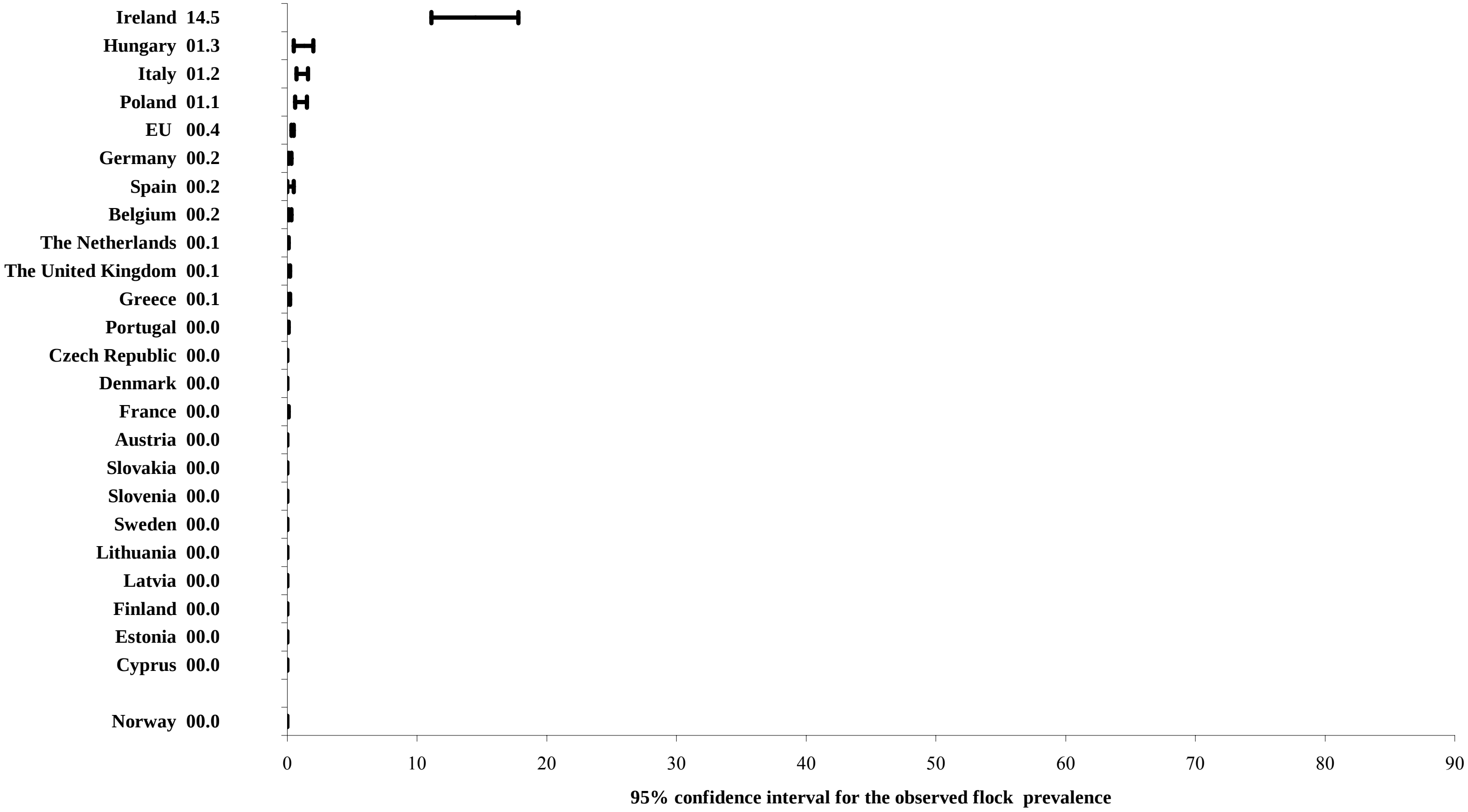
*: Broiler flock prevalence estimate (proportion of the total number of broiler flocks over the one year period that are positive)

Figure 5. Observed prevalence* of *S.* Infantis - positive broiler flocks, with 95% confidence intervals, in the EU, 2005-2006



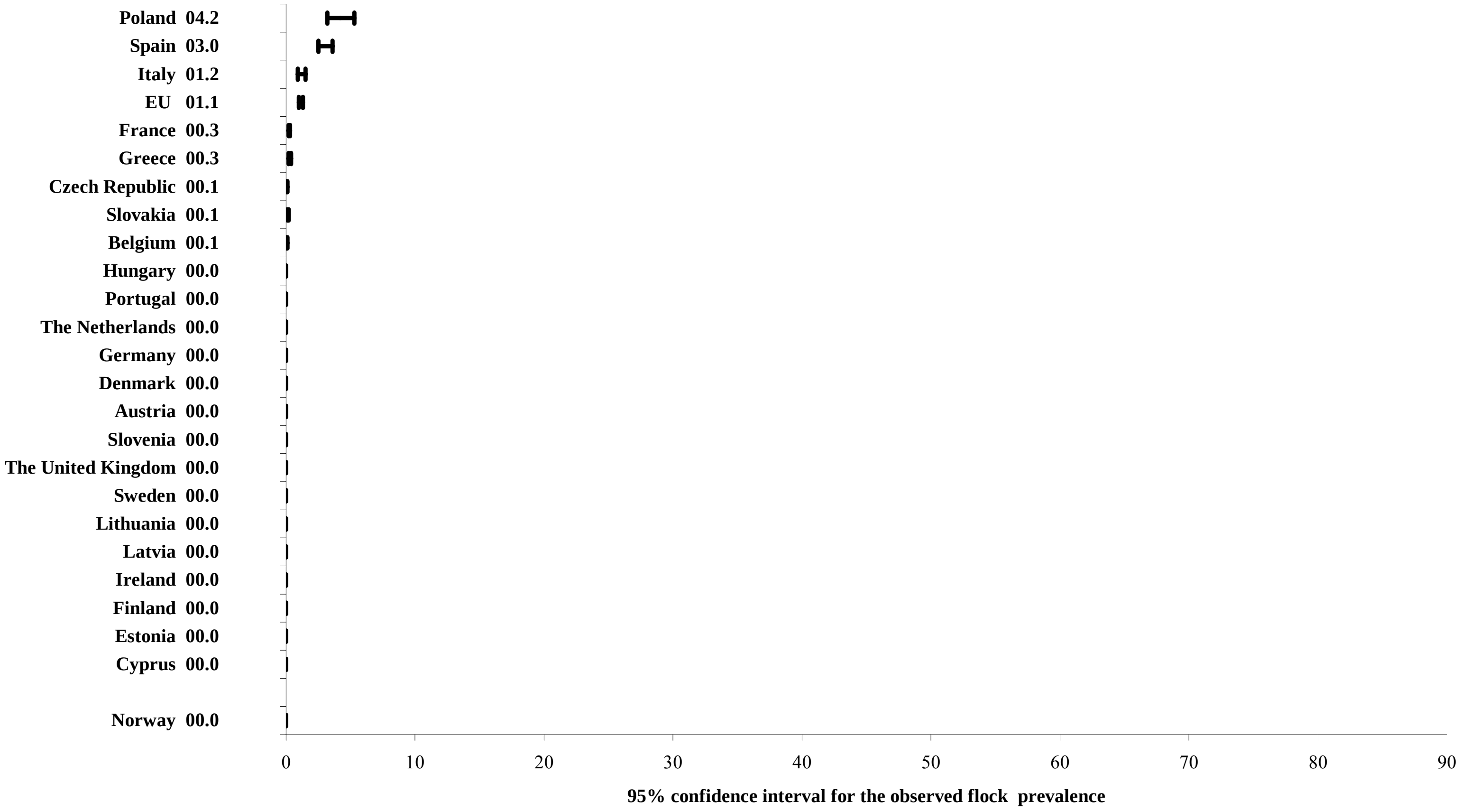
*: Broiler flock prevalence estimate (proportion of the total number of broiler flocks over the one year period that are positive)

Figure 6. **Observed prevalence* of *S.* Mbandaka - positive broiler flocks, with 95% confidence intervals, in the EU, 2005-2006**



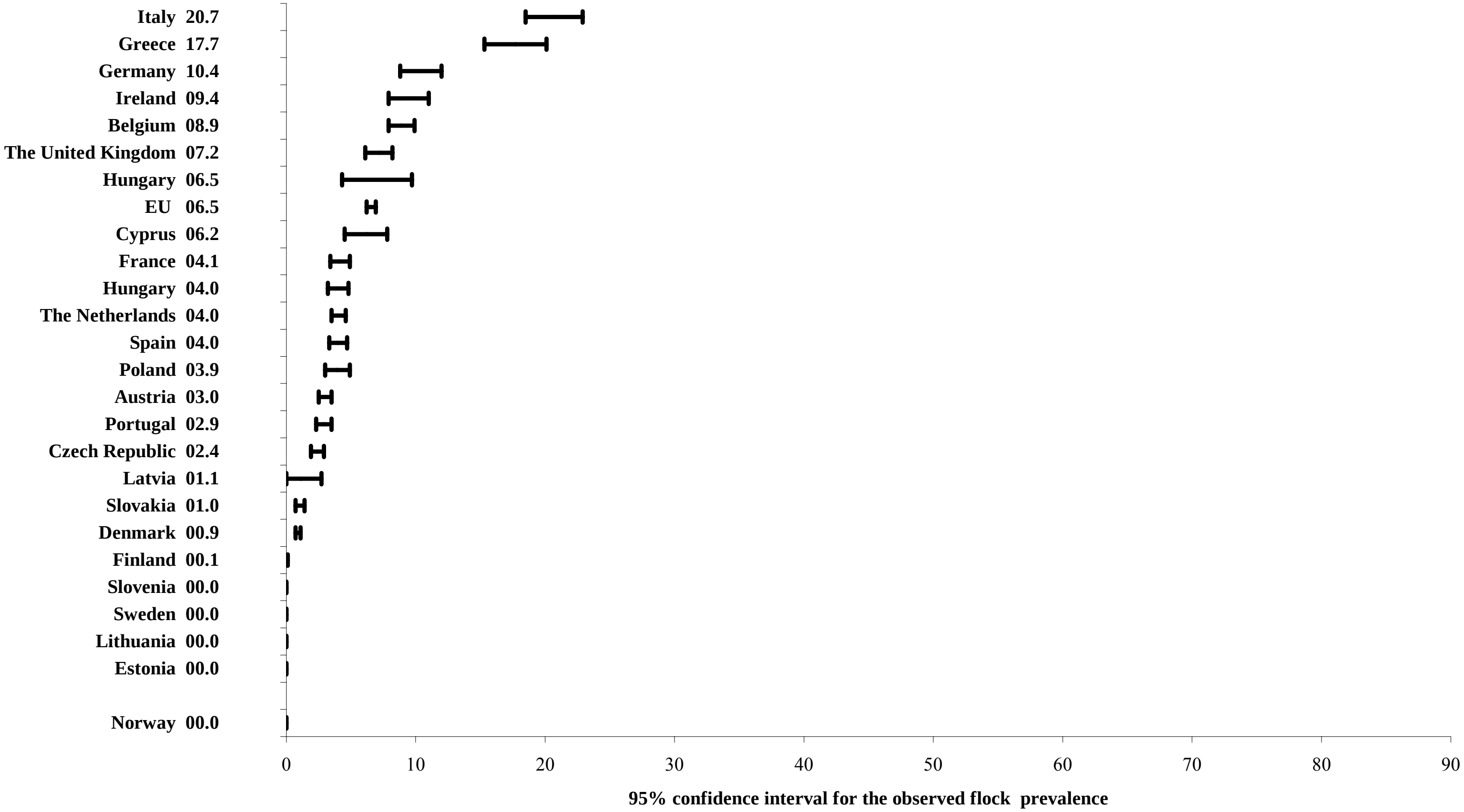
*: Broiler flock prevalence estimate (proportion of the total number of broiler flocks over the one year period that are positive)

Figure 7. Observed prevalence* of *S.* Hadar - positive broiler flocks, with 95% confidence intervals, in the EU, 2005-2006



*: Broiler flock prevalence estimate (proportion of the total number of broiler flocks over the one year period that are positive)

Figure 8. Observed prevalence* of broiler flocks positive to serovars other than *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Mbandaka and *S.* Hadar, with 95% confidence intervals, in the EU, 2005-2006



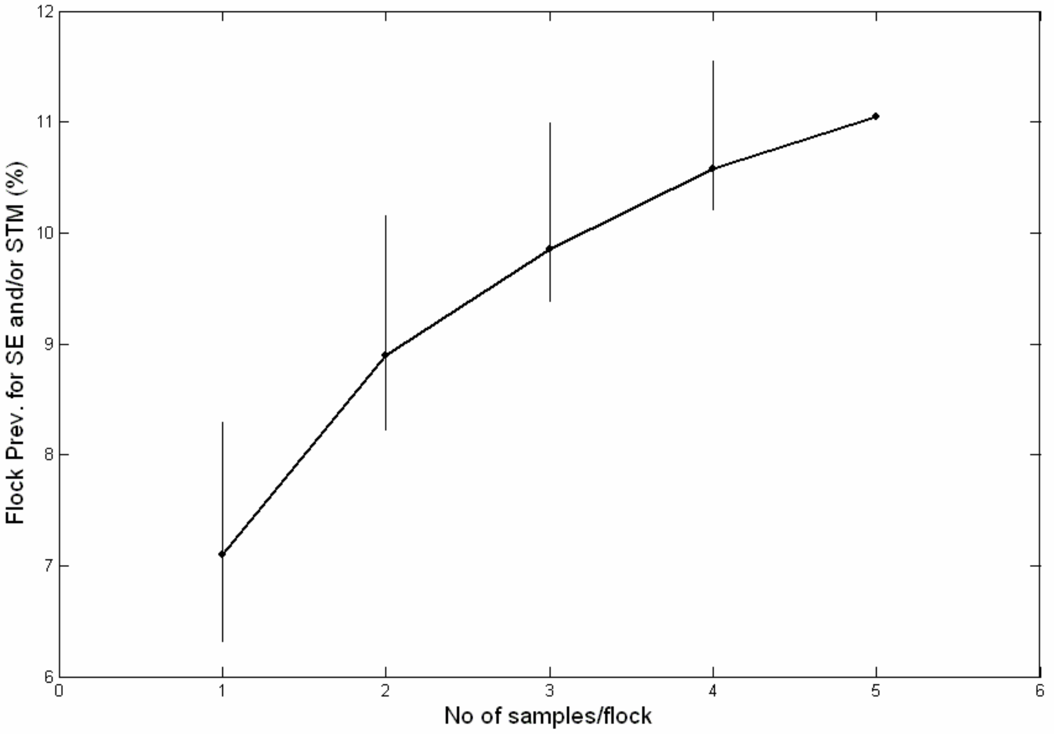
*: Broiler flock prevalence estimate (proportion of the total number of broiler flocks over the one year period that are positive)

4.2.3. Sensitivity analysis with respect to number of samples per flock (*S.* Enteritidis and/or *S.* Typhimurium EU flock observed prevalence)

4.2.3.1 Simulation-based evaluation of designs with fewer samples per flock

Figure 9 represents the simulated EU prevalence of *S.* Enteritidis and/or *S.* Typhimurium -positive broiler flocks with different number of samples taken per flock. The averaged estimate over the simulations is represented by a black spot, and the 95% confidence interval is plotted around it. As expected, the sensitivity of the sampling decreases with a lower within-flock sample size. On average over the simulations, the EU flock prevalence decreases from 11% based on 5 samples taken per flock to 9% based on 2 samples per flock and even to 7% with only one sample per flock.

