SCIENTIFIC REPORT

EFSA Journal

APPROVED: 21 November 2016

doi: 10.2903/j.efsa.2016.4634

The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2015

European Food Safety Authority and
European Centre for Disease Prevention and Control

Abstract

This report of EFSA and the European Centre for Disease Prevention and Control presents the results of the zoonoses monitoring activities carried out in 2015 in 32 European countries (28 Member States (MS) and four non-MS). Campylobacteriosis was the most commonly reported zoonosis and the increasing European Union (EU) trend for confirmed human cases since 2008 continued. In food, the occurrence of *Campylobacter* remained high in broiler meat. The decreasing EU trend for confirmed human salmonellosis cases since 2008 continued, but the proportion of human *Salmonella* Enteritidis cases increased. Most MS met their *Salmonella* reduction targets for poultry. More *S.* Enteritidis isolates were reported and *S.* Infantis was confirmed as the most frequent serovar isolated from domestic fowl. In foodstuffs, the EU level *Salmonella* non-compliance for minced meat and meat preparations from poultry was low. Despite the significant increasing trend since 2008, the number of human listeriosis cases stabilised in 2015. In ready-to-eat foods, *Listeria monocytogenes* seldom exceeded the EU food safety limit. The decreasing EU trend for confirmed yersiniosis cases since 2008 continued. Positive findings for *Yersinia* were mainly reported in pig meat and products thereof. The number of confirmed shiga toxin-producing *Escherichia coli* (STEC) infections in humans was similar to 2014. In food, STEC was most frequently reported in meat from ruminants. A total of 4,362 food-borne outbreaks, including waterborne outbreaks, were reported. Bacteria were the most commonly detected causative agents, followed by bacterial toxins, viruses, other causative agents and parasites. The causative agent remained unknown in 33.5% of all outbreaks. As in previous years, *Salmonella* in eggs continued to represent the highest risk agent/food combination. The report further summarises trends and sources for tuberculosis due to *Mycobacterium bovis*, *Brucella*, *Trichinella*, *Echinococcus*, *Toxoplasma*, rabies, *Coxiella burnetii* (Q fever), West Nile virus and tularaemia.

Keywords: zoonoses, monitoring, *Salmonella*, *Campylobacter*, *Listeria*, parasites, food-borne outbreaks

Requestor: European Commission

Question number: EFSA-Q-2015-00656

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Acknowledgements: EFSA and the ECDC wish to thank the members of the Scientific Network for Zoonoses Monitoring Data and the Food and Waterborne Diseases and Zoonoses Network, who provided the data and reviewed the report; the members of the Scientific Network for Zoonoses Monitoring Data for their endorsement of this scientific report; the EFSA staff members (Frank Boelaert, Giusi Amore, Yves Van der Stede, Krisztina Nagy, Valentina Rizzi, Ivanova Mirena, Anca Stoicescu, Francesca Riolo, Andrea Gervelmeyer), the ECDC staff members (Taina Niskanen, Ines Reulet, Joana Gomes Dias, Herve Zeller, Laurence Marrama, Vahur Hollo and Csaba Ködmön) and the EFSA contractors: the Istituto Zooprofilattico Sperimentale delle Venezie, Italy (and staff members: Antonia Ricci, Lisa Barco, Simone Belluco, Marzia Mancin, Ilaria Patuzzi and Carmen Losasso), the Istituto Superiore di Sanità, Italy (and staff members: Stefano Morabito, Gaia Scavia, Ida Luzzi, Arnold Knijn, Claudia Lucarelli, Edoardo Pozio and Adriano Casulli) and the School of Veterinay Medicine – Aristotle University of Thessaloniki, Greece (and staff members: Apostolos Angelidis) for the support provided to this scientific report.

Suggested citation: EFSA (European Food Safety Authority) and ECDC (European Centre for Disease Prevention and Control), 2016. The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2015. EFSA Journal 2016;14(12):4634, 231 pp. doi:10.2903/j.efsa.2016.4634

ISSN: 1831-4732

The EFSA Journal is a publication of the European Food Safety Authority, an agency of the European Union.

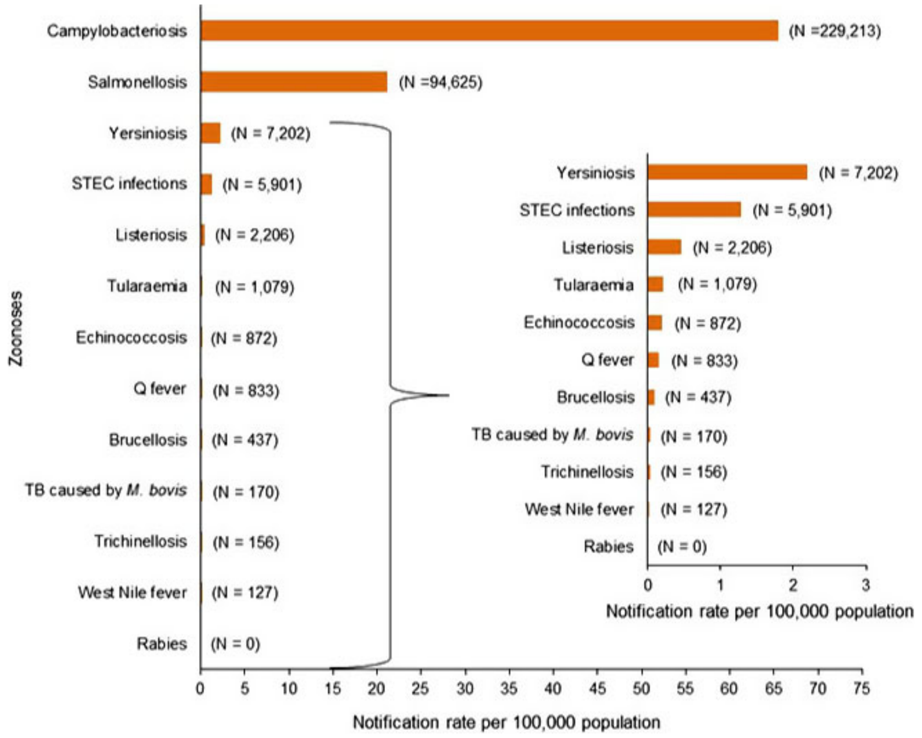
Summary

The report presents the results of the zoonoses monitoring activities carried out in 2015 in 32 European countries: 28 Member States (MS) and four non-Member States (non-MS) Iceland, Liechtenstein, Norway (European Economic Area (EEA) countries) and Switzerland. The European Food Safety Authority (EFSA) and the European Centre for Disease Prevention and Control (ECDC) summarised all submitted data on the occurrence of zoonoses and food-borne outbreaks.

Campylobacter

Humans

In 2015, *Campylobacter* continued to be the most commonly reported gastrointestinal bacterial pathogen in humans in the European Union (EU) and has been so since 2005. The number of reported confirmed cases of human campylobacteriosis was 229,213 (Figure 1) with an EU notification rate of 65.5 per 100,000 population, a 5.8% decrease compared with the rate in 2014. The 12-month moving average showed a statistically significant increasing trend over the 8-year period 2008–2015. The majority of the MS reported increasing notification rates in 2015 with almost half of the MS reporting significant increases between 2008 and 2015. Despite the high number of human campylobacteriosis cases, their severity in terms of reported case fatality was low (0.03%) (Table 1).



Total number of confirmed cases is indicated in parenthesis at the end each bar. Exception is made for West Nile fever where total number of cases was used.

Figure 1: Reported numbers and notification rates of confirmed human zoonoses cases in the EU, 2015

Foodstuffs

Twenty-one MS and one non-MS countries reported 2015 data on *Campylobacter* in food with generally lower sample sizes compared to 2014. Broiler meat is considered to be the most important single source of human campylobacteriosis. In 2015, 46.7% of the 6,707 samples of fresh broiler meat (single or batch, aggregated data from all sampling stages) were found to be *Campylobacter*-positive, which was higher than in 2014. There was, however, variation in the countries reporting *Campylobacter* monitoring data between the 2 years. *Campylobacter* was not detected in the tested units (single or batch) of raw cow's milk intended for direct human consumption or for manufacture of pasteurised/ultra-high temperature (UHT) products.

Table 1: Reported hospitalisation and case fatality rates due to zoonoses in confirmed human cases in the EU, 2015

Disease	Number of confirmed(a)	Hospitalisation				Deaths			
	Human cases	Status available (%)	Number of reporting MS(b)	Reported hospitalised cases	Proportion hospitalised (%)	Outcome available (%)	Number of reporting MS(b)	Reported Deaths	Case Fatality (%)
Campylobacteriosis	229,213	27.0	17	19,302	31.2	73.7	16	59	0.03
Salmonellosis	94,625	34.0	16	12,353	38.4	55.6	16	126	0.24
Yersiniosis	7,202	23.9	14	530	30.9	59.8	14	0	0.0
STEC infections	5,901	39.4	14	853	36.3	56.2	15	8	0.24
Listeriosis	2,206	44.9	18	964	97.4	69.1	20	270	17.7
Tularaemia	1,079	14.9	9	89	55.6	15.6	10	0	0.0
Echinococcosis	872	20.5	13	107	59.8	23.5	13	1	0.49
Q fever	833	NA(c)	NA	NA	NA	47.7	12	3	0.36
Brucellosis	437	42.8	8	130	69.5	31.1	8	1	0.74
Trichinellosis	156	72.5	7	30	34.5	75.0	8	0	0.0
West Nile fever(a)	127	51.2	7	54	83.1	51.2	5	2	1.57
Rabies	0	NA(c)	NA	NA	NA	0.0	0	0	0.0

(a): Exception made for West Nile fever where the total number of cases was included.
(b): Not all countries observed cases for all diseases.
(c): NA-not applicable as the information is not collected for this disease.

Animals

Fifteen MS and three non-MS reported 2015 data on *Campylobacter* in animals, which are fewer compared to 2014. *Campylobacter* was found in 19.3% of the 10,063 units of broilers tested in the MS. This overall proportion of positives is lower than in 2014. Since the reporting countries differed across years, data were not comparable across these years. Only a few MS reported *Campylobacter* data for other animals.

Salmonella

Humans

In 2015, a total of 94,625 confirmed salmonellosis cases were reported by 28 EU MS, resulting in an EU notification rate of 21.2 cases per 100,000 population. This represented a 1.9% increase in the EU notification rate compared with 2014. There was a statistically significant decreasing trend of salmonellosis in the 8-year period between 2008 and 2015. Ten MS reported 126 fatal cases among the 16 MS that provided data on the outcome of their cases. This gives an EU case fatality rate of 0.24% among the 52,605 confirmed cases for which this information was available (Table 1).

As in previous years, the two most commonly reported *Salmonella* serovars in 2014 were *Salmonella* Enteritidis and *Salmonella* Typhimurium, representing 45.7% and 15.8%, respectively, of all reported serovars in confirmed human cases. The proportion of *S.* Enteritidis increased compared with 2014. *S.* Typhimurium cases decreased, while its monophasic variant strains 1,4,[5],12:i:- returned to the level of 2013 after a decrease in 2014. Cases of *Salmonella* Infantis, the fourth most common serovar continued to decrease in 2015. Cases of *Salmonella* Stanley still remained, as in the last 2 years, at a higher level than before the large outbreak reported in 2011–2012.

Foodstuffs

Generally, there were no major changes as regards *Salmonella*-contaminated foodstuffs as compared to the previous year. The highest occurrence of samples not-compliant with *Salmonella* criteria was found in foods of meat origin which are intended to be cooked before consumption. Among these foods, 'minced meat and meat preparations from poultry' had a notable level of non-compliance (6.8% of single samples and 5.1% of batches), with values similar to the previous year. *Salmonella* was most frequently detected in broiler meat (6.5%) and turkey meat (4.6%), whereas a lower number of positive samples were found in pig meat (1.7%) and bovine meat (0.2%). *Salmonella* was rarely found in table eggs (0.9%, in single samples). Ready-to-eat (RTE) foods pose a direct risk to consumers, and 1.1% and 0.7% positive samples were found for RTE food from meat from broilers and pig meat, respectively, whereas one positive sample and no positive samples were found for RTE food from turkey and cattle meat. A notable *Salmonella* prevalence of 4.3% was described for dried seeds in 2015, mainly associated with samples collected during border inspection activities by two MS, Greece and the Netherlands.

Animals

In 2015, the EU level prevalence of *Salmonella* target serovars-positive flocks was very low, as in 2014, for all animal categories covered by the implementation of National Control Programs: breeding flocks of *Gallus gallus*, laying hen flocks, broiler flocks, and breeding and fattening turkey flocks. Since the implementation of these programs since many years, a statistically significant declining trend in the EU level prevalence of *Salmonella* target serovars-positive flocks was observed for all categories with the exception of breeding turkey flocks.

The EU level prevalence of *Salmonella* target serovars-positive flocks in breeding flocks of *G. gallus* was very low (0.34%) with only two MS not meeting the target (< 1%) for the five target serovars (*S*. Enteritidis, *S*. Typhimurium, *S*. Infantis, *S*. Virchow and *Salmonella* Hadar). In the case of flocks of laying hens, the EU level prevalence of *Salmonella* target serovar-positive flocks was 1.0% with only one MS not meeting the reduction target for the two serovars (*S*. Enteritidis, *S*. Typhimurium). In broilers, the *Salmonella* target serovars-positive flock prevalence was 0.3% and two MS did not meet the target of 1% or less of broiler flocks positive for these two target serovars. Still, compared to 2014, the 2015 EU prevalence of *S.* Enteritidis-positive flocks increased in laying hens and also slightly in broilers. As regards turkeys, the overall *Salmonella* target serovars-positive flock prevalence for breeding and fattening flocks was 0.4% and 0.3%, respectively. All the MS met the target for breeding turkeys, whereas two MS did not meet the target of 1% for fattening turkeys.

Data about the other animal species should be interpreted with caution due to the absence of harmonised control programs. The overall herd prevalence was 12.4% for pigs and 2.1% for cattle.

Feedingstuffs

The overall level of *Salmonella*-positive units in animal- and vegetable-derived feed material in 2015 was 5.13% out of 4,546 units reported by 21 MS. Compared to 2014 (3.8%) and 2013 (1.4%), a slight increase was observed.

Among different matrices reported by 21 MS and one non-MS, the most commonly tested feed material was soya (bean)-derived feed material with 3,404 samples tested and a mean *Salmonella* prevalence of 3.7%. High prevalence was reported for meat meal (290 tested, 16.7% positives). In the finished feed for animals (compound feedingstuffs), the prevalence of *Salmonella*-positive units in 2015 was low to very low for all animal species: 1.20% of 2,248 tested samples for cattle, 0.51% of 2,754 tested samples for pigs and 0.67% of 7,961 tested samples for poultry.

Serovars

The most frequent serovar among reports from *G. gallus* was *S*. Infantis, accounting for 1,859 or 33.6% of all reported isolates, followed by *S*. Enteritidis (875 isolates; 15.8%) and *Salmonella* Mbandaka (373 isolates; 6.7%). These three serovars were confirmed for the fourth year as those most frequently isolated from *G. gallus*. At the EU level, a substantial increase (of about 35%) of *S*. Enteritidis isolates occurred in 2015 (875 isolates) compared to 2014 (641 isolates) as well as for *S*. Typhimurium (321 isolates in 2015 and 209 in 2014). However, these increases were due to a limited number of MS; France, Germany, Poland and the United Kingdom for *S*. Enteritidis, and mainly France for *S*. Typhimurium. This reporting might have been strongly influenced by the differences in reporting of serovars from the MS among the years, rather than by a real evolution of the epidemiological situation.

With regard to laying hens, *S.* Enteritidis and *S.* Typhimurium were the two most frequent reported serovars, accounting for 41.2% and 11.1% of the isolates from this source.

As for *G. gallus*, *S*. Infantis, *S*. Enteritidis and *S*. Mbandaka were confirmed as the most frequent serovars from broilers, accounting for 38.7%, 11.6% and 7.2% of the isolates. *S.* Infantis and *S*. Enteritidis were the two most common serovars isolated from broiler meat, accounting for 594 (54.1%) and 136 isolates (12.4%), respectively. This was in line with the serovars reported from *G. gallus* and broilers, where *S*. Infantis and *S*. Enteritidis were by far the most commonly reported serovars too.

With regard to turkeys, serovars reported in high numbers from this source seem to cluster in one country only and *Salmonella* Derby, which was the most common serovar from turkey flocks, was reported exclusively by the United Kingdom. From turkey meat, *S*. Stanley, *Salmonella* Newport and *Salmonella* Bredeney were the most commonly reported serovars.

In pigs, *S*. Typhimurium accounted for 56.9% of the 2,401 isolates reported in 2015, and *S*. Derby was the second most common serovar, accounting for 13.7% of isolates. The proportion of isolates that belong to the group of monophasic strains of *S*. Typhimurium has not changed substantially over the last years and ranged between 9.0% of isolates in 2015 and 14.0% in 2013. The same serovars were identified as the most frequent from pig meat. *S*. Derby accounted for 22.9% of the isolates from this source, followed by monophasic strains of *S*. Typhimurium (22.3%) and *S*. Typhimurium (20.6%).

As reported in the previous year for cattle, the most common serovar was *S*. Typhimurium (43.2% of all 3,243 reported isolates). *S*. Dublin (26.0% of isolates) was the second most common serovar across the EU, and *S*. Coeln accounted for 6.7% of isolates. In 2015, 21.3% of isolates from bovine meat were *S.* Typhimurium and 10.7% were *S*. Derby.

Listeria

Humans

In 2015, 28 MS reported 2,206 confirmed human cases of listeriosis. The EU notification rate was 0.46 cases per 100,000 population, which was similar to 2014. There was a statistically significant increasing trend of listeriosis over 2008–2015. Nineteen MS reported 270 deaths due to listeriosis in 2015, which was the highest annual number of deaths reported since 2008. The EU case fatality was 17.7% among the 1,524 confirmed cases with known outcome (Table 1). Listeriosis infections were most commonly reported in the elderly population in the age group over 64 years old and particularly in the age group over 84 years.

Foodstuffs

In 2015, the non-compliance for the different RTE food categories was generally at levels comparable to previous years, with non-compliance being highest in samples of fishery products (mainly smoked fish), dairy products (other than cheeses) and heat-treated meat products collected at processing. At retail, non-compliance was highest in batches of fishery products and 'soft and semi-soft cheeses'.

Animals

In 2015, several MS reported data on *Listeria* spp. in various animal species. Most of the tested samples were from domestic ruminants (cattle, sheep and goats) and positive findings were most often reported in these three animal species. However, *Listeria* spp. (mainly *Listeria monocytogenes*) were also reported in pigs, solipeds, broilers, cats, dogs, foxes, and other wild and zoo animals.

Shiga toxin-producing *E. coli*

Humans

In 2015, 5,901 confirmed cases of shiga toxin-producing *Escherichia coli* (STEC) infections were reported in the EU. The EU notification rate was 1.27 cases per 100,000 population, which was slightly lower than the notification rate in 2014. The EU notification rate following the large outbreak in 2011 was higher in 2012–2015 than before the outbreak but stabilised in the last 2 years in 2014–2015. In 2015, eight deaths due to STEC infection were reported in the EU which resulted in an EU case fatality of 0.2% among the 3,352 confirmed cases for which this information was provided (Table 1).

As in previous years, the most commonly reported STEC serogroup in 2015 was O157 (41.7%), although its relative proportion compared to other serogroups declined. This is possibly an effect of increased awareness and of more laboratories testing for other serogroups. Serogroup O157 was followed by serogroups O26, O103, O91, O145, O146 and O128. The proportion of non-typable STEC strains continued to increase in 2015.

Foodstuffs and animals

STEC were detected in 2.9% of the food samples and in 6.8% of the animal samples tested. The highest proportion of STEC-positive food samples was detected in meat from ruminants (primarily sheep and goat, but also wild ruminants and cattle), followed by raw milk and dairy products, whereas the proportion of positive samples in fruit and vegetables was very low. As for sprouted seeds, the sole category for which microbiological criteria for STEC have been established in the EU, only two positive samples were reported out of the 925 analysed by 12 MS.

Among animals, the reported proportion of STEC-positive samples was higher for sheep and goats than for cattle.

Compared with the previous years, in 2015, higher proportions of STEC-positive samples were reported for both food and animal samples. This finding may be due to the increased adoption of the ISO TS 13136:2012 standard method, which is able to detect any STEC, regardless of the serogroup.

A large spectrum of STEC serogroups was reported in food, with STEC O157 being the most frequent. Similarly, this STEC serogroup prevailed in animal samples, where only five STEC serogroups have been identified. However, it should be considered that many of the MS's surveillance and monitoring programmes are traditionally focused on STEC O157 and this may have introduced a bias in the estimates of the frequency of STEC serogroups. It is important to note that the proportion of STEC O26 was similar to that of STEC O157 in the food samples tested using the ISO/TS 13136:2012 standard method. In the EU, these two STEC serogoups are the most reported STEC serogroups causing the severe Haemolytic Uremic Syndrome.

Yersinia

Humans

Twenty-six MS reported 7,202 confirmed cases of yersiniosis in 2015, making it the third most commonly reported zoonosis in the EU. The EU notification rate was 2.20 cases per 100,000 population which was 6.8% higher than in 2014. There was a statistically significant decreasing 8-year trend in 2008–2015. The highest country-specific notification rates were observed in the MS in north-eastern Europe. *Yersinia enterocolitica* was the most common species reported to be isolated from human cases. The most common serotype was O:3 followed by O:9 and O:5,27.

No fatalities were reported among the 4,304 confirmed yersiniosis cases for which this information was reported in 2015 (Table 1).

Food and animals

Only very few MS report data from the surveillance of *Yersinia* in food and animals. In 2015, three MS reported positive findings for *Yersinia* in pig meat and products thereof (11.3% of the 952 units tested), and two MS reported positive findings in pigs (11.0% of the 2,050 samples tested). Positive units were also reported in other foods (bovine meat, raw cow's and raw goat's milk, and RTE salad) and in other animals (cattle, cats, dogs, deer, foxes, hares, marten, Steinbock, Cantabrian chamois, wild boar and other wild animals). *Yersinia enterocolitica* was the most common species reported in food and animals. The most common biotypes/serotypes were biotype 1A in food, and serotypes O:9 followed by O:3, O:8, O:5 and O:1,2,3 in animals.

Tuberculosis due to *Mycobacterium bovis*

Humans

Tuberculosis due to *M. bovis* is a rare infection in humans in the EU, with 170 confirmed human cases reported in 2015 and a notification rate of 0.03 cases per 100,000 population. The notification rates in the EU have been stable in 2011–2014. There was no clear association between a country's status as officially free of bovine tuberculosis in cattle (OTF) and notification rates in humans.

Animals

The 2015 monitoring data on bovine tuberculosis in the EU cattle demonstrate that the current situation in Europe regarding bovine tuberculosis infection, detection and control is heterogeneous. The prevalence ranges from absence of infection in most OTF regions to a regional prevalence of test-positive cattle herds of 17.7% within the United Kingdom in Wales and England. In the non-OTF regions in the EU, the overall prevalence of bovine tuberculosis-positive cattle herds has increased slowly during the last years from 1.05% in 2010 to 1.49% in 2015. This slight increase might be explained by the gradual declaration of few MS as OTF and of regions within non-OTF MS as OTF.

Brucella

Humans

Brucellosis is a rare infection in humans in the EU with 437 confirmed cases reported in 2015. The highest notification rates and the majority of the domestic cases were reported from three countries (Greece, Portugal and Italy) that are not officially brucellosis-free in cattle (OBF), sheep or goats (ObmF). Almost 70% of the human brucellosis cases were hospitalised, with one death reported in 2015.

Foodstuffs

There were two *Brucella*-positive samples in an investigation of 'milk from other animal species or unspecified' collected at retail in Italy. The other two MS (Portugal and Spain) that reported surveillance results in food did not have any positive sample.

Animals

In 2015, in non-OBF/non-ObmF regions of non-OBF/non-ObmF MS, the overall prevalence of bovine, ovine and caprine brucellosis was very low, about 0.3%. For bovine brucellosis, the overall prevalence of *Brucella*-positive or -infected cattle herds has been increasing in the non-OBF regions of the non-OBF MS during the years 2012–2015, from 0.10% in 2012 to 0.28% in 2015. This is mainly due to the decrease of number of cattle herds in these non-OBF regions while the total number of *Brucella*-positive or -infected cattle herds only decreased slightly. Italy reported some hundreds of *Brucella*-positive herds and Greece 199 infected herds in 2015. The overall prevalence of *Brucella melitensis*-positive sheep and goat herds in the non-ObmF regions of the non-ObmF MS decreased during the years 2012–2015, from 0.45% in 2012 to 0.29% in 2015. Italy and Portugal still reported some hundreds of *Brucella* test-positive sheep and goat herds in 2015.

Trichinella

Humans

In 2015, 156 confirmed trichinellosis cases were reported in the EU. The EU notification was 0.03 cases per 100,000 population, and decreased by 57.1% compared with 2014 when the highest notification rate was reported since 2010. Lithuania reported the highest notification rate followed by Romania and Bulgaria. The EU trend for trichinellosis was greatly influenced by a number of smaller and larger outbreaks with peaks often occurring in January and February. The most commonly reported species was *Trichinella spiralis* followed by *Trichinella britovi.*

Animals

In 2015, 27 MS and three non-MS provided information on *Trichinella* in domestic animals (pigs, farmed wild boar and/or horses). No positive results were reported in pigs raised under controlled housing conditions and no positive animals were detected among farmed wild boar and domestic solipeds. Five MS (Croatia, Lithuania, Romania, Poland and Spain) reported 106 positive findings from more than 50 million fattening pigs raised under not controlled housing conditions. Twenty-one MS and two non-MS provided data on hunted wild boar, and 14 MS and one non-MS reported 672 positive findings out of 877,122 animals tested (0.08%). Sixteen MS and one non-MS reported data on *Trichinella* in 18 different wildlife species other than wild boar, and reported a total of 354 (3.7%) positive findings in nine host species of 10 MS from approximately 10,000 animals tested.

Echinococcus

Humans

In 2015, a total of 872 laboratory-confirmed echinococcosis cases were reported in the EU. The EU notification rate was 0.20 cases per 100,000 population, which was the same as in 2014. The *Echinococcus granulosus* (cystic echinococcosis) trend in number of cases decreased since 2008 but stabilised in 2015. In contrast, *Echinococcus multilocularis* (alveolar echinococcosis) showed a statistically significant increasing trend since 2008. One death due to echinococcosis (species not specified) was reported in 2015.

Animals

In 2015, five MS (Finland, Ireland, Malta, Norway and the United Kingdom) confirmed their free status of *E. multilocularis* (Regulation (EU) No 1152/2011). In 2015, 24 MS and two non-MS provided data on *Echinococcus* in animals. Eleven MS reported data on 5,720 foxes examined for *E. multilocularis*, and eight MS reported positive findings with a total prevalence of 10%. For *E. granulosus*, 23 MS reported data from more than 78 million animals, mainly domestic animals. Twelve MS reported a total of 113,517 positive samples.

Toxoplasma

Humans

In 2015, in total, 41 cases of congenital toxoplasmosis were reported in the EU (in the Czech Republic, Germany, Hungary, Ireland, Lithuania, Poland, Slovenia and the United Kingdom). France reported data with 2-year delay, 216 confirmed congenital toxoplasmosis cases in 2014.

Animals

In 2015, 13 MS and two non-MS provided data on *Toxoplasma* in animals. Positive findings via serology were detected in sheep and goats (11 MS and two non-MS with overall 39.4% of the tested samples positive), pigs (three MS and one non-MS, 3.7% positive), cattle (seven MS and two non-MS, 5.9% positive), and dogs and cats (seven MS and one non-MS; 15.5% of the 1,896 cats and 17.9% of 2,065 tested dogs were positive for *Toxoplasma*). Only in small ruminants and cats was *Toxoplasma* detected by direct diagnostic methods such as polymerase chain reaction (PCR) and histology. In addition, nine MS and two non-MS reported *Toxoplasma*-positive samples from hares, Cantabrian chamois, red and roe deer, foxes, lamas, dolphin, wolves, alpacas, ducks, domestic fowl, and zoo animals.

Rabies

Humans

In 2015, no case of rabies in humans was reported in the EU.

Animals

In 2015, total 17 MS and two non-MS reported *Lyssavirus* in bats. In eight MS, 26 positive cases were found out of 1,391 bats examined. Twenty-two MS and two non-MS reported data on foxes, and in total, 99 rabies cases in foxes were reported from four MS (Lithuania, Romania, Poland and Slovakia) out of the 46,588 tested. Three rabies cases were reported in raccoon dogs in 2015 by two MS. Eighteen MS and two non-MS reported approximately 3,600 samples tested in wildlife other than bats, foxes and raccoon dogs and only 13 animals tested positive from two MS (Poland and Romania). In domestic farm animals, positive samples were reported in cattle and solipeds by these two MS.

Q fever

Humans

In 2015, a total of 833 confirmed cases of Q fever were reported in the EU. The EU notification rate was 0.16 per 100,000 population. The highest notification rate (0.54 cases per 100,000 population) was observed in Spain, followed by Croatia (0.49) and Cyprus (0.47). The highest numbers of confirmed cases were reported by Germany and France (311 and 250, respectively), as in 2014.

Overall, a decreasing trend in confirmed Q fever cases was observed over the period 2008–2015 in the EU/EEA. Three deaths due to Q fever were reported in 2015 in the EU (one case in the Netherlands and two cases in Hungary), resulting in an EU case fatality of 0.36%.

Animals

The 2015 monitoring data for Q fever in animals demonstrate that the *Coxiella burnetii* was found in cattle, sheep, goats, pigs, farmed water buffaloes and pet dogs.

West Nile virus

Humans

In 2015, 127 cases of West Nile fever (WNF) in humans were reported in the EU. The EU notification rate was 0.02 per 100,000 population, identical to 2014. The highest numbers of cases have been reported from Italy, where provinces with high population were affected, particularly Milano, a province without previous history of local transmission. In Hungary and Romania, the transmission season was rather similar to the 2014 season. Greece did not report any case.

There were two deaths reported in 2015, one in Romania (neuroinvasive manifestation) and one in Bulgaria (clinical manifestation unknown).

Animals

Test-positive birds and solipeds were reported by Croatia, Italy, Hungary and Spain. Additionally positive solipeds were reported by the Czech Republic, Portugal and Romania.

Tularaemia

Humans

In 2015, 1,079 confirmed cases of tularaemia in humans were reported in the EU. The EU notification rate was 0.21 cases per 100,000 population, a significant increase compared with 2014. The highest notification rate was observed in Sweden (7.41 confirmed cases per 100,000 population), as the country experienced an outbreak with a higher number of confirmed cases compared with the 2012 outbreak. No deaths due tularaemia were reported in the EU.

Animals

In 2015, occurrence of *Francisella tularensis* was reported by one MS (Sweden) and one non-MS, in wild hares, beavers and monkeys. Only hares were found positive.

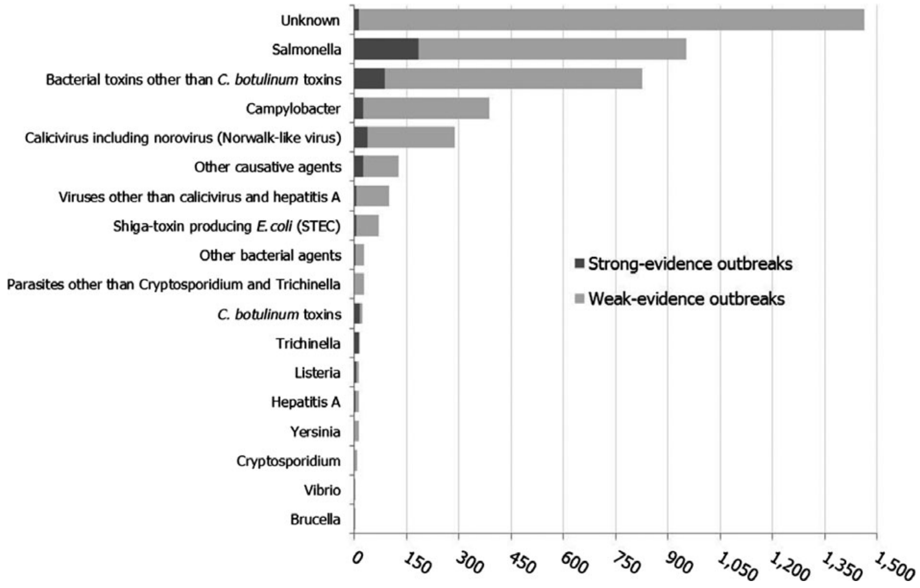
Other zoonoses and zoonotic agents

The findings of *Anisakis* spp. (one MS), *Chlamydia* spp. (one MS), *Bacillus cereus* (one MS), *Taenia saginata* cysts in bovine carcases (one MS) and of *Taenia solium* cysts in pig carcases (two MS) and *Sarcocystis* (one MS) were reported in 2015.

Food-borne outbreaks

In 2015, 26 MS reported a total of 4,362 food-borne outbreaks, including waterborne outbreaks. Overall, these outbreaks caused 45,874 cases of illness (209 more than 2014), 3,892 hospitalisations (2,546 less than 2014) and 17 deaths (10 less than 2014). In addition, two non-MS reported data on 50 food-borne outbreaks involving 1,853 cases and 7 hospitalisations. The overall reporting rate of food-borne outbreaks in the EU was 0.95 per 100,000 population, which represents a slight decrease compared with data provided for 2014.

Most of the outbreaks reported in 2015 were caused by bacterial agents (33.7% of all outbreaks), in particular *Salmonella* (21.8% of all outbreaks) and *Campylobacter* (8.9% of all outbreaks), even though the reporting of outbreaks involving these agents has been declining over the recent years. Bacterial toxins ranked second among the causative agents in food- and waterborne outbreaks and were reported in 19.5% of the total outbreaks while viruses, which were the agents most frequently reported in 2014, accounted for 9.2% of total outbreaks in 2015. Parasites and other causative agents, in particular histamine, were reported in less than 3% of the outbreaks. It is important to note that the vast majority of outbreaks caused by bacterial toxins and other causative agents (87.2% and 81.1%, respectively) were reported from a single MS, and therefore, the respective findings are to be interpreted with caution, as they cannot be considered representative of the EU. Furthermore, for a third of the reported outbreaks (34%) the causative agent remained unknown. The distribution of food-borne and waterborne outbreaks per causative agent reported by EU Member States in 2015 is shown in Figure 2.



Other bacterial agents include *Francisella*, *Shigella*, pathogenic *E. coli* other than shiga toxin-producing *E. coli*, and other unspecified bacteria. Bacterial toxins other than *Clostridium botulinum* toxins include toxins produced by *Bacillus*, *Clostridium* other than *C. botulinum* and *Staphylococcus* and other unspecified bacterial toxins. Viruses other than calicivirus and hepatitis A virus include adenovirus, flavivirus, rotavirus and other unspecified viruses. Other causative agents include chemical agents, histamine, marine biotoxins, mushroom toxins and scrombotoxin. Parasites other than *Trichinella*, *Cryptosporidium*, *Anisakis*, include *Giardia* and other unspecified parasites.

Figure 2: Distribution of food-borne and waterborne outbreaks per causative agent in the EU Member States, 2015

For 422 outbreaks accounting for 9.7% of total food-borne outbreaks reported in 2015, the link with the implicated suspected vehicle could be established based on strong evidence. The implicated food vehicles were mostly of animal origin, in particular eggs and egg products and pig meat (both accounting for 10% of all strong-evidence outbreaks), broiler meat (9%) and cheese (8%) followed by fish and fish products (7%), milk and dairy products (5%), bovine meat (4%) and crustaceans (3%). *Salmonella* in eggs remained a public health problem. In 2015, *Salmonella* in eggs was associated with the highest number of reported food-borne outbreaks and was among the top-5 food-pathogen combinations in terms of the overall number of cases of illness and hospitalisations in outbreaks. However, the number of reported outbreaks caused by *Salmonella* and associated with the consumption of 'eggs and egg products' has been decreasing in the last 5 years.

Information on place of exposure was provided in 2015 by the MS for 409 strong-evidence outbreaks. Household was by far the most frequent place of exposure. In strong-evidence food-borne outbreaks, *Salmonella* was the most common agent reported in private households whereas 'bacterial toxins other than *C. botulinum* toxins', calicivirus and other causative agents were more frequently reported in public settings such as canteens, workplace catering, restaurants and pubs.

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Legal basis

The EU system for the monitoring and collection of information on zoonoses is based on the Zoonoses Directive 2003/99/EC,[1] which obliges the European Union (EU) Member States (MS) to collect relevant and, where applicable, comparable data on zoonoses, zoonotic agents, antimicrobial resistance and food-borne outbreaks. In addition, the MS are required to assess trends and sources of these agents, as well as outbreaks in their territory, submitting an annual report each year by the end of May to the European Commission covering the data collected. The European Food Safety Authority (EFSA) is assigned the tasks of examining these data and publishing the EU annual Summary Reports. In accordance with Article 9 of the Zoonoses Directive 2003/99/EC, EFSA shall examine the submitted national reports of the EU MS and publish by the end of November a summary report on the trends and sources of zoonoses, zoonotic agents and antimicrobial resistance in the EU.

The data collection on human diseases from the MS is conducted in accordance with Decision 1082/2013/EU[2] on serious cross-border threats to health, which in October 2013 replaced Decision 2119/98/EC on setting up a network for the epidemiological surveillance and control of communicable diseases in the EU. The case definitions to be followed when reporting data on infectious diseases to the European Centre for Disease Prevention and Control (ECDC) are described in Decision 2012/506/EU.[3] The ECDC has provided data on zoonotic infections in humans, as well as their analyses, for the EU Summary Reports since 2005. Since 2007, data on human cases have been received via The European Surveillance System (TESSy), maintained by the ECDC.

About EFSA

EFSA, located in Parma, Italy, and established and funded by the EU as an independent agency in 2002, provides objective scientific advice, in close collaboration with national authorities and in open consultation with its stakeholders, with a direct or indirect impact on food and feed safety, including animal health and welfare and plant protection. EFSA is also consulted on nutrition in relation to the EU legislation. EFSA's risk assessments provide risk managers (the European Commission, the European Parliament and the Council) with a sound scientific basis for defining policy-driven legislative or regulatory measures required to ensure a high level of consumer protection with regard to food and feed safety. EFSA communicates to the public in an open and transparent way on all matters within its remit. Collection and analysis of scientific data, identification of emerging risks and scientific support to the European Commission, particularly in the case of a food crisis, are also part of EFSA's mandate, as laid down in founding Regulation (EC) No 178/2002[4] of 28 January 2002.

About ECDC

The ECDC, an EU agency based in Stockholm, Sweden, was established in 2005. The objective of the ECDC is to strengthen Europe's defences against infectious diseases. According to Article 3 of founding Regulation (EC) No 851/2004[5] of 21 April 2004, the ECDC's mission is to identify, assess and communicate current and emerging threats to human health posed by infectious diseases. In order to achieve this goal, the ECDC works in partnership with national public health bodies across Europe to strengthen and develop the EU-wide disease surveillance and early warning systems. By working with experts throughout Europe, the ECDC pools Europe's knowledge in health to develop authoritative scientific opinions about the risks posed by current and emerging infectious diseases.

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

[2] Decision No 1082/2013/EU of the European Parliament and of the Council of 22 October 2013 on serious cross-border threats to health and repealing Decision No 2119/98/EC. OJ L 293, 5.11.2013, p. 1–15.

[3] Commission Decision 2012/506/EU amending Decision 2002/253/EC laying down case definitions for reporting communicable diseases to the Community network under Decision No 2119/98/EC of the European Parliament and of the Council. OJ L 262, 27.9.2012, p. 1–57.

[4] Regulation (EC) No 178/2002 of the European Parliament and of the Council of 28 January 2002 laying down the general principles and requirements of food law, establishing the EFSA and laying down procedures in matters of food safety. OJ L 31, 1.2.2002, p. 1–24.

[5] Regulation (EC) No 851/2004 of the European Parliament and of the Council of 21 April 2004 establishing an European centre for disease prevention and control. OJ L 142, 30.4.2004, p. 1–11.

1. Introduction

This European Union (EU) Summary Report 2015 on zoonoses, zoonotic agents and food-borne outbreaks was prepared by the European Food Safety Authority (EFSA) in collaboration with the European Centre for Disease Prevention and Control (ECDC). The Member States (MS), other reporting countries, the European Commission, members of EFSA's Scientific Panels on Biological Hazards (BIOHAZ) and Animal Health and Welfare (AHAW) and the relevant EU Reference Laboratories (EURLs) were consulted while preparing the report.

The efforts made by the MS, the reporting non-MS and the European Commission in the reporting of zoonoses data and in the preparation of this report are gratefully acknowledged.

The 2015 data on antimicrobial resistance in zoonotic agents submitted and validated by the MS are published in a separate EU Summary Report.

The present EU Summary Report on zoonoses and food-borne outbreaks focuses on the most relevant information on zoonoses and food-borne outbreaks within the EU in 2015. If substantial changes compared with the previous year were observed, they have been reported.

1.1. The structure of the report

The current report, the EU Summary Report 2015, includes an abstract, a summary, an introduction to the zoonoses reporting, a description of materials and methods and an EU assessment of the specific zoonoses. It is available in printable format. The Appendix A lists all data summarised in tables and figures for the production of this report, for humans, foods, animals, feed and food-borne outbreaks. Also, summary tables and figures that did not trigger any marked observation and were not included in this printable report are available in the supporting information files published.

Monitoring and surveillance schemes for most zoonotic agents covered in this report are not harmonised among the MS, and findings presented in this report must, therefore, be interpreted with care. The data presented may not have been derived from sampling plans that were statistically designed, and, thus, findings may not accurately represent the national situation regarding zoonoses. Regarding data on human infections, please note that the numbers presented in this report may differ from national zoonoses reports due to differences in case definitions used at the EU and national level or because of different dates of data submission and extraction. Results are generally not directly comparable between the MS and sometimes not even between different years in one country.

The national zoonoses reports submitted in accordance with Directive 2003/99/EC are published on the EFSA website together with the EU Summary Report. They are available online at http://www.efsa.europa.eu/en/biological-hazards-data/reports

2. Materials and methods

2.1. Data received in 2015

2.1.1. Human data

The human data analyses in the EU Summary Report for 2015 were prepared by the Food- and Waterborne Diseases and Zoonoses programme at the ECDC and were based on the data submitted via The European Surveillance System (TESSy), hosted at the ECDC. Please note, as explained above, that the numbers presented in the report may differ from national reports owing to differences in case definitions used at the EU and national level or to different dates of data submission and extraction. The latter may also result in some divergence in case numbers presented in the different ECDC reports.

TESSy is a software platform that has been operational since April 2008 and in which data on 52 diseases and special health issues are collected. Both aggregated and case-based data were reported to TESSy. Although aggregated data did not include individual case-based information, both reporting formats were included where possible to calculate country-specific notification rates, case fatality rates, proportion of hospitalised cases and trends in diseases. Human data used in the report were extracted from TESSy as of 3 November 2016, except for human tuberculosis due to *Mycobacterium bovis* as of 3 October 2016. The denominators used for the calculation of the notification rates were the human population data from EUROSTAT 1 January 2016 update.

Data on human zoonoses cases were received from 28 MS and also from two non-MS, Iceland and Norway. Switzerland sent its data on human cases directly to EFSA. The human data for Switzerland also include the ones from Liechtenstein.

The data should be interpreted with caution and taking into account data quality issues and differences between the MS surveillance systems. The reader should refrain from making direct comparisons between countries without taking into account the limitations in the data which may differ between countries depending on the characteristics of their surveillance systems.

2.1.2. Data on food, animals and feed

In 2015, 28 MS submitted data and national zoonoses reports. In addition, data and reports were submitted by the four non-MS: Iceland, Norway, Switzerland and Liechtenstein.[6] All the MS and the four non-MS submitted data on animals, food and food-borne outbreaks electronically to the EFSA zoonoses database, through EFSA's Data Collection Framework (DCF). The MS could also update data from previous years, before 2015.

In 2015, data were collected on a mandatory basis for the following eight zoonotic agents in animals, food and feed: *Salmonella*, *Campylobacter*, *Listeria monocytogenes*, shiga toxin-producing *Escherichia coli* (STEC), *M. bovis*, *Brucella*, *Trichinella* and *Echinococcus*. In addition, based on the epidemiological situations in the MS, data were reported on the following agents and zoonoses: *Yersinia*, *Mycobacterium caprae*, *Toxoplasma*, *Lyssavirus* (rabies), *Coxiella burnetii* (Q fever), West Nile virus (WNV), *Cysticercus*, *Francisella*, *Chlamydia* and *Sarcocystis*, and *Bacillus*. Data on *Staphylococcus*, meticillin-resistant *Staphylococcus aureus* (MRSA) and antimicrobial resistance in indicator *E. coli* and enterococci isolates were also submitted. Furthermore, the MS provided data on certain other microbiological contaminants in food – histamine, staphylococcal enterotoxins and *Cronobacter sakazakii* (before *Enterobacter sakazakii*), for which food safety criteria are set down in the EU legislation.

The deadline for data submission was 31 May 2016. Two data validation exercises were implemented, by 3 June 2016 and by 1 July 2016. Validated data on food, animals, and feed used in the report were extracted from the EFSA zoonoses database on 13 July 2016.

The draft EU Summary Report was sent to the MS for consultation on 17 October 2016 and comments were collected by 28 October 2016. The utmost effort was made to incorporate comments and data amendments within the available time frame. The report was finalised by 16 November 2016 and published online by EFSA and the ECDC on 15 December 2016.

In this report, data are presented on the eight mandatory zoonotic agents and also on rabies, *Toxoplasma*, Q fever, WNV, *Yersinia*, *Francisella*, *Cysticercus* and *Sarcocystis*, and microbiological contaminants.

For each pathogen, an overview table presenting all the MS reported data is available. However, for the summary tables, data from industry own-control programmes and hazard analysis and critical control point (HACCP) sampling and, unless stated otherwise, data from suspect sampling, selective sampling and outbreak or clinical investigations are excluded. Specifically, the following criteria have been applied:

- data from industry own-control programmes and HACCP sampling are excluded in all the summary tables;
- data from suspect sampling, selective sampling and outbreak or clinical investigations are excluded in the summary tables for *Salmonella*, *Campylobacter*, *Listeria*, STEC, *Yersinia* and *Trichinella*;
- data from suspect sampling, selective sampling and outbreak or clinical investigations are included in the summary tables for *Echinococcus*, rabies, *Toxoplasma*, *Francisella tularensis*, WNV, *Brucella*, *M. bovis, Coxiella burnetii*.

More details regarding the 2015 zoonoses models for data entry and the picklists (qualitative classifications) of variables are available online (http://www.efsa.europa.eu/en/supporting/pub/992e)

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[6] Based on the customs union treaty of the Principality of Liechtenstein with Switzerland, Liechtenstein is part of the Swiss customs territory. Due to the tight connection between the veterinary authorities of Liechtenstein and Switzerland as well as Liechtenstein's integration into the Swiss system in the veterinary field, in principal, all legislation, rules and data concerning contagious diseases are identical for both Switzerland and Liechtenstein. If not mentioned otherwise, the Swiss data include also the data from Liechtenstein.

and in an EFSA supporting publication (EFSA, 2016c). As regards the number of samples of investigations, there was no restriction and also smaller sample sizes, of fewer than 25 units, are included in all tables. It is acknowledged that sampling biases and imprecision due to limited numbers of specimens examined preclude extending findings to reflect actual prevalence or accurate prevalence estimations.

The detailed description of the terms used in the report is available in the EFSA's manual for reporting on zoonoses (EFSA, 2016b).

2.1.3. Data on food-borne outbreaks

Twenty-six MS and three non-MS reported 2015 data on food-borne outbreaks. No outbreak data were reported by Malta and Spain. The non-reporting of food-borne outbreak data does not necessarily mean that no outbreaks were notified in non-reporting countries.

If in rare cases, the MS do not provide any information on the number of human cases, hospitalisation and/or deaths the numbers are assumed to be zero.

Data on food-borne outbreaks used in the report were extracted from the EFSA zoonoses database on 14 November 2016.

The detailed description of the terms used in the report is available in the EFSA's manual for reporting on food-borne outbreaks (EFSA, 2016a).

2.2. Statistical analysis of trends over time

2.2.1. Human data

Routine surveillance data from TESSy were used to describe two components of the temporal pattern (secular trend and seasonality) of human zoonoses cases for the EU and by the MS.

Only confirmed human cases (with the exception of West Nile fever (WNF), for which total numbers of cases were used) reported consistently by the MS, throughout the study period 2008–2015, were included in the time series analysis. Diseases were analysed by month. Of the date variables available (date of onset, date of diagnosis, etc.), the date chosen by the MS as the official 'Date used for statistics' was selected.

For assessing the temporal trends at the EU level and by the MS, moving averages were applied. Linear regression was applied where appropriate to test the significance of trends. The level of statistical significance was set at 5%. All analyses were performed using Stata®14.

2.2.2. Data on animals

Statistical trend analyses were carried out in order to evaluate the significance of temporal variations in the EU level prevalence of *Salmonella* target serovar-positive flocks for poultry species since the start of implementation of national control programmes.

To take into account the potential correlation among observations in the same MS in subsequent years, marginal models via generalised estimating equations were fitted (EFSA, 2009a).

Exchangeable (EXCH) and autoregressive (AR1) correlation matrices were considered as possible types of correlation matrix. The interpretation of the parameters obtained through these methods is at the population level (i.e. the EU), whereas no inference is directly made at the level of an individual MS. For this reason, a generalised linear mixed model for binary data was proposed as an alternative approach, where heterogeneity among the MS (in the probability of finding target serovars) is explicitly evaluated and expressed in the form of an additional parameter in the model (EFSA, 2011). Given that the MS highlighted different levels (baselines) of risk to have target serovars but similar patterns over time, only a random MS-specific intercept effect was included in the model.

Additionally, the analysis of temporal patterns was carried out applying a more complex generalised linear mixed model that takes into account both the heterogeneity among the MS and the correlation among repeated observations in the same MS in subsequent years (AR1).

Temporal trends and spatial trends over time, of the proportions of *Salmonella*-positive sampling units in food and animals, of the percentage of *Salmonella* isolates of serovars in food and animals, of the prevalence of bovine tuberculosis, as well as of brucellosis in cattle and small ruminants were descriptively visualised using the R software (www.r-project.org); packages ggplot2, lattice and tmap.

2.3. Cartographic and other representation of data

2.3.1. Animal data

ArcGIS from the Economic and Social Research Institute (ESRI) was used to map animal data. Choropleth maps with graduated colours over a continuous scale of values were used to map the proportion of positive sample units across the EU and other reporting countries.

A Sankey diagram of reported *Salmonella* serovar isolates was produced using the open source data visualisation website: http://app.raw.densitydesign.org/#%2F

For *Lyssavirus* and WNV, the number of positive samples, rather than the proportion, was displayed using proportional circles, while for *Trichinella* in wild animals a simple absence/presence map was produced.

For disease status data, a simple colour code was selected to represent the official status of each country as defined in the legislation (officially free or not free).

2.4. Data sources

In the following sections, the types of data submitted by the reporting countries are briefly described. Information on human surveillance systems is based on the countries reporting data to the ECDC for 2015.

2.4.1. *Salmonella* data

Humans

The notification of non-typhoidal salmonellosis in humans is mandatory in most MS, Iceland, Norway and Switzerland, except for six MS where reporting is based on a voluntary system (Belgium, France Luxembourg and the Netherlands) or other system (Spain and the United Kingdom). In the United Kingdom, although the reporting of food poisoning is mandatory, isolation and specification of the organism is voluntary. The surveillance systems for salmonellosis have full national coverage in all the MS except four (Belgium, France, the Netherlands and Spain). The coverage of the surveillance system is estimated to be 48% in France, 64% in the Netherlands and 45% in Spain. These proportions of populations were used in the calculation of notification rates for these three MS. No estimation for population coverage in Belgium was provided so notification rate was not calculated. Diagnosis of human *Salmonella* infections is generally done by culture from human stool samples. The majority of countries perform serotyping of strains (ECDC, 2012).

Food

Salmonella in food is notifiable in 17 MS (Austria, Belgium, Bulgaria, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Hungary, Italy, Latvia, Romania, Slovakia, Slovenia, Spain and Sweden) and in two non-MS (Norway and Iceland). Information was not provided from Cyprus, Croatia, Greece, Lithuania, Luxembourg, Malta, the Netherlands, Poland, Portugal and Switzerland.

Commission Regulation (EC) No 2073/2005[7] on microbiological criteria for food lays down food safety criteria for *Salmonella* in several specific food categories. This Regulation came into force in January 2006 and was modified by Regulation (EC) No 1441/2007[8], entering into force in December 2007. Sampling schemes for monitoring *Salmonella* in food, e.g. place of sampling, sampling frequency and diagnostic methods, vary between the MS and according to food types, as do sampling objectives. For a full description of monitoring schemes and diagnostic methods in an individual MS, please refer to the national reports. The monitoring schemes are based on various types of samples, such as neck skin samples, carcase swabs and meat cuttings; these samples were collected at slaughter, at processing plants, at meat cutting plants and at retail. Several MS reported data collected as part of HACCP programmes based on sampling at critical control points. These targeted samples could not be directly compared with those that were randomly collected for monitoring/surveillance purposes and were not included in data analysis and tables, unless stated otherwise.

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[7] Commission Regulation (EC) No 2073/2005 of 15 November 2005 on microbiological criteria for foodstuffs. OJ L 338, 22.12.2005, p. 1–26.

[8] Commission Regulation (EC) No 1441/2007 of 5 December 2007 amending Regulation (EC) No 2073/2005 on microbiological criteria for foodstuffs. OJ L 322, 7.12.2007, p. 12–29.

Animals

Salmonella in *Gallus gallus* (fowl) and/or other animal species is notifiable in all the MS, except for Hungary, and also in three non-MS (Iceland, Norway and Switzerland). In France, *Salmonella* notification is mandatory only for breeding flocks and laying hens of *Gallus gallus*, and in Malta for broilers and laying hen flocks of *G. gallus*. In Poland and in Romania, the notification of *Salmonella* is mandatory only in poultry; in Poland only findings of *Salmonella* Enteritidis, *Salmonella* Typhimurium, *Salmonella* Pullorum and *Salmonella* Gallinarum, and in Romania findings of *S.* Enteritidis and *S.* Typhimurium.

The monitoring of *Salmonella* in animals is mainly conducted through active routine monitoring of flocks of breeding and production animals in different age groups, and tests on organs during meat inspection, but also includes passive, laboratory-based surveillance of clinical samples. Regulation (EC) No 2160/2003[9] with subsequent amendments prescribes a harmonised sampling plan for the control of *S.* Enteritidis, *S.* Typhimurium, *Salmonella* Infantis, *Salmonella* Virchow and *Salmonella* Hadar in breeding flocks of *G. gallus* and for the control of *S.* Enteritidis and *S.* Typhimurium in laying hen flocks and broiler flocks of *G. gallus* and for turkey flocks to ensure comparability of data among the MS. The reporting to the EU of the results of this monitoring of *Salmonella* in poultry is also harmonised; results and any additional relevant information must be reported by the MS as part of the report on trends and sources provided for in Article 9(1) of the Zoonoses Directive 2003/99/EC.[1] The non-MS European Economic Area (EEA) members) must also apply the Regulation in accordance with the Decision of the EEA Joint Committee No 101/2006.[10] No specific requirements for the monitoring and control of other commercial poultry production systems or in other animals were applicable in 2015.

Details of monitoring programmes and control strategies in breeding flocks of *G. gallus*, laying hen flocks, broiler flocks and breeding and production turkey flocks are available in the national reports.

Feed

There is no common sampling scheme for feed materials in the EU. Results from compulsory and voluntary monitoring programmes, follow up investigations and industry quality assurance programmes, as well as from surveys, are reported. The MS monitoring programmes often include both random and targeted sampling of feed that are considered at risk. Samples of raw material, materials used during processing and final products are collected from batches of feed of domestic and imported origin. The reported epidemiological units were either 'batch' (usually based on pooled samples) or 'single' (often several samples from the same batch). As in previous years, most MS did not report separately data from the different types of monitoring programmes or data from domestic and imported feed. Therefore, it must be emphasised that the data related to *Salmonella* in feed cannot be considered national prevalence estimates. Moreover, owing to the lack of a harmonised surveillance approach, information is not comparable among countries. Nevertheless, data at country level are presented in the same tables. Information was requested on feed materials of animal and vegetable origin and on compound feed (mixture of feed materials intended for feeding specific animal groups). Data on the detection of *Salmonella* in feed material of land animal origin, marine animal origin, cereals, oil seeds and products, and compound feed for cattle, pigs and poultry in 2015 are presented. Single sample and batch-based data from the different monitoring systems are summarised.

2.4.2. *Campylobacter* data

Humans

The notification of campylobacteriosis is mandatory in most MS, Iceland, Norway and Switzerland, except for seven MS, where notification is based on a voluntary system (Belgium, France, Italy, Luxembourg and the Netherlands) or other system (Spain and the United Kingdom). No surveillance system exists in Greece. Portugal reported for the first time in 2015. The surveillance systems for campylobacteriosis have full national coverage in all the MS except five (Belgium, France, Italy, the Netherlands and Spain). The coverage of the surveillance system is estimated to be 20% in France,

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[9] Regulation (EC) No 2160/2003 of the European Parliament and of the Council and Regulation of 17 November 2003 on the control of *Salmonella* and other specified food-borne zoonotic agents. OJ L 325, 12.12.2003, p. 1–15.

[10] Decision of the EEA Joint Committee No 101/2006 of 22 September 2006 amending Annex I (Veterinary and phytosanitary matters) to the EEA Agreement. OJ L 333, 30.11.2006, p. 6–9.

52% in the Netherlands and 45% in Spain. These proportions of populations were used in the calculation of notification rates for these three MS. No estimation for population coverage in Belgium and Italy was provided so notification rate was not calculated. Diagnosis of human infection is generally based on culture from human stool samples and both culture and non-culture methods (polymerase chain reaction (PCR)-based) are used for confirmation. Biochemical tests or molecular methods are used for species determination of isolates submitted to the National Reference Laboratory.

Food

In food, *Campylobacter* is notifiable in the following 12 MS: Austria, Belgium, the Czech Republic, Estonia (only *Campylobacter jejuni*), Germany, Italy, Latvia, the Netherlands, Poland, Slovakia, Slovenia and Spain. *Campylobacter* is also notifiable in Iceland and Norway. Information on *Campylobacter* notification was not provided from Croatia, Cyprus, France, Lithuania, Luxembourg, Malta, Portugal and Romania. Bulgaria did not test for *Campylobacter*. At processing, cutting and retail, sampling was predominantly carried out on fresh meat. Food samples were collected in several different contexts, i.e. continuous monitoring or control programmes, surveys and as part of HACCP programmes implemented within the food industry. Samples reported as HACCP or own controls were not included for analysis and, unless stated differently in the specific section, data from suspect and selective sampling and outbreak or clinical investigations were also excluded.

Animals

Campylobacter is notifiable in *G. gallus* in the Czech Republic, Finland, Slovenia, Sweden, Iceland and Norway, in cattle in Germany and in all animals in Belgium, Estonia (only *C. jejuni*), Ireland, Latvia, the Netherlands, Spain and Switzerland. Information on *Campylobacter* notification was not provided from Bulgaria, Croatia, Cyprus, France, Lithuania, Malta and Poland. The most frequently used methods for detecting *Campylobacter* in animals at farm, slaughter and in food were bacteriological methods (ISO, 2006; Nordic Committee on Food Analysis (NMKL), 2007) as well as PCR methods. In some countries, isolation of the organism is followed by biochemical or other tests for speciation. For poultry sampled prior to slaughter, faecal material was collected either as cloacal swabs or as sock samples (faecal material collected from the floor of poultry houses by pulling gauze over footwear and walking through the poultry house). At slaughter, several types of samples were collected, including cloacal swabs, caecal contents and/or neck skin.

2.4.3. *Listeria* data

Humans

The notification of listeriosis in humans is mandatory in most MS, Iceland, Norway and Switzerland, except for four MS, where notification is based on a voluntary system (Belgium, Luxembourg and the United Kingdom) or other system (Spain). Portugal reported for the first time in 2015. The surveillance systems for listeriosis have full national coverage in all the MS except Spain, where the estimated coverage is 45%. This population proportion was used in the calculation of notification rates for Spain. Diagnosis of human infections is generally done by culture from blood, cerebrospinal fluid and vaginal swabs.

Food

Notification of *L. monocytogenes* in food is required in 12 MS (Austria, Belgium, Estonia, France, Germany, Hungary, Italy, Latvia, the Netherlands, Slovakia, Slovenia and Spain); however, several other MS reported data. Commission Regulation (EC) No 2073/2005 on microbiological criteria for foodstuffs lays down food safety criteria for *L. monocytogenes* in ready-to-eat (RTE) foods. This Regulation came into force in January 2006. Surveillance in RTE foods was performed in most MS. However, owing to differences in sampling and analytical methods, comparisons from year to year were difficult.

Assumptions, uncertainties and data limitations

The data presented in the section on *L. monocytogenes* in food should be considered in the light of certain assumptions and decisions made by EFSA because of some underlying uncertainties and limitations in the reported data. These assumptions/decisions and related data uncertainties/limitations are outlined below:

- **Unknown dates of sampling and testing with respect to the foods' shelf lives**. According to Regulation 2073/2005, the criterion of less or equal to 100 colony-forming units (CFU)/g applies during the entire shelf life of RTE foods on the market. However, for RTE foods sampled at retail by the reporting MS, no information was provided regarding the sampling and testing dates with respect to the foods' shelf lives on the market. Therefore, it is possible that some of the tested products at retail that are able to support the growth of *L. monocytogenes* and which were found to contain less than 100 colony forming units per gram (CFU/g) at the time of testing (and which were therefore classified as compliant) may had not been characterised as compliant, had they been tested at the end of their shelf life.
- **Unknown status of RTE foods in terms of their ability to support *L. monocytogenes* growth**. For many of the data, it was not evident whether the RTE foods tested were able to support the growth of *L. monocytogenes* or not, because data on crucial physicochemical parameters, such as pH, a_w, and levels and types or preservatives present in the sampled foods were not reported. For assessing compliance of samples collected at the processing stage, the criterion of 'absence in 25 g' was applied, except for samples from hard cheeses and fermented sausages that were assumed to be unable to support the growth of *L. monocytogenes*, where the criterion '≤ 100 CFU/g' was applied. Therefore, it is possible that some of the foods that were considered as able to support the growth of *L. monocytogenes* (and for which the criterion of 'absence in 25 g' was applied to assess compliance at processing) may, actually not be permissive to the pathogen's growth. Such foods could be misclassified as non-compliant in the event of a detection-positive result at processing.
- **Incorporation of the 'unspecified' sampling stage into 'retail' for purposes of compliance assessment**. In cases where the sampling stage for certain of the reported investigations was not specified, EFSA assumed that the investigations were conducted at the retail level. This assumption could, in certain occasions (e.g. for food listed as 'unspecified' but actually sampled at the processing level), lead to overestimating of compliance. For instance, for foods able to support the growth of *L. monocytogenes*, the Regulation's criterion at retail (≤ 100 CFU/g) is more 'lenient' than the corresponding criterion at processing ('absence in 25 g', i.e. < 0.04 CFU/g).
- **Reporting and analysis of aggregated data – dichotomous classification of foods containing enumerable populations of *L. monocytogenes***. The *L. monocytogenes* data from enumeration analyses of RTE foods that are submitted to EFSA by the reporting MS are aggregated (no detailed information on individual units within each reported investigation is available) and include only two categories: ≤ 100 CFU/g and > 100 CFU/g. This categorisation does not fully address or account for the risk for humans associated with the different levels of contamination of RTE foods. In particular, the potential risk for human health originating from 'compliant' RTE foods at retail containing enumerable populations (≤ 100 CFU/g) is not accounted for.
- **Performance characteristics of the EN ISO 11290-2 method**. Regulation 2073/2005 specifies the enumeration EN/ISO 11290-2 method as the analytical reference method for determining the populations of *L. monocytogenes* in RTE food products placed on the market during their shelf life. However, limitations regarding the ability of this method (and other enumeration methods used in food microbiology which are based on colony counts in Petri dishes) to precisely enumerate populations of *L. monocytogenes* around 100 CFU/g in RTE foods (particularly in solid foods) have been documented (ISO, 1996a; Loncarevic et al., 2008). It should be noted that the vast majority of the enumeration data submitted to EFSA are derived from analyses of solid RTE foods.
- **Varying and/or limited data reported for some food (sub)categories**. In certain cases, only limited data (either in terms of the number of MS reporting data, or in terms of the sample size of the respective investigations, or both) were available for some RTE food (sub)categories. Therefore, in such instances, the reported prevalence values may not be adequately accurate or precise, may not be directly comparable for a given food (sub)category across reporting years, or may not be representative of the EU as a total.
- **Consideration of data from investigations irrespective of their sample size.** In 2015, EFSA considered, validated and analysed (both in the summary tables and in the compliance assessment) the reported investigations, irrespective of their sample size. However, it should be noted that until 2012, EFSA considered and analysed only investigations including at least

25 tested units. This change in the amount of data considered may affect the comparisons of prevalence estimates and compliance assessment before and after 2012.

- **Consideration of RTE foods tested quantitatively irrespective of sample weight**. According to ISO 6887-1 (ISO, 1999), a minimum of 10 g or 10 mL of food should be used as the test portion for the microbiological examinations of products intended for human consumption. However, due to the aforementioned data limitations and in order to prevent further uncertainty of the reported estimates by data exclusion, it was considered preferable to not exclude data that may provide useful information, even when they were not fully in line with the ISO recommendations. Hence, EFSA did not exclude data submitted by the MS on RTE foods tested quantitatively (using the EU reference method EN/ISO 11290-2) using less than the minimum specified sample weight (e.g. 1 g).
- **Assessment of compliance at the processing plant level**. As previously mentioned, for the assessment of compliance of RTE foods collected at the processing stage (except for hard cheeses and fermented sausages that are assumed to be unable to support the growth of *L. monocytogenes*, and for which the criterion of '≤ 100 CFU/g' was applied), the criterion of 'absence in 25 g' was applied and the results of the detection method were used to classify foods as compliant or non-compliant. For some investigations, the MS reported quantitative (enumeration) data for RTE foods sampled at processing without, or in addition to reporting qualitative (detection) data. However, in such cases, due to the aggregated nature of the reported data and/or the lack of information of the independence status of the qualitative and quantitative data from the same investigation, quantitative data for foods tested at processing were not utilised by EFSA in assessing compliance. In practice, the vast majority of RTE foods testing positive in enumeration analyses, would have also tested positive upon being subjected to detection analyses. However, EFSA applies a single and uniform rule for assessing compliance of RTE foods from all reported investigations by only considering results from the detection method. In addition, given the risk for double-reporting (overestimating non-compliance upon usage of non-independent data), quantitative data from foods sampled at processing were excluded from the assessment of compliance with the microbiological criteria.
- **Non-Compliance of single samples (units) with the food safety limits**. According with the Regulation 2073/2005, *L. monocytogenes* food safety criteria are set for batch sampling with 5 or 10 units comprising the sample (n). There is a single microbiological limit (m = M) and the maximum allowable number of sample units yielding unsatisfactory test results is 0 (c). EFSA has classified batches as non-compliant based on the number of positive batches reported by the MS although the number of units comprising each batch sampled is unknown. In addition, EFSA classified single samples (units) based on their test results. This 'classification' of single samples (units) is based on the rationale that any batch sample (comprised of 5 or 10 units) containing even one unit with *L. monocytogenes* counts above the microbiological limit would have made the corresponding batch unsatisfactory.

Animals

Listeria in animals was notifiable in 13 MS (Belgium, the Czech Republic, Estonia, Finland, Germany, Greece, Latvia, Lithuania, the Netherlands, Slovakia, Slovenia, Spain and Sweden), Switzerland and Norway. In Ireland and Iceland, *Listeria* is not notifiable in animals. Information is missing from Bulgaria, Croatia, Cyprus, Malta and Poland. The monitoring of *Listeria* in animals is mainly conducted through passive, laboratory-based surveillance of clinical samples, active routine monitoring or random national surveys.

2.4.4. STEC data

Humans

The notification of STEC infections is mandatory in most MS, Iceland, Norway and Switzerland, except for six MS, where notification is based on a voluntary system (Belgium, France, Italy, Luxembourg and Spain) or other system (the United Kingdom). Portugal reported for the first time in 2015. The surveillance systems for STEC infections have full national coverage in all the MS except two (Belgium and France). The STEC surveillance in France is centred on paediatric haemolytic uraemic syndrome (HUS) surveillance, and in Italy is primarily based on the National registry of HUS. Diagnosis of human STEC infections is generally done by culture from stool samples and indirect diagnosis by the detection of antibodies against the O-lipopolysaccharides *E. coli* in serum in case of HUS. Diagnosis by direct detection of the toxin or the toxin genes by PCR without strain isolation is increasing.