Figure 9. Simulated EU prevalence of *S.* Enteritidis and/or *S.* Typhimurium -positive broiler flocks and 95% uncertainty intervals for sample sizes less than 5 per flock



Similarly, results for each Member States are reported in Table 4 and the corresponding curves plotted in Figure 9 (black curves). At the Member States' level, the general tendency follows a similar pattern as for the EU level. However, variability across Member States is very large. For example, the flock prevalence in Portugal decreases from about 40% based on 5 samples taken per flock down to less than 20% when taking only 1 sample per flock, whereas Italy only drops from 2.3% to 1.8%. Such variability is linked to the (diagnostic and analytical) test sensitivity but also to the within-flock prevalence. The more sensitive the test is, the less the estimated flock prevalence should decrease when taking fewer samples. Similarly, the more homogeneous is the sampled flock (in terms of infection), the less the estimated flock prevalence should decrease when taking fewer samples. Moreover for some countries, taking fewer samples per flocks does not make any difference in the estimated prevalence. This happens when outcomes of the test are always the same for every sample taken. It is either due to the fact that no positive samples were observed (for Finland, Ireland, Sweden) or due to either very sensitive analytical method and/or very homogeneous flocks (Austria and Cyprus mainly). For Cyprus, a (non-significant) increase is even observed in the average prevalence estimates when taking fewer samples. This is actually made possible by the model-based estimation but such small fluctuations and sometimes deviations from common sense remain within the confidence interval and are therefore meaningless.

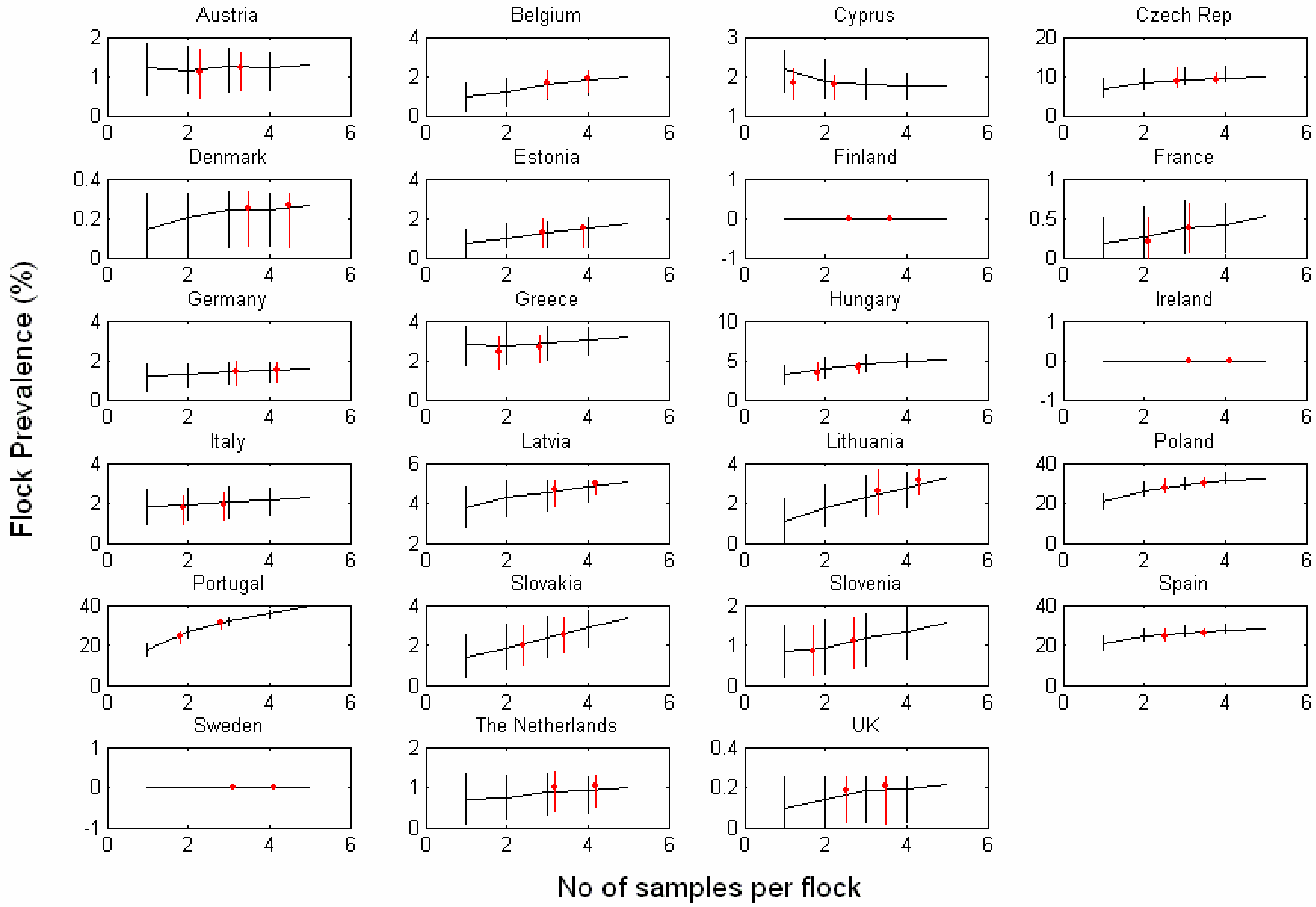
Table 4. Simulated prevalence of *S.* Enteritidis and/or *S.* Typhimurium -positive broiler flocks and 95% uncertainty intervals for sample sizes less than 5, at the EU and at the MS-specific level

		Number of samples per flock												
		N=1		N=2		N=2.5*		N=3		N=3.5**		N=4		N=5
Member State	**N**	**%pos**	**CI 95%**	**%pos**	**CI 95%**	**%pos**	**CI 95%**	**%pos**	**CI 95%**	**%pos**	**CI 95%**	**%pos**	**CI 95%**	
Austria	365	1.2	0.5 - 1.9	1.1	0.6 - 1.8	1.1	0.4 - 1.7	1.2	0.6 - 1.8	1.2	0.6 - 1.6	1.2	0.6 - 1.6	1.3
Belgium	373	0.9	0.2 - 1.8	1.2	0.5 - 1.9	1.6	0.9 - 2.3	1.6	0.8 - 2.3	1.9	1.2 - 2.4	1.8	1 - 2.4	2.0
Cyprus	248	2.2	1.6 - 2.7	1.9	1.5 - 2.4	1.8	1.4 - 2.2	1.8	1.4 - 2.2	1.8	1.4 - 2.1	1.8	1.4 - 2.1	1.7
Czech Republic	334	6.9	4.9 - 9.6	8.4	6.6 - 12.2	8.6	7.2 - 12.5	9.0	7.8 - 12.7	9.1	8.2 - 11.2	9.5	8.6 - 13	9.6
Denmark	295	0.1	0 - 0.3	0.2	0 - 0.3	0.3	0.1 - 0.3	0.2	0.1 - 0.3	0.3	0 - 0.3	0.2	0.1 - 0.3	0.3
Estonia	139	0.8	0 - 1.5	1.0	0.5 - 1.8	1.3	0.5 - 2.1	1.2	0.5 - 1.8	1.5	0.5 - 1.7	1.5	0.5 - 2.1	1.7
Finland	360	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0
France	381	0.2	0 - 0.5	0.3	0 - 0.7	0.2	0 - 0.5	0.4	0 - 0.7	0.4	0.1 - 0.7	0.4	0.1 - 0.7	0.5
Germany	377	1.2	0.4 - 1.9	1.3	0.6 - 1.9	1.4	0.8 - 2	1.4	0.8 - 2	1.5	0.9 - 1.9	1.5	0.9 - 1.9	1.6
Greece	245	2.8	1.7 - 3.8	2.7	1.8 - 3.9	2.4	1.5 - 3.3	2.9	2 - 3.8	2.6	1.8 - 3.4	3.1	2.3 - 3.8	3.2
Hungary	359	3.1	1.9 - 4.4	3.9	2.7 - 5.5	3.5	2.4 - 4.9	4.4	3.5 - 5.8	4.2	3.4 - 4.9	4.8	4.1 - 6	5.1
Ireland	351	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0
Italy	313	1.8	1 - 2.7	2.0	1.2 - 2.8	1.8	0.9 - 2.5	2.1	1.3 - 2.9	2.0	1.2 - 2.6	2.2	1.4 - 2.8	2.3
Latvia	121	3.8	2.8 - 4.9	4.3	3.4 - 5.2	4.7	3.9 - 5.2	4.5	3.6 - 5.2	5.0	4.4 - 5.2	4.9	4.1 - 5.2	5.1
Lithuania	156	1.1	0 - 2.3	1.8	0.8 - 2.9	2.6	1.5 - 3.7	2.3	1.3 - 3.4	3.2	2.5 - 3.7	2.8	1.8 - 3.6	3.3
Poland	357	20.4	17.1 - 25.2	26.3	23.6 - 31.6	27.6	25.2 - 32.7	29.1	27 - 33.3	30.1	28.3 - 33.7	31.2	29.5 - 35.8	32.4
Portugal	367	17.7	14.4 - 21.5	26.7	23.6 - 30	24.4	21 - 27.9	32.0	29.4 - 34.6	31.2	28.3 - 33.8	36.0	33.6 - 38	39.3
Slovakia	230	1.4	0.4 - 2.6	1.9	0.8 - 3.1	2.0	1 - 3.1	2.4	1.4 - 3.5	2.6	1.6 - 3.4	2.9	1.9 - 3.8	3.3
Slovenia	326	0.8	0.2 - 1.5	0.9	0.3 - 1.7	0.9	0.2 - 1.5	1.2	0.5 - 1.8	1.1	0.4 - 1.7	1.4	0.7 - 1.9	1.6
Spain	388	20.8	17.9 - 25	24.3	22.1 - 28.9	24.5	22.5 - 29.3	26.1	24.4 - 30.4	26.1	24.6 - 28.8	27.5	26.1 - 31.3	28.2
Sweden	291	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0
The Netherlands	362	0.7	0.1 - 1.4	0.7	0.2 - 1.3	1.0	0.4 - 1.4	0.9	0.3 - 1.4	1.0	0.5 - 1.3	0.9	0.4 - 1.3	1.0
The United Kingdom	382	0.1	0 - 0.3	0.1	0 - 0.3	0.2	0 - 0.3	0.2	0 - 0.3	0.2	0 - 0.3	0.2	0 - 0.3	0.2
EU	**7,120**	**7.1**	**6.3 - 8.3**	**8.9**	**8.2 - 10.2**	**8.9**	**8.4 - 10.3**	**9.9**	**9.4 - 11**	**9.9**	**9.5 - 10.7**	**10.6**	**10.2 - 11.6**	**11.0**
Norway	**320**	**0.0**	**0 - 0.3**	**0.1**	**0 - 0.3**	**0.0**	**0 - 0.3**	**0.1**	**0 - 0.3**	**0.1**	**0 - 0.3**	**0.2**	**0 - 0.3**	**0.2**

*= average number of samples per flock, when taking 1 sample where flock size cat.=1, 2 samples where flock size cat.=2 etc…

**= average number of samples per flock, when taking 2 samples where flock size cat.=1, 3 samples where flock size cat.=2 etc…

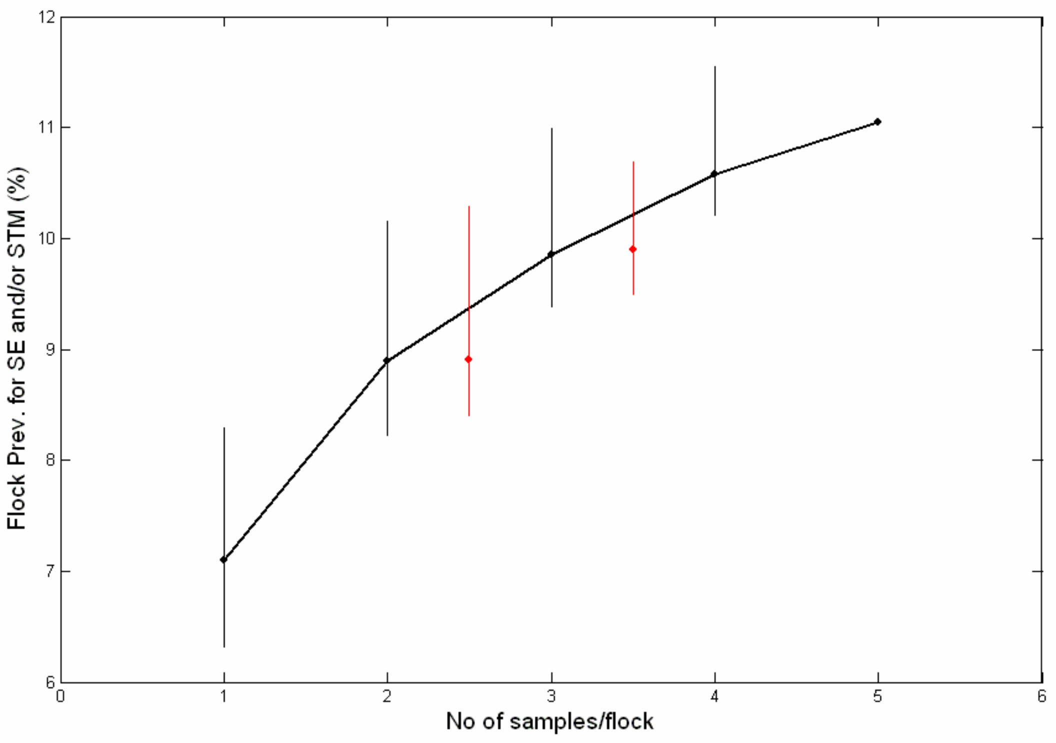
Figure 10. **Simulated MS-specific prevalence of *S.* Enteritidis and/or *S.* Typhimurium -positive broiler flocks and 95% uncertainty intervals for sample sizes less than 5: the red plots are the prevalence when the sample size is accounting for flock size**



4.2.3.2 Sampling less than five samples per flock and accounting for flock size

Results of the simulations using flock size-dependent number of samples are reported in red in Figure 9 and Figure 11, for the two designs investigated. Figure 11 shows the curve at the EU level, where the designs correspond to respectively an average number of samples per flock equal to 2.5 for design 1 and 3.5 for design 2. The plot demonstrates that estimated flock prevalence using such designs is even a bit below the curve drawn using the same number of samples for every flock. Considering the confidence intervals, it can be concluded that taking more samples in larger flocks does not increase the sensitivity of the testing. Similar graphical analysis was made at the Member States level in Figure 9. For each Member State, the average number of samples per flock was derived for both designs in order to be able to compare the flock size dependent designs (in red) with the normal ones (in black). It appears that for some Member States, such as the Netherlands or the United Kingdom, the designs bring slightly more sensitivity, whereas for some others it does the opposite. In both cases, the change compared to standard designs is negligible and not significant with respect to the confidence intervals. The overall conclusion of this simulation exercise is that taking more samples in larger flocks and fewer samples in smaller ones does not increase the sensitivity of the flock prevalence estimation, neither at the Member States-level, nor at the EU level.

Figure 11. Simulated EU prevalence of *S.* Enteritidis and/or *S.* Typhimurium -positive broiler flocks and 95% uncertainty intervals for sample sizes less than 5, while accounting for flock size (marked red)



4.2.4. *Salmonella* within-flock number positive samples

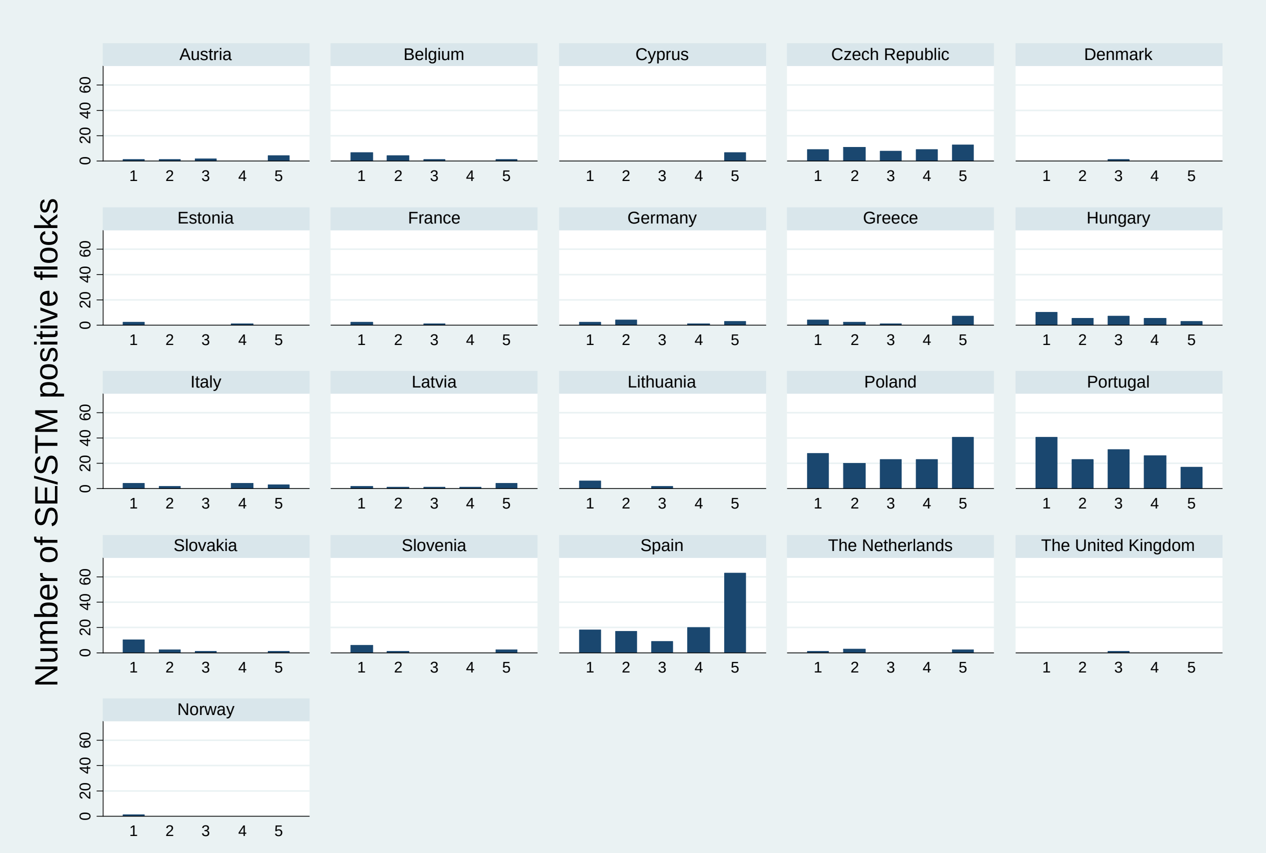
A total of five samples were taken from each broiler flock sampled, and in positive flocks one to five samples were positive. In this dataset there were 1,448 broiler flocks positive for *Salmonella* whereas 597 flocks were positive to *S.* Enteritidis and/or *S.* Typhimurium.

The number of samples positive for *Salmonella* in the positive flocks varied between one and five. The overall proportions of *Salmonella* positive flocks found positive on the basis of one, two, three, four and five positive samples was not evenly distributed but was 20%; 13%; 12%; 13% and 42%, respectively. The MS-specific distribution of the within-flock number of *Salmonella*-positive samples in the positive flocks varied importantly between countries and is shown in Figure 12. A large number of MSs, such as Hungary, Ireland, Poland, Spain and The Netherlands, had a major part of their *Salmonella* positive flocks with all five samples positive.

Figure 12. Distribution of the within-flock number of *Salmonella* positive samples in *Salmonella* positive broiler flocks observed in the EU MSs, 2005-2006

The overall proportions of *S.* Enteritidis and/or *S.* Typhimurium positive flocks found positive on the basis of one, two, three, four and five positive samples was more evenly distributed. The proportions were respectively, 25%; 16%; 15%; 15% and 29%. The MS-specific distribution of the within-flock number of positive samples in the positive flocks varied importantly and is shown in Figure 13. Some MSs had a relative important number of positive flocks where only one or two samples were positive while other MSs had many *S.* Enteritidis and/or *S.* Typhimurium positive flocks where four or five samples were positive.

Figure 13. Distribution of the within-flock number of *Salmonella* Enteritidis and/or Typhimurium positive samples in *Salmonella* Enteritidis and/or Typhimurium positive broiler flocks observed in the EU MSs, 2005-2006



4.3. Frequency distribution of *Salmonella* serovars

The serotyping of *Salmonella* isolates was mandatory according to the technical specifications of the survey. At least one isolate from each positive sample was to be typed according to the Kaufmann-White Scheme. Results from any flock where the serovar information was not available for any isolate were excluded from the final dataset. Together there were 4,962 *Salmonella*- positive samples (13.3% of 37,200 samples) originating from 1,448 positive flocks, which corresponded to 1,407 positive holdings. Two different *Salmonella* serovars were isolated from 12 *Salmonella*-positive samples.

The ten most frequently isolated *Salmonella* serovars in the EU are listed in Table 5. This table is ranked based on the percentages of specific *Salmonella* serovar-positive flocks, as flock is the epidemiological unit of interest. The serovar frequency distribution for the EU as well as for each MS was based on the number of typed isolates, including non-typeable isolates. MS-specific overviews of the most frequently isolated serovars are shown in Annex IX. Sweden was the only country not to detect any *Salmonella* positive sample.

S. Enteritidis was the most frequently reported serovar from the broiler flocks in EU with 37.1% proportion of the *Salmonella* positive flocks. The two next most frequent serovars were *S.* Infantis and *S.* Mbandaka (20.4% and 7.9% of the *Salmonella* positive flock, respectively). *S.* Typhimurium was the 4th most frequent serovar followed by *S.* Hadar.

The distribution of the serovars varied strongly amongst the MSs. *S.* Enteritidis was the dominant serovar in less than half of (10 of the 23) MSs reporting *Salmonella* findings. *S.* Infantis was the leading serovar in 3 MSs, and *S.* Mbandaka and *S.* Typhimurium both in one MS.

Six MSs (Belgium, Denmark, Finland, Ireland, Sweden and the United Kingdom) did not detect any *S.* Enteritidis isolates among their *Salmonella* findings while 2 MSs (Estonia and Lithuania) only isolated *S.* Enteritidis serovar.

The proportion of *S.* Infantis-positive flocks in relation to the total number of *Salmonella*-positive flocks ranged from 1.1% (Italy) to 88.6% (Hungary) in the 14 MSs that identified this serovar. For *S.* Mbandaka this proportion varied from 1.2% (Spain) to 56.1% (Ireland) in the 12 MSs reporting this serovar. In case of *S.* Typhimurium, the range was from 1.1% (Italy) to 22.8% (Belgium) in the 15 MSs that isolated the serovar.

Figure 14 displays the geographical distribution of the most frequently isolated *Salmonella* serovars in the MSs.

Figure 14. Most frequently identified *Salmonella* serovars (the percentage of the *Salmonella* positive units) in the EU broiler flocks, 2005 – 2006

The number between brackets indicates the number of *Salmonella* positive broiler flocks in the Member States. In case that the second or third highest percentage positive flocks were the same for more than one serovar, these percentages were not displayed. The *Salmonella* Group B figure for Germany includes the not fully typed *Salmonella* serovar with (incomplete) antigenic formula 4,12:d:- and does not include *S.* Typhimurium.

Table 5. Frequency distribution of isolated *Salmonella* serovars in the broilers baseline survey, 2005-2006

Serovars (N totl = 4,962)			Holdings with serovars (N totl = 1,407)		Flocks with serovars (N totl = 1,448)		No of Member States
	N	%	N	%	N	%	reporting the serovar
S. Enteritidis	1677	33.8	523	37.1	538	37.1	17
S. Infantis	1090	22.0	283	20.1	295	20.4	14
S. Mbandaka	400	8.1	106	7.5	114	7.9	12
S. Typhimurium	150	3.0	64	4.6	65	4.6	15
S. Hadar	186	3.7	59	4.2	59	4.1	8
S. Kentucky	130	2.6	43	3.1	44	3.0	5
S. Livingstone	105	2.1	39	2.8	39	2.7	8
S. Anatum	90	1.8	32	2.3	32	2.2	8
S. Montevideo	84	1.7	31	2.2	31	2.1	6
S. Virchow	93	1.9	30	2.1	30	2.1	11
Other serovars	969	19.5					
Salmonella spp.	26	0.5	10				

4.4. Overview of the quality of the bacteriological testing

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

The CRL-*Salmonella* reported on the quality of the serotyping of non-typable *Salmonella* isolates from the baseline survey on broiler flocks performed by the NRL's.

Seven of the 25 NRL's-*Salmonella* sent in some non-typable isolates to the CRL; 16 NRL's indicated that they had not found any non-typable isolates and two NRL's-*Salmonella* gave no response.

Only a very low number of non-typable *Salmonella* strains were found during this baseline survey by the NRL's-*Salmonella*. A total of 36 strains were sent to the CRL-*Salmonella*, of which four were in fact typable strains (although mixed cultures in two cases). Of the remaining 32 strains, CRL-*Salmonella* was able to further identify (only) six strains to serovar names. Although the CRL-*Salmonella* also followed the Kauffmann-White scheme for serotyping the strains, extra or alternative culture steps were used, which are in most cases not routinely used at the NRL's-*Salmonella*. Because of this 'special treatment' the CRL-*Salmonella* was able to further identify the strains where the NRL was not able to do so. Still 19 isolates could only be identified to the level of subspecies and seven isolates could only biochemically be identified as *Salmonella* while serotyping was not possible as the strains were rough.

5. Discussion

5.1. Observed prevalence of *Salmonella*

Rationale for estimating the flock prevalence

The study design laid down by technical specifications for the broiler baseline survey prescribed sampling of one flock per holding. This design has not proven to be optimal for the estimation of the prevalence for the reasons explained in Annex V and also reported for the *Salmonella* in laying hens baseline study[1]. The holding (observed) prevalence estimates are not a robust measure of infection from a statistical point of view.

The fact that approximately two thirds of the Member States sampled at least once more than one flock in the holdings in this survey, made it possible to estimate the flock prevalence. This prevalence is epidemiologically more relevant estimate since flocks constitute separate epidemiological units, even though there may be some clustering of infection in flocks from same holding.

Furthermore, since the flocks were randomly selected for sampling and the *Salmonella* status of the holding did not per se influence the proportion of flocks selected per holding, the flock prevalence estimate should not be significantly biased by the fact that some holdings had a larger proportion of flocks sampled.

For the above mentioned reasons the flock prevalence was chosen as the main outcome variable of the analyses performed. The flock prevalence estimation is understood to mean the 'proportion of *Salmonella* positive flocks out of the total number of broiler flocks over one year period in the MS or in the EU'.

Observed prevalence in the broiler flocks

The *Salmonella* spp. EU weighted flock observed prevalence is 23.7%. This means that on average one in four broiler flocks were infected with a *Salmonella* serovar during the last three weeks prior to slaughter.

The EU weighted observed prevalence of flocks positive to *S.* Enteritidis and/or *S.* Typhimurium was 11.0%. This observed prevalence means that on average one in ten broiler flocks were positive to these serovars during the last three weeks before slaughter.

Differences in the MS-specific flock prevalence were considerable, with the result that an EU weighted mean can be regarded as arbitrary and of little practical use. For example, the observed *Salmonella* spp. and observed *S.* Enteritidis/*S.* Typhimurium flock prevalences at the MS level range from 0% to 68.2% and 0% to 39.3%, respectively.

For *Salmonella* spp. positive flocks all prevalence scenarios were present in the MSs, ranging from very low to moderate, up to a high prevalence.

It is noteworthy that in case of the specific *Salmonella* serovar prevalence, a few MSs accounted for most of the positive findings while large proportion of the other MSs had very low or low

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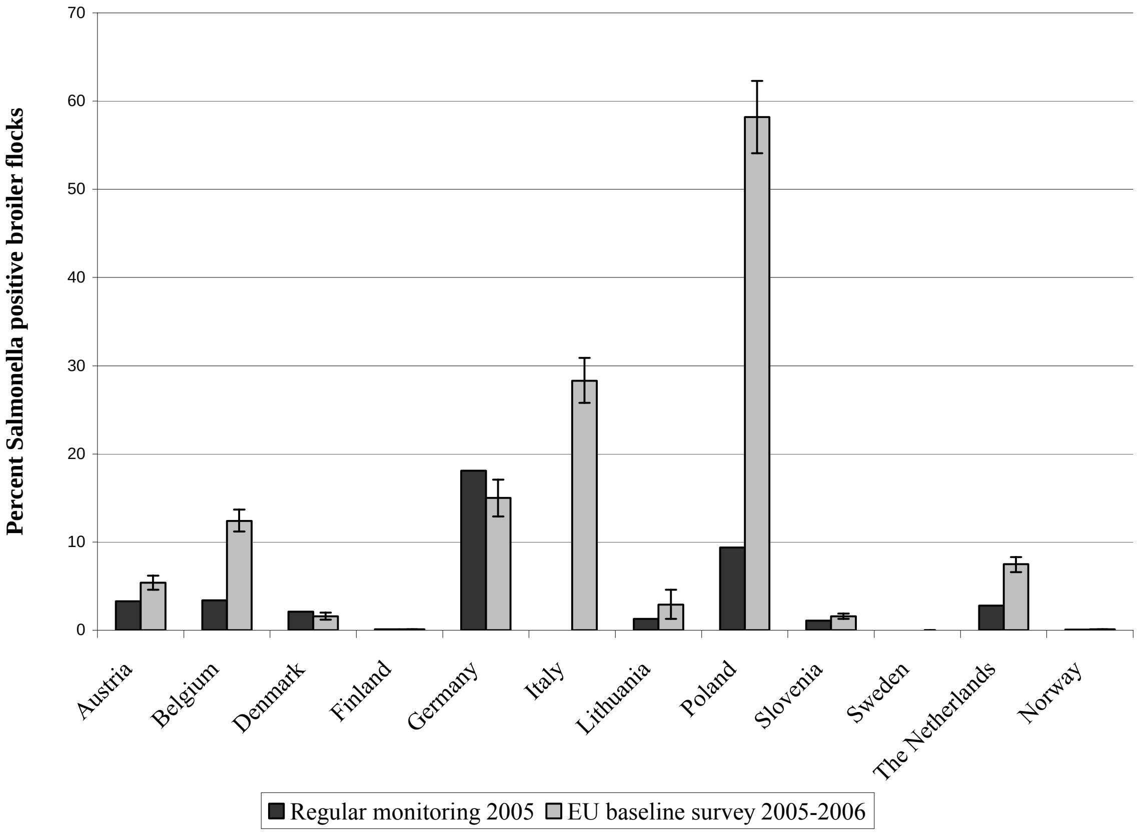
[1] Report of the Task Force on Zoonoses Data Collection on the Analysis of the baseline study on the prevalence of Salmonella in holdings of laying hen flocks of Gallus gallus, The EFSA Journal (2007), 97.

prevalence. This is in particular the case for S. Enteritidis, S. Infantis and S. Mbandaka, where some MSs had outlying high prevalence figures. This shows that in addition to large variation in the *Salmonella* prevalence, the serovar distribution also varies remarkably between the MSs.

When compared to the *Salmonella* prevalence deriving from the routine monitoring of broiler flocks that MSs reported in the annual Community Summary Report on Zoonoses in 2005[1], the prevalence in the baseline survey are comparable or substantially higher (Figure 15). The substantially higher prevalence results may be explained by the more sensitive sampling design applied in the baseline survey or the increased sensitivity of the ISO 6579 Annex D analytical method used. Also the fact that the period of sampling was not exactly the same may have contributed to this difference.

Figure 15. Comparison of the proportion of *Salmonella* positive broiler flocks found as part of the regular monitoring in 2005 and the *Salmonella* flock prevalence observed in the EU baseline study conducted from October 2005 to September 2006



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[1] The Community Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents, Antimicrobial Resistance and Foodborne Outbreaks in the European Union in 2005, *The EFSA Journal* (2006), 94.