Food and animals

STEC is notifiable in food in 11 MS (Austria, Belgium, Estonia, Germany, Italy, Latvia, the Netherlands, Romania, Slovakia, Slovenia and Spain) and in animals in eight MS (Belgium, the Czech Republic, Estonia, Finland, Latvia, Lithuania, Spain and Sweden). In Ireland, STEC is not notifiable in animals. Information is missing from Bulgaria, Croatia, Cyprus, the Czech Republic, Denmark, Greece, Hungary, Lithuania, Malta, Poland, Portugal and Switzerland for food, and from Bulgaria, Cyprus, France, Germany, Greece, Malta, Poland, Portugal and Romania for animals.

Samples were collected in a variety of settings, such as slaughterhouses, cutting plants, dairies, wholesalers and at retail level, and included different types of samples such as carcase surface swabs, cuts of meats, minced meat, milk, cheese and other products. The majority of investigated products were raw but intended to undergo preparation before consumption. The samples were taken as part of official control and monitoring programmes as well as random national surveys. The number of samples collected and types of food sampled varied among the individual MS. Most of the animal samples were collected at the slaughterhouse or at the farm.

Analyses of the occurrence of STEC in food and animals

For the estimation of the proportion of samples positive for STEC in the different food and animal categories data from industry own-control programmes, HACCP, suspect sampling, selective sampling and outbreak or clinical investigations were excluded.

Analyses of the STEC serogroups

The analyses of the data concerning the distribution of the STEC serogroups in the different food and animal categories, as well as on the analytical approaches used by the different reporting countries, were performed using the entire data set with some adjustments in terms of data aggregation in order to ease the discussion. The data in the 'anMethCode' field have been aggregated as presented in Table 2.

Table 2: Aggregation of the information reported for STEC under the 'anMethCode' field

Aggregation	Values in the field 'anMethCode'
Other methods based on the immunochemical detection of VT	Detection method – presence in x g (with specification in the ResComm and footnote fields)
ISO/TS 13136:2012	EURL method_food_2. Rev. 2 – O104:H4
ISO/TS 13136: 2012	ISO/PRF TS 13136 – *E. coli*
ISO/TS 13136: 2012	Microbiological tests – ISO/PRF TS 13136 – *E. coli*
ISO/TS 13136: 2012 (Recoding done based on the content of the field ResComm)	PCR (with specification in the ResComm)
ISO 16654:2001 or NMKL 164:2005 or DIN 10167	Microbiological tests – ISO 16654:2001
ISO 16654:2001 or NMKL 164:2005 or DIN 10167	Microbiological tests – ISO 16654:2001 – *E. coli*
ISO 16654:2001 or NMKL 164:2005 or DIN 10167	Microbiological tests – NMKL 164:2005
ISO 16654:2001 or NMKL 164:2005 or DIN 10167	Microbiological tests
ISO 16654:2001 or NMKL 164:2005 or DIN 10167	Microbiological tests – Microbiological standard tests
Recoding done based on the content of the field ResComm and footnote	Classification not possible (with specification in the ResComm and footnote fields)
Other methods based on PCR detection of *vtx* genes	PCR (w/o specification in the ResComm and footnote fields)
In house real time PCR methods based on ISO/TS 13136:2012	Real-time PCR
Unspecified	Detection method
Unspecified	Detection method – presence in x g
Unspecified	Unknown
Unspecified	Classification not possible (w/o specification in the ResComm and footnote fields)

EURL: European Union Reference Laboratory; ISO: International Organization for Standardization; NMKL: Nordic Committee on Food Analysis; DIN: Deutsches Institut für Normung e.V.; PCR: polymerase chain reaction.

Trends in the reporting of STEC serogroups in food and animal categories

For the analysis of trends in serogroups reporting, only the samples with serogroups identified by the MS and obtained with any method but the ISO 16654:2001 (ISO, 2001) or NMKL 164:2005 (NMKL, 2005) or DIN 10167:2004-03 (DIN, 2004), were included. The samples positive for the STEC O157 serogroup on the basis of the application of method(s) ISO 16654:2001 or NMKL 164:2005 or DIN 10167:2004-03 were excluded since they have been obtained with methods biased towards the detection of one single STEC serogroup. No STEC-positive samples with the serogroup specified and analysed with 'unspecified' method were reported.

2.4.5. *Yersinia* data

Humans

Notification of yersiniosis in humans is mandatory in most MS, Iceland and Norway. Belgium, France, Italy and Luxembourg have a voluntary notification system and the United Kingdom has another system. No surveillance system exists in Greece, and the Netherlands. Portugal reported for the first time in 2015. The surveillance systems for *Yersinia* infections have full national coverage in all the MS except three (Belgium, France and Italy). In Switzerland, yersiniosis in humans is not notifiable, since 1999. The estimated coverage of the sentinel surveillance for yersiniosis in Spain is 45%, and this population proportion was used in the calculation of notification rates. Diagnosis of human gastrointestinal infections is generally done by culture from human stool samples.

Food and animals

Yersinia is notifiable in food in 10 MS (Austria, Belgium, Estonia, Germany, Italy, Latvia, the Netherlands, Slovakia, Slovenia and Spain) and Norway, and in animals in seven MS (Belgium, Ireland, Latvia, Lithuania, the Netherlands, Slovenia and Spain) and two non-MS (Norway and Switzerland). Information was not provided from Bulgaria, Croatia, Cyprus, the Czech Republic, Denmark, France, Greece, Hungary, Lithuania, Malta, Portugal, Romania and Switzerland for food, and from Bulgaria, Croatia, Cyprus, France, Germany, Greece, Malta and Poland for animals. Only eight MS reported data on *Yersinia,* and primarily, domestic animals were tested. The reporting of specific human pathogenic serotypes/biotypes found in food and animals is often lacking and differences in sampling and analytical methods make comparison between countries difficult.

2.4.6. Tuberculosis data

Humans

The notification of tuberculosis in humans is mandatory in all the EU MS, Iceland, Norway and Switzerland with full national coverage. Greece and France do not report all the species of the *Mycobacterium tuberculosis* complex separately to TESSy; therefore, no human *M. bovis* data are available from these two countries.

Animals

Tuberculosis in animals is notifiable in 25 MS, Norway and Switzerland (information was not provided from Bulgaria and Malta). Tuberculosis in bovine animals and avian tuberculosis in birds is notifiable in Iceland. In Cyprus, Greece, Hungary, Poland and Romania, only bovine tuberculosis is notifiable, and in Ireland, only tuberculosis in ruminant animals is notifiable. Rules for intra-EU bovine trade, including requirements for cattle herds and country qualification as officially free from tuberculosis (OTF), are laid down in Council Directive 64/432/EC,[11] as last amended by Commission Decision 2007/729/EC.[12] More detailed information regarding the status of the EU MS, Norway and Switzerland and regions thereof in relation to cattle tuberculosis can be found in European Commission's DG SANCO's annual reports on bovine and swine diseases (European Commission, online). For the first time in the EU annual summary reports on trends and sources of zoonoses, monitoring data from cattle of the specific types of bacteria that are part of the *Mycobacterium*

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[11] Council Directive 64/432/EEC of 26 June 1964 on animal health problems affecting intra-Community trade in bovine animals and swine. OJ L 121, 29.7.1964, p. 1977–2012.

[12] Commission Decision 2007/729/EC of 7 November 2007 amending Council Directives 64/432/EEC, 90/539/EEC, 92/35/EEC, 92/119/EEC, 93/53/EEC, 95/70/EC, 2000/75/EC, 2001/89/EC, 2002/60/EC, and Decisions 2001/618/EC and 2004/233/EC as regards lists of national reference laboratories and State institutes. OJ L 294, 13.11.2007, p. 26–35.

tuberculosis complex were taken account of to summarise the EU situation on bovine tuberculosis. Previously the separate reporting of bacterial species of the *M. tuberculosis* complex in the EFSA Disease status data model was not possible. In this chapter a distinction is made descriptively, whenever possible, of reporting by MS on *Mycobacterium tuberculosis* complex, *M. bovis* and *M. caprae*.

2.4.7. *Brucella* data

Humans

The notification of brucellosis in humans is mandatory in all the MS, Iceland, Norway and Switzerland except in Belgium, Denmark and the United Kingdom. The voluntary surveillance systems in Belgium and the United Kingdom have full national coverage. In Denmark, no surveillance system is in place.

Food

The notification of *Brucella* in food is mandatory in 10 MS (Austria, Belgium, Finland, Germany, Italy, Latvia, the Netherlands, Slovenia, Spain and the United Kingdom). Information was not provided from Bulgaria, Cyprus, the Czech Republic, Denmark, France, Greece, Lithuania, Luxembourg, Malta, Poland, Portugal, Romania, Slovakia and Switzerland.

Animals

Brucellosis in animals is notifiable in 24 MS, Iceland, Norway and Switzerland (information was not provided from Bulgaria, Cyprus and Malta). Rules for the intra-EU bovine trade, including requirements for cattle herds and country qualification as officially free from brucellosis (OBF), are laid down in Council Directive 64/432/EC, as last amended by Commission Decision 2007/729/EC. Rules for the intra-EU trade of ovine and caprine animals and country qualification as officially free from ovine and caprine brucellosis, caused by *Brucella melitensis* (official *Brucella melitensis*-free in sheep and goats (ObmF)), are laid down in Council Directive 91/68/EEC,[13] as last amended by Council Directive 2008/73/EC.[14] More detailed information regarding the status of the EU MS, Norway and Switzerland and regions thereof in relation to cattle brucellosis can be found in European Commission's DG SANCO's annual reports on bovine and swine diseases (European Commission, online).

2.4.8. *Trichinella* data

Humans

The notification of *Trichinella* infections in humans is mandatory in all the MS, Iceland, Norway and Switzerland, except in three MS (Belgium, France and the United Kingdom, having voluntary surveillance systems). No surveillance system for trichinellosis exists in Denmark. The surveillance systems for trichinellosis have full national coverage in all the MS except one (Belgium). In humans, diagnosis of *Trichinella* infections is primarily based on clinical symptoms and serology (indirect enzyme-linked immunosorbent assay (i-ELISA) and western blot). Histopathology on muscle biopsies is rarely performed.

Food and animals

Trichinella in food is reported to be notifiable in 18 MS, Iceland and Norway. Ireland and Switzerland report that *Trichinella* is not notifiable. Information was not provided from Bulgaria, Croatia, Cyprus, the Czech Republic, Denmark, Lithuania, Luxembourg and Malta.

Trichinella infections in animals are notifiable in all the MS except Hungary. It is also notifiable in Iceland and Switzerland. Information was not provided from Croatia and Malta.

According to Commission Regulation (EC) No 2075/2005[15], carcases of domestic pigs, horses, wild boar and other farmed or wild animal species that are susceptible to *Trichinella* infestation should be

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[13] Council Directive 91/68/EEC of 28 January 1991 on animal health conditions governing intra-Community trade in ovine and caprine animals. OJ L 46, 19.2.1991, p. 19–36.

[14] Council Directive 2008/73/EC of 15 July 2008 simplifying procedures of listing and publishing information in the veterinary and zootechnical fields and amending Directives 64/432/EEC, 77/504/EEC, 88/407/EEC, 88/661/EEC, 89/361/EEC, 89/556/EEC, 90/426/EEC, 90/427/EEC, 90/428/EEC, 90/429/EEC, 90/539/EEC, 91/68/EEC, 91/496/EEC, 92/35/EEC, 92/65/EEC, 92/66/EEC, 92/119/EEC, 94/28/EC, 2000/75/EC, Decision 2000/258/EC Directives 2001/89/EC, 2002/60/EC and 2005/94/EC. OJ L 219, 14.8.2008, p. 40–54.

[15] Commission Regulation (EC) No 2075/2005 of 5 December 2005 laying down specific rules on official controls for *Trichinella* in meat. OJ L 338, 22.12.2005, p. 60–82.

systematically sampled at slaughter as part of the meat inspection process and are tested for *Trichinella*. Animals (both domestic and wild) slaughtered for own consumption are not included in the Regulation, but are subject to national rules, which differ per MS, as each MS can decide how to control *Trichinella* in this population (e.g. test or not, freeze or not). Therefore, data from animals slaughtered for own consumption might not be comparable between the MS since there is no information if these animals were included among data provided to EFSA for 2015. From 10 August 2015, Commission Regulation (EU) No 1375/2015[16] repealing the Commission Regulation (EC) No 2075/2005 came into force. Among other requirements, the Regulation states that the reporting of data regarding domestic swine shall, at least, provide specific information related to number of animals raised under controlled housing conditions as well as the number of breeding sows, boars and fattening pigs tested. Further, the Regulation states that a negligible risk status for a country or region is no longer recognised in an international context by the World Organisation for Animal Health (OIE). Instead, such recognition is linked to compartments of one or more holdings applying specific controlled housing conditions. Belgium and Denmark have had such a status since 2011, and the holdings and compartments of domestic swine in those two MS complied with the conditions for controlled housing at the date of entry into force of this Regulation. Therefore, these two MS are allowed to apply for the status as negligible risk without additional prerequisites.

Assumptions, uncertainties and data limitations

In case MS did not report for domestic pigs (breeding, fattening pigs and farmed wild boar), the housing conditions for one or for all categories of pigs, EFSA assumed that these animals came from premises where the animals were not kept under controlled housing conditions. This assumption was taken to summarise the number of *Trichinella* positive in EU in 2015 for each of the housing conditions (controlled or not controlled).

2.4.9. *Echinococcus* data

Humans

Cases of both cystic and alveolar echinococcosis are reported jointly to the ECDC as echinococcosis since the EU case definition does not distinguish between the two forms of the disease. The ECDC can differentiate between the two forms in the data only by analysing the reported species. The notification of echinococcosis in humans is mandatory in most MS, Iceland and Norway. In three MS, reporting is based on a voluntary surveillance system (Belgium, the Netherlands and the United Kingdom). In one MS (France), the type of reporting system is not specified. Denmark and Italy have no surveillance system for echinococcosis. In Switzerland, echinococcosis in humans is not notifiable.

Food and animals

Echinococcus is notifiable in food in 10 MS (Belgium, Estonia, Finland, Hungary, Italy, Latvia, the Netherlands, Slovenia, Spain and Sweden) and Norway, and not notifiable in food in Austria, Ireland, Slovakia and the United Kingdom. Information was not provided from Bulgaria, Croatia, Cyprus, the Czech Republic, Denmark, France, Greece, Germany, Lithuania, Luxembourg, Malta, Poland, Portugal, Romania and Switzerland.

Echinococcus is notifiable in animals in 17 MS (Austria, Belgium, Denmark, Estonia, Finland, Germany, Greece, Italy, Latvia, Lithuania, the Netherlands, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden), Iceland, Norway and Switzerland and not notifiable in animals in the Czech Republic, France, Hungary, Luxembourg and the United Kingdom (information was not provided from Bulgaria, Croatia, Cyprus, Ireland, Malta and Poland).

Surveillance for *Echinococcus multilocularis* is usually carried out on the main European definitive hosts, the red fox (*Vulpes vulpes*), using mainly parasitological (sedimentation and counting technique, SCT) or molecular PCR-based methods for the identification of adult worms.

Four MS (Finland, Ireland, Malta and the United Kingdom) are considered free from *E. multilocularis* and according to Regulation (EU) No 1152/2011[17], these MS require an annual surveillance programme in place to monitor the absence of *E. multilocularis*. One EEA State, mainland Norway

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[16] Commission Implementing Regulation (EU) 2015/1375 of 10 August 2015 laying down specific rules on official controls for *Trichinella* in meat. OJ L 212, 11.8.2015, p. 7–34.

[17] Commission Delegated Regulation (EU) No 1152/2011 of 14 July 2011 supplementing Regulation (EC) No 998/2003 of the European Parliament and of the Council as regards preventive health measures for the control of *Echinococcus multilocularis* infection in dogs. OJ L 296, 15.11.2011, p. 6–12.

(Svalbard excluded), has also claimed freedom from *E. multilocularis* and implements a surveillance programme in line with Regulation (EU) No 1152/2011[18].

Guidelines for the control of *Echinococcus granulosus* through inspection at slaughtering are provided through Council Directive 64/433/EC,[19] whereby visual inspection of all slaughtered animals is carried out by official veterinarians examining organs. Organs are destroyed in cases where *Echinococcus* cysts are found.

Assumptions, uncertainties and data limitations

In case MS did not specify the species of *Echinococcus* (*Echinococcus* spp. or unspecified) in one or all animals species tested, EFSA assumed that for each of these MS *E. multilocularis* could be assigned for investigated animals if it is known that *E. multilocularis* is circulating in the concerned MS; otherwise, the species *E. granulosus sensu lato* is assigned.

2.4.10. *Toxoplasma* data

Humans

National surveillance systems for toxoplasmosis differ from each other between countries. Only congenital toxoplasmosis is reported to the ECDC. Three MS (the Czech Republic, France and Slovakia) have active surveillance of congenital cases with full national coverage. France reports cases with a 2-year delay. In 17 MS and Iceland, a compulsory surveillance system is implemented and two countries have a voluntary system (Spain and the United Kingdom). The surveillance systems for toxoplasmosis have full national coverage in all the MS except one (Spain). Surveillance systems in some countries focus on severe cases in all age groups. No surveillance system for toxoplasmosis exists in eight MS (Austria, Belgium, Denmark, Greece, Italy, the Netherlands, Portugal and Sweden), Norway and Switzerland.

Data on congenital toxoplasmosis in the EU in 2015 are not analysed in this report but the data will be available in the ECDC Surveillance Atlas of Infectious Diseases at: http://atlas.ecdc.europa.eu/public/index.aspx?Instance=GeneralAtlas

Animals

Toxoplasmosis is a notifiable disease in animals in Latvia, Poland, the Netherlands, Iceland and Switzerland. In Finland, *Toxoplasma gondii* is classified as a monthly reported animal disease in pigs, sheep, goats, dogs, cats and ferrets, but is not notifiable in hares, rabbits and rodents. No active monitoring programmes are in place in Switzerland. In Germany, toxoplasmosis is notifiable in pigs, dogs and cats. In Austria, Denmark, Ireland, Sweden and the United Kingdom, toxoplasmosis is not notifiable (information is missing from Belgium, Bulgaria, Cyprus, the Czech Republic, Estonia, France, Greece, Hungary, Italy, Lithuania, Luxembourg, Malta, the Netherlands, Portugal, Romania, Slovakia, Slovenia and Spain).

2.4.11. Rabies data

Humans

The notification of rabies in humans is mandatory in most MS, Iceland, Norway and Switzerland. Belgium and France have a voluntary notification system and the United Kingdom has another system, unspecified. Most countries use the EU case definition apart from Belgium, Denmark, Finland, France, Germany and Italy who have other/non-specified case definitions. Most countries examine saliva and neck skin biopsy for diagnosis of rabies ante-mortem. In the case of post-mortem examinations, the central nervous system is sampled. Identification is mostly based on antigen detection, viral genome detection by real time reverse transcriptase-polymerase chain reaction (RT-PCR) and/or isolation of virus. Serum and spinal fluid are used to test antibodies to rabies virus.

Animals

Rabies is a notifiable disease in all the MS, Iceland and Switzerland. In animals, most countries test samples from the central nervous system. The identification is mostly carried out using the fluorescent

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[18] Decision of the EEA Joint Committee No 103/2012 of 15 June 2012 amending Annex I (Veterinary and phytosanitary matters) to the EEA Agreement. OJ L 270, 4.10.2012, p. 1–2.

[19] Council Directive 64/433/EC of 26 June 1964 on health problems affecting intra-Community trade in fresh meat. OJ L 121, 29.7.1964, p. 2012–2032.

antibody test (FAT), which is recommended by both World Health Organization (WHO, 1996) and OIE (Terrestrial Manual), and the cell isolation virus test. However, PCR and real-time PCR are also used.

2.4.12. Q fever data

Humans

The notification of Q fever in humans is mandatory in 23 MS, Iceland, Norway and Switzerland. The disease is not notifiable in Austria and Italy. Belgium, France, Spain and the United Kingdom have a voluntary system, while in the case of Belgium and Spain is based on sentinel surveillance. The population covered by the sentinel surveillance system is estimated to be 30% for Spain and unknown for Belgium, but is reported constantly over the study years. Cases are reported in an aggregated format by Belgium, Bulgaria and Croatia, and case-based for the other countries. Countries use the EU case definitions apart for Belgium, Denmark, Finland, France, Germany and Romania (not specified).

Animals

C. burnetii in animals is notifiable in 15 MS (Bulgaria, the Czech Republic, Denmark, Finland, France, Germany, Greece, Italy, Latvia, Lithuania, the Netherlands, Poland, Slovenia, Spain and Sweden), Iceland and Switzerland. In Austria and the United Kingdom, *C. burnetii* in animals is not notifiable (information is missing from the remaining MS and Norway).

Data reported are mostly based on suspect sampling due to an increase in abortions in the herd and identification is mostly carried out using serological testing methods, such as ELISA or immunofluorescence assay (IFA) tests, or direct identification methods such as real-time PCR.

2.4.13. West Nile virus data

Humans

The notification of WNF in humans is mandatory in 23 MS, Norway and Switzerland. Croatia did not report 2015 data. The disease is not notifiable in Denmark and Germany. Belgium, France and the United Kingdom have a voluntary system: in Belgium, it is based on the sentinel surveillance; in France and in the United Kingdom, it is based on the comprehensive system. The population covered by the sentinel surveillance systems is unknown, but in both cases is reported constantly over the study years. Italy has no national coverage. The EU case definitions are used by most countries apart from Belgium, Finland, Italy and the United Kingdom (not specified). The reporting is case-based in all countries.

Total case numbers for WNF were used because case confirmation according to the EU case definition is usually carried out only when cases occur in previously unaffected areas. Subsequently, some of the cases are diagnosed with laboratory methods for probable cases. Thus, both probable and confirmed cases reflect more accurately the epidemiological situation. This approach is also used for the seasonal real-time monitoring of West Nile cases in the EU carried out by the ECDC.

Animals

WNV infection is notifiable in horses in Great Britain and in animals in Sweden, Iceland and Switzerland.

2.4.14. Tularaemia data

Humans

The notification of tularaemia in humans is mandatory in most MS, Norway and Switzerland. The disease is not notifiable in Denmark and Liechtenstein. Two MS (Belgium and the United Kingdom) have a voluntary surveillance system for tularaemia in humans, and it is not specified for the Netherlands. Reporting is in aggregated format for Belgium, Bulgaria and Croatia, case-based for the other countries. Most countries use the EU case definition; Belgium, Finland, France, Germany and the Netherlands use another non-specified case definition.

Animals

The notification of tularaemia in animals is mandatory in the Netherlands, Sweden, Iceland and Switzerland.

2.4.15. Other zoonoses and zoonotic agent data

Food and animals

Cysticercus in food and animals: Monitoring is carried out as a visual inspection (macroscopic examination) of carcases at the slaughterhouse by meat inspection according to Regulation (EC) No 854/2004[20].

2.4.16. Food-borne outbreak data

Food-borne outbreaks are incidents of two or more human cases of the same disease or infection in which the cases are linked or are probably linked to the same food vehicle. Situations in which the observed human cases exceed the expected number of cases and where the same food source is suspected are also indicative of a food-borne outbreak.

Since the reporting of 2014 monitoring data, the MS had the possibility of providing the same information for 'weak-evidence' food-borne outbreaks as for the 'strong-evidence' food-borne outbreaks. For all outbreaks the type of evidence should be reported, and if available, information on food vehicle and its origin, nature of evidence linking the outbreak cases to the food vehicle, type of outbreak, setting, place of origin of the problem and contributory factors should be reported. All food-borne outbreaks are included in the general tables and figures. The denominators used for the calculation of the reporting rates were the human populations from EUROSTAT 26 July 2016 update.

2.4.17. Non-zoonotic microbiological contaminants

Monitoring of non-zoonotic microbiological contaminants (histamine, *C. sakazakii* and staphylococcal enterotoxins) in food is carried out according the EU Regulation (EC) No 2073/2005[7].

2.5. Terms used to describe prevalence or proportion positive values

In the report, a set of standardised terms are used to characterise the proportion of positive sample units or the prevalence of zoonotic agents in animals and food:

Rare:	< 0.1%
Very low:	0.1–1%
Low:	> 1–10%
Moderate:	> 10–20%
High:	> 20–50%
Very high:	> 50–70%
Extremely high:	> 70%

3. Assessment

This report section provides a descriptive and qualitative EU assessment of the specific zoonoses for the year 2015.

3.1. *Salmonella*

The Appendix A lists all summaries made for the production of this section, for humans, foods, animals and feed, including *Salmonella* summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.1.1. *Salmonellosis* in humans

A total of 96,144 salmonellosis cases were reported by 28 EU MS for 2015, with 94,625 confirmed cases resulting in an EU notification rate of 21.2 cases per 100,000 (Table 3). This represented a small increase, by 1.9%, in the EU notification rate compared with 2014 (20.8 cases per 100,000). As in the previous year, the highest notification rates in 2015 were reported by the Czech Republic (117.7 per 100,000) and Slovakia (89.3 per 100,000), while the lowest rates were reported by Portugal and

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[20] Regulation (EC) No 854/2004 of the European Parliament and of the Council of 29 April 2004 laying down specific rules for the organisation of official controls on products of animal origin intended for human consumption. OJ L 139, 30.4.2004, p. 206–320.

Greece (≤ 4.5 per 100,000). The large increase in notification rate in Bulgaria (48.3%), and France (15.0%) was accompanied by an increase in the number of *Salmonella* outbreaks in these countries and in addition was associated with changes in the laboratory and reporting procedures in France. In Spain, the improved surveillance system for salmonellosis in 2015 resulted in an increase of confirmed cases by 36.5%.

The proportion of domestic versus travel-associated cases varied markedly between countries, with the highest proportions of domestic cases, ranging from 85.9% to 100%, reported in the Czech Republic, Germany, Greece, Hungary, Latvia, Lithuania, Malta, the Netherlands, Portugal and Slovakia. The highest proportions of travel-related cases were reported by three Nordic countries – Finland (72.6%), Sweden (68.1%), and Norway (69.4%). Among 9,489 travel-associated cases, Thailand, Turkey, and Spain were most frequently stated as the probable country of infection (22.0%, 15.5% and 7.3%, respectively, of the imported cases with known probable country of infection).

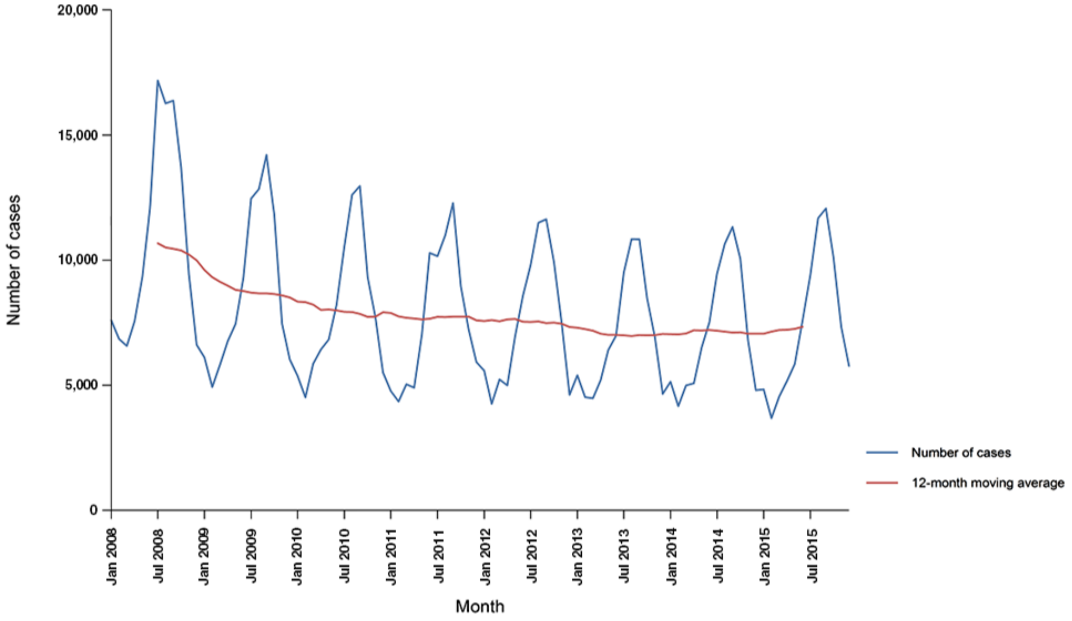
Table 3: Reported human cases of salmonellosis and notification rates per 100,000 population in the EU/EEA, by country and year, 2011–2015

Country	2015					2014		2013		2012		2011	
	National coverage[a]	Data format[a]	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	1,546	1,544	18.0	1,654	19.4	1,404	16.6	1,773	21.1	1,432	17.0
Belgium[b]	N	A	3,170	3,170	–	2,698	–	2,528	–	3,101	–	3,177	–
Bulgaria	Y	A	1,109	1,076	14.9	730	10.1	766	10.5	839	11.5	924	12.5
Croatia	Y	A	1,593	1,593	37.7	1,494	35.2	0	0.0	0	0.0	–	–
Cyprus	Y	C	65	65	7.7	88	10.3	79	9.1	90	10.4	110	13.1
Czech Republic	Y	C	12,612	12,408	117.7	13,255	126.1	9,790	93.1	10,056	95.7	8,499	81.0
Denmark	Y	C	925	925	16.3	1,124	20.0	1,137	20.3	1,207	21.6	1,170	21.0
Estonia	Y	C	118	112	8.5	92	7.0	183	13.9	249	18.8	375	28.2
Finland	Y	C	1,650	1,650	30.2	1,622	29.8	1,984	36.6	2,210	40.9	2,098	39.0
France[c]	N	C	10,305	10,305	32.3	8,880	28.1	8,927	28.4	8,705	27.8	8,685	27.8
Germany	Y	C	13,821	13,667	16.8	16,000	19.8	18,696	22.8	20,493	25.1	23,982	29.4
Greece	Y	C	466	466	4.3	349	3.2	414	3.7	404	3.6	471	4.2
Hungary	Y	C	5,069	4,894	49.7	5,249	53.1	4,953	50.2	5,462	55.2	6,169	62.8
Ireland	Y	C	270	270	5.8	259	5.6	326	7.1	309	6.7	311	6.8
Italy	Y	C	3,840	3,821	6.3	4,462	7.3	5,042	7.8	4,829	8.1	4,467	7.5
Latvia	Y	C	430	380	19.1	278	13.9	385	19.0	547	26.8	995	48.0
Lithuania	Y	C	1,082	1,082	37.0	1,145	38.9	1,199	40.4	1,762	58.7	2,294	75.2
Luxembourg	Y	C	106	106	18.8	110	20.0	120	22.3	136	25.9	125	24.4
Malta	Y	C	126	126	29.3	132	31.0	84	19.9	88	21.1	129	31.1
Netherlands[d]	N	C	974	974	9.0	970	9.0	979	9.1	2,199	20.5	1,284	12.0
Poland	Y	A	8,661	8,245	21.7	8,042	21.2	7,315	19.2	7,959	20.6	8,400	21.8
Portugal	Y	C	333	325	3.1	244	2.3	167	1.6	185	1.8	174	1.7
Romania	Y	C	1,518	1,330	6.7	1,512	7.6	1,302	6.5	698	3.5	989	5.0
Slovakia	Y	C	5,103	4,841	89.3	4,078	75.3	3,807	70.3	4,627	85.6	3,897	72.3
Slovenia	Y	C	401	401	19.4	597	29.0	316	15.4	392	19.1	400	19.5
Spain[e]	N	C	9,047	9,045	43.3	6,633	31.7	4,537	32.4	4,224	36.1	3,786	32.5
Sweden	Y	C	2,312	2,312	23.7	2,211	22.9	2,842	29.7	2,922	30.8	2,887	30.7
United Kingdom	Y	C	9,492	9,492	14.6	8,099	12.6	8,465	13.2	8,812	13.9	9,455	15.1
EU Total	–	–	**96,144**	**94,625**	**21.2**	**92,007**	**20.8**	**87,747**	**20.2**	**94,278**	**21.8**	**96,685**	**22.7**

Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Iceland	Y	C	44	44	13.4	40	12.3	48	15.2	38	11.9	45	14.1
Norway	Y	C	928	928	18.0	1,118	21.9	1,361	26.9	1,371	27.5	1,290	26.2
Switzerland(f)	Y	C	1,375	1,375	16.6	1,241	15.0	1,265	15.5	1,242	15.6	1,301	16.5

(a): Y: yes; N: no; A: aggregated data; C: case-based data;-: no report.
(b): Sentinel surveillance; no information on estimated coverage. Thus, notification rate cannot be estimated.
(c): Sentinel system; notification rates calculated with an estimated population coverage of 48%.
(d): Sentinel system; notification rates calculated with an estimated population coverage of 64%.
(e): Sentinel system; notification rates calculated with an estimated population coverage of 45% in 2014–2015, 30% in 2013 and 25% in 2009–2012.
(f): Switzerland provided data directly to EFSA. The human data for Switzerland also include the ones from Liechtenstein.

A seasonal trend was observed for the number of confirmed salmonellosis cases in the EU/EEA in 2008–2015, with most cases reported during summer months (Figure 3). Over the same 8-year period, despite the overall increase in reported cases in the 2-year period 2014–2015, there was a statistically significant ($p < 0.01$) decreasing overall trend for salmonellosis in the EU/EEA. Twelve MS (Austria, Cyprus, Denmark, Estonia, Finland, Germany, Ireland, Italy, Lithuania, Luxembourg, Slovenia and Sweden) reported declining trends from 2008 to 2015. In contrast, a significant increasing trend was observed in three MS (the Czech Republic, France and Spain).



Source: Austria, Cyprus, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Portugal, Slovakia, Slovenia, Spain, Sweden and the United Kingdom. Belgium, Bulgaria, Croatia, Latvia and Romania did not report data to the level of detail required for the analysis.

Figure 3: Trend in reported confirmed human cases of non-typhoidal salmonellosis in the EU/EEA, by month, 2008–2015

Sixteen MS provided information on hospitalisation for some or all of their cases of salmonellosis. Lithuania and Slovenia reported hospitalisation status for the first time in 2015, increasing the proportion of confirmed cases at the EU level with known hospitalisation status from 32.2% to 34.0% and resulting in an increase in the proportion of hospitalised cases from 34.4% to 38.4%. The highest hospitalisation proportions (74–95%) were reported in Cyprus, Greece, Latvia, Lithuania, Portugal, Romania and the United Kingdom. Four of these countries (57%) also reported the lowest notification rates of salmonellosis, which indicates that the surveillance systems in these countries primarily capture the more severe cases.

Sixteen MS provided data on the outcome of salmonellosis, and among them, 10 MS reported a total of 126 fatal cases. The EU case fatality was 0.24%. More than half of the fatal cases (65 cases; 51.6%) were reported by the United Kingdom.

Information on *Salmonella* serovars was available from 24 MS (Belgium, Bulgaria, Croatia and Poland reported no case-based serovar data) and Iceland and Norway. As in previous years, the three most commonly reported *Salmonella* serovars in 2015 were *S.* Enteritidis and *S.* Typhimurium, and monophasic *S.* Typhimurium 1,4,[5],12:i:-, representing 69.8%, among 69,663 confirmed human cases with known serovar in 2015 (Table 4). The proportion of *S.* Enteritidis increased compared with 2013 and 2014, the proportion of *S.* Typhimurium decreased while its monophasic variant strains 1,4,[5],12:i:- were at the same stable level than in 2014. Cases of *S.* Infantis continued to decline in 2015. *S.* Stanley cases slightly increased in 2015 but remained at a lower level compared with 2013. Two 'new' serovars (*Salmonella* Panama and *Salmonella* Thompson) entered the top 20 list in 2015.

Table 4: Distribution of reported confirmed cases of human salmonellosis in the EU/EEA, 2013–2015, by the 20 most frequent serovars in 2015

Serovar	2015			2014			2013		
	Cases	**MS**	**%**	**Cases**	**MS**	**%**	**Cases**	**MS**	**%**
Enteritidis	31,829	26	45.7	32,874	27	44.4	29,090	27	39.5
Typhimurium	10,997	26	15.8	12,866	27	17.4	14,852	27	20.2
Monophasic Typhimurium 1.4.[5].12:i:-	5,770	15	8.3	5,773	13	7.8	6,313	14	8.6
Infantis	1,585	24	2.3	1,841	26	2.5	2,225	26	3.0
Stanley	763	22	1.1	757	23	1.0	813	21	1.1
Newport	725	19	1.0	752	20	1.0	714	21	1.0
Derby	648	21	0.9	753	23	1.0	818	21	1.1
Kentucky	506	18	0.7	605	21	0.8	651	23	0.9
Virchow	504	21	0.7	509	22	0.7	571	22	0.8
Paratyphi B var. Java	434	17	0.6	388	15	0.5	348	16	0.5
Agona	374	15	0.5	378	23	0.5	581	24	0.8
Bovismorbificans	372	20	0.5	440	21	0.6	412	20	0.6
Napoli	366	13	0.5	333	14	0.4	434	14	0.6
Oranienburg	305	15	0.4	261	17	0.4	274	17	0.4
Saintpaul	274	17	0.4	374	19	0.5	401	19	0.5
Thompson	262	17	0.4	167	18	0.2	255	19	0.3
Chester	260	13	0.4	294	18	0.4	111	13	0.2
Panama	258	13	0.4	244	15	0.3	352	16	0.5
Braenderup	238	15	0.3	276	17	0.4	245	19	0.3
Hadar	235	19	0.3	286	16	0.4	267	20	0.4
Other	12,958	–	18.6	13,845	–	18.7	13,900	–	18.9
Total	**69,663**	**26**	**100.0**	**74,016**	**27**	**100.0**	**73,627**	**27**	**100.0**

MS: Member State. Source: 25 MS and two non-MS; Austria, Belgium (2013–2014), Cyprus, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden and the United Kingdom.

3.1.2. *Salmonella* in food, animals and feedingstuffs

It is important to note that results from different countries are not directly comparable owing to between-country variation in the sampling and testing methods used. In addition, at the EU level, overall results are highly influenced by the reporting MS and the sample sizes in their investigations, both of which vary importantly between the years. Only results for the most important food products and animals that might serve as a source for human infection in the EU are presented.

3.1.2.1. Food

Compliance with microbiological criteria

The *Salmonella* criteria laid down by Regulation (EC) No 2073/2005 on microbiological criteria in foodstuffs have been in force since 1 January 2006 (revised by Regulations (EC) No 1441/2007[8], 1086/2011[21], and 217/2014[22]). The regulations prescribe sampling and testing requirements, and set limits for the presence of *Salmonella* in specific food categories. These specified foods have a rather diverse marketing pattern across the EU, leading to the fact that not all MS reporting on them. Prescribed samples are to be taken by food business operators; however, competent authorities are obliged to verify correct implementation by following the same sampling strategy with a reduced frequency. According to these food safety criteria, *Salmonella* must be absent in these products when placed on the market, during their shelf life. The absence is defined by testing five or, depending on the food category, 30 sampling units of 10 or 25 g per batch. According to Regulation ((EC) No 1086/2011[21]) that has been in force since December 2011, the absence is required for *S*. Enteritidis and *S*. Typhimurium (including monophasic *S*. Typhimurium strains with the antigenic formula 1,4,[5],12:i:-) that are the regulated serovars in the context of the EU control programmes for poultry populations, in fresh poultry meat (including fresh meat from breeding flocks of *G. gallus*, laying hens, broilers and breeding and fattening flocks of turkeys).

With regard to the comparability of data, it is important to note that the definition of a batch varies widely and, in official controls, often only single samples are taken to verify compliance with the criteria. An evaluation of non-compliance with the *Salmonella* criteria at the EU level for 2011–2015 is summarised in Figure 4 and in Table 2015_SALMCOMPL. The evaluation includes only investigations where the sampling unit (single samples or batches) and sampling stage at the retail level have been reported for the relevant food types. The number of reporting MS differs among the matrices and ranges from a single MS reporting data for mechanically separated meat (both single samples and batches) and 13 MS reporting data for minced meat and meat preparations from other species than poultry intended to be eaten cooked. With regard to single samples, the highest numbers of samples collected were for ice cream (6,715), minced meat and meat preparations from other species than poultry intended to be eaten cooked (3,585), fresh poultry meat (2,232), meat products intended to be eaten raw (1,533) and minced meat and meat preparations from poultry intended to be eaten cooked (1,511). For batch samples, the matrices most represented were minced meat and meat preparations from species other than poultry intended to be eaten cooked (1,456) and fresh poultry meat (778).

As in previous years, the highest levels of non-compliance with *Salmonella* criteria generally occurred in foods of meat origin which are intended to be cooked before consumption. Among these foods, minced meat and meat preparations from poultry had the highest level of non-compliance (6.8% of single samples and 5.1% of batches). These data are similar to 2014 when non-compliant samples were 8.1% and 3.2%, respectively. Low non-compliance was also reported for meat products from poultry meat (2.1% of single samples and 0% of batches) and for minced meat and meat preparations from animal species other than poultry (0.9% of single samples and 2.3% of batches).

As regards foods of meat origin intended to be eaten raw, all sampling units (single samples and batches) in the product category minced meat and meat preparations were compliant in 2015, compared to 1.8% single samples non-compliant in 2014. In meat products intended to be eaten raw there were only a few non-compliant findings (0.2% for single samples and 0.6% for batch samples). The occurrence of *Salmonella* in these foods of meat origin intended to be eaten raw is of particular relevance because of the risk such foods pose to human health.

In minced meat and meat preparations from poultry to be eaten cooked before consumption, in meat products from poultry intended to be eaten cooked and in minced meat and meat preparations from other animal species than poultry intended to be eaten cooked, there were no important variations in the proportions of non-compliant units during the last 5 years.

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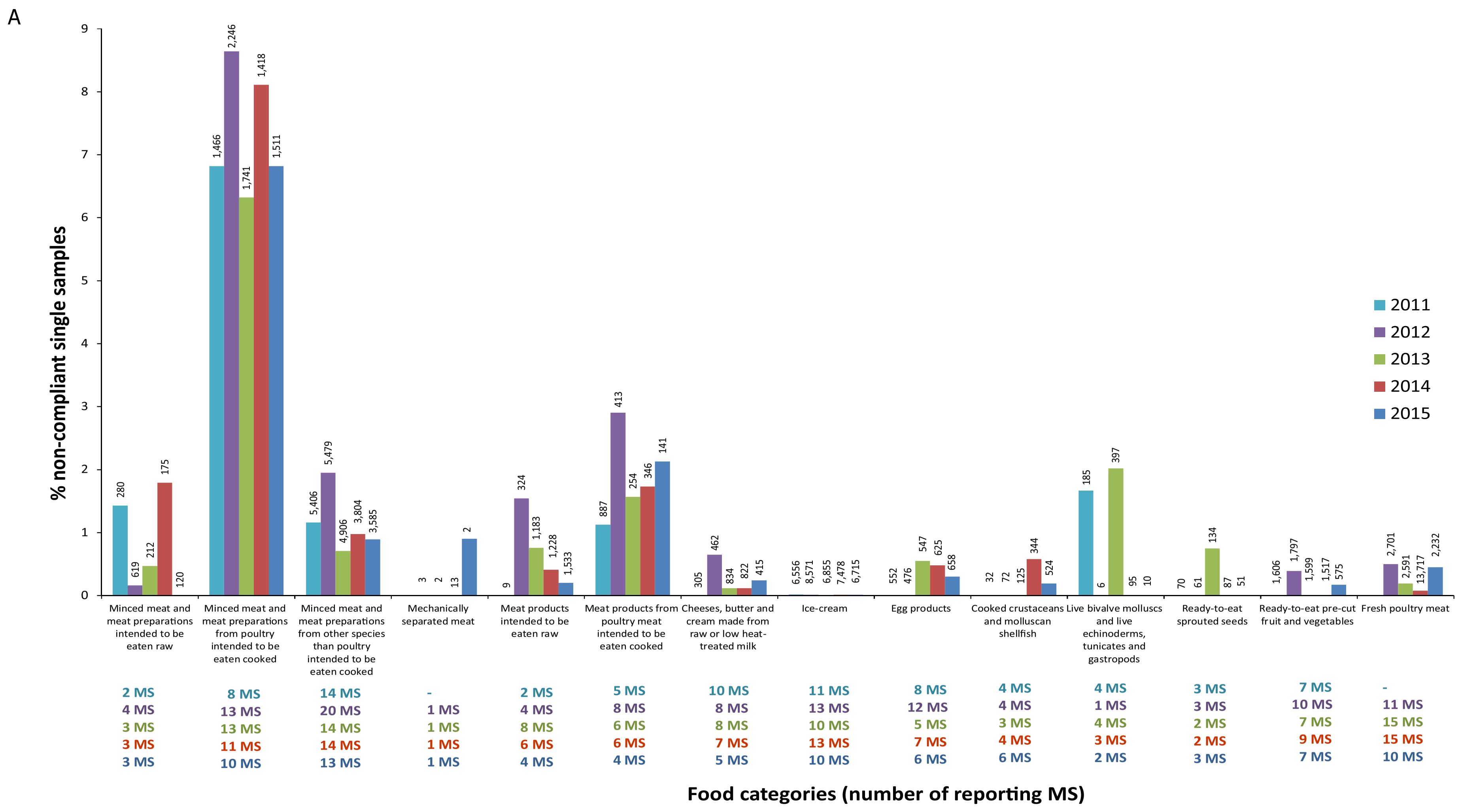
[21] Commission Regulation (EU) No 1086/2011 of 27 October 2011 amending Annex II to Regulation (EC) No 2160/2003 of the European Parliament and of the Council and Annex I to Commission Regulation (EC) No 2073/2005 as regards *Salmonella* in fresh poultry meat. OJ L 281, 28.10.2011, p. 7–11.

[22] Commission Regulation (EU) No 217/2014 of 7 March 2014 amending Regulation (EC) No 2073/2005 as regards *Salmonella* in pig carcasses. OJ L 69, 8.3.2014, p. 93–94.

The reported non-compliance for fresh poultry meat remained very low even though with a slight increase compared to 2014; 0.4% of single samples and 0.8% of batches were non-compliant in 2015 as compared to, respectively, 0.1% and 0.2% in 2014.

For egg products, non-compliance with the microbiological criteria was low as only two *Salmonella*-positive samples (0.3%) were found in a total of 658 single samples, and none of 15 batches was found positive.

All samples/batches of dried infant formulae and dried dietary foods for medical purposes, milk and whey powder, unpasteurised fruit and vegetable juices (RTE), RTE foods containing raw eggs, live bivalve molluscs, live echinoderms, tunicates and gastropods were found to be compliant with the *Salmonella* criteria. Very low to low levels of non-compliance were reported for cooked crustaceans and molluscan shellfish (0.2% of single samples and 1.8% of batches). In 2014, all batches of cooked crustaceans and molluscan shellfish were compliant, whereas for single samples 0.6% were non-compliant. The proportion of non-compliant samples for the other food categories was very low or rare, as observed in previous years.



The number of tested units (sample size) at the EU level is indicated at the top of each bar. MS: Member States.

Figure 4: Proportion of units ((A) single samples; (B) batches) not complying with the EU *Salmonella* criteria, per food category, MS, 2011–2015

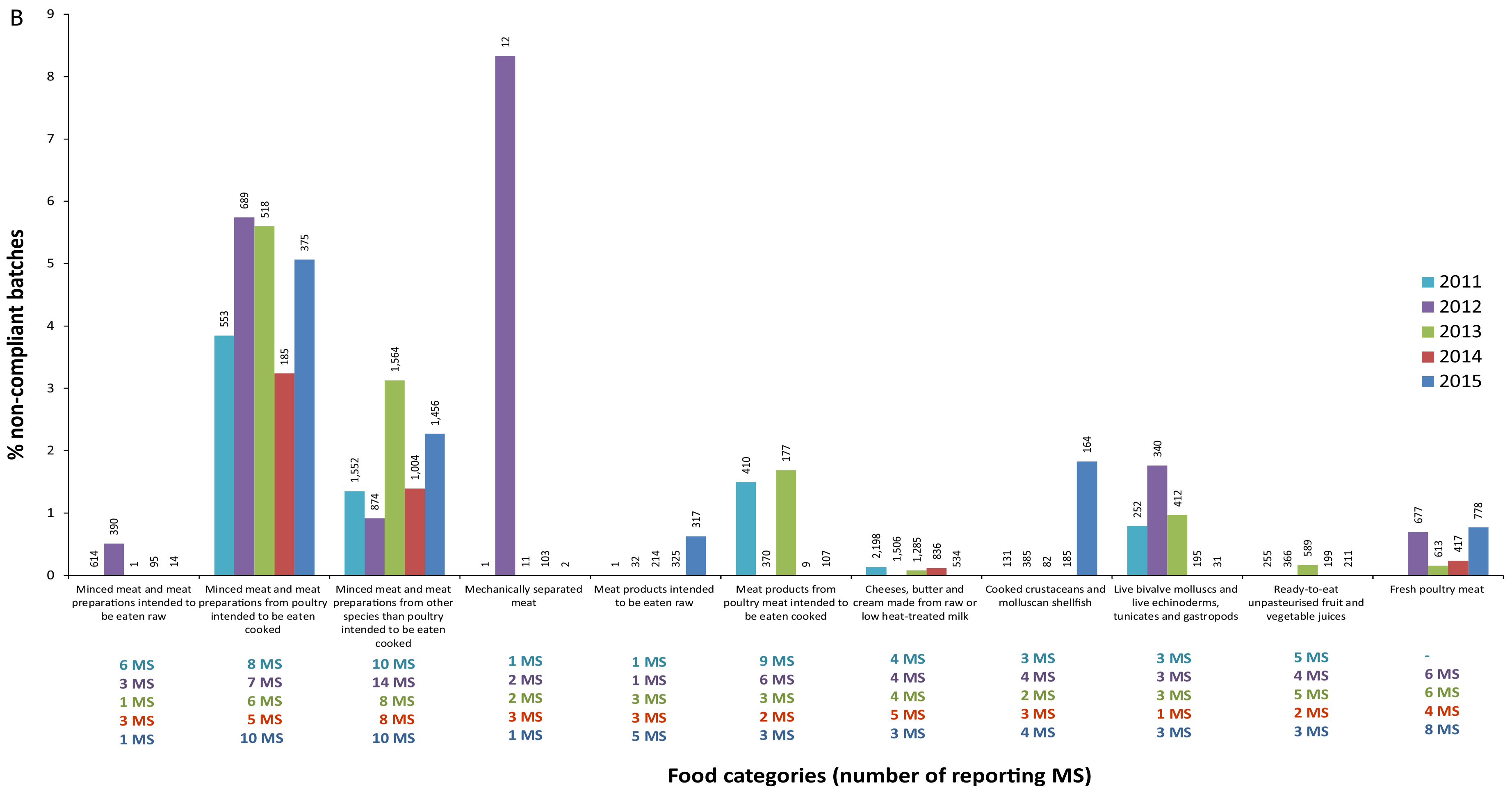


Figure 4: (Continued)

Results for the most important food categories that might serve as a source for human infection in the EU are presented below.

Broiler meat and products thereof

Monitoring activities and control programmes for *Salmonella* in fresh broiler meat are based on sampling at the slaughterhouse, where mainly neck skin samples are taken, and/or at processing or cutting plants and at retail, where usually meat samples are collected.

Overall, *Salmonella* was detected in 6.5% of the 16,981 units tested in 2015 (5.3% of single samples, up from 2.2% in 2014 and 5.7% of batches, down from 9.5% in 2014). The overall proportion of *Salmonella*-positive samples at retail was 7.4%, which was higher than at the slaughterhouse (6.3%) and at the processing plant (6.7%) levels (Table 2015_SALMBROILMEAT). In 2015, *Salmonella* was found in 1.1% of the 1,122 units of RTE broiler meat products tested at retail or at processing (0.4% of single samples and 2.3% of batches; Table 2015_SALMRTEBROIL).

Turkey meat and products thereof

In total, 1,747 units of fresh turkey meat were sampled and tested and, overall, 4.6% were *Salmonella*-positive (6.4% of single samples and 1.8% of batches) (Table 2015_SALMTURKMEAT). Most of the samples were taken at slaughterhouse (606 units) and processing plants (606 units). The majority of the tested turkey meat samples were from Hungary, which reported 32.2% of all the EU samples. Compared to 2014, in the last year a substantial decrease in the number of turkey meat samples was reported (7,482 in 2014 and 1,747 in 2015), whereas the prevalence of positive samples was comparable between the two consecutive years (3.5% in 2014 and 4.6% in 2015). Poland, that contributed in 2014 with the great majority of the turkey meat samples (60.9% of all units tested), contributed in 2015 with 16.3% of all units tested.

Salmonella was found in 1 out of 457 (0.2%) RTE turkey meat products and the majority of the tested units were from Hungary, which reported 45.9% of all units tested in the MS (Table 2015_SALMRTETURK). The overall results for 2015 are comparable with 2014, when 0.3% of the RTE products from turkey meat were positive.

Eggs and egg products

In 2015 in total, 0.7% of the 5,619 tested table egg units were *Salmonella*-positive (0.9% of single samples and 0% of batches) (Table 2015_SALMEGGS). Most of the tested units were reported by Germany (61%). In 2014, a total of 13,394 units of table eggs were reported, 0.4% of which were *Salmonella*-positive. It is interesting to note that at farm level, where the lowest amount of samples was collected (44 samples), the prevalence of positive sample was 9.1% and all positive samples (4) were reported by Slovakia. Generally, the proportion of positive units has been very low for the last 2 years, although only few MS report data and the reporting MS have changed over the years. Further, it should be noted that what constituted a batch or single sample varied considerably in terms of weight (1–600 g) and content (white, yolk or whole eggs) among the MS. Samples with weights other than 25 g accounted for 3.4% of the total number of samples and so this, together with the variation in sample content, should be kept in mind when comparing the results.

Pig meat and products thereof

Within the EU in 2015, a total of 47,038 units of fresh pig meat were tested, of which 1.7% were *Salmonella*-positive (Table 2015_SALMPIGMEAT). In comparison, in 2014, a total of 68,134 units of pig meat were examined and 0.5% was *Salmonella*-positive. Most of these samples were tested at the slaughterhouse level (81%). Of the total number of samples tested in 2015, 20.3% were from Denmark. These were process hygiene criteria samples (investigations at the slaughterhouse level). Samples collected at slaughterhouses were carcase swabs, at retail were mainly meat samples, while the sample types at processing plants were not specified. The comparability of data is hampered by the high heterogeneity among reporting MS in terms of sample weights that range from 10 to 100 g or from 1 to 1,400 cm^2.

Related to the monitoring of *Salmonella* on pig carcasses, in 2015 an amendment of Regulation 854/2004[20] came into force. The amendment, Regulation (EU) No 218/2014, obliges the MS to report separate monitoring data with the total number of samples taken and the number of *Salmonella*-positive samples (1) taken by the Competent Authority, (2) taken by the Food Business Operators and collected by the Competent Authority and (3) of other national sampling plans in countries with special guarantees. This surveillance has been set up in order to reinforce Competent Authority's verification of the correct implementation by Food Business Operators of the process hygiene criterion for *Salmonella* on pig carcases as foreseen by Regulation (CE) No 2073/2005.

The first year of implementation was 2015, and the results show that few MS did yet already comply with these new reporting requirements. Croatia, Slovenia and the United Kingdom reported on sampling investigations by the Competent Authority. A total of 7,448 samples were collected, 4,873 slaughter batches and 2,575 single samples. Overall, 1.24% of the units were *Salmonella*-positive (Table 2015_SALMPIGCARCAS). Nine MS, Bulgaria, Estonia, France, Italy, Luxembourg, Portugal, Romania, Slovenia and Spain, reported on investigations based on sampling investigations taken by the food business operator and collected by the Competent Authority ('HACCP', Table 2015_SALMPIGCARCASHACCP). A total of 25,730 samples were collected, 4,277 slaughter batches, 1,093 batches and 20,360 single samples. Overall, 5.1% of the units were *Salmonella*-positive, which is higher compared to the monitoring results for *Salmonella* on pig carcases based on sampling investigations by the Competent Authority. However, these results are based on the reports of only few MS and may not be representative yet for the EU.

In 2015, 0.7% of the 9,854 tested samples of RTE minced meat, meat preparations and meat products from pig meat were *Salmonella*-positive (Table 2015_SALMRTEPIG). Sixteen MS tested 3,359 samples at the retail level (34% of all samples of RTE pig meat). In 2014, 20,259 samples of RTE pig meat were examined for *Salmonella*, with 0.7% of samples positive.

Bovine meat and products thereof

Data from the testing of fresh bovine meat mainly originates from surveillance programmes, where samples are collected mainly at slaughterhouses (carcase swabs or meat samples). Among the 22,413 samples of fresh bovine meat tested in the MS, 0.2% was *Salmonella*-positive (Table 2015_SALMBOVINEMEAT). Most of the samples were tested at the slaughterhouse (73%). Sample sizes at slaughterhouses varied considerably (1–100 g, 400–1,600 cm^2), which should be taken into account when assessing the results. None of the 557 units of RTE minced meat, meat preparations and meat products from bovine meat tested were found to be *Salmonella*-positive (Table 2015_SALMRTEBOVINE).

Salmonella in other foodstuffs

Altogether, 4.3% of the 650 samples of dried seeds (Table 2015_SALMDRIEDSEED) were *Salmonella*-positive in 2015, most of which were collected during border inspection activities (93%) by Greece (19 out of 26 samples) and the Netherlands (7 out of 26 samples).

Out of the 365 tested units of sprouted seeds, one sample at retail was reported to be *Salmonella*-positive by Belgium (Table 2015_SALMSPRSEED).

Of the 3,117 units of vegetables tested, 0.2% were *Salmonella*-positive (Table 2015_SALMVEGET). Most units were tested at retail (85%) and at that sampling stage only three *Salmonella*-positive samples were obtained by three MS: Cyprus, Germany and the Netherlands.

In fruits, of the 1,500 tested units, none were positive for *Salmonella,* and the same applied to the 329 samples reported as 'Fruit and vegetables' (Table 2015_SALMFRUITVEG).

Of 1,610 units of spices and herbs tested for *Salmonella*, 1.1% were *Salmonella*-positive. The 18 positive samples originated from Sweden (eight samples, from an unspecified sampling stage) and the Netherlands (10 samples, from retail) (Table 2015_SALMHERBS).

Lastly, 1,267 units of live bivalve molluscs were reported to be tested in 2015. Only two positive samples were found by Greece and Spain (Table 2015_SALMBIVMOLLUSC).

3.1.2.2. Animals

According to EU Regulation (EC) No 2160/2003, the MS have to set up national control programmes aimed at reducing the prevalence of *Salmonella* serovars which are considered relevant for public health, in certain animal populations, in order to protect human health against *Salmonella* infections transmissible between animals and humans. Currently, prevalence reduction targets have been defined for breeding flocks of *G. gallus*, laying hens, broilers and breeding and fattening turkeys. National control programmes are established in an individual MS to achieve the EU prevalence targets in the aforementioned animal populations at the primary production level. National control programmes have to be approved by the European Commission, which evaluates the compliance of the programmes with the relevant EU legislation. The results of the programmes have to be reported to the European Commission and EFSA in the framework of the annual EU zoonoses monitoring.

Complementary to the mandatory control programmes for *Salmonella* in poultry, MS can have compulsory or voluntary *Salmonella* control or monitoring programmes in place for a number of farm animal species. These programmes, which are based on national requirements, may fluctuate over time.

Statistical trend analyses

Trend analysis (see Section 2) was carried out using the EU *Salmonella* flock prevalence data shown in Figure 5. Given that the MS highlighted different levels (baselines) of risk to have target serovars but similar patterns over time, only a random MS-specific intercept effect was included in the model (see Figures 2015_SALMBREEDTRENDMS, 2015_SALMLAYTRENDMS, 2015_SALMBROIBSTRENDMS, 2015_SALMBREEDTURKTRENDMS and 2015_SALMFATTURKTRENDMS).

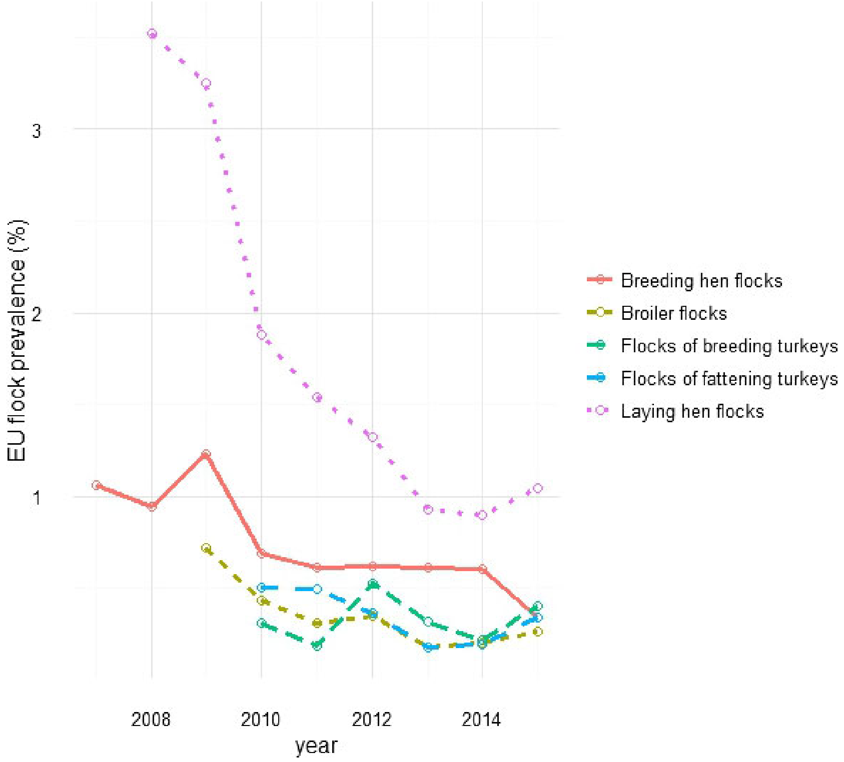


Figure 5: Prevalence of *S*. Enteritidis, *S*. Typhimurium, *S*. Infantis, *S*. Virchow and/or *S*. Hadar-positive breeding flocks of *Gallus gallus* during production in the EU, 2007–2015; of *S*. Enteritidis and/or *S*. Typhimurium-positive laying hen flocks, broiler flocks, flocks of breeding and fattening turkeys, during the production period in the EU, 2008–2015

All models indicated that the EU prevalence of *Salmonella* target serovars-positive flocks has significantly decreased during the years of implementation of the national control programmes for breeding hens, broilers, fattening turkeys and laying hens. In breeding turkeys, however, no significant trend was evidenced.

Looking in detail at the results obtained from the final generalised mixed model, the logit of the probability that flocks will be positive for target serovars has decreased significantly of 0.1677, 0.1491, 0.1128 and 0.2453 for each additional year of national control programme application, in breeding flocks of *G. gallus*, broiler, fattening turkeys and laying hens, respectively. Consequently, the odds of flocks being positive for target serovars decreases by 15.4%, 13.8%, 10.7% and 21.7% – for every year of national control programme application in, respectively, breeding flocks of *G. gallus*, broiler, fattening turkeys and laying hens. The results of the applied models are reported in Appendix A (2015_OUTCTRENDANAL).

In conclusion, the application of national control programmes in poultry has given satisfactory results, since a decreasing trend in the EU prevalence of *Salmonella* target serovars-positive flocks is observed over time for all poultry species except breeding turkeys.

Breeding flocks of Gallus gallus

The year 2015 was the ninth year in which MS were obliged to implement *Salmonella* control programmes in breeding flocks of *G. gallus* in accordance with Regulation (EC) No 2160/2003. The control programmes, based on Regulation (EC) No 200/2010[23], target a prevalence of 1% or less of positive flocks for the following serovars: *S.* Enteritidis, *S.* Typhimurium (including monophasic *S.* Typhimurium), *S.* Infantis, *S.* Virchow and *S.* Hadar. The target has been set for all commercial-scale adult breeding flocks, during the production period, comprising at least 250 birds. However, MS with fewer than 100 breeding flocks would attain the target if only one adult breeding flock was positive.

In 2015, 25 MS and three non-MS reported data within the framework of the programme. This is because Luxembourg and Malta do not have breeding flocks of *G. gallus* and Lithuania did not report validated data. In 2015, *Salmonella* was found in 1.42% of breeding flocks in the EU during the production period (Table 5), compared with 1.73% in 2014.

Table 5: *Salmonella* in breeding flocks of *Gallus gallus* during the production period (all types of breeding flocks, flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2015

Country	Tested	Per cent positive	Five target serovars %	*S.* Enteritidis %	*S.* Typhimurium %	*S.* Infantis %	*S.* Virchow %	*S.* Hadar %	Other than target %
Austria	149	3.36	0.67	0	0.67	0	0	0	3.36
Belgium	584	2.4	0.34	0	0.17	0.17	0	0	2.23
Bulgaria	237	1.27	1.27	0	0.42	0.84	0	0	0
Croatia	178	1.69	0	0	0	0	0	0	1.69
Cyprus	34	2.94	0	0	0	0	0	0	2.94
Czech Republic	657	0.46	0	0	0	0	0	0	0.46
Denmark	308	0.32	0.32	0.32	0	0	0	0	0
Estonia	9	0	0	0	0	0	0	0	0
Finland	158	0	0	0	0	0	0	0	0
France	2,222	0.23	0.23	0.18	0.05	0	0	0	0
Germany	848	2.24	0.59	0.59	0	0	0	0	1.65
Greece	280	1.43	0.71	0.36	0.36	0	0	0	0.71
Hungary	890	0.22	0.22	0	0	0.22	0	0	0
Ireland	165	0	0	0	0	0	0	0	0
Italy	1,097	1.91	0	0	0	0	0	0	1.91
Latvia	36	0	0	0	0	0	0	0	0
Netherlands	1,646	1.09	0	0	0	0	0	0	1.09
Poland	1,599	1.81	1.5	1.13	0.13	0.19	0.06	0	0.31
Portugal	535	0.56	0.19	0.19	0	0	0	0	0.37
Romania	318	3.46	0	0	0	0	0	0	3.46
Slovakia	119	0	0	0	0	0	0	0	0
Slovenia	132	3.03	0.76	0	0	0.76	0	0	2.27
Spain	1,750	4	0.29	0	0.23	0	0	0.06	3.83
Sweden	154	0.65	0.65	0	0.65	0	0	0	0
United Kingdom	1,725	0.46	0.06	0.06	0	0	0	0	0.41

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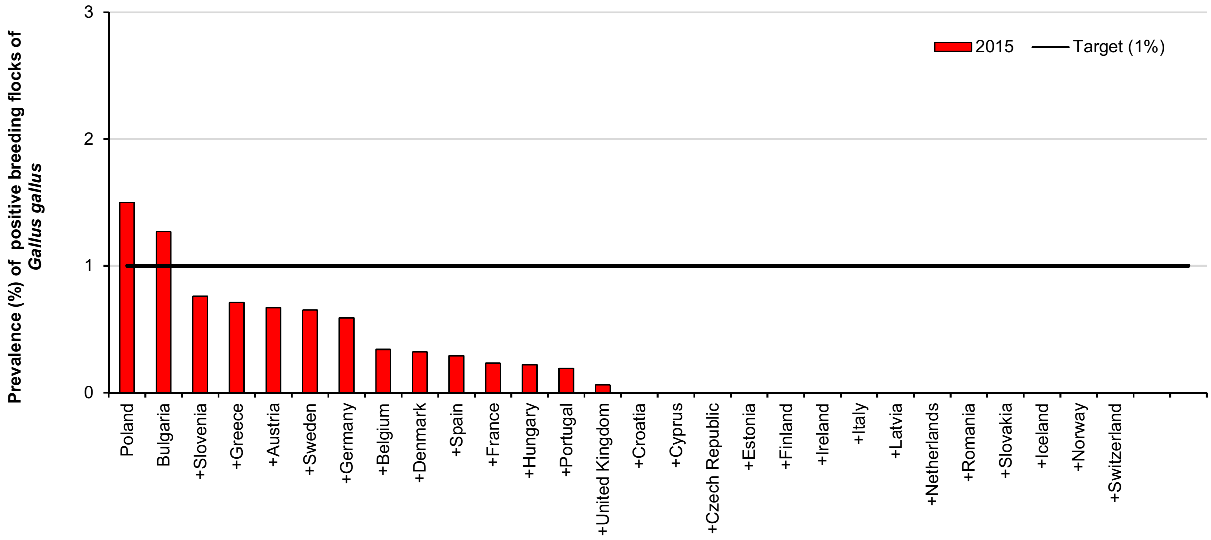
[23] Commission Regulation (EC) No 200/2010 of 10 March 2010 implementing Regulation (EC) No 2160/2003 of the European Parliament and of the Council as regards a Union target for the reduction of the prevalence of *Salmonella* serotypes in adult breeding flocks of *Gallus gallus*. OJ L 61, 11.3.2010, p. 1–9.