5.2. Within-flock *Salmonella* number of positive samples and expected results if fewer samples had been taken per flock

In this survey an important proportion of the flocks positive for *Salmonella* spp. were positive in all the five sample taken. This could indicate that the within-flock *Salmonella* prevalence tends to be high in broiler flocks, and a reduction in the number of samples taken from a flock is not likely to change substantially the numbers of flocks found positive. However, there were important MS-specific variations in this distribution of the within-flock number of *Salmonella*-positive samples, and therefore this general conclusion does not necessarily apply to all MSs.

The situation was different for *S.* Enteritidis and/or *S.* Typhimurium positive flocks, where the positivity of samples was more evenly distributed. This may indicate, at the EU-level, that a within-flock sample size reduction would impact more on the numbers of flocks found positive. This observation is consistent with the findings of the simulation which indicated that, at the EU-level, a within-flock sample size reduction would impact on the sensitivity of the sampling scheme, and thereby the accuracy of the prevalence estimates. This impact seemed to be significant when the number of samples was reduced from five to two or one sample. The adjusting of the number of samples according to the size of the flock did not improve the sensitivity of the sampling.

These findings may be considered when assessing the accuracy of prevalence estimates from future routine monitoring of broiler flocks. However, it should be bared in mind that direct comparison between different numbers of faecal dropping samples is difficult, because fewer samples are usually collected correspondingly from a larger area.

5.3. Frequency of isolated *Salmonella* serovars

S. Enteritidis was the main serovar isolated in broiler flocks in the survey accounting approximately one third of the positive flocks. However, the dominance of this serovar was not as strong as in the *Salmonella* baseline study in laying hens, where 60% of the *Salmonella*-positive holdings were positive for *S.* Enteritidis. Indeed, more varied serovar distributions were apparent in the broiler baseline survey. The contribution of serovars other than *S.* Enteritidis and *S.* Typhimurium was greater, especially that of *S.* Infantis and *S.* Mbandaka[1].

Together six out of the 10 most frequently reported serovars in the broiler flocks are amongst the 10 most commonly reported serovars in human salmonellosis cases in 2005 in EU (the Community Summary Report 2005). These serovars include *S.* Enteritidis, *S.* Infantis, *S.* Hadar, *S.* Typhimurium, *S.* Virchow and *S.* Anatum. In the salmonellosis cases in humans the three most frequent serovar in 2005 were *S.* Enteritidis (52.5% of the cases), *S.* Typhimurium (9.1%) and *S.* Infantis (0.8%), and all the other serovars accounted less than 0.5% of the cases each (data from Basic Surveillance Network).

The results of the survey show that in some Member States broiler flocks form an important reservoir of *S.* Enteritidis infections. The relatively frequent findings of other serovars of public

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[1] *S.* Mbandaka was isolated most frequently in Ireland. According to the Irish Authorities the frequent isolation of this serovar in their country during the period of the baseline survey was to a large extend attributable to the high prevalence of this specific serovar in one single integrated company. This fairly isolated event importantly influenced the Community frequency of *S.* Mbandaka isolates in the survey.

health importance, such as *S.* Infantis, *S.* Typhimurium and *S.* Hadar, from the broiler flocks indicate that broilers may be a relevant reservoir for these serovars as well in relation to human infections. As the serovar distribution greatly varied between the MSs, the situations are likely to be MS specific. For example, in a number of Member States *S.* Enteritidis was detected in only a small proportion of broiler flock/holdings (including six Member States and Norway where it was not detected at all).

A more in depth analyses of the *Salmonella* serovars including the phage types will be presented in the Part B report.

5.4. Relevance of the findings to human health

Salmonella is an important cause of food-borne diseases in humans in the Europe (Community Summary Report 2005). Salmonellosis can range from a mild to severe gastroenteritis and in some people, invasive disease, which can be fatal. Long term sequelae such as reactive arthritis can also result from *Salmonella* infections.

In 2005, the reported number of human salmonellosis cases in the EU was 176,395 corresponding to an incidence of 38.2 cases per 100,000 inhabitants (Community Summary Report 2005). Broiler meat is considered an important source of human salmonellosis in Europe[1]. Indeed, in the EU, broiler meat was the second most frequently reported source of food-borne outbreaks caused by *Salmonella* in 2005 (Community Summary Report 2005).

In this baseline survey, broiler flocks were sampled within 3 weeks prior to slaughter. The flocks found infected with *Salmonella* at that stage are also likely to be infected at the time of slaughter. During the slaughter process of infected flocks the broiler carcasses are subject to *Salmonella* contamination and also cross-contamination between infected and non-infected slaughter batches may take place. This results in *Salmonella* contaminated meat being placed on the market. According to the Community Summary Report 2005, 0-18% of the fresh (raw) broiler meat samples were found to be *Salmonella* positive in the investigations carried out by the MSs.

Thorough cooking destroys the *Salmonella* bacteria present in meat. As broiler meat is typically consumed in a well cooked form, properly prepared broiler meats do not pose a health risk for consumers. The *Salmonella* infection risk arises from undercooking of the broiler meat or from cross-contamination from raw broiler meat to other dishes during preparation in the kitchen (e.g. via food handlers, utensil or food contact surfaces). Good kitchen hygiene and thorough cooking of broiler meat will prevent or reduce the risk. Consumer education campaigns and strict hygiene measures and HACCP-principles implemented by mass catering and restaurants would further contribute to the reduction of the risk.

5.5. The *Salmonella* reduction target

The Regulation (EC) No 2160/2003 foresees setting of the *Salmonella* reduction target for broiler flocks for only two serovars, *S.* Enteritidis and *S.* Typhimurium, for a transitional 3 year period. These are the two most frequently reported *Salmonella* serovars in salmonellosis cases in humans

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[1] SCVPH, (2003). Opinion of the Scientific Committee on Veterinary Measures relating to Public Health on *Salmonellae* in Foodstuffs. Adopted on 14-15 April.

in EU and therefore agreed to be of special public health importance. The scope of the target could be extended to other serovars having public health importance, but only after risk-benefit analyses. As these risk benefit analyses are not currently available at the EU level, it is likely that the reduction target will be set to only *S.* Enteritidis and *S.* Typhimurium at this stage.

However, MSs are free to consider addressing other serovars of public health importance in their national *Salmonella* control programmes in order to protect their consumers, when deemed necessary. MSs may consider doing this for example in case of high *S.* Infantis or *S.* Hadar prevalence in their country.

6. Conclusions

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

- The observed flock prevalence of *Salmonella* spp. varied widely amongst MSs from 0% to 68.2%. The weighted prevalence of *Salmonella* spp. in broiler flocks within the EU was estimated to be 23.7%. The weighted flock prevalence of *S.* Enteritidis and/or *S.* Typhimurium was 11.0%.
- The 5 most frequently isolated *Salmonella* serovars from the broiler flocks were *S.* Enteritidis (37.1% of the positive flocks), *S.* Infantis (20.1%), *S.* Mbandaka (7.9%), *S.* Typhimurium (4.6%) and *S.* Hadar (4.1%). Out of these, *S.* Enteritidis, *S.* Infantis, *S.* Typhimurium and *S.* Hadar serovars are amongst the most commonly reported serovars in human *Salmonella* infections.
- The serovar distribution varied amongst the MSs, many of them having a specific distribution pattern of their own. Often, for a specific *Salmonella* serovar, a few MSs accounted for the majority of the positive flocks.
- Reducing the number of samples taken from a flock is likely to have a stronger impact on *S.* Enteritidis and/or *S.* Typhimurium prevalence than *Salmonella* spp. prevalence. Reducing the number of samples from 5 to 2 samples per flock would lead to significantly lower prevalence estimate of *S.* Enteritidis and/or *S.* Typhimurium. Adjusting the sample size according to the size of the flock would not improve the sensitivity.
- *Salmonella* infected broiler flocks contribute to consequent contamination of fresh broiler meat. Broiler meat is an important source of human salmonellosis in EU. The infection may result from undercooking of the meat or cross-contamination to other foods. Thorough cooking of the broiler meat and strict kitchen hygiene would prevent or reduce the risk posed by *Salmonella* contaminated broiler meat.

7. Recommendations

- It is recommended that MSs would address in their national *Salmonella* control programmes also other serovars than *S.* Enteritidis and *S.* Typhimurium when these other serovars are of public health importance in their country.
- Consumer education campaigns about good hygiene practices in handling of broiler meat and strict implementation of the food hygiene legislation in mass catering would increase the protection of consumers.

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Abbreviations

CI	Confidence Interval
EEA	European Economic Area
EFSA	European Food Safety Authority
EU	European Union
MS(s)	Member State(s)

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Annexes

Annex I. List of criteria used to identify non-valid and non-plausible information in the *Salmonella* broiler database

The variables are uniquely identified using the 'item integer' mentioned in the ad hoc Data Dictionary.

Step 1

In step one records were selected.

Criterion No	**Rationale for the criterion**
1	**007 Broilers in holding: < 100** This criterion excludes all records containing less than 100 broilers in the holding.
2	**007 Broilers in holding: < values for 011 Number of broilers in flock** This criterion excludes all records containing a number of broilers in the holding that is smaller than the number of broilers in the flock. A 10% difference (in case '007 broilers in holding' is a smaller number compared to '011 Number of broilers in flocks') is allowed.
3	**008 Number of flocks: <= 0** This criterion excludes all records containing a number of flocks equal to, or lower than, zero.
4	**008 Number of flocks: > 42 and no comments under 003** This criterion excludes all records containing a number of flocks higher than 42 unless comments are provided.
5	**008 Number of flocks: values: = 1 and value for 007 Broilers in holding IS NOT EQUAL TO value for 011 Number of broilers in flock** This criterion excludes all records with one flock in the holding where the number of broilers in that holding does not equal the number of broilers in the flock. A 10% difference in either direction is allowed for.

Criterion No	**Rationale for the criterion**
6	**010 Date of sampling: < 15 September 2005** This criterion excludes all records containing a date of sampling before 15 September 2005.
7	**010 Date of sampling: > 15 October 2006** This criterion excludes all records containing a date of sampling after 15 October 2006.
8	**011 Number of broilers in flock: < 100** This criterion excludes all records containing flocks with less than 100 broilers.
9	**013 Age of broilers at sampling: > 126** This criterion excludes all records containing broilers aged more than 126 days.
10	**014 Number of cycles (crop) per year in this flock: > 13** This criterion excludes all records of flocks with more than 13 cycles per year.
11	**015 Expected slaughter age: > 147 days** This criterion excludes all records containing an expected slaughter age of more than 147 days.
12	**015 Expected slaughter age: < value of 013 Age of broilers at sampling** This criterion excludes all records containing an expected slaughter age before the age of sampling.
13	**016 Expected slaughter age accuracy: no and [difference between (015 Expected slaughter date and 013 Date of sampling) > 21]** This criterion excludes all records containing flocks sampled more than 3 weeks before slaughter.
14	**017 Vaccination status: no and 018 Vaccination type: IS NOT NULL** This criterion excludes all records containing unvaccinated flocks with information of the type of vaccination.
15	**017 Vaccination status: unknown and 018 Vaccination type: IS NOT NULL** This criterion excludes all records containing flocks with an unknown vaccination status with information of the type of vaccination.

Criterion No	Rationale for the criterion
16	**017 Vaccination status: no and 019 Vaccination period: IS NOT NULL** This criterion excludes all records containing unvaccinated flocks with information of the vaccination period.
17	**017 Vaccination status: unknown and 019 Vaccination period: IS NOT NULL** This criterion excludes all records containing flocks with an unknown vaccination status with information of the vaccination period.
18	**017 Vaccination status: no and 020 Vaccination name: IS NOT NULL** This criterion excludes all records containing unvaccinated flocks with information of the vaccination name.
19	**017 Vaccination status: unknown and 020 Vaccination name: IS NOT NULL** This criterion excludes all records containing flocks with an unknown vaccination status with information of the vaccination name.
20	**021 Medication status: no and 022 Medication-antimicrobial name IS NOT NULL** This criterion excludes all records containing flocks where no antimicrobials were used during the last two weeks, with information of the antimicrobial name.
21	**026 Date of bacteriological detection testing: < value of 010 Date of sampling** This criterion excludes all records containing a date of primary testing in the laboratory before the date of sampling
22	**032 Reference of laboratory for serotyping: IS NULL (EMPTY) and 030 Test result is 'positive'** This criterion excludes all records containing positive test results without information of the reference laboratory.
23	**032 Reference of laboratory for serotyping: IS NOT NULL (NOT EMPTY)** and **030 Test result is 'negative'** This criterion excludes all records containing negative test results with information of the reference laboratory.
24	**033 Isolate (Salmonella serovar): IS NULL (EMPTY) and 030 Test result is 'positive'** This criterion excludes all records containing positive test results with no information of the isolate.
25	**033 Isolate (Salmonella serovar): IS NOT NULL (NOT EMPTY) and 030 Test result is 'negative'** This criterion excludes all records containing negative test results with information of the isolate.

Criterion No	**Rationale for the criterion**
26	**Difference date between: '010 Date of sampling' and '026 Date of bacteriological detection testing' : > 7** This criterion excludes all records containing a 'days to bacteriological start of test' above 7 days.

Step 2

In a second step holdings with less than 5 samples were excluded, which were those holdings where at least one sample did not meet one of the aforementioned exclusion criteria.

Annex II. Overview of the number of holdings per Member State after data validation and cleaning

Member States	Number of holdings having at least 5,000 broilers		
	Total[1]	Actually sampled and validated by EFSA N	Validated sampled proportion[2] %
Austria	378	359	95.0
Belgium	817	373	45.7
Cyprus	128	91	71.1
Czech Republic	309	333	107.8
Denmark	263	228	86.7
Estonia	4	4	100.0
Finland	216	196	90.7
France	6,060	381	6.3
Germany	986	377	38.2
Greece	1,180	245	20.8
Hungary	310	336	108.4
Ireland	240	263	109.6
Italy	2,213	313	14.1
Latvia	2	3	150.0
Lithuania	18	20	111.1
Poland	2,788	357	12.8
Portugal	1,700	366	21.5
Slovakia	127	187	147.2
Slovenia	362	323	89.2
Spain	4,139	388	9.4
Sweden	120	121	100.8
The Netherlands	975	359	36.8
The United Kingdom	1,295	382	29.5
EU[3]	24,630	6,005	24.4
Norway	458	320	69.9

[1]: Based on Technical specifications 'Baseline survey on the prevalence of *Salmonella* in broilers of Gallus gallus in the EU', updated by the figures provided by the Member States' during a consulation in January-February 2007.

[2]: Validated sampled proportion = actually sampled and validated by EFSA / Total * 100

[3]: These EU figures do not include data for Malta and Luxembourg

Annex III. Overview of the number of flocks per Member State after data validation and cleaning

Member States	Number of flocks having at least 5,000 broilers		
	Total[1]	Actually sampled and validated by EFSA N	Validated sampled proportion[2] %
Austria	3,145	365	11.6
Belgium	5,099	373	7.3
Cyprus	2,728	248	9.1
Czech Republic	4,326	334	7.7
Denmark	3,330	295	8.9
Estonia	288	139	48.3
Finland	3,020	360	11.9
France	66,112	381	0.6
Germany	14,909	377	2.5
Greece	9,016	245	2.7
Hungary	3,310	359	10.8
Ireland	2,525	351	13.9
Italy	24,249	313	1.3
Latvia	382	121	31.7
Lithuania	978	156	16.0
Poland	30,444	357	1.2
Portugal	15,360	367	2.4
Slovakia	480	230	47.9
Slovenia	2,025	326	16.1
Spain	45,529	388	0.9
Sweden	3,000	291	9.7
The Netherlands	6,424	362	5.6
The United Kingdom	35,542	382	1.1
EU[3]	282,221	7,120	2.5
Norway	3,854	320	8.3

[1]: Based on Technical specifications 'Baseline survey on the prevalence of *Salmonella* in broilers of Gallus gallus in the EU', updated by the figures provided by the Member States' during a consulation in January-February 2007.

[2]: Validated sampled proportion = actually sampled and validated by EFSA / Total * 100

[3]: These EU figures do not include data for Malta and Luxembourg

Annex IV. Overview of the number of records with non-plausible characteristics in the final dataset received by the European Commission

	Number of the exclusion criterion																										
Member State	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**TOTAL (no redundancy)**
	number of samples with non-plausible characteristics																										
Austria																											
Belgium																					15						15
Cyprus		5																			4					30	39
Czech Republic	5	5						20													37					5	67
Denmark	5	10		20				10													17					31	83
Estonia																					5					50	55
Finland																											
France			5						5		5																10
Germany																								1			1
Greece				5				5	5	5		5									53					161	229
Hungary																					1						1
Ireland		10			5																1			1		7	19
Italy		15												5		5		5		60			1		1		81
Latvia																											
Lithuania																											
Poland		5			5			5		10		40									14					20	94
Portugal		10		10	10																20					14	49
Slovakia	10	10						10													1					11	32
Slovenia				20																	10						30
Spain																											
Sweden												5														13	13
The Netherlands		5			5																26					3	34
The United Kingdom																					5						5
EU	20	75	5	55	25			50	10	15	5	50		5		5		5		60	212		1	2	1	350	857
Norway																											

Annex V. Description of the statistical model fitted to estimate the EU *Salmonella* flock prevalence

General assumptions and remarks;

- Only observed prevalence is investigated, meaning that one flock observed as negative is assumed to be truly negative (no false negative cases allowed),
- Member States without positive flocks or holdings were excluded from the analysis, and the corresponding prevalence estimates and confidence intervals were set to zero,
- The EU weighting was computed according to the final population sizes, i.e. total number of holdings and total number of flocks,
- Norway was excluded from the EU weighting.

Holding prevalence

For each outcome variable, data were aggregated at the holding level and analyzed independently for each Member State. A holding was considered to be positive whenever at least one of its flocks was found positive. Next a simple logistic distribution was fitted to the holding data, using PROC LOGISTIC in SAS version 9.1. Such an approach is consistent with previous baseline study analyses as well as with the flock prevalence analysis of this broilers baseline survey. The 95%-confidence intervals were directly available from the SAS output. The EU holding prevalence was derived from the Member States' prevalence using linear weighting according to numbers of holdings per Member State. Confidence intervals at the EU level were derived using the same weighting under the assumption of normality of prevalence estimates at MS level.

By definition, such an estimation procedure aims at evaluating not the observed proportion of positive holdings, but the probability (or "true proportion") of positive holdings. However, for consistency with previous baseline studies, it was decided that in case of census sampling, the confidence intervals were reduced to the point estimates.

Member States with no positive flock were excluded from the analysis; and their holding prevalence set to 0, with a confidence interval reduced to [0, 0].

There are various sources of bias in the determination of the holding prevalence, mainly due to the design, the main ones originating from:

- the randomness at the sample level which is not accounted for: cases of false positive flocks are neglected,
- the randomness at the flock level which is not accounted for: cases of false negative holdings are neglected,
- the fact that one third of the Member States (8 out of 23) had only one flock per holding is sampled, independently from the size of holdings, implying that prevalence estimates for Member States with smaller holdings are likely to be more biased than those for Member States with larger holdings,

- the fact that two thirds of the Member States (15 out of 23) had more flocks sampled per holding, implying that their estimates are likely to be less or differently biased than the other Member States.

For all those reasons, holding prevalence estimates are not a robust measure of infection from a statistical point of view. This sums up with the biological rationale to favour instead flock prevalence estimation.

Flock prevalence

For each outcome variable, a mixed effect model was fitted to the data independently. A logistic regression with a random effect on the holding was evaluated using PROC NLMIXED in SAS version 9.1. For this purpose, the epidemiological unit of interest called "flock" was defined as a physical flock for a given holding in a given cycle. As a consequence, one physical flock over a year of 6 cycles for example corresponds to 6 different flocks in that sense. The random effect was taken as Gaussian on the probit scale (as usual, the probit function is defined as the inverse of the Cumulative Distribution Function of the normalized Gaussian distribution). The choice of probit versus any other link function (e.g. logit) was based on the convergence, but the results were not sensitive to that choice. For any holding *j* in a given country *i*, the number of positive flocks $Y_{i,j}$ was assumed to follow a binomial distribution:

$$Y_{i,j} \sim' Bin(p_{ij}, n_{ij})$$

Where $p_{i,j}$ is the flock prevalence in this holding and $n_{i,j}$ is the number of sampled flocks in this holding. $p_{i,j}$ was defined via a holding (random) effect on the probit scale, namely:

$$\text{probit}(p_{i,j}) = \eta_{ij}$$

$$\text{And } \eta_{ij} \sim \text{N}(\eta_i, s^2) \text{ for every holding } j$$

η_i represents then the flock prevalence for a typical holding in the country *i*. In order to estimate the inter-holding variance s^2, this was assumed to be the same for all countries. However, in some cases, this variance was defined as increasing with η_i, to account for the fact that countries with high prevalence may show larger inter-holding variability than those with smaller prevalence. In such cases, *s* was then specific to the country *i* (therefore denoted by s_i) and defined as:

$$s_i = \alpha + \beta\eta_i$$

With α and β being 2 positive regression parameters. To determine whether s^2 should depend on η_i, or not, the convergence of estimation algorithms was checked and also visual evaluation of any relationship between s and η_i was made. Only *S.* Enteritidis and *S.* Enteritidis and/or Typhimurium and *S.* Infantis were found to be in this case. The final results were not very sensitive to the model choice (s dependent or not on η_i), and the value *0* was included in the confidence interval of the estimate of β except for *S.* Infantis which was then the most significant case. However, since this choice of model is meaningful from an epidemiological point of view it was kept for the 3 mentioned outcome variables.

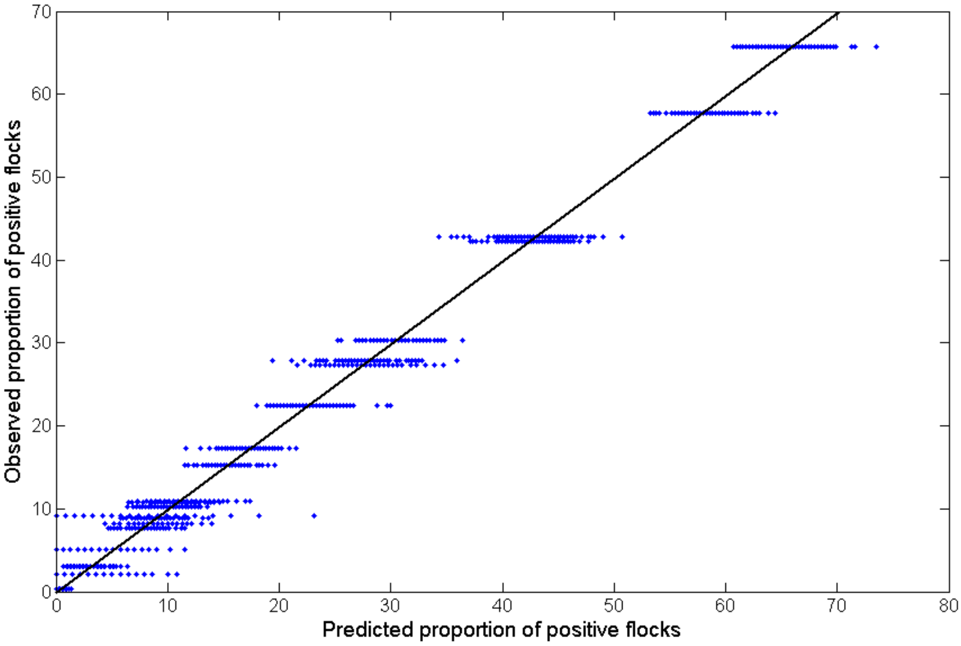
Note that for *S.* Hadar and serovars other than *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Mbandaka and *S.* Hadar, the model-based estimation was not possible due to the lack of data. As a consequence, s was then fixed for these two outcome variables to $s = 0.6$, as this was found to be an average value consistent across all the other variables investigated (see table below).

Outcome variable	**Estimate of s (inter-holding std in the probit scale)**
All *Salmonella*	0.59
S. Enteritidis	0.57*
S. Typhimurium	0.59
S. Enteritidis and/or Typhimurium	0.95*
serovars other than *S.* Enteritidis or *S.* Typhimurium	0.55
S. Infantis	0.23*
S. Mbandaka	0.89

*: those values are estimates derived from the formula $s_i = \alpha + \beta\eta_i$ averaged over the countries

Finally, to derive the flock prevalence estimate for each country, that accounts for the various holding sizes, estimates of every η_{ij} were weighted by the number of flocks corresponding to the holding *j* in the country *i*. To define such a number of flocks per holding, the number of cycles per holding was computed as the mean over all sampled flock for each holding. The related 95% confidence intervals were derived under the normal assumption of estimates (mean +/- 1.96 × standard deviation). When the lower bound of a confidence interval was found to be negative, this was adjusted to 0. Then, the EU weighted average was derived similarly to the holding prevalence case, using available population sizes by Member States.

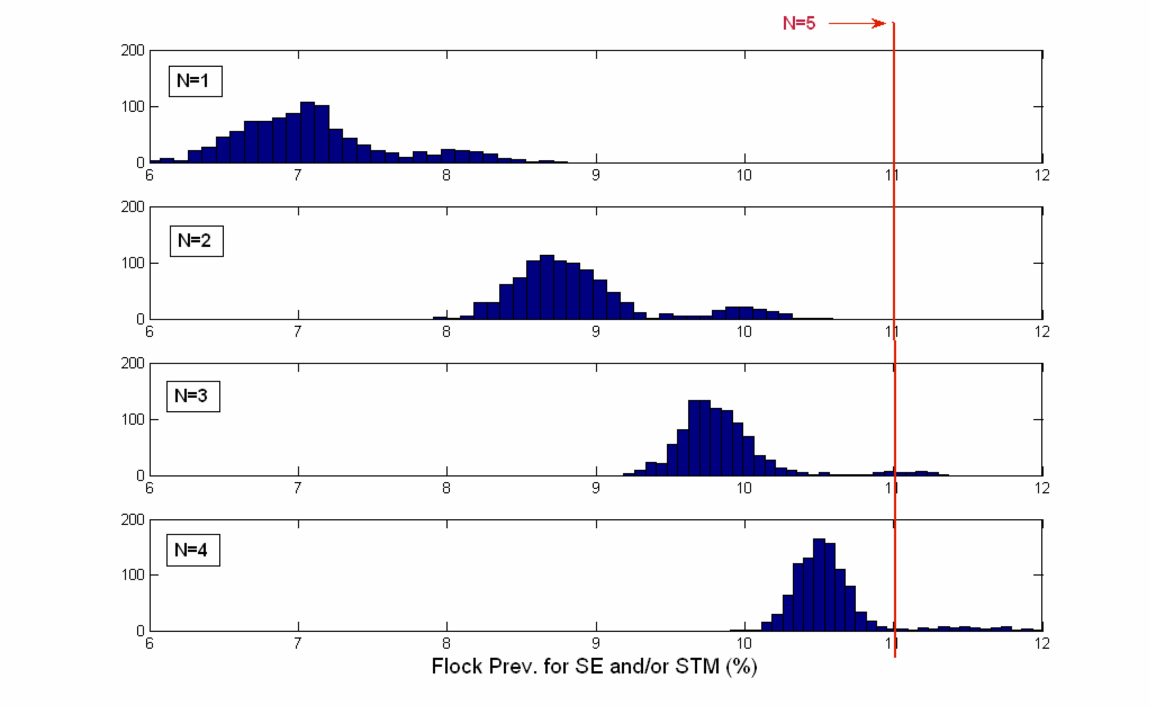
In order to check the model estimations, it was decided to re-simulate the baseline study 100 times, using exactly the same designs (same number of flocks and holdings sampled by country). The simulated (or "predicted") values were assessed only using the statistical model and the country-level parameters (η_i and s). Then out of these 100 simulated studies, the observed proportion of positive flocks among the surveyed flocks were plotted by country against the one actually observed in the data base. The plot corresponding to all *Salmonella* is reported below, overlaid by the diagonal line ("y = x"). It shows that the model can actually reproduce the observed proportion of positive flocks, in a quite accurate way for most countries.



This model-based approach enabled the evaluation of flock prevalence and the reduction of various design biases as much as possible, making the estimates much more reliable than the holding prevalence ones. Note that randomness at the sample level was again neglected (no false negative flocks allowed), although a model with one level more (random effect on the flock level) would have permitted to account for it. Because of time constrains, this was not investigated, a simulation-based sensitivity analysis was done instead.

Simulations

Simulations for the evaluation of sensitivity of results with respect to number of samples per flock were performed in SAS version 9.1, using an *ad hoc* macro. The simulations did not use the fitted model but only resample from available data. The designs investigated were respectively 4, 3, 2 and 1 sample(s) per flock instead of 5. Then, the 2 flock size dependent designs were also similarly investigated. For each design, 1000 baseline studies were resimulated using the database and randomly censoring 1, 2, 3 or 4 samples out of the 5 samples per flock. For each simulated study, the model-based flock prevalence estimation is conducted for *S.* Enteritidis and/or Typhimurium. Therefore, the final outcome is, for each design, a histogram of estimates representing the randomness in the data. The confidence intervals shown in the plotted curves in the core report are derived from those histograms. Such intervals only include data randomness (variability) not the uncertainty of estimates. The histograms of estimated flock prevalence at the EU level for 1, 2, 3 and 4 samples per flock are plotted in the figure below.



It shows that the distributions are slightly skewed (or bimodal) upwards. This explains why the mean is not centred in the 95% confidence interval.

Annex VI. General features of the European broiler population

An overview of the European broiler holdings, broiler flocks and of the broilers population is given in Table 6. The figures for numbers of the holdings and flocks originate from the baseline survey whereas the ones for the broilers population were provided by EUROSTAT (2005). The figures pertain to the holdings and flocks having at least 5,000 birds, exception made of Estonia and Latvia whose figures also refer to holdings with less then 5,000 broilers. No data for Luxembourg and Malta are included in this overview.

In the EU there were in 2005 24,630 broiler holdings. France has the highest number of broiler holdings (6,060), whereas Latvia had the smallest number (2).

France has also the highest number of broiler flocks (66,112), whereas Estonia has the smallest number (288).

In the subpopulation 'holding size above 5,000' there were approximately 714 million broilers in the EU. France has the highest number of broilers (approximately 113 million broilers), whereas Estonia had the smallest number (980,000).

In addition, the density of the broiler holdings, flocks and broiler population in the MSs was determined by dividing the aforementioned number of holdings, flocks and broilers, by the amount of utilized agricultural area in km^2. Data on the amount of agricultural land per MS were obtained from EUROSTAT.

Figure 16 displays the broilers flock density. Cyprus, Portugal, Slovenia, Belgium and The Netherlands are the MSs were the density of broiler flocks is highest, respectively 218, 40, 40, 37 and 34 broiler flocks per 100 km^2. It is lowest in Slovakia, Latvia, Estonia and Lithuania (less than 4 broiler flocks per 100 km^2).

Figure 17 displays the broiler holding density. Cyprus, Slovenia, Belgium, The Netherlands and Portugal are those MSs were the density of broiler holdings is highest, respectively 10, 7, 6, 5 and 5 broiler holdings per 100 km^2. It is lowest in Latvia, Estonia and Lithuania (less than 0.1 broilers per 100 km^2).

Figure 18 displays the broiler population density. In Cyprus and The Netherlands the density of broilers is highest, respectively 2,627 and 2,324 broilers per km^2. It is lowest in Latvia, 73.