Country	Tested	Per cent positive	Five target serovars %	*S.* Enteritidis %	*S.* Typhimurium %	*S.* Infantis %	*S.* Virchow %	*S.* Hadar %	Other than target %
Iceland	46	0	0	0	0	0	0	0	0
Norway	155	0	0	0	0	0	0	0	0
Switzerland	118	0	0	0	0	0	0	0	0
Eu Total	**15,830**	**1.42**	**0.34**	**0.2**	**0.08**	**0.06**	**< 0.01**	**< 0.01**	**1.11**

The prevalence of the five target *Salmonella* serovars was 0.34% in 2015 (Table 5). A total of 11 MS and three non-MS reported no positive flocks for the target serovars in 2015. The EU level prevalence of breeding flocks of *G. gallus* positive to the target *Salmonella* serovars decreased further compared to 2014 (0.6%) (2015_SALMTRENDBREED), and decreased significantly since 2007, the first year of implementation of the national control programme for breeding hens.

In 2015 the number of breeding flocks tested was higher (883 more) compared to 2014. Austria, Belgium, Bulgaria, Croatia, the Czech Republic, Denmark, France, Germany, Greece, Ireland, Latvia, the Netherlands, Portugal, Spain, the United Kingdom, Iceland and Switzerland reported a higher number of tested flocks; this was particularly evident for Bulgaria (237 against 87 in 2014 and 2015, respectively), Croatia (178 against 112), Denmark (308 against 153), Greece (280 against 234), Latvia (36 against 26) and the United Kingdom (1,725 against 1,464).

All reporting countries except Bulgaria and Poland met the target of a maximum of 1% of breeding flocks being positive for *Salmonella* in 2015 (Figure 6). The overall situation improved compared to 2014 when four MS did not meet the target (Belgium, Denmark, Greece and Poland). In the case of Bulgaria in 2015, one flock was positive for *S.* Typhimurium and two flocks for *S.* Infantis; as regards Poland, 18 flocks were positive for *S.* Enteritidis, two for *S.* Typhimurium, three for *S.* Infantis and one for *S.* Virchow.



MS are ordered by prevalence of *S*. Enteritidis, *S*. Typhimurium, *S*. Infantis, *S*. Virchow and/or *S*. Hadar-positive fowl breeding flocks. No data for Luxembourg and Malta as they had no fowl breeding flocks. Lithuania did not report validated data for 2015. Twenty-one MS and three non-MS met the target in 2015, indicated with a '+'.

Figure 6: Prevalence of *S*. Enteritidis, *S*. Typhimurium, *S*. Infantis, *S*. Virchow and/or *S*. Hadar-positive breeding flocks of *Gallus gallus* during the production period and target for MS, Iceland, Norway and Switzerland, 2015

The most commonly reported of the five target serovars in breeding flocks of *G. gallus* in 2015 was *S.* Enteritidis (0.2% compared to 0.31% in 2014), reported by seven MS, followed by *S.* Typhimurium including the monophasic variants (0.08%) and *S.* Infantis (0.06%); just one flock tested positive to *S.* Virchow and *S.* Hadar, respectively.

Laying hen flocks

In the context of Regulation (EC) No 2160/2003, the EU target for laying hens has been defined in Regulation (EC) No 517/2011[24] and consists of an annual minimum percentage of reduction in the number of adult laying hen flocks (i.e. in the production period) remaining positive for *S.* Enteritidis and/or *S.* Typhimurium by the end of the following year. The annual targets are proportionate, depending on the prevalence in the preceding year, but the ultimate EU target is defined as a maximum of 2% of laying hen flocks remaining *Salmonella*-positive. Any reporting of monophasic *S.* Typhimurium is included within the *S.* Typhimurium total and as such is counted as a target serovar. However, MS with fewer than 50 flocks of adult laying hens would attain the target if only one flock remained positive.

In 2015, the eighth year in which MS were obliged to implement *Salmonella* control programmes, 27 MS and three non-MS reported data within the framework of the laying hen flock programme. Lithuania did not report validated data for laying hen flocks.

In 2015, *Salmonella* was found in 2.7% of adult laying hen flocks in the EU (Table 6), in line with 2014 data when the prevalence was 2.5%. In 2015, the overall number of flocks tested was comparable to 2014 (15 flocks more in 2015), although some differences can be noticed looking at the data at national level; a notable inferior number of flocks tested in 2015 compared to 2014 is highlighted in particular for Bulgaria (243 against 679), Hungary (466 against 966), Italy (2,321 against 3,059).

The prevalence of the two targeted *Salmonella* serovars was 1% in 2015 (Table 6). Seven MS and two non-MS reported no flocks positive for *S.* Enteritidis and/or *S.* Typhimurium. The EU level prevalence of laying hen flocks positive to the target *Salmonella* serovars increased slightly compared to 2014 (0.9%) (2015_SALMTRENDLAY), but decreased overall significantly since 2008, the first year of implementation of the national control programme for laying hens.

All reporting MS except Poland met their 2015 reduction targets (Figure 7, 2015_SALMMAPLAY), while in 2014, three MS (Belgium, Malta and Portugal) did not meet their targets. Among the target serovars in laying hen flocks, *S.* Enteritidis (0.8% compared to 0.7% in 2014) was more common than *S.* Typhimurium (0.2%, including the monophasic variants; Table 6). In Poland, 2.84% of the 2,290 tested laying hen flocks were positive for S. Enteritidis while none was positive for S. Typhimurium.

Table 6: *Salmonella* in laying hen flocks of *Gallus gallus* during the production period (flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2015

Country	Tested	Per cent positive	*S.* Enteritidis *S.* Typhimurium %	*S.* Enteritidis %	*S.* Typhimurium %	Other than SET %
Austria	2,768	0.94	0.36	0.14	0.22	0.58
Belgium	716	5.17	1.26	1.26	0	4.47
Bulgaria	243	2.06	1.65	1.23	0.41	0.41
Croatia	387	7.24	1.81	1.81	0	5.43
Cyprus	121	7.44	0	0	0	8.26
Czech Republic	428	1.4	1.4	1.4	0	0
Denmark	344	0	0	0	0	0
Estonia	35	2.86	0	0	0	2.86
Finland	939	0.11	0.11	0.11	0	0
France	5,243	1.2	1.18	0.63	0.55	0.02
Germany	5,947	2.17	1.18	0.79	0.39	0.99
Greece	476	3.78	0.42	0.21	0.21	3.36
Hungary	651	1.69	1.69	1.54	0.15	0
Ireland	165	0	0	0	0	0
Italy	2,321	5.95	0.95	0.39	0.56	5
Latvia	47	0	0	0	0	0

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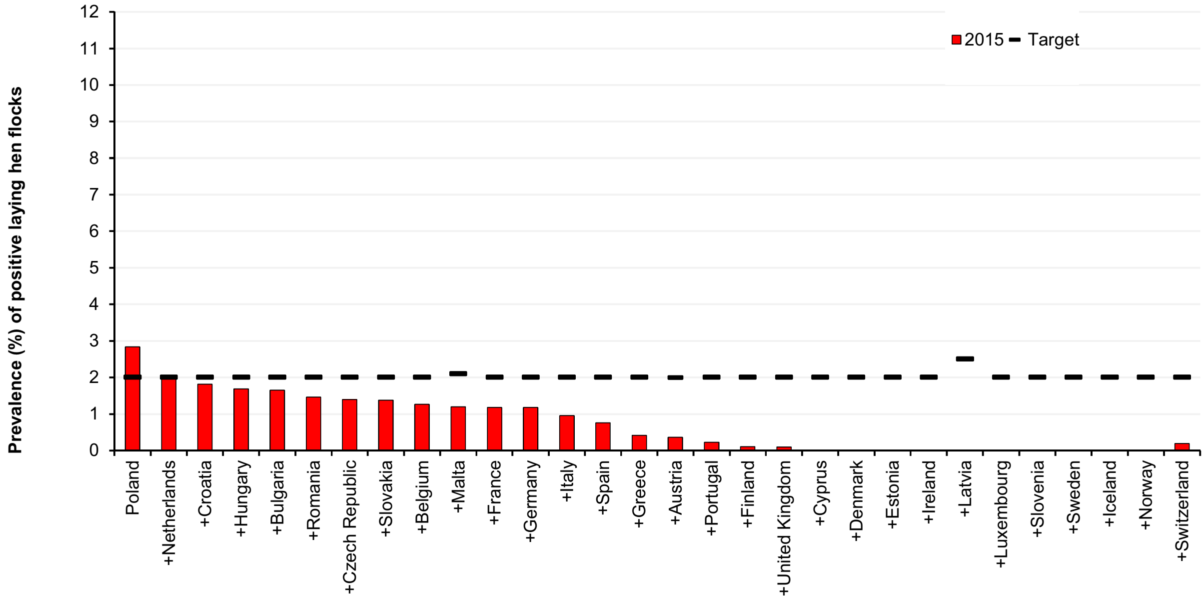
[24] Commission Regulation (EU) No 517/2011 of 25 May 2011 implementing Regulation (EC) No 2160/2003 of the European Parliament and of the Council as regards a Union target for the reduction of the prevalence of certain *Salmonella* serotypes in laying hens of *Gallus gallus* and amending Regulation (EC) No 2160/2003 and Commission Regulation (EU) No 200/2010. OJ L 138, 26.5.2011, p. 45–51.

Country	**Tested**	**Per cent positive**	***S.* Enteritidis *S.* Typhimurium %**	***S.* Enteritidis %**	***S.* Typhimurium %**	**Other than SET %**
Luxembourg	31	0	0	0	0	0
Malta	83	1.2	1.2	1.2	0	0
Netherlands	2,816	1.99	1.99	1.95	0.04	0
Poland	2,290	3.62	2.84	2.84	0	0.79
Portugal	426	3.99	0.23	0	0.23	4.46
Romania	683	9.81	1.46	1.46	0	8.49
Slovakia	218	1.38	1.38	1.38	0	0
Slovenia	186	3.76	0	0	0	4.3
Spain	2,491	7.83	0.76	0.56	0.2	7.35
Sweden	661	0.3	0	0	0	0.3
United Kingdom	4,056	0.67	0.1	0.02	0.07	0.57
Iceland	42	0	0	0	0	0
Norway	848	0	0	0	0	0
Switzerland	1,063	0.19	0.19	0.09	0.09	0
EU Total	**34,772**	**2.67**	**1.04**	**0.8**	**0.24**	**1.68**



MS are ordered by prevalence of *S.* Enteritidis and/or *S.* Typhimurium-positive laying hen flocks. Lithuania did not report validated data for 2015. Twenty-six MS and three non-MS met the target in 2015, indicated with a '+'.

Figure 7: Prevalence of *S.* Enteritidis, *S.* Typhimurium positive laying hen flocks of *Gallus gallus* during the production period and targets for MS, Iceland, Norway and Switzerland, 2015

Broiler flocks

According to Regulation (EC) No 200/2012[25] the EU target for broiler flocks is defined as a maximum percentage of broiler flocks being positive for the target serovars *S.* Enteritidis and/or *S.* Typhimurium (including monophasic *S.* Typhimurium) of 1% or less.

In 2015, the seventh year of mandatory implementation of *Salmonella* control programmes in broiler flocks, 27 MS and three non-MS reported data. In 2015, the EU level prevalence of *Salmonella*-positive broiler flocks positive was 2.22% (Table 7), compared with 3.37% in 2014 (2015_SALMTRENDBROIBS).

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[25] Commission Regulation (EC) No 200/2012 of 8 March 2012 concerning a Union target for the reduction of *Salmonella* Enteritidis and *Salmonella* Typhimurium in flocks of broilers, as provided for in Regulation (EC) No 2160/2003 of the European Parliament and of the Council. OJ L 71, 9.3.2012, p. 31–36.

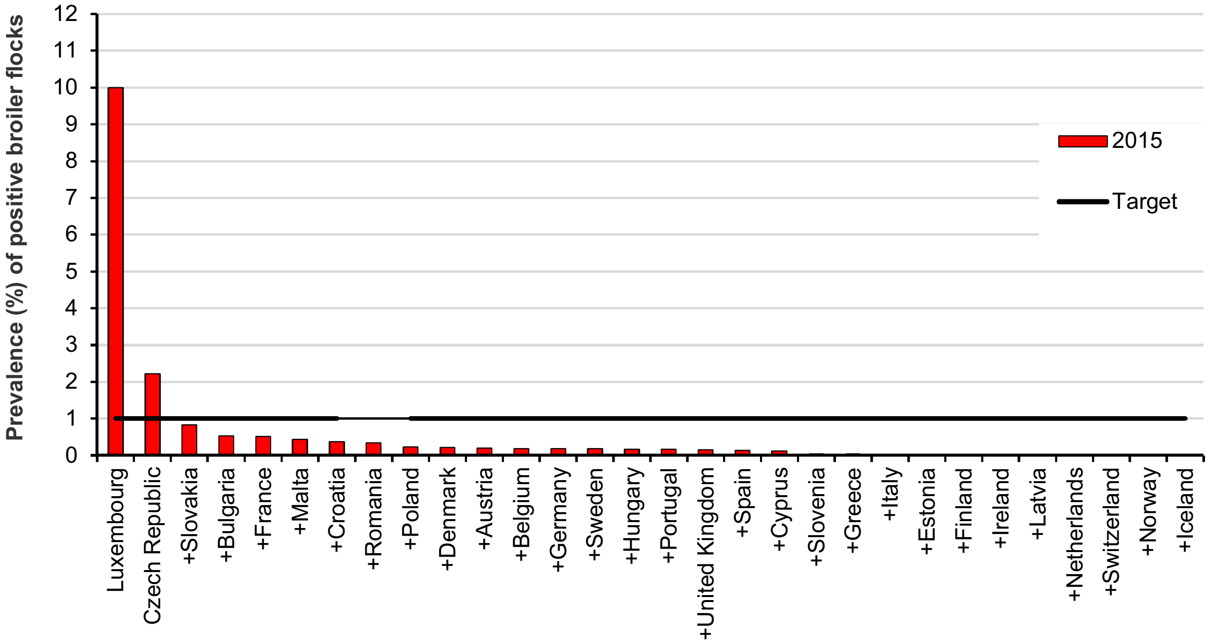
In 2015, the overall number of broiler flocks tested was higher than in 2014 (67,312 flocks more in 2015). This was mainly due to data received from France. France reported 67,268 tested broiler flocks in 2015, as opposed to 2014 when no data for France were included, as the number of tested broiler flocks was not known, because the French IT system could not disentangle the number of broiler and of fattening turkey flocks. A general small increase in the number of tested flocks was observed in 2015 except for in some few countries; in particular, a considerable decrease in the number of flocks tested was noticed for Italy (16,301 and 26,431 flocks tested in 2015 and 2014, respectively).

The reported prevalence of *S.* Enteritidis and *S.* Typhimurium in broiler flocks in the EU was 0.26%, slightly higher than in 2014 (0.20%) (2015_SALMTRENDBROIBS), but decreased overall significantly since 2009, the first year of implementation of the national control programme for broilers. Five MS and all the three non-MS reported no flocks positive for *S.* Enteritidis and/or *S.* Typhimurium (Table 7).

In 2015, all reporting MS except Luxembourg and the Czech Republic met the target of 1% or less of broiler flocks positive for *S.* Enteritidis and/or *S.* Typhimurium. As regards Luxembourg, the high prevalence of 10% is due to one *S.* Typhimurium-positive flock out of the 10 tested (Figure 8 and 2015_SALMBROIBSMAP). The most common of the target serovars in broiler flocks was *S.* Enteritidis (0.17%, compared to 0.13% in 2014) compared with 0.10% of flocks being positive for *S.* Typhimurium including the monophasic variants.

Table 7: *Salmonella* in broiler flocks of *Gallus gallus* before slaughter (flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2015

Country	Tested	Per cent positive	*S.* Enteritidis *S.* Typhimurium %	*S.* Enteritidis %	*S.* Typhimurium %	Other than SET %
Austria	4,146	3.11	0.02	0.02	0	3.11
Belgium	9,483	1.43	0.19	0.06	0.13	1.24
Bulgaria	382	1.05	0.52	0.52	0	0.52
Croatia	3,261	5.49	0.37	0.37	0	5.12
Cyprus	933	3.22	0.11	0	0.11	3.11
Czech Republic	4,751	3.26	2.21	2.21	0	1.05
Denmark	3,631	0.63	0.22	0	0.22	0.44
Estonia	520	0	0	0	0	0
Finland	3,648	0.05	0	0	0	0.05
France	67,268	0.54	0.51	0.23	0.28	0.02
Germany	19,850	1.97	0.19	0.13	0.06	1.79
Greece	6,824	0.4	0.03	0.01	0.01	0.37
Hungary	7,507	0.17	0.17	0.04	0.13	0
Ireland	37	0	0	0	0	0
Italy	16,301	8.37	0.01	0	0.01	8.36
Latvia	641	0	0	0	0	0
Luxembourg	10	10	10	0	10	0
Malta	456	0.44	0.44	0	0.44	0
Netherlands	15,725	0.52	0	0	0	0.52
Poland	38,465	0.33	0.23	0.22	< 0.01	0.1
Portugal	11,359	2.64	0.17	0.11	0.05	2.47
Romania	11,619	8.99	0.34	0.29	0.04	8.65
Slovakia	2,279	0.83	0.83	0.83	0	0
Slovenia	2,291	7.68	0.04	0	0.04	7.64
Spain	38,870	4.68	0.13	0.02	0.11	4.59
Sweden	3,390	0.38	0.18	0	0.18	0.21
United Kingdom	44,091	1.48	0.15	0.13	0.02	1.35
Iceland	686	1.9	0	0	0	1.9
Norway	4,437	0.02	0	0	0	0.02
Switzerland	620	0	0	0	0	0
EU Total	**317,738**	**2.22**	**0.26**	**0.17**	**0.1**	**1.96**



MS are ordered by prevalence of *S*. Enteritidis and/or *S*. Typhimurium-positive broiler flocks. Lithuania did not report validated data for 2015. Twenty-five MS and three non-MS met the target in 2015, indicated with a '+'.

Figure 8: Prevalence of *S*. Enteritidis, *S*. Typhimurium positive broiler flocks of *Gallus gallus* during the production period and targets for MS, Iceland, Norway and Switzerland, 2015

Breeding and fattening turkeys

Salmonella control programmes in turkey flocks have been mandatory since 2010. Regulation (EU) No 1190/2012[26] introduced a final annual *Salmonella* reduction target of 1% defined as the maximum percentage of breeding and fattening turkey flocks being positive for the target serovars *S.* Enteritidis and/or *S.* Typhimurium (including monophasic *S.* Typhimurium). However, for MS with less than 100 flocks of adult breeding or fattening turkeys, the target is that no more than one flock of adult breeding or fattening turkeys is positive.

For breeding turkeys, 14 MS and two non-MS reported data from *Salmonella* testing in adult flocks in 2015 (Table 8). France reported data belonging to 975 tested flocks (49% of the total flocks tested), whereas smaller numbers of flocks were tested by other countries. The overall EU prevalence of *Salmonella* in turkey flocks was 1.41%, a decreasing trend considering the 3.3% prevalence observed in 2014.

Eight flocks were positive for target *Salmonella* serovars resulting in a reported prevalence of *S.* Enteritidis and *S.* Typhimurium in the EU of 0.40%, which was higher than in 2014 (0.22%) (2015_SALMTRENDBREEDTURK). Since 2010, the first year of implementation of the national control programme for breeding turkeys, no statistically significant trend was evident.

Only two MS (France and Croatia) reported breeding turkey flocks positive for the target serovars in 2015. Seven flocks were reported by France (5 flocks *S.* Typhimurium-positive and two flocks *S*. Enteritidis-positive), whereas one *S.* Enteritidis-positive flock was reported by Croatia.

The prevalence of target *Salmonella* serovars continued to be low in reporting countries and all 14 reporting MS and the two non-MS met their target prevalence of *S.* Enteritidis and/or *S.* Typhimurium set for adult turkey breeding flocks in 2015. Croatia met the target even though the proportion of positive flocks was higher than 1%, as they reported only one positive flock out of the three tested (Table 8 and Figure 9).

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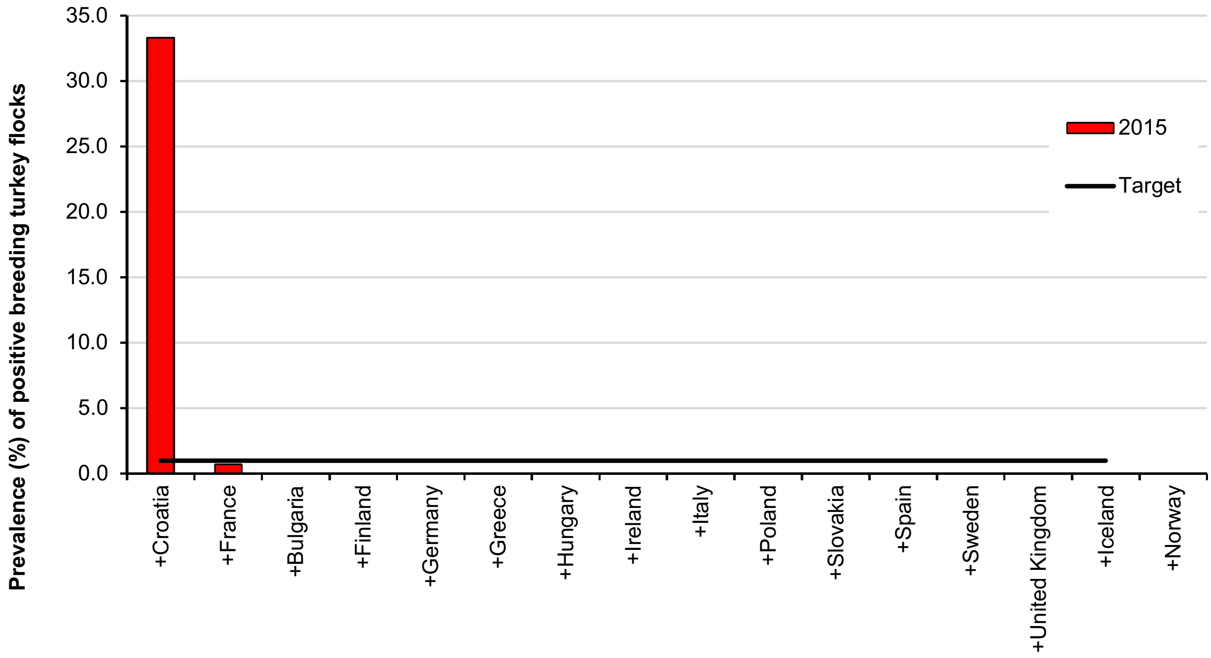
[26] Commission Regulation (EU) No 1190/2012 of 12 December 2012 concerning a Union target for the reduction of *Salmonella* Enteritidis and *Salmonella* Typhimurium in flocks of turkeys, as provided for in Regulation (EC) No 2160/2003 of the European Parliament and of the Council. OJ L 340, 13.12.2012, p. 29–34.

Table 8: *Salmonella* in breeding flocks of turkeys (adults, flock-based data) in countries running control programmes, 2015

Country	Tested	Per cent positive	*S.* Enteritidis *S.* Typhimurium %	*S.* Enteritidis %	*S.* Typhimurium %	Other than SET %
Bulgaria	3	0	0	0	0	0
Croatia	3	33.33	33.33	33.33	0	0
Finland	7	0	0	0	0	0
France	975	0.72	0.72	0.21	0.51	0
Germany	80	0	0	0	0	0
Greece	3	0	0	0	0	0
Hungary	168	0	0	0	0	0
Ireland	4	0	0	0	0	0
Italy	213	6.1	0	0	0	6.1
Poland	152	0.66	0	0	0	0.66
Slovakia	34	0	0	0	0	0
Spain	85	1.18	0	0	0	1.18
Sweden	4	0	0	0	0	0
United Kingdom	256	1.95	0	0	0	1.95
Iceland	4	0	0	0	0	0
Norway	17	0	0	0	0	0
EU Total	**1,987**	**1.41**	**0.4**	**0.15**	**0.25**	**1.01**



MS are ordered by prevalence of *S*. Enteritidis and/or *S*. Typhimurium-positive breeding flocks of turkeys. Fourteen MS and two non-MS met the target in 2015, indicated with a '+'.

Figure 9: Prevalence of *S*. Enteritidis, *S*. Typhimurium positive breeding turkey flocks during the production period and targets for MS, Iceland and Norway, 2015

For fattening turkeys, in total, 23 MS and three non-MS provided data from flocks before slaughter. In 2015, the EU level prevalence of *Salmonella*-positive turkey fattening flocks spp. was 3.6% (Table 9), which confirms a decreasing trend compared to 2013 and 2014, when prevalence was 11.1% and 9.3%, respectively. However, prevalence at the EU level for the target serovars was 0.34%, which was a slight increase over the 0.2% prevalence reported for 2014 (Figure 2015_SALMTRENDFATTURKBS). Despite this, prevalence decreased significantly overall since 2010, the first year of implementation of the national control programme for fattening turkeys. Ten MS and three non-MS reported no fattening turkey flocks positive for *S.* Enteritidis and/or *S.* Typhimurium.

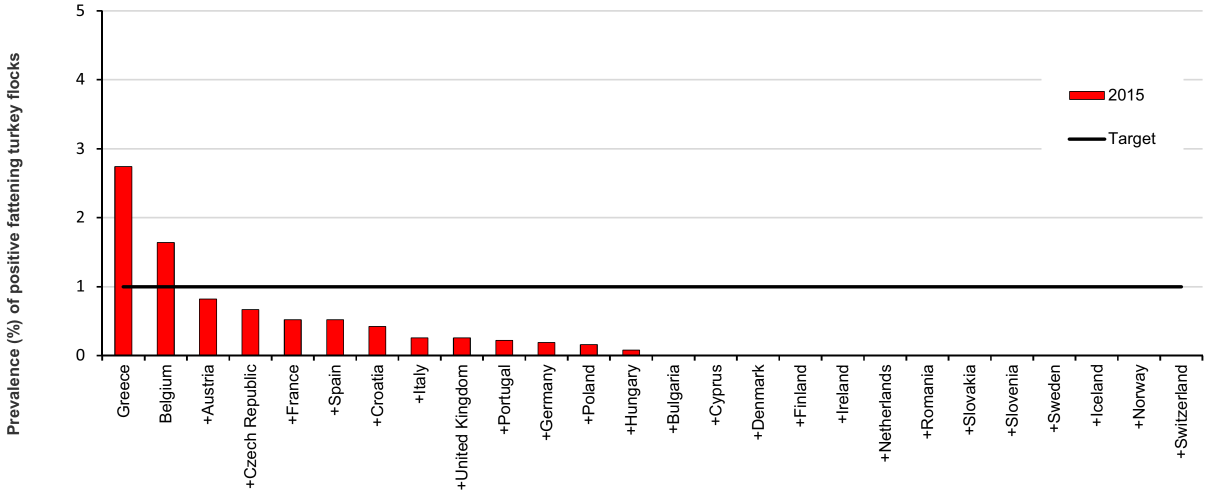
Two MS, Belgium and Greece, did not meet the target of 1% for fattening turkeys (Figure 10 and 2015_SALMFATTURKBS map). In the case of Belgium, this target was not met in 2014 either, whereas for Greece, non-achievement occurred for the first time in 2015.

In 2015, France tested 11,871 flocks which comprises more than a quarter of total EU tested flocks. Previously, no 2014 data of France were included, as the number of tested turkey fattening flocks was not known, because the French IT system could not disentangle the number of broiler and of fattening turkey flocks.

The prevalence of target serovars *S.* Typhimurium (including the monophasic strains) and *S*. Enteritidis in fattening turkey flocks was 0.25% and 0.09%, respectively.

Table 9: *Salmonella* in fattening flocks of turkeys before slaughter (flock-based data) in countries running control programmes, 2015

Country	Tested	Per cent positive	*S.* Enteritidis *S.* Typhimurium %	*S.* Enteritidis %	*S.* Typhimurium %	Other than SET %
Austria	365	3.84	0.82	0	0.82	3.01
Belgium	183	4.92	1.64	0	1.64	3.28
Bulgaria	3	0	0	0	0	0
Croatia	240	12.08	0.42	0.42	0	11.67
Cyprus	10	30	0	0	0	30
Czech Republic	298	3.02	0.67	0.67	0	2.35
Denmark	80	1.25	0	0	0	1.25
Finland	333	0	0	0	0	0
France	11,871	0.55	0.52	0.24	0.29	0.03
Germany	4,758	0.63	0.19	0.02	0.17	0.44
Greece	73	2.74	2.74	0	2.74	0
Hungary	2,419	0.08	0.08	0.04	0.04	0
Ireland	7	0	0	0	0	0
Italy	3,063	10.09	0.26	0	0.26	9.83
Netherlands	289	0	0	0	0	0
Poland	6,272	0.94	0.16	0	0.16	0.78
Portugal	905	0.33	0.22	0	0.22	0.11
Romania	320	0	0	0	0	0
Slovakia	12	0	0	0	0	0
Slovenia	141	2.84	0	0	0	2.84
Spain	3,442	16.53	0.52	0	0.52	16.1
Sweden	144	0	0	0	0	0
United Kingdom	3,057	8.8	0.26	0.03	0.23	8.67
Iceland	26	0	0	0	0	0
Norway	199	0	0	0	0	0
Switzerland	40	0	0	0	0	0
EU Total	**38,285**	**3.6**	**0.34**	**0.09**	**0.25**	**3.28**



MS are ordered by prevalence of *S*. Enteritidis and/or *S*. Typhimurium-positive fattening flocks of turkeys. Twenty-one MS and three non-MS met the target in 2015, indicated with a '+'.

Figure 10: Prevalence of *S*. Enteritidis, *S*. Typhimurium positive fattening turkey flocks during the production period and targets for MS, Iceland, Norway and Switzerland, 2015

Ducks and geese

In 2015, the overall flock *Salmonella* prevalence in ducks and geese was 49.46% and 2.76% for *S*. Enteritidis and *S*. Typhimurium combined (Table 2015_SALMDUCKGEESE). Only four MS reported data for ducks and two MS reported data for geese. In addition, owing to variations in types of flocks submitted to sampling (breeding or meat production flocks), sampling strategy and sample type and size, prevalence is not comparable across MS.

Pigs

Nine MS reported *Salmonella* prevalence data for pigs. The overall proportion of *Salmonella*-positive samples from pigs was 11.5%, which is higher than in 2014 (7.9%). Prevalence was similar at animal and herd levels with values of 11.3% and 12.4%, respectively (Table 2015_SALMPIGSBACT).

Data belong to both breeding and fattening pig systems, and were obtained at farm or at the slaughterhouse level. Sample types reported were: faeces, lymph nodes, organ or tissue samples, carcass swabs and environmental samples. Due to the different number of animals tested and to differences among MS in the choice of sampling matrices, comparisons between MS and between years should be made with caution.

Cattle

Ten MS reported data *Salmonella* prevalence data for cattle with an overall prevalence of *Salmonella*-positive samples from cattle of 3.3%, compared to 3.9% for 2014. The *Salmonella* prevalence was similar at the herd and animal levels with values of 2.1% and 3.5%, respectively (Table 2015_SALMCATBACT).

Animal samples (faeces, tissues or unspecified matrices) belonged to different production categories encompassing both, meat and dairy production with sampling plans based on animals or herds generally in the context of official sampling.

3.1.2.3. Feedingstuffs

The overall level of *Salmonella*-positive units in animal- and vegetable-derived feed material in 2015 was 5.13% of 4,546 units reported by 21 MS. In addition, Norway reported data from 4,257 samples which showed 0.4% of samples positive for *Salmonella* (Table 2015_SALMDERIVEDFEED). In 2014 and 2013, prevalence of 3.8% and 1.4% were reported, respectively, and thus, a slight increase in prevalence of *Salmonella*-positive units in feed material was observed in 2015.

Data reported from feed material of vegetable or animal (both land and marine) origin, as well as the number of batches or samples tested, was highly variable among MS, ranging from 1,184, as reported by Poland, to 9 and 7 reported by Latvia and Slovenia, respectively. Among different matrices reported by 21

MS and one non-MS, the most commonly tested feed material was soya (bean)-derived feed material with 3,404 samples tested and a mean *Salmonella* prevalence of 3.7%. High prevalence was reported for meat meal (290 tested, 16.7% positives) as well as for rice–derived materials, by-products of brewing, and blood products, but in these cases the number of tested samples was very low (< 10).

High levels of *Salmonella*-positive samples were observed at all sampling stages except for farm level. The highest proportion of positive samples in individual investigations was reported for the feed category 'Feed material of oil seed or fruit origin', which is mainly soya (bean)-derived and sunflower seed-derived feed. *Salmonella* contamination was also detected in 'Feed material of marine animal origin (fish meal)' and 'Feed material of land animal origin (meat meal)', as well as in feed of cereal origin. In meat and bone meal, *Salmonella* contamination is to be considered only an indicator, and it does not pose any risk to food-producing animals because meat and bone meal is still prohibited for feeding food-producing animals, although it is used in pet foods.

In the finished feed for animals (compound feedingstuffs), the prevalence of *Salmonella*-positive units in 2015 was low to very low for all animal species: 1.20% of 2,248 tested samples for cattle, 0.51% of 2,754 tested samples for pigs and 0.67% of 7,961 tested samples for poultry (Tables 2015_SALMCOMPFEEDCATTLE, 2015_SALMCOMPFEEDPIGS and 2015_SALMCOMPFEEDPOULTRY). It should be highlighted that the reported prevalence of *Salmonella*-positive samples might not always be representative of compound feedingstuffs on the national markets, as some reports might reflect intensive sampling of high-risk products, and representative sampling of feedingstuffs is difficult.

3.1.2.4. Serovars in food and animals

In this following section, data relating to *Salmonella* serovars isolated in 2015 from animals and foods of animal origin are analysed. These analyses are underpinned by *Salmonella* serovar frequency distribution tables of the most commonly isolated serovars, specific to every matrix (category). These data are compared with data from previous years.

In order to interpret the data presented it should be noted that some MS do not necessarily fully serotype all isolates, or report all serotyped isolates to EFSA. MS are obliged to report the five regulated serovars (*S*. Enteritidis, *S*. Typhimurium, *S*. Hadar, *S*. Virchow and *S*. Infantis) for breeding chickens. For other poultry production sectors, only *S*. Enteritidis and *S*. Typhimurium (including the monophasic variants) have to be compulsorily reported, while for the remaining production categories, serotyping is not mandatory. Also for the food sector, according to the current legislation, the food safety criteria are the absence of *Salmonella* spp. for all matrices considered except for fresh poultry meat that has the absence of *S*. Typhimurium (including the monophasic variant) and *S*. Enteritidis as criterion. Hence, some MS only report on the presence of regulated serovars, without identifying the serovar for the strains that did not belong to the regulated serovars. This results in a possible bias towards the reporting of regulated serovars (*S*. Enteritidis and *S*. Typhimurium) for poultry populations and for fresh poultry meat. It also implies that the true occurrence of serovars other than the regulated ones is uncertain when analysing these poultry data as a whole. For the remaining matrices, the data collected could be strongly biased by what the MS actually serotyped and reported. The number of isolates reported in the different categories varied greatly between MS and between categories. Substantial variations in terms of reporting for the different serovars/matrices observed along the years could be related to the evolution of the epidemiological situation, but could also be influenced by *ad hoc* monitoring activities carried out by MS, which may lead to the overestimation or underestimation of specific serovars from certain matrices. These biases make it difficult to directly compare the serovar data, especially when the comparisons are made among different years or among different sources.

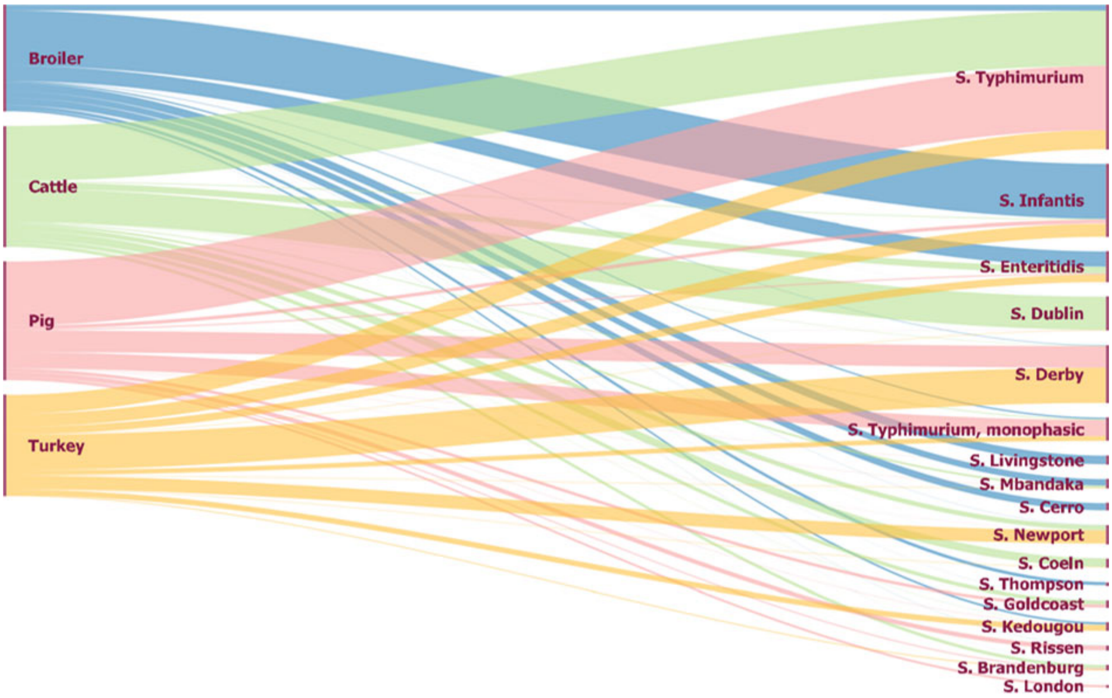
In the following paragraphs the discussion refers exclusively to the isolates serotyped and reported by MS for the different matrices.

Data reported by MS in 2015 were collated into the following eight matrices (Table 2015_SERALLMATRIX): broiler flocks, broiler meat, turkeys, turkey meat, pigs, pig meat, cattle and bovine meat. A total of 14,596 *Salmonella* serotyped isolates were reported from these matrices, considering isolates reported by MS from all monitoring activities.

Among the serotyped isolates the most common serovar was *S*. Typhimurium (3,409 isolates; 23.4% of the serotyped isolates), followed by *S*. Infantis (3,397 isolates; 23.3%), *S*. Enteritidis (1,136 isolates; 7.8%), *S*. Dublin (858 isolates; 5.9%) and *S*. Derby (779 isolates; 5.3%). *S*. Typhimurium, *S*. Infantis, *S*. Enteritidis and *S*. Derby were isolated from all the matrices taken into account, whereas *S*. Dublin was isolated from six out of the eight matrices even though the great majority of isolates was from cattle (98.3%) (Table 2015_SERALLMATRIX).

The Sankey diagram (Figure 11 illustrates the overall distribution of the most common *Salmonella* serovars across different food, animal and meat sectors in the EU in 2015. Since the aim of the diagram is to show association between the most common serovars and matrices, animal and food data from the same species were merged. Hence, 'broiler' refers to data from chickens and broiler meat, 'cattle' refers to data from cattle and bovine meat, 'pig' refers to data from pigs and pig meat and 'turkey' refers to data from turkeys and turkey meat. The selection of serovars was obtained by considering the seven most reported serovars for each source. Some serovars were common to more than one source, so those shared serovars were listed once. The final list included a total of 17 serovars.

Even though *S*. Typhimurium was related to all sources taken into account, it was specifically associated with pigs and cattle. *S*. Infantis was associated mainly with poultry (both broiler and turkey) as was *S*. Enteritidis, but this last serovar was also associated with cattle. *S*. Dublin was associated exclusively with cattle, whereas *S*. Livingstone and *S*. Cerro were associated with broiler. *S*. Derby was equally associated with turkey and pig, and the monophasic variant of *S*. Typhimurium was also associated with these two sources.



The left side of the diagram shows the sources considered: broiler (blue), cattle (green), pig (red) and turkey (yellow); animal and food data from the same source were merged (broiler includes isolates from chicken flocks and broiler meat, cattle includes data from bovine herds and bovine meat, pig includes data from pig herds and pig meat, turkey includes data from turkey flocks and turkey meat. On the right side, the list of the 17 most reported serovars from each matrix (combined animal and food) is reported. Included serovars are the outcome of a merging procedure involving the seven most reported serovars for each source. The width of the coloured bands linking sources and serovars is proportional to the percentage of isolation of each serovar in each source.

Figure 11: Sankey diagram of the 17 most reported *Salmonella* serovars, in animal species and foods of animal origin, by source, EU, 2015

Serovars in poultry production

Gallus gallus (breeding hens, laying hens and broilers)

The distribution of the most commonly isolated *Salmonella* serovars from domestic fowl (*G. gallus*) (including data from breeding hens, laying hens and broilers collected in the context of national control programmes) in 2015 is shown in Table 2015_SERGAL. In 2015, 25 MS (all MS except Ireland, Lithuania and Latvia) reported the serovar of *Salmonella* isolates from *G. gallus*. Of all categories described in this chapter, this was the category with the highest number of countries reporting the serovars of *Salmonella* isolates. This is due to the fact that *Salmonella* control in *G. gallus* is a statutory requirement for all MS.

In the context of national control programmes, a total of 5,535 serotyped isolates were reported in 2015, which is an increase of 2.9% compared to 2014, when 5,377 serotyped isolates were recorded, and it is comparable to the number of isolates reported in 2013 (5,660). The highest increase in terms of isolates reported in 2015 compared to 2014 was for France (81 isolates in 2014 and 462 isolates in 2015), Croatia (43 isolates in 2014 and 210 isolates in 2015) and Portugal (72 isolates in 2014 and 315 in 2015).

The number of isolates varied greatly between the MS. As in 2014, in 2015, Italy and Romania reported the highest number of isolates (1,131 and 1,123, respectively), followed by the United Kingdom (931 isolates). These three MS together accounted for 57.5% of all serotyped isolates.

Altogether, 1,196 isolates (21.6%) were either *S*. Enteritidis or *S*. Typhimurium, which are regulated serovars for all production types. Since monophasic variants of *S*. Typhimurium were not among the 'top ten' serovars in *G. gallus* in 2015, the number of isolates belonging to regulated serovars was likely higher than that. Compared to 2014, when 850 out of 5,377 isolates (15.9%) belonged to regulated serovars, an increase in the proportion of regulated serovars was reported in 2015 and this increase was substantial in France which reported five times more regulated serovars in 2015 compared to 2014.

The most frequent serovar among reports from *G. gallus* was *S*. Infantis, accounting for 1,859 or 33.6% of isolates, followed by *S*. Enteritidis (875 isolates; 15.8%) and *S*. Mbandaka (373 isolates; 6.7%). These three serovars were confirmed for the fourth year as those most frequently isolated from *G. gallus*. *S*. Typhimurium and *S*. Livingstone accounted for 321 (5.8%) and 256 isolates (4.6%), respectively.

Since 2013, *S*. Infantis has been confirmed as the most frequent serovar isolated from *G. gallus*. In 2015, it was reported by 14 MS, and it was notified with highest numbers by Italy (719 isolates), Romania (682 isolates), Slovenia (166 isolates), Croatia (94 isolates) and Austria (86 isolates). For the other reporting MS, a lower number of *S*. Infantis was notified. However, compared to the previous year, in 2015, about 10% fewer reports of *S*. Infantis were reported (1,859 isolates in 2015 and 2,057 in 2014).

S. Enteritidis, with 875 isolates (15.8%), was the second most frequent serovar isolated from *G. gallus* in 2015. It was reported from 20 MS, with France (216), Poland (169), the Czech Republic (111), Germany (78) and the United Kingdom (71) reporting the highest numbers. For all these countries except the Czech Republic, a substantial increase in the notification of *S*. Enteritidis was reported in 2015 compared to 2014. In the Netherlands 98.2% of the serotyped isolates from G. gallus were reported as S. Enteritidis, in Poland 82%, in Germany 69.6%, in the Czech Republic 67.7% and In France 46.7%. At the EU level, a substantial increase (of about 35%) of *S*. Enteritidis isolates occurred in 2015 (875 isolates) compared to 2014 (641 isolates). However, this increase in the *S*. Enteritidis isolation was attributed to a limited number of MS, for which there was a substantial increase in the number of isolates notified. In particular, France reported 47 isolates in 2014 and 216 isolates in 2015, Germany 28 in 2014 and 78 in 2015, Poland 118 in 2014 and 169 in 2015, the United Kingdom 3 in 2014 and 71 in 2015. The remaining MS reported a lower number of *S*. Enteritidis isolates in 2015 compared to 2014. However, it is noteworthy that France, for which the highest increase in term of *S*. Enteritidis reporting occurred, technically was not able to submit *Salmonella* prevalence data for broilers or for turkeys in 2014, whereas in 2015, this MS contributed a substantial proportion of the flocks tested at the EU level. This notable difference between the two consecutive years in terms of *Salmonella* prevalence reporting from France for these species could have influenced the reporting of the *Salmonella* serovars from the same sources. Hence, the increase of *S*. Enteritidis, which occurred in the last year, might have been strongly influenced by the variations in the serovars reporting from MS among years rather than by a real evolution of the epidemiological situation.

S. Mbandaka, was the third most frequent serovar from *G. gallus* (6.7% of the isolates) and it was reported in large numbers from the United Kingdom (72.9% of the isolates were from the United Kingdom) and from eight additional MS, but with a reduced number of isolates. Also notable is that Italy, which was one of the leading countries in terms of reports of *S*. Mbandaka from *G. gallus* in previous years, did not report any isolate of this serovar in 2015.

S. Typhimurium accounted for 5.8% of the isolates from *G. gallus* in 2015, and it was reported from 21 MS. Compared to the two previous years (2013–2014), in 2015, a substantial increase in the number of isolates was seen (321 isolates in 2015 and 209 in 2014). France, Spain and Germany notified 52.3%, 14% and 10.6% of the *S*. Typhimurium isolates and the increase described in the current year should be attributed mainly to France, which reported 29 *S*. Typhimurium isolates in 2014 and 168 in 2015.

Monophasic variants of *S*. Typhimurium were not among the 'top ten' serovars from *G. gallus* in 2015 and are, therefore, not discussed here.

Other serovars, which occurred in a limited number of MS, were *S*. Livingstone (256 isolates), *S*. Thompson (193 isolates) and *S*. Senftenberg (157 isolates). *S*. Livingstone was notified by eight MS, and Italy accounted for 77.3% of the isolates, *S*. Thompson by five MS and in this case too, Italy notified the majority of the isolates (63.7%), *S*. Senftenberg by seven MS and the majority of isolates were reported by the United Kingdom (43.9) and Romania (40.8). These serovars are persistent at hatcheries and at farm level and for this reason during recent years they were constantly reported among the top ten serovars from *G. gallus*.

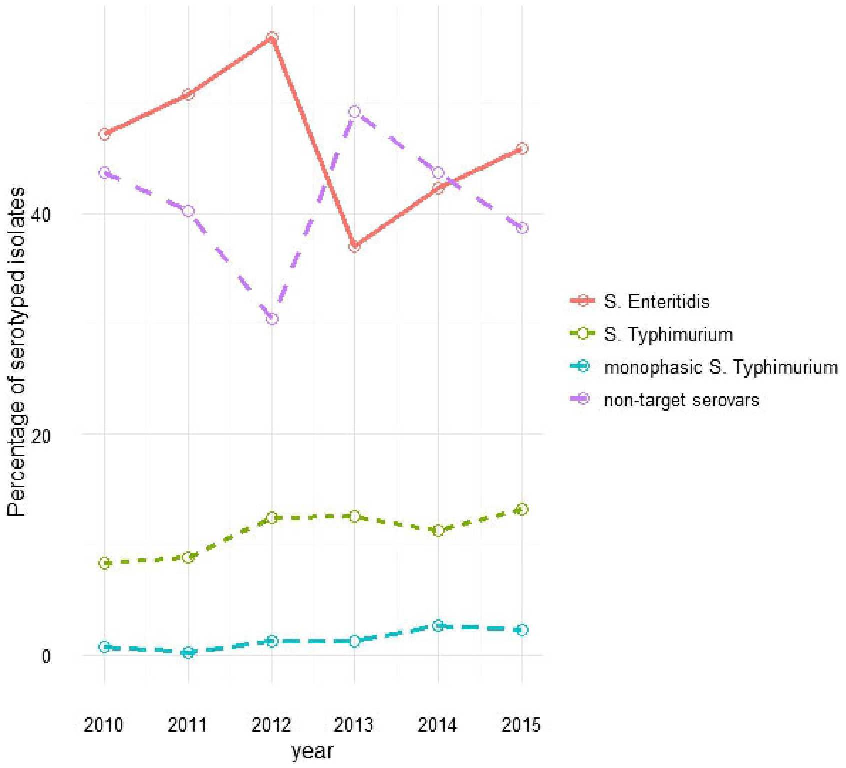
The other serovars were reported almost exclusively by a single country. *S*. Cerro was notified by Portugal (209 out of the 211 notified isolates). As in 2014, in 2015, *S*. 12,23:i:- (185 isolates) and *S*. Kedougou (127 isolates) were reported in significant numbers only by the United Kingdom. These two serovars, which seem to be related since *S*. 12,23:i:- has been described as a monophasic variant of *S.* Kedougou, are generally associated with feed sources.

In contrast to 2014, *S*. Kentucky, which is an important public health concern, because of its high levels of multidrug-resistance and in particular for its resistance to fluoroquinolones, did not feature among the 'top 10' serovars from *G. gallus* in 2015. This was the third most frequent serovar from laying hens (56 isolates) and it was reported almost exclusively from Italy (55 out of 56 isolates). However, it is not clear if this is the real picture since some isolates of non-regulated serovars may not have been fully serotyped in some MS and, therefore, not have been identified to serovar level in all cases.

Laying hens

Table 2015_SERLAY shows the distribution of the 10 most common *Salmonella* serovars in laying hen isolates by MS in 2015 in the context of national control programmes. A total of 721 isolates were reported from 23 MS, and *S.* Enteritidis and *S.* Typhimurium were the two most frequent reported serovars. *S*. Enteritidis accounted for 41.2% of the isolates from laying hens, but only 15.8% of the isolates from *G. gallus*, indicating that this serovar was more prevalent in laying hen flocks than in broilers or breeding chickens. A similar picture was found for *S*. Typhimurium, which accounted for 11.1% of the isolates from laying hens and 5.8% of the isolates from *G. gallus*, confirming that this relevant serovar was more frequently isolated from laying hens than from the other *G. gallus* production categories. The monophasic variant of *S*. Typhimurium was also among the 'top ten' serovars from laying hens, although it was reported exclusively by France (13 isolates).

The annual trend (percentage of isolates per serovar out of the total number of isolates serotyped each year) from laying hens between 2010 and 2015 is displayed in Figure 12.



All isolates reported by MS were included in this analysis.

Figure 12: *Salmonella* regulated and non-regulated serovars (percentage of isolates per serovar out of the total number of isolates serotyped each year) from laying hens, EU, 2010–2015

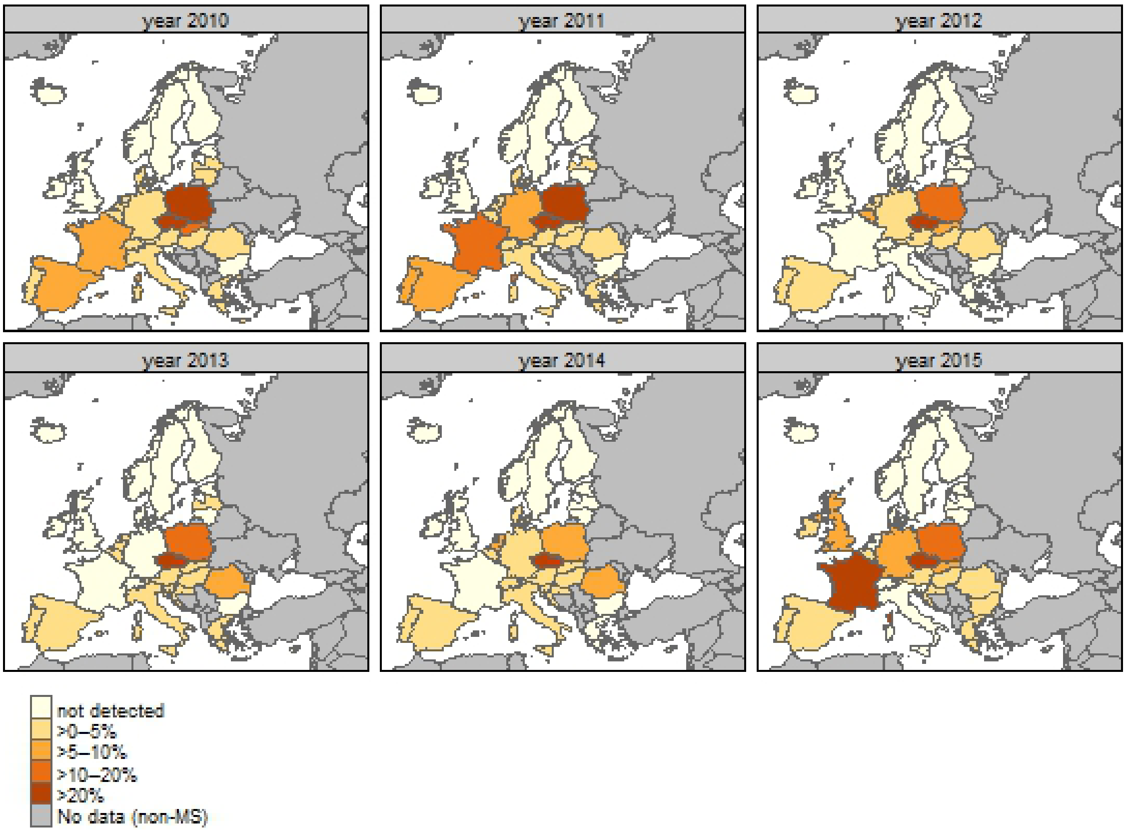
The annual percentage of *S*. Enteritidis, which was by far the most frequent serovar isolated from laying hens, has displayed remarkable fluctuations over the last 6 years. An increase in the percentage occurred from 2010 up to 2012, then in the next year there was a sharp decrease and again in the last 2 years (2014, 2015) the trend for this serovar increased to reach a percentage comparable to that which occurred in 2010. An opposite trend was seen for the non-regulated serovars, considered as a whole, with a decrease from 2010 to 2012, an increase in 2013 and again a decrease in the last 2 years. For *S*. Typhimurium, the annual percentage reported was fairly constant over the entire 6-year period, even though a slight increase was seem from 2010 to 2012 and from 2014 to 2015.

Broilers

Table 2015_SERBRO shows the distribution of the 10 most common *Salmonella* serovars in broiler flocks in 2015 in the context of national control programmes and reported from 23 MS.

The majority of *Salmonella* serotyped isolates from *G. gallus* originated from broiler chickens (4,668 out of the 5,535 isolates). The distribution of most of the 'top ten' serovars was fairly similar between *G. gallus* and broiler flocks. *S*. Infantis, *S*. Enteritidis and *S*. Mbandaka were also confirmed as the most frequent serovars from broilers, accounting for 38.7%, 11.6% and 7.2% of the isolates. *S*. Cerro, *S*. Kedougou, *S*. Infantis and *S*. Thompson were almost exclusively isolated from broilers, accounting for 99.5%, 97.6%, 97.3% and 95.3% of the isolates from *G. gallus*.

As has already been discussed for *G. gallus*, a substantial increase in the number of reports of *S*. Enteritidis and *S*. Typhimurium was also reported for broilers in 2015 compared to 2014, and this trend was strongly influenced by the reporting of just a few MS. In particular France, which was technically not able to report *Salmonella* isolates from broilers at all in 2014, reported 158 isolates of *S*. Enteritidis and 140 isolates of *S*. Typhimurium in 2015. As shown in Figure 13, displaying annual MS-specific percentages out of the total number of serotyped isolates over the last 6 years, a consistent increase in the percentage of *S*. Enteritidis isolates has been noted in several countries over the last few years. Poland and the Czech Republic continuously reported the highest percentages of *S*. Enteritidis isolates from broilers up to 2014, when France contributed with the great majority of *S*. Enteritidis isolates from this source.



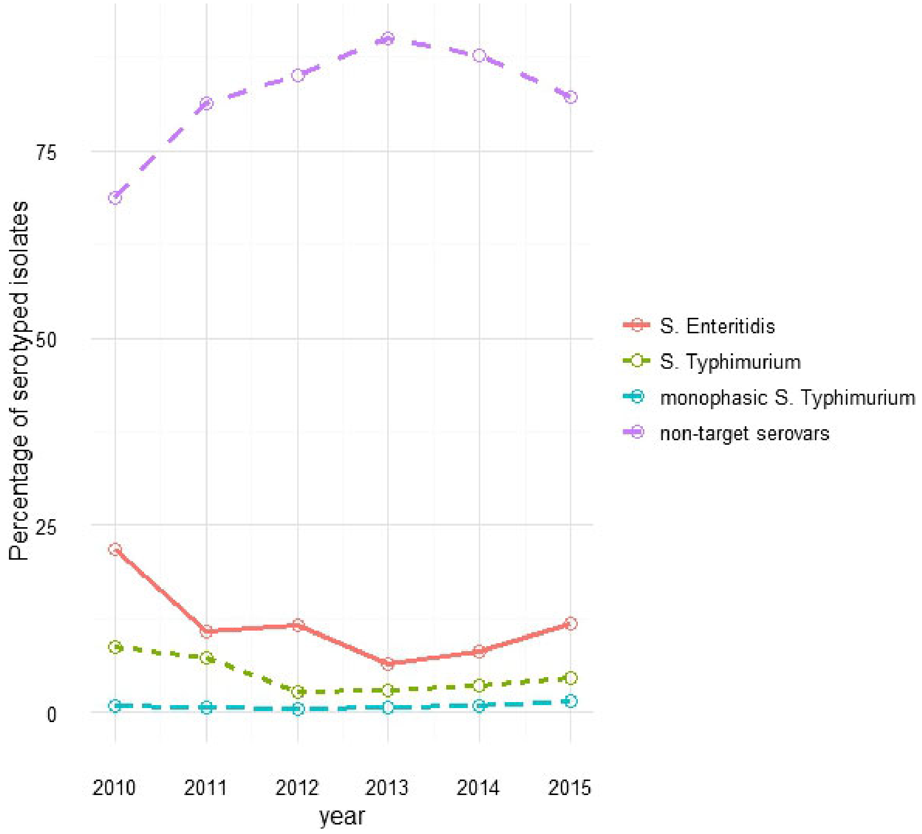
All isolates reported by MS were included in this analysis.

Figure 13: Distribution of *S*. Enteritidis (percentage out of the total number of serotyped isolates per year) reported from broilers, Europe, 2010–2015. Countries coloured in grey did not report *S*. Enteritidis isolates from broilers

For *S.* Infantis, a decrease of the number of isolates was reported in 2015 (1,809 isolates) compared to 2014 (2,011 isolates).

The annual trend (percentage of isolates per serovar out of the total number of isolates serotyped each year) from broilers between 2010 and 2015 is displayed in Figure 14.

A decrease in the annual percentage of *S.* Enteritidis occurred from 2010 up to 2013, but in the following 2 years, an opposite trend was observed and in 2015, this serovar accounted for 11.8% of serovars, with a percentage comparable to 2012. Similarly, for *S.* Typhimurium over the period 2010–2012, a decreasing trend was reported, whereas the percentage of this serovar remained substantially stable from 2012 onwards. For the monophasic variant of *S.* Typhimurium, the annual percentage was constant and negligible over the entire period.



All isolates reported by the MS were included in this analysis.

Figure 14: *Salmonella* regulated and non-regulated serovars (percentage of isolates per serovar out of the total number of isolates serotyped each year) from broilers, EU, 2010–2015

Broiler meat

Table 2015_SERBROMEAT shows the distribution of the 10 most common *Salmonella* serovars in broiler meat notified by MS reporting serovars data. This type of matrix is not sampled in the context of an EU harmonised programme and all isolates reported by MS (from all monitoring activities) were considered for the analysis.

Reporting, especially for some non-regulated serovars, seems to be inconsistent among MS over the years. This may be due to changes in reporting serovars and changes in serotyping priorities. Moreover, the current food safety criterion for fresh broiler meat, according to Regulation (EC) No 1086/2011, is the absence of *S.* Enteritidis and *S.* Typhimurium (including monophasic *S.* Typhimurium strains), hence, MS could serotype and report exclusively these serovars leading to an overestimation of regulated serovars and an underestimation of the reporting of all the other serovars not considered for the criterion. These limitations should be taken into account since they could hamper the consistency of the data reported over the years and the comparison among sources.

In 2015, 20 MS reported a total of 1,097 serotyped isolates from broiler meat. This was a decrease of 32.5% from 2014, when 1,626 serotyped isolates were reported.

The Czech Republic (245 isolates), Hungary (176 isolates), Romania (134 isolates) and the Netherlands (127 isolates) together accounted for 62.2% of all reported isolates.

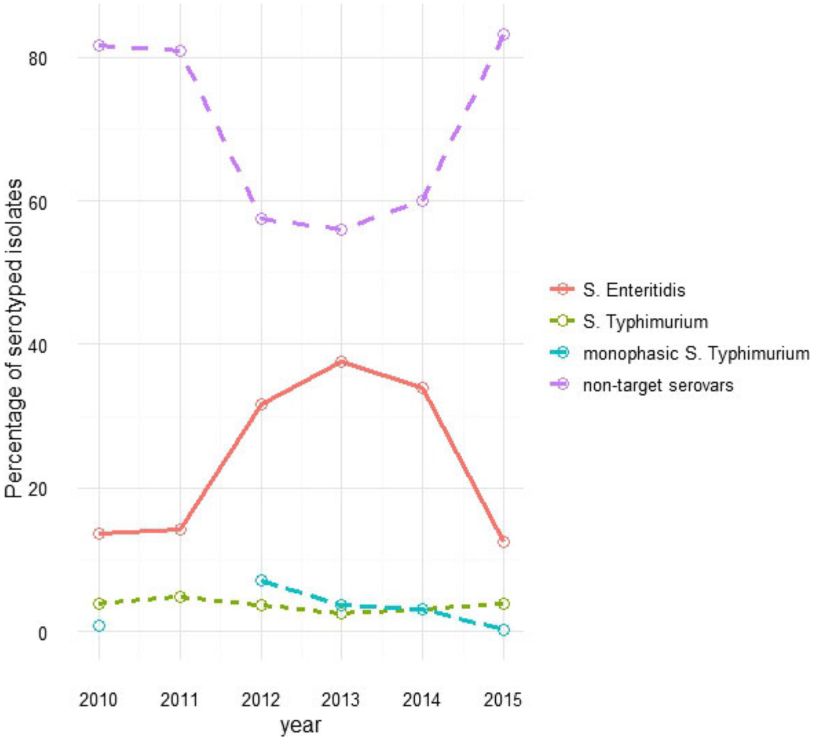
S. Infantis and *S*. Enteritidis were the two most common serovars isolated from broiler meat, accounting for 594 (54.1%) and 136 isolates (12.4%), respectively. This was in line with the serovars reported from *G. gallus* and broilers, where *S*. Infantis and *S*. Enteritidis were by far the most commonly reported serovars too. The third most common serovar from broiler meat was *S*. Ohio (54 isolates), which was notified almost exclusively from the Czech Republic (53 isolates); this serovar did not appear among the 'top ten' serovars for *G. gallus* and broiler flocks in 2015.

The number of *S*. Infantis from broiler meat was comparable to that reported in 2014 (594 in 2015 and 582 in 2014), and for this emergent serovar, although numbers fluctuate over the years, a sharp increase has been noted during recent years, from 217 isolates in 2012 to 594 isolates in 2015. Hungary, the Czech Republic and the Netherlands reported a negligible number of *S*. Infantis isolates from *G. gallus* in the framework of their national control programmes (2, 14 and 0 isolates, respectively), but notified a significant number of isolates of this serovar from broiler meat (162, 93 and 83, respectively). Romania reported a remarkable number of *S*. Infantis isolates both from *G. gallus* (682) and broiler meat (102). Italy, which reported the highest number of *S*. Infantis from *G. gallus* (719), did not report any *Salmonella* from broiler meat at all.

Compared to 2014, in 2015, a substantial decrease in the number of *S*. Enteritidis isolates was reported from broiler meat, reducing from 551 isolates in 2014, to 136 isolates in 2015. However, it should be noted that in 2014, the majority of *S*. Enteritidis isolates (412; 74.8%) originated from Poland and, in 2015, although Poland remained the country with the greatest number of *S*. Enteritidis isolates from broiler meat, it notified a considerably lower number of isolates than previously (50; 36.8%).

The third and the fourth most common serovars isolated from broiler meat, *S.* Ohio (54 isolates) and *S*. Indiana (46 isolates), were reported from two or three MS and for both serovars, the great majority of isolates was notified by the Czech Republic.

Nine MS reported a total of 43 *S*. Typhimurium isolates, with Poland (24 isolates) reporting the majority of these (55.8%), Greece, Latvia and Spain reporting four isolates each and another five MS reporting one or two isolates each.



All isolates reported by MS were included in this analysis.

Figure 15: *Salmonella* regulated and non-regulated serovars (percentage of isolates of regulated and non-regulated serovars out of the total number of isolates serotyped per year) from broiler meat, EU, 2010–2015

The annual trend (percentage of isolates per serovar out of the total number of isolates serotyped each year) from broiler meat between 2010 and 2015 is displayed in Figure 15.

For *S*. Enteritis, an increase in the annual percentage occurred from 2011 to 2013 and the next year it remained essentially stable, whereas in 2015, a drop in the percentage of *S.* Enteritidis was documented. An opposite trend was described for non-target serovars compared to that for *S*. Enteritidis. The percentage of non-target serovars markedly decreased from 2011 to 2012, then it remained reasonably stable up to 2014, but sharply increased in 2015. This trend for non-target serovars, opposite to the trend for *S*. Enteritidis, did not seem to be largely influenced by *S*. Infantis reports, since for this emergent poultry-related serovar, a constant increase was reported over the last 4 years. The annual percentage reports of *S.* Typhimurium remained constant over the entire period.

A 'population pyramid' was constructed to investigate any dissimilarities in the distribution of frequency of serovars from animals and foodstuffs. The percentages of the most frequently reported serovars from broiler flocks and broiler meat was reported in Figure 16. *S*. Infantis and *S*. Enteritidis, which were the two most frequent serovars from broiler chickens, were reported with comparable frequencies from broiler flocks and broiler meat, indicating that these serovars tend to persist along the broiler chain. Also, *S*. Livingstone, *S*. Mbandaka and *S*. Typhimurium were reported both from animals and food, although they were more frequent among animal rather than food isolates. Finally, *S.* Cerro was isolated exclusively from animals; however, this serovar was reported in broiler flocks exclusively by Portugal, which notified only five serotyped isolates from broiler meat.

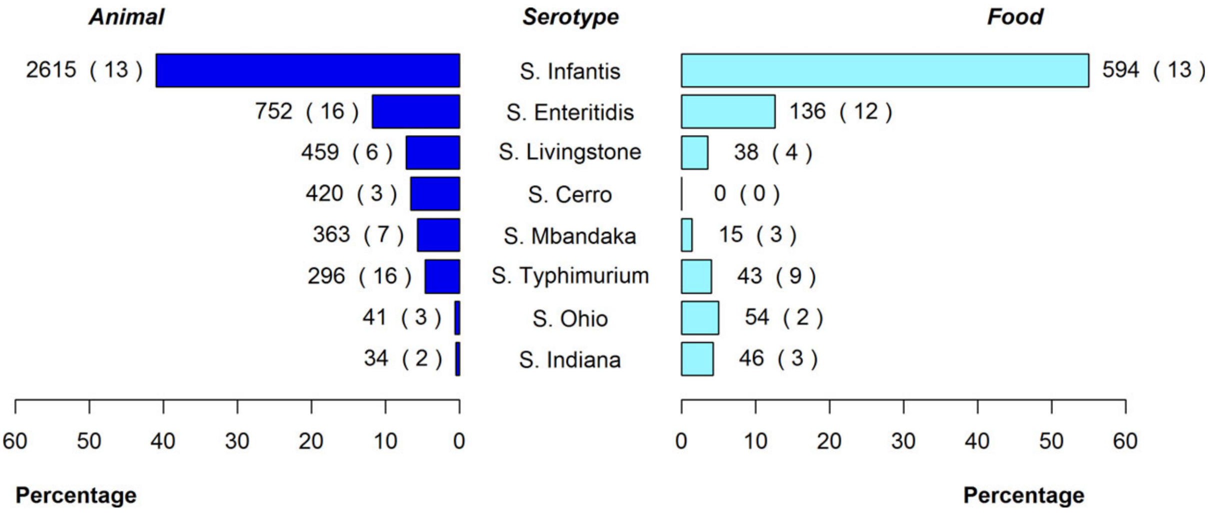


Figure 16: Pyramid plot showing the distribution of the most common *Salmonella* serovars between broilers and broiler meat, EU, 2015.The percentages are calculated on the total number of isolates for each category (animal and food). The values at the side of each bar represent the number of isolates for each serotype and the number of reporting MS is indicated in parenthesis.

Eggs

Table 2015_SEREGGS shows the distribution of the 10 most common *Salmonella* serovars in eggs in 2015. Five MS provided information on *Salmonella* serovars from eggs, with a total of 51 isolates being reported.

For this matrix, all isolates reported by MS from all monitoring activities were considered.