Table 6. Overview of the broiler population in the EU and Norway

Member States	Broiler holdings with at least 5,000 birds		
	No of broilers**	No of broiler holdings	No of broiler flocks
Austria	5,260,000	378	3,145
Belgium	20,670,000	817	5,099
Cyprus	3,280,000	128	2,728
Czech Republic	16,140,000	309	4,326
Denmark	11,780,000	263	3,330
Estonia*	980,000	4	288
Finland	5,200,000	216	3,020
France	112,680,000	6,060	66,112
Germany	56,460,000	986	14,909
Greece	17,370,000	1,180	9,016
Hungary	9,330,000	310	3,310
Ireland	7,970,000	240	2,525
Italy	88,490,000	2,213	24,249
Latvia*	1,170,000	2	382
Lithuania	3,050,000	18	978
Poland	70,450,000	2,788	30,444
Portugal	15,780,000	1,700	15,360
Slovakia	7,310,000	127	480
Slovenia	1,580,000	362	2,025
Spain	95,860,000	4,139	45,529
Sweden	7,470,000	120	3,000
The Netherlands	44,450,000	975	6,424
The United Kingdom	111,270,000	1,295	35,542
EU	714,000,000	24,630	282,221
Norway	8,840,000	458	3,854

** Source: EUROSTAT 2005
* Holdings with < 5,000 broilers

Figure 16. Broiler flocks density in the EU and Norway

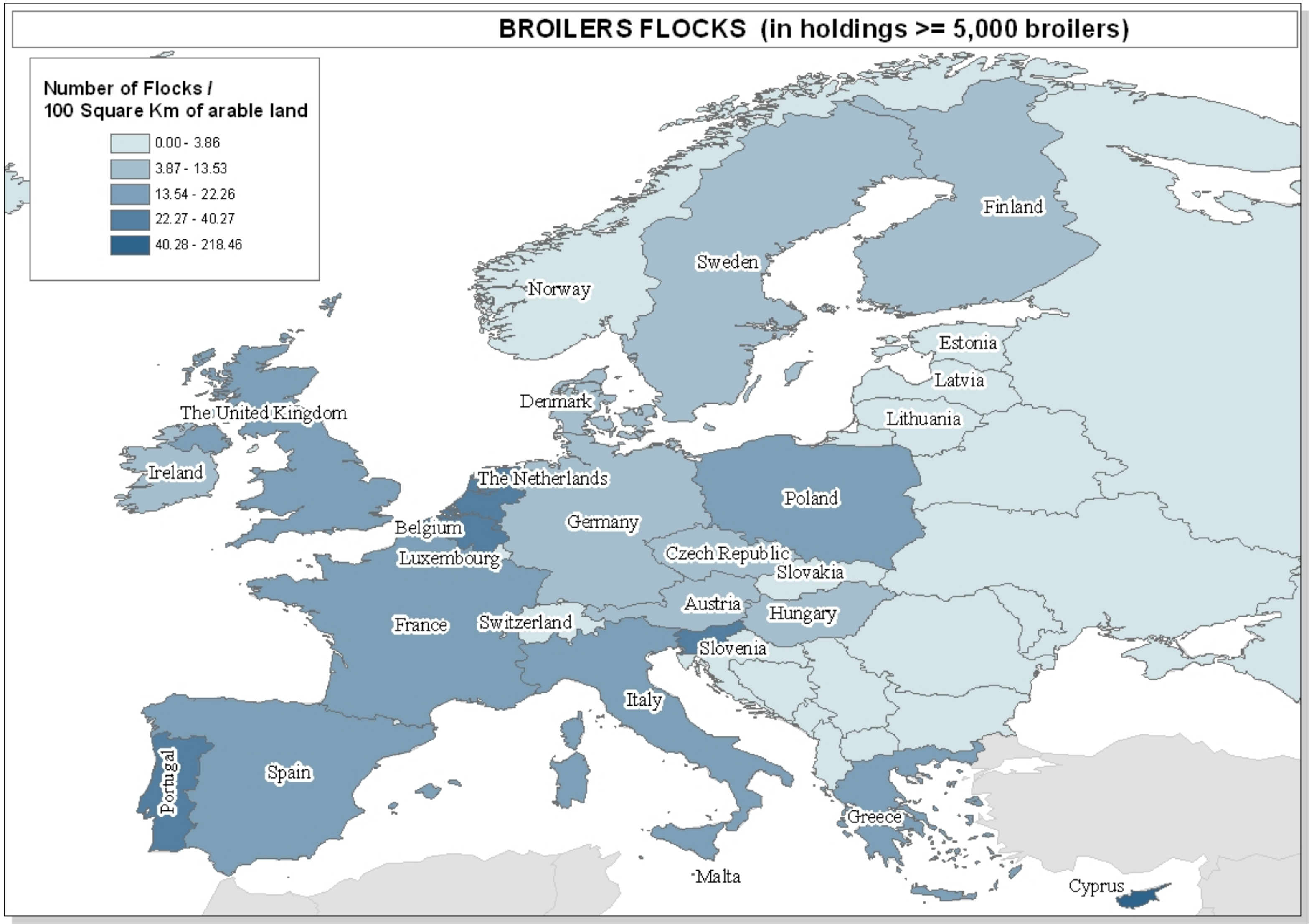


Figure 17. Broiler holdings density in the EU and Norway

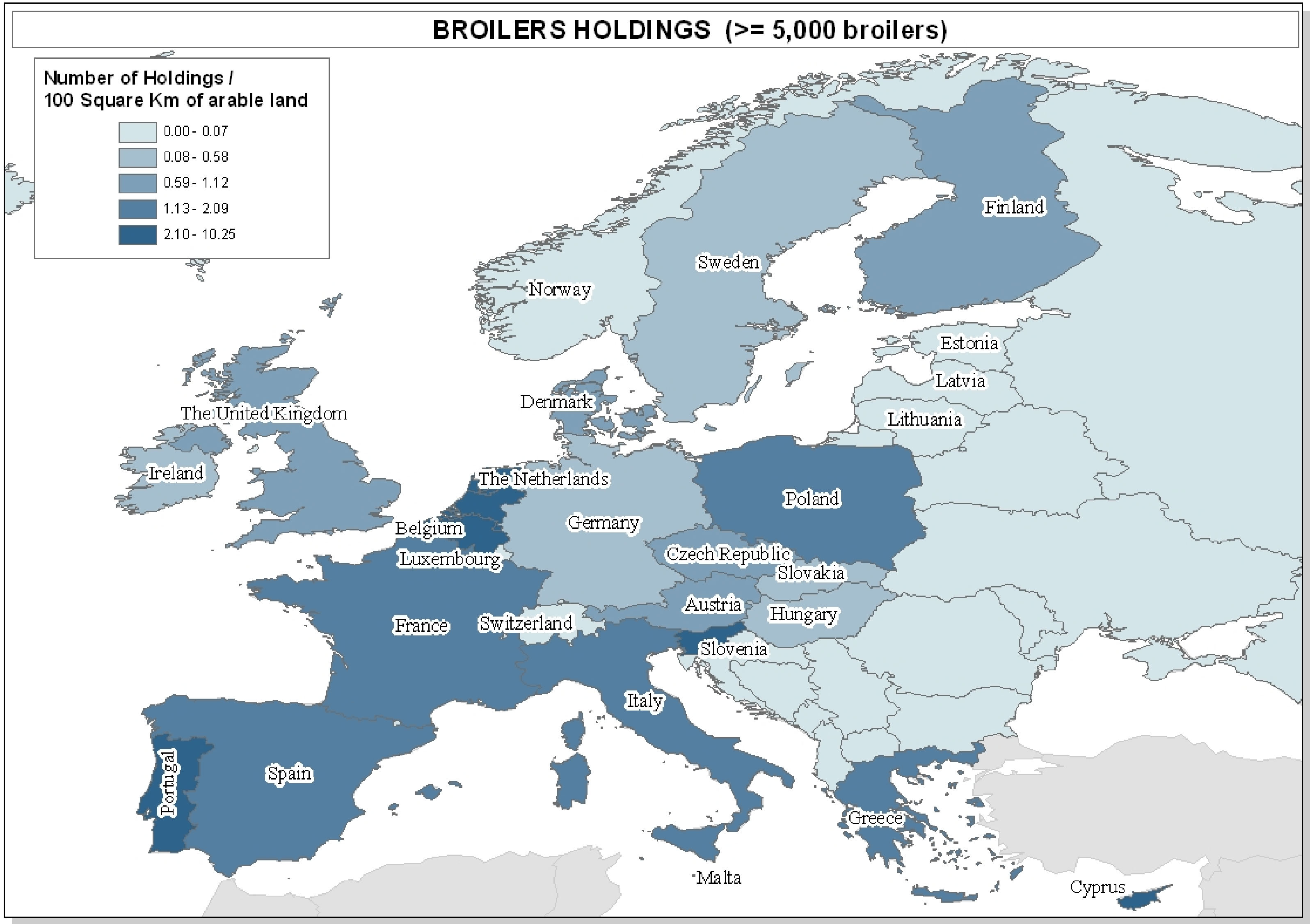
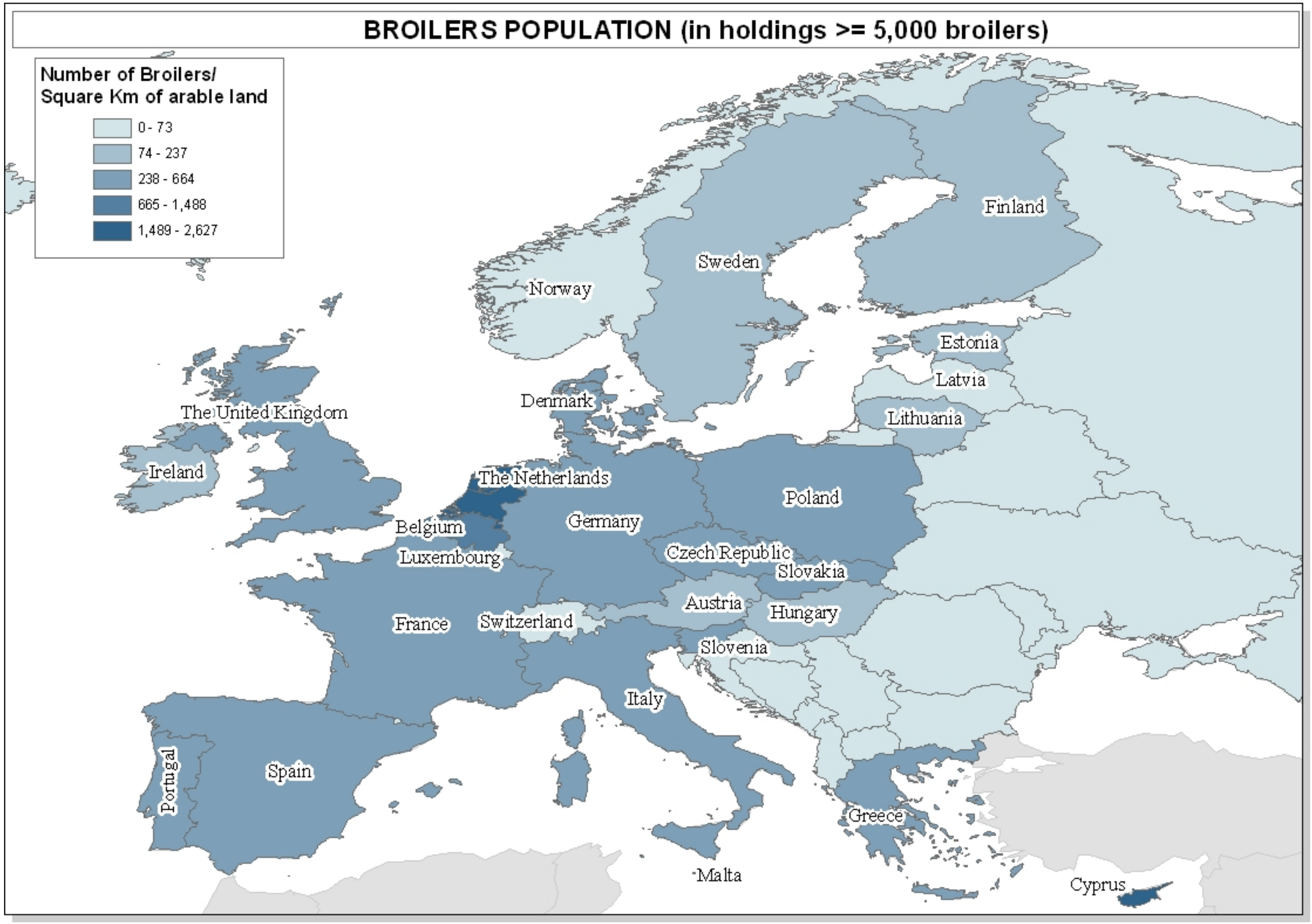


Figure 18. Broiler population density in the EU and Norway



Annex VII. Observed proportion of *Salmonella* positive broiler flocks and *Salmonella* broiler flock prevalence, in the EU, 2005-2006

		***Salmonella* spp.**			***S.* Enteritidis**			***S.* Typhimurium**			***S.* Enteritidis and/or *S.* Typhimurium**		
Member State	**N**	**%pos***	**prev est****	**CI 95%**	**%pos**	**prev est**	**CI 95%**	**%pos**	**prev est**	**CI 95%**	**%pos**	**prev est**	**CI 95%**
Austria	365	7.7	5.4	4.6 - 6.2	1.6	0.9	0.7 - 1.1	0.5	0.2	0.1 - 0.2	2.2	1.3	1 - 1.5
Belgium	373	15.3	12.4	11.2 - 13.7	0.0	0.0	0 - 0	3.5	1.9	1.6 - 2.3	3.5	2.0	1.7 - 2.3
Cyprus	248	10.9	9.1	7 - 11.3	2.8	1.9	1.2 - 2.5	0.0	0.0	0 - 0	2.8	1.7	1.1 - 2.4
Czech Republic	334	22.5	19.3	17.2 - 21.5	14.4	11.3	9.8 - 12.8	0.6	0.2	0.1 - 0.2	15.0	9.6	7.8 - 11.5
Denmark	295	3.1	1.6	1.2 - 2	0.0	0.0	0 - 0	0.3	0.1	0 - 0.1	0.3	0.3	0.2 - 0.3
Estonia	139	2.2	2.0	0 - 4	2.2	1.9	0 - 3.9	0.0	0.0	0 - 0	2.2	1.7	0 - 3.7
Finland	360	0.3	0.1	0 - 0.1	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0
France	381	8.9	6.2	5.2 - 7.2	0.5	0.2	0.2 - 0.3	0.3	0.1	0 - 0.1	0.8	0.5	0.4 - 0.6
Germany	377	17.2	15.0	12.9 - 17.1	1.1	0.5	0.4 - 0.7	1.6	0.7	0.4 - 1.1	2.7	1.6	1.1 - 2
Greece	245	27.3	24.0	21.2 - 26.9	3.7	2.3	1.8 - 2.8	2.0	0.9	0.6 - 1.2	5.7	3.2	2.4 - 4
Hungary	359	65.7	68.2	65.4 - 71	5.0	3.3	2.7 - 3.8	3.3	1.9	1.4 - 2.3	8.4	5.1	4 - 6.2
Ireland	351	27.9	27.6	24.5 - 30.6	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0
Italy	313	30.4	28.3	25.8 - 30.9	3.8	2.4	2 - 2.8	0.3	0.1	0 - 0.1	4.2	2.3	1.8 - 2.8
Latvia	121	9.1	6.2	2.7 - 9.7	7.4	5.2	1.9 - 8.5	0.0	0.0	0 - 0	7.4	5.1	1.8 - 8.3
Lithuania	156	5.1	2.9	1.3 - 4.6	5.1	3.2	1.5 - 5	0.0	0.0	0 - 0	5.1	3.3	1.4 - 5.2
Poland	357	57.7	58.2	54.1 - 62.3	34.5	31.8	27.8 - 35.9	4.2	2.3	1.7 - 3	37.8	32.4	26.9 - 37.8
Portugal	367	42.8	43.5	40.2 - 46.8	37.6	37.8	34 - 41.5	0.3	0.1	0 - 0.1	37.6	39.3	34.1 - 44.5
Slovakia	230	8.3	5.7	4.5 - 6.9	5.7	3.7	2.9 - 4.5	0.4	0.1	0.1 - 0.2	6.1	3.3	2.4 - 4.3
Slovenia	326	3.1	1.6	1.3 - 1.9	2.8	1.6	1.3 - 1.9	0.0	0.0	0 - 0	2.8	1.6	1.3 - 1.9
Spain	388	42.3	41.2	38.3 - 44.1	32.0	29.5	26.6 - 32.3	0.8	0.3	0.2 - 0.4	32.7	28.2	24.4 - 31.9
Sweden	291	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0
The Netherlands	362	10.2	7.5	6.6 - 8.3	1.4	0.7	0.6 - 0.9	0.3	0.1	0 - 0.1	1.7	1.0	0.8 - 1.1
The United Kingdom	382	10.7	8.2	7.1 - 9.4	0.0	0.0	0 - 0	0.3	0.1	0 - 0.1	0.3	0.2	0.2 - 0.3
EU	**7,120**		**23.7**	**23 - 24.5**		**10.9**	**10.2 - 11.6**		**0.5**	**0.4 - 0.5**		**11.0**	**10.2 - 11.9**
Norway	320	0.3	0.1	0 - 0.1	0.0	0.0	0 - 0	0.3	0.1	0 - 0.1	0.3	0.2	0.2 - 0.3