S. Enteritidis (21 isolates) followed by *S*. Typhimurium (8 isolates) and *S*. Rissen (8 isolates) were the most common serovars isolated from eggs. *S*. Rissen appeared in the 'top ten' list from this matrix, even though it has never been listed among the 'top ten' serovars from *G. gallus* during the last 6 years. *S*. Typhimurium was reported by Spain and Austria, *S*. Rissen exclusively by Spain, whereas *S*. Enteritidis occurred in four (Germany, Spain, Slovakia and Romania) out of the five MS who reported *Salmonella* from eggs. Five serovars (*S*. Enteritidis, *S*. Typhimurium, *S*. Infantis, *S*. Kentucky and *S*. Mbandaka) were listed among the 'top ten' serovars both from laying hens and eggs.

Turkeys

Table 2015_SERTURK shows the distribution of the 10 most common *Salmonella* serovars in turkeys in 2015. In this context, the serovars reported by MS in the framework of the national control programmes were considered.

Sixteen MS provided information on *Salmonella* serovars from turkey flocks, with a total of 629 isolates being reported. This was a marked increase (of 68.2%) compared to 2014, when 374 *Salmonella* isolates were reported from turkey flocks. This increase in the reporting was evident especially for France, which reported 4 isolates in 2014 and 76 in 2015, the United Kingdom (132 isolates in 2014 and 305 isolates in 2015) and Croatia (4 isolates in 2014 and 30 isolates in 2015).

As already mentioned, in 2014, serovars reported in high numbers from turkeys seem to cluster in one country only.

S. Derby, which was the most common serovar from turkey flocks, was reported exclusively by the United Kingdom (217 isolates). This serovar was reported by the United Kingdom from turkey flocks also in 2014, but in 2015, the number of notifications increased by more than five times.

With regard to the regulated serovars, *S*. Typhimurium, with 74 isolates serotyped (reported especially by France and Spain with 29 and 16 isolates, respectively), was the second most common serovar from turkey flocks, whereas *S*. Enteritidis with 40 isolates serotyped (33 in France) was the fifth most common of the 'top ten' from turkey flocks. For these serovars, the number of isolates reported in 2015 was almost three times that notified in 2014 and their increases were substantially influenced by the increased number of isolates reported by France. As already mentioned, this increase in the reporting of regulated serovars might have been strongly influenced by the variations in the reporting from MS among years rather than by a substantial evolution of the epidemiological situation.

The annual trend (percentage of isolates per serovar out of the total number of isolates serotyped each year) from turkey flocks between 2010 and 2015 is displayed in Figure 17.

Also, 20 isolates of the monophasic variant of *S*. Typhimurium were reported (11 in France, 7 in the United Kingdom and 2 in Spain) from turkey flocks.

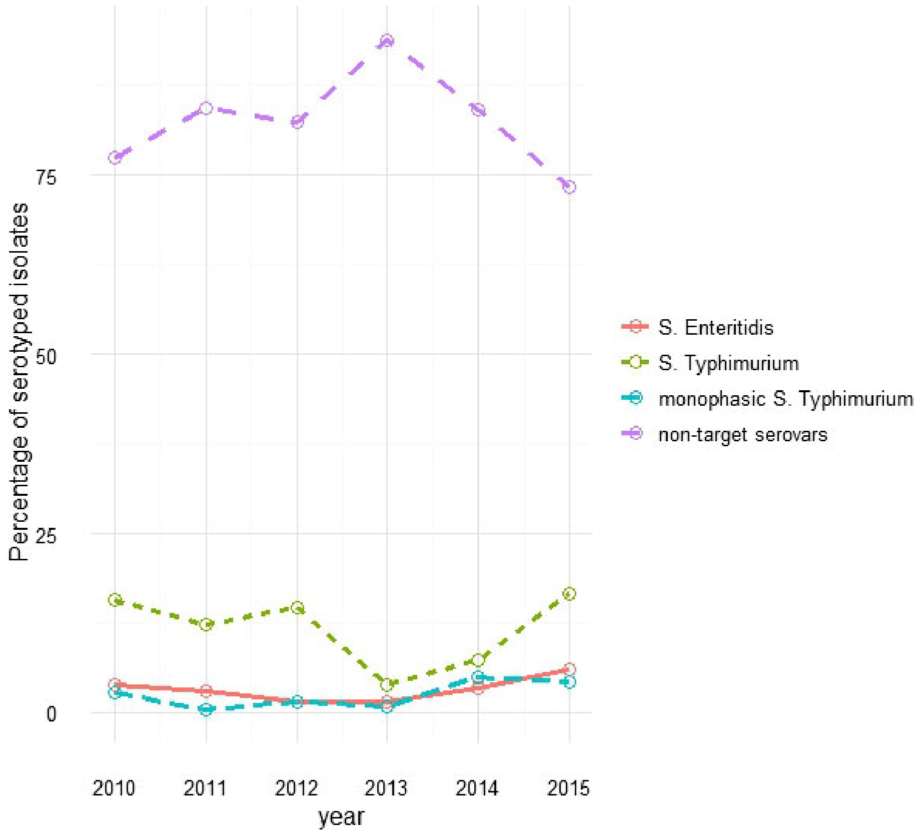
Another frequent serovar from turkeys was *S*. Newport (69 isolates), which was reported from three MS and Italy in particular notified the great majority of the isolates (62).

Similarly, only three MS reported *S*. Infantis (67 isolates) from turkey flocks and Italy also accounted for the majority of isolates (45).

As in 2014*, S*. Kedougou remained a frequent serovar from turkey flocks (36 isolates) in 2015, even though notifications were limited to the United Kingdom, where it was also found in high numbers from *G. gallus*. These data could suggest common sources of infections between chickens and turkeys in this country.

Twenty isolates of *S*. Senftenberg were reported from turkey flocks by four MS and the majority of the notifications were from the United Kingdom (14 isolates). This serovar has come to be more common in poultry production and it has also achieved a place among the 'top ten' for *G. gallus*, likely because it is often associated with hatcheries.

For *S*. Typhimurium, the annual percentage of reports remained essentially stable from 2010 to 2012, then in 2013 it decreased and, during the following 2 years, the percentage of *S*. Typhimurium isolates progressively increased to reach values comparable to those from 2010. These fluctuations were markedly correlated with the notifications from Germany, France and Spain, which reported the great majority of *S*. Typhimurium isolates from turkey flocks in this context. For *S*. Enteritidis and the monophasic variant of *S*. Typhimurium, the number of isolates was rather limited and the annual percentages reported have remained fairly constant, even though a limited increase *S*. Typhimurium was seen during the last 3 years.



All isolates reported by MS were included in this analysis.

Figure 17: *Salmonella* regulated and non-regulated serovars (percentage of isolates of each regulated and non-regulated serovars per year out of the total number of isolates serotyped per year) from turkey flocks, EU, 2010–2015

Turkey meat

Table 2015_SERTURKMEAT shows the distribution of the 10 most common *Salmonella* serovars in turkey meat in 2015. This type of matrix is not sampled in the context of an EU harmonised programme and all isolates provided (from all monitoring activities) by MS were considered for the analysis.

Eight MS reported a total of 87 serotyped isolates from turkey meat in 2015, and this represents a substantial decrease compared to 2014, when 10 reporting MS notified 162 serotyped isolates. Hungary (61 isolates) accounted for 70.1% of all isolates reported from this matrix in the last year. As already remarked in 2014, in 2015 too, the low number of isolates and the low number of reporting countries make it difficult to assess the true incidence of *Salmonella* serovars found in turkey meat across the EU.

S. Newport, *S*. Stanley and *S*. Bredeney with 15 isolates each were the most frequent serovars, followed by *S*. Infantis and *S*. Kentucky with 13 and 9 isolates, respectively. With regard to regulated serovars, five isolates of *S*. Enteritidis and two isolates of *S*. Typhimurium were reported; hence, the isolation of these serovars from turkey meat seem to be less frequent than from turkey flocks.

S. Stanley, after the outbreak related to the turkey production chain reported in 2011–2013 involving 10 MS and the additional turkey-related outbreaks reported later and in some cases caused by strains showing concerning antimicrobial resistances (Hugas and Beloeil, 2014; Springer et al., 2014), continues to be one of the most frequent serovars associated with this matrix.

S. Derby, which was the most frequent serovar from turkey flocks, did not achieve a place among the 'top ten' serovars from turkey meat in 2015. However, it should be noted that *S*. Derby from turkey flocks was reported exclusively by the United Kingdom, which did not report *Salmonella* serovars from turkey meat at all.

A ‘population pyramid’ was constructed to investigate any dissimilarities in the distribution of frequency of serovars from animals and foodstuffs. The percentages of the most frequently reported serovars from turkey flocks and turkey meat was reported in Figure 18. As already mentioned, the number of serotyped *Salmonella* isolates from turkey meat and the reporting MS for this matrix were rather limited, and hence, it is difficult to compare the frequencies of serovars from turkey flocks and turkey meat.

S. Derby and *S*. Typhimurium, the two most frequent serovars from turkey flocks, were reported with a low frequency from turkey meat. This finding could indicate that these serovars are not easily transmitted from animal populations to foodstuffs. However, to interpret these data it is important to note that the United Kingdom, which reported the total amount of *S.* Derby isolates from turkey flocks, and France, which reported the great majority of the *S*. Typhimurium isolates from turkey flocks, did not report serovar data from turkey meat at all. The frequency of reporting of *S*. Newport, *S*. Infantis and *S*. Enteritidis was comparable between turkey flocks and turkey meat. *S*. Stanley and *S.* Bredeney, the most frequently reported serovars from turkey meat, were rarely or never reported from animals. These isolates from turkey meat were reported by Hungary.

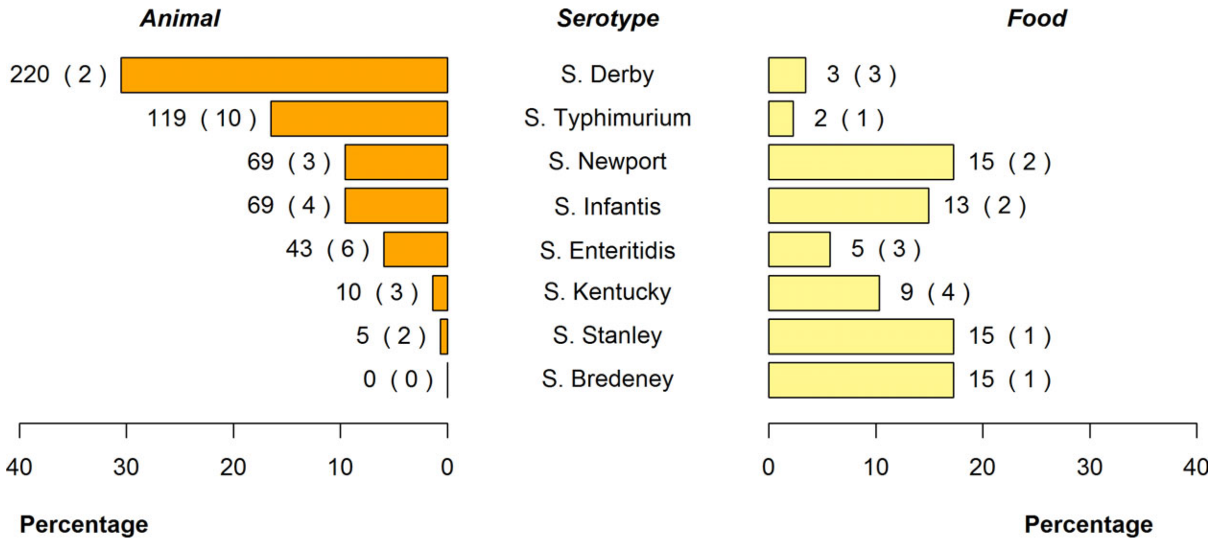


Figure 18: Pyramid plot showing the distribution of the most common *Salmonella* serovars between turkey and turkey meat, EU, 2015. The percentages are calculated on the total number of isolates for each category (animal and food). The values at the side of each bar represent the number of isolates for each serotype and the number of reporting MS is indicated in parenthesis

Serovars in pig production

Pigs

Table 2015_SERPIGS shows the distribution of the 10 most common serovars in pigs in 2015. Reports on *Salmonella* serovars in pigs tend to be less comprehensive compared to poultry, as there are no statutory requirements to regularly test pigs in primary production for the presence of *Salmonella.* Since there is not an EU harmonised programme for *Salmonella* in pigs, all isolates provided (from all monitoring activities) by MS were considered for analysis.

Twelve MS submitted reports on *Salmonella* in pigs for 2015, compared with 10 in 2014 and 16 each year in 2011–2013.

As has been the case since 2012, Germany continued to report the great majority of serotyped *Salmonella* isolates (73% in 2015), which leads to a substantial bias towards one MS. For the above mentioned reasons, it is difficult to analyse trends of serovars over time.

In total, 2,401 serotyped *Salmonella* isolates were reported from pigs in 2015, of which 56.9% were *S*. Typhimurium. Compared to 2014, when 2,037 serotyped isolates were reported from pigs, notifications increased by 15.2% in 2015.

As has occurred during previous years, *S*. Typhimurium continued to be the predominant serovar in pigs in 2015. It was found in all reporting MS in 2015, confirming its widespread diffusion in pig herds.

This serovar accounted for 87.5% of the isolates (7) reported in Finland, 70.7% of the isolates (53) in Ireland and 67.7% of the isolates in Germany (1186).

S. Derby was the second most common serovar, accounting for 329 isolates (13.7% of serotyped isolates), and was found in eight out of the twelve reporting MS. *S*. Derby has been reported as the second most frequent serovar from pigs for the last 3 years. Interestingly, *S*. Derby was the most common serovar isolated from pigs in Denmark (54.2% of serotyped isolates) and in Italy (47.2% of serotyped isolates).

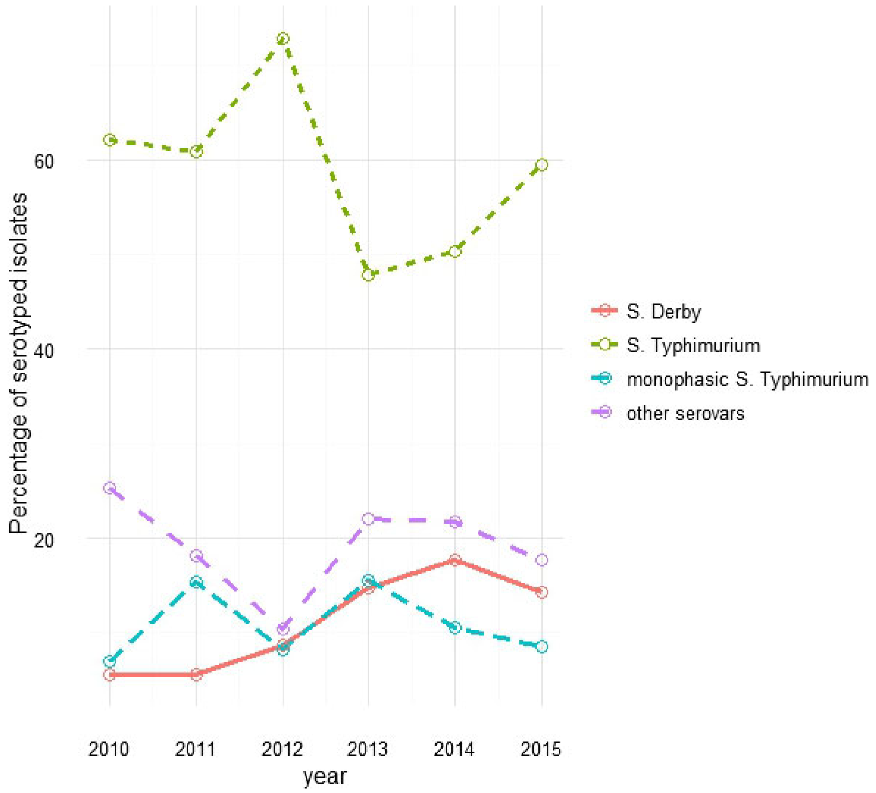
Isolates belonging to the group of monophasic strains of *S*. Typhimurium were reported with different designations (*S*.1,4,5,12:i:-, *S*.1,4,12:i:-, *S*. Typhimurium monophasic) in three MS (Italy, Spain and the United Kingdom) and accounted for 9.0% of serotyped isolates (8.4% of isolates in 2014 and 14.0% in 2013). In the three MS which reported the presence of these isolates, they accounted for a large proportion of pig isolates: 27.8%, 31.3% and 58.9% in Italy, Spain and the United Kingdom, respectively. The high level of molecular correlation between *S*. Typhimurium monophasic isolates from pigs at the slaughterhouse and human clinical cases was recently confirmed by a study conducted in Italy (Bonardi et al., 2016).

Other reported serovars, although below 5% at the EU level, were *S*. Goldcoast in Germany and Italy, *S*. Rissen in Denmark, Germany, Italy and Spain, *S*. Infantis in Denmark, Germany and Slovakia, and *S*. London in Germany, Italy, Spain and the United Kingdom.

S. Goldcoast has been associated with pigs and it was responsible for important outbreaks, likely associated with the pork production chain, in Hungary (Horvath et al., 2014) and Italy (Scavia et al., 2014) from 2009 to 2010. However, it has never been reported among the 'top ten' serovars from pigs to date, although in 2015 it accounted for 3.0% of serotyped isolates and was the fourth most common serovar from this source.

The annual trend (percentage of isolates per serovar out of the total number of isolates serotyped each year) from pigs between 2010 and 2015 is displayed in Figure 19.

For *S*. Typhimurium, which was by far the most common serovar from pigs, significant fluctuations occurred over the last 6 years, with the highest annual percentage reported in 2012 and the lowest in 2013. Also, the monophasic variants of *S*. Typhimurium did not display a clear trend, even though for this serovar a progressive decrease in the percentage of reports from pigs occurred during the last 3 years. For *S.* Derby, the other major pig-related serovar, a constant increase in the annual percentage reported occurred from 2011 to 2014, whereas during the last year, an opposite trend was seen.



All isolates reported by MS were included in this analysis.

Figure 19: Three most frequent *Salmonella* serovars (number of isolates of each serovar per year out of the total number of isolates serotyped per year) from pigs, EU, 2010–2015

Pig meat

Table 2015_SERPIGMEAT shows the distribution of the 10 most common *Salmonella* serovars in pig meat in 2015. Twenty-one MS submitted reports on *Salmonella* from pig meat, but the overall number of reports is lower compared to the number of isolates obtained from pigs. This may be due to the fact that it is not compulsory to serotype isolates that are obtained from carcase swabs taken to fulfil the requirements of the EU Process Hygiene and Microbiological Criteria testing programmes. For this type of matrix all isolates provided (from all monitoring activities) by MS were considered for analysis.

In 2015, a total of 803 serotyped *Salmonella* isolates were reported from 21 MS, whereas in 2014, 533 isolates were reported from 17 MS. In the last 5 years, the number of reports of serotyped *Salmonella* from pig meat ranged from 392 in 2011 to 803 in 2015.

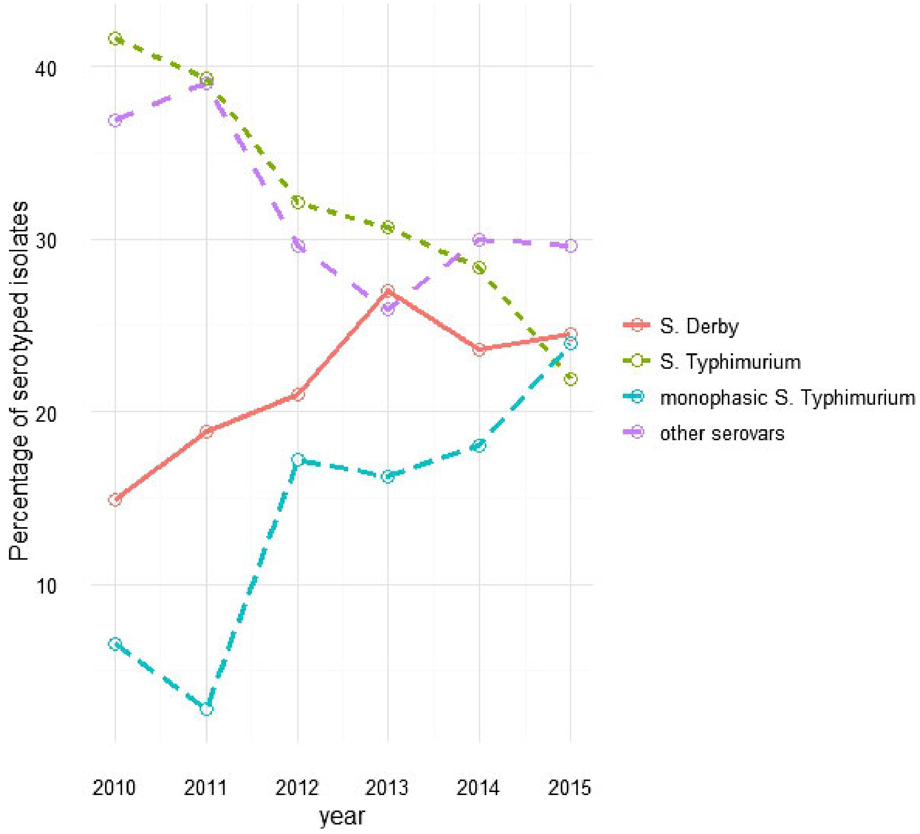
Spain reported the highest number of serotyped *Salmonella* isolates (169), followed by Denmark (95), Belgium (93), Romania (72) and Croatia (68). A consistent number of MS did not report serovar data in 2015 from pigs even though they notified serovars from pig meat. Germany, which reported by far the highest number of serotyped isolates from pigs, accounted for just 8.5% of serotyped *Salmonella* isolates from pig meat.

The percentage of *S*. Typhimurium isolates has decreased from 39.3% of serotyped isolates in 2011 to 27.8% in 2014 and 23.0% in 2015. This contrasts with the percentage of reported monophasic strains of *S*. Typhimurium, which has increased from 2.6% in 2011, to 18.0% in 2014 and 22.3% in 2015. *S*. Derby accounted for 18.8% of serotyped isolates in 2011, 27.0% in 2013, 24.4% in 2014 and 22.9% in 2015, showing a more stable pattern.

Across the EU, *S*. Derby was the most commonly reported serovar (22.9%) from pig meat in 2015, followed by monophasic strains of *S*. Typhimurium (22.3%) and *S*. Typhimurium (20.6%). In Italy, Portugal and the United Kingdom, monophasic strains of *S*. Typhimurium comprised more than 50% of *Salmonella* isolates in pig meat (52.4%, 57.7% and 55.6%, respectively). In Italy and Spain, these strains were very frequent among pig isolates as well, whereas Portugal did not report *Salmonella* serovars from pigs. *S*. Derby was the most common serovar isolated in Denmark both from pig meat (42.1%) and pig herds (54.2%).

The annual trend of the most frequent serovars (percentage of isolates per each serovar out of the total number of isolates serotyped) from pig meat between 2010 and 2015 is displayed in Figure 20.

Over the period 2010–2015, a progressive decrease of the annual percentage of *S*. Typhimurium isolates was reported. For the monophasic variants of *S*. Typhimurium an opposite trend occurred, since this serovar showed a marked increase in annual percentage reports from 2011 to 2012, then the annual percentage remained essentially stable for 3 years. In 2015, however, there was a new increase and the monophasic variants of *S.* Typhimurium overtook *S*. Typhimurium. The same trend was not seen in pigs, where *S*. Typhimurium was the most frequently reported serovar in 2015. Additionally, for *S*. Derby a constant increase in annual percentage occurred between 2010 and 2013, but in the following 2 years the percentage of isolates of this serovar remained reasonably constant.



All isolates reported by MS were included in this analysis.

Figure 20: The three most frequent *Salmonella* serovars (number of isolates of each serovar per year out of the total number of isolates serotyped per year) from pig meat, EU, 2010–2015

A 'population pyramid' was constructed to investigate any dissimilarities in the distribution of frequency of serovars from animals and foodstuffs. The percentages of the most frequently reported serovars from pigs and pig meat was reported in Figure 21.

S. Typhimurium, *S*. Derby and the monophasic variant of *S.* Typhimurium were the three most frequent serovars reported both from pigs and pig meat even though the actual order differed. The frequency of isolation of *S*. Typhimurium from pigs was close to 60%, whereas the frequency from pig meat was about 20%. For *S*. Derby and the monophasic variant of *S*. Typhimurium, the frequency of isolation was higher from foods (close to 30% for both serovars) than from animals (about 15% for *S*. Derby and 10% for monophasic variant of *S*. Typhimurium). *S*. Goldcoast, that was the fourth most common serovar reported in pigs and reported almost exclusively by Germany, was reported to be isolated only once in pig meat (Figure 21).

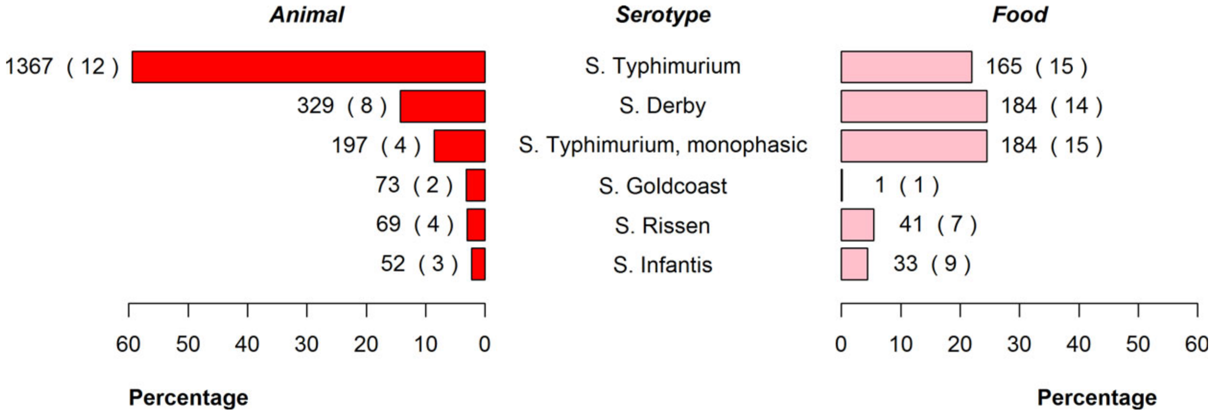


Figure 21: Population pyramid showing the distribution of the most common *Salmonella* serovars between pig and pig meat, EU, 2015. The percentages are calculated on the total number of isolates for each category (animal and food). The values at the side of each bar represent the number of isolates for each serotype and the number of reporting MS is indicated in parenthesis

Serovars in cattle production

Cattle

Table 2015_SERBOV shows the distribution of the 10 most common serovars in cattle in 2015, and considers all isolates provided (from all monitoring activities) by MS.

Thirteen MS submitted *Salmonella* serovar data from cattle, reporting information on a total of 3,243 isolates.

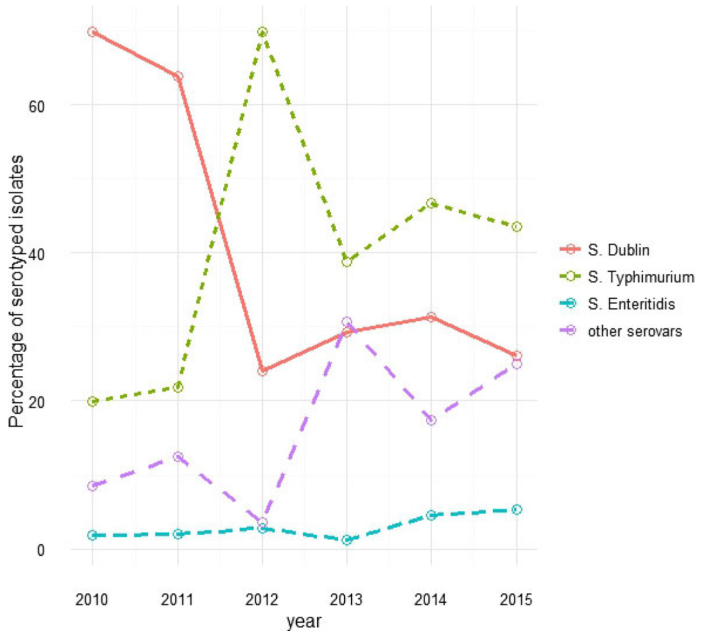
As in 2014, the vast majority of those isolates came from Germany (2,138; 65.9% of all serotyped cattle isolates) in 2015. The United Kingdom reported 446 isolates, followed by the Netherlands (318 isolates) and Ireland (235 isolates). Hence, the data reported refer mainly to the situation of only a few MS.

At the EU level, the most common serovar was *S*. Typhimurium (1,401 isolates; 43.2%), followed by *S*. Dublin (843 isolates, 26%). However, the proportion between these two serovars was very different in individual countries: in Germany and the Netherlands, *S*. Typhimurium accounted, respectively, for 51.2% and 76.4% of serotyped isolates from cattle, whereas in the United Kingdom and Ireland *S*. Dublin was by far the most commonly isolated serovar, accounting for 67.0% and 92.8% of all serotyped isolates, respectively. The third most common serovar in 2015 was *S*. Coeln (6.7%), while *S*. Enteritidis was the fourth (5.2%).

The trends of *Salmonella* serovars from cattle over the past 5 years are difficult to interpret, as the total number of notifications varies greatly between years and ranges from 1,150 in 2011 to 4,859 in 2013. The reasons for the fluctuations may be related to specific surveys carried out in some MS during 1 year which were not continued in the following years, but also due to the fact that there are no harmonised monitoring schemes for *Salmonella* in cattle at the EU level and there is not consistency among years in terms of reporting MS. Some MS did not submit any cattle data in some years, which may have an impact on the overall number of serovars as well as the proportions of serovars reported. The same consideration should be done also for all the other sources for which harmonised programmes have not been implemented at the EU level.

The annual trend of the most frequent serovars (percentage of isolates per serovar out of the total number of serotyped isolates) from cattle between 2010 and 2015 is displayed in Figure 22.

These data are markedly influenced by the reporting of two countries (Germany and the Netherlands), which have notified the great majority of isolates from this source since 2012. *S.* Dublin, which was the most common serovar from cattle in 2010 to 2012, showed a progressive decrease in the annual percentage reported up to 2012 and then notifications remained fairly stable. For *S*. Typhimurium, the other major serovar from cattle, an increase in the annual percentage occurred from 2010 to 2012, but thereafter, no clear trend was evident as notifications fluctuated over the years. *S*. Enteritidis was rather stable over the years even though a slight increase was reported during the last 3 years (2013–2015).



All isolates reported by MS were included in this analysis.

Figure 22: The most frequent *Salmonella* serovars (percentage of isolates of each serovar out of the total number of isolates serotyped per year) from cattle, EU, 2010–2015

Bovine meat

Table 2015_SERBOVMEAT shows the distribution of the 10 most common serovars in bovine meat in 2015. The data discussed took into account all isolates provided (from all monitoring activities) by MS.

Although thirteen MS submitted data relating to *Salmonella* serovars from bovine meat, the total number of isolates was only 75, of which 22 were reported from the Czech Republic, 15 from Spain and 11 from Croatia. These low numbers make it difficult to assess the data in depth or to compare them to previous years.

Considering the MS that reported the vast majority of serotyped *Salmonella* isolates from cattle, Germany and the United Kingdom reported few isolates from bovine meat, whereas the Netherlands and Ireland did not report isolates from this matrix at all.

S. Typhimurium was the most prevalent serovar in bovine meat (21.3% of all serotyped isolates) as well as in cattle, but other serovars were isolated from bovine meat but were not reported in cattle, such as *S*. Derby (10.7%), and *S*. Stanleyville (5.3%). *S*. Enteritidis accounted for 2.7% of serotyped *Salmonella* isolates from bovine meat in 2015, showing a remarkable decrease compared to previous years (20.7% in 2013 and 17.8% in 2014).

The number of isolates reported from bovine meat was also very limited, and hence, it is quite hard to draw conclusions about the frequency of serovars along the bovine chain. In cattle, *S.* Typhimurium was the most frequently reported serovar, and was confirmed as the predominant serovar from bovine meat as well. Conversely, for *S*. Dublin the frequency of isolation was remarkable from cattle and negligible from bovine meat. *S*. Coeln and *S*. Newport were reported from cattle exclusively by Germany and for these serovars, no isolates were reported from bovine meat. *S*. Derby, the third most frequent serovar from bovine meat, was only rarely reported from cattle and *S*. Stanleyville was completely absent from cattle (Figure 23).

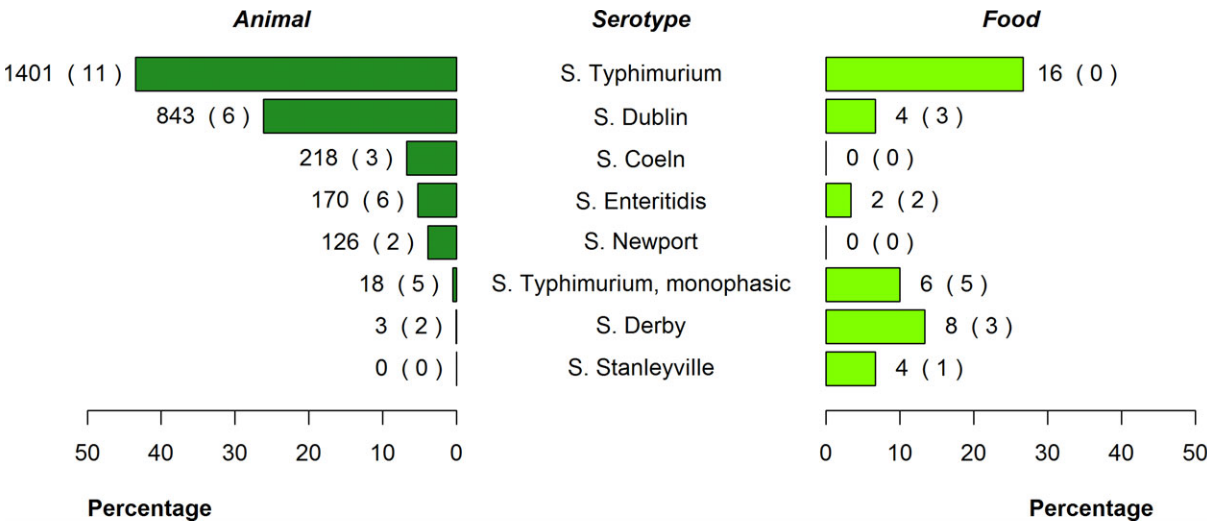


Figure 23: population pyramid showing the distribution of the most common *Salmonella* serovars between cattle and bovine meat, EU, 2015. The percentages are calculated on the total number of isolates for each category (animal and food). The values at the side of each bar represent the number of isolates for each serotype and the number of reporting MS is indicated in parenthesis

3.1.3. Discussion

3.1.3.1. Human

Salmonellosis remains the second most common zoonosis in humans in the EU despite a significant decreasing 8-year trend in salmonellosis cases since 2008. In 2014 and 2015 there was a small increase in the number of reported cases and the EU notification rate, partly attributable to increased and comprehensive reporting to the ECDC (Croatia, Italy) as well as improvements in the surveillance of salmonellosis (France, Spain). Two of these countries (France and Spain) had significant increasing trends since 2008.

The decrease of salmonellosis has been mainly attributed to *S*. Enteritidis, but the cases of *S*. Enteritidis seemed to have stabilised in recent years. *S.* Typhimurium continued to decrease in 2015. Together, *S*. Enteritidis and *S.* Typhimurium accounted for about 70% of human cases as in previous years. *S.* Infantis cases have decreased steadily since 2013, albeit still being the fourth most commonly reported serovar. An outbreak of *S*. Stanley, which started in 2011 and peaked in 2012, affected several MS and was linked to the turkey meat production chain. The number of cases associated with this outbreak strain increased again in Austria in 2015, and five other MS also reported the same strain suggesting a continued circulation of the strain in the food chain (ECDC and EFSA, 2014a; ECDC, 2015).

Salmonellosis notification rates for human infections vary between MS, reflecting variations in, for example, quality, coverage and severity focus of the surveillance systems, practices in sampling and testing, disease prevalence in the production animal population, food and animal trade between MS, and the proportion of travel-associated cases. The variation in national surveillance systems is reflected for example by the fact that countries reporting the lowest notification rate for salmonellosis had the highest proportions of hospitalisation, suggesting that the surveillance systems in these countries are focusing on the most severe cases.

3.1.3.2. Foodstuffs

Generally, there were no major changes as regards *Salmonella*-contaminated foodstuffs as compared to the previous year. The highest occurrence of non-compliant samples was found in foods of meat origin which are intended to be cooked before consumption with a potential for consumer infection linked to cross contamination or improper preparation. Among these foods, 'minced meat and meat preparations from poultry' had a notable level of non-compliance (6.8% of single samples and 5.1% of batches), with values similar to the previous year. As regards foods of meat origin intended to be eaten raw, in the product category minced meat and meat preparations, all sampling units were compliant in 2015. In meat products intended to be eaten raw there were only a few non-compliant findings (0.2% for single samples and 0.6% for batch samples). Despite the low levels, the presence of *Salmonella* in these foods is of particular relevance because of the absence of applied mitigation strategies, such as cooking, before consumption.

Considering the RTE products, which clearly pose the highest risk for consumers, the non-compliances were less frequent than in previous years and in particular for meat products intended to be consumed raw, a decrease was observed compared to previous years. Also, for some other RTE categories such as cheeses, butter and cream, cooked crustaceans and molluscan shellfishes and RTE precut fruits and vegetables, some non-compliances were reported, although with very low frequencies. Ice-cream continued to be the most commonly sampled of the RTE matrices, and, as confirmed in the previous years, *Salmonella* was almost always not detected in this food.

Regulation (EC) No 2073/2005 specifies that *Salmonella* has to be absent in minced meat and meat preparations made from poultry meat. However, for fresh poultry meat, according to Regulation (EC) No 1086/2011, the food safety criterion considers exclusively *S*. Enteritidis and *S*. Typhimurium. In 2015, for these two serovars, the number of non-compliant fresh poultry meat samples was limited (0.4% of single samples and 0.8% of batches were non-compliant), even though a slight increase in the number of non-compliant samples was reported compared to the previous year, when the number of samples collected for this matrix was six times higher. The percentage of non-compliant samples among minced meat and meat preparations from poultry to be cooked (6.8% of single samples and 5.1% of batches) and among meat products from poultry to be cooked (2.1% of single samples and 0% of batches) were somewhat higher than among samples of fresh poultry meat. The low level of non-compliance for fresh poultry meat could be directly related to the positive effects of the application of control programmes at primary production level. In the following steps of the production chain this positive effect could become less evident, not only as a direct effect of further processing, but also because at these later steps, the regulation covers all *Salmonella* serovars.

With regard to the analyses of non-compliance with the EU *Salmonella* criteria, important fluctuations were noted from year to year. The analyses for such data should take into account different factors which could strongly influence the conclusions drawn. In particular, the number of units tested annually, the weight each individual MS represents in the EU scenario across all years, the fact that the reporting MS have varied over the years and the inclusion of data from *ad hoc* surveillance activities implemented by the different reporting MS in different matrices could lead to significant temporal variability in the frequency of non-compliance for the different matrices. The data originating from the reporting obligations of MS under the EU regulation on microbiological criteria (EC No 2073/2005) lack harmonisation, because, although the matrices sampled are harmonised and the sampling and analytical methods are harmonised to a certain extent, the sampling objectives, the place of sampling and the sampling frequency vary or are interpreted differently between MS and according to food types. As such, these data are not comparable across MS (Boelaert et al., 2016).

Related to occurrence monitoring activities, *Salmonella* was most frequently detected in broiler meat (6.5%) and turkey meat (4.6%), whereas a lower number of positive samples was found in pig meat (1.7%) and bovine meat (0.2%). *Salmonella* was rarely found in table eggs (0.9%, in single samples). Ready-to-eat (RTE) foods pose a direct risk to consumers and 1.1% and 0.7% of positive samples were found for RTE food from meat from broilers and pig meat, respectively, whereas one positive sample and no positive samples were found for RTE food from turkey and cattle meat. A notable *Salmonella* prevalence of 4.3% was described for dried seeds in 2015, mainly associated with samples collected during border inspection activities by two MS.

Related to the monitoring of *Salmonella* on pig carcasses, in 2015 an amendment of Regulation 854/2004[20] came into force. The amendment, Regulation (EU) No 218/2014, obliges MS to report separate monitoring data with the total number of samples taken and the number of *Salmonella*-positive samples (1) taken by the Competent Authority, (2) taken by the Food Business Operators and collected by the Competent Authority, and (3) of other national sampling plans in countries with special guarantees. This surveillance has been set up in order to reinforce Competent Authority's verification of the correct implementation by Food Business Operators of the process hygiene criterion for *Salmonella* on pig carcases as foreseen by Regulation (CE) No 2073/2005. The first year of implementation was 2015 and the results show that few MS did yet already comply with these new reporting requirements.

3.1.3.3. Animals

In 2015, the EU level prevalence of *Salmonella* target serovars-positive flocks was very low, as in 2014, for all animal categories covered by the implementation of National Control Programs: breeding flocks of *G. gallus*, laying hen flocks, broiler flocks, and breeding and fattening turkey flocks. Since the implementation of these programs since many years, a statistically significant declining trend in the EU level prevalence of *Salmonella* target serovars-positive flocks was observed for all categories with the exception of breeding turkey flocks. The EU level prevalence of Salmonella target serovars-positive flocks in breeding flocks of *G. gallus* was very low (0.34%) with Bulgaria and Poland not meeting the target (< 1%) for the five target serovars (*S*. Enteritidis, *S*. Typhimurium, *S*. Infantis, *S*. Virchow and *S*. Hadar). In the case of flocks of laying hens, the EU level prevalence of Salmonella target serovar-positive flocks was 1.0% with only Poland not meeting the reduction target for the two serovars (*S*. Enteritidis, *S*. Typhimurium). Still, compared to 2014, the 2015 EU prevalence of *S*. Enteritidis-positive flocks increased in laying hens and also slightly in broilers. The Polish breeding flocks of *G. gallus* and laying hen flocks found positive to target serovars, were mostly positive to *S*. Enteritidis. In broilers, the *Salmonella* target serovars-positive flock prevalence was 0.3% and Czech Republic and Luxembourg did not meet the target of 1% or less of broiler flocks positive for these two target serovars. As regards turkeys, the overall Salmonella target serovars-positive flock prevalence for breeding and fattening flocks was 0.4% and 0.3%, respectively. All the MS met the target for breeding turkeys, whereas Belgium and Greece did not meet the target of 1% for fattening turkeys.

Data about the other animal species should be interpreted with caution due to the absence of harmonised control programs. The overall herd prevalence in 2015 was 12.4% for pigs and 2.1% for cattle.

3.1.3.4. Serovars

With regard to the reported *Salmonella* serovars in chickens, an increase in the notifications of relevant serovars was seen in 2015 despite the ongoing reduction in prevalence of target serovars in the context of national control programmes. The most important change seen in the last year was the increase in reports of *S*. Enteritidis, but also, to a more limited extent, of *S*. Typhimurium, compared to the previous year. This situation was confirmed both in broilers and turkeys. However, this increase was attributed to relatively few MS. In particular in 2014, French prevalence data were not included neither for broilers nor for turkeys, whereas in 2015, this MS contributed with a substantial number of flocks tested as well as with the reporting of *Salmonella* serovars. Hence, the increase of notifications of the target *Salmonella* serovars which occurred in the last year, and which is not consistent with the constantly decreasing EU level prevalence of target *Salmonella* serovars in poultry, might have been strongly influenced by the variations in the reporting from MS over the years rather than by a substantial evolution of the epidemiological situation. Considering the human side, for both these relevant serovar a decrease in the number of isolates from human salmonellosis was evidenced and the decrease (14.5%) was substantial for *S.* Typhimurium.

S. Infantis has been confirmed in 2015 as the highest ranked serovar isolated from *G. gallus*. With regard to human isolates, *S*. Infantis was confirmed as the fourth most commonly isolated serovar from human salmonellosis cases, confirming data of previous years. In 2015, this serovar accounted for 1,585 confirmed cases of human salmonellosis (2.3%) with a slight reduction compared to previous years (1,841, 2.5% in 2014 and 2,225 3.0% in 2013). A high level of concern still remains for the public health relevance of this serovar related to the high level of multidrug-resistance, including to critical antimicrobials, displayed by some clones of this serovar. According to the last summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food (EFSA and ECDC 2016), *S*. Infantis contributed significantly to the overall numbers of multidrug-resistant *Salmonella* in Europe and especially in Italy, isolates from broilers displayed resistance to third generation cephalosporins and high resistance to ciprofloxacin (Franco et al., 2015). As confirmed during recent years, this emergent serovar seems to be spreading throughout the poultry chain and currently it is one of the most frequent serovars in broilers flocks and broiler meat, but also in turkey flocks and turkey meat. The increasing frequency of isolation of *S.* Infantis from different sources confirms the remarkable adaptation of this serovar to various environmental niches, a condition that has trigged its epidemiological success.

S. Enteritidis was the second most frequent serovar isolated from *G. gallus* in 2015. A substantial increase (of about 35%) of *S*. Enteritidis isolates, occurred in 2015 (875 isolates) compared to 2014 (641 isolates) and it was attributed to a limited number of MS. As mentioned before, the 2015 EU prevalence of *S.* Enteritidis-positive flocks increased in laying hens and also slightly in broilers as compared to 2014. Analysis of the serovar data reported over the last years, confirmed that the increase of *S*. Enteritidis from *G. gallus*, might have been strongly influenced by the variations in the serovars reporting from MS among years rather than by a real evolution of the epidemiological situation. This hypothesis was supported also by human data. In 2015 *S*. Enteritidis was confirmed as the first serovars responsible for human salmonellosis (31,829 isolates representing 45.7% of the serotyped isolates from human salmonellosis), but compared to the previous year, when 32,874 isolates were reported, there was a slight decrease (3.2%) of the isolates of this serovar. However, different multistate outbreaks of *S.* Enteritidis, related to the consumption of eggs and egg products (ECDC and EFSA, 2014b; Inns et al., 2015, 2016) as well as several outbreaks related to broiler flocks (Lawes et al., 2016), have been documented during the last few years. Hence, it is pivotal not to underestimate the potential risk posed by this relevant serovar. Premature relaxation of effective control measures as vaccination should be avoided. The high level of measures implemented to control *Salmonella* should be maintained also because it has been demonstrated that the sensitivity of the sampling programme carried out using current harmonised monitoring programmes could be affected by several factors, such as the difficulties in obtaining representative sampling, particularly in large colony cage houses, deficiencies in laboratory testing standards (EFSA, 2014b) and the farming system (e.g. cage and non-cage flocks) that has a clear effect on the sensitivity of the sampling strategy for a given within- flock prevalence (Arnold et al., 2014).

S. Mbandaka, was another serovar commonly isolated from *G. gallus* (6.7% of the isolates) and it was reported in large numbers especially from the United Kingdom (72.9% of the isolates were from UK). This serovar, which has gained epidemiological importance in several EU countries, is associated with animal feed sources. Based on recent studies, the reasons for its epidemiological success might be related to its ability to produce biofilm, its pathogenicity and also the ability to persist and grow in the external environment (Hayward et al., 2016). A recent study conducted in Poland comparing *S*. Mbandaka isolates of human and poultry origin demonstrated that animals and food act as primal human infection routes for this serovar (Hoszowski et al., 2016). Looking at human data, *S*. Mbandaka was not among the ‘top 20 serovars’, hence its diffusion is limited to some MS.

With regard to turkeys, serovars reported in high numbers from turkey flocks seem to cluster in one country only. *S.* Derby, for instance, was the first serovar from turkey flocks and it was reported exclusively by the United Kingdom. It is notable that in the United Kingdom two distinct lineages of *S*. Derby, which differ genotypically and phenotypically, coexist and these two lineages are adapted to pigs and turkeys, respectively (Hayward et al., 2016). According to the data reported by MS, it can be speculated that the swine lineage is likely widespread across several MS, whereas the turkey lineage has remained confined to the United Kingdom. Considering the serovars reported from turkey meat, as already remarked in 2014, in 2015 too, the low number of isolates and the low number of reporting countries make it difficult to assess the true incidence of *Salmonella* serovars found in turkey meat across the EU. *S*. Stanley, which has been responsible for multicountry outbreaks in the past, was one of the most frequent serovars associated with this source and it was the fifth most reported serovar causing human salmonellosis (763 isolates). Another prominent serovar causing human infection was *S*. Newport (725 isolates), which was also among the most common serovars from turkey meat.

An increase has occurred in the number of *Salmonella* reports from pigs, where *S*. Typhimurium has been confirmed as by far the most common serovar, followed by *S*. Derby and monophasic variants of *S*. Typhimurium. Notably, looking at the temporal trend of *S*. Typhimurium in pig meat, a decreasing number of isolates was reported during previous years, whereas for the monophasic variants, the number of isolates reported has constantly increased. In 2015, the prevalence of *S*. Derby and *S*. Typhimurium from pigs was similar. A high level of resistance to antimicrobials and heavy metals for the different clones of monophasic strains of *S*. Typhimurium was documented by several MS. This evidence combined with the epidemiological success of this serovar, especially along the swine chain, indicate the validity of remarkable concerns related to this emerging serovar (Petroska et al., 2016). With regard to the human isolates, the monophasic variant of *S*. Typhimurium, with 5,770 isolates from human salmonellosis remained substantially stable compared to 2014 (5,773 isolates), whereas compared to 2013 there was a decrease (8.6%) of human isolates belonging to this serovar. Over the last years a progressive reduction of the number of isolates was reported also for *S*. Derby (648 isolates in 2013 and 818 in 2015). Another serovar associated with the pig chain is *S*. Rissen and it accounted for 25.6% of serotyped pig isolates in Spain. A recent study demonstrated the high frequency of resistance and multidrug-resistance among *S*. Rissen isolates obtained from different sources and mainly from pigs (Garcia-Fierro et al., 2016). Moreover, the authors described a successful clone of *S*. Rissen that is circulating among humans, pigs and other sources in the Iberian Peninsula and in other countries (Garcia-Fierro et al., 2016).

Looking at the distribution of the most common serovars among animal and food source, for *S*. Derby and the monophasic variant of *S*. Typhimurium, the frequency of isolation was higher from pig and pork (close to 30% for both serovars) than from pigs (about 15% for *S*. Derby and 10% for monophasic variant of *S*. Typhimurium). These data suggest that some pig-adapted serovars could have developed adaptive mechanisms which favour their survival *ex vivo*, including when the environment is less favourable for their growth, as happens in many foods. The same analysis was done also for the most common serovars isolated along the turkey chain and in this case the behaviour of *S*. Derby described for pig sources is different from that found for turkey sources, where the frequency of *S*. Derby was also about 15% in animals but was negligible in food. However, it is important to note that the absence of *S*. Derby from turkey meat could be due to the fact the United Kingdom, which reported almost all *S*. Derby from turkey flocks, did not report serovars from turkey meat at all. Another hypothesis to explain the different behaviour of this serovar in the two animal species, is that different clones of the same serovar have colonised different niches, as recently confirmed for a selection of *S*. Derby isolates from pigs and turkey flocks in the United Kingdom (Hayward et al., 2016).

Data about *Salmonella* serovars from cattle are not clear, since the reporting is inconsistent over the years. However, *S.* Dublin and *S.* Typhimurium were confirmed as the predominant serovars from cattle in 2015, although their prevalence has fluctuated significantly over the years.

3.2. *Campylobacter*

The Appendix A lists all summaries made for the production of this section, for humans, food and animals, including *Campylobacter* summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.2.1. Campylobacteriosis in humans

For 2015, campylobacteriosis data were reported by 27 MS, for the first time also including Portugal. The number of confirmed cases of human campylobacteriosis in the EU in 2015 was 229,213 which represents a decrease of 7,605 cases (3.2%) compared with 2014 (Table 10). The EU notification rate was 65.5 per 100,000 population in 2015, a decrease by 5.8% compared with 2014 (69.5 per 100,000 population), but at a similar level as in 2012–2013.

The highest country-specific notification rates in 2015 were observed in the Czech Republic (198.9 cases per 100,000), Slovakia (128.2), Sweden (94.2) and the United Kingdom (92.2). The lowest rates were reported in Bulgaria, Cyprus, Latvia, Poland, Portugal and Romania (≤ 3.7 per 100,000) in 2015. In Spain, improved coverage of the surveillance system for campylobacteriosis in 2015 resulted in an increase of confirmed cases by 15.3%.

In several MS, campylobacteriosis was mainly a domestically acquired infection with ≥ 90% of cases reported as domestic. The highest proportions of travel-associated cases (≥ 40%) were reported in Finland and Sweden as well as in Iceland and Norway. Among the 16,529 travel-associated cases, Spain, Turkey and Thailand were most often stated as the probable country of infection (21.3%, 8.8% and 7.6%, respectively).

Table 10: Reported human cases of campylobacteriosis and notification rates per 100,000 in the EU/EEA, by country and year, 2011–2015

Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	6,259	6,258	73.0	6,514	76.6	5,731	67.8	4,710	56.0	5,129	61.0
Belgium(b)	N	A	6,096	6,096	–	8,098	–	8,148	–	6,607	–	7,716	–
Bulgaria	Y	A	227	227	3.2	144	2.0	124	1.7	97	1.3	73	1.0
Croatia	Y	A	1,393	1,393	33.0	1,647	38.8	0	0.0	0	0.0	–	–
Cyprus	Y	C	29	29	3.4	40	4.7	56	6.5	68	7.9	62	7.4
Czech Republic	Y	C	21,102	20,960	198.9	20,750	197.4	18,267	173.7	18,287	174.1	18,743	178.7
Denmark	Y	C	4,327	4,327	76.5	3,773	67.0	3,772	67.3	3,720	66.7	4,060	73.0
Estonia	Y	C	364	318	24.2	285	21.7	382	28.9	268	20.2	214	16.1
Finland	Y	C	4,588	4,588	83.8	4,889	89.7	4,066	74.9	4,251	78.7	4,267	79.4

Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
France(c)	N	C	6,074	6,074	45.7	5,958	45.2	5,198	39.6	5,079	38.9	5,538	42.6
Germany	Y	C	70,190	69,829	86.0	70,571	87.4	63,280	78.6	62,548	77.9	70,811	88.3
Greece(d)	–	–	–	–	–	–	–	–	–	–	–	–	–
Hungary	Y	C	8,366	8,342	84.6	8,444	85.5	7,247	73.5	6,367	64.4	6,121	62.4
Ireland	Y	C	2,454	2,453	53.0	2,593	56.3	2,288	49.8	2,391	52.2	2,433	53.2
Italy(b)	N	C	1,014	1,014	–	1,252	–	1,178	–	774	–	468	–
Latvia	Y	C	77	74	3.7	37	1.8	9	0.4	8	0.4	7	0.3
Lithuania	Y	C	1,186	1,186	40.6	1,184	40.2	1,139	38.3	917	30.5	1,124	36.8
Luxembourg	Y	C	254	254	45.1	873	158.8	675	125.7	581	110.7	704	137.5
Malta	Y	C	249	248	57.8	288	67.7	246	58.4	220	52.7	220	53.0
Netherlands(e)	N	C	3,778	3,778	43.0	4,159	47.5	3,702	42.4	4,248	48.8	4,408	50.9
Poland	Y	C	653	653	1.7	650	1.7	552	1.4	431	1.1	354	0.9
Portugal	Y	C	273	271	2.6	–	–	–	–	–	–	–	–
Romania	Y	C	311	311	1.6	256	1.3	218	1.1	92	0.5	149	0.7
Slovakia	Y	C	7,040	6,949	128.2	6,744	124.5	5,845	108.0	5,704	105.5	4,565	84.7
Slovenia	Y	C	1,328	1,328	64.4	1,184	57.4	1,027	49.9	983	47.8	998	48.7
Spain(f)	N	C	13,227	13,227	63.3	11,481	54.9	7,064	50.4	5,548	47.4	5,469	46.9
Sweden	Y	C	9,180	9,180	94.2	8,288	85.9	8,114	84.9	7,901	83.3	8,214	87.2
United Kingdom	Y	C	59,846	59,846	92.2	66,716	103.7	66,382	103.9	72,500	114.2	72,139	114.5
EU Total	–	–	**229,885**	**229,213**	65.5	**236,818**	**69.5**	**214,710**	**64.3**	**214,300**	**65.4**	**223,986**	**69.2**
Iceland	Y	C	119	119	36.2	142	43.6	101	31.4	60	18.8	123	38.6
Norway	Y	C	2,318	2,318	44.9	3,386	66.3	3,291	65.2	2,933	58.8	3,005	61.1
Switzerland(g)	Y	C	7,055	7,055	85.3	7,565	92.9	7,481	93.1	8,432	106.0	7,963	101.2

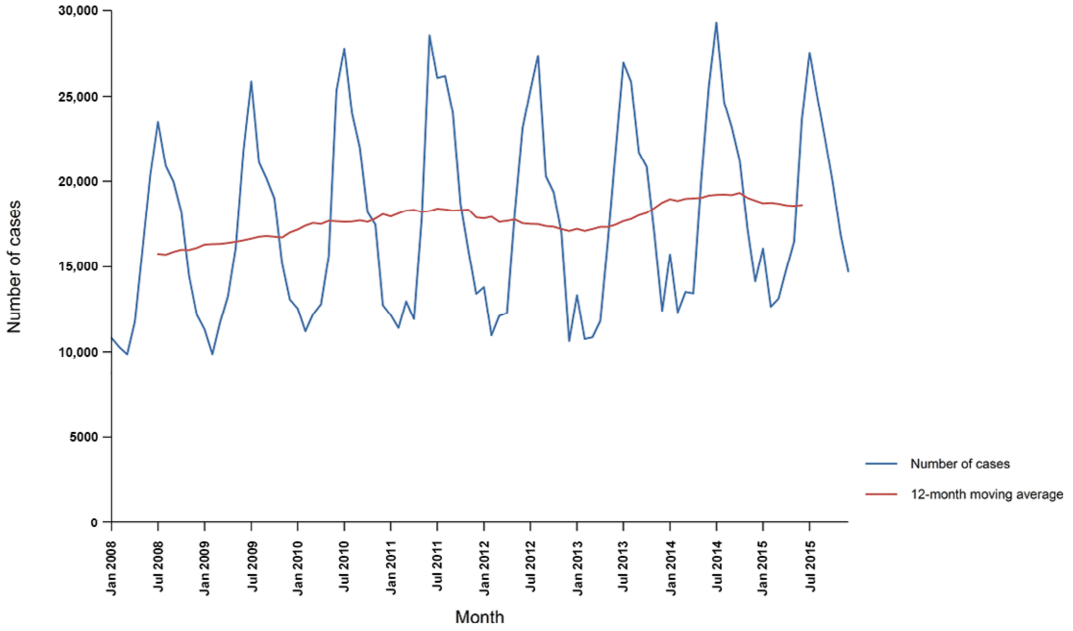
(a): Y: yes; N: no; A: aggregated data; C: case-based data; –: no report.
(b): Sentinel surveillance; no information on estimated coverage. Thus, notification rate cannot be estimated.
(c): Sentinel surveillance; notification rates calculated with estimated coverage of 20%.
(d): No surveillance system.
(e): Sentinel surveillance; notification rates calculated with estimated coverage 52%.
(f): Sentinel system; notification rates calculated with estimated population coverage of 45% in 2014–2015, 30% in 2013 and 25% in 2009–2012.
(g): Switzerland provided data directly to EFSA. The human data for Switzerland also include the ones from Liechtenstein.

Between 2008 and 2015, there was a clear seasonal variation of confirmed campylobacteriosis cases reported in the EU/EEA with sharp peaks in the summer months. Small annual winter peaks were also observed in January starting from 2011. Over the eight-year period, a statistically significant increasing trend was observed in the EU/EEA ($p < 0.05$) (Figure 24). At the country-level, 13 MS (Austria, Estonia, France, Hungary, Ireland, Italy, Latvia, Lithuania, Malta, Poland, Slovakia, Slovenia and Spain) reported significantly increasing trends between 2008 and 2015 while none of the MS observed a decreasing trend.

Seventeen MS provided information on hospitalisation, for 27.0% of all campylobacteriosis cases in 2015. Of cases with known hospitalisation status, 31.2% were hospitalised. The highest hospitalisation rates (72.4–94.2%) were reported in Cyprus, Latvia, Lithuania, Poland, Romania and the United Kingdom.

Outcome was reported for 73.7% of all cases. The number of reported deaths attributed to campylobacteriosis increased from 25 deaths in 2014 to 59 deaths in 2015 resulting in an EU case fatality of 0.03%. This was similar to the average percentage of fatal outcome observed over the last 5 years.

Campylobacter species information was provided for 45.3% of confirmed cases reported in the EU, which was less than in 2014 (52.6%). Of these, 81.0% were *C. jejuni*, 8.4% *C. coli*, 0.2% *C. fetus*, 0.1% *C. lari*, and 0.09% *C. upsaliensis*. 'Other' *Campylobacter* species accounted for 10.3%, but the large majority of those cases were reported at the national level as '*C. jejuni*/*C. coli*/*C. lari* not differentiated'.



Source: Austria, Cyprus, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Slovakia, Slovenia, Spain, Sweden and the United Kingdom. Belgium, Bulgaria, Croatia, Portugal and Romania did not report data to the level of detail required for the analysis. In Greece, campylobacteriosis is not under surveillance.

Figure 24: Trend in reported confirmed human cases of campylobacteriosis in the EU/EEA, by month, 2008–2015

3.2.2. *Campylobacter* in food and animals

At present there is no harmonised surveillance of *Campylobacter* in the EU and, when interpreting the data on *Campylobacter* in foods and animals, it is important to note that there is variation in the countries reporting *Campylobacter* monitoring data each year, and that data from different investigations are not necessarily directly comparable owing to differences in sampling strategies and testing methods. In addition, the proportion of positive samples observed could have been influenced by the sampling season because, in most countries, *Campylobacter* infections are known to be more prevalent in poultry during the summer than during the winter (EFSA, 2010). Therefore, these monitoring data do not allow trend analysis at the EU level.

Only results for the most important food products and animals that might serve as a source for human infection in the EU are presented.

3.2.2.1. Food

Fewer countries reported 2015 data on *Campylobacter* in food with generally lower sample sizes compared to 2014; 21 MS and one non-MS reported in 2015, compared to 26 MS and three non-MS in 2014. The number of samples tested within each food category ranged from one to several hundreds. Most of the MS reported data on food of animal origin, where the majority of tested units were from broiler meat.

Broiler meat and products thereof

Monitoring programmes and other activities for *Campylobacter* in fresh broiler meat are based on sampling at the slaughterhouse (caeca, neck skin, skin or meat samples), at processing or cutting plants and at retail, where meat samples are usually collected.

Broiler meat is considered the most important single source of human campylobacteriosis. In 2015, the overall occurrence of *Campylobacter* in fresh broiler meat, reported by 14 MS, sampled at slaughter, processing and retail was 46.7% of the 6,707 tested units (single or batch, aggregated data from all sampling stages) (Table 11). For reasons stated above, the proportion of positive samples reported in 2015 was not comparable to that in 2014, when 38.4% of samples were found to be positive (n = 6,703, 18 MS). The proportion of *Campylobacter*-positive samples of broiler meat varied greatly between reporting MS. With regard to single samples, *Campylobacter* was detected in 58.9%

of samples collected at retail and in 37.7% of the single samples at slaughterhouse level. Overall, 46.1% of the tested single samples were *Campylobacter* positive.

Two MS had tested 169 single samples of RTE broiler products, of which 13.0% tested positive. The positive samples originated from a German investigation at retail. No batches were found positive out of 33 tested (Table 2015_CAMPBROILPROD).

Table 11: *Campylobacter* in fresh broiler meat, 2015

Sampling stage	Country	Matrix	Description	Sample origin	Sampling unit	Sample weight	Tested	Positive	Per cent positive
Retail	Austria	Fresh	Food sample, Surveillance	Austria	Single	25 g	67	38	56.7
				European Union	Single	25 g	20	13	65
				Unknown	Single	25 g	4	2	50
	Hungary	Fresh	Food sample – meat, Monitoring		Single	25 g	228	72	31.6
	Italy	Fresh	Food sample, Surveillance	Italy	Single	25 g	1	0	0
	Netherlands	Fresh, chilled	Surveillance		Single	25 g	597	206	34.5
	Slovakia	Fresh	Food sample, Surveillance	European Union	Single	10 g	7	0	0
	Slovenia	Fresh, chilled	Food sample, Monitoring		Batch	25 g	30	20	66.7
	Spain	Fresh	Monitoring		Single	25 g	8	4	50
			Food sample – meat, Surveillance	Spain	Single	25 g	60	14	23.3
			Food sample, Monitoring		Single	100 g	5	4	80
			Food sample, Surveillance	Spain	Single	150 g	100	59	59
	United Kingdom	Fresh, chilled	Food sample – meat, Monitoring		Single	25 g	2,525	1,721	68.2
Slaughter batch							0	0	0
Batch							30	20	66.7
Single							3,622	2,133	58.9
Total Retail							3,652	2,153	59.0
Processing plant	Austria	Fresh	Food sample, Surveillance	Austria	Single	25 g	28	20	71.4
				European Union	Single	25 g	1	1	100
	Hungary	Fresh	Food sample – meat, Monitoring		Single	25 g	198	72	36.4
	Italy	Fresh	Food sample, Surveillance	Italy	Single	25 g	6	0	0
			Food sample, Survey	Italy	Single	25 g	4	0	0
	Portugal	Carcase	Food sample – meat, Surveillance	Portugal	Single	25 g	17	5	29.4
		Fresh	Food sample – meat, Surveillance	Portugal	Single	25 g	41	13	31.7
	Spain	Fresh	Monitoring		Single	25 g	2	1	50

Sampling stage	Country	Matrix	Description	Sample origin	Sampling unit	Sample weight	Tested	Positive	Per cent positive
Slaughter batch							0	0	0
Batch							0	0	0
Single							297	112	37.7
Total Processing plant							297	112	37.7
Slaughterhouse	Austria	Fresh	Food sample, Surveillance	Austria	Single	25 g	10	9	90
	Belgium	Carcase	Surveillance		Single	1 g	548	116	21.2
	Croatia	Carcase, chilled	Survey		Slaughter batch		974	489	50.2
	Denmark	Fresh, chilled	Food sample – meat, Monitoring	Denmark	Single	10 g	960	193	20.1
	Estonia	Carcase	Food sample – neck skin, Monitoring	Estonia	Batch	25 g	12	0	0
	Hungary	Carcase	Food sample – neck skin, Monitoring		Single	25 g	208	39	18.75
	Spain	Fresh, laying hens	Food sample, Monitoring	Spain	Batch	25 g	4	0	0.0
		Fresh, skinned	Food sample, Monitoring	Spain	Batch	25 g	38	20	52.6
Slaughter batch							974	489	50.2
Batch							54	20	37.0
Single							1,726	357	20.7
Total Slaughterhouse							2,754	866	31.5
Unspecified	Sweden	Fresh	Food sample, Surveillance		Single	25 g	4	0	0
Slaughter batch							0	0	0
Batch							0	0	0
Single							4	0	0
Total Unspecified							4	0	0
Slaughter batch							974	489	50.2
Batch							84	40	47.6
Single							5,649	2,602	46.1
EU Total							**6,707**	**3,131**	**46.7**

Other foods

Other foods of animal origin were also analysed for the presence of *Campylobacter*. Six MS reported data on fresh turkey meat (Table 2015_CAMPTURKMEAT) and 15.7% of the 293 tested units (single and batch) were found to be *Campylobacter*-positive.

The proportion of *Campylobacter*-positive single samples or batches of fresh pig or fresh bovine meat was generally low (3.4% positive sampling units) to very low (0.4% positive sampling units) (Tables 2015_CAMPBOVMEAT and 2015_CAMPPIGMEAT). *Campylobacter* was not detected in any of the 111 RTE pig or 21 RTE bovine meat products tested (Tables 2015_CAMPBOVPROD and 2015_CAMPPIGPROD).

Campylobacter was not detected in the tested units (single or batch) of raw cow's milk intended for direct human consumption or for manufacture of pasteurised/UHT products. In single samples of milk from other animal species or unspecified the proportion positive sampling units was low to very low, except for one Italian investigation at processing plant where 10 out of 18 samples (55.6%) were positive. The proportion of *Campylobacter*-positive units of milk from other animals or of unspecified origin was low to very low (Table 2015_CAMPMILK). No *Campylobacter*-positive samples were reported from the 423 tested cheese samples.

Detailed information on the data reported and on the occurrence of *Campylobacter* in the different food categories have been included in specific tables referenced in the Appendix A.

3.2.2.2. Animals

Fewer countries reported 2015 data on *Campylobacter* in animals compared to 2014; 15 MS and three non-MS reported in 2015, compared to 22 MS and three non-MS in 2014. Data reported were about broiler flocks, turkeys, pigs, cattle, goats, sheep, horses, cats, dogs and a range of wild animals.

Broilers

Only five MS reported 2015 monitoring data on *Campylobacter* in broilers. *Campylobacter* was found in 19.3% of the 10,063 units tested in MS with 28.4% of the tested broiler slaughter batches found positive and 15.3% of the tested flocks (Table 2015_CAMPBROILERS). This overall proportion of positive is lower than in 2014, when 30.7% of sample units were found to be positive. As stated before, since the reporting countries differ across years, data are not comparable. The largest investigations were carried out in the Nordic countries. Samples obtained in Denmark, Finland and Sweden constituted 88.6% of the reported samples in the EU and these MS reported a low to moderate prevalence. The two other reporting MS, the Czech Republic and the United Kingdom, reported extremely high prevalences.

Other animals

One MS and one non-MS reported data on *Campylobacter* in turkeys in 2015 (Table 2015_CAMPTURKEYS). The one MS, Germany, found 13% of the sampling units to be positive to *Campylobacter*. Five MS and one non-MS reported data for *Campylobacter* in pigs (animal and herd); overall 46.8% of the sampling units (941 out of the 2,010 tested) were positive, ranging from 0% to 73.1%. Six MS reported prevalence data for cattle; overall 6.8% (843 out of the 12,265 tested) of the sampling units were positive, ranging from 0% to 64.2% (animal and herd samples) (Table 2015_CAMPCATTLE).

Eight MS and two non-MS reported data on *Campylobacter* in cats and dogs. The proportion of *Campylobacter*-positive samples varied greatly between MS from 0 to 59.1 proportions of positives. (Table 2015_CAMPCATDOG).

A wide range of investigations of *Campylobacter* in other animals was reported by three MS (Germany, Italy and Spain). Italian data on a wide range of different animal populations accounted for 45.6% of 2,696 samples. Results can be found in Table 2015_CAMPOTHERAN.

Details on the data reported and on the occurrence of *Campylobacter* in the various animal species have been included in tables referenced in the Appendix A.

3.2.3. Discussion

Campylobacteriosis has been the most commonly reported zoonosis in humans in the EU since 2005. There was a statistically significant increasing trend in case numbers at the EU/EEA level and at country-level in half of the MS between 2008 and 2015. In the last 5 years, the EU notification rate, however has been quite stable. A serology-based study in the EU/EEA population showed that the reported number of human cases only represents a small proportion of all clinical *Campylobacter* infections (Gibbons et al., 2014). The increase in reported cases in some countries in the last few years may therefore not only reflect changes in exposure but also improvements in MS surveillance systems (Emborg et al., 2015).

Campylobacter has a characteristic seasonality with a sharp increase of cases in summer and early autumn. A smaller but distinct winter peak has become pronounced in the past few years. It was mainly caused by an increase of cases in five MS (Austria, Belgium, Germany, Luxembourg and the Netherlands) covering more than 45% of all cases reported in January. The observed winter peak in *Campylobacter* infections in Switzerland has been partly attributed to a traditional meal, meat fondue, especially if served with chicken meat (Bless et al., 2014). This meal is typically consumed also in several other countries at festive occasions in wintertime like Christmas and New Year.

The proportion of hospitalised campylobacteriosis cases was higher than expected in some MS, which also reported the lowest notification rates. In some countries, the surveillance is known to focus mainly on severe cases. In others, hospitalisation status is reported only for a fraction of cases. This fraction most likely represents cases ascertained and reported by hospitals, while for cases reported from other sources, e.g. laboratories, hospitalisation status is often missing. Both these factors result in an overestimation of the proportion of hospitalised cases.

Fewer countries reported 2015 monitoring data regarding investigations of *Campylobacter* in food and in animals, compared to the reporting year 2014.

Broiler meat is considered to be the main source of human campylobacteriosis and overall 46.7% of the tested fresh broiler meat units (single or batch) were *Campylobacter*-positive. The variation between MS was large. Also, some MS collect more samples during the high-prevalence summer period and thus do not report an overall annual prevalence. Thus, monitoring results are not comparable between reporting countries. Furthermore, the overall prevalence is not directly comparable between years, as not all MS report data every year and the number of samples reported by each MS varies, influencing the estimate differently. *Campylobacter* was not detected in the tested units (single or batch) of raw cow's milk intended for direct human consumption or manufacture of raw or minimal heat-treated products, except in one Italian investigation.

Monitoring data from animals were reported on broiler flocks, turkeys, pigs, cattle, goats, sheep, horses, cats, dogs and a range of wild animals. The overall proportions of units tested and found *Campylobacter*-positive was low in cattle, moderate in broilers and high in pigs. The high proportion of positives in pigs was not reflected in fresh pig meat.

The non-harmonised nature of the food and animal monitoring data collection does not allow confirmation of hypotheses explaining the increase observed in human case numbers at the EU/EEA level or at country-level in the 8-year period 2008–2015.

Differently from the previous years, in 2015 the most frequently food vehicle associated with strong-evidence *Campylobacter* outbreaks was raw milk (14 outbreaks), followed by broiler meat (6 outbreaks.

In 2014, an EU project (CamCon) that aimed to improve the control of *Campylobacter* in primary poultry production in Europe and thereby enable the production of 'low-risk broilers' was finalised. The project ran under the seventh framework with a consortium consisting of partners from six MS (Denmark, the Netherlands, Poland, Portugal, Spain and the United Kingdom) and one non-MS (Norway) representing different parts of Europe. The project results showed that biosecurity initiatives helped reducing the *Campylobacter* prevalence in Nordic countries and as well in countries in southern Europe. The project provided an E-learning programme (currently available in Danish, English, German and Spanish) and a Best Practice Manual for poultry producers which are freely available online.[27] Very recently, the United Kingdom Food Standards Agency welcomed signs of progress with the reduction of *Campylobacter* on fresh shop-bought chickens.[28] UK data showed 15% of chickens tested positive for the highest level of contamination (more than 1,000 colony-forming units per gram (CFU/g)), down from 22% in July to September 2014. In the United Kingdom, these most heavily contaminated birds are the focus of the current target agreed by industry, which is equivalent to no more than 7% of chickens at retail having the highest levels of contamination. Research has shown that reducing the proportion of birds in this category will have the biggest positive impact on public health.

3.3. *Listeria*

The Appendix A lists all summaries made for the production of this section, for humans, foods and animals, including *Listeria* summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.3.1. Listeriosis in humans

In 2015, 28 MS reported 2,206 confirmed human cases of listeriosis (Table 12). Portugal reported listeriosis for the first time in 2015. The EU notification rate was 0.46 cases per 100,000 population,

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[27] Available online: http://www.camcon-eu.net

[28] https://www.food.gov.uk/news-updates/news/2015/14701/campylobacter-survey

very similar to 2013 and 2014. The highest notification rates were observed in Spain, Malta, Sweden, Estonia and Finland: 0.99, 0.93, 0.90, 0.84 and 0.84 cases per 100,000 population, respectively. Spain improved the surveillance system for listeriosis in 2015, which resulted in an increase of reported confirmed cases by 36.5%. The lowest rates were reported by Bulgaria, Croatia, and Romania (< 0.1 per 100,000). Cyprus and Luxembourg reported zero cases.

The vast majority (> 98%) of listeriosis cases were reported to be domestically acquired.

Table 12: Reported human cases of listeriosis and notification rates per 100,000 in the EU/EEA, by country and year, 2011–2015

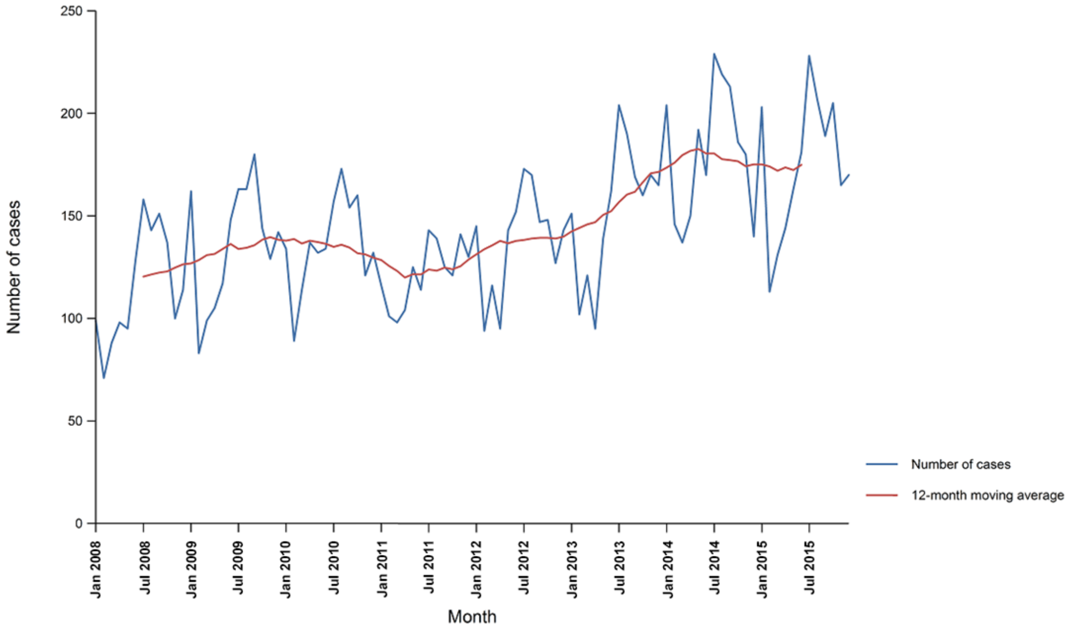
Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	38	38	0.44	49	0.58	36	0.43	36	0.43	26	0.31
Belgium	Y	A	83	83	0.74	84	0.75	66	0.59	83	0.75	70	–
Bulgaria	Y	A	5	5	0.07	10	0.14	3	0.04	10	0.14	4	0.05
Croatia	Y	A	2	2	0.05	4	0.09	0	0.00	0	0.00	–	–
Cyprus	Y	C	0	0	0.00	0	0.00	1	0.12	1	0.12	2	0.24
Czech Republic	Y	C	36	36	0.34	38	0.36	36	0.34	32	0.30	35	0.33
Denmark	Y	C	44	44	0.78	92	1.64	51	0.91	50	0.90	49	0.88
Estonia	Y	C	11	11	0.84	1	0.08	2	0.15	3	0.23	3	0.23
Finland	Y	C	46	46	0.84	65	1.19	61	1.12	61	1.13	43	0.80
France	Y	C	412	412	0.62	373	0.57	369	0.56	346	0.53	282	0.43
Germany	Y	C	662	580	0.71	598	0.74	463	0.57	414	0.52	331	0.41
Greece	Y	C	31	31	0.29	10	0.09	10	0.09	11	0.10	10	0.09
Hungary	Y	C	38	37	0.38	39	0.40	24	0.24	13	0.13	11	0.11
Ireland	Y	C	19	19	0.41	15	0.33	8	0.17	11	0.24	7	0.15
Italy	Y	C	153	153	0.25	132	0.22	143	0.24	112	0.19	129	0.22
Latvia	Y	C	8	8	0.40	3	0.15	5	0.25	6	0.29	7	0.34
Lithuania	Y	C	5	5	0.17	7	0.24	6	0.20	8	0.27	6	0.20
Luxembourg	Y	C	0	0	0.00	5	0.91	2	0.37	2	0.38	2	0.39
Malta	Y	C	4	4	0.93	1	0.24	1	0.24	1	0.24	2	0.48
Netherlands	Y	C	71	71	0.42	90	0.54	72	0.43	73	0.44	87	0.52
Poland	Y	C	70	70	0.18	87	0.23	58	0.15	54	0.14	62	0.16
Portugal	Y	C	28	28	0.27	–	–	–	–	–	–	–	–
Romania	Y	C	12	12	0.06	5	0.03	9	0.05	11	0.05	1	0.01
Slovakia	Y	C	18	18	0.33	29	0.54	16	0.30	11	0.20	31	0.57
Slovenia	Y	C	13	13	0.63	18	0.87	16	0.78	7	0.34	5	0.24
Spain(b)	N	C	207	206	0.99	161	0.77	140	1.00	109	0.93	91	0.78
Sweden	Y	C	88	88	0.90	125	1.30	93	0.97	72	0.76	56	0.59
United Kingdom	Y	C	187	186	0.29	201	0.31	192	0.30	183	0.29	164	0.26
EU Total	–	–	**2,291**	**2,206**	**0.46**	**2,242**	**0.47**	**1,883**	**0.45**	**1,720**	**0.42**	**1,516**	**0.36**
Iceland	Y	C	0	0	0.00	4	1.23	1	0.31	4	1.25	2	0.63
Norway	Y	C	18	18	0.35	29	0.57	21	0.42	30	0.60	21	0.43
Switzerland(c)	Y	C	54	54	0.65	98	1.20	64	0.80	39	0.49	47	0.60

(a): Y: yes; N: no; A: aggregated data; C: case-based data; –: no report.

(b): Sentinel system; notification rates calculated with an estimated population coverage of 45% in 2014–2015, 30% in 2013 and 25% in 2009–2012.

(c): Switzerland provided data directly to EFSA. The human data for Switzerland also include information from Liechtenstein.

In the period 2008–2015, a seasonal pattern was observed in the listeriosis cases reported in the EU/EEA, with large summer peaks followed by smaller winter peaks (Figure 25). Despite the significant increasing trend ($p < 0.01$) over this period, the number of cases stabilised in 2015. Twelve MS (France, Germany, Greece, Hungary, Malta, the Netherlands, Poland, Romania, Slovakia, Slovenia, Spain and Sweden) had increasing trends ($p < 0.01$) since 2008. None of the MS observed any decreasing trend between 2008 and 2015.



Source: Austria, Cyprus, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Malta, the Netherlands, Norway, Poland, Romania, Slovakia, Slovenia, Spain, Sweden and the United Kingdom. Belgium, Bulgaria, Croatia, Lithuania, Luxembourg and Portugal did not report data to the level of detail required for the analysis.

Figure 25: Trend in reported confirmed human cases of listeriosis in the EU/EEA, by month, 2008–2015

Eighteen MS, for the first time including Portugal, provided information on hospitalisation for all or the majority of their cases, an increase from 38.0% of all confirmed cases in 2014 to 44.9% in 2015. Among the cases with known hospitalisation, 97.4% were hospitalised. Listeriosis has the highest proportion of hospitalised cases of all zoonoses under the EU surveillance.

The outcome was reported for 1,524 confirmed cases (69.1%). Nineteen MS reported 270 deaths due to listeriosis in 2015, the highest number of annual deaths recorded since 2008 (annual average: 166). The overall EU case fatality among cases with a known outcome was 17.7%. France reported the highest number of fatal cases (75), followed by Germany (45).

Listeria infections were most commonly reported in the age group over 64 years. The proportion of cases in this age group has steadily increased from 56.2% in 2008 to 64.1% in 2015, and especially in the age group over 84 years with an increase from 7.3% to 12.8%. Case fatality in the age group over 64 years was 20.3% and in the age group over 84 years 26.7% in 2015. The proportion of fatal cases in those over 84 years of age increased from 7.5% in 2008 to 19.3% in 2015.

3.3.2. *Listeria* in food and animals

It is important to note that results from different countries are not directly comparable owing to the variation, among the reporting countries, in the sampling and testing methods used. Therefore, the totals in the summary tables might not be representative of the EU level, because results are highly influenced by the reporting MS and the sample sizes in their investigations, both of which vary among reporting years.

Only results for the most important food products and animals that might serve as a source for human infection in the EU are presented.

3.3.2.1. Food

In 2015, 27 MS and three non-MS (Iceland, Norway and Switzerland) reported data on investigations of *L. monocytogenes* in food. Malta did not report any data on *L. monocytogenes* in food.

The number of samples tested within each food category ranged from one to several thousand. The data presented in this section focus on RTE foods, in which *L. monocytogenes* was detected in either qualitative investigations (absence or presence, using detection methods) and/or quantitative investigations (counts of colony-forming units per gram (CFU/g) or per mL (CFU/mL) using enumeration methods).

Regulation (EC) No 2073/2005 lays down the food safety criteria for *L. monocytogenes* in RTE foods. This regulation came into force in January of 2006 and the criteria are described below. The data reported reflect the obligations of MS under this Regulation and the investigations have, therefore, focused on testing RTE foods for compliance with the legal microbiological criteria for food safety.

Microbiological criteria

A wide range of foodstuffs can be contaminated with *L. monocytogenes*. The limit for the EU food safety criterion for *L. monocytogenes* was set at 100 CFU/g for RTE products on the market.

The reported results of RTE food samples testing for *L. monocytogenes* were evaluated in accordance with the *L. monocytogenes* criteria indicated in the EU legislation applying certain assumptions, where appropriate.

Regulation (EC) No 2073/2005 covers primarily RTE food products and specifies the following food safety criteria for *L. monocytogenes*:

- For RTE foods intended for infants and RTE foods for special medical purposes placed on the market during their shelf life, absence of *L. monocytogenes* is required in 25 g of sample (n = 10, c = 0).[29]
- For RTE foods able to support the growth of *L. monocytogenes*, other than those intended for infants and for special medical purposes, absence of *L. monocytogenes* is required in 25 g of sample (n = 5, c = 0) before the food has left the immediate control of the food business operator, who has produced it. This criterion shall apply to products when the operator is not able to demonstrate, to the satisfaction of the competent authority, that the product will not exceed the limit of 100 CFU/g throughout the shelf life. For products placed on the market during their shelf life the limit is 100 CFU/g (n = 5, c = 0) if the manufacturer is able to demonstrate, to the satisfaction of the competent authority, that the product will not exceed the limit 100 CFU/g throughout the shelf life.
- For RTE foods unable to support the growth of *L. monocytogenes* (based on their pH and water activity values) and for products with a shelf life of less than five days, other than those intended for infants and for special medical purposes, the limit is 100 CFU/g (n = 5, c = 0) during their shelf life on the market.

The results from qualitative examinations using the detection method EN ISO 11290-1:1996 amended in 2004 (ISO, 1996b, 2004a) have been used to assess the compliance with the criterion of 'absence in 25 g of sample', and the results from quantitative analyses using the enumeration method EN ISO 11290-2:1998 amended in 2004 (ISO, 1998, 2004b) have been used to assess compliance with the criterion of '≤ 100 CFU/g'.

For many of the reported data, it was not evident whether the RTE food tested was able to support the growth of *L. monocytogenes* or not. For the non-compliance analysis of samples collected at processing, the criterion of absence in 25 g was applied, except for samples from hard cheeses and fermented sausages (assumed to be unable to support the growth of *L. monocytogenes*), where the limit ≤ 100 CFU/g was applied. For samples collected at retail, the limit ≤ 100 CFU/g was applied, except for RTE products intended for infants and for special medical purposes, where the presence of *L. monocytogenes* must not be detected in 25 g of sample.

According with the Regulation 2073/2005, *L. monocytogenes* food safety criteria are set for batch sampling (n = 5 or n = 10 units) and testing. In the present report, non-compliance of single samples (units) is also presented. The classification of single samples as non-compliant with the *L. monocytogenes* food safety criteria is based on the rationale that any sample (comprised of 5 or 10

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[29] n = number of units comprising the sample (number of sample units per food batch that are required for testing); c = the maximum allowable number of sample units yielding unsatisfactory test results. In a two-class attributes sampling plan defined by n = 10, c = 0 and a microbiological limit of 'absence in 25 g', in order for the food batch to be considered acceptable, *L. monocytogenes* must not be detected in qualitative (detection) analyses of 25 g food portions obtained from each one of 10 sample units from the batch.

units) containing even one unit with *L. monocytogenes* counts above the microbiological limit would have made the corresponding batch unsatisfactory (c = 0). Results from single samples are therefore considered informative for the analysis of non-compliance with the *L. monocytogenes* food safety criteria in RTE food categories.

For a detailed description of the assumptions, uncertainties and limitations of the data on *L. monocytogenes* in food, with a particular focus on the compliance data, refer to the section on Materials and Methods.

Non-compliance in ready-to-eat products

In total, 25 MS reported data which were included in the assessment of compliance with the EU food-safety criteria. The data submitted to EFSA by Denmark[30] and France were not included in the compliance assessment because the sampling was conducted entirely under a selective and a suspect sampling strategy, respectively. Non-compliance with the *L. monocytogenes* food safety criteria in RTE food categories in 2015 is presented in Table 13.

Table 13: Non-compliance with the *L. monocytogenes* food safety criteria laid down by Regulation (EC) No 2073/2005 in RTE food categories in the EU, 2015

Food category	Sampling stage	Sampling unit	Tested detection[(a)]	Detection (%)[(b)]	Tested enumeration[(c)]	> 100 CFU/g (%)[(d)]
Fishery products, RTE	Border inspection activities	Batch	58	3.45		
	Processing plant	Batch	455	2.86		
		Single	2,627	3.46		
	Retail	Batch			488	1.43
		Single			1,688	0.3
	Unspecified	Batch			32	0
		Single			110	0
Soft and semi-soft cheeses, RTE	Border inspection activities	Single	1	0		
	Processing plant	Batch	1,678	0.6		
		Single	4,790	1.32		
	Retail	Batch			489	1.02
		Single			1,039	0.19
	Unspecified	Single			21	0
Hard cheeses, RTE	Processing plant	Batch			2	0
		Single			220	0
	Retail	Batch			215	0
		Single			607	0
	Unspecified	Single			12	0
Unspecified cheeses	Processing plant	Batch	7	0		
		Single	4,264	0.38		
	Retail	Batch			3	0
		Single			383	0
	Unspecified	Single			3	0

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[30] Although not included in the tables, the information on positive findings in food from selected sampling reported by Denmark have been presented in the text within the specific sections on 'ready-to-eat fish and fishery products', 'pig meat' and 'other ready-to-eat products'.

Food category	Sampling stage	Sampling unit	Tested detection(a)	Detection (%)(b)	Tested enumeration(c)	> 100 CFU/g (%)(d)
Other Dairy products, RTE	Border inspection activities	Batch	1	0		
	Processing plant	Batch	4,338	2.7		
		Single	1,388	1.01		
	Retail	Batch			154	0
		Single			1,805	0
	Unspecified	Batch			13	0
		Single			79	0
Milk, RTE	Processing plant	Batch	981	6.12		
		Single	111	0		
	Retail	Batch			18	0
		Single			61	0
	Unspecified	Single			1	0
RTE products of meat origin other than fermented sausage	Border inspection activities	Batch	2	0		
	Processing plant	Batch	6,553	1.62		
		Single	5,853	2.07		
	Retail	Batch			864	0
		Single			2,766	0.04
	Unspecified	Batch			274	0
		Single			498	0.6
RTE products of meat origin, fermented sausage	Processing plant	Batch			4	0
		Single			311	0.64
	Retail	Batch			151	0
		Single			738	0.27
RTE food intended for infants and for medical purposes	Processing plant	Batch	13	0		
		Single	23	0		
	Retail	Batch	32	0		
		Single	386	0		
	Unspecified	Single	2	0		
Other RTE products	Border inspection activities	Batch	1	0		
	Processing plant	Batch	2,377	2.27		
		Single	2,397	1.79		
	Retail	Batch			4,152	0.07
		Single			12,126	0.07
	Unspecified	Batch			706	0
		Single			1,433	0.07

RTE: ready-to-eat.
(a): Number of units tested qualitatively (using the detection method) for the presence of *L. monocytogenes*.
(b): Percentage of units tested qualitatively (using the detection method) that was reported as positive for *L. monocytogenes*.
(c): Number of units tested quantitatively (using the enumeration method) for *L. monocytogenes*.
(d): Percentage of units tested quantitatively (using the enumeration method) that was reported to contain *L. monocytogenes* above 100 CFU/g.

For RTE products on the market, less than 0.3% of single samples and 0–1.4% of batches were found not to comply with the criterion of '≤ 100 CFU/g'. However, higher and varying (depending on food type) levels of non-compliance (primarily presence in 25 g) were reported in samples of RTE products at the processing stage, ranging from 0% to 3.5% in single samples and from 0% to 6.1% in batch samples.

Among samples of RTE fish and fishery products collected at the processing plant stage (15 MS), the level of non-compliance (3.5% of single samples and 2.9% of batches) was lower compared to previous years, particularly in batch samples, and mainly concerned smoked fish. However, RTE fish and fishery products remain the food category with the highest level of non-compliance at processing. Similar to 2014, most of the data on RTE fish and fishery products tested at processing were provided by Poland. At retail, the levels of non-compliance (0.3% of single samples and 1.4% of batches) were much lower than those observed at processing plants. More than half of the data on fish and fishery products tested at retail were provided from Belgium and Germany.

For soft and semi-soft cheeses, low levels of non-compliance were observed in investigations at processing (1.3% of single samples and 0.6% of batches). Sixteen MS provided data from processing and eight MS reported results not compliant with the food safety criterion ('absence in 25 g') in a few of their investigations. Non-compliance was primarily related to soft and semi-soft cheeses made from pasteurised milk and the majority of the non-compliant samples were reported from Poland. At retail, the levels of non-compliance were low (1.0%) in batches and very low (0.2%) in single samples, and the non-compliant products were reported from three out of the 16 MS reporting data.

Hard cheeses are assumed not to support the growth of *L. monocytogenes*. All tested units complied with the criterion of '≤ 100 CFU/g' both at processing and at retail.

Among samples of unspecified cheeses, very low levels of non-compliance were observed in single samples at processing (0.4%), whereas all batches sampled at processing and all samples obtained from retail were found to be compliant. Data were mainly reported by Italy.

All samples from other dairy products, excluding cheeses, tested at retail (14 MS) were found to be compliant. However, at processing a low number of samples (2.7% of batches and 1.0% of single units) was found not to be compliant. Most of the data (75.1%) on batch samples at processing were reported from Poland. In addition, all except one (116 out of the 117 detection-positive batches, 99.1%) of the non-compliant batch samples at processing were reported from Poland and concerned mainly butter and yogurt.

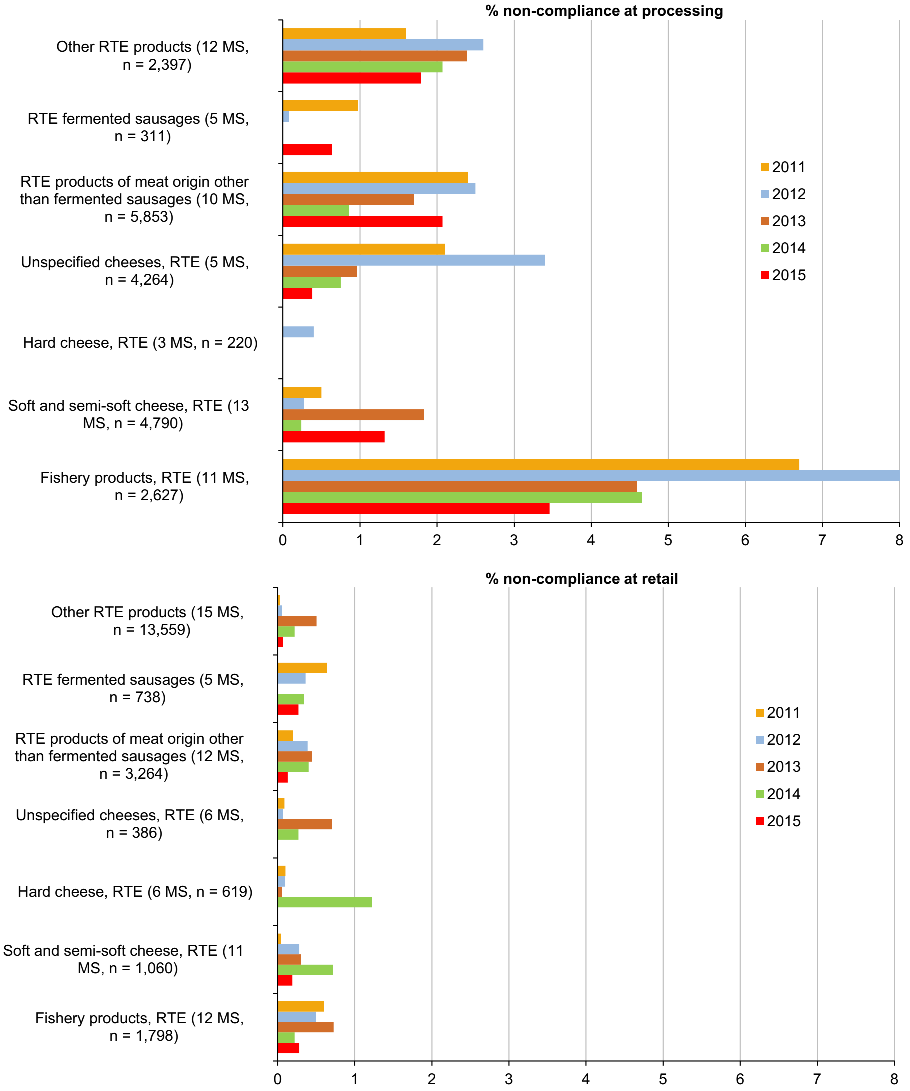
All RTE milk samples (batch or single) collected at retail (eight MS) were found to be compliant. However, at the processing plant level (11 MS), whereas all single samples were found to be compliant, 60 batch samples were not (6.1% non-compliance). All these non-compliant batches were reported from investigations in Poland, in which the pathogen was detected in 6.0% of 747 tested batches of pasteurised cow's milk and in 16.7% of 90 tested batches of raw goat's milk intended for direct human consumption.

Among samples of RTE products of meat origin, other than fermented sausages, low levels of non-compliance were observed at processing (2.1% of single samples and 1.6% of batches), where non-compliance (in some of their investigations) was reported from 14 out of the 16 MS reporting data. Poland reported the majority of the batch units tested at processing (75.5%). At retail, all tested batches were found to be compliant and very low levels of non-compliance were reported in single samples (< 0.1%).

Fermented sausages are assumed not to support the growth of *L. monocytogenes*, and all tested products were found to meet the food safety criterion (no levels exceeding 100 CFU/g) at both processing and retail, except for two single samples at processing and two single samples at retail.

As in previous years, all samples of RTE food intended for infants and for special medical purposes were compliant with the *L. monocytogenes* food safety criteria both at processing (three MS) and at retail (seven MS).

The percentage of non-compliant single units from the main RTE food categories, at processing and at retail, are visualised in Figure 26.



RTE: ready-to-eat. In parentheses, the number of MS reporting data on the specific food category in 2015 and the total number of tested units (n). This graph includes data where sampling stage at retail (also catering, hospitals and care homes) and at processing (also cutting plants) have been specified for the relevant food types. Data collected at the 'unspecified' sampling stage are included into the data reported at retail. The category 'other RTE products' includes RTE food other than: 'RTE fishery products', 'soft and semi-soft cheeses', 'hard cheeses', 'unspecified cheeses', 'other RTE dairy products', milk, 'RTE products of meat origin other than fermented sausage', 'RTE products of meat origin, fermented sausage' and 'RTE food intended for infants and for medical purposes'. For the non-compliance analysis of samples collected at the processing stage, the food safety criterion of 'absence in 25 g' was applied, except for samples of hard cheeses and fermented sausages that were assumed to be unable to support the growth of *L. monocytogenes* and for which the criterion of '≤ 100 CFU/g' was applied. For the non-compliance analysis of samples collected at the retail level, the food safety criterion of '≤ 100 CFU/g' was applied. Only information on the main RTE food categories (RTE fishery products, RTE cheeses and RTE meat products) is included in this graph. For the detailed information on non-compliance with the EU *L. monocytogenes* food safety criteria refer to Table 13.

Figure 26: Proportion of single samples at processing and retail non-compliant with the EU *L. monocytogenes* food safety criteria, 2011–2015

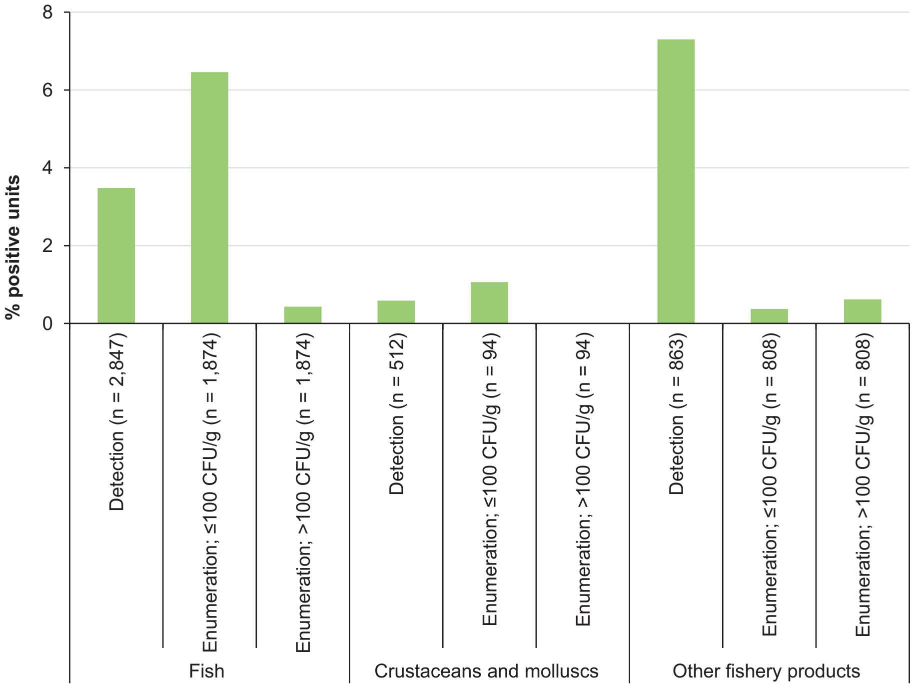
Ready-to-eat fish and fishery products

In 2015, 21 MS and one non-MS reported data on *L. monocytogenes* in RTE fish (Table 2015_LISTERIAFISH). The number of samples tested was much smaller than in 2014. However, similar to the 2014 data, most of the tested units were from smoked fish and the majority were sampled at the processing plant level. *L. monocytogenes* was detected in 3.5% of the 2,847 tested fish units (Figure 27) but, as more than half (56.8%) of the tested units were sampled in two MS (Poland and Finland), the lack of representativeness should be taken into account when interpreting the overall results. This proportion of detection-positive units (3.5%) is appreciably lower than that reported in 2014 (10.6%) and 2013 (15.2%). In addition, in 2015, 1,874 units of fish were tested by enumeration and 0.4% had counts of *L. monocytogenes* > 100 CFU/g (Figure 27 and Table 2015_LISTERIAFISH), which is much less than what was reported in 2014 (2.5%) and 2013 (1.6%). In addition, Denmark reported that *L. monocytogenes* was detected in one out of 20 batches and in five out of 100 single samples of smoked fish, which were obtained, via selective sampling, from the processing plant level.

Considering only single units of RTE fish sampled at retail (and excluding heat-treated fish), a low proportion tested positive in qualitative analyses (5.9%; n = 625), whereas among the fish units tested quantitatively (n = 870) 8.5% contained *L. monocytogenes* counts ≤ 100 CFU/g and 0.2% contained counts > 100 CFU/g. The 2015 prevalence estimate of *L. monocytogenes* in fish was lower than the respective prevalence estimates obtained during the 2010–2011 EU baseline survey (EFSA, 2013a), corresponding to RTE smoked and gravad fish sampled at retail and tested at the time of sampling and at the end of shelf life (10.3–10.4%). In addition, whereas the 2015 estimate for the percentage of fish units with *L. monocytogenes* counts > 100 CFU/g was also appreciably smaller than the corresponding estimates from the EU survey (1.0–1.7%), the 2015 proportion of RTE fish units with counts ≤ 100 CFU/g was much higher than the corresponding EU-survey estimates (1.2–1.5%).

In 2015, 21 MS reported data on *L. monocytogenes* in RTE fishery products (crustaceans and molluscs and other fishery products) (Table 2015_LISTERIAFISHPR). *L. monocytogenes* was detected in 4.8% of the 1,375 units tested qualitatively. Nine MS reported *L. monocytogenes* detection-positive samples (mostly unspecified fishery products). The vast majority (49 out of 66) of the *L. monocytogenes* detection-positive samples were reported by a single Polish investigation at the processing level. In addition, 902 units of fishery products were tested by enumeration, and among these, five (0.6%) units (three single samples and two batches reported by Belgium and Slovenia, respectively) of unspecified products sampled at retail had counts of *L. monocytogenes* > 100 CFU/g (Table 2015_LISTERIAFISHPR).

A summary of the proportion of *L. monocytogenes*-positive units in different types of fishery products is presented in Figure 27. Unlike previous years when *L. monocytogenes* was most often detected in RTE fish (mainly smoked fish), in 2015 the subcategory in which the pathogen was most frequently detected in qualitative analyses was 'other fishery products' (7.3% of 863 tested units). This result should be interpreted with caution because 77.8% of positive units (49 out of the 63 detection-positive 'other fishery products') were reported by the aforementioned Polish investigation. Despite the decrease in the proportion of RTE fish units found positive for *L. monocytogenes* in qualitative analyses in 2015 compared with the previous years, a small increase was noted in the proportion of RTE fish containing ≤ 100 CFU/g (6.5% of the units tested in 2015 vs. 4.3 and 5.1% in 2014 and 2013, respectively) in 2015. Finally, unlike previous years when RTE fish was the subcategory with the highest percentage (ca 1.5–2.5%) of units containing *L. monocytogenes* counts exceeding 100 CFU/g, in 2015 this percentage was quite smaller (0.4%).



Test results obtained by detection and enumeration methods are presented separately. Data are pooled for all sampling units (single and batch), for all sampling stages and for all reporting MS. As data were mostly reported by a limited number of MS, the findings presented in this figure should not be considered representative of the EU level.

Fish includes data from Austria, Bulgaria, Croatia, Cyprus, the Czech Republic, Estonia, Finland, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, the Netherlands, Poland, Portugal, Slovakia, Slovenia, Spain and Sweden (Detection: 17 MS, Enumeration: 18 MS).

Crustacean and molluscs includes data from Austria, Bulgaria, Hungary, Ireland, the Netherlands, Poland, Portugal and Spain (Detection: 8 MS, Enumeration: 4 MS).

Other fishery products (including unspecified fishery products and surimi) includes data from Austria, Belgium, Bulgaria, Croatia, the Czech Republic, Estonia, Germany, Ireland, Italy, Latvia, Lithuania, Luxembourg, Poland, Portugal, Romania, Slovakia, Slovenia, Spain and Sweden (Detection: 14 MS, Enumeration: 15 MS).

Figure 27: Proportion of *Listeria monocytogenes*-positive units in ready-to-eat fishery products categories in the reporting EU Member States, 2015

Ready-to-eat meat products

In 2015, 20 MS reported data from investigations of *L. monocytogenes* in RTE meat products. A summary of the proportions of units positive for *L. monocytogenes* in RTE products of meat origin is presented in Figure 28.

In 2015, except for RTE pig meat where findings were comparable with those reported in 2014, some differences were noted in the percentages of positive units among the tested RTE products of meat origin. Hence, an increase was noted in the proportions of detection-positive units from bovine and broiler meat. Increases were also noted in the proportions of units containing enumerable (≤ 100 CFU/g) populations of *L. monocytogenes*, particularly in RTE products made from broiler and turkey meat. However, the proportion of positive units from RTE turkey meat is strongly influenced by two small quantitative investigations, which reported high percentages of positive values (one Spanish investigation at retail in which three out of the three units tested were reported to contain ≤ 100 CFU/g, and one Polish investigation at processing in which two out of the four units tested were reported to contain ≤ 100 CFU/g).

When considering only single units of meat products sampled at retail (and excluding fermented sausages and raw meat products intended to be eaten raw), a low proportion tested positive in qualitative analyses (4.0%; n = 2,366), and, among the units tested quantitatively (n = 2,304), a very low proportion (0.7%) was found to contain populations of *L. monocytogenes* ≤ 100 CFU/g, whereas the occurrence of units with counts > 100 CFU/g was rare (0.04%). The 2015 prevalence estimate of *L. monocytogenes* in meat products was almost two times higher than the percentage of 2.1% reported from the 2010–2011 EU baseline survey (RTE heat-treated meat products sampled at retail and tested at the end of shelf life). In addition, the 2015 estimate for the proportion of meat product units with *L. monocytogenes* counts ≤ 100 CFU/g was slightly higher than that from the EU survey (0.5%), and the 2015 estimate for the proportion of units with counts > 100 CFU/g was almost 10-fold lower than that reported from the EU survey (0.4%).

Poultry meat

In 2015, 13 MS reported data on *L. monocytogenes* in RTE broiler meat (Table 2015_LISTERIARTEBROIL) and 11 MS reported data on *L. monocytogenes* in RTE products of turkey meat (Table 2015_LISTERIARTETURK).

Compared to the data reported to EFSA in 2014, in 2015 a much lower number of units of RTE broiler meat products were tested both at retail as well as at the processing stage. In 2015 *L. monocytogenes* was not detected in any of the 342 RTE meat products from broilers tested qualitatively at retail, but it was isolated from 3.4% of the 1,245 units sampled at processing. Most (73.8%) of the detection-positive units at processing were reported by Poland. In addition, a total of 1,339 units were tested by enumeration and *L. monocytogenes* was reported at levels above 100 CFU/g in five units originating from three investigations of broiler meat products reported by Poland and Ireland (Table 2015_LISTERIARTEBROIL).

In turkey-meat products, *L. monocytogenes* was only detected in two investigations (one at processing reported by Spain and one at retail reported by Hungary); the overall percentage of detection-positive units was 1.5% (1.7% at retail and 1.4% at processing) out of the 332 units tested with the qualitative method. None of the 208 units of turkey-meat products tested by enumeration were found to contain *L. monocytogenes* in excess of 100 CFU/g (Table 2015_LISTERIARTETURK).

Bovine meat

In 2015, data on *L. monocytogenes* in RTE bovine meat products were reported by 13 MS and are summarised in Table 2015_LISTERIARTEBOVINE.

L. monocytogenes was detected in 4.4% of the 180 tested units sampled at retail and in 2.0% of the 1,519 tested units sampled at processing. However, 93.5% of the detection-positive units at processing originated from a single Polish investigation.

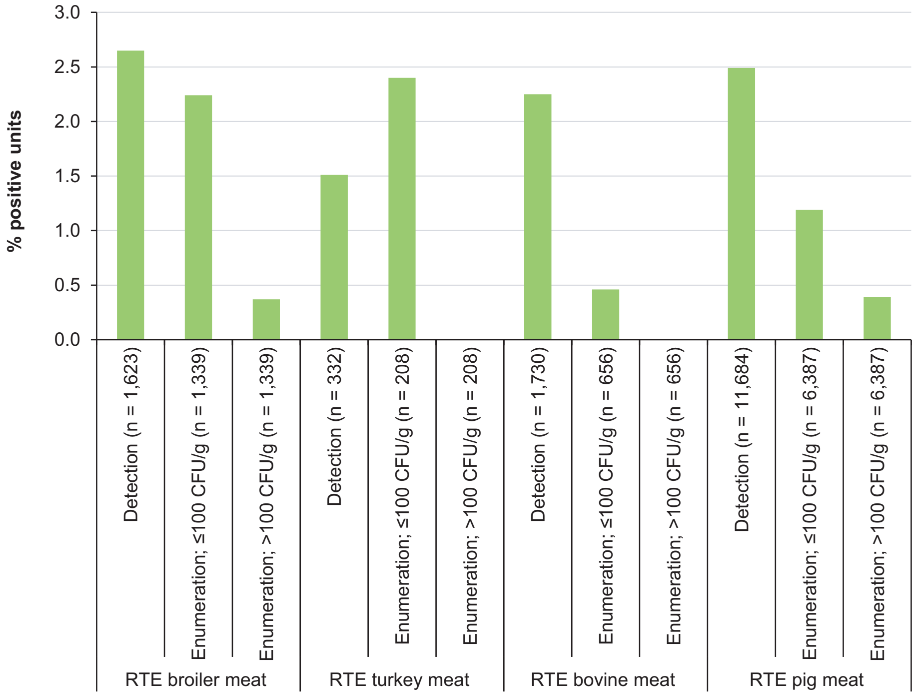
None of the quantitative investigations from 10 MS reported any RTE bovine meat products with *L. monocytogenes* counts above 100 CFU/g, although enumerable populations of the pathogen (≤ 100 CFU/g) were noted in two investigations from Germany (one at retail and one at processing), corresponding only to 0.5% of the 656 units tested using the enumeration method (Table 2015_LISTERIARTEBOVINE).

Pig meat

In 2015, 20 MS reported data on *L. monocytogenes* in RTE meat products from pig.

Eighteen MS reported data on *L. monocytogenes* in RTE meat products from pig using the detection method. *L. monocytogenes* was detected in 4.2% of the 2,382 tested units sampled at retail and in 2.1% of the 9,226 tested units sampled at processing. Overall, 14 MS reported positive results in 38 investigations of RTE meat products from pig tested qualitatively. In addition, Denmark reported that *L. monocytogenes* was detected in one out of two batches and in two out of five single samples of fermented sausages from pig meat, which were obtained, via selective sampling, from the processing plant level.

Counts of *L. monocytogenes* > 100 CFU/g were found in eight investigations from six MS, corresponding to 0.4% of the 6,387 units tested quantitatively (Table 2015_LISTERIARTEPIG); all except one of the RTE pig product units found to contain counts of *L. monocytogenes* > 100 CFU/g were tested at processing. In addition, 19 investigations from five MS reported enumerable (≤ 100 CFU/g) populations of *L. monocytogenes*, corresponding to 1.2% of the 6,387 units tested quantitatively.



Test results obtained by detection and enumeration methods are presented separately. Data are pooled for all sampling units (single and batch), for all sampling stages and for all reporting MS. Since data were mostly reported by a few MS, the findings presented in this figure should not be considered representative of the EU level.

RTE broiler meat includes data from Bulgaria, the Czech Republic, Estonia, Greece, Hungary, Ireland, Italy, Poland, Portugal, Romania, Slovakia, Spain and Sweden (Detection: 13 MS; Enumeration: 10 MS).

RTE turkey meat includes data from Austria, Cyprus, Estonia, Hungary, Ireland, Italy, Poland, Portugal, Slovakia, Spain and Sweden (Detection: 10 MS; Enumeration: 8 MS).

RTE bovine meat includes data from Austria, Bulgaria, the Czech Republic, Estonia, Germany, Hungary, Ireland, Italy, Luxembourg, Poland, Romania, Spain and Sweden (Detection: 12 MS; Enumeration: 10 MS).

RTE pig meat includes data from Austria, Belgium, Bulgaria, Cyprus, the Czech Republic, Estonia, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, Luxembourg, Poland, Portugal, Romania, Slovakia, Spain and Sweden (Detection: 18 MS; Enumeration: 20 MS).

Figure 28: Proportion of *Listeria monocytogenes*-positive units in ready-to-eat meat categories in the reporting EU Member States, 2015

Ready-to-eat cheeses

In 2015, 17 MS reported data from investigations on *L. monocytogenes* in cheeses, mainly cheeses made from cow's milk.

A summary of the proportion of units positive for cheeses is presented in Figure 29. Based on the results of qualitative investigations, a comparable frequency of detection of *L. monocytogenes* across the different cheese subcategories was noted, although the occurrence of the pathogen was smaller in hard cheeses made from pasteurised milk. It is important to note that half of the data on units tested qualitatively were reported by Poland, and therefore the results may not be representative of the EU level.

Soft and semi-soft cheeses

Overall, in the reporting EU MS in 2015, 5,830 units of soft and semi-soft cheeses were tested using the detection method (less than half of those tested in 2014) and 2,018 units were tested by the enumeration method. Detailed results are presented in specific tables referenced in the Appendix A for each type of soft and semi-soft cheese (made either from raw or low heat-treated milk or from pasteurised milk originating from cows, sheep and/or goats).

In 2015, the occurrence of *L. monocytogenes* in soft and semi-soft cheeses made from raw or low heat-treated milk (1.4% of the 707 units tested by detection) was only slightly higher than in soft and semi-soft cheeses made from pasteurised milk (1.3% of the 5,123 units tested by detection). It should be noted that almost half (49%) of the data on soft and semi-soft cheeses were reported from Poland. For instance, in a single Polish investigation 2,664 units of cheese made from pasteurised goat milk were sampled at processing and 1.8% (49 units) was reported as positive.

When using the enumeration method, counts of *L. monocytogenes* > 100 CFU/g were reported in three investigations of soft and semi-soft cheeses from raw milk (1.2% of 809 units tested) and in two investigations of soft and semi-soft cheeses from pasteurised milk (0.4% of 1,209 units tested). In addition, low proportions of units (1.0% and 4.1% of soft and semi-soft cheeses from raw milk and pasteurised-milk, respectively) were found to contain enumerable (≤ 100 CFU/g) populations of *L. monocytogenes*. However, it is important to note that the proportion of units from soft and semi-soft cheeses from pasteurised milk containing ≤ 100 CFU/g of *L. monocytogenes* may be biased by the results reported by Poland in one investigation, where 49 units were reported as having been tested using the enumeration method and 45 were reported to contain *L. monocytogenes* populations ≤ 100 CFU/g. Furthermore, it is important to note that Poland tested for enumeration only the 49 units of soft and semi-soft cheeses from pasteurised milk that resulted positive with the detection method, leading to an overestimation of the positivity for enumeration.

When considering only single units of soft and semi-soft cheeses sampled at retail (and excluding fresh cheeses), a low proportion tested positive in qualitative analyses (1.3%; n = 306), and, among the units tested quantitatively (n = 848), very low proportions were found to contain populations of *L. monocytogenes* ≤ 100 CFU/g (0.9%) or > 100 CFU/g (0.2%). Compared to the corresponding estimate (0.5%) obtained from the 2010–2011 EU baseline survey (RTE soft and semi-soft cheeses sampled at retail and tested at the end of shelf life), the 2015 prevalence estimate of *L. monocytogenes* in soft cheeses was more than two-times higher. In addition, the 2015 estimates for the percentage of units with counts ≤ 100 CFU/g and > 100 CFU/g were higher compared to the corresponding estimates from the EU survey (both *ca.* 0.06%).

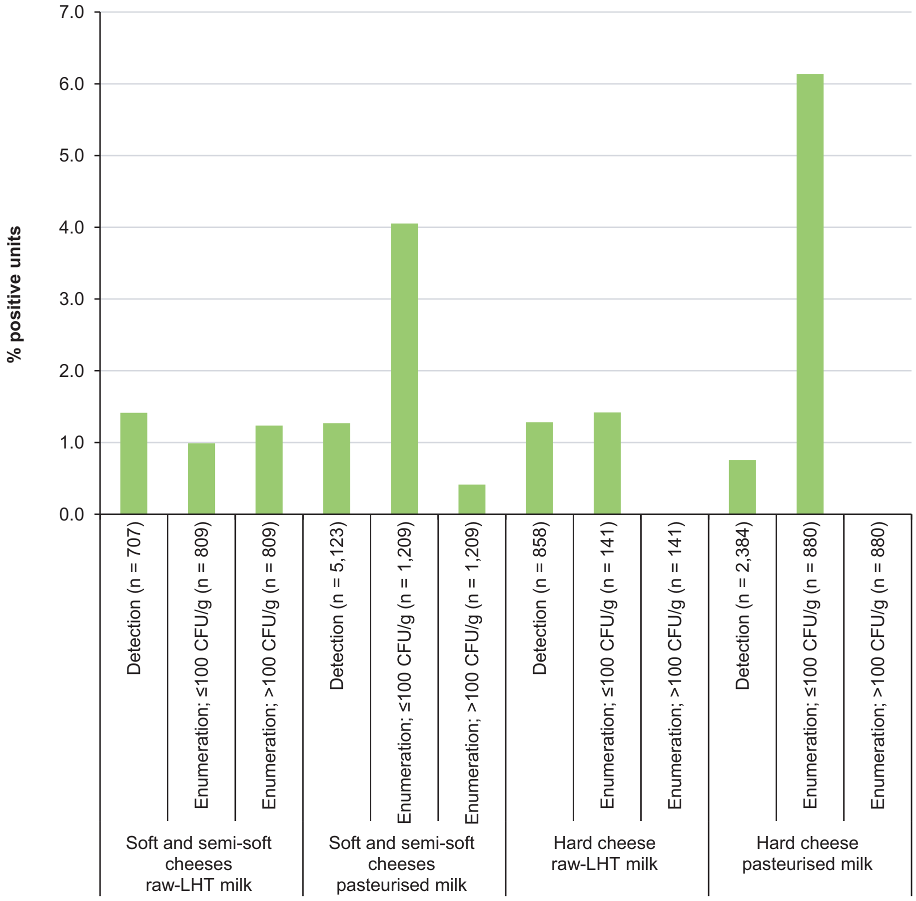
Hard cheeses

Overall, in 2015, 3,242 units of hard cheeses were reported as tested using the detection method (about 4.5 times less than the number of units tested in 2014) and 1,021 units were reported as tested by the enumeration method, in the reporting EU MS. Detailed results are presented in specific tables referenced in the Appendix A for each type of hard cheese (made either from raw or low heat-treated milk or from pasteurised milk originating from cows, sheep and/or goats).

In 2015, *L. monocytogenes* was detected (in qualitative analyses) in 1.3% of the 858 units of hard cheeses made from raw or low heat-treated milk and in 0.8% of the 2,384 units made from pasteurised milk. Both of these estimates are higher than the respective estimates in 2014. It should be noted that 50% of the data on hard cheeses were reported from a single MS (Poland) and, although detection-positive results in hard cheeses were reported from four MS (Bulgaria, Croatia, Ireland and Poland, from eight qualitative investigations conducted at the processing plant level), 20 out of the 29 total detection-positive units were reported by Poland from three investigations.

When using the enumeration method, no counts of *L. monocytogenes* > 100 CFU/g were reported in hard cheeses made either from pasteurised or raw milk. However, enumerable populations of *L. monocytogenes* (≤ 100 CFU/g) were reported, corresponding to 1.4% and 6.1% of the raw and pasteurised hard cheese units tested quantitatively, respectively. Both these estimates are much higher than the corresponding estimates in 2014 (0.3% and 0.8% of raw and pasteurised hard cheese units, respectively). It is important to note that all the units containing ≤ 100 CFU of *L. monocytogenes* per gram were reported by Germany, which also sampled the majority (70%) of the hard cheeses tested using the enumeration method.

Detailed information on the data reported and on the occurrence of *L. monocytogenes* in the different cheese categories has been presented in specific tables referenced in the Appendix A.



Test results obtained by detection and enumeration methods are presented separately. LHT: low heat-treated milk. Data are pooled for all sampling units (single and batch), for all sampling stages and for all reporting MS. Since data were mostly reported by a few MS, the findings presented in this figure should not be considered representative of the EU level.

Soft and semi-soft cheeses, made from raw-LHT milk includes data from Austria, Belgium, Bulgaria, Croatia, the Czech Republic, Estonia, Germany, Ireland, Poland, Portugal, Romania, Slovakia and Spain (Detection: 12 MS, Enumeration: 9 MS).

Soft and semi-soft cheeses, made from pasteurised milk includes data from Austria, Belgium, Bulgaria, Croatia, Cyprus, the Czech Republic, Estonia, Germany, Greece, Ireland, Latvia, Poland, Portugal, Romania, Slovakia and Spain (Detection: 14 MS, Enumeration: 13 MS).

Hard cheese, made from raw-LHT milk includes data from Austria, Estonia, Germany, Ireland, Poland, Portugal, Romania, Slovakia, Spain and Sweden (Detection: 7 MS, Enumeration: 7 MS).

Hard cheese, made from pasteurised milk includes data from Austria, Bulgaria, Croatia, Cyprus, the Czech Republic, Estonia, Germany, Greece, Ireland, Poland, Portugal, Romania, Slovakia and Spain (Detection: 13 MS, Enumeration: 9 MS).

Figure 29: Proportion of *Listeria monocytogenes*-positive units in soft and semi-soft cheeses, and in hard cheeses made from raw or low heat-treated milk and pasteurised milk in reporting EU Member States, 2015

Other ready-to-eat products

Results from a considerable number of investigations on *L. monocytogenes* in other RTE products such as bakery products, fruits and vegetables, salads, milk, sauces and dressings, spices and herbs, other processed food products and prepared dishes were reported.

As in 2015, most of the data on bakery products were from samples collected at retail and based on single samples (Table 2015_LISTERIABAKERY). Overall, nine MS reported on 1,539 units of bakery products tested using the detection method and 0.5% was positive for *L. monocytogenes*. *L. monocytogenes* populations > 100 CFU/g were not reported in any of the 2,144 units analysed using the enumeration method by the 15 MS which reported results from quantitative analyses.

However, 2.0% of the units tested quantitatively were found to contain enumerable (≤ 100 CFU/g) populations of *L. monocytogenes*; all these enumeration-positive units were sampled at retail (90.7% from a single German investigation).

Similar to the data reported in 2014, most of the reported data on fruits and vegetables in 2015 were from retail and were based on single samples (Table 2015_LISTERIAFRUITVEG). In 2015, 13 MS provided data on 2,238 units of RTE fruit and vegetables tested using the detection method. Italy reported 45.6% of all units tested qualitatively, followed by Spain (11.7%) and Hungary (10.5%). Eight MS reported positive findings with detection analyses and 1.4% of the total number of units tested qualitatively (a percentage exactly twofold lower than in 2014) was positive for *L. monocytogenes*. In addition, 18 MS reported data on 2,858 units tested using the enumeration method and only one unit (0.03%) from a retail investigation in Belgium had *L. monocytogenes* populations > 100 CFU/g. Thirty-three units (all from single samples tested at retail) contained enumerable (≤ 100 CFU/g) populations of *L. monocytogenes* and the majority (23 units) were reported from a single German investigation.

Regarding RTE salads, nine MS reported data on 1,196 units tested using the detection method and 2.3% was reported as positive (seven MS reported detection-positive results). Twelve MS provided information on 2,332 units tested using the enumeration method and 0.04% had counts of *L. monocytogenes* > 100 CFU/g. In addition, 0.6% of units tested quantitatively contained ≤ 100 CFU of *L. monocytogenes* per g (Table 2015_LISTERIASALAD).

In 2015, 13 MS reported data on *L. monocytogenes* in milk. Most of the units tested were sampled by Poland at the processing level. *L. monocytogenes* was found in 4.1% of the 1,508 milk units tested using the detection method. Sixty out of the 61 detection-positive units originated from two Polish investigations at processing. In the first investigation *L. monocytogenes* was detected in 6% of 747 batches of pasteurised milk and in the second investigation the pathogen was detected in 15 out of 90 batches of raw milk intended for direct human consumption. Out of the 175 units tested using the enumeration method, no findings of units with counts > 100 CFU/g were reported, and only a single sample (0.6%) of pasteurised milk (reported by Germany) contained enumerable populations (≤ 100 CFU/g) of *L. monocytogenes*. (Table 2015_LISTERIAMILK). In addition, Denmark reported that *L. monocytogenes* was detected in one out of 14 batches and in one out of 65 single samples of pasteurised cow's milk which were obtained, via selective sampling, from the processing plant level.

Regarding sauces and dressings, eight MS reported information on 230 units tested using the detection method and *L. monocytogenes* was not detected in any of the tested units. Similarly, no positive findings were reported from enumeration analyses in investigations conducted from five MS on 351 units (Table 2015_LISTERIASAUCE).

Regarding spices and herbs, four MS reported information on 87 units tested using the detection method with no positive findings. Similarly, none of the quantitative investigations by six MS reported any positive findings in the 261 units tested (Table 2015_LISTERIASPICES).

In other processed food products and prepared dishes, 10 MS submitted qualitative data and six reported positive findings: *L. monocytogenes* was detected in 2.8% of 3,604 units tested using the detection method. The majority of these detection-positive units (84 out of the 101 total detection-positive units) were sandwiches sampled at retail in the United Kingdom. In addition, 13 MS reported quantitative data on 4,172 units tested using the enumeration method. Enumeration-positive findings were provided by three MS from two retail investigations on sandwiches (Hungary and Poland) and one investigation at the processing plant level on sushi (Poland). Overall, 0.5% of the units tested quantitatively had counts of *L. monocytogenes* ≤ 100 CFU/g and less than 0.1% (three out of the 2,867 units of sandwich products from the UK study) had counts > 100 CFU/g (Table 2015_LISTERIAPREPDISH). In addition, Denmark reported that *L. monocytogenes* was detected in one out of three batches and in one out of 15 single samples of sandwiches containing meat, which were obtained, via selective sampling, from the processing plant level.

L. monocytogenes was not found in any of the reported qualitative (166 units, five MS) or quantitative (600 units, five MS) investigations of confectionery products and pastes (Table 2015_LISTERIACONF), nor in any of the reported qualitative (29 units, two MS) or quantitative (93 units, three MS) investigations of egg products (Table 2015_LISTERIAEGGPR).

3.3.2.2. Animals

In 2015, 15 MS and one non-MS reported qualitative data on several animal categories (food-producing, wild-, zoo- and pet animals, including birds and marine mammals) and animal species tested for *Listeria* spp. In total, 31,490 units were tested for *Listeria* spp. and 3.0% were positive.

Reported data were mainly at animal level (93.8%). However, the sample size of the investigations, the sampling strategy and the proportion of positive samples varied considerably among reporting countries and animal species. Almost half (48.4%) of the total EU data on animals were reported from Germany, but, among the reporting countries, Italy reported on the greatest variety of animal categories and species. It is important to note that all the data reported by the United Kingdom relate to positive findings, with a consequent overestimation of the proportion of positive units reported.

Among the 951 units found positive for *Listeria* spp., 80.9% (769 units) were reported as being positive for *L. monocytogenes*. As MS testing for *Listeria* spp. in animals was expected to concentrate on *L. monocytogenes* (EFSA, 2016b), only limited findings on other *Listeria* species were reported (mainly on unspecified *Listeria* spp. and *Listeria* spp. other than *L. ivanovii* and *L. innocua*).

Findings of *Listeria* spp. were most often reported in domestic ruminants (cattle, sheep, goats; 67.1%), pigs (9.4%) and solipeds (7.5%), but *Listeria* spp. were also detected in broilers, cats, dogs, foxes, and other wild and zoo animals.

Further details on the findings of *Listeria* spp. in animals are included in Table 2015_LISTERIAANIMALS.

3.3.3. Discussion

The human listeriosis trend has been increasing since 2008 but seemed to stabilise in 2015. The EU notification rate and case numbers remained at a stable level in comparison with 2014, despite the fact that one additional country (Portugal) started reporting in 2015 and another country (Spain) improved its surveillance system.

While still relatively rare, human listeriosis is one of the most serious food-borne diseases under the EU surveillance causing high morbidity, hospitalisation and mortality, particularly among the elderly. The EU surveillance of listeriosis focuses on severe, invasive forms of the disease, for which the risk groups are mainly elderly and immunocompromised persons as well as pregnant women and infants. All years from the beginning of the EU level surveillance, the majority of listeriosis cases have been reported in persons over 64 years of age. The number of reported cases and their proportion has steadily increased from 2008 to 2015 in the age group over 64 and almost doubled in those over 84 years.

As in previous years, almost all (97%) reported listeriosis cases were hospitalised, while 2015 marked the highest proportion of fatal cases reported since 2007. The majority of fatal cases were in the elderly (over 64 years) and the proportion of fatal cases, particularly in age group over 84 years, has steadily increased over the years. The increase of *Listeria* infections may be partially explained by the ageing population in the EU, which will continue in most MS (Eurostat, 2016). It is therefore important to raise awareness of listeriosis and risky foods, especially among the elderly.

L. monocytogenes is widespread in the environment and has the ability to withstand and adapt to various environmental stresses. The pathogen can colonise, in the form of biofilms, food-processing equipment and food-contact surfaces and can therefore persist for prolonged time periods in food-handling environments. Hence, a wide range of foodstuffs can get contaminated during the food-harvesting stage, but mostly during the food-processing stage. The EU microbiological limit for *L. monocytogenes* in RTE food products on the market is set at 100 CFU/g. Although delicatessen meats and soft cheeses were initially considered as the primary high-risk food categories for listeriosis in humans, results from food-testing surveys and outbreak investigations around the world in the past decade have significantly expanded the list of implicated foods (RTE meat-, dairy-, fish- and fishery products but also produce, fruits, salads and other RTE products) (Garner and Kathariou, 2016).

In 2015, at the processing plant level, the food category with the highest levels of non-compliance was 'fishery products' (3.5% of single samples and 2.9% of batches), followed by 'other RTE products' (1.8% of single samples and 2.3% of batches), 'meat products other than fermented sausages' (2.1% of single samples and 1.6% of batches) and 'other RTE dairy products' (1.0% of single samples and 2.7% of batches). However, the highest level of non-compliance at processing was observed for 'RTE milk' (6.1% of batches), but this estimate is heavily influenced by findings from investigations in a single MS (Poland). With the exception of batch samples of soft and semi-soft cheeses, the proportion of non-compliant units at retail was lower than at processing for all food categories. The RTE food categories with the highest levels of non-compliance at retail were 'fishery products' (0.3% of single samples and 1.4% of batches) and 'soft and semi-soft cheeses' (0.2% of single samples and 1.0% of batches).

In 2015, the non-compliance for most RTE food categories was generally at levels comparable to those reported in 2014, with some noticeable exceptions pertaining mainly to batch samples collected at the processing stage. Hence, whereas the level of non-compliance in batch samples of 'fishery products' and 'other RTE products' at processing was appreciably smaller than those reported in 2014 (10.8% and 6.4%, respectively), the levels of non-compliance (batch samples at processing) in 'other dairy products' and 'RTE milk' were much higher than those reported in 2014 (1.0% and 0.5%, respectively).

The 2015 data (single units sampled at retail) for RTE fish, meat products and soft cheeses were considered and compared with the corresponding data from the EU baseline survey on *Listeria* in RTE foods conducted during 2010–2011 (EFSA, 2013a). For RTE smoked and marinated fish, both the prevalence of *L. monocytogenes* (detection analyses) as well as the proportion of units with counts exceeding 100 CFU/g (enumeration analyses) were appreciably lower than the estimates obtained during the EU baseline survey. In contrast, the proportion of units with counts ≤ 100 CFU/g was much higher in 2015. For RTE meat products, the prevalence of *L. monocytogenes* (detection analyses) was almost twice as high, whereas the proportion of units with counts exceeding 100 CFU/g (enumeration analyses) was almost 10-fold lower than the respective EU baseline survey estimates. Finally, for RTE soft and semi-soft cheeses, all three 2015 estimates (detection-positive, '≤ 100 CFU/g' and '> 100 CFU/g') were higher than the respective EU baseline survey estimates, and in particular the proportion of units with counts ≤ 100 CFU/g. All these comparisons should be interpreted with caution because, besides the differences in the design of the investigations (the EU baseline survey and 2015 EU data), the 2015 estimates are based on significant smaller sample sizes (particularly the estimates of RTE fish and cheeses).

Several MS reported findings of *Listeria* spp. in animals. Most of the tested samples were from domestic ruminants (cattle, sheep and goats) and positive findings were most often reported in these three animal species. However, *Listeria* spp. (mainly *L. monocytogenes*) were also reported in pigs, solipeds, broilers, cats, dogs, foxes and other wild- and zoo animals. *Listeria* spp. are widespread in the environment; therefore, their isolation from animals is to be expected and increased exposure to pathogenic *Listeria* spp. may lead to clinical disease in some animals.

3.4. Shiga toxin-producing *Escherichia coli*

The Appendix A lists all summaries made for the production of this section, for humans, foods and animals, including STEC summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.4.1. Shiga toxin-producing *Escherichia coli* in humans

In 2015, 6,025 cases of STEC[31] infections, including 5,901 confirmed cases, were reported in the EU (Table 14). Twenty-two MS reported at least one confirmed STEC case and six MS reported zero cases. Portugal reported STEC data for the first time in 2015. The EU notification rate was 1.27 cases per 100,000 population, which was slightly lower than the rate in 2014. The highest country-specific notification rates were observed in Ireland, Sweden, the Netherlands and Denmark (12.92, 5.65, 5.08, and 3.06 cases per 100,000 population, respectively). Nine countries (Bulgaria, Croatia, Cyprus, Greece, Lithuania, Poland, Portugal, Romania and Slovakia) reported ≤ 0.1 cases per 100,000 population.

Most of the STEC cases reported in the EU were infected within their own country (64.4% domestic cases, 13.8% travel-associated and 21.8% of unknown origin). Finland was the only MS reporting a higher proportion (56.8%) of travel-associated cases than domestic cases. Among 810 travel-associated cases, Turkey, Egypt and Spain were most frequently reported as the probable country of infection (21.1%, 8.4% and 6.9% of the imported cases, respectively).

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[31] Also known as verotoxigenic, verocytotoxigenic, verotoxin-producing, verocytotoxin-producing *E. coli* (VTEC) or Shiga toxin-producing *E. coli* (STEC).