*= Proportion of sampled broiler flocks that are positive

**= Estimate of the broiler flock prevalence (proportion of the total number of broiler flocks over the one year period that are positive)

Annex VII. (continued) Observed proportion of *Salmonella* positive broiler flocks and *Salmonella* broiler flock prevalence, in the EU, 2005-2006

		S. Infantis			*S.* Mbandaka			*S.* Hadar			Other serovars than *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Mbandaka and *S.* Hadar		
Member State	**N**	**%pos***	**prev est****	**CI 95%**	**%pos**	**prev est**	**CI 95%**	**%pos**	**prev est**	**CI 95%**	**%pos**	**prev est**	**CI 95%**
Austria	365	0.5	0.5	0.5 - 0.6	0.0	0.0	0 - 0	0.0	0.0	0 - 0	4.9	3.0	2.5 - 3.5
Belgium	373	0.3	0.1	0 - 0.2	1.1	0.2	0.1 - 0.3	0.3	0.1	0 - 0.1	11.8	8.9	7.9 - 9.9
Cyprus	248	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0	8.1	6.2	4.5 - 7.8
Czech Republic	334	3.0	2.5	2.2 - 2.8	0.0	0.0	0 - 0	0.3	0.1	0 - 0.1	4.2	2.4	1.9 - 2.9
Denmark	295	0.7	0.7	0.6 - 0.8	0.0	0.0	0 - 0	0.0	0.0	0 - 0	2.0	0.9	0.7 - 1.1
Estonia	139	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0
Finland	360	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.3	0.1	0 - 0.1
France	381	0.5	0.5	0.4 - 0.6	0.5	0.0	0 - 0.1	0.8	0.3	0.2 - 0.3	6.6	4.1	3.4 - 4.9
Germany	377	1.6	1.5	1.4 - 1.6	1.6	0.2	0.1 - 0.3	0.0	0.0	0 - 0	13.0	10.4	8.8 - 12
Greece	245	0.0	0.0	0 - 0	0.8	0.1	0 - 0.2	0.8	0.3	0.2 - 0.4	21.2	17.7	15.3 - 20.1
Hungary	359	58.2	64.0	60.1 - 67.9	3.1	1.3	0.5 - 2	0.0	0.0	0 - 0	6.1	4.0	3.2 - 4.8
Ireland	351	0.0	0.0	0 - 0	15.7	14.5	11.1 - 17.8	0.0	0.0	0 - 0	12.3	9.4	7.9 - 11
Italy	313	0.3	0.2	0.1 - 0.3	3.5	1.2	0.7 - 1.6	2.6	1.2	0.9 - 1.5	23.3	20.7	18.5 - 22.9
Latvia	121	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0	1.7	1.1	0 - 2.7
Lithuania	156	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0
Poland	357	10.6	8.0	6.2 - 9.8	3.9	1.1	0.6 - 1.5	6.4	4.2	3.2 - 5.3	6.2	3.9	3 - 4.9
Portugal	367	3.0	2.5	2.2 - 2.8	0.5	0.0	0 - 0.1	0.0	0.0	0 - 0	4.9	2.9	2.3 - 3.5
Slovakia	230	0.4	0.4	0.2 - 0.5	0.0	0.0	0 - 0	0.4	0.1	0.1 - 0.2	2.2	1.0	0.7 - 1.4
Slovenia	326	0.3	0.2	0.1 - 0.3	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0
Spain	388	0.8	0.8	0.7 - 0.8	0.5	0.2	0 - 0.5	5.2	3.0	2.5 - 3.6	6.4	4.0	3.3 - 4.7
Sweden	291	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0
The Netherlands	362	2.2	2.0	1.8 - 2.1	0.6	0.1	0 - 0.1	0.0	0.0	0 - 0	6.4	4.0	3.5 - 4.6
The United Kingdom	382	0.0	0.0	0 - 0	0.8	0.1	0 - 0.2	0.0	0.0	0 - 0	9.7	7.2	6.1 - 8.2
EU	**7,120**		**2.2**	**2 - 2.4**		**0.4**	**0.3 - 0.5**		**1.1**	**1 - 1.3**		**6.5**	**6.2 - 6.9**
Norway	320	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0	0.0	0.0	0 - 0

*= Proportion of sampled broiler flocks that are positive

**= Estimate of the broiler flock prevalence (proportion of the total number of broiler flocks over the one year period that are positive)

Annex VIII. Observed *Salmonella* broiler holding prevalence (with 95% confidence intervals) in the EU, 2005-2006

		***Salmonella* spp.**		***S.* Enteritidis**		***S.* Typhimurium**		**S. Enteritidis and/or S. Typhimurium**	
	N	**prev est***	**CI 95%**	**prev est**	**CI 95%**	**prev est**	**CI 95%**	**prev est**	**CI 95%**
Member States that sampled strictly one flock per holding									
Belgium	373	15.3	12 - 19.3	0.0	0 - 0	3.5	2 - 5.9	3.5	2 - 5.9
France	381	8.9	6.4 - 12.2	0.5	0.1 - 2.1	0.3	0 - 1.8	0.8	0.3 - 2.4
Germany	377	17.2	13.8 - 21.4	1.1	0.4 - 2.8	1.6	0.7 - 3.5	2.7	1.4 - 4.9
Greece	245	27.3	22.1 - 33.3	3.7	1.9 - 6.9	2.0	0.9 - 4.8	5.7	3.4 - 9.4
Italy	313	30.4	25.5 - 35.7	3.8	2.2 - 6.6	0.3	0 - 2.2	4.2	2.4 - 7
Poland	357	57.7	52.5 - 62.7	34.5	29.7 - 39.5	4.2	2.5 - 6.9	37.8	32.9 - 43
Spain	388	42.3	37.4 - 47.2	32.0	27.5 - 36.8	0.8	0.2 - 2.4	32.7	28.2 - 37.6
The United Kingdom	382	10.7	8 - 14.3	0.0	0 - 0	0.3	0 - 1.8	0.3	0 - 1.8
MS group	**2,816**	**27.4**	**25.6 - 29.1**	**12.6**	**11.3 - 13.9**	**1.3**	**0.7 - 1.8**	**13.7**	**12.4 - 15**
Member States that did not strictly sampled one flock per holding									
Austria	365	7.8	5.4 - 11.1	1.7	0.8 - 3.7	0.6	0.1 - 2.2	2.2	1.1 - 4.4
Cyprus	248	29.7	21.2 - 39.8	7.7	3.7 - 15.3	0.0	0 - 0	7.7	3.7 - 15.3
Czech Republic	334	22.5	18.4 - 27.3	14.4	11 - 18.6	0.6	0.2 - 2.4	15.0	11.6 - 19.3
Denmark	295	3.9	2.1 - 7.4	0.0	0 - 0	0.4	0.1 - 3	0.4	0.1 - 3
Estonia[1]	139	50.0	-	50.0	-	0.0	-	50.0	12.3 - 87.7
Finland	360	0.5	0.1 - 3.5	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
Hungary	359	66.1	60.8 - 70.9	5.4	3.4 - 8.3	3.3	1.8 - 5.8	8.6	6.1 - 12.1
Ireland	351	33.8	28.4 - 39.8	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
Latvia[1]	121	33.3	-	33.3	-	0.0	-	33.3	4.3 - 84.6
Lithuania[1]	156	10.0	-	10.0	-	0.0	-	10.0	2.5 - 32.4
Portugal	367	42.9	37.9 - 48	37.7	32.9 - 42.8	0.3	0 - 1.9	37.7	32.9 - 42.8
Slovakia	230	10.2	6.6 - 15.4	7.0	4.1 - 11.6	0.5	0.1 - 3.7	7.5	4.5 - 12.2
Slovenia	326	3.1	1.7 - 5.7	2.8	1.5 - 5.3	0.0	0 - 0	2.8	1.5 - 5.3
Sweden	291	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
The Netherlands	362	10	7.3 - 13.6	1.4	0.6 - 3.3	0.3	0 - 1.9	1.7	0.8 - 3.7
MS group	**4,304**	**25.0**	**23.2 - 26.9**	**14.7**	**13 - 16.4**	**0.5**	**0.1 - 0.9**	**15.0**	**13.3 - 16.7**
Norway	320	0.3	0 - 2.2	0.0	0 - 0	0.3	0 - 2.2	0.3	0 - 2.2

*= Estimate of the broiler holding prevalence (= proportion of the sampled broiler holdingsthat are positive)

[1]: No confidence interval for Estonia, Latvia and Lithuania since all holdings in these MSs were sampled

Annex VIII (continued). Observed *Salmonella* broiler holding prevalence (with 95% confidence intervals) in the EU, 2005-2006

		***S.* Infantis**		***S.* Mbandaka**		***S.* Hadar**		**Other serovars than *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, *S.* Mbandaka and *S.* Hadar**	
	N	**prev est***	**CI 95%**	**prev est**	**CI 95%**	**prev est**	**CI 95%**	**prev est**	**CI 95%**
Member States that sampled strictly one flock per holding									
Belgium	373	0.3	0 - 1.9	1.1	0.4 - 2.8	0.3	0 - 1.9	11.8	8.9 - 15.5
France	381	0.5	0.1 - 2.1	0.5	0.1 - 2.1	0.8	0.3 - 2.4	6.6	4.5 - 9.5
Germany	377	1.6	0.7 - 3.5	1.6	0.7 - 3.5	0.0	0 - 0	13.0	10 - 16.8
Greece	245	0.0	0 - 0	0.8	0.2 - 3.2	0.8	0.2 - 3.2	21.2	16.6 - 26.8
Italy	313	0.3	0 - 2.2	3.5	2 - 6.2	2.6	1.3 - 5	23.3	19 - 28.3
Poland	357	10.6	7.8 - 14.3	3.9	2.3 - 6.5	6.4	4.3 - 9.5	6.2	4.1 - 9.2
Spain	388	0.8	0.2 - 2.4	0.5	0.1 - 2	5.2	3.3 - 7.9	6.4	4.4 - 9.4
The United Kingdom	382	0.0	0 - 0	0.8	0.3 - 2.4	0.0	0 - 0	9.7	7.1 - 13.1
MS group	**2,816**	**2.0**	**1.4 - 2.6**	**1.5**	**0.9 - 2**	**2.6**	**1.9 - 3.3**	**10.0**	**8.8 - 11.2**
Member States that did not strictly sampled one flock per holding									
Austria	365	0.6	0.1 - 2.2	0.0	0 - 0	0.0	0 - 0	5.0	3.2 - 7.8
Cyprus	248	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	22.0	14.6 - 31.6
Czech Republic	334	3.0	1.6 - 5.5	0.0	0 - 0	0.3	0 - 2.1	4.2	2.5 - 7
Denmark	295	0.9	0.2 - 3.4	0.0	0 - 0	0.0	0 - 0	2.6	1.2 - 5.7
Estonia[1]	139	0.0	-	0.0	-	0.0	-	0.0	-
Finland	360	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.5	0.1 - 3.5
Hungary	359	58.6	53.3 - 63.8	3.3	1.8 - 5.8	0.0	0 - 0	6.5	4.3 - 9.7
Ireland	351	0.0	0 - 0	17.9	13.7 - 23	0.0	0 - 0	16.0	12 - 20.9
Latvia[1]	121	0.0	-	0.0	-	0.0	-	0.0	-
Lithuania[1]	156	0.0	-	0.0	-	0.0	-	0.0	-
Portugal	367	3.0	1.7 - 5.3	0.5	0.1 - 2.2	0.0	0 - 0	4.9	3.1 - 7.7
Slovakia	230	0.5	0.1 - 3.7	0.0	0 - 0	0.5	0.1 - 3.7	2.7	1.1 - 6.3
Slovenia	326	0.3	0 - 2.2	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
Sweden	291	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0
The Netherlands	362	2.2	1.1 - 4.4	0.6	0.1 - 2.2	0.0	0 - 0	6.4	4.3 - 9.5
MS group	**4,304**	**5.2**	**4.5 - 6**	**1.3**	**0.9 - 1.8**	**0.0**	**0 - 0.1**	**5.4**	**4.4 - 6.4**
Norway	320	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0	0.0	0 - 0

*= Estimate of the broiler holding prevalence (= proportion of the sampled broiler holdingsthat are positive)

[1]: No confidence interval for Estonia, Latvia and Lithuania since all holdings in these MSs were sampled

Annex IX. **Frequency distribution of Salmonella serovars in broiler holdings and flocks in EU MSs and Norway, 2005-2006**

Austria	**Serovars (N=93)**			**Holdings with serovars (N=28)**		**Flocks with serovars (N=28)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Montevideo	53	56.99	15	53.57	15	53.57
	S. Enteritidis	21	22.58	6	21.43	6	21.43
	S. Typhimurium	8	8.60	2	7.14	2	7.14
	S. Infantis	4	4.30	2	7.14	2	7.14
	S. Virchow	5	5.38	1	3.57	1	3.57
	S. Tennessee	1	1.08	1	3.57	1	3.57
	S. Senftenberg	1	1.08	1	3.57	1	3.57
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	93	100.00				

Belgium	**Serovars (N=164)**			**Holdings with serovars (N=57)**		**Flocks with serovars (N=57)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Typhimurium	23	14.02	13	22.81	13	22.81
	S. Senftenberg	18	10.98	8	14.04	8	14.04
	S. Paratyphi B/variant Java	27	16.46	7	12.28	7	12.28
	S. Mbandaka	7	4.27	4	7.02	4	7.02
	S. Anatum	10	6.10	4	7.02	4	7.02
	S. Virchow	7	4.27	3	5.26	3	5.26
	S. Rissen	8	4.88	3	5.26	3	5.26
	S. Havana	2	1.22	2	3.51	2	3.51
	S. Cubana	3	1.83	2	3.51	2	3.51
	S. Agona	5	3.05	2	3.51	2	3.51
	S. Indiana	4	2.44	2	3.51	2	3.51
	Other serovars	42	25.61				
	Salmonella spp.	8	4.88	5			
	Total	164	100.00				

Cyprus	**Serovars (N=139)**		**Holdings with serovars (N=27)**		**Flocks with serovars (N=27)**	
	N	**%**	**N**	**%**	**N**	**%**
S. Enteritidis	35	25.18	7	25.93	7	25.93
S. Newport	20	14.39	4	14.81	4	14.81
S. Senftenberg	10	7.19	2	7.41	2	7.41
S. Blockley	5	3.60	1	3.70	1	3.70
S. Brandenburg	5	3.60	1	3.70	1	3.70
S. Duisburg	5	3.60	1	3.70	1	3.70
S. Kalamu	5	3.60	1	3.70	1	3.70
S. Agona	5	3.60	1	3.70	1	3.70
S. Muenchen	5	3.60	1	3.70	1	3.70
Salmonella Group E4	5	3.60	1	3.70	1	3.70
S. subsp. salamae	4	2.88	1	3.70	1	3.70
S. Virchow	5	3.60	1	3.70	1	3.70
Salmonella Group B	5	3.60	1	3.70	1	3.70
Salmonella Group C	5	3.60	1	3.70	1	3.70
Salmonella Group E	5	3.60	1	3.70	1	3.70
S. Massenya	5	3.60	1	3.70	1	3.70
Other serovars	0	0.00				
Salmonella spp.	10	7.19	2			
Total	139	100.00				