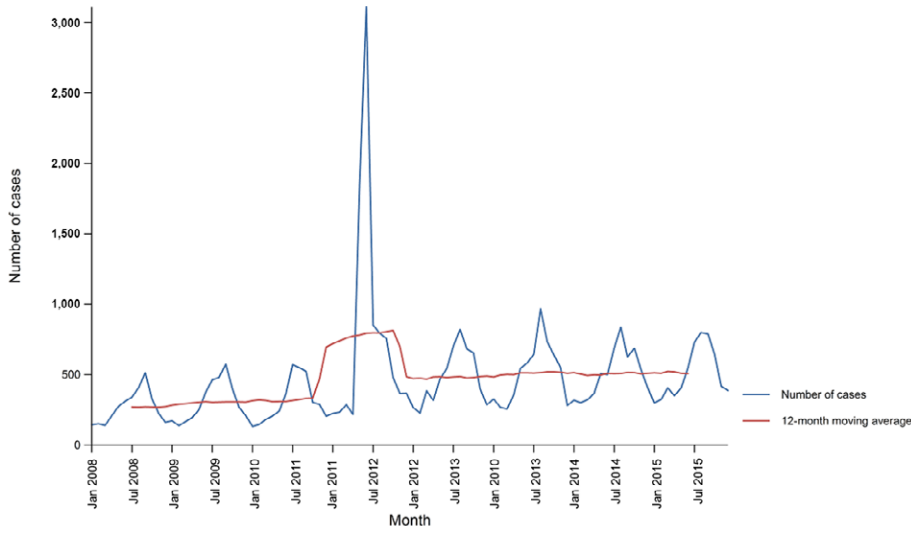
Table 14: Reported human cases of STEC infections and notification rates per 100,000 population in the EU/EEA, by country and year, 2011–2015

Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	107	107	1.27	131	1.54	130	1.54	130	1.55	120	1.43
Belgium(a)	N	A	100	100	–	85	–	117	–	105	–	100	–
Bulgaria	Y	A	0	0	0.00	0	0.00	1	0.01	0	0.00	1	0.01
Croatia	Y	A	0	0	0.00	4	0.09	0	0.00	0	0.00	–	–
Cyprus	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Czech Republic	Y	C	26	26	0.25	29	0.28	17	0.16	9	0.09	7	0.07
Denmark	Y	C	228	173	3.06	229	4.07	191	3.41	199	3.57	215	3.87
Estonia	Y	C	8	8	0.61	6	0.46	8	0.61	3	0.23	4	0.30
Finland	Y	C	74	74	1.35	64	1.17	98	1.81	32	0.59	27	0.50
France(b,c)	N	C	262	262	–	221	–	218	–	208	–	221	–
Germany	Y	C	1,647	1,616	1.99	1663	2.06	1,639	2.00	1,573	1.93	5,558	6.82
Greece	Y	C	1	1	0.01	1	0.01	2	0.02	0	0.00	1	0.01
Hungary	Y	C	15	15	0.15	18	0.18	13	0.13	3	0.03	11	0.11
Ireland	Y	C	625	598	12.92	572	12.42	564	12.29	412	8.99	275	6.02
Italy(c)	Y	C	68	59	–	68	–	64	–	50	–	51	–
Latvia	Y	C	4	4	0.20	0	0.00	0	0.00	0	0.00	0	0.00
Lithuania	Y	C	3	3	0.10	1	0.03	6	0.20	2	0.07	0	0.00
Luxembourg	Y	C	4	4	0.71	3	0.55	10	1.86	21	4.00	14	2.74
Malta	Y	C	4	4	0.93	5	1.18	2	0.48	1	0.24	2	0.48
Netherlands	Y	C	858	858	5.08	919	5.46	1,184	7.06	1,049	6.27	845	5.07
Poland	Y	C	2	0	0.00	5	0.01	5	0.01	3	0.01	5	0.01
Portugal	Y	C	0	0	0.00	–	–	–	–	–	–	–	–
Romania	Y	C	0	0	0.00	2	0.01	6	0.03	1	0.01	2	0.01
Slovakia	Y	C	1	1	0.02	2	0.04	7	0.13	9	0.17	5	0.09
Slovenia	Y	C	23	23	1.11	29	1.41	17	0.83	29	1.41	25	1.22
Spain	Y	C	86	86	0.19	50	0.11	28	0.06	32	0.07	20	0.04
Sweden	Y	C	551	551	5.65	472	4.89	551	5.77	472	4.98	477	5.07
United Kingdom	Y	C	1,328	1,328	2.05	1324	2.06	1,164	1.82	1,337	2.11	1,501	2.40
EU Total	–	–	**6,025**	**5,901**	**1.27**	**5903**	**1.32**	**6,042**	**1.35**	**5,680**	**1.29**	**9,487**	**2.21**
Iceland	Y	C	1	1	0.30	3	0.92	3	0.93	1	0.31	2	0.63
Norway	Y	C	221	221	4.28	151	2.96	103	2.04	75	1.50	47	0.96
Switzerland(c)	Y	C	308	308	3.72	125	1.51	82	1.00	66	0.82	76	0.97

(a): Y: yes; N: no; A: aggregated data; C: case-based data; –: no report.
(b): Sentinel surveillance; no information on estimated coverage; thus, notification rate cannot be estimated.
(c): Sentinel surveillance; only cases with HUS are notified.
(d): Switzerland provided the data directly to EFSA. The human data for Switzerland also include the ones from Liechtenstein.

There was a clear seasonal trend in confirmed STEC (Figure 30). A dominant peak in the summer of 2011 was due to a large outbreak of enteroaggregative STEC O104:H4 in Germany with linked cases in additional 15 countries.

There was an increasing trend observed over the 8-year-period in the EU/EEA (Figure 30), however, statistical testing for trend is not suitable due to the outbreak peak in 2011. A significant increasing trend ($p < 0.05$) was observed in 11 countries (Austria, Finland, France, Hungary, Ireland, Italy, Lithuania, the Netherlands, Norway, Slovenia and Sweden). No decreasing trend was observed in any of the MS.



Source: Austria, Cyprus, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Iceland, Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Slovakia, Slovenia, Sweden and the United Kingdom. Belgium, Bulgaria, the Czech Republic, Croatia, Portugal, Romania and Spain did not report data to the level of detail required for the analysis.

Figure 30: Trend in reported confirmed cases of human STEC infection in the EU/EEA, by month, 2008–2015

Data on STEC serogroups (based on O antigens) were reported by 22 MS, Iceland and Norway in 2015. As in previous years, the most commonly reported serogroup was O157 accounting for 41.7% of cases with known serogroup, although its proportion continue to decline (Table 15). Serogroup O157 was followed by serogroups O26, O103, O91, O145, O146 and O128. Three new serogroups entered the top 20 list in 2015: O182, O177 and O78. Serogroup O78 was reported by seven countries in 2015 compared with four and five countries in the previous two years. The proportion of non-typed[32] STEC strains continued to increase in 2015 representing 11.9% of the reported cases with known serogroup. Only three cases of O104:H4 (*eae*-, *aggr* not specified) were reported by one country (France) in 2015. Germany and the United Kingdom reported cases of O104 with unknown H-group, no case associated with this serogroup was reported to have had a fatal outcome.

Table 15: Distribution of reported confirmed cases of human STEC infections in the EU/EEA, 2013–2015, by the 20 most frequent serogroups in 2015

Serogroup	2015			2014			2013		
	Cases	MS	%	Cases	MS	%	Cases	MS	%
O157	1,510	21	41.7	1,692	23	46.3	1,828	23	48.9
O26	537	16	14.8	444	16	12.2	476	17	12.7
NT[(a)]	430	10	11.9	315	9	8.6	298	10	8.0
O103	171	14	4.7	193	12	5.3	160	12	4.3
O91	114	12	3.1	105	11	2.9	94	11	2.5
O145	95	12	2.6	105	11	2.9	96	11	2.6
O146	74	10	2.0	83	9	2.3	75	9	2.0
O128	49	12	1.4	47	11	1.3	41	8	1.1
O-rough[(b)]	45	8	1.2	55	7	1.5	41	5	1.1
O111	42	11	1.2	54	11	1.5	78	13	2.1
O76	31	9	0.9	21	7	0.6	22	9	0.6

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[32] Non-typable STEC include those strains where the laboratory tried, but was not able to define the O-serogroup. This depends on how many sera/molecular tools are included in the typing panel. O-rough strains lack the O-chains in the lipopolysaccharide, leading to autoagglutination in the agglutination tests used to determine serogroup or serotype.

Serogroup	2015			2014			2013		
	Cases	MS	%	Cases	MS	%	Cases	MS	%
O55	29	8	0.8	42	11	1.1	12	6	0.3
O113	28	7	0.8	37	10	1.0	36	6	1.0
O182	25	5	0.7	13	5	0.4	18	5	0.5
O80	24	4	0.7	15	3	0.4	8	4	0.2
O117	24	7	0.7	24	8	0.7	27	8	0.7
O177	23	5	0.6	14	8	0.4	23	7	0.6
O5	23	6	0.6	16	7	0.4	15	5	0.4
O78	21	7	0.6	8	4	0.2	5	5	0.1
O8	21	9	0.6	15	7	0.4	11	5	0.3
Other	308	–	8.5	356	–	9.7	373	–	10.0
Total	**3,624**	**21**	**100.0**	**3,654**	**24**	**100.0**	**3,737**	**24**	**100.0**

(a): Non-typable STEC include those strains where the laboratory tried, but was not able to define the O-serogroup. This depends on how many sera/molecular tools are included in the typing panel.

(b): O-rough strains lack the O-chains in the lipopolysaccharide, leading to autoagglutination in the agglutination tests used to determine serogroup or serotype.

Source: 22 MS and two non-MS: Austria, Belgium, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Lithuania, Luxembourg, the Netherlands, Norway, Poland, Romania, Slovakia, Slovenia, Spain, Sweden, and the United Kingdom.

Fourteen MS provided information on hospitalisation for 39.4% of all confirmed STEC cases in the EU in 2015. Of the 2,350 cases with known hospitalisation status, 36.3% were hospitalised. The highest proportions of hospitalised cases (90–100%) were reported in Greece, Italy and Latvia. Two hundred and eighty-three cases of HUS were reported, with the majority in patients.

0–4 years (184 cases; 65%) and 5–14 years of age (58 cases; 20%). The most common serogroups among HUS cases were O157 and O26 (both 27.9%), O80 (8.8%) and O55 (5.9%), while 14.2% were untypable.

In 2015, eight deaths due to STEC infection were reported in the EU compared with seven in 2014. Six MS reported one to three fatal cases each, and nine MS reported no fatal cases. This resulted in an EU case fatality of 0.2% among the 3,352 confirmed cases with known outcome (56.2% of all reported confirmed cases). The serogroups associated with fatal cases were O157 (two cases), O182 (one case), O111 (one case), O91 (one case), O55 (one case) and O-rough (one case). For one fatal case, the serogroup was not specified.

3.4.2. Shiga toxin-producing *Escherichia coli* in food and animals

Data on STEC detected in food and animals are reported annually on a mandatory basis by the EU MS to the European Commission and EFSA, in compliance with the EU Directive 2003/99/EC. In order to improve the quality of the data from STEC monitoring in the EU, EFSA issued technical specifications for the monitoring and reporting of STEC in animals and food in 2009 (EFSA, 2009b). Those guidelines were developed to facilitate the generation of data which would enable a more thorough analysis of STEC in food and animals in the future. The specifications encourage MS to monitor and report data on STEC serogroups that are considered by the BIOHAZ Panel as an important indicator of human pathogenicity (EFSA BIOHAZ Panel, 2013a).

When interpreting the STEC data it is important to note that results from different investigations may be not directly comparable owing to differences in sampling strategies and the analytical methods applied. Monitoring criteria and analytical methods for STEC are not yet fully harmonised across the different countries. Therefore, a non-uniform distribution of sampled units per country or the use of analytical methods selecting one specific STEC serogroup may have introduced artefacts in the calculation of STEC prevalence or STEC serogroup distribution when data were analysed at the EU level.

As in the previous year, the analysis of the data provided by the reporting countries in 2016, concerning STEC detected in food and animal samples in 2015, have been carried out by dividing the analytical methods used in two main categories:

a) Methods aiming at detecting any STEC, regardless of the serotype. These methods are mainly based on PCR screening of sample enrichment cultures for the presence of *stx* genes followed by the characterisation of the isolated STEC strains. This category includes the method ISO/TS 13136:2012 (ISO, 2012) and other PCR-based methods as well as methods based on the detection of verocytotoxin production by immunoassays.

b) Methods designed to detect only STEC O157, such as the method ISO 16654:2001 (ISO, 2001) and the equivalent methods NMKL 164:2005 (NMKL, 2005) and DIN 1067:2004-03 (DIN, 2004). STEC O157 is the serotype most commonly reported in the EU as a cause of both outbreaks and sporadic cases in humans and has also been identified as a major cause of HUS in children (EFSA BIOHAZ Panel, 2013a; EFSA and ECDC, 2015b). The focus has therefore traditionally been on this serotype in many of the MS surveillance programmes.

The standard methods ISO/TS 13136:2012 (ISO, 2012), ISO 16654:2001 (ISO, 2001), NMKL 164:2005 (NMKL, 2005) and DIN 1067:2004-03 (DIN, 2004) are intended for testing food and feed, but have been adapted to test animal samples by many reporting countries, following the EFSA recommendations (EFSA, 2009b).

The proportion of food and animal samples reported by the EU MS and non-MS and tested for STEC by the different analytical methods is presented in the Table 2015_STECANMETH.

It is important to note that, for the estimation of the proportion of samples positive for STEC in the different food and animal categories referenced in this section and in the Appendix A, data from industry own-control programmes, HACCP, suspect sampling, selective sampling and outbreak or clinical investigations were excluded. The whole data set was instead used for any other descriptive analysis on STEC findings in food and animals, including those on the methods used and the serogroups' frequency distribution.

Detailed information on the data reported and on the occurrence of STEC in the different food and animal categories has been included in specific tables referenced in the Appendix A.

3.4.2.1. Shiga toxin-producing *Escherichia coli* in food

In 2015, data on STEC in food were reported by 20 MS, Iceland and Switzerland, for a total of 20,886 samples.

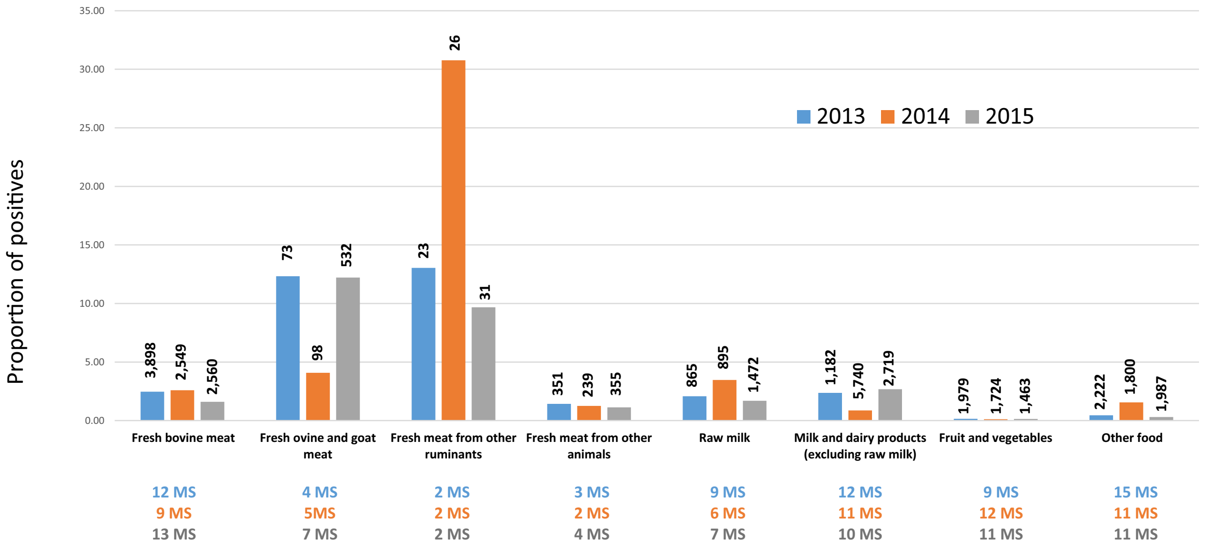
The EFSA technical specifications for the monitoring and reporting of STEC (EFSA, 2009b) were followed by 18 MS and Switzerland, indicating a moderate improvement of the way the 2015 data were reported compared with previous years. The use of the standard method for the detection of STEC in food, ISO/TS 13136:2012 (ISO, 2012) or equivalent methods, was reported by 17 MS and Switzerland, and used to analyse 82.8% of the 20,886 units tested (Table 2015_STECANMETH). The international standard ISO 16654:2001 or the equivalent national methods NMKL 164:2005 and DIN 10167:2004-03 (ISO, 2001; DIN, 2004; NMKL, 2005), which detect only STEC O157, were used by five MS, and accounted for 8.8% of the total samples tested. The use of other PCR-based methods was reported by three MS and Iceland. Some MS reported the use of more than one type of method. Detailed information on the use of the different analytical methods for testing food samples is presented in specific tables, as indicated in the Appendix A.

Overall, 15 MS reported 602 positive samples, corresponding to 2.9% of the 20,886 food samples tested in the EU. Those MS also provided information on STEC O157. Overall, 271 samples positive for STEC O157 (1.3% of total food samples examined by MS) were reported by eight MS, with the majority of the reports (88.6%) from one MS (Spain). In addition, Switzerland and Iceland provided information on, respectively, 844 and two food samples tested for any STEC, without positive findings (2015_STECFOODCOUNTRY).

The proportion of STEC-positive samples in the main food categories, regardless of the analytical method employed, is shown in Figure 31, in comparison with those reported in 2013 and 2014. The highest proportion of positive samples was observed for fresh ovine and goat meat (12.2%) followed by meat from other ruminants (deer, 9.7%). The proportion of STEC-positive samples in meat from sheep and goats was about three times higher than the same figure from the previous year. However, it was comparable to the proportion reported in 2013 for the same food commodity. It is noteworthy that the number of samples analysed in this food category was much higher in 2015 than in the two previous years (Figure 31) and that 389 from the 532 samples of ovine meat tested in 2015 were reported by a single MS (Belgium). The proportion of STEC-positive samples in meat from deer was much lower than that reported in 2014 but was only slightly lower than in 2013. The number of deer meat samples assayed for STEC was comparable, although very limited, being n = 23, n = 26 and n = 31 for 2013, 2014 and 2015, respectively. As in 2014, these figures were reported by two MS (Austria and the Netherlands), with one contributing the majority of the data (Austria).

As far as the other food categories are concerned, STEC were reported in proportions varying between 0.2% and 2.7% of the samples tested. In particular, STEC was isolated from milk (other than raw milk) and dairy products (2.7% of 2,719 samples), followed by raw milk (1.7% of 1,472 samples), fresh bovine meat (1.6% of 2,560 samples) and fresh meat from other animals (1.1% of 355 samples). 'Fruit and vegetables' and the category 'other food' showed percentages of positivity far below 1% (0.1% and 0.3% of 1,463 and 1,987 samples, respectively).

In 2015, two out of the 925 sprouted seeds samples were reported to contain STEC. As a whole, 12 MS reported data on STEC in this food category.



Data from industry own-control programmes, Hazard Analysis and Critical Control Point (HACCP), suspect sampling, selective sampling and outbreak or clinical investigations are not included in this graph. 'Fresh meat from other ruminants' includes meat from deer. 'Fresh meat from other animals' includes meat from horse, rabbit, wild boar, meat from poultry, meat from other poultry, meat from other animal species or not specified. Sprouted seeds are included in the fruit and vegetables food category. Pig meat (not included in the figure): 0% (N = 447) in 2013, 0.73% (N = 274) in 2014 and 4.9% (N = 308) in 2015. Broiler meat (2015: 0.8%, N = 609) and turkey meat (2015: 0%, N = 84) not included in the figure. Source 2013: 14 reporting MS (Austria, Belgium, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Hungary, Italy, the Netherlands, Poland, Slovakia and Spain); Source 2014: 19 reporting MS (Austria, Belgium, Cyprus, the Czech Republic, Denmark, Estonia, France, Germany, Hungary, Ireland, Italy, the Netherlands, Poland, Portugal, Slovakia, Slovenia, Spain, Sweden and the United Kingdom); Source 2015: 19 reporting MS (Austria, Belgium, the Czech Republic, Denmark, Estonia, France, Germany, Hungary, Ireland, Italy, Latvia, Luxembourg, the Netherlands, Portugal, Slovakia, Slovenia, Spain, Sweden and the United Kingdom).

Figure 31: Proportion of STEC-positive samples in food categories in the reporting Member States, 2013–2015

Results for the most important food categories that might serve as a source for human infection in the EU are presented below.

Fresh bovine meat

Cattle are the main recognised STEC reservoirs and bovine meat is considered to be a major source of food-borne STEC infections in humans. In 2015, 13 MS provided data from 2,560 units of fresh bovine meat tested for STEC (283 batches and 2,277 single samples), and 1.6% were positive (0.2% for STEC O157). The proportion of positive samples ranged from 0.7% of those taken at retail to 5.5% for samples taken at the processing plant. The proportion of STEC-positive samples at the slaughterhouse was 1.5%. The figure for positive samples was lower than those reported in 2014 for the samples taken at the slaughterhouse (2.4% in 2014) and at retail (3.5% in 2014), while that reported for the processing plant sampling stage was more than twice what was observed in 2014 (2.1%).

The 283 batch-based samples were all reported by one MS from slaughterhouses. One of them was positive for STEC O26. The remaining 2,277 single samples were collected at the slaughterhouse, processing plant and retail, as well as during border inspection activities. Twenty samples were reported by one MS (Sweden) collected at the latter sampling stage, with six samples positive for STEC (30%). Comparisons with similar data from previous years were not possible since this sampling stage was reported in 2015 only.

In 2015, the serogroups most frequently reported in bovine meat (including all types of bovine meat) were O157 (16 isolates), O26 (14), O148 (7 isolates), O145 (4), O8 (4), O103 (3), O91 (3), O130 (3), O174 (3) and O113 (2). The majority of these STEC serogroups are reported as cause of human disease (EFSA and ECDC, 2015b), confirming the importance of this food category in the epidemiology of STEC infections.

Fresh ovine and goat meat

Seven MS reported on 528 units of fresh ovine meat tested for STEC (all single samples) with 12.1% positive (Table 2015_STECOVINEMEAT). The proportion of STEC-positive samples reported in 2015 was much higher than how reported for the previous year (4.9%) (Figure 31). It is important to note that this figure might have been affected by the sample size. The total number of samples tested in 2015 was more than six times higher than in 2014, with more than 70% of these samples reported by a single MS (Belgium). Nevertheless, the proportion of positive samples in 2015 was comparable to what was observed in 2013.

Eight samples from ovine meat were positive for STEC O157, but serogroups O26 (8 samples), O103 (4) and O91 (2), all frequently reported in human infections (3), were also reported.

In 2014, two MS reported on fresh goat meat with one carcase positive for STEC O157 out of four analysed (Table 2015_STECGOATMEAT).

Fresh meat from other ruminants

In 2015, two MS provided information on fresh deer meat with 9.7% positive samples out of 31 tested in Austria (30 units) and the Netherlands (1). All the positive units were reported by Austria (Table 2015_STECOTHERMEAT). The proportion of STEC-positive samples from fresh deer meat was slightly lower than what was reported in 2013 and 2014 (Figure 31).

The main STEC serogroup reported in deer meet in 2015 (including all types of deer meat) was O146 (2 samples).

Fresh meat from other animal species

Six MS provided information from 296 single samples and 12 batches of pig meat tested, with 57.5% of the samples being carcases at the slaughterhouse. A total of 15 positive samples were reported (4.9%) with three STEC O157-positive samples from carcases (Table 2015_STECPIGSMEAT).

Information on meat from other animal species (meat from horse, rabbit, wild boar, meat from poultry, meat from other poultry, meat from other animal species or not specified) was provided by four MS (Italy, Austria, the Netherlands and Spain), and totalled 355 units tested (25 batches and 330 single samples). Non-O157 STEC were detected in three single samples of unspecified meat and in one wild boar sample (see Table 2015_STECOTHERMEAT). The findings are similar to those reported in previous years (Figure 31).

Data on the presence of STEC in meat from broilers and turkeys have been reported by three MS. A total of 84 samples from meat from turkeys and 609 from meat from broilers were tested with only five STEC O157-positive samples reported in broilers (2015_STECTURKMEAT and 2015_STECBROIMEAT).

Milk and dairy products

In 2015 seven MS reported data on STEC in samples of raw cow's milk (63 batches and 554 single samples), with 1.8% positive samples out of 617 tested (Table 2015_STECRAWCOWMILK). Two batch samples were positive for STEC O157, nine single samples were positive for STEC, with STEC O26 reported from two of them, while for the remaining seven positive single samples the STEC serogroup was not specified. Three MS provided information on 12 single units of raw milk from goats with STEC O103 detected in one sample (8.3%) (Table 2015_STECRAWGOATSMILK). No MS reported on raw milk from sheep. In addition, two MS provided information on 843 samples of raw milk from other animal species or unspecified, from which 13 STEC-positive samples were reported. Overall, the proportion of STEC-positive samples from raw milk was lower in 2015 than in 2014 and similar (although slightly lower) to what was reported in 2013 (Figure 31).

Ten MS reported on 2,719 samples of milk (excluding raw milk) and dairy products (1 batch and 2,718 single samples), and 2.7% were positive for STEC (Table 2015_STECDAIRY). The samples were mainly collected from cheese (84.5%), followed by milk (10.8%) and other types of dairy products

(4.7%). The proportion of positive units was higher for cheese samples (2.9%) than for milk samples (1.4%). Two positive samples were reported from the other dairy products. Six milk samples and one cheese sample were positive for STEC O157, as reported by two MS (Italy and Slovenia).

Sprouted and dry seeds

This food commodity is regulated by Regulation (EU) 209/2013[33] which establishes microbiological criteria for STEC in sprouted seeds. As an effect of the implementation of this regulation, a positive trend in the number of samples tested was observed in 2014 and confirmed in 2015. This figure increased from 616 samples, tested in 2013 by eight MS, to 761, reported by eight MS in 2014 up to 925 samples tested in 2015 by 12 MS (Table 2015_STECSEED). Two samples positive for STEC were reported in 2015, with one report of STEC O104:H4. This STEC serotype matched that of the STEC that caused the large German outbreak in 2011 (EFSA BIOHAZ Panel, 2013a) and its presence in sprouted seeds constitutes a non-compliance with regard to the EC regulation 209/2013. However, the MS reporting these data did not provide information on the presence of the enteroaggregative *E. coli* adhesion determinants, which characterised the German outbreak strain (EFSA BIOHAZ Panel, 2013a).

Vegetables and fruits

In 2015, 11 MS reported data on 1,069 vegetable units tested for STEC (96 batches and 973 single samples), of which only two samples from unspecified vegetables reported by Belgium were positive for STEC. There were no reports of STEC O157 from vegetables (Table 2015_STECVEGETABLE).

Six MS reported STEC-negative data from 394 units of fruits tested (37 batch and 357 single samples) (Table 2015_STECFRUITS).

Analysis of STEC serogroups in food

As previously done with 2014 monitoring data, the estimation of the proportion of food samples positive for the STEC serogroups most commonly reported in the EU (EFSA BIOHAZ Panel, 2013; EFSA and ECDC, 2015b) as a cause of HUS in children (O157, O26, O103, O111, and O145, the so called 'top five' serogroups), was achieved by considering only the analysis carried out using the method ISO/TS 13136:2012. This standard method is able to detect any STEC, and allows the identification of the STEC strains belonging to the 'top 5' serogroups. This subset of data can be considered homogeneous and may facilitate a more comparable estimation of the level of contamination with these STEC serogroups in the different food categories. In 2015, the proportion of food samples tested using the ISO TS 13136:2012 standard doubled that reported in 2014 reaching 82.8% (2015_STECANMETH), providing a solid base for estimating the prevalence of these STEC serogroups in food.

Among the 17,291 food samples tested by 17 MS and Switzerland using the ISO/TS 13136:2012, 319 (1.8%) were positive for STEC (Table 16), a proportion lower than that obtained for food samples tested by any analytical method (2.9%). Nevertheless, a methodological bias could have caused such a discrepancy. As a matter of fact, it has to be noted that 223 out of the 271 total samples positive for STEC O157 were detected by using the method ISO 16654:2001 or NMKL 164:2005 or DIN 10167:2004-03 (ISO, 2001; DIN, 2004; NMKL, 2005), which specifically aims at identifying STEC O157 through the immunomagnetic separation technique that it is also included in the ISO TS 13136:2012 standard. Therefore, it is conceivable that these latter samples would have also been found positive with the ISO TS 13136:2012. These 223 STEC O157-positive samples have not been included in the analysis of the top 5 STEC serogroups in food as the method(s) used for their detection did not allow detect other STEC serogroups possibly present in the food samples.

The top five STEC serogroups most frequently reported were O157 (31 samples) and O26 (29), followed by O103 (10), O145 (5) and O111 (1). The reported positive samples were mainly in meat-related food categories, including bovine, ovine and other ruminant meat, pig meat, followed by milk and dairy products, including raw milk (Table 16).

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[33] Commission Regulation (EU) No 209/2013 of 11 March 2013 amending Regulation (EC) No 2073/2005 as regards microbiological criteria for sprouts and the sampling rules for poultry carcases and fresh poultry meat. OJ L 68, 12.3.2013, p. 19–23.

Table 16: Proportion of positive samples for any STEC and STEC belonging to the 'top-5' serogroups in food categories in the Member States and non-Member States, 2015(a)

Food category(b)	Samples tested by ISO 13136	Samples positive for											
		Any STEC		**O157**		**O26**		**O103**		**O145**		**O111**	
	n	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**	**n**	**%**
Bovine meat	4,625	82	1.77	11	0.24	13	0.28	3	0.06	4	0.09	1	0.02
Ovine and goat meat	621	79	12.72	8	1.29	8	1.29	4	0.64	1	0.16	0	0.00
Other ruminants meat(c)	45	5	11.11	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Pig meat	859	22	2.56	1	0.12	0	0.00	0	0.00	0	0.00	0	0.00
Other meat(d)	2,743	43	1.57	2	0.07	2	0.07	0	0.00	0	0.00	0	0.00
Mixed meat	206	13	6.31	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Milk and dairy products(e)	3,185	41	1.29	4	0.13	4	0.13	1	0.03	0	0.00	0	0.00
Raw milk(f)	1,312	24	1.83	5	0.38	2	0.15	2	0.15	0	0.00	0	0.00
Fruit and vegetable	1,479	2	0.14	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Seeds(g)	942	2	0.21	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Other food	1,274	6	0.47	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Total	**17,291**	**319**	**1.84**	**31**	**0.18**	**29**	**0.17**	**10**	**0.06**	**5**	**0.03**	**1**	**0.01**

n: number of samples; STEC: Shiga toxin-producing *Escherichia coli*.
(a): Only samples tested by the ISO/TS 13136 method.
(b): The different meat categories presented in this table include all type of meat (not only fresh);
(c): Includes meat from deer.
(d): Includes meat from other animals (other than ruminants);
(e): Includes any type of dairy product, cheese and milk other than raw milk;
(f): Includes raw milk from different species, but the majority of the tested and all the positive samples were from cows;
(g): The majority of samples were sprouted seeds, but dry seeds are also included in this category.

The relative frequency of all the serogroups reported in the different food categories was estimated by computing the data reported for food samples obtained by applying any analytical method. In total, 612 STEC isolates from food samples were reported. For 434 of these, information on the serogroup was reported by 14 MS.

For 46 isolates, only the information that they did not belong to O157 serogroup (9 isolates) or that they did not belong to O157, O26, O103, O111 and O145 serogroups (37 isolates) was reported, while the STEC serogroup was determined for the remaining 388 isolates. Overall, the most frequently reported serogroup was STEC O157 with 271 isolates (44.3% of the total 612 STEC isolates). STEC O157 was reported in pig meat (74 isolates), and other meat (121 positive samples) categories followed by milk and dairy products (44), bovine meat (16), ovine meat (9), raw milk (6) and other food (1).

After O157, the second most reported serogroup was STEC O26 (4.7% of the total 612 STEC isolates, 7.5% of the 388 strains with an identified serogroup), followed by O103 (1.6% of the total 612 STEC isolates, 2.6% of the 388 strains with an identified serogroup), O145 (5 isolates) and O111 (1 isolate) among the top five STEC serogroups. Other STEC serogroups represented included O8 (9 isolates), O91 (7), O148 (7). It is important to observe that all the mentioned serogroups, with the possible exception of O148, are among the 20 most commonly reported in human infections in the EU in the period 2012–2014 (EFSA and ECDC, 2015b). Thirty other STEC serogroups were reported with a relative frequency below 1%.

The relative frequency distribution of the non-O157 STEC serogroups in the different food categories is shown in Table 17. STEC O26 and O103 were mainly isolated from milk, including raw milk, dairy product, ovine and bovine meat, while STEC O91 and O113 were mainly reported from meat products.

Table 17: Frequency distribution of non-O157 STEC serogroups in food categories in the Member States, 2015(a)

Food category(b)	STEC isolates with serogroup reported	STEC serogroups														
		% of total STEC isolates with serogroup reported in the specific food category														
	n	O26	O103	O145	O111	O146	O91	O76	O113	O5	O174	O87	O116	O6	Other serogroups (list)	
Bovine meat	53	26.4	5.7	7.5	1.9	0.0	5.7	0.0	3.8	0.0	5.7	1.9	1.9	0.0	39.6	(O128, O130, O136, O148, O153, O172, O178, O55, O79, O8)
Ovine and goat meat	27	29.6	14.8	3.7	0.0	7.4	7.4	0.0	0.0	3.7	0.0	0.0	0.0	7.4	25.9	(O104, O117, O128, O178, O38, O75, O8)
Other ruminants meat(c)	5	0.0	0.0	0.0	0.0	40.0	0.0	20.0	0.0	0.0	0.0	0.0	0.0	0.0	40.0	(O110, O8)
Pig meat	3	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	100.0	(O141, O179, O74)
Other meat(d)	16	12.5	0.0	0.0	0.0	6.3	12.5	6.3	0.0	0.0	6.3	0.0	0.0	0.0	56.3	(O21, O27, O38, O55, O8, O88)
Mixed meat	1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	
Milk and dairy products(e)	5	80.0	20.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
Raw milk(f)	4	50.0	50.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
Fruit and vegetable	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	0.0	0.0	
Seeds	1	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	100.0	(O104)
Other food	2	0.0	0.0	0.0	0.0	0.0	0.0	50.0	0.0	0.0	0.0	0.0	0.0	0.0	50.0	(O149)
Total	**117**	**25.6**	**8.5**	**4.3**	**0.9**	**4.3**	**6.0**	**2.6**	**1.7**	**0.9**	**3.4**	**0.9**	**1.7**	**1.7**	**37.6**	**(O104, O110, O117, O128, O130, O136, O141, O148, O149, O153, O172, O178, O179, O21, O27, O38, O55, O74, O75, O79, O8, O88)**

Note: data originating from any analytical method are included.

(a): Non-O157 STEC serogroups are listed according to their public health relevance as a cause of human infections in the EU.

(b): The different meat categories presented in this table include all type of meat (not only fresh).

(c): Includes meat from deer.

(d): Includes meat from animals other than ruminants and pigs.

(e): Includes any type of dairy product, cheese and milk other than raw milk.

(f): Includes raw milk from different species, but the majority of tested samples and all the positive samples were from cows.

Trends in the reporting of STEC serogroups in food

The proportion of food samples positive for the STEC serogroups most frequently reported by MS and non-MS between 2012 and 2015 was analysed and is reported in Figure 32. Due to the low number of positive samples for each food category, data were presented aggregated for the total of all food samples tested. The increasing trend of reporting for STEC O26 in food observed in 2014 was confirmed in 2015. STEC O8 was not reported in the previous years, but is one of the 20 most frequent STEC serogroups isolated from human disease and reported to the ECDC (EFSA and ECDC, 2015b). A decreasing trend in the reporting of STEC O157 in the last 3 years can be observed in parallel with the increase in the reporting of STEC O26 (Figure 32).

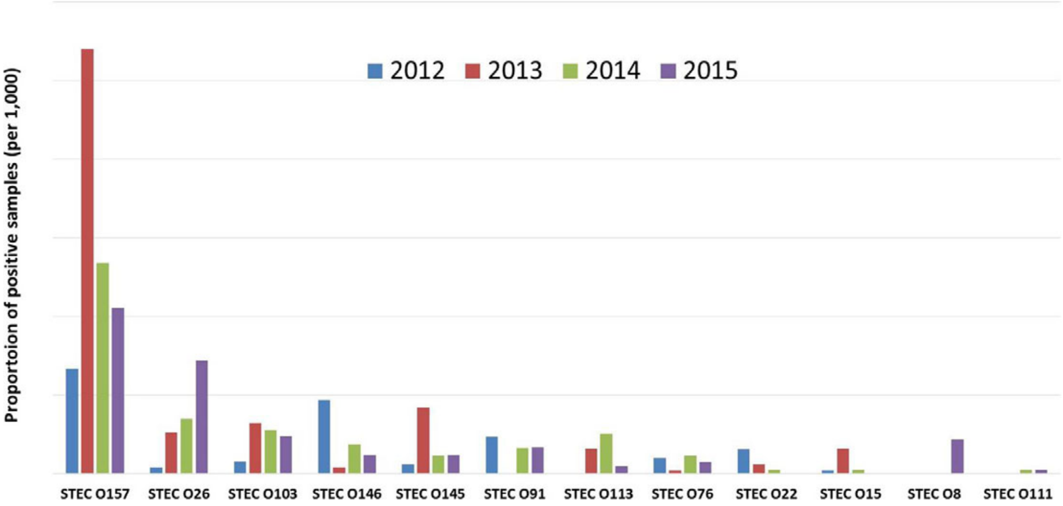


Figure 32: Proportion of food samples positive for the most frequent STEC serogroups (per 1,000 samples tested), reported by the Member States and non-Member States, 2012–2015

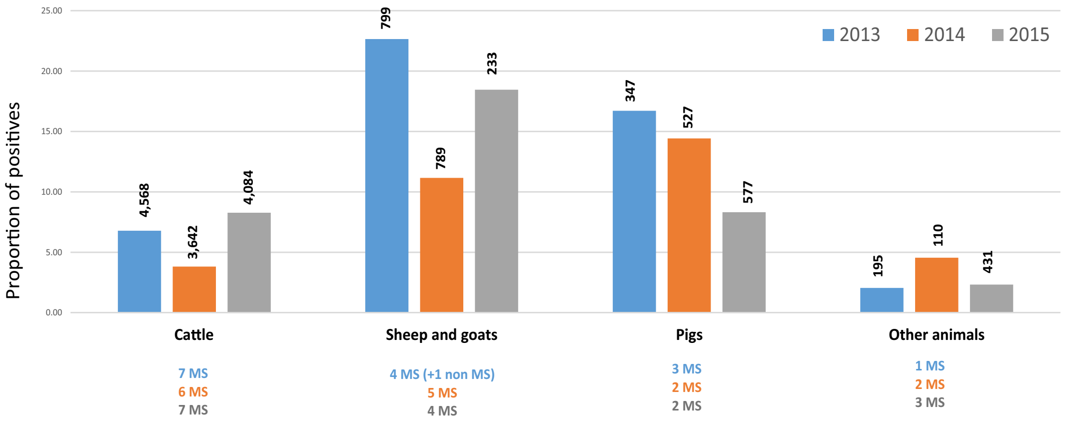
3.4.2.2. Shiga toxin-producing *Escherichia coli* in animals

Overall, data on STEC in animals were provided by 11 MS (6,881 samples tested in total) (Table 2015_STECANMETH), 10 of which followed the EFSA technical specifications for the monitoring and reporting of STEC (2) and adapted the standard methods ISO/TS 13136:2012, ISO 16654:2001 NMKL 164:2005 and DIN 10167:2004-3 (ISO, 2012, 2001; NMKLz, 2005; DIN, 2004) to test animal samples. A total of 6,510 samples (94.6%) were tested by these methods, while the use of in house PCR-based methods and unspecified microbiological tests were reported for 4.1% and 1.3% of the samples, respectively. Detailed information on the use of the different analytical methods for testing samples from animals is presented in specific tables, as indicated in Appendix A.

The proportion of STEC-positive samples in the main animal species, regardless the analytical method employed, is shown in Figure 33, in comparison with the proportions reported in 2013 and 2014.

Overall the presence of STEC was reported in 6.8% of the 6,881 animal samples tested in 2015. The highest prevalence was reported in sheep and goats (18.5%), followed by cattle (8.3%) and pigs (8.3%). The proportion of positive samples in pigs was lower than that reported in 2014 and 2013, while for cattle an increase in the number of samples positive for STEC was observed in comparison with the previous years (Figure 33). As in the previous year, the testing results may have been influenced by MS-specific results, as most data on pigs were reported by a single MS (Germany). All the samples from pigs were tested with the adaptation of the ISO TS 13136:2012 to animal samples, but no details were provided on the serogroups and virulence genes (*stx1*, *stx2*, *eae*) of the STEC strains isolated.

Results for the animal categories most relevant for the epidemiology of STEC infections are presented below.



Data from suspect sampling, selective sampling, and clinical investigations were not included in this graph. Other animals include: cats, dogs, horses, donkeys, pigeons, deer, pheasant, shellfish, steinbock, turkeys and other animals. Source 2013: Austria, Belgium, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Hungary, Italy, the Netherlands, Poland, Slovakia, Spain and Norway. Source 2014: Austria, Denmark, Estonia, Finland, Germany, Italy, the Netherlands and the United Kingdom. Source 2015: Denmark, Finland, Germany, Ireland, Italy, the Netherlands, Spain, Sweden and the United Kingdom.

Figure 33: Proportion of STEC-positive samples in animal categories in the Member States and non-Member States, 2013–2015

Cattle

Seven MS reported 4,084 units of cattle tested for STEC (3,321 animals, 5 herds and 758 slaughter batches) and six MS reported positive findings. In total, 8.3% of the samples was positive for STEC and 2.7% for STEC O157 (Figure 33 and Table 2015_STECCATTLE). The overall proportion of STEC-positive units found in cattle was higher than that reported in the previous 2 years (Figure 33). As a matter of fact, the number of positive units follows the rate of adoption of the method, with 43.4% of the animal samples tested with the ISO TS 13136:2012 in 2015, compared to the 1.2% and 8.5% of samples tested in 2014 and 2013, respectively.

Finland and Sweden reported STEC O157-positive results for 2.9% of 625 units and 2.2% of 1,492 units, respectively. In both countries, the specimens from cattle were specifically tested for STEC O157. Spain reported 13.8% of STEC O157 positive units from 383 specimens, all tested using the adaptation of the ISO TS 13136:2012. Of the 92 samples analysed in Denmark, 10 were reported as being positive for STEC, with six of them of O157 serogroup. Germany reported that 18.6% of the 980 cattle samples were positive for STEC, but did not report information on the serogroup. Italy reported 29.2% of STEC-positive samples, among the 144 analysed with no STEC O157. Finally, Ireland found no STEC-positive samples among the total 368 units assayed.

A total of five STEC serogroups were reported among the STEC-positive cattle samples. These included O1, O2, O103, O121 and O157. STEC O157 represented the most frequent serogroup. Among the STEC non-O157, the STEC serogroup O2 was the most frequently reported in cattle.

Sheep and goats

In 2015, four MS reported 233 units of sheep and goats tested for STEC (167 animals and 66 herds), and 18.4% was positive. Thirteen samples were positive for STEC O157 (5.6%) (Figure 33; Table 2015_STECOVINEGOAT). In sheep, 41 out of 207 tested units (19.8%) were positive, compared with 2 out of 26 tested units in goats (7.7%). The highest prevalence of STEC was reported by Spain in the caecal content of sheep (53.7% positive out of 54 animals tested), among which 24.1% were STEC O157.

Pigs

Pigs were tested for STEC in two MS (Germany and Italy), which reported on 577 units from single animals (Figure 33). In particular, Germany found 10.1% of 475 animals positive for STEC (Table 2015_STECPIGS). However, no information on the serogroup of the isolated strains was reported. All the 102 animals tested in Italy were negative for STEC.

Other animal species

Three MS reported data on 431 units tested for STEC and sampled from cats, dogs, solipeds (horses and donkeys), pheasant, pigeons, poultry including *G. gallus* and turkey, steinbock and water buffaloes. Positive findings were reported by Germany in dogs (2 out of 46 samples tested) horses (2 out of the 17 samples tested) and poultry (1 out of the 23 samples tested). Italy reported on the presence of five unspecified STEC out of 39 water buffaloes sampled. The overall proportion of STEC-positive units was 2.3%. STEC O157 was not reported (Table 2015_STECOTHERANIMAL). However, when the whole set of submitted data was used for serogroup analyses, STEC O157 (n = 3) were reported in dogs and cats sampled in Slovakia, together with one report of a STEC O2 in three deer samples in Italy (Table 18). Moreover, five STEC of unspecified serogroup were reported by Germany in different animal categories.

STEC serogroups in animals

Eight MS provided information on 467 STEC-positive samples from animals (6.8% of the total 6,881 animal samples tested). Overall, 145 STEC O157-positive samples from animals were reported by seven MS (2.1% of the total 6,881 animal samples tested) (Table 18). The proportion of STEC O157-positive samples in cattle was 2.5%. A higher prevalence of STEC O157 was reported for sheep and goats (4.6%) while for 'other animals' category this figure was below 1%.

The information on the STEC serogroups was provided for 226 strains out of the total 467 positive samples obtained using any analytical method. For 16 samples the generic description of the non-O157 serogroup was reported. STEC O157 was the most common serogroup (69% of the 210 strains with an identified serogroup). As for the non-O157 sergroups identified in STEC from animals, O2 was the most reported with more than 50% of the non-O157 isolates with serogroup reported falling within this serogroup (Table 19). STEC O2, was mainly detected in cattle and represented the only serogroup other than O157 reported in other ruminants. STEC O1 was the second most common reported serogroup in non-O157 animals isolates, representing the 24.6% of the non-O157 isolates with serogroup reported. Sixteen STEC O1 strains were reported from 15 cattle and one from pigs. Other serogroups reported were O121 (13.8% with 9 isolates, eight from cattle and one from sheep and goat) and O103 (4.6% with three isolates from cattle) (Table 19). The latter two serogroups are among those most commonly found as a cause of human infections in the EU/EEA in the preceding years (EFSA and ECDC, 2015).

Table 18: Frequency distribution of STEC serogroups in animals in the Member States, 2015

Animal category	Samples tested for STEC by any method				
		Positive (any STEC)		Positive for STEC O157	
	n total	n	%	n	%
Cattle	5,037	355	7.0	127	2.5
Goat and sheep	281	45	16.0	13	4.6
Other ruminants(a)	208	3	1.4	0	0.0
Pigs(b)	598	49	8.2	0	0.0
Other animals(c)	757	15	2.0	5	0.7
Total	**6,881**	**467**	**6.8**	**145**	**2.1**

Note: data originating from any analytical method are included.
(a): Includes only deer.
(b): Includes also wild boar.
(c): Includes birds, cats, dogs, fowl, solipeds and turkeys.

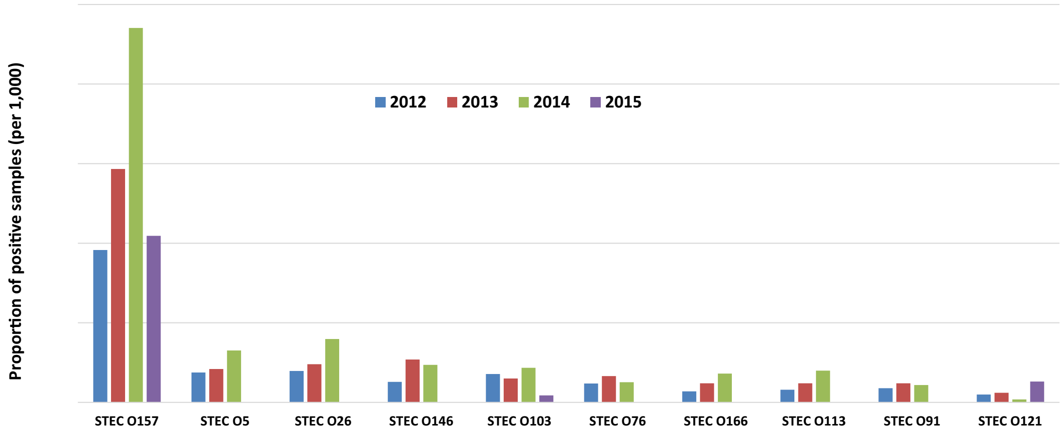
Table 19: Frequency distribution of non-O157 STEC serogroups in animals in the Member States, 2015[(a)]

Animal category	STEC isolates with serogroup reported	STEC serogroups % of total STEC isolates with serogroup reported in the specific animal category			
	n	O2	O1	O121	O103
Cattle	60	56.7	25.0	13.3	5.0
Goat and sheep	1	0.0	0.0	100.0	0.0
Other ruminants[(b)]	3	100.0	0.0	0.0	0.0
Pigs[(c)]	1	0.0	100.0	0.0	0.0
Other animals[(d)]	0	0.0	0.0	0.0	0.0
Total	**65**	**56.9**	**24.6**	**13.8**	**4.6**

Note: data originating from any analytical method are included.
(a): Non-O157 STEC serogroups are listed according to their occurrence in the animal samples tested.
(b): Includes only deer.
(c): Includes also wild boar.
(d): Includes birds, cats, dogs, fowl, solipeds and turkeys.

Trends in the reporting of STEC serogroups in animals

The proportion of animal samples positive for the STEC serogroups most frequently reported by MS and non-MS between 2012 and 2015 was analysed and is shown in Figure 34. Due to the low number of positive samples for each animal category, data were presented aggregated for the total animal samples tested. In 2015 only five STEC serogroups were reported in animal samples. Three of them, STEC O157, O103 and O121, matched those most frequently reported in the previous years and are among the STEC serogroups most involved in human infections in the EU (EFSA and ECDC, 2015b). Additional serogroups reported in 2015 in animal samples include O1 and O2.



Serogroups O1 and O2 were not included in the figure as they were only reported in 2015. Serogroups O166, O113 and O91 were not reported in 2015.

Figure 34: Proportion of animal samples positive for the most frequent STEC serogroups (per 1,000 samples tested), reported by the Member States and non-Member States, 2012–2015

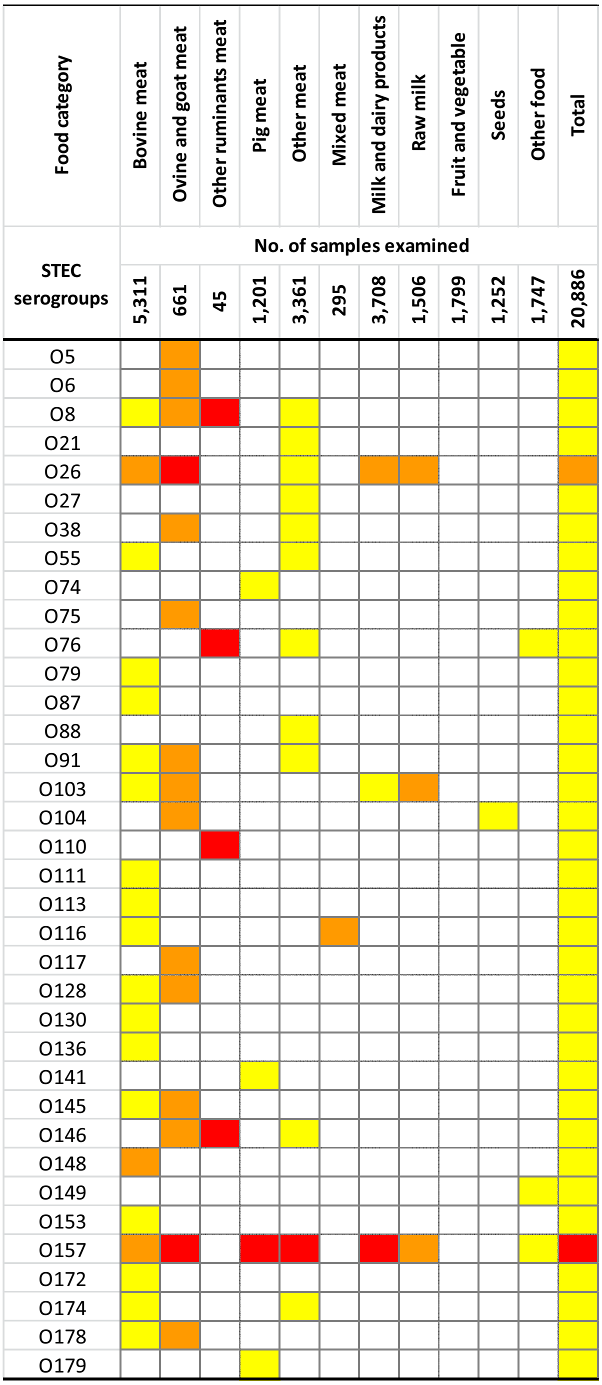
3.4.2.3. Atlas of the STEC serogroups reported in food and animals in the EU in 2015

The data on the STEC serogroups provided by MS in 2015 were used to generate an 'atlas' of the presence/absence of the STEC serogroups. Information on the reporting of the different STEC serogroups in food and animal samples in the EU between 2011 and 2015 is presented in Figure 35. The relative presence and absence of STEC serogroups reported in 2015 in the different food and animal categories is presented in Figures 36 and 37.

Food	2011	2012	2013	2014	2015	Animals	2011	2012	2013	2014	2015
	No of samples tested						No of samples tested				
STEC serogroups	32,767	25,547	25,008	21,671	20,886	STEC serogroups	8,392	10,134	6,683	5,526	6,881
O1						O1			🟥		🟥
O2			🟥			O2	🟥		🟥		🟥
O5				🟥	🟥	O5	🟥	🟥	🟥	🟥	
O6				🟥	🟥	O6	🟥	🟥		🟥	
O8	🟥			🟥	🟥	O8			🟥		
O13					🟥	O13	🟥				
O15		🟥	🟥	🟥		O15		🟥			
O17		🟥				O17	🟥				
O21		🟥		🟥	🟥	O21					
O22		🟥	🟥	🟥		O22	🟥	🟥	🟥	🟥	
O26	🟥	🟥	🟥	🟥	🟥	O26	🟥	🟥	🟥	🟥	
O27	🟥	🟥			🟥	O27		🟥			
O36		🟥				O36		🟥			
O38					🟥			🟥			
O39						O39	🟥	🟥	🟥		
O43				🟥	🟥	O43		🟥			
O46						O46		🟥			
O50						O50			🟥		
O51		🟥				O51					
O55		🟥		🟥	🟥	O55			🟥		
O74		🟥		🟥	🟥	O74		🟥			
O75		🟥			🟥	O75	🟥	🟥	🟥	🟥	
O76		🟥	🟥	🟥	🟥	O76	🟥	🟥	🟥	🟥	
O78			🟥			O78					
O79					🟥	O79		🟥		🟥	
O81						O81		🟥	🟥	🟥	
O82						O82	🟥		🟥	🟥	
O87			🟥	🟥	🟥	O87	🟥	🟥	🟥	🟥	
O88				🟥	🟥	O88					
O89						O89		🟥			
O91	🟥	🟥		🟥	🟥	O91	🟥	🟥	🟥	🟥	
O96						O96	🟥				
O103	🟥	🟥	🟥	🟥	🟥	O103	🟥	🟥	🟥	🟥	🟥
O104[a]	🟥	🟥			🟥	O104[b]	🟥			🟥	
O105	🟥					O105					
O107		🟥				O107	🟥	🟥	🟥		
O108						O108	🟥				
O109						O109		🟥		🟥	
O110		🟥			🟥	O110					
O111				🟥	🟥	O111	🟥	🟥		🟥	
O112						O112	🟥	🟥	🟥	🟥	
O113			🟥	🟥	🟥	O113	🟥	🟥	🟥	🟥	
O116				🟥	🟥	O116				🟥	
O117					🟥	O117	🟥				
O121						O121		🟥	🟥	🟥	🟥
O128		🟥			🟥	O128	🟥	🟥	🟥	🟥	
O129						O129		🟥			
O130		🟥		🟥	🟥	O130					
O132						O132			🟥		
O136			🟥		🟥	O136					
O137						O137		🟥			
O139				🟥		O139				🟥	
O141					🟥	O141				🟥	
O142				🟥		O142					
O143		🟥				O143					
O145	🟥	🟥	🟥	🟥	🟥	O145	🟥		🟥	🟥	
O146		🟥	🟥	🟥	🟥	O146	🟥	🟥	🟥	🟥	
O148					🟥	O148				🟥	
O149					🟥	O149			🟥	🟥	
O150						O150		🟥			
O153		🟥		🟥	🟥	O153			🟥		
O157	🟥	🟥	🟥	🟥	🟥	O157	🟥	🟥	🟥	🟥	🟥
O160						O160	🟥				
O166		🟥				O166	🟥	🟥	🟥	🟥	
O168						O168	🟥	🟥	🟥		
O172	🟥				🟥	O172					
O174		🟥		🟥	🟥	O174	🟥	🟥	🟥	🟥	
O176				🟥		O176		🟥	🟥	🟥	
O177						O177	🟥			🟥	
O178			🟥		🟥	O178	🟥	🟥	🟥	🟥	
O179					🟥	O179	🟥	🟥	🟥	🟥	
O181		🟥				O181	🟥			🟥	
O182				🟥		O182					
O183				🟥		O183	🟥	🟥	🟥	🟥	
O185						O185		🟥	🟥	🟥	
O186						O186	🟥				

Presence (red boxes) and absence of STEC serogroups in foods (left) and animals (right). (a) *E. coli* O104:H4 *stx*2+ *eae*- isolated from sprouted seeds in 2015. No information was provided on the H type and genotype of the *E. coli* O104 strains isolated from food in the previous years. (b) An *E. coli* O104:H8 strain, with the genotype *stx*1-, *stx*2+, *eae*- isolated in 2011 from cattle; an *E. coli* O104:H7 strain, with the genotype *stx*1+, *stx*2-, *eae*- isolated in 2014 from sheep.

Figure 35: Trend in the presence of the different STEC serogroups in food and animals reported in the EU and non-MS between 2011 and 2015

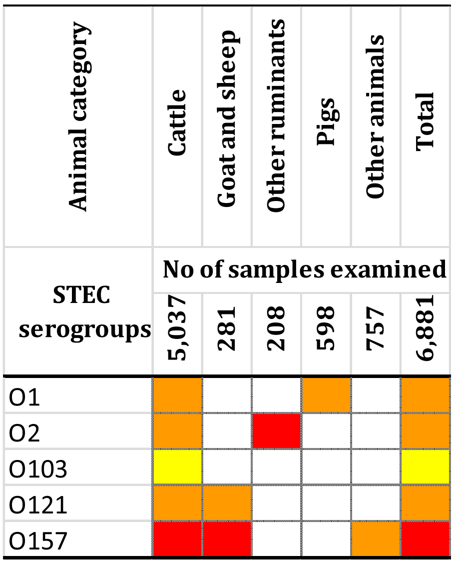


Food category	Bovine meat	Ovine and goat meat	Other ruminants meat	Pig meat	Other meat	Mixed meat	Milk and dairy products	Raw milk	Fruit and vegetable	Seeds	Other food	Total
	No. of samples examined											
STEC serogroups	5,311	661	45	1,201	3,361	295	3,708	1,506	1,799	1,252	1,747	20,886
O5		🟧										🟨
O6		🟧										🟨
O8	🟨	🟧	🟥		🟨							🟨
O21					🟨							🟨
O26	🟧	🟥			🟨		🟧	🟧				🟧
O27					🟨							🟨
O38		🟧			🟨							🟨
O55	🟨				🟨							🟨
O74				🟨								🟨
O75		🟧										🟨
O76			🟥		🟨						🟨	🟨
O79	🟨											🟨
O87	🟨											🟨
O88					🟨							🟨
O91	🟨	🟧			🟨							🟨
O103	🟨	🟧					🟨	🟧				🟨
O104		🟧								🟨		🟨
O110			🟥									🟨
O111	🟨											🟨
O113	🟨											🟨
O116	🟨					🟧						🟨
O117		🟧										🟨
O128	🟨	🟧										🟨
O130	🟨											🟨
O136	🟨											🟨
O141				🟨								🟨
O145	🟨	🟧										🟨
O146		🟧	🟥		🟨							🟨
O148	🟧											🟨
O149											🟨	🟨
O153	🟨											🟨
O157	🟧	🟥		🟥	🟥		🟥	🟧			🟨	🟥
O172	🟨											🟨
O174	🟨				🟨							🟨
O178	🟨	🟧										🟨
O179				🟨								🟨

Presence and proportions of STEC serogroups in food categories, sampled in 21 MS and in Iceland and Switzerland in 2015. Total number of samples examined per each food category is also reported. Proportions of STEC serogroups: red boxes > 1%, orange boxes > 0.1% and ≤ 1%, yellow boxes > 0.0001% and ≤ 0.1% of positive samples. White boxes indicate absence of the serogroup. 'Other ruminants meat' includes meat from deer. 'Other meat' includes meat from other animals (other than ruminants). 'Milk and dairy products' include any type of dairy product, cheese and milk other than raw milk. 'Raw milk' includes raw milk from different species, but the majority of the tested and all the positive samples were from cows. 'Seeds' include mostly sprouted seeds, but dry seeds are also included.

Figure 36: Relative presence (coloured boxes) and absence of STEC serogroups in foods, sampled in the EU in 2015

It is important to underline that the differences in the sampling strategies and analytical methods applied by reporting countries do not allow confirmation of the existence of specific trends in the geographical distribution of STEC serogroups.



Animal category	Cattle	Goat and sheep	Other ruminants	Pigs	Other animals	Total
	No of samples examined					
STEC serogroups	5,037	281	208	598	757	6,881
O1	🟧	⬜	⬜	🟧	⬜	🟧
O2	🟧	⬜	🟥	⬜	⬜	🟧
O103	🟨	⬜	⬜	⬜	⬜	🟨
O121	🟧	🟧	⬜	⬜	⬜	🟧
O157	🟥	🟥	⬜	⬜	🟧	🟥

Presence and proportions of STEC serogroups in animals sampled in 11 MS in 2015. Total number of samples examined per each food category is also reported. Proportions of STEC serogroups: red boxes > 1%, orange boxes > 0.1% and ≤ 1%, yellow boxes > 0.0001% and ≤ 0.1% of positive samples. White boxes indicate absence of the serogroup. The animal category 'other ruminants' includes deer, capricorns and mouflons. The Pigs category includes also wild boars. The Other animal category comprises birds, cats, dogs, fowl, solipeds, turkeys.

Figure 37: Relative presence (coloured boxes) and absence of STEC serogroups in animals sampled in the EU in 2015

3.4.3. Discussion

STEC was the fourth most commonly reported zoonosis in the EU in 2015, with 5,901 confirmed human cases. The EU/EEA trend for STEC infections has increased from 2008 to 2013, but it seems have stabilised since then. Part of the increase may be explained by increased general awareness of STEC following the largest ever reported STEC outbreak in 2011. One year after the outbreak, a 1.8-fold increase in the EU/EEA notification rate was observed compared to the year before the outbreak. Other contributing factors are probably the increasing number of laboratories testing for serogroups other than O157 and the shift in diagnostic methods with PCR being more commonly used for detection of STEC. The EU notification rate was 1.27 cases per 100,000 population. In 2015, one new country (Portugal) started to report, so the overall population denominator increased, leading to a slightly lower rate compared with 2014.

Of the STEC cases with known hospitalisation status, more than one-third was hospitalised. Some countries reported very high proportions of hospitalised cases, but had notification rates that were among the lowest, indicating that the surveillance systems in these countries primarily capture the most severe cases. However, the reported case fatality of STEC cases was low. As in previous years, the most commonly reported serogroup was O157, followed by O26, and, less commonly, O103, O91, O145, O146 and O128. In addition, a high proportion of non-typed STEC strains were reported. Serogroups O157 and O26 were also the most common among HUS cases.

In 2015, data on the presence of STEC in food and animals were reported by 21 MS and two non-MS. As in the previous year, the lack of data from seven MS still represents a critical aspect of the data collection. STEC are, in fact, included among the pathogens with the highest priority, as laid down in the EU Directive 99/2003/EC.

Most reporting countries (19 MS and one non-MS) provided data obtained by applying the analytical methods indicated by the EFSA technical specifications for the monitoring and reporting of STEC (EFSA, 2009b). Notably, the methods indicated in the EFSA technical specifications were used to analyse 92.3% of the total number of samples, respectively, constituting 91.6% of the food samples and 94.6% of the animal samples. Only for 8.4% of food samples and 5.4% of animal samples the method used was different from that specified in the EFSA technical specifications or not reported. For these samples the method used remained not classified.

More importantly, the proportion of food samples tested by the ISO TS 13136:2012 standard, the reference method for the detection of STEC in food, or equivalent methods reached 82.8% in 2015. This is a notably increase compared with 2014, when 41.4% of the food samples were tested using ISO TS 13136:2012 standard or equivalent methods (EFSA and ECDC, 2015). The use of a common method meets the principles of standardisation and allows a more homogenous analysis of the results. However, the number of samples tested by the reporting countries for each food and animal category was highly variable, and such an unequal distribution may have introduced selection bias in the estimates of STEC prevalence or STEC serogroup distribution.

Overall, the presence of STEC was reported in 2.9% of the 20,886 tested food samples and in 6.8% of the 6,881 animal samples tested. The highest proportion of STEC-positive food samples was reported for fresh meat from sheep and goat (12.2% of the samples tested), followed by meat from other ruminants (9.7%), although for the latter category the figure referred to a limited number of samples of deer meat reported by two MS only. Positive samples were also reported in cheese (2.9%), 'raw milk' from different animal species (1.7%), 'milk and dairy products' (2.7%) as well as fresh bovine meat (1.6%), whereas the proportion of positive samples in fruit, vegetables and sprouted seeds was below 0.2%. For the latter category, the sole for which microbiological criteria for STEC have been established in the EU, only two positive samples were reported out of the 925 analysed. For one sample, STEC O104:H4 was reported. This STEC serotype matched that of the STEC that caused the large German outbreak in 2011 (EFSA BIOHAZ Panel, 2013a) and its presence in sprouted seeds constitutes a non-compliance with regard to the EC regulation 209/2013. However, the MS reporting this data did not provide information on the presence of the enteroaggregative *E. coli* adhesion determinants, which characterised the German outbreak strain (EFSA BIOHAZ Panel, 2013a).

Among animals, the reported proportion of STEC-positive samples was higher for sheep and goats (18.5%) than for cattle (8.3%) and pigs (8.3%). The figures related with the same animal categories were lower in 2013 and 2014 except for pigs, for which a higher proportion of STEC-positive samples was reported in 2014. As far as pigs are concerned, the data from both 2014 and 2015 may have been influenced by MS-specific results, being reported by only two MS with the majority of the positive reports from one single MS in both years.

Generally, higher proportions of STEC-positive samples were reported in 2015 for both food and animals (2.9% and 6.8%, respectively), compared to the same figures described in 2014 (1.6% and 6.3%, respectively). This finding may be due to the increased adoption of the ISO TS 13136:2012 standard. More than 80% of food samples and 43.4% of the animal samples were tested with the ISO TS 13136:2012 in 2015. This method allows detection of STEC without selecting for specific serogroups representing an unbiased approach for the detection of STEC.

A wide range of STEC serogroups was reported in food, with STEC O157 being the most frequent. Similarly, this STEC serogroup prevailed in animal samples. However, it should be noted that many of the MS's surveillance and monitoring programmes are traditionally focused on this serogroup and this may have introduced a bias in the estimates of the frequency of STEC serogroups. In this respect, it is important to note that the trend of reporting of STEC O26 increased in the last 3 years in parallel with a decrease in the reporting of STEC O157 and that in 2015 the proportion of STEC of serogroup O26 matched that of STEC O157 in the food samples that were tested using the ISO/TS 13136:2012 standard method. Such a picture can be explained by the replacement of the STEC O157-based methods (ISO, 2001; DIN, 2004; NMKL, 2005) with the unbiased ISO TS 13136:2012 international standard. In contrast with the variety of STEC serogroups reported in food, only four serogroups other than O157 (O2, O1, O121 and O103) were reported from animal samples in 2015.

The analysis of the data on the presence of STEC in food and animals in 2015 and the comparison with the same data from the previous years indicates that a step forward has been taken towards the harmonisation of analytical process for food and animal testing in the EU. The large adoption of the ISO TS 13136:2012 method has caused the data to be more homogenous and returned a more sensitive and comprehensive picture of the circulation of this pathogen in the different food and animal categories.

3.5. *Yersinia*

The Appendix A lists all summaries made for the production of this section, for humans, foods and animals, including *Yersinia* summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.5.1. Yersiniosis in humans

A total of 7,202 confirmed cases of yersiniosis were reported in the EU for 2015 by 26 MS (Table 20). The number of confirmed cases increased by 8.7% compared with 2014. Portugal reported data for the first time in 2015. In Spain, improved coverage of the surveillance system for yersiniosis has resulted in an increase of confirmed cases by 77.8% since 2013. The EU notification rate was 2.2 cases per 100,000 population, which was 6.8% higher than in 2014. The highest country-specific notification rates were observed in Finland and Denmark (10.64 and 9.54 cases per 100,000 population, respectively).

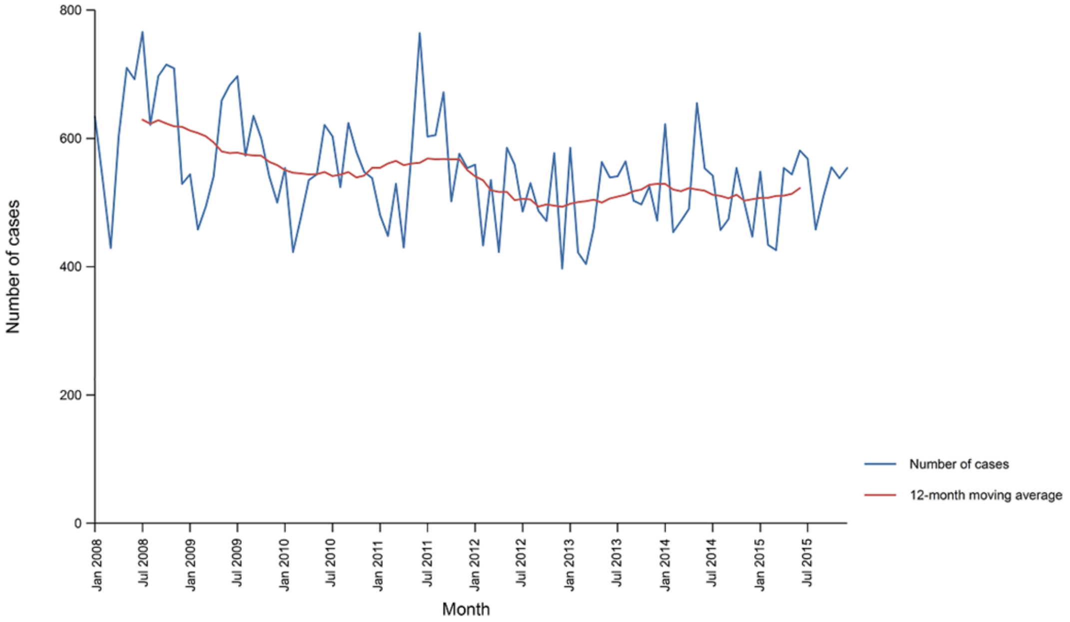
Most of the yersiniosis cases reported in the EU acquired the infection within their own country (53.8% domestic cases, 5.2% travel-associated and 40.9% of unknown origin). Among the 206 travel-associated cases, Turkey and Spain were the most common probable countries of infection, representing 14.6% and 11.2% of the travel-associated cases, respectively.

Table 20: Reported human cases of yersiniosis and notification rates in the EU/EEA, by country and year, 2011–2015

Country	2015					2014		2013		2012		2011	
	National coverage$^{(a)}$	Data format$^{(a)}$	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	118	118	1.38	107	1.26	158	1.87	130	1.55	119	1.42
Belgium$^{(b)}$	N	A	350	350	–	309	–	350	–	256	–	214	–
Bulgaria	Y	A	12	12	0.17	20	0.28	22	0.30	11	0.15	4	0.05
Croatia	Y	A	16	16	0.38	20	0.47	0	0.00	0	0.00	–	–
Cyprus	Y	C	0	0	0.00	0	0.00	1	0.12	0	0.00	0	0.00
Czech Republic	Y	C	678	678	6.39	557	5.30	526	5.00	611	5.82	460	4.39
Denmark	Y	C	540	540	9.54	434	7.71	345	6.16	291	5.22	225	4.05
Estonia	Y	C	53	53	4.04	62	4.71	72	5.45	47	3.55	69	5.19
Finland	Y	C	582	582	10.64	579	10.62	549	10.12	565	10.46	554	10.31
France$^{(b)}$	N	A	624	624	–	574	–	430	–	314	–	294	–
Germany	Y	C	2,752	2,739	3.37	2,470	3.06	2,579	3.15	2,690	3.29	3,381	4.21
Greece$^{(c)}$	–	–	–	–	–	–	–	–	–	–	–	–	–
Hungary	Y	C	41	41	0.42	43	0.44	62	0.63	53	0.54	93	0.93
Ireland	Y	C	13	13	0.28	5	0.11	4	0.09	2	0.04	6	0.13
Italy$^{(b)}$	N	C	16	16	–	18	–	25	–	14	–	15	–
Latvia	Y	C	67	64	3.22	28	1.40	25	1.24	28	1.37	28	1.35
Lithuania	Y	C	165	165	5.65	197	6.69	262	8.82	276	9.19	370	12.12
Luxembourg	Y	C	15	15	2.66	19	3.46	15	2.79	28	5.33	14	2.74
Malta	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Netherlands$^{(c)}$	–	–	–	–	–	–	–	–	–	–	–	–	–
Poland	Y	C	172	172	0.45	212	0.56	199	0.52	201	0.52	235	0.62
Portugal	Y	C	24	24	0.23	–	–	–	–	–	–	–	–
Romania	Y	C	25	25	0.13	32	0.16	43	0.22	26	0.13	47	0.23
Slovakia	Y	C	226	224	4.13	172	3.18	164	3.03	181	3.35	166	3.08
Slovenia	Y	C	10	10	0.48	19	0.92	26	1.26	22	1.07	16	0.78
Spain$^{(d)}$	N	C	475	432	2.07	436	2.08	243	1.73	221	1.89	264	2.26
Sweden	Y	C	245	245	2.51	248	2.57	313	3.28	303	3.20	350	3.72
United Kingdom	Y	C	44	44	0.07	58	0.09	59	0.09	54	0.09	59	0.09
EU Total	–	–	**7,263**	**7,202**	**2.20**	**6,619**	**2.06**	**6,472**	**2.05**	**6,324**	**2.05**	**6,983**	**2.33**
Iceland	Y	C	1	1	0.03	3	0.92	0	0.00	–	–	–	–
Norway	Y	C	76	76	1.47	211	4.13	55	1.09	43	0.86	60	1.22

(a): Y: yes; N: no; A: aggregated data; C: case-based data; –: no report.
(b): Sentinel surveillance; no information on estimated coverage; thus, notification rate cannot be estimated.
(c): No surveillance system.
(d): Sentinel system; notification rates calculated with estimated population coverage of 45% in 2014–2015, 30% in 2013 and 25% in 2009–2012.

The case reports showed some seasonality with most of the cases reported between May and August. Despite a decreasing 8-year trend from 2008 to 2015 ($p < 0.01$), the rate has stabilised in the past few years and increased slightly in 2014–2015 (Figure 38). Among 18 MS with data available for the whole period, the Czech Republic and Denmark reported increasing trends ($p < 0.01$), while Germany and Sweden reported declining trends ($p < 0.01$) from 2008 to 2015.



Source: Austria, Cyprus, the Czech Republic, Denmark, Estonia, Finland, Germany, Hungary, Ireland, Luxembourg, Malta, Norway, Poland, Slovakia, Slovenia, Spain, Sweden and the United Kingdom. Belgium, Bulgaria, Croatia, France, Iceland, Italy, Latvia, Lithuania, Portugal and Romania did not report data to the level of detail required for the analysis. Greece and the Netherlands do not have any formal surveillance system for the disease.

Figure 38: Trend in reported confirmed human cases of yersiniosis in the EU/EEA, by month, 2008–2015

Species information was reported by 20 countries for 6,039 (83.9%) of the confirmed yersiniosis cases in the EU/EEA in 2015. *Y. enterocolitica* was the most common species reported in all countries, with the isolation percentage being 99.5% at the EU level. Information about the *Y. enterocolitica* serotypes was provided for 2,797 (38.9%) of confirmed *Y. enterocolitica* cases by 14 countries. The most common serotype was O:3 (82.2%), followed by O:9 (11.07%) and O:5,27 (1.6%). Biotype information was provided for 616 (8.6%) confirmed cases by five countries (Austria, Denmark, Finland, Lithuania and Poland); two countries more than in 2014 resulting in a 71.1% increase of biotyped cases compared with 2014. The most commonly reported biotypes in 2015 were biotype 4 (45.5%) followed by biotype 1A (42.2%) and biotype 2 (11.2%). *Y. enterocolitica* biotype 1A was mainly (98.8%) reported by Denmark, which reported biotype data for the first time. This biotype included almost half (47.6%) of all *Y. enterocolitica* isolates reported by Denmark.

Y. pseudotuberculosis represented 0.5% of cases reported by eight countries (Austria, the Czech Republic, Finland, Ireland, Poland, Sweden, Slovakia and the United Kingdom). Ireland and the United Kingdom reported the highest proportion of *Y. pseudotuberculosis* infections, representing 7.7% and 6.8% of all their confirmed yersiniosis cases, respectively.

Fourteen MS, for the first time including the Czech Republic and Portugal, provided information on hospitalisation. Of 1,717 cases with known hospitalisation status, 30.9% were hospitalised, less than in 2014 (44.0%). As in previous years, the highest hospitalisation rates (57.7%–100% of cases) were reported in Lithuania, Poland and Romania. No fatalities were reported in 2015 among the 4,304 confirmed yersiniosis cases with known outcome (59.8% of all confirmed cases).

3.5.2. *Yersinia* in food and animals

At present there is no harmonised surveillance of *Yersinia* in the EU and, when interpreting the data on *Yersinia* in foods and animals, it is important to note that data from different investigations are not necessarily directly comparable owing to variations in sampling strategies and testing methods. A scientific report of EFSA suggested technical specifications for the harmonised monitoring and reporting of *Y. enterocolitica* in slaughter pigs in the EU (EFSA, 2009c). Few MS provided detailed information on the microbiological test used; Austria and Spain reported using the method ISO 10273:2003 (ISO, 2003). Germany reported using a 'microbiological standard test'. Only results for the most important food categories and animal species that might serve as a source for human infection in the EU are presented.

3.5.2.1. Food

In 2015, six MS provided information on *Yersinia* in food samples; more MS than in 2014 (four MS). Data were mostly reported from meat samples (mainly pig meat), milk and other dairy products. Additionally, MS provided data on vegetables, fruits, RTE salads, fish, dried infant formula intended for infants below 6 months, and other processed food products and prepared dishes.

Five MS (Austria, Belgium, Germany, Italy, Spain) reported data from 22 investigations on pig meat and products thereof from different sampling stages. Only eleven investigations included at least 10 samples. The majority of the investigations were reported by Italy and Germany (63.6%). *Yersinia* was found in 11.3% of the 952 units tested (Table 2015_YERSPIGMEAT). Three MS (Belgium, Germany and Spain) reported findings of *Yersinia* ranging from 5.3% to 54.1%; most of the positive findings were reported at retail, but positive findings were also reported at slaughterhouse and at processing. Minced meat was the food item with the majority of the positive findings. The remaining positive samples were fresh meat samples at retail and carcases at slaughterhouse. *Y. enterocolitica* was identified in 98 out of 108 positive samples (10.3% of the tested samples); in addition, *Y. frederiksenii* and *Y. intermedia* were reported from 10 single samples of one investigation at retail. Sampling was mainly carried out as part of surveillance programmes or surveys.

Three MS (Belgium, Germany, Italy) reported results from seven investigations on *Yersinia* in bovine meat and products thereof (Table 2015_YERSBOVINEMEAT) at processing plant and at retail. *Yersinia* was found in 5.3% of the 76 samples tested. Two retail investigations, one in minced meat and a second one in an unspecified matrix, included more than 10 samples and were the only ones with positive findings (2.2% and 17.7% positive samples for *Y. enterocolitica*). No data on ovine meat were reported in 2015.

Three MS (Austria, Germany, Italy) reported data from 12 investigations of *Yersinia* in milk and dairy products, all with less than 10 samples. *Yersinia* was found in 5.9% of 34 samples tested. One MS detected *Y. enterocolitica* in two investigations in processing plants (one positive sample in each) for raw cow's milk for manufacture of raw or low heat-treated products and raw goat's milk, respectively (Table 2015_YERSMILKDAIRY). The investigations of cheeses and other dairy products had no positive findings.

Out of the samples of products other than meat and dairy products (159 samples), only one sample of RTE salads at retail was positive for *Y. enterocolitica.*

Information about biotype and/or serotype of the food isolates was provided for more than 70% (74.6%) of *Y. enterocolitica* isolates by two MS. Three biotypes were reported: biotype 1A that was the most common (83 isolates from pig meat, bovine meat and mixed bovine and pig meat samples), biotype 1B (1 isolate from pig meat) and biotype 4 (3 isolates from pig meat). The serogroup was only reported for a few isolates: serogroup O:3 in combination with biotype 4 (3 isolates from pig meat) and O:5 (2 isolates from meat from other animal species or not specified).

3.5.2.2. Animals

In 2015, four MS provided monitoring data for *Yersinia* from animals, which are fewer reporting MS compared to 2014 when six MS provided animal data for *Yersinia*. Data were mostly reported from domestic animals.

Three MS (Germany, Italy, Spain) provided information from four investigations in pigs and *Yersinia* was reported by two MS (Germany and Spain) in 11.0% of 2,050 samples tested (positive findings ranging from 3.8% to 41.7%) (Table 2015_YERSPIGS).

Two MS (Germany, Italy) reported data from 20 investigations in domestic animals other than pigs (cattle, poultry, goats, sheep, horses, rabbit and turkeys). Overall, 1.4% of 5,796 samples tested were *Yersinia*-positive (positive findings ranging from 0.4% to 33.3%). Germany reported 70% of the investigations, all with more than 10 samples. All investigations from Italy had < 10 samples except one. With regard to cattle, three of eight investigations reported had positive findings for *Yersinia* (1.6%, 1.9% and 27.2%) and all positive samples were *Y. enterocolitica* except in one investigation where two samples were positive for *Y. frederiksenii* and *Yersinia* spp., respectively (Table 2015_YERSDOMAN). Information on *Yersinia* in sheep and goats were reported from seven investigations, and four of these had positive findings (all for *Y. enterocolitica*) ranging from 0.7% to 33.3%. One investigation in poultry was reported with 0.4% of positive findings for *Y. enterocolitica*. No positive findings were reported in horses, rabbits and turkeys.

Three MS (Germany, Hungary, Italy) reported data from 29 investigations in other animal species, 15 having less than 10 samples. Overall, 1.8% of the 4,847 tested single samples was *Yersinia*-positive (Table 2015_YERSOTHERAN). *Y. enterocolitica* was found in cats, dogs, deer, foxes, hares, marten, steinbock Cantabrian chamois, wild boar and other wild animals. Italy reported also *Y. frederiksenii* in bats, deer, foxes and wild boar, *Y. kristensenii* in deer and hares, *Y. pseudotuberculosis* in foxes and *Yersinia* spp. in deer and wild boar.

For animal isolates, information about biotype and/or serotype was provided for 28.9% of *Y. enterocolitica* isolates. One biotype was reported – biotype 1B with one isolate from wild boar. Four serotypes were also reported: serotype O:9 was the most commonly reported as in 2014 (64 isolates), O:3 (16 isolates), O:8 (14 isolates), O:5 (11 isolates); O:1,2,3 (4 isolates). Serotype O:9 was mainly reported from cattle, but was also found in sheep, pigs, deer, foxes, hares and wild boar. Serotype O:3 was reported from cattle, dogs, pigs, and wild boar. Serotype O:8 was reported from deer, foxes, Cantabrian chamois, steinbock and wild boar; serotype O:5 from deer, hares, foxes, marten and wild boar; serotype O:1,2,3 from deer and wild boar.

3.5.3. Discussion

Yersiniosis remains the third most commonly reported bacterial food-borne zoonosis in the EU, despite the significantly decreasing trend between 2008 and 2015. However, the trend in number of reported cases appeared to increase slightly in 2014–2015. The highest notification rates were reported in MS in north-eastern Europe. This increase was partly due to improvements in surveillance systems (Denmark, Spain) and two countries (Croatia and Portugal) starting to report yersiniosis cases for the first time. *Y. enterocolitica* was the dominating species in all countries.

To assess the public health significance and pathogenicity for humans, it is recommended to report information on the biotype of each *Y. enterocolitica* isolate and preferably also serotyping data. *Y. enterocolitica* represents six biotypes (1A, 1B, 2–5) of which biotype 1A is largely considered non-pathogenic for humans. There are conflicting reports on the pathogenicity of biotype 1A strains as they have been isolated from clinical samples from yersiniosis patients (Stephan et al., 2013) even though these strains have been considered to be largely non-pathogenic. Serotype information is provided more frequently, but biotype information is only available for a small fraction of the yersiniosis cases reported in the EU. The most frequently reported bioserotypes since the beginning of EU/EEA yersiniosis surveillance have been 4/O:3 followed by 2/O:9. In 2015, biotype 1A (combined with several different serotypes) was the second most commonly reported biotype after biotype 4. Almost all biotype 1A cases were reported by Denmark, where the increase of yersiniosis cases in recent years is solely driven by the increase in non-pathogenic variant biotype 1A (SSI, 2016). Since the biotype information is rarely reported, a proportion of the non-typed isolates will also belong to biotype 1A in other countries. According to the EU case definition, only human-pathogenic *Y. enterocolitica* or *Y. pseudotuberculosis* cases should be reported.[34]

Only very few MS report data from surveillance of *Yersinia* in food and animals. In 2015, three MS reported positive findings for *Yersinia* in pig meat and products thereof (11.3% of the 952 units

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[34] Decision 2012/506/EU. Commission implementing Decision of 8 August 2012 amending Decision 2002/253/EC laying down case definitions for reporting communicable diseases to the Community network under Decision No 2119/98/EC of the European Parliament and of the Council. Available at: http://eur-lex.europa.eu/LexUriServ/LexUriServ.do?uri=OJ:L:2012:262:0001:0057:EN:PDF

tested), and two MS reported positive findings in pigs (11.0% of the 2,050 samples tested). Positive units were also reported in other foods (bovine meat, raw cow's and raw goat's milk, and RTE salad) and in other animals (cattle, cats, dogs, deer, foxes, hares, marten, steinbock, Cantabrian chamois, wild boar and other wild animals).

According to the Scientific Opinion published by the BIOHAZ Panel in 2007 (EFSA, 2007a), it is well-documented that pigs can harbour human-pathogenic *Y. enterocolitica,* especially in the tonsils, with a very high prevalence, especially biotype 4 (serotype O:3). Reservoirs other than pigs may also play a role in the epidemiology of human yersiniosis. Evidence suggests that ruminants (e.g. cattle) may be reservoirs for biotype 2 (serotype O:9). The opinion further concluded that the majority of human pathogenic *Y. enterocolitica* strains in Europe belong to biotype 4 (serotype O:3), followed by biotype 2 (serotype O:9). Biotypes 1B, 3 and 5 are also pathogenic in humans, whereas biotype 1A is considered to be largely non-pathogenic. Therefore, it is important that information is provided on the biotype of each *Y. enterocolitica* isolate in order to assess its public health significance. It is recommended that biotyping, and preferably also serotyping, is increased in the future.

Information about biotype and/or serotype of the food isolates was provided for more than 70% (74.6%) of *Y. enterocolitica* isolates in food and for only 28.9% isolates in animals. The most common biotypes/serotypes were biotype 1A in food, and serotypes O:9 followed by O:3, O:8, O:5 and O:1,2,3 in animals. Hopefully, an increased focus on the reported *Yersinia* data and more sensitive methods will improve the detailed information on *Yersinia* in the future.

3.6. Tuberculosis due to *Mycobacterium bovis*

The Appendix A lists all summaries made for the production of this section, for humans and animals, including bovine tuberculosis summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.6.1. *Mycobacterium bovis* in humans

In 2015, 170 confirmed cases of tuberculosis due to *M. bovis* in humans were reported by 26 EU MS (Table 21). Eleven MS reported at least one confirmed case and 15 MS reported zero cases. The EU notification rate was 0.03 cases per 100,000 population, the same as in previous years. Most cases were reported in Germany, the United Kingdom and Spain, while the highest notification rate (0.11 cases per 100,000 population) was observed in Ireland. There was no clear association between a country's OTF status (OTF; Officially bovine tuberculosis free in cattle) and its notification rate in humans. The notification rate of human cases for both country group (OTF and non-OTF) was 0.03 per 100 000 population.

Table 21: Reported human cases of tuberculosis due to *M. bovis* and notification rates per 100,000 population in the EU/EEA, by country and year, 2011–2015

Country	2015				2014		2013		2012		2011	
	National coverage[(a)]	Data format[(a)]	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
			Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria (OTF)[(b)]	Y	C	3	0.03	1	0.01	1	0.01	1	0.01	0	0.00
Belgium (OTF)[(c)]	Y	C	9	0.08	10	0.09	10	0.09	4	0.04	5	0.05
Bulgaria	Y	C	1	0.01	0	0.00	0	0.00	0	0.00	2	0.03
Croatia	Y	C	0	0.00	0	0.00	–	–	–	–	–	–
Cyprus	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Czech Republic (OTF)	Y	C	1	0.01	0	0.00	0	0.00	0	0.00	4	0.04
Denmark (OTF)	Y	C	0	0.00	1	0.02	0	0.00	0	0.00	1	0.02
Estonia (OTF)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Finland (OTF)	Y	C	0	0.00	0	0.00	1	0.02	0	0.00	0	0.00
France (OTF)[(d)]	Y	C	–	–	–	–	–	–	–	–	–	–

Country	2015				2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
			Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Germany (OTF)	Y	C	49	0.06	50	0.06	43	0.05	45	0.05	43	0.05
Greece	Y	C	–	–	–	–	–	–	–	–	–	–
Hungary (OTF)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Ireland	Y	C	5	0.11	3	0.07	6	0.13	4	0.09	6	0.13
Italy(e),(f)	Y	C	17	0.03	18	0.03	14	0.02	10	0.02	14	0.02
Latvia (OTF)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Lithuania (OTF)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Luxembourg (OTF)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Malta (OTF)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Netherlands (OTF)	Y	C	9	0.05	8	0.05	10	0.06	8	0.05	11	0.07
Poland (OTF)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Portugal(g)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Romania	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	1	0.00
Slovakia (OTF)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Slovenia (OTF)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Spain	Y	C	28	0.06	33	0.07	28	0.06	14	0.03	23	0.05
Sweden (OTF)	Y	C	6	0.06	4	0.04	0	0.00	5	0.05	2	0.02
United Kingdom(h)	Y	C	42	0.06	39	0.06	30	0.05	41	0.06	40	0.06
EU Total	–	–	**170**	**0.03**	**167**	**0.03**	**143**	**0.03**	**132**	**0.03**	**152**	**0.03**
Iceland(i)	Y	C	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Norway (OTF)	Y	C	1	0.02	4	0.08	0	0.00	2	0.04	2	0.04
Switzerland (OTF)(j)	Y	C	6	0.07	2	0.02	2	0.02	5	0.06	13	0.17

(a): Y: yes; N: no; A: aggregated data; C: case-based data; –: no report.
(b): OTF: Officially bovine tuberculosis free (status regarding freedom from bovine tuberculosis, in cattle).
(c): There is an under estimation of the number of *M. bovis* in human cases in Belgium because the identification within the M. tuberculosis complex strains is not performed systematically by all the laboratories.
(d): Not reporting species of the *M. tuberculosis* –complex.
(e): In Italy, seven regions and 14 provinces are OTF.
(f): 36 cases, 80% of all reported human *M. bovis* cases from Italy to TESSy in 2010–2013 were without laboratory results but were still included in the table since reported as *M. bovis.*
(g): In Portugal, all administrative regions within the superior administrative unit of the Algarve are OTF.
(h): In the United Kingdom, Scotland and the Isle of Man are OTF (in cattle).
(i): In Iceland that has no special agreement concerning animal health (status) with the EU, the last outbreak of bovine tuberculosis was in 1959.
(j): Switzerland provided data directly to EFSA. The human data for Switzerland also include the ones from Liechtenstein (OTF).

As tuberculosis is a chronic disease with a long incubation period, it is not possible to assess travel-associated cases in the same way as diseases with acute onset. Instead, the distinction is made between individuals with the disease born in the reporting country (native infection) and those moving there at a later stage (foreign infection). In a few cases, the distinction is also made based on the nationality of the cases. On average, 60.6% of the cases reported in 2015 were native to the reporting country, 34.1% were foreign and 5.3% were of unknown origin. Among cases with known origin, there was a larger proportion (78.2%) of native cases in countries not free of bovine tuberculosis (non-OTF) than in countries that were officially *M. bovis*-free (OTF) (47.3%).

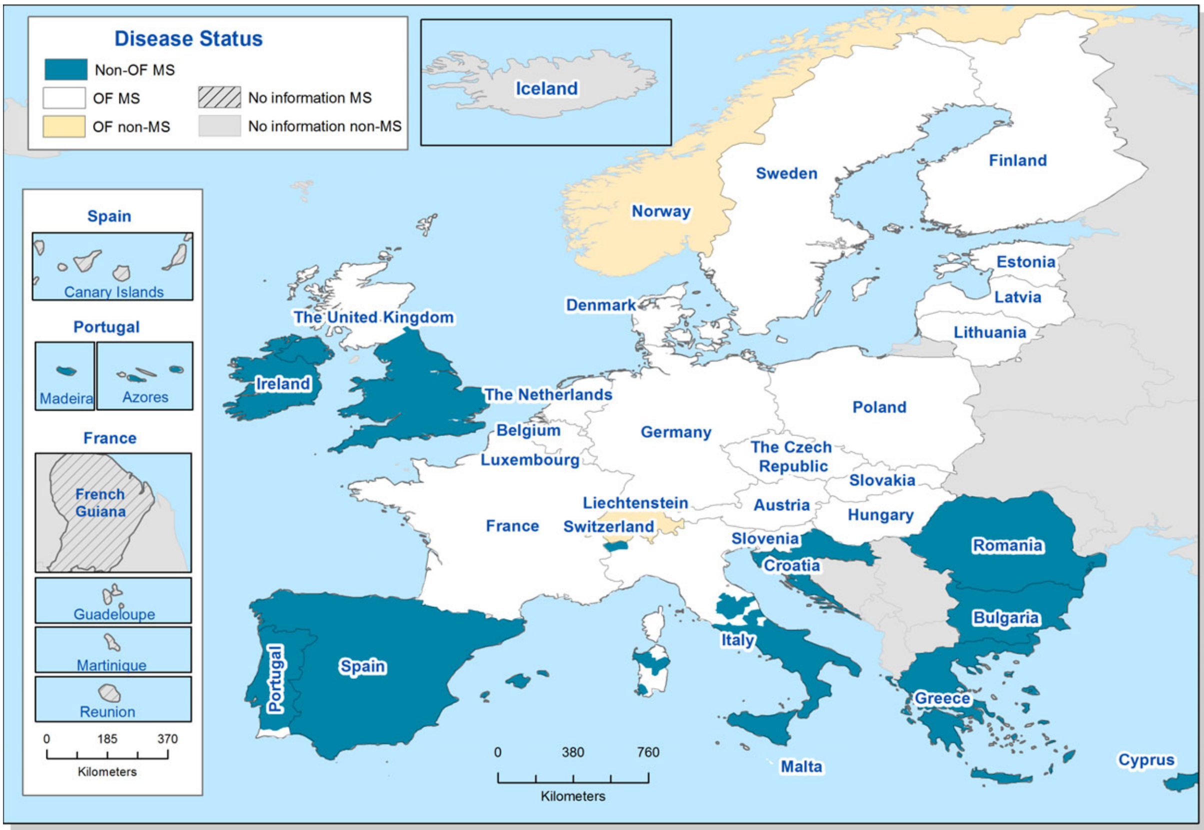
Treatment outcome after 12 months of treatment was reported for 151 (90.4%) of 167 human *M. bovis* cases reported in 2014. Successful treatment was reported for 91 cases (60.3%); while, 26 cases (17.2%) died during the treatment, 3 cases (2.0%) were lost to follow-up, 13 cases (8.6%) were still on treatment and treatment outcome was not evaluated for 18 cases (11.9%).

3.6.2. Bovine tuberculosis in cattle

For the first time in the EU annual summary reports on trends and sources of zoonoses, monitoring data from cattle of the specific types of bacteria that are part of the *Mycobacterium tuberculosis* complex were taken account of to summarise the EU situation on bovine tuberculosis. Previously the separate reporting of bacterial species of the *M. tuberculosis* complex in the EFSA Disease status data model was not possible. In this chapter a distinction is made descriptively, whenever possible, of reporting by MS on *Mycobacterium tuberculosis* complex, *M. bovis* and *M. caprae*.

The status regarding freedom from bovine tuberculosis (OTF) and occurrence of the disease at region or national levels for MS and non-MS in 2015 are presented in Figures 39 and 40, respectively. In 2015, Lithuania and Malta acquired OTF status. Therefore, the 2015 list of countries and regions OTF was: Austria, Belgium, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Hungary, seven regions and 14 provinces in Italy, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, all administrative regions within the superior administrative unit of the Algarve in Portugal, Poland, Slovakia, Slovenia, Sweden, Scotland and the Isle of Man in the United Kingdom, Norway and Switzerland, in accordance with EU legislation (Decision 2014/91/EU[35]). Liechtenstein has the same status (OTF) as Switzerland. In Iceland, which has no special agreement concerning animal health status with the EU, the last outbreak of bovine tuberculosis was reported in 1959.

Bulgaria, Croatia, Cyprus, Greece, Ireland, Italy, Portugal, Romania, Spain and the United Kingdom had not yet achieved the country-level OTF status in 2015.



OF: Officially bovine tuberculosis free in cattle.

Figure 39: Status of countries regarding bovine tuberculosis, 2015

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[35] Commission implementing Decision 2014/91/EU of 14 February 2014 amending Annex II to Decision 93/52/EEC as regards the recognition of certain regions of Italy and Spain as officially free of brucellosis (*B. melitensis*) and amending Annexes I, II and III to Decision 2003/467/EC as regards the declaration of Hungary as officially tuberculosis-free, Romania and certain regions of Italy as officially brucellosis-free, and certain regions of Italy as officially enzootic-bovine-leukosis-free. OJ 46, 18.2.2014, p. 12–17.

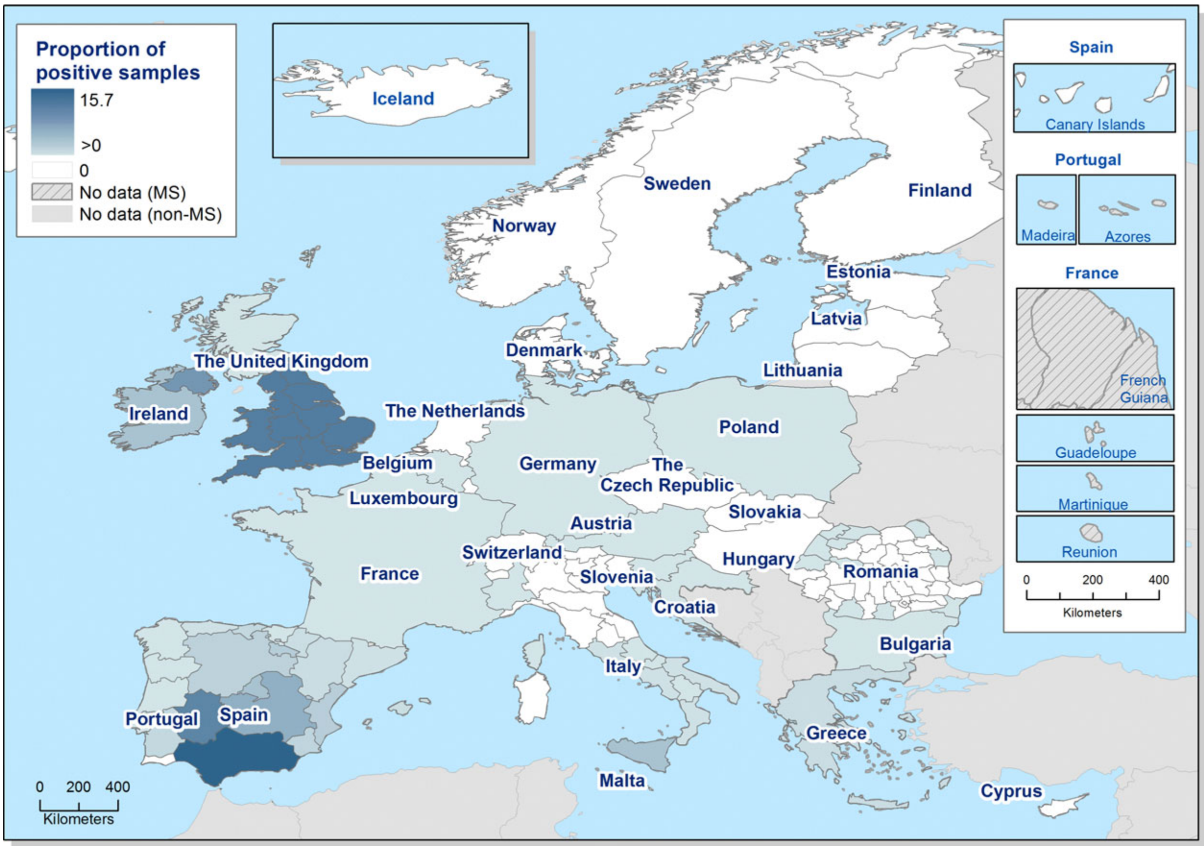

Figure 40: Proportion of cattle herds infected with or positive for bovine tuberculosis, 2015

The overall proportion of cattle herds infected with, or positive for, bovine tuberculosis, considering all the EU regions, remained very low EU (0.7% of the cattle herds in the EU), although there is a heterogeneous distribution of bovine tuberculosis in Europe with a pronounced spatial clustering (Figure 40). The prevalence ranges from absence of infected/positive animals in most OTF regions to a regional prevalence in non-OTF regions of 15.8% in Andalusia, Spain, considering all herds, or a reported regional prevalence of test-positive cattle herds of 17.7% within the United Kingdom in Wales and England.

In the 18 OTF MS and in the regions declared OTF in the three non-OTF MS Italy, Portugal and the United Kingdom, which represent a total a population of 1,314,645 cattle herds, annual surveillance programmes are carried out to confirm freedom from bovine tuberculosis. Their reporting requirements are, among other indicators, the number of infected herds and the total number of herds existing (Table 2015_DSTUBOFNCOFCAT). Eight of these MS reported a total of 155 bovine tuberculosis-infected herds; six MS reported infection with *M. bovis* (Belgium, 3 herds; Germany, 12; Italy, 3; Poland, 28; Slovenia, 1; and the United Kingdom, 2), whereas Austria[36] reported 4 herds infected with *M. caprae* and France declared 102 herds infected with *Mycobacterium tuberculosis* complex. The prevalence of bovine tuberculosis-infected herds in these OTF regions of 21 MS in 2015 was 0.012%, compared to 0.011% during 2014 in the OTF regions of 19 MS (Figure 41). From 2010 to 2015, the number of cattle herds reported infected in the OTF regions of the EU per year was 227, 200, 209, 197, 139 and 155, respectively (Figure 41).

Bovine tuberculosis was not detected in 2015 in the non-MS Iceland, Norway, Switzerland and Liechtenstein.

In 2015 there were a total of 1,167,945 cattle herds in the non-OTF regions of the 10 MS with non-OTF status. National eradication programme for bovine tuberculosis are in place in all these regions. In 2015, six of these MS (Croatia, Ireland, Italy, Portugal, Spain and the United Kingdom) received the EU cofinancing for eradication programmes. These MS reported on the prevalence situation in their non-OTF regions by the number of positive herds, the number of herds tested under

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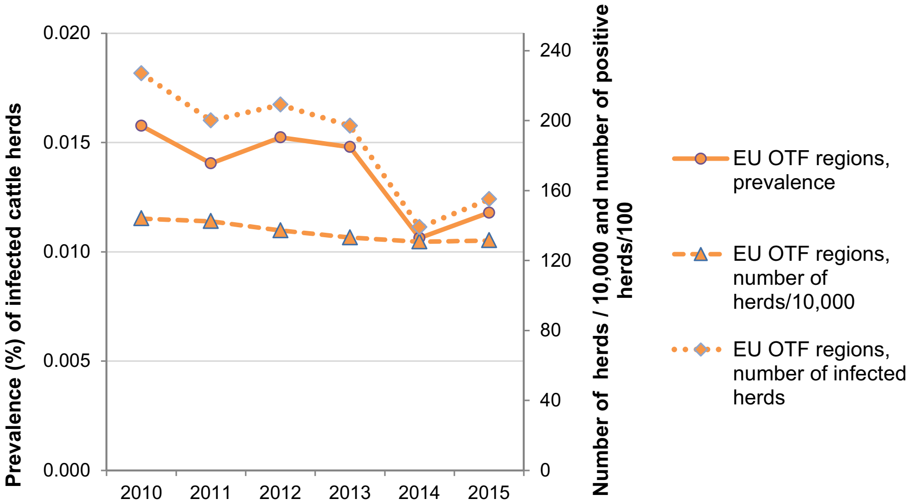
[36] During 2015, Austria was an OTF MS for all its regions and also covered by an EU cofinanced eradication programme for some single regions.

the eradication programme, and the total number of herds existing. The number of positive herds reported was 21 in Croatia (53 in 2014), 4,002 in Ireland (4,293 in 2014), 433 in Italy (380 in 2014), 94 in Portugal (108 in 2014), 3,070 in Spain (1,867 during 2014) and 9,628 in the United Kingdom (10,172 in 2014) (Table 2015_DSTUBCOF). Reports concerned *M. bovis* (Ireland, Italy, Portugal and the United Kingdom) or *Mycobacterium tuberculosis* complex (Croatia and Spain).

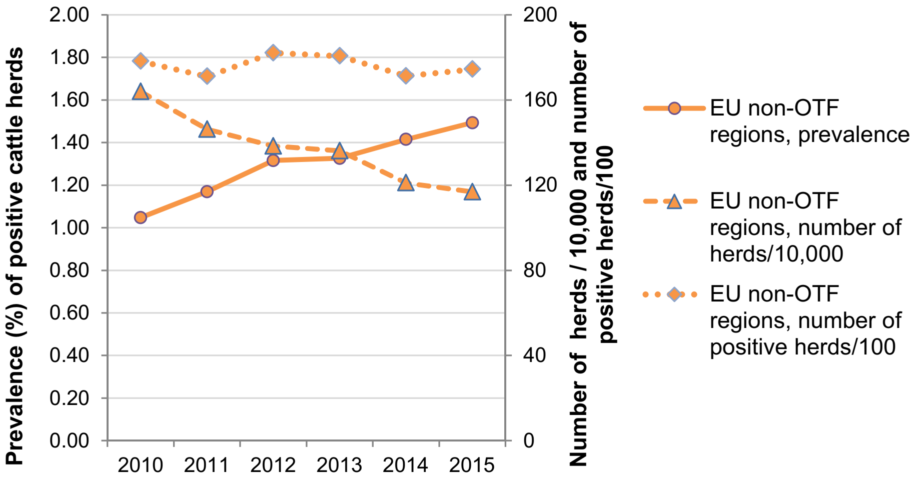


OTF: Officially bovine tuberculosis free in cattle.

Figure 41: Proportion of cattle herds infected with or positive for bovine tuberculosis, in OTF regions, EU, 2010–2015

The four other non-OTF MS did not receive cofinancing by the EU for their eradication programmes during 2015. They reported, among other indicators, the number of infected herds and the total number of herds existing (Table 2015_DSTUBOFNCOFCAT). Of these MS, Cyprus did not report any infected herds for the year 2015, like in 2014, whereas Bulgaria reported six (10 in 2014) and Greece 187 (203 in 2014) *M. bovis*-positive herds. Romania reported 36 *M. caprae*-positive herds (36 also in 2014).

From 2010 to 2015, the total number of test-positive cattle herds in these EU non-OTF regions remained at the same level and 17,814; 17,102; 18,208; 18,059; 17,122; and 17,441 were reported from 2010 to 2015, respectively. The overall prevalence of that period is increasing going from 1.05% to 1.49% in 2015. Concomitantly, the total number of cattle herds decreased importantly from 1,638,694 in 2010 to 1,167,945 in 2015 (Figure 42).



OTF: Officially bovine tuberculosis free in cattle.

Figure 42: Proportion of cattle herds infected with or positive for bovine tuberculosis, in non-OTF regions, EU, 2010–2015

Figure 43 displays the MS-specific trends of the prevalence of bovine tuberculosis test-positive cattle herds in the non-OTF regions of six MS with the EU cofinanced eradication programmes, during 2004–2015. Croatia, MS since 1 July 2013, had its programme cofinanced for 2014 and 2015. A moderate prevalence (> 10–20%) is reported by the United Kingdom in Wales and England, with a reported highest regional prevalence in the EU of 17.7%. When considering all herds, the regional prevalence was 12.0% (Figure 40). For Northern Ireland a low prevalence (> 1–10%) of test-positive herds was reported, but with a slightly increasing trend. Also Ireland and Spain reported a low prevalence with a decreasing (Ireland) and a slightly increasing trend (Spain) in recent years. When considering all herds, Spain reported a regional prevalence of 15.8% in Andalusia, Figure 40). Italy and Portugal reported very low prevalences (> 0.1–1%) in their remaining non-OTF regions.

Greece, a non-OTF MS without an EU cofinanced eradication programme, reported a very low prevalence of infected cattle herds (*M. bovis*) with a slightly increasing trend from 0.44% in 2006 to 0.85% in 2015 (Table 2015_DSTUBNONCOF).

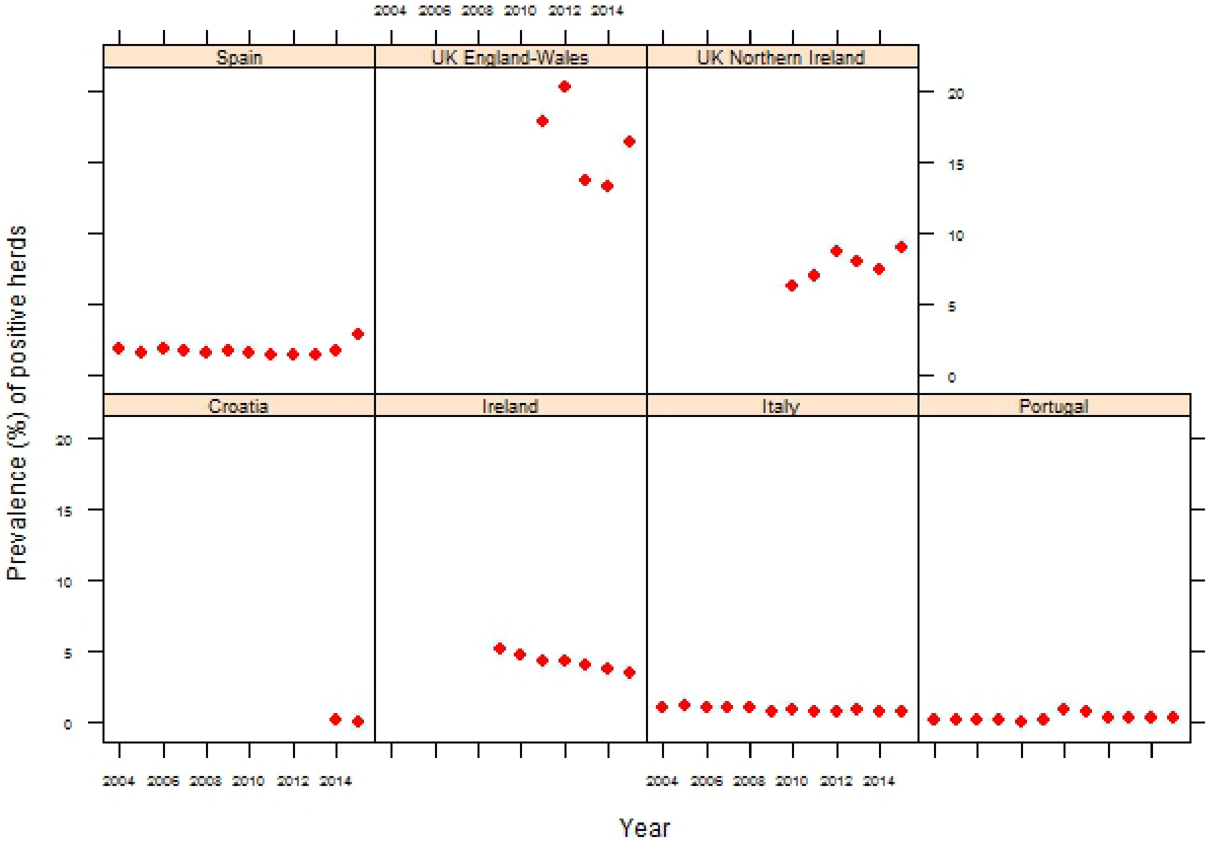


Figure 43: Prevalence of bovine tuberculosis test-positive cattle herds, in non-OTF regions of six non-OTF cofinanced Member States, 2004–2015

In 2015, 12 MS and two non-MS investigated *M. bovis* in other animals and it was reported in 2,375 animals: water buffalos (1,343), wild boar (398), badgers (311), deer (195), alpacas (35), cats (34), zoo animals (21), pigs (20), foxes (8), sheep (8) and lamas (2). Thirteen MS and two non-MS investigated animals for *Mycobacterium* species other than *M. bovis*. *M. tuberculosis* complex was reported in cattle, but also from wild alpacas (4), goats (4,022), cat (1), sheep (2), wild boars (31 slaughter batches), wild deer (45) and zoo animals (4) among which elephants. *M. caprae* was reported, in addition to the *M. caprae*-positive herds in Austria and in Romania (see above), in 177 animals by three MS (Germany, Hungary and Spain): cattle (169), wild boars (5), wild deer (2), and a fox (Table 2015_TUBALL).

3.6.3. Discussion

Tuberculosis due to *M. bovis* is a rare infection in humans in the EU, with 170 confirmed human cases reported in 2015. The EU notification rate has been stable between 2011 and 2015. There was no clear association between a country's OTF status as and its notification rate in humans. This could be due to many of the cases in both OTF and non-OTF countries having immigrated to the country, thus, the infection might have been acquired in the country of origin. Cases native to the country could also have been infected before the disease was eradicated from the animal population, as it may take years before disease symptoms develop.

Bovine tuberculosis is a zoonotic animal disease regulated by Directive 64/432/EEC. According to Directive 2003/99/EC on the monitoring of zoonoses and zoonotic agents, the zoonosis and zoonotic agent to be included in monitoring of bovine tuberculosis is tuberculosis due to *M. bovis* (Annex I, A). Additionally to *M. bovis, M. caprae* is recognised since 2003 as a distinct bacterial species and causative agent of bovine tuberculosis and of tuberculosis in humans and animals other than cattle (Aranaz et al., 2003). Disease caused by *M. caprae* is not considered to be substantially different from that caused by *M. bovis*, and the same tests can be used for its diagnosis (OIE Terrestrial Manual). In the meeting of 7 May 2013 of the Committee on the Food Chain and Animal Health (Section Animal Health and Welfare),[37] the European Commission circulated and presented a working document (SANCO/7059/2013) on the subject matter. Without prejudice to the exclusive competence of the European Court of Justice to authoritatively interpret Union legislation, the document concluded that all provisions explicitly referring to *M. bovis* in Directive 64/432/EEC should be understood as also applicable to *M. caprae*. Based on the above, a distinction is descriptively made for the first time in the EU annual summary reports on trends and sources of zoonoses, of reporting by MS on *Mycobacterium tuberculosis* complex, *M. bovis* and *M. caprae*.

The 2015 monitoring data on bovine tuberculosis in EU cattle demonstrate that the current situation in Europe regarding bovine tuberculosis infection, detection and control is heterogeneous, as recently substantiated by EFSA (EFSA AHAW Panel, 2014). The prevalence ranges from absence of infection in most OTF regions to a regional prevalence of 15.8% in Andalusia, Spain, considering all herds, or a reported regional prevalence of test-positive cattle herds of 17.7% by the United Kingdom in Wales and England.

In the EU OTF regions of 21 MS (with OTF status or with non-OTF status but with OTF regions), the remaining prevalence in 2015 of bovine tuberculosis-infected herds was 0.012% and remained a rare event like in the previous years. Eight of these MS reported a total of 155 bovine tuberculosis-infected herds; six MS (Belgium, Germany, Italy, Poland, Slovenia and the United Kingdom) reported infection with *M. bovis*, whereas Austria and France reported herds infected with *M. caprae* and with *Mycobacterium tuberculosis* complex, respectively.

In the non-OTF regions in the EU, the overall prevalence of bovine tuberculosis-positive cattle herds has increased slowly during the last years from 1.05% in 2010 to 1.49% in 2015. This slight increase might be explained by the gradual declaration of few MS as OTF and of regions within non-OTF MS as OTF, resulting in the total number of remaining cattle herds in non-OTF regions decreasing importantly from 2010 to 2015, whereas the total number of remaining positive cattle herds decreased only slightly. At MS-level, the United Kingdom reported a moderate prevalence for Wales and England like in previous years and for Northern Ireland a low, yet slightly increasing prevalence. Also Ireland and Spain reported a low prevalence with, respectively, a decreasing and a slightly increasing trend in recent years. Italy and Portugal reported very low prevalences in their remaining non-OTF regions. Reports were on *M. bovis* (Ireland, Italy, Portugal and the United Kingdom) or *Mycobacterium tuberculosis* complex (Croatia and Spain). Greece reported a slightly increasing trend of very low prevalence of infected cattle herds. Stagnating or increasing trends in prevalence of bovine tuberculosis-positive cattle herds demonstrate that control and eradication of bovine tuberculosis is a challenge and owing to the complex interactions between the pathogen, hosts and the local environments (EFSA AHAW Panel, 2014).

More information on the EU approved and cofinanced eradication programmes for bovine tuberculosis in cattle carried out by the MS is available online at: http://ec.europa.eu/dgs/health_food-safety/funding/cff/animal_health/vet_progs_en.htm

In 2015 *M. bovis* was reported to be isolated from a wide range of animal species, domestic ones and wild animals, reflecting this causative agent of tuberculosis in cattle and has a broad host range. *M. caprae*, recognised to cause bovine tuberculosis (see above) was reported in cattle, wild boars, wild deer, and a fox.

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[37] http://ec.europa.eu/food/animals/docs/reg-com_ahw_20130507_sum.pdf

3.7. *Brucella*

The Appendix A lists all summaries made for the production of this section, for humans, foods and animals, including *Brucella* summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.7.1. Brucellosis in humans

In 2015, 27 EU MS provided information on brucellosis in humans. In total, 449 cases, were reported in the EU. They included 437 confirmed cases, with a notification rate of 0.09 cases per 100,000 population (Table 22). This represents a stable rate compared with the notification rate in the last 5 years. Thirteen MS (Cyprus, Croatia, the Czech Republic, Estonia, Finland, Hungary, Ireland, Latvia, Lithuania, Luxembourg, Malta, Romania and Slovenia) and Iceland reported no human cases. As in previous years the highest notification rates of brucellosis were reported in three countries that were not officially brucellosis-free in cattle, sheep or goats: Greece (1.0 per 100,000 population), Portugal (0.44) and Italy (0.17) together accounting for 59.5% of all confirmed cases reported in 2015 (Table 22). The high notification rate (0.5 per 100,000 population) observed in Bulgaria in 2015, was due to an outbreak in July–August in the southwestern region of the country, involving 33 cases infected with *Brucella melitensis*.

The lowest notification rates were observed in MS with the status 'officially free of bovine brucellosis' (OBF, Table 22, Figure 45) and/or officially free of ovine and caprine brucellosis (*B. melitensis*) (ObmF, Table 22, Figure 49). The majority of brucellosis cases in these countries were travel-associated. Sweden, which has the status OBF/ObmF and had a relatively high notification rate (0.13 cases per 100,000 population), reported all confirmed brucellosis cases as travel-associated. Among 71 travel-associated cases, Iraq, Syria and Turkey were stated as the probable country of infection (19.7%, 9.9% and 5.6% of the imported cases, respectively).

Table 22: Reported human cases of brucellosis and notification rates per 100,000 in the EU/EEA, by country and year, 2011–2015

Country	2015					2014		2013		2012		2011	
	National coverage[a]	Data format[a]	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria (OBF/ObmF)[b]	Y	C	1	1	0.01	1	0.01	7	0.08	2	0.02	5	0.06
Belgium (OBF/ObmF)	Y	A	9	9	0.08	1	0.01	0	0.00	4	0.04	5	0.05
Bulgaria	Y	A	37	36	0.50	2	0.03	0	0.00	1	0.01	2	0.03
Cyprus (ObmF)	Y	C	0	0	0.00	1	0.02	0	0.00	0	0.00	–	–
Croatia	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	–	–
Czech Republic (OBF/ObmF)	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Denmark[c] (OBF/ObmF)	–	–	–	–	–	–	–	–	–	–	–	–	–
Estonia (OBF/ObmF)	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Finland (OBF/ObmF)	Y	C	0	0	0.00	1	0.02	0	0.00	1	0.02	0	0.00
France[d] (OBF)	Y	C	19	17	0.03	14	0.02	19	0.03	28	0.04	21	0.03
Germany (OBF/ObmF)	Y	C	44	44	0.05	45	0.06	26	0.03	28	0.03	24	0.03
Greece	Y	C	110	109	1.00	135	1.24	159	1.44	123	1.11	98	0.88
Hungary (ObmF)	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Ireland (OBF/ObmF)	Y	C	0	0	0.00	3	0.07	1	0.02	2	0.04	1	0.02
Italy[e]	Y	C	106	105	0.17	121	0.22	141	0.24	184	0.31	166	0.28
Latvia (OBF/ObmF)	Y	C	0	0	0.00	0	0.00	1	0.05	0	0.00	0	0.00
Lithuania (OBF/ObmF)	Y	C	0	0	0.00	0	0.00	2	0.07	0	0.00	0	0.00
Luxembourg (OBF/ObmF)	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	1	0.20
Malta (OBF)	Y	C	0	0	0.00	0	0.00	1	0.24	0	0.00	0	0.00

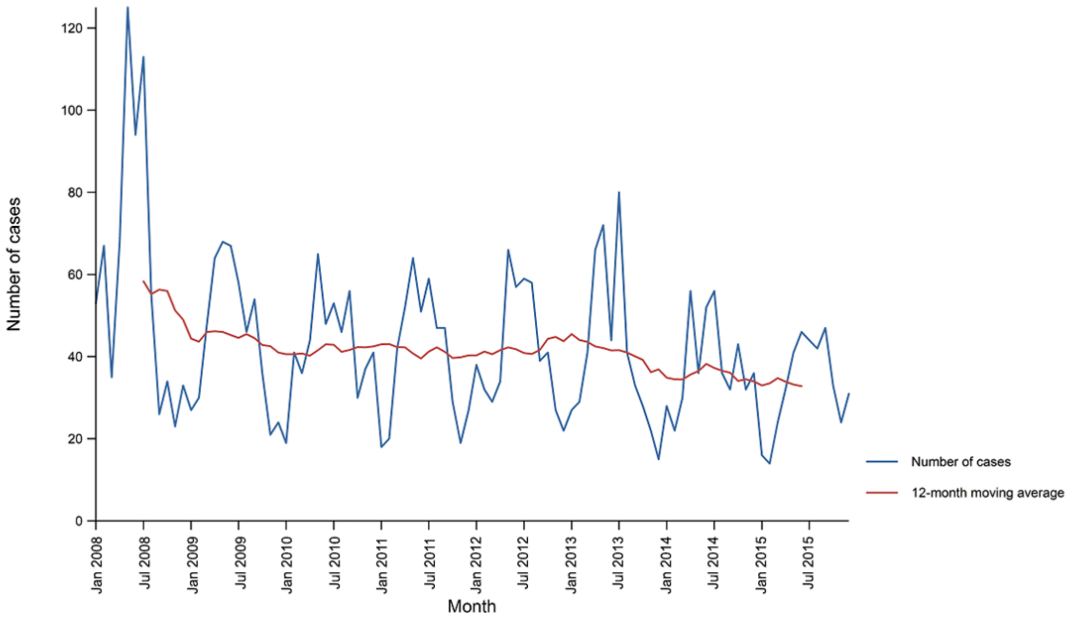
Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Netherlands (OBF/ObmF)	Y	C	7	7	0.04	1	0.01	5	0.03	3	0.02	1	0.01
Poland (OBF/ObmF)	Y	C	4	4	0.01	1	0.00	1	0.00	0	0.00	0	0.00
Portugal(f)	Y	C	47	46	0.44	50	0.48	22	0.21	37	0.35	76	0.73
Romania (OBF/ObmF)	Y	C	0	0	0.00	2	0.01	0	0.00	0	0.00	1	0.01
Slovakia (OBF/ObmF)	Y	C	1	1	0.02	0	0.00	1	0.02	1	0.02	0	0.00
Slovenia (OBF/ObmF)	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	1	0.05
Spain(g)	Y	C	39	33	0.07	56	0.12	87	0.19	62	0.13	43	0.09
Sweden (OBF/ObmF)	Y	C	13	13	0.13	16	0.17	10	0.11	13	0.14	11	0.12
United Kingdom(h) (ObmF)	Y	C	12	12	0.02	11	0.02	15	0.02	14	0.02	25	0.04
EU Total	–	–	**449**	**437**	**0.09**	**461**	**0.09**	**498**	**0.10**	**503**	**0.10**	**481**	**0.10**
Iceland(i)	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Norway (OBF/ObmF)	Y	C	2	2	0.04	2	0.04	2	0.04	4	0.08	2	0.04
Switzerland(j) (OBF/ObmF)	Y	C	1	1	0.01	3	0.04	4	0.05	3	0.04	8	0.10

(a): Y: yes; N: no; A: aggregated data; C: case-based data; –: no report.
(b): OBF/ObmF: Officially Brucellosis-free in cattle/Officially *B. melitensis* free in sheep and goats.
(c): No surveillance system.
(d): In France, all but one of the 96 metropolitan departments (due to Rev.1 vaccination against *Brucella ovis*) are ObmF and no cases of brucellosis have been reported in small ruminants since 2003.
(e): In Italy, 11 regions and nine provinces are OBF and also 13 regions and three provinces are ObmF.
(f): In Portugal, six islands of the Azores and the superior administrative unit of Algarve are OBF whereas the whole of the Azores are ObmF.
(g): In Spain, the Canary Islands, the Balearic Islands, Basque Country, and Navarre are OBF/ObmF; Murcia and La Rioja are OBF, whereas are Asturias, Cantabria, Castile and Leon, and Galicia are ObmF.
(h): In the United Kingdom, England, Scotland and Wales in Great Britain and the Isle of Man were OBF at the start of 2015. Northern Ireland was declared as OBF on 6 October 2015, whereas the Channel Islands Jersey and Guernsey are not yet OBF. The whole of the United Kingdom is ObmF.
(i): In Iceland, which has no special agreement concerning animal health (status) with the EU, brucellosis (*B. abortus, B. melitensis, B. suis*) has never been reported.
(j): Switzerland provided data directly to EFSA. The human data for Switzerland also include the ones from Liechtenstein.

A clear seasonality was observed in the number of confirmed brucellosis cases in the EU/EEA with more cases reported from April to September (Figure 44). There was a significantly ($p < 0.01$) declining 8-year trend from 2008 to 2015. Six MS (Greece, Italy, Portugal, Romania, Slovenia and Spain) reported decreasing trends ($p < 0.01$) and Germany reported an increasing trend ($p < 0.01$) during this same period. A dominant peak in 2008 was due to a large outbreak on the Greek island of Thassos in which 126 people fell ill with brucellosis.

Eight MS provided data on hospitalisation, accounting for 42.8% of confirmed cases in the EU. On average, 69.5% of the confirmed brucellosis cases with known status were hospitalised. One death due to brucellosis was reported in 2015 among 136 confirmed cases (31.1% of all confirmed cases) from eight MS reporting outcome.

Brucella species information was missing for 79.8% of the 437 confirmed cases reported in the EU. Of the 82 cases with known species, 90.2% were infected by *B. melitensis*, 4.9% by *B. abortus* and 4.9% by other *Brucella* species.



Source: Austria, Cyprus, the Czech Republic, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden and the United Kingdom. Belgium, Bulgaria, Croatia, Lithuania and Luxembourg did not report data to the level of detail required for the analysis. Denmark does not have a surveillance system for this disease.

Figure 44: Trend in reported confirmed human cases of brucellosis in the EU/EEA, by month, 2008–2015

3.7.2. *Brucella* in food and animals

3.7.2.1. Food

Three MS (Italy, Portugal and Spain) provided 2015 *Brucella* monitoring data in food (single samples), in the following categories: raw milk from cows, sheep and goats, milk from other animal species, cheese, and other dairy products excluding cheeses. A total of 282 samples taken in processing plants, farms and at retail level were tested in these MS. Portugal and Spain did not find any positive sample. Italy accounted for 59% of the samples reported and two samples were found positive in 'milk from other animal species or unspecified' collected at retail (Table 2015_BRUCFOOD).

3.7.2.2. Animals

Cattle

The status regarding freedom from bovine brucellosis (OBF) and occurrence of the disease at regional or national levels for MS and non-MS in 2015 are presented in Figures 45 and 46, respectively. In 2015, Malta acquired OBF status. Therefore, the 2015 list of countries and regions OBF was: Austria, Belgium, the Czech Republic, Denmark, Estonia, Finland, France, Germany, 11 regions and 9 provinces in Italy, Ireland, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, all administrative regions within the superior administrative unit of the Algarve as well as six of the nine islands of the Azores in Portugal, Poland, Romania, Slovakia, Slovenia, Sweden, England, Scotland, Wales, Northern Ireland[38] and the Isle of Man in the United Kingdom, the Canary Islands, the Balearic Islands, Basque Country, Murcia, La Rioja and Navarre in Spain. The nine MS that did not yet gain country-level OBF status by the end of 2015 were: Bulgaria, Croatia, Cyprus, Greece, Hungary, Italy, Portugal, Spain and the United Kingdom (Channel Islands Jersey and Guernsey are not yet OBF). Norway and Switzerland were OBF in accordance with the EU legislation and Liechtenstein had the same status (OBF) as Switzerland. Iceland, which has no special agreement on animal health (status) with the EU, has never reported brucellosis due to *B. abortus, B. melitensis* or *B. suis*.

In the 19 MS declared OBF and in the regions declared OBF of the four non-OBF MS Italy, Portugal, Spain and the United Kingdom, which represents a total population of 2,126,033 cattle herds, annual surveillance programmes are carried out to confirm the freedom from bovine brucellosis. In these OBF regions bovine

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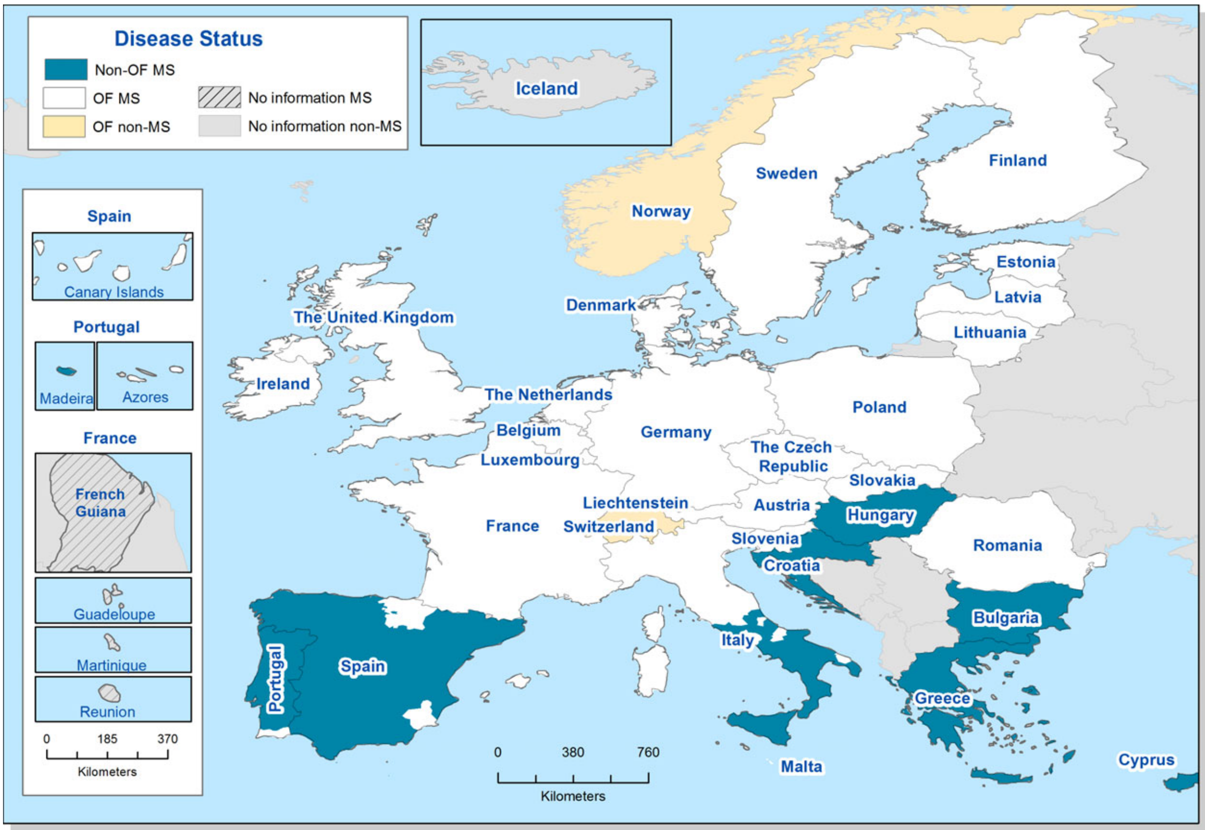
[38] Northern Ireland was declared as OBF on 6 October 2015 (Commission Implementing Decision ((EU) 2015/1784).

brucellosis was only detected in 2015 in four German cattle herds (Table 2015_DSBRUOFNCOFCAT). Bovine brucellosis was not detected in the non-MS Iceland, Norway, Switzerland and Liechtenstein.



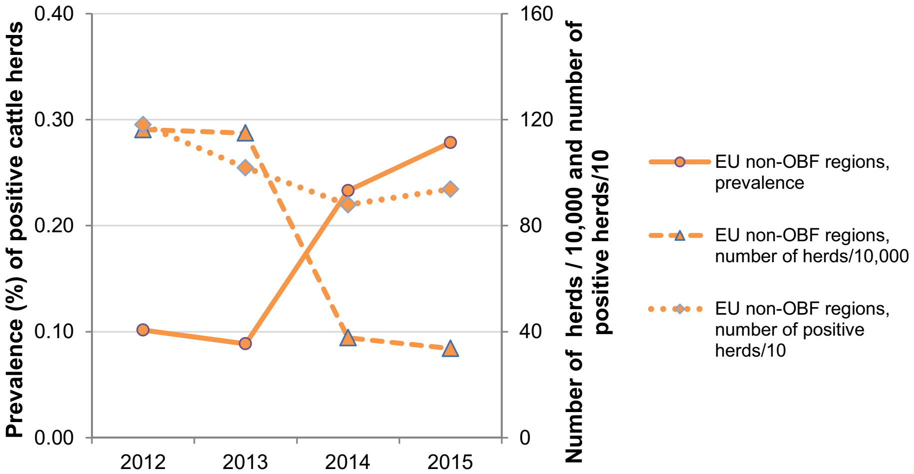
OF: Officially Brucellosis-free in cattle.

Figure 45: Status of countries regarding bovine brucellosis, 2015

In total, there are 336,741 cattle herds in the non-OBF regions of the nine non-OBF MS. Five of the nine non-OBF countries, namely, Croatia, Italy, Portugal, Spain and the United Kingdom had their eradication programmes for bovine brucellosis in their non-OBF regions approved and cofinanced during 2015 by the EU. These MS reported on the prevalence situation in their non-OBF regions by the number of positive herds, the number of herds tested under the eradication programme, and the total number of herds existing. The number of positive herds reported in non-OBF regions was 19 in Croatia (four in 2014), 598 in Italy (510 in 2014), 73 in Portugal (88 in 2014), 47 in Spain (58 during 2014) and none in the United Kingdom (8 in 2014) (Table 2015_DSBRUCOFCAT). The four non-OBF MS with eradication programmes that were not cofinanced by the EU during 2015 reported the number of infected herds and the total number of herds existing. Of these MS, Cyprus and Hungary did not report any cases of infected herds for the year 2015, whereas Bulgaria reported 2 (0 in 2014) and Greece reported 199 infected herds (211 in 2014). Therefore, for 2015, 938 positive or infected cattle herds were reported in total in the non-OBF regions of the non-OBF MS (967 in 2014).

During the years 2012–2015, there were, respectively, 9, 2, 2 and 4 cattle herds reported infected in the OBF MS or OBF regions of non-OBF MS, meaning it was an extremely rare event. In the non-OBF regions of the non-OBF MS the overall prevalence of *Brucella*-positive or -infected cattle herds increased during those years from 0.10% in 2012 to 0.28% in 2015 (Figure 47). Concomitantly the total number of cattle herds in this period decreased steadily from 1,162,978 to 336,741 while the total number of *Brucella*-positive or -infected cattle herds decreased slightly from 1,181 to 938. The overall increase in the prevalence of *Brucella*-positive or -infected cattle herds is mainly due to the decrease of number of cattle herds in the non-OBF regions of the non-OBF MS. In addition, Romania – with 619,591 cattle herds – became OBF MS from 2014 onwards. In some non-OBF MS or non-OBF regions in OBF MS, especially regions in Italy as well as in Greece, there seems not to be an important decrease in the number of positive or infected cattle herds compared to 2014.

Figure 46: Proportion of cattle herds infected with or positive for *Brucella*, 2015



OBF: Officially Brucellosis free in cattle.

Figure 47: Proportion of *Brucella*–positive cattle herds, in non-OBF regions, EU, 2012–2015

Indeed, Figure 48 displays the trends in *Brucella* test-positive cattle herds in the non-OBF regions of the four MS with the EU cofinanced eradication programmes for bovine brucellosis, during 2004–2015. In Croatia (cofinanced since 2014), Portugal and Spain, 19, 73 and 47 test-positive herds, respectively, remained in their non-OBF regions in the year 2015 resulting in a very low to rare prevalence of, respectively, 0.07%, 0.24% and 0.04%. In Italy 598 test-positive herds remained leading to a prevalence of 1.85% in its non-OBF regions, with a reported highest regional prevalence in Sicilia (3.2%) (Figure 46).

Greece, a non-OBF MS without its eradication programme cofinanced by the EU reported 199 *Brucella*-infected cattle herds in their national herd of 21,941 units, resulting in a prevalence of 0.91% (Table 2015_DSBRUOFNCOFCAT) as compared to 211 (prevalence of 1.21%) in 2014. The other non-cofinanced non-OBF MS gradually reported, these last years, to have no infected herds any more or only very few (Bulgaria).

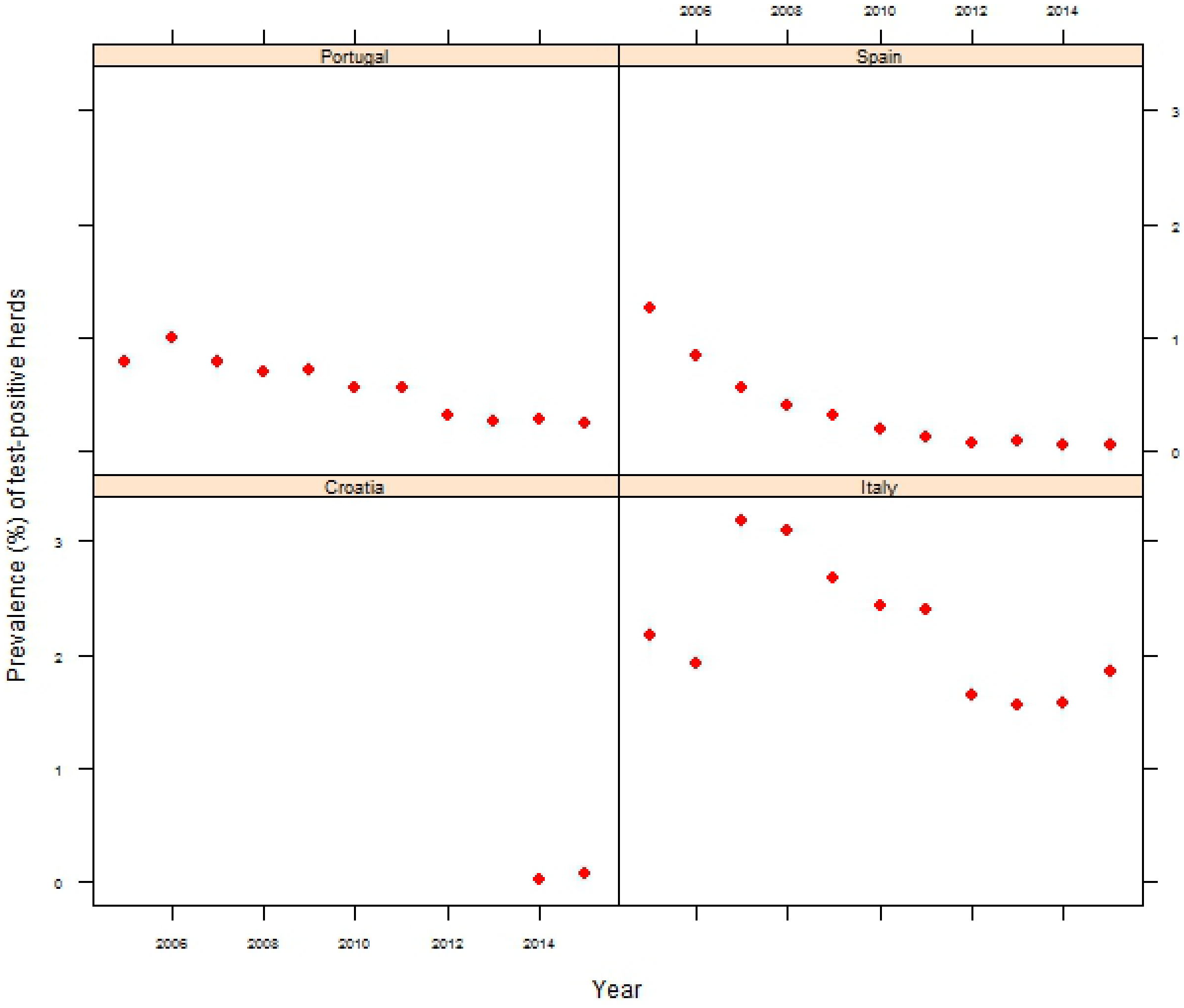
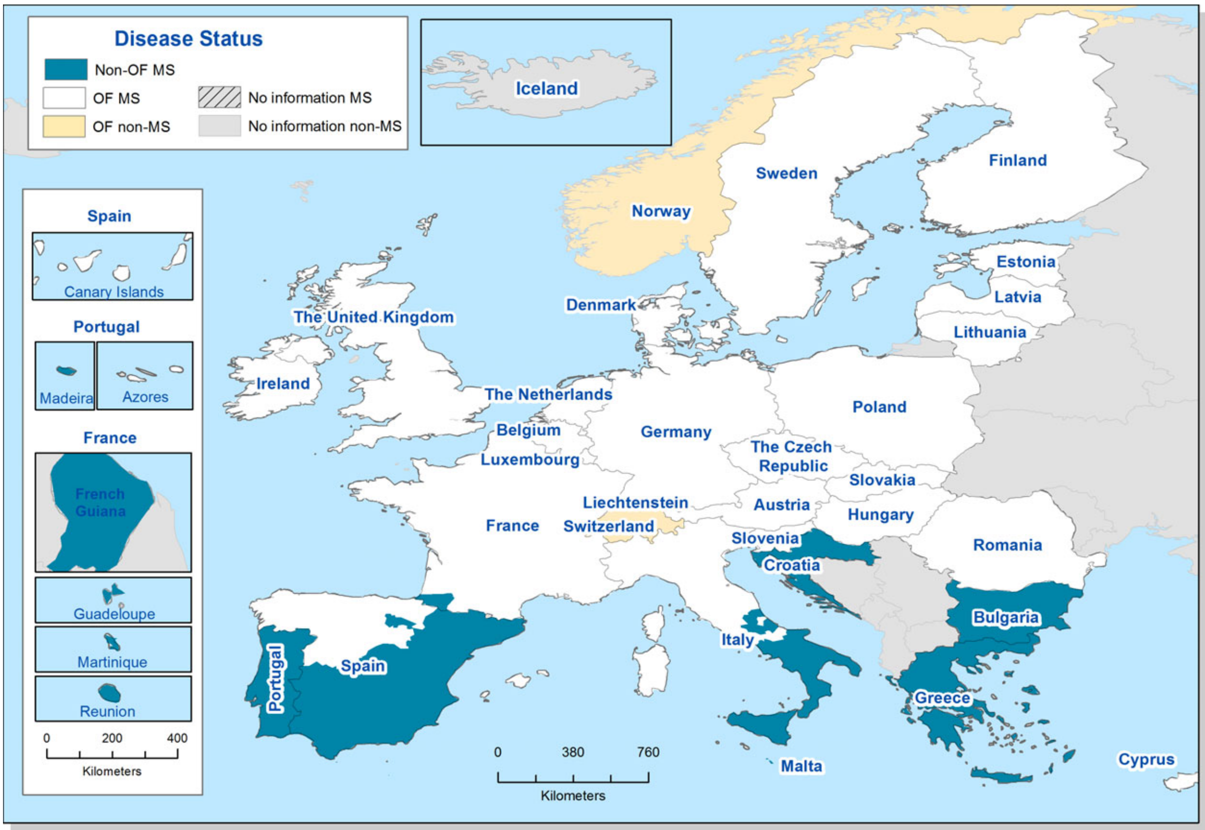


Figure 48: Prevalence of *Brucella* test-positive cattle herds, in non-OBF regions of four non-OBF cofinanced Member States, 2004–2015

Sheep and goats

The status regarding freedom from ovine and caprine brucellosis caused by *B. melitensis* (ObmF) and occurrence of the disease at regional or national levels for MS and non-MS in 2015 are presented in Figures 49 and 50, respectively. In 2015, Cyprus acquired ObmF status. Therefore, the 2015 list of countries and regions ObmF was: Austria, Belgium, Cyprus, the Czech Republic, Denmark, Estonia, Finland, all but one of the 96 metropolitan departments in France (Perrin et al., 2015), Germany, Hungary, 13 regions and three provinces in Italy, Ireland, Latvia, Lithuania, Luxembourg, the Netherlands, the Azores in Portugal, Poland, Romania, Slovakia, Slovenia, the Canary Islands, Asturias, Cantabria, Castile and Leon, Galicia, Navarre, Basque Country and the Balearic Islands in Spain, Sweden and the United Kingdom. The eight MS that by the end of 2015 had not yet gained a country-level ObmF status are Bulgaria, Croatia, France, Greece, Italy, Malta, Portugal and Spain. Norway and Switzerland were ObmF in accordance with the EU legislation and Liechtenstein had the same status (ObmF) as Switzerland. Iceland, which has no special agreement concerning animal health (status) with the EU, has never reported brucellosis due to *B. abortus, B. melitensis* or *B. suis*.



OF: Officially *B. melitensis* free in sheep and goats. In France, all but one of the 96 metropolitan departments (due to Rev.1 vaccination against *Brucella ovis*) are ObmF and no cases of brucellosis have been reported in small ruminants since 2003.

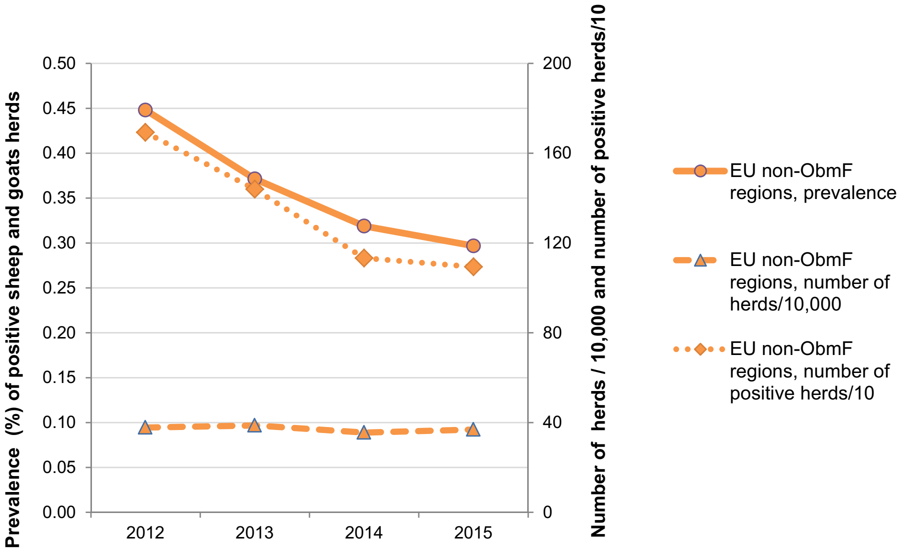
Figure 49: Status of countries and regions regarding ovine and caprine brucellosis, 2015

In the 20 MS declared ObmF and in the regions declared ObmF in the four non-ObmF MS France, Italy, Portugal and Spain, which total a population of 1,041,570 sheep and goat herds, annual surveillance programmes are carried out to confirm freedom from sheep and goat brucellosis. In these 20 ObmF MS and ObmF regions of the four non-ObmF MS, brucellosis due to *B. melitensis* was only detected in 10 sheep and goat herds in Italy (Table 2015_DSBRUOFNCOFOV). It was not detected in the non-MS Iceland, Norway, Switzerland and Liechtenstein.

In 2015 there were a total of 368,436 sheep and goat herds in the non-ObmF regions of the eight non-ObmF MS. Five of the eight non-ObmF countries, namely Croatia, Greece, Italy, Portugal and Spain, had their eradication programmes for ovine and caprine brucellosis in their non-ObmF regions during 2015 approved and cofinanced by the EU. These MS reported on the prevalence situation in their non-ObmF regions by the number of positive herds, the number of herds tested under the eradication programme, and the total number of herds existing. The number of positive herds reported in non-ObmF regions was, respectively, 482 in Portugal (529 in 2014), 465 in Italy (444 in 2014), 77 in Spain (113 in 2014), 28 herds in Croatia (25 in 2014) and 5 in Greece (22 in 2014) (Table 2015_DSBRUCOFOV). The three non-ObmF MS with eradication programmes that were not cofinanced by the EU during 2015 reported the number of infected herds and the total number of herds existing. Of these MS Bulgaria reported 37 infected herds (0 in 2014), whereas France and Malta reported no positive case of infected flocks (Table 2015_DSBRUOFNCOFOV). Therefore, for 2015, 1,094 positive or infected sheep and goats herds were reported in total in the non-ObmF regions of the non-ObmF MS (1,133 in 2014).

During the years 2012–2015, there were, respectively, 5, 4, 3 and 10 sheep and goat herds reported infected in the ObmF MS or ObmF regions of non-ObmF MS, meaning it was an extremely rare event. In the non-ObmF regions of the non-ObmF MS, the overall prevalence of *B. melitensis* -positive sheep and goat herds decreased from 0.45% in 2012 to 0.29% in 2015 (Figure 51). This is due to the decrease in the total number of positive sheep and goat herds from 1,693 in 2012 to 1,094 in 2015, while the total number of sheep and goat herds remained quite stable in these non-ObmF regions and was 377,690 in 2012 and 368,436 in 2015.

Figure 50: Proportion of sheep and goat herds infected with or positive for brucellosis, 2015



ObmF: Officially *B. melitensis* free in sheep and goats.

Figure 51: Proportion of sheep and goat herds infected with or positive for *B. melitensis*, in non-ObmF regions, EU, 2012–2015

Figure 52 displays the trends in *B. melitensis* test-positive sheep and goat herds in the non-ObmF regions of the five MS with the EU cofinanced eradication programmes for small ruminant brucellosis, during 2005–2015. In Croatia (cofinanced since 2014), Greece and Spain 28, 5 and 77 test-positive herds remained in 2015 resulting in a very low prevalence in 2015 of 0.15%, 0.40% and 0.11%, respectively. Italy and Portugal reported, respectively, 465 and 482 test-positive herds leading to a low to very low prevalence of 1.24% and 0.83% in their non-ObmF regions, with a reported highest regional prevalence in Sicilia (3.5%) (Figure 50).

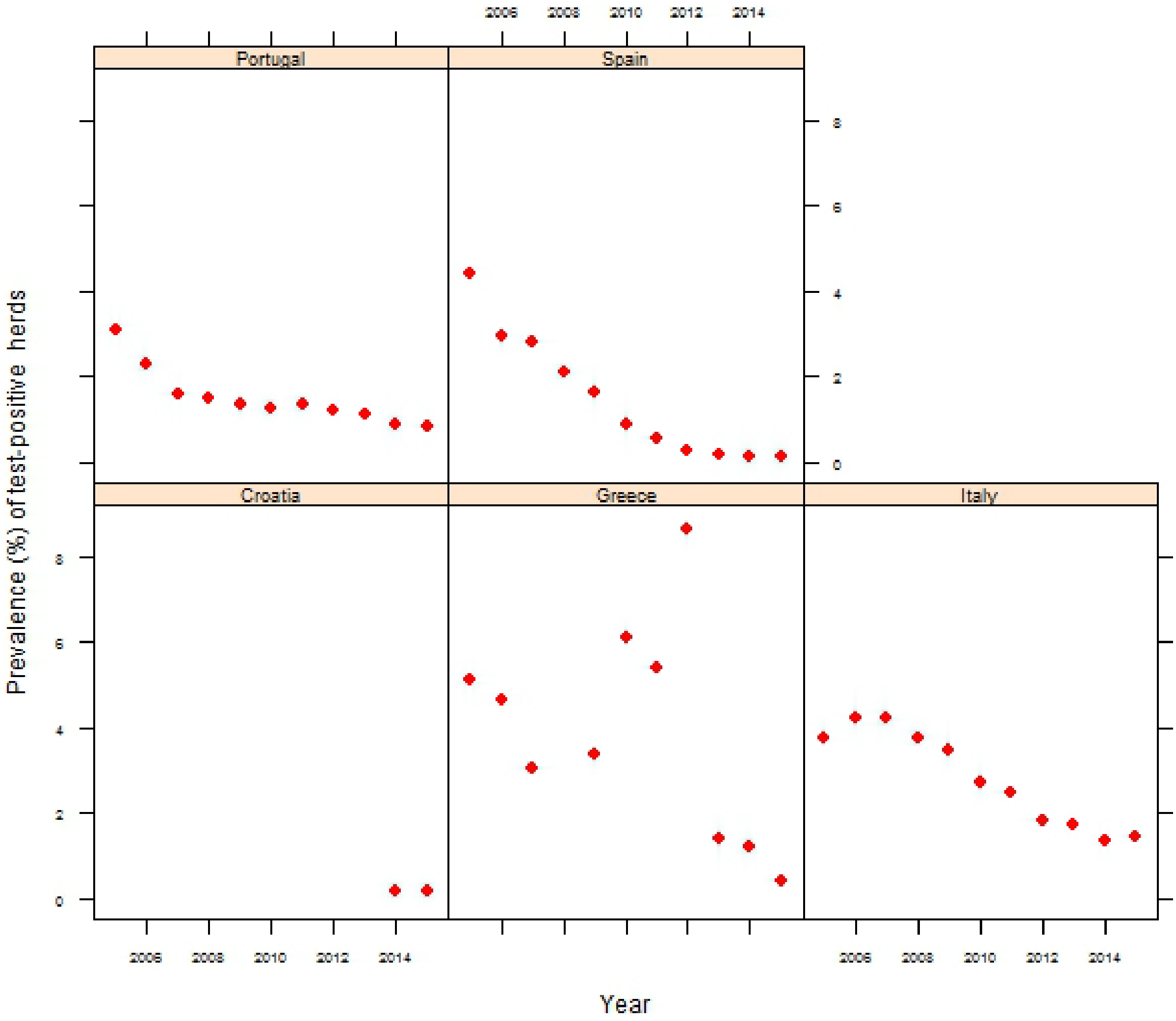


Figure 52: Prevalence of *Brucella melitensis* test-positive sheep and goat herds, in non-ObmF regions of five cofinanced Member States, 2004–2015

Other animals

In 2015, 16 MS sampled animal species other than cattle, sheep or goats. *B. suis*-positive non-farmed wild boars were reported by Finland, Germany, Italy and Spain and *B. suis*-positive pigs by Croatia and Germany. *Brucella* unspecified-positive tests were reported from pigs and wild boars by Germany, from dogs (pet), water buffalos, farmed wild boars and hunted wild boars by Italy, in hunted wild boars by Romania. Finland reported a *B. pinnipedialis*-positive wild seal (Table 2015_BRUCOTHERAN).

3.7.3. Discussion

Brucellosis is rare in humans in the EU. The highest notification rates and the majority of domestic cases were reported as in previous years from three MS (Greece, Italy and Portugal) which are not officially brucellosis-free in cattle, sheep or goats. Also Bulgaria, not officially brucellosis-free in cattle, sheep or goats, reported a high notification rate due to an outbreak involving 33 cases infected with

Brucella melitensis. The majority of brucellosis cases in the officially brucellosis-free countries were travel-associated. Nearly 70% of the human brucellosis cases were hospitalised with one fatal case in 2015.

There was a *Brucella*-positive investigation with two samples of 'milk from other animal species or unspecified' at retail found positive for *Brucella* in Italy. The other two MS (Portugal and Spain) that reported surveillance results in food did not report any positive finding.

The EU MS have national surveillance and/or eradication programmes for brucellosis in place. In animals, bovine brucellosis and ovine and caprine brucellosis have been widely eradicated by most MS[39] since some years now. As a result, outbreaks thereof have become less frequent in large areas of the EU. The 2015 reports of positive cases of brucellosis demonstrate that they are very much clustered and that there are only few MS, and within these countries few regions, that still report detecting *Brucella* in domestic ruminants.

In the EU OF regions no bovine brucellosis or ovine and caprine brucellosis was reported for the year 2015, except for four *Brucella*-infected cattle herds in Germany and 10 *B. melitensis*–infected sheep and goat herds in Italy. Bovine brucellosis and ovine and caprine brucellosis have remained an extremely rare event in the EU OF regions since many years.

In the EU non-OF regions of non-OF MS, the overall prevalence of bovine, ovine and caprine brucellosis was very low, about 0.3%, for the year 2015. For bovine brucellosis, the overall prevalence of *Brucella*-positive or -infected cattle herds has been increasing in the non-OBF regions of the non-OBF MS during the years 2012–2015, from 0.10% in 2012 to 0.28% in 2015. This is mainly due to the decrease of number of cattle herds in these non-OBF regions of the non-OBF MS while the total number of *Brucella*-positive or -infected cattle herds only decreased slightly. Italy reported some hundreds of *Brucella*-positive herds and Greece 199 infected herds, respectively, leading to a remaining low (Italy) to very low (Greece) prevalence of bovine brucellosis in non-OBF regions of these MS. Croatia, Portugal and Spain reported a very low to rare prevalence. The overall prevalence of *B. melitensis* -positive sheep and goat herds in the non-ObmF regions of the non-ObmF MS decreased during the years 2012–2015, from 0.49% in 2012 to 0.29% in 2015. Italy and Portugal still reported some hundreds of *Brucella* test-positive sheep and goat herds leading to a remaining low to very low prevalence, whereas Croatia, Greece and Spain reported a very low prevalence. Bulgaria reported two positive cattle herds and some tenths of sheep and goat herds infected with *Brucella melitensis* while the public health authorities reported an outbreak of *Brucella melitensis* in humans (see above).

The findings in humans of highest notification rates of brucellosis in the non-OBF and non-ObmF MS Greece, Italy and Portugal as well as the reporting of the majority of domestic cases of brucellosis in humans in the EU by these three MS, might be explained by the *Brucella* monitoring and surveillance findings in the cattle and small ruminant populations of these three MS, which disclosed some hundreds of *Brucella*-positive or -infected herds still.

More information on the EU approved and cofinanced eradication programmes for brucellosis in cattle and small ruminants carried out by the MS is available online at: http://ec.europa.eu/dgs/health_food-safety/funding/cff/animal_health/vet_progs_en.htm

3.8. *Trichinella*

The Appendix A lists all summaries made for the production of this section, for humans and animals, including *Trichinella* summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

Nematodes of the genus *Trichinella* are parasites circulating among wild carnivore and omnivore animals. When humans fail in the management of wildlife and domestic animals, these parasites can be transmitted from wild to domestic animals (mainly swine) and from these animals to humans. In addition, some species can transfer in a reversible path from domestic animals to wildlife.

According to data of the International *Trichinella* Reference Center (ITRC, online) and published reports and publications (EFSA, 2007b; EFSA and ECDC, 2009; Pozio et al., 2009; EFSA and ECDC, 2010, 2012, 2013; Boutsini et al., 2014; EFSA and ECDC, 2014; Pozio, 2014; EFSA and ECDC, 2015a, b; Lopes et al., 2015; Pozio, 2016a,b) four species of *Trichinella* (*T. spiralis*, *T. nativa*, *T. britovi* and *T. pseudospiralis*) have circulated in European wildlife during the last 20 years. *T. spiralis* has patchy

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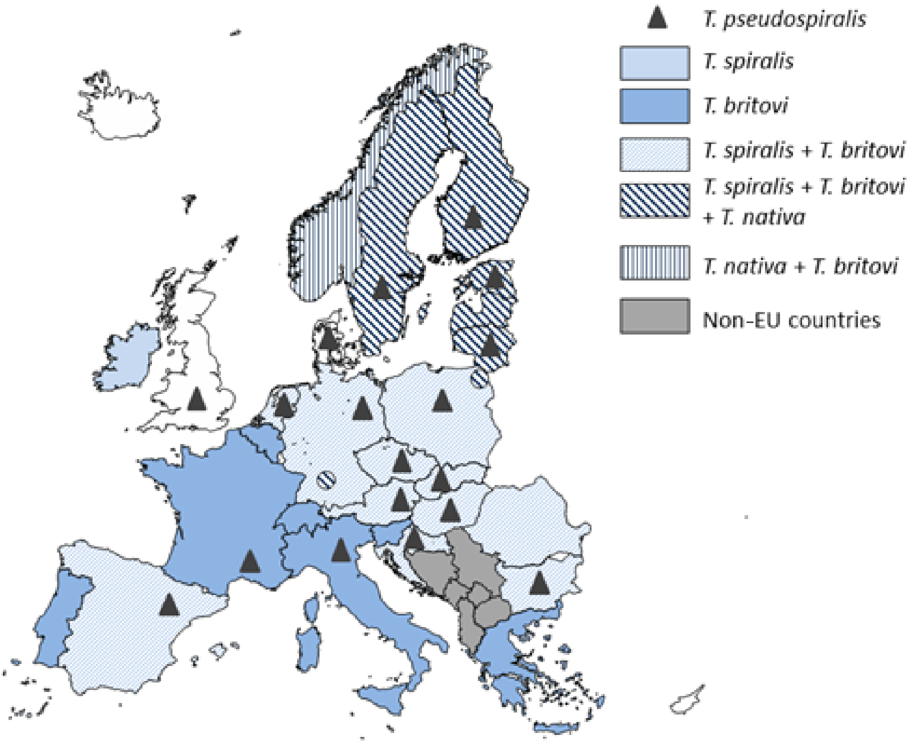
[39] Commission Implementing Decision of 27 November 2012 amending Annexes I and II to Council Directive 82/894/EEC on the notification of animal diseases within the Community.

distribution in the EU and is found predominantly in wild boar, but can also be detected in carnivore mammals; *T. nativa* infects almost exclusively carnivore mammals of northern EU countries; *T. britovi* is prevalent among carnivore mammals, but can also be detected in wild boar in the EU MS non-EU MS; *T. pseudospiralis* has been detected in both carnivore and omnivore mammals and in some birds in small foci of 18 MS (Figure 53). According to data of the International *Trichinella* Reference Center, *Trichinella* spp. infections in domestic animals reflect the host preference of these parasites and their circulation among wildlife of MS. In domestic pigs the species most commonly detected during the last 20 years has been *T. spiralis* (79.2%), followed by *T. britovi* (20.6%) and *T. pseudospiralis* (0.2%).



The distribution map is based on data obtained from the International *Trichinella* Reference Center, EFSA reports and recently published papers.

Figure 53: Distribution of *Trichinella* spp. in wildlife of 28 MS and 3 non-MS (IC, NO and CH) in the last 20 years

3.8.1. Trichinellosis in humans

In 2015, 243 cases of trichinellosis, including 156 confirmed cases, were reported in 27 MS (Table 23). The EU notification rate in 2015 was 0.03 cases per 100,000 population which represented a decrease of 57.1% compared with 2014 (0.07 per 100,000), when the highest notification rate in the last 5 years was reported. The decrease in 2015 was mainly due to a reduced number of trichinellosis cases reported by Romania and Bulgaria, which in previous years had reported the highest numbers of cases. In 2015, Lithuania had the highest notification rate in the EU (0.72 cases per 100,000), followed by Bulgaria and Romania with 0.31 and 0.28 cases per 100,000, respectively. Together, these three countries accounted for 63.3% of all confirmed cases reported at the EU level in 2015. Increase of cases in Lithuania was attributed to an outbreak with 20 cases caused by wild board meat. Thirteen MS reported zero confirmed cases in 2015 including four MS (Cyprus, Luxembourg, Malta and Portugal) that have never reported any trichinellosis cases. Five countries (Austria, the Czech Republic, Finland, the Netherlands and the United Kingdom) have reported only one each case since the beginning of the EU level surveillance in 2007.

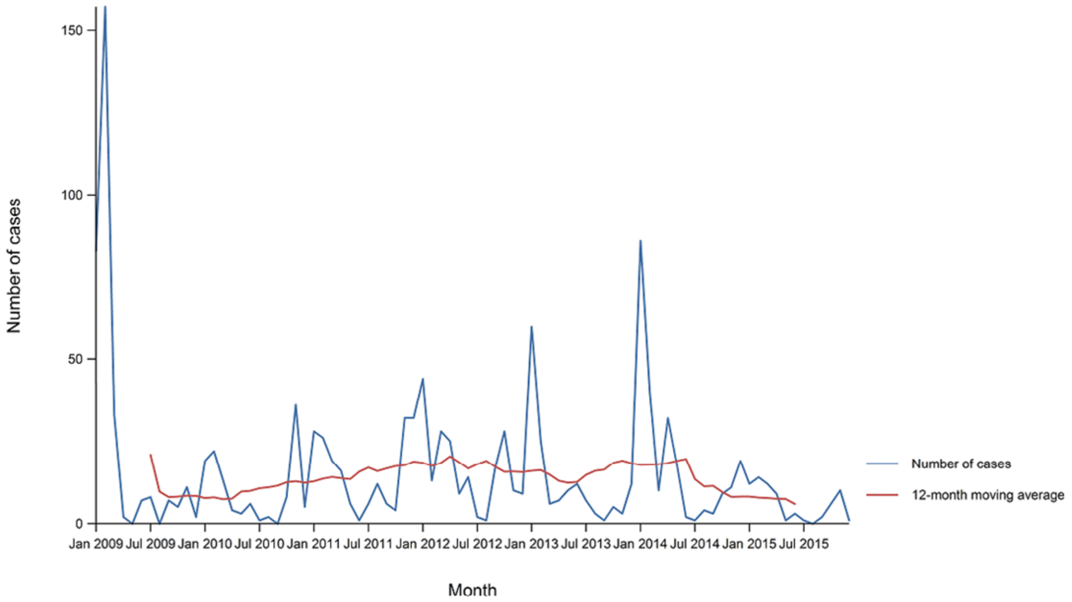
One case of trichinellosis was reported as travel-associated with unknown travel destination by Sweden. The remaining 94 cases reported with travel information were either reported as domestically-acquired (94.7%) or of unknown travel-status (4.2%).

Table 23: Reported human cases of trichinellosis and notification rates per 100,000 population in the EU/EEA, by country and year, 2011–2015

Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	1	0.01
Belgium(b)	N	A	2	0	–	16	–	1	–	0	–	0	–
Bulgaria	Y	A	22	22	0.31	60	0.83	36	0.49	30	0.41	27	0.37
Croatia	Y	A	3	3	0.07	3	0.07	0	0.00	0	0.00	–	–
Cyprus	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Czech Republic	Y	C	0	0	0.00	0	0.00	0	0.00	1	0.01	0	0.00
Denmark(c)	–	–	–	–	–	–	–	–	–	–	–	–	–
Estonia	Y	C	2	2	0.15	0	0.00	0	0.00	0	0.00	0	0.00
Finland	Y	C	1	1	0.02	0	0.00	0	0.00	0	0.00	0	0.00
France	Y	C	3	3	0.00	0	0.00	0	0.00	0	0.00	2	0.00
Germany	Y	C	8	3	0.00	1	0.00	14	0.02	2	0.00	3	0.00
Greece	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Hungary	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Ireland	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Italy	Y	C	36	36	0.06	4	0.01	–	–	33	0.06	6	0.01
Latvia	Y	C	4	4	0.20	5	0.25	11	0.54	41	2.01	50	2.41
Lithuania	Y	C	38	21	0.72	5	0.17	6	0.20	28	0.93	29	0.95
Luxembourg	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Malta	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Netherlands	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	1	0.01
Poland	Y	C	27	1	0.00	6	0.02	4	0.01	1	0.00	10	0.03
Portugal	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Romania	Y	C	92	55	0.28	221	1.11	116	0.58	149	0.74	107	0.54
Slovakia	Y	C	1	1	0.02	0	0.00	5	0.09	5	0.09	13	0.24
Slovenia	Y	C	0	0	0.00	0	0.00	1	0.05	1	0.05	1	0.05
Spain	Y	C	3	3	0.01	1	0.00	23	0.05	10	0.02	18	0.04
Sweden	Y	C	1	1	0.01	1	0.01	0	0.00	0	0.00	0	0.00
United Kingdom	Y	C	0	0	0.00	1	0.00	0	0.00	0	0.00	0	0.00
EU Total	–	–	**243**	**156**	**0.03**	**324**	**0.07**	**217**	**0.05**	**301**	**0.06**	**268**	**0.06**
Iceland	Y	C	0	0	0.00	0	0.00	0	0.00	–	–	–	–
Norway	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Switzerland(d)	Y	C	2	2	0.02	0	0.00	1	0.01	1	0.01	0	0.00

(a): Y: yes; N: no; A: aggregated data; C: case-based data; –: no report.
(b): Disease not under formal surveillance.
(c): No surveillance system.
(d): Switzerland provided data directly to EFSA. The human data for Switzerland also include the ones from Liechtenstein.

The seven-year EU/EEA trend from 2009 to 2015 in confirmed cases of trichinellosis was substantially influenced by a number of smaller and larger outbreaks, often with peaks in January-February, Figure 54). The sharp peak at the beginning of 2009 was attributed to Romania, which reported 243 confirmed cases in January–March only. For January-February 2014, Romania reported 221 cases. No significant increasing or decreasing trends were observed for any country from 2009 to 2015.



Source: Austria, Cyprus, the Czech Republic, Estonia, Finland, France, Greece, Hungary, Ireland, Latvia, Luxembourg, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Sweden and the United Kingdom. Bulgaria, Croatia, Germany, Iceland, Italy, Lithuania and Spain did not report data to the level of detail required for the analysis. Belgium and Denmark do not have any formal surveillance system for the disease.

Figure 54: Trend in reported confirmed human cases of trichinellosis in the EU/EEA by month, 2009–2015

Of the 14 MS reporting confirmed cases for 2015, seven provided information on hospitalisation for all their cases (72.5% of all confirmed cases reported in the EU) with 34.5% of these cases reported as hospitalised. Eight MS provided information on the outcome of their cases (75.0% of all confirmed cases). No deaths due to trichinellosis were reported in 2015 among the 90 confirmed cases for which this information was available.

Species information was available for 81.5% of the reported confirmed cases from 12 MS. The most commonly reported species was *T. spiralis* (77.6%) followed by *T. britovi* (22.4%). Bulgaria reported all 22 cases infected by *T. britovi.*

3.8.2. *Trichinella* in animals

According to Commission Regulation (EC) No 1375/2015, carcases of domestic pigs, horses, wild boar and other farmed or wild animal species that are susceptible to *Trichinella* infestation should be systematically sampled at slaughter as part of the meat inspection process and tested for *Trichinella*. Animals (both domestic and wild) slaughtered for own consumption are not included in the Regulation, but are subject to national rules, which differ per MS, as each MS can decide how to control *Trichinella* in this population (e.g. test or not, freeze or not). Therefore, data from animals slaughtered for own consumption might not be comparable between MS since there is not always information if these animals were included or not in the data provided to EFSA for 2015.

From 10 August 2015, Commission Regulation (EU) No 1375/2015 joining the Commission Regulation (EC) No 2075/2005 and all the further amendments came into force. Among other requirements, the Regulation state that the reporting of data regarding domestic swine shall, at least, provide specific information related to number of animals tested that were raised under controlled housing conditions as well as the number of breeding sows, boars and fattening pigs tested. Further, the Regulation states that a negligible risk status for a country or region is no longer recognised in an international context by the OIE. Instead, such recognition is linked to compartments of one or more holdings applying specific controlled housing conditions. Belgium and Denmark have had such a status since 2011, and the holdings and compartments of domestic swine in those two MS complied with the conditions for controlled housing at the date when this Regulation came into force. Therefore, these two MS are allowed to apply for the status as negligible risk without additional prerequisites.

Domestic and wild swine, as well as different wildlife species, are the most important potential sources for human infection or may serve as *Trichinella* spp. reservoirs in the EU. Therefore, detailed information on the data reported by MS and non-MS on the occurrence of *Trichinella* in pigs raised under controlled housing conditions, pigs and farmed wild boar not raised under controlled housing conditions has been summarised in Table 24 and data for wild animals are presented in Table 25.

In 2015, 27 MS and three non-MS provided information on *Trichinella* in domestic animals (pigs, farmed wild boar and/or horses) and 5 MS reported positive findings.

Eighteen MS reported data on breeding and fattening pigs raised under controlled housing conditions, no positive findings were reported (Table 24).

Table 24: Number of *Trichinella* positive/tested (% positive) in pigs in the EU and non-MS in 2015

Country	**Farmed wild boar**	**Fattening pigs**	**Breeding pigs(b)**	**Fattening pigs**	**Breeding pigs(b)**
	Not raised under controlled housing conditions or not specified(a)		**Not raised under controlled housing conditions or not specified**	**Raised under Controlled housing conditions**	
Austria	0/25,406	0/5,289,607	0/92,082		
Belgium				0/11,918,904	
Bulgaria			0/10,866	0/957,886	0/7,079
Croatia(c)		9/1,391,070 (< 0.01%)			
Cyprus		0/561,969	0/11,058		
Denmark	0/414	0/691,426	0/304,190	0/17,474,755	0/213,430
Estonia		0/498,661		0/8937	
Finland	0/376	0/2,026,355	0/42,329		
France				0/2,011,461	
Germany	0/381			0/55,017,355	
Greece	0/1,619	0/4,685		0/1,089,787	0/23,578
Hungary				0/4,641,960	
Ireland				0/3,124,438	0/103,615
Italy	0/1,763	0/5,966,951		0/3,708,405	
Latvia		0/407,228			
Lithuania		1/841,348 (< 0.01%)			
Luxembourg				0/163,234	
Malta		0/59,639	0/1,199		
Netherlands	0/1,111			157,684	
Poland		8/21,973,398 (< 0.01%)			
Portugal		0/248,980	0/1,508	0/4,281,310	0/28,768
Romania	0/149	87/137,338 (0.06%)	0/12,655	0/4,606,626	0/37,284
Slovakia		0/519,684	0/10,412		
Slovenia		0/242,497			
Spain(d)		1/8,908,509 (< 0.01%)	0/3,383,709	0/107,404	0/883,854
Sweden		0/379,332	0/21,441	0/1,039,058	0/26,510
United Kingdom	0/1,120	0/497,298	0/249,798	0/5,155,331	0/210,571
EU Total	**0/32,339**	**106/50,645,975 (< 0.01%)**	**0/4,141,247**	**0/115,464,535**	**0/1,534,689**
Iceland				0/81,561	
Norway		0/1,605,000			
Switzerland		0/2,573,450			
Total non-MS		**0/4,178,450**		**0/81,561**	

(a): Fattening pigs for which the housing conditions were not specified, have been arbitrarily included in the category of fattening pigs under not raised under controlled housing conditions.

(b): Breeding pigs represents the sum of boars and sows if these are reported separately.

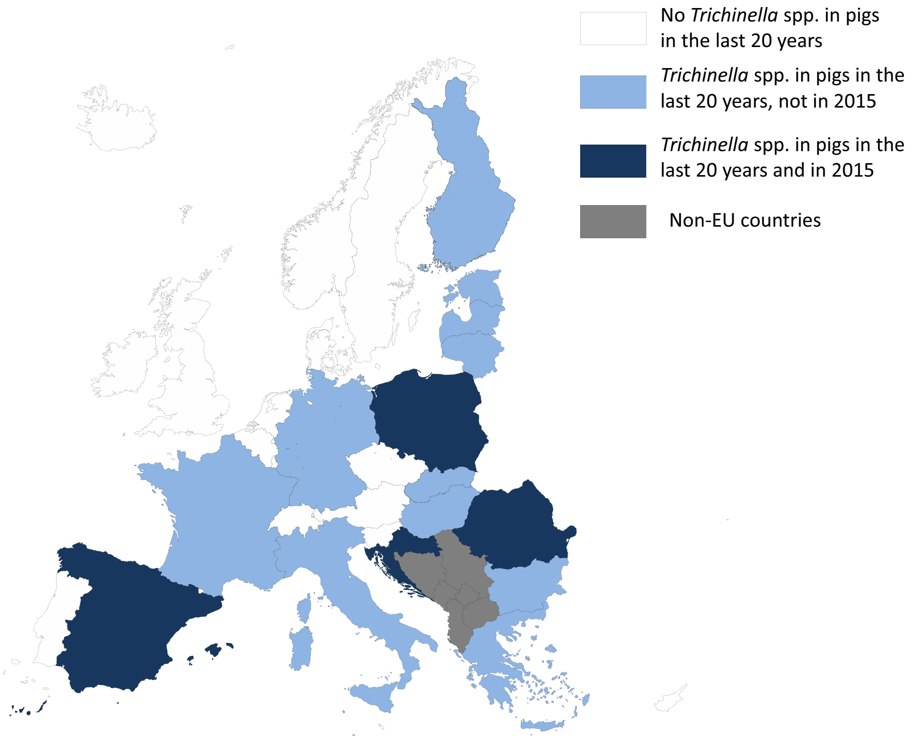
(c): In Croatia, three meat products made with pork from pigs not raised under controlled housing tested positive for *Trichinella* spp.; the number of fattening pigs from not raised under controlled housing conditions includes also pigs for which housing conditions were not reported (number of animals obtained from mixed herds).

(d): In Spain, 1,579,156 slaughtered batches of fattening pigs not raised under controlled housing and 883, 854 batches of breeding pigs raised under controlled housing tested negative for *Trichinella* spp.

In total, data on 115,464,535 fattening pigs, 1,534,689 breeding pigs and 1,579,156 slaughtered batches from pigs raised under controlled housing conditions were tested for *Trichinella* spp. in 17 MS. Norway and Switzerland tested 4,178,450 fattening pigs raised under not controlled housing conditions and all were negative. In Iceland no positives were found and all fattening pigs tested had been housed under controlled housing conditions (Table 24).

Twenty-two MS and two non-MS reported data on breeding and fattening pigs or farmed wild boar that were not raised under controlled housing conditions and five MS reported positive findings among fattening pigs (Table 24). In fattening pigs, five MS (Romania accounting for most reports followed by Croatia, Poland, Spain and Lithuania) reported in total 106 positive findings out of 50,645,975 tested animals. No positive animals were detected among 4,141,247 breeding pigs of 12 reporting MS. A total of 1,605,000 and 2,573,450 breeding pigs not raised under controlled housing condition were tested for *Trichinella* spp. in Norway and Switzerland, respectively. None of these animals tested positive. No positive animals were detected among 32,339 farmed wild boars reported by 8 MS.

As shown in Figure 55, from 1995 to 2014 (20-year period), *Trichinella* spp. were not documented in domestic pigs in 13 MS (Austria, Belgium, Cyprus, the Czech Republic, Denmark, Ireland, Luxembourg, Malta, the Netherlands, Portugal, Slovenia, Sweden and the United Kingdom) while this was the case in the other 15 MS (Bulgaria, Croatia, Estonia, Finland, France, Germany, Greece, Hungary, Italy, Latvia, Lithuania, Poland, Romania, Slovak Republic and Spain). For the latter, Figure 55 also indicates for which MS positive *Trichinella* findings were confirmed or not using the current surveillance in 2015.



This distribution map has been built based on data from the International *Trichinella* Reference Center (https://w3.iss.it/site/Trichinella/), EFSA reports and published papers.

Figure 55: *Trichinella* spp. in domestic pigs of 28 MS and 3 non-MS (IC, NO and CH) in the last 20 years and in 2015

In total in the EU, more than 171 million animals (breeding pigs, fattening pigs and unspecified pigs kept under controlled or not controlled housing conditions and farmed wild boar) were tested for *Trichinella* and 106 were positive (0.6 per million) (Tables 2015_TRICHPIGS, 2015_TRICHPIGSNOT, 2015_TRICHFARMEDWILDBOAR). Most (82.85%) of the positive findings were reported by Romania followed by Croatia, Poland, Lithuania and Spain (Table 24). All *Trichinella* spp. infected pigs originated from animals kept under not controlled housing conditions. Most (63.8%) of *Trichinella* spp. isolates from swine were not identified at the species level; however, when larvae were identified (36.2% of cases), 77.4% of the isolates were *T. spiralis*, and 22.6% were *T. britovi.*

No positive findings were reported from ± 137,000 domestic solipeds (mainly horses, but also donkeys) and 10,477 slaughtered soliped batched tested in 20 MS (Austria, Belgium, Croatia, Denmark, Estonia, Finland, France, Hungary, Ireland, Italy, Latvia, Luxembourg, Malta, the Netherlands, Portugal, Romania, Slovenia, Spain, Sweden, and the United Kingdom) and in three non-MS (Iceland, Norway, Switzerland) (Table 2015_TRICHHORSE).

Twenty-one MS and two non-MS provided data on hunted wild boar (Table 25). Fourteen MS reported 672 positive findings out of 877,122 animals tested, with an overall EU proportion of positive samples of 0.08%. Most of the positive animals were reported by Spain (47%), Romania (14.0%), Bulgaria (13.2%), Estonia (12.2%), Latvia (6.0%) and Croatia (3.1%). Most of the findings were reported as *Trichinella* spp. followed by *T. britovi*, and *T. spiralis*. There were also a small number of findings of *T. nativa* and *T. pseudospiralis* (Table 2015_TRICHWILDWILDBOAR)*.*

Sixteen MS and one non-MS reported data on *Trichinella* in 18 different wildlife species other than wild boar, and reported a total of 354 (3.7%) positive findings in nine host species of 10 MS from almost 10,000 animals. *Trichinella* is found in wildlife in large parts of Europe and 13 MS reported positive findings (Table 25). The highest prevalence has been detected among wild carnivores at the top of the food chain and/or with a scavenger behaviour (33.7% in raccoon dogs, 25.0% in lynxes, 19.5% in wolves, and 9.5% in bears). The prevalence of infection in red foxes (Table 2015_TRICHFOX) is highly variable from 33.7% in Finland, 7.7% in Slovakia, 3.3% in Croatia, 1.4% in Hungary, and less than 1% in the Czech Republic, Germany and Italy, and with a total prevalence (1.6%) lower than that of other carnivore mammals (Table 25).

No positive findings were reported from 35 wild carnivore and omnivore birds tested in two MS (Finland and the United Kingdom).

Table 25: Number of *Trichinella* positive/tested (% positive) in wild animals in the EU and non-MS in 2015

	Badger	Bear	Beaver	Golden jackal	Red fox	Lynx	Marten	Mink	Otter	Polecat	Raccoon dog	Seal	Wolf	Wolverine	Carnivore total	Wild boar
Austria	0/1															0/769
Belgium																1/6,546 (0.01%)
Bulgaria[(a)]																89/6,790 (1.31%)
Croatia	0/2	0/50			20/609 (3.3%)											21/26,650 (< 0.1%)
Cyprus					0/9											
Czech Republic					5/2,245 (0.2%)											2/185,040 (< 0.01%)
Denmark								0/29				0/33				
Estonia	1/2	13/58 (22.41%)				2/2										82/8,570 (1%)
Finland[(b)]	0/10	3/44 (6.81%)	0/2		60/178 (33.7%)	11/53 (20.8%)	2/7	0/8	3/47 (6.4%)	0/4	116/300 (38.7%)	0/11	13/36 (36.1%)	4/4		0/5
France																0/42,598
Germany[(c)]	0/35				1/1,860 (0.05%)						0/44					6/137,599 (< 0.01%)
Greece																0/95
Hungary[(d)]				4/20 (20%)	12/838 (1.43%)											5/63,992 (< 0.01%)
Italy[(e)]	1/157 (0.63%)				17/1,900 (0.9%)		0/40			0/1			20/87 (23%)			6/114,618 (< 0.01%)
Latvia						1/1										38/7,947 (0.5%)
Luxembourg					0/27											0/3,513
Netherlands																0/512
Portugal																0/67
Romania		29/131 (22.14%)														94/19,731 (0.5%)
Slovakia	0/1	0/21			15/195 (7.7%)											7/16,343 (0.04%)

	Badger	Bear	Beaver	Golden jackal	Red fox	Lynx	Marten	Mink	Otter	Polecat	Raccoon dog	Seal	Wolf	Wolverine	Carnivore total	Wild boar
Slovenia[f]																
Spain[g]																316/146,226 (0.21%)
Sweden	0/5	1/180 (0.55%)	0/2		0/2							0/1	0/46			1/89,497 (< 0.01%)
United Kingdom[h]	0/114				0/39											0/14
EU Total	**2/327 (0.6%)**	**46/484 (9.5%)**	**0/4**	**4/20 (20%)**	**130/7,902 (1.6%)**	**14/56 (25%)**	**2/47 (4.3%)**	**0/37**	**3/47 (6.4%)**	**0/5**	**116/344 (33.7%)**	**0/45**	**33/169 (19.5%)**	**4/4**	**354/9,491 (3.7%)**	**672[i]/ 877,122 (0.08%)**
Norway																1/1
Switzerland	0/2					1/10							0/1			0/4,278
Total non-MS	**0/2**					**1/10**							0/1			1/4,279

(a): Hunted wild boar and Fresh meat from hunted wild boar were aggregated; Bulgaria tested additional 303 wild boars in zoo with no positives.
(b): In addition to the reported animals in the table, 13 eagles, 4 falcons, 10 owls, and one crow tested negative.
(c): In addition to the reported animals in the table, no positive raccoon was detected among the 67 tested animals; and no positive among 240 other unspecified wild animals.
(d): In addition to the reported animals in the table, two rats were tested with a negative result.
(e): In addition to the reported animals in the table, one stray dog in Slovenia four weasels and four wild cats were tested with a negative result.
(f): Out of 988 tested bears and wild boar in Slovenia, four wild boars tested positive for *Trichinella.*
(g): 16/5191 (0.31%) slaughtered wild boar batches tested positive for *Trichinella*, but the number of infected animals is unknown.
(h): No one of 14 slaughtered wild boar batches tested positive for *Trichinella*; none of 232 the synanthropic rats tested positive for *Trichinella*; 7 gulls tested negative.
(i): Includes the four positive wild boar from Slovenia.

3.8.3. Discussion

Trichinellosis is a rare but serious human disease, which is still present in the EU. Almost half of the MS reported zero cases including four MS that have never reported any trichinellosis cases since 2007. In 2015, the majority of cases were reported from a few MS mainly in Eastern Europe and domestically-acquired. The EU/EEA trend was greatly affected by the number and size of disease outbreaks since the beginning of EU surveillance of trichinellosis. The EU notification rate decreased in 2015 and was the lowest rate reported in 5 years. This was mainly due to a decline in cases reported from Bulgaria and Romania, which had experienced the majority of *Trichinella* outbreaks in previous years. In 2015, these two countries together with Lithuania, reported more than half of the confirmed cases. The recurring peak in trichinellosis cases in January and February may reflect the consumption of various pork products during Christmas as well as the wild boar hunting season. On average, one-third of the confirmed human trichinellosis cases were hospitalised with no fatal outcomes.

Uncontrolled hunting activities play an important role to spread *Trichinella* by infected game carcasses and offal, which can be ingested by wild or domestic animals. Other rearing practices involved in transmission of *Trichinella* spp. to domestic pigs are the introduction of new pigs on a farm without any information on the farm of origin and previous farming conditions; cannibalism due to a high mortality rate; feed on garbage containing pork or wild animal scraps; feed on pork scraps from pigs slaughtered at the farm; feed on carcasses or scraps from farmed fur animals; feed on rats, which can play the role of *Trichinella* spp. 'vector' from one farm to another; feed origin and correct daily feed intake not always controlled; and lack of mechanical barriers to prevent entry of synanthropic and wild animals (both mammals and birds) into the pigsty. Pork scraps and offal from domestic pigs infected by *Trichinella* spp. represent a source of infection not only for other domestic pigs but also for synanthropic and wild animals.

These zoonotic parasites circulate among wild animals in large parts of Europe and only Cyprus, Luxembourg and Malta had never reported any findings. In 2015, 17 MS and two non-MS reported positive findings in animals. The lack of positive findings or confirmation of previous findings in other MS during 2015 is simply due to the lack of surveys, inadequacy of sample sizes, or investigation in regions where the environmental conditions do not favour the transmission of these zoonotic nematodes among wildlife. In the EU, most pigs are subject to official meat inspection at slaughter in accordance with Regulation (EC) No 1375/2015; only pigs slaughtered for own consumption are not covered by the regulation.

Only five out of 27 MS reported *Trichinella* in pigs in 2015, with an overall prevalence of 0.00006%. The positive findings were from pigs not raised under controlled housing conditions. Indeed, Romania account for 82% of the reported positive findings in pigs and all of these were related to pigs not raised under controlled housing conditions or for which the raising conditions were unknown. Comparison of the *Trichinella* prevalence in pigs not raised under controlled conditions with the prevalence of the previous years, shows a permanent decrease in the number of infected animals. However, the true underlying prevalence and spread could be higher and underestimated. Furthermore, most of *Trichinella* infections in domestic pigs for own consumption, i.e. the pigs at higher risk for this infection, are not registered or are not provided to EFSA. EFSA has identified that non-controlled housing condition is the single main risk factor for *Trichinella* infections in domestic pigs, and the risk of *Trichinella* infection in pigs from well-managed officially recognised controlled housing conditions is considered negligible (EFSA and ECDC, 2011). Most humans become infected when consuming undercooked meat from pigs or wild boar that have not been tested for *Trichinella* spp.

In 2015, *Trichinella* spp. have not been detected in farmed wild boar, which are assumed to be reared as pigs not raised under controlled conditions.

No positive findings were reported from solipeds in 2015. In the last decade, there was a strong reduction of *Trichinella* infections in solipeds due to the reduction of *Trichinella* in domestic pigs, since pig scraps and offal were the main source of infection for horses.

In the EU MS, *Trichinella* spp. are widespread and commonly reported in wildlife, especially by some eastern and north-eastern European MS. The proportion of positive samples from wildlife, other than wild boar, was highest in raccoon dogs, followed by lynxes, wolves and bears, but the prevalence of infection is also influenced by the environmental characteristics and human behaviour. In 2015, *Trichinella* spp. was also reported from red foxes, golden jackals, badgers, martens and otters. Carnivore mammals at the top of the food chain and with a life span longer than that of other animals are more likely to be infected (e.g. lynxes, wolves, bears); however, the population size and the distribution in Europe of these animals are generally limited. The red foxes, with a much larger and widespread population, can be considered as the main natural reservoirs for these pathogens through Europe. The lower prevalence of infection in red foxes (1.6%) than that detected in other carnivores is probably related to the spread of this mammal in populated areas where it feeds mainly on garbage resulting from human activities, where *Trichinella* spp. are not transmitted. It follows that only a percentage of tested foxes originated from regions where *Trichinella* spp. are circulating. In support of this, the prevalence of infection in red foxes (33.7%) in Finland, a MS with a very low human density, is very similar to the prevalence recorded in raccoon dogs (38.7%). In the next years, it will be important to acquire information on the regions of origin of foxes and other carnivores to better define the transmission risk areas for pigs not reared under controlled conditions in the MS.

Since the population size for each of the wild host species varies along the years and regions of sampling and has never been reported nor estimated, any comparison with data from previous years is difficult. However, infected animals have been detected in the MS where the circulation of these pathogens had been already reported in the previous years. For the next years, it is recommended that data are collected per region, province, county or NUTS (Nomenclature of Units for Territorial Statistics) and information on the estimated target population needs to be provided to increase the value of the data.

Identification of *Trichinella* larvae at the species level carried out in 2015, confirms that *T. spiralis* is more prevalent than *T. britovi* in swine and the opposite occurs in carnivores. However, since *T. spiralis* is patchy distributed (Figure 53), only *T. britovi* has been detected in swine in some countries. *T. nativa* has been documented in wild carnivores and seldom in wild boar of northern MS. *T. pseudospiralis* has been documented only in few animals confirming the extremely low frequency of this zoonotic nematodes in target animals (Pozio, 2016b). Double infections with *T. spiralis* and *T. britovi* have been also documented.

The increasing number of wild boar and red foxes and the spread of the raccoon dog from eastern to western Europe may increase the prevalence of *Trichinella* circulating among wild animals (Alban et al., 2011). Therefore, it is important to continue educating hunters and others eating wild game about the risk of eating undercooked game meat.

Indeed, in 2015, 15 *Trichinella* outbreaks were reported by eight MS (reporting rate < 0.01 outbreak per 100.000 population). In total 119 people were affected of which 34 were hospitalised. Twelve of the outbreaks were reported with strong evidence, and nine of these were associated with 'pig meat and products thereof' (including four outbreaks involving meat from hunted wild boar).

Generally, *Trichinella* is considered a medium risk for public heath related to the consumption of pig meat, and integrated preventative measures and controls on farms and at slaughterhouses can ensure effective control of *Trichinella* (EFSA BIOHAZ, CONTAM and AHAW Panels, 2011). In pigs raised indoors, the risk of infection is mainly related to the lack of compliance with rules on the treatment of animal waste. Pigs raised outdoors are at risk of contact with potentially *Trichinella*-infected wildlife (Rosenthal et al., 2008). In the last decades in the MS, investigations carried out to identify the source of *Trichinella* infections in domestic pigs, identified direct (free-raging pigs) or indirect (e.g. farmers, who were hunters) contacts with wild animals, which are the reservoir of these zoonotic nematodes (Pozio, 2014).

3.9. *Echinococcus*

The Appendix A lists all summaries made for the production of this section, for humans and animals, including *Echinococcus* summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

Alveolar (AE) and cystic echinococcosis (CE) are food-borne zoonotic parasitic diseases transmitted to humans through the ingestion of eggs of the tapeworm *Echinococcus (E.) multilocularis* and *E. granulosus sensu* lato (s.l.), respectively, shed in the faeces of canids. For *E. granulosus* s.l. the definitive hosts (DH) are dogs and, rarely, other canids, while the intermediate hosts (IH) are mainly livestock. For *E. multilocularis*, in Europe the transmission cycle is predominantly sylvatic and is wildlife-based. IHs for *E. multilocularis* are wild small rodents (microtine or arvicolid), while DH in Europe are mainly red foxes, raccoon dogs and, to a lesser extent, dogs and wolves. Although *E. multilocularis* and *E. granulosus* s.l. belong to the same genus, they cause different pathologies in humans.

Despite of that, case definitions of 'Echinococcosis' in Europe, according to Commission Decision 2012/506/EU, do not make distinction between AE and CE and consequently between *E. multilocularis* and *E. granulosus* s.l., respectively. For this reason, the data collection on human diseases from the MS is conducted in accordance with Decision 1082/2013/EU7 on serious cross-border threats to health, which in October 2013, replaced Decision 2119/98/EC on setting up a network for the epidemiological surveillance and control of communicable diseases in the EU. As data on *E. multilocularis* vary geographically (across countries as well as within countries) and timely, reported cases of *E. multilocularis* are difficult to compare within and between countries.

3.9.1. Cystic and alveolar echinococcosis in humans

In 2015, 872 laboratory-confirmed echinococcosis cases were reported in the EU (Table 26). Twenty-two MS reported at least one confirmed case and four MS reported zero cases, Malta being the only MS reporting zero cases in the previous 5-year period. The EU notification rate was 0.20 cases per 100,000 population, which was the same stable level than in the previous 5 years. The highest notification rate was observed in Bulgaria with 4.35 cases per 100,000, followed by Lithuania, Latvia and the Netherlands with 1.13, 0.50 and 0.38 cases per 100,000, respectively. In Romania, the number of cases and the rate reported in the EU summary reports have decreased in the three previous years.

Table 26: Reported human cases of cystic and alveolar echinococcosis and notification rates per 100,000 population in the EU/EEA, by country and year, 2011–2015. Depending to the country, the confirmed cases could be autochthonous and/or imported cases

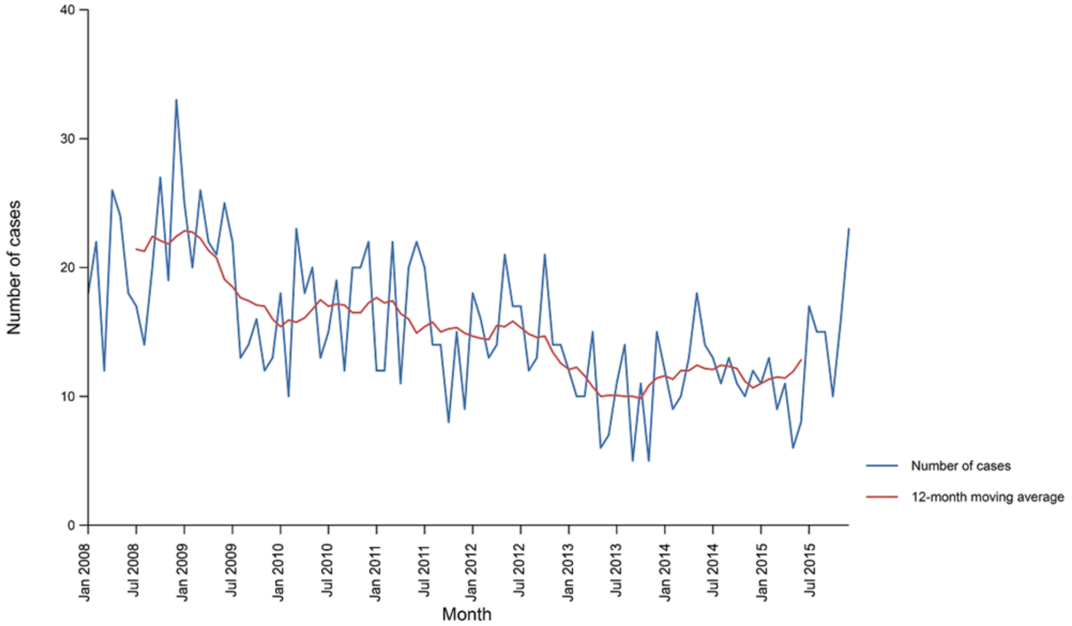
Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	8	8	0.09	14	0.17	11	0.13	3	0.04	7	0.08
Belgium	Y	A	6	6	0.05	15	0.13	15	0.13	6	0.05	1	0.01
Bulgaria	Y	A	313	313	4.35	302	4.17	278	3.82	320	4.37	307	4.17
Croatia	Y	A	7	7	0.17	20	0.47	0	0.00	0	0.00	–	–
Cyprus	Y	C	2	2	0.24	0	0.00	0	0.00	0	0.00	2	0.24
Czech Republic	Y	C	3	3	0.03	6	0.06	2	0.02	0	0.00	0	0.00
Denmark(b)	–	–	–	–	–	–	–	–	–	–	–	–	–
Estonia	Y	C	0	0	0.00	1	0.08	3	0.23	3	0.23	0	0.00
Finland(c)	Y	C	2	2	0.04	0	0.00	4	0.07	3	0.06	1	0.02
France	Y	C	48	48	0.07	32	0.05	34	0.05	49	0.08	45	0.07
Germany	Y	C	145	145	0.18	127	0.16	132	0.16	119	0.15	142	0.17
Greece	Y	C	13	13	0.12	13	0.12	10	0.09	21	0.19	17	0.15
Hungary	Y	C	2	2	0.02	2	0.02	5	0.05	6	0.06	11	0.11
Ireland(c)	Y	C	0	0	0.00	0	0.00	1	0.02	0	0.00	0	0.00
Italy(b)	–	–	–	–	–	–	–	–	–	–	–	–	–
Latvia	Y	C	10	10	0.50	13	0.65	7	0.35	8	0.39	10	0.48
Lithuania	Y	C	33	33	1.13	22	0.75	23	0.77	23	0.77	24	0.79
Luxembourg	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	1	0.20
Malta(c)	Y	C	0	0	0.00	0	0.00	0	0.00	0	0.00	0	0.00
Netherlands	Y	A	64	64	0.38	30	0.18	33	0.20	50	0.30	49	0.29
Poland	Y	C	47	47	0.12	48	0.13	39	0.10	28	0.07	19	0.05
Portugal	Y	C	4	4	0.04	4	0.04	3	0.03	2	0.02	1	0.01
Romania	Y	C	18	18	0.09	31	0.16	55	0.28	96	0.48	53	0.27
Slovakia	Y	C	5	5	0.09	8	0.15	20	0.37	3	0.06	2	0.04
Slovenia	Y	C	7	7	0.34	5	0.24	6	0.29	6	0.29	8	0.39
Spain	Y	C	83	83	0.18	77	0.17	94	0.20	96	0.21	53	0.11
Sweden	Y	C	26	26	0.27	21	0.22	16	0.17	16	0.17	19	0.20

Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
United Kingdom(c)	Y	C	26	26	0.04	25	0.04	14	0.02	7	0.01	9	0.01
EU Total	–	–	**872**	**872**	**0.20**	**816**	**0.20**	**805**	**0.18**	**865**	**0.20**	**781**	**0.18**
Iceland	Y	C	0	0	0.0	0	0.0	0	0.00	–	–	–	–
Norway(c)	Y	C	2	2	0.0	0	0.00	2	0.04	2	0.04	3	0.06

(a): Y: yes; N: no; A: aggregated data; C: case-based data; –: no report.
(b): No surveillance system.
(c): Finland, Ireland, Malta, the United Kingdom and mainland Norway have been declared free of *E. multilocularis*.

In 2015, species information was provided for 601 confirmed echinococcosis cases (68.9%) by 19 of 22 MS. This was an increase of 15.4% compared with the previous year.

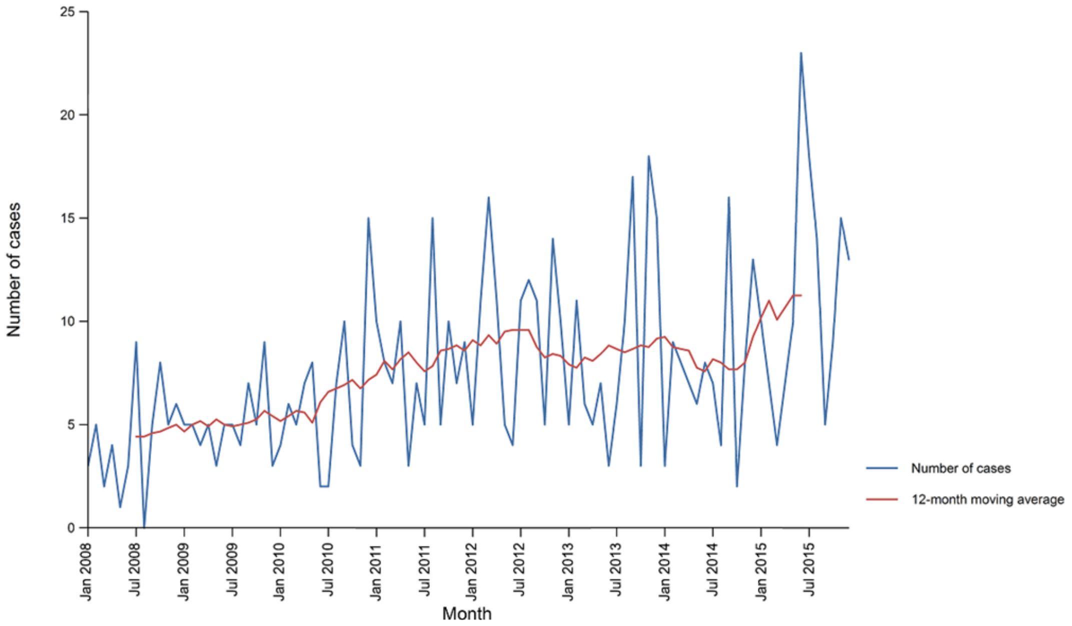
E. granulosus accounted for 466 cases (58.6%) of those with species information available, and majority (67.2%; 313 cases) of these were from Bulgaria. There was a decreasing 8-year trend ($p < 0.01$) in 2008–2015 in the EU/EEA (Figure 56). The trend seemed to stabilise in 2015. In spite of the decreasing EU trend, no significant trends were seen in any of 19 individual countries which data were available for the whole period from 2008 to 2015. Bulgaria, which reported majority of the cases in the EU in 2008–2015 (all cases were *E. granulosus*) was not included in the EU trend calculations since no monthly data were available. Cases from Bulgaria decreased by 18.9% from 2008 to 2015.



Source: Austria, Estonia, Finland, Germany, Greece, Hungary, Ireland, Latvia, Lithuania, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden and the United Kingdom. Belgium, Bulgaria, Croatia, Cyprus, the Czech Republic, Denmark, France, Iceland, Italy, Luxembourg and Malta did not report data to the level of detail required for the analysis.

Figure 56: Trend in reported confirmed human cases of *E. granulosus* in the EU/EEA, by month, 2008–2015

E. multilocularis accounted for 135 cases (17.0%), which was an increase by 64.6% compared with 2014. This was mainly due to an increase of cases in three MS (France, Germany and Poland), explaining 87.4% of all reported *E. multilocularis* cases in the EU in 2015. There was a significant increasing 8-year trend ($p < 0.01$) in the EU/EEA (Figure 57). For 13 MS with available data for the whole period, two countries (Germany and Poland) reported increasing national trends ($p < 0.01$). None of the MS observed declining trends from 2008 to 2015.



Source: Austria, Estonia, France, Germany, Hungary, Latvia, Lithuania, the Netherlands, Poland, Romania, Sweden, Slovakia, and Slovenia. Belgium, Bulgaria, Croatia, Cyprus, the Czech Republic, Denmark, Finland, Greece, Iceland, Italy, Ireland, Luxembourg, Malta, Norway, Portugal, Spain and the United Kingdom did not report data to the level of detail required for the analysis.

Figure 57: Trend