Czech Republic		Serovars (N=236)		Holdings with serovars (N=75)		Flocks with serovars (N=75)	
		N	**%**	**N**	**%**	**N**	**%**
	S. Enteritidis	154	65.25	48	64.00	48	64.00
	S. Infantis	37	15.68	10	13.33	10	13.33
	S. Montevideo	17	7.20	7	9.33	7	9.33
	S. Kentucky	10	4.24	3	4.00	3	4.00
	S. Typhimurium	2	0.85	2	2.67	2	2.67
	S. Ohio	1	0.42	1	1.33	1	1.33
	S. Newport	1	0.42	1	1.33	1	1.33
	S. Hadar	4	1.69	1	1.33	1	1.33
	S. Derby	5	2.12	1	1.33	1	1.33
	S. Agona	5	2.12	1	1.33	1	1.33
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	236	100.00				

Denmark	**Serovars (N=33)**			**Holdings with serovars (N=9)**		**Flocks with serovars (N=9)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Infantis	6	18.18	2	22.22	2	22.22
	S. Derby	7	21.21	2	22.22	2	22.22
	Salmonella Group B	5	15.15	1	11.11	1	11.11
	S. Typhimurium	3	9.09	1	11.11	1	11.11
	S. Meleagridis	5	15.15	1	11.11	1	11.11
	S. Kentucky	2	6.06	1	11.11	1	11.11
	S. Agona	5	15.15	1	11.11	1	11.11
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	33	100.00				

Estonia	**Serovars (N=6)**			**Holdings with serovars (N=2)**		**Flocks with serovars (N=3)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Enteritidis	6	100.00	2	100.00	3	100.00
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	6	100.00				

Finland	**Serovars (N=3)**			**Holdings with serovars (N=1)**		**Flocks with serovars (N=1)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Livingstone	3	100.00	1	100.00	1	100.00
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	3	100.00				

France	**Serovars (N=99)**			**Holdings with serovars (N=34)**		**Flocks with serovars (N=34)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Montevideo	4	4.04	3	8.82	3	8.82
	S. Hadar	12	12.12	3	8.82	3	8.82
	S. Anatum	8	8.08	3	8.82	3	8.82
	S. Virchow	6	6.06	3	8.82	3	8.82
	S. Enteritidis	2	2.02	2	5.88	2	5.88
	S. Indiana	6	6.06	2	5.88	2	5.88
	S. Infantis	3	3.03	2	5.88	2	5.88
	S. Mbandaka	8	8.08	2	5.88	2	5.88
	S. Kottbus	1	1.01	1	2.94	1	2.94
	S. Braenderup	4	4.04	1	2.94	1	2.94
	S. Veneziana	1	1.01	1	2.94	1	2.94
	S. Typhimurium	3	3.03	1	2.94	1	2.94
	S. Heidelberg	4	4.04	1	2.94	1	2.94
	S. subsp. (di-)arizonae 48:z4,z23:-	1	1.01	1	2.94	1	2.94
	S. Livingstone	5	5.05	1	2.94	1	2.94
	S. Kedougou	4	4.04	1	2.94	1	2.94
	S. Ohio	5	5.05	1	2.94	1	2.94
	S. Lexington	1	1.01	1	2.94	1	2.94
	S. Senftenberg	1	1.01	1	2.94	1	2.94
	S. Schwarzengrund	5	5.05	1	2.94	1	2.94
	S. Paratyphi B/variant Java	5	5.05	1	2.94	1	2.94
	S. Napoli	5	5.05	1	2.94	1	2.94
	S. Newport	4	4.04	1	2.94	1	2.94
	S. subsp. (di-)arizonae 21:k:z	1	1.01	1	2.94	1	2.94
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	99	100.00				

Germany	**Serovars (N=220)**			**Holdings with serovars (N=65)**		**Flocks with serovars (N=65)**	
		N	**%**	**N**	**%**	**N**	**%**
	Salmonella Group B *	52	23.64	20	30.77	20	30.77
	S. Anatum	31	14.09	13	20.00	13	20.00
	S. Paratyphi B/variant Java	34	15.45	7	10.77	7	10.77
	S. Infantis	20	9.09	6	9.23	6	9.23
	S. Mbandaka	16	7.27	6	9.23	6	9.23
	S. Typhimurium	19	8.64	6	9.23	6	9.23
	S. Enteritidis	10	4.55	4	6.15	4	6.15
	Salmonella Group C1	3	1.36	3	4.62	3	4.62
	S. Ohio	6	2.73	3	4.62	3	4.62
	Salmonella subsp. enterica rough	2	0.91	2	3.08	2	3.08
	S. Virchow	7	3.18	2	3.08	2	3.08
	S. Indiana	5	2.27	2	3.08	2	3.08
	S. Heidelberg	7	3.18	2	3.08	2	3.08
	Other serovars	8	3.64				
	Salmonella spp.	0	0.00				
	Total	220	100.00				

* Including the not fully typed *Salmonella* serovar with (incomplete) antigenic formula 4,12:d:-

Greece	**Serovars (N=187)**			**Holdings with serovars (N=67)**		**Flocks with serovars (N=67)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Blockley	45	24.06	23	34.33	23	34.33
	S. Enteritidis	30	16.04	9	13.43	9	13.43
	S. Typhimurium	16	8.56	5	7.46	5	7.46
	S. Indiana	9	4.81	5	7.46	5	7.46
	S. Muenchen	4	2.14	4	5.97	4	5.97
	S. Livingstone	9	4.81	3	4.48	3	4.48
	S. Senftenberg	6	3.21	3	4.48	3	4.48
	S. Bredeney	10	5.35	2	2.99	2	2.99
	S. Hadar	4	2.14	2	2.99	2	2.99
	S. Kottbus	5	2.67	2	2.99	2	2.99
	S. Mbandaka	6	3.21	2	2.99	2	2.99
	S. Meleagridis	10	5.35	2	2.99	2	2.99
	Other serovars	26	13.90				
	Salmonella spp.	7	3.74	2			
	Total	187	100.00				

Hungary	**Serovars (N=991)**			**Holdings with serovars (N=222)**		**Flocks with serovars (N=236)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Infantis	837	84.46	197	88.74	209	88.56
	S. Enteritidis	51	5.15	18	8.11	18	7.63
	S. Typhimurium	25	2.52	11	4.95	12	5.08
	S. Mbandaka	30	3.03	11	4.95	11	4.66
	Salmonella spp. rough	13	1.31	10	4.50	10	4.24
	S. Cubana	14	1.41	4	1.80	4	1.69
	S. Bredeney	7	0.71	3	1.35	3	1.27
	S. Senftenberg	2	0.20	1	0.45	1	0.42
	S. Schleissheim	1	0.10	1	0.45	1	0.42
	S. Havana	1	0.10	1	0.45	1	0.42
	S. Bovismorbificans	2	0.20	1	0.45	1	0.42
	S. Blockley	5	0.50	1	0.45	1	0.42
	S. Anatum	2	0.20	1	0.45	1	0.42
	S. Abony	1	0.10	1	0.45	1	0.42
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	991	100.00				

Ireland	Serovars (N=360)			Holdings with serovars (N=89)		Flocks with serovars (N=98)	
		N	%	N	%	N	%
	S. Mbandaka	225	62.50	47	52.81	55	56.12
	S. Kentucky	101	28.06	34	38.20	35	35.71
	S. Indiana	19	5.28	5	5.62	5	5.10
	S. Agona	4	1.11	3	3.37	3	3.06
	S. Senftenberg	6	1.67	2	2.25	2	2.04
	S. Livingstone	3	0.83	1	1.12	1	1.02
	S. Dublin	1	0.28	1	1.12	1	1.02
	S. Bredeney	1	0.28	1	1.12	1	1.02
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	360	100.00				

Italy	**Serovars (N=300)**			**Holdings with serovars (N=95)**		**Flocks with serovars (N=95)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Livingstone	58	19.33	22	23.16	22	23.16
	S. Enteritidis	38	12.67	12	12.63	12	12.63
	S. Mbandaka	30	10.00	11	11.58	11	11.58
	S. Thompson	24	8.00	9	9.47	9	9.47
	S. Hadar	21	7.00	8	8.42	8	8.42
	S. Emek	26	8.67	7	7.37	7	7.37
	S. Bredeney	14	4.67	4	4.21	4	4.21
	S. subsp. enterica	4	1.33	4	4.21	4	4.21
	S. Heidelberg	11	3.67	4	4.21	4	4.21
	S. Agona	5	1.67	4	4.21	4	4.21
	S. Montevideo	4	1.33	4	4.21	4	4.21
	Other serovars	64	21.33				
	Salmonella spp.	1	0.33	1			
	Total	300	100.00				

Latvia		**Serovars (N=33)**		**Holdings with serovars (N=1)**		**Flocks with serovars (N=11)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Enteritidis	31	93.94	1	100.00	9	81.82
	S. Derby	2	6.06	1	100.00	2	18.18
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	33	100.00				

Lithuania		**Serovars (N=12)**		**Holdings with serovars (N=2)**		**Flocks with serovars (N=8)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Enteritidis	12	100.00	2	100.00	8	100.00
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	12	100.00				

Norway		**Serovars (N=1)**		**Holdings with serovars (N=1)**		**Flocks with serovars (N=1)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Typhimurium	1	100.00	1	100.00	1	100.00
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	1	100.00				

Poland	Serovars (N=723)			Holdings with serovars (N=206)		Flocks with serovars (N=206)	
		N	**%**	**N**	**%**	**N**	**%**
	S. Enteritidis	397	54.91	123	59.71	123	59.71
	S. Infantis	107	14.80	38	18.45	38	18.45
	S. Hadar	66	9.13	23	11.17	23	11.17
	S. Typhimurium	37	5.12	15	7.28	15	7.28
	S. Mbandaka	48	6.64	14	6.80	14	6.80
	S. Virchow	24	3.32	7	3.40	7	3.40
	S. Derby	19	2.63	6	2.91	6	2.91
	S. Senftenberg	4	0.55	2	0.97	2	0.97
	S. Indiana	7	0.97	2	0.97	2	0.97
	S. Albany	6	0.83	2	0.97	2	0.97
	Other serovars	8	1.11				
	Salmonella spp.	0	0.00				
	Total	723	100.00				

Portugal	**Serovars (N=453)**			**Holdings with serovars (N=157)**		**Flocks with serovars (N=157)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Enteritidis	368	81.24	138	87.90	138	87.90
	S. Infantis	27	5.96	11	7.01	11	7.01
	S. Anatum	28	6.18	8	5.10	8	5.10
	S. Heidelberg	12	2.65	3	1.91	3	1.91
	S. Mbandaka	6	1.32	2	1.27	2	1.27
	S. Havana	3	0.66	2	1.27	2	1.27
	Salmonella Group C1	1	0.22	1	0.64	1	0.64
	S. Typhimurium	1	0.22	1	0.64	1	0.64
	S. Thompson	1	0.22	1	0.64	1	0.64
	S. Tennessee	1	0.22	1	0.64	1	0.64
	S. Senftenberg	4	0.88	1	0.64	1	0.64
	S. Agona	1	0.22	1	0.64	1	0.64
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	453	100.00				

Slovakia	Serovars (N=46)			Holdings with serovars (N=19)		Flocks with serovars (N=19)	
		N	%	N	%	N	%
	S. Enteritidis	21	45.65	13	68.42	13	68.42
	S. Kentucky	15	32.61	4	21.05	4	21.05
	S. Typhimurium	1	2.17	1	5.26	1	5.26
	S. Lille	3	6.52	1	5.26	1	5.26
	S. Infantis	1	2.17	1	5.26	1	5.26
	S. Hadar	5	10.87	1	5.26	1	5.26
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	46	100.00				

Slovenia	Serovars (N=19)			Holdings with serovars (N=10)		Flocks with serovars (N=10)	
		N	%	N	%	N	%
	S. Enteritidis	18	94.74	9	90.00	9	90.00
	S. Infantis	1	5.26	1	10.00	1	10.00
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	19	100.00				

Spain	Serovars (N=629)			Holdings with serovars (N=164)		Flocks with serovars (N=164)	
		N	%	N	%	N	%
	S. Enteritidis	471	74.88	124	75.61	124	75.61
	S. Hadar	73	11.61	20	12.20	20	12.20
	S. Ohio	13	2.07	5	3.05	5	3.05
	S. subsp. salamae 4,12:b:-	19	3.02	4	2.44	4	2.44
	S. Virchow	12	1.91	4	2.44	4	2.44
	S. Infantis	11	1.75	3	1.83	3	1.83
	S. Typhimurium	3	0.48	3	1.83	3	1.83
	S. Senftenberg	3	0.48	2	1.22	2	1.22
	S. Mbandaka	5	0.79	2	1.22	2	1.22
	S. Agona	2	0.32	1	0.61	1	0.61
	S. Anatum	5	0.79	1	0.61	1	0.61
	S. Dabou	1	0.16	1	0.61	1	0.61
	S. Eko	1	0.16	1	0.61	1	0.61
	S. Grumpensis	1	0.16	1	0.61	1	0.61
	S. Aarhus	3	0.48	1	0.61	1	0.61
	S. London	1	0.16	1	0.61	1	0.61
	S. Mikawasima	1	0.16	1	0.61	1	0.61
	S. Newport	1	0.16	1	0.61	1	0.61
	S. subsp. salamae 13,22 : z29 : -	2	0.32	1	0.61	1	0.61
	S. Hayindogo	1	0.16	1	0.61	1	0.61
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	629	100.00				

The Netherlands	**Serovars (N=121)**			**Holdings with serovars (N=36)**		**Flocks with serovars (N=37)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Infantis	28	23.14	8	22.22	8	21.62
	S. Paratyphi B/variant Java	34	28.10	7	19.44	7	18.92
	S. Virchow	15	12.40	5	13.89	5	13.51
	S. Livingstone	7	5.79	5	13.89	5	13.51
	S. Enteritidis	12	9.92	5	13.89	5	13.51
	S. Mbandaka	4	3.31	2	5.56	2	5.41
	S. Agona	4	3.31	2	5.56	2	5.41
	S. Yoruba	2	1.65	1	2.78	1	2.70
	S. Typhimurium	5	4.13	1	2.78	1	2.70
	S. Saintpaul	2	1.65	1	2.78	1	2.70
	S. Indiana	5	4.13	1	2.78	1	2.70
	S. Goldcoast	1	0.83	1	2.78	1	2.70
	S. Derby	1	0.83	1	2.78	1	2.70
	S. Anatum	1	0.83	1	2.78	1	2.70
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	121	100.00				

The United Kingdom	**Serovars (N=107)**			**Holdings with serovars (N=41)**		**Flocks with serovars (N=41)**	
		N	**%**	**N**	**%**	**N**	**%**
	S. Ohio	14	13.08	9	21.95	9	21.95
	S. Kedougou	18	16.82	7	17.07	7	17.07
	S. Livingstone	15	14.02	5	12.20	5	12.20
	S. Senftenberg	10	9.35	5	12.20	5	12.20
	S. Orion	8	7.48	4	9.76	4	9.76
	S. Mbandaka	15	14.02	3	7.32	3	7.32
	S. Thompson	5	4.67	1	2.44	1	2.44
	S. Oslo	1	0.93	1	2.44	1	2.44
	Salmonella spp. rough	2	1.87	1	2.44	1	2.44
	S. Typhimurium	3	2.80	1	2.44	1	2.44
	S. Idikan	5	4.67	1	2.44	1	2.44
	S. Montevideo	1	0.93	1	2.44	1	2.44
	S. London	4	3.74	1	2.44	1	2.44
	S. Virchow	2	1.87	1	2.44	1	2.44
	Salmonella Group B *	3	2.80	1	2.44	1	2.44
	S. Newport	1	0.93	1	2.44	1	2.44
	Other serovars	0	0.00				
	Salmonella spp.	0	0.00				
	Total	107	100.00				

* Not fully typed *Salmonella* serovar (incomplete antigenic formula 4,12:d:-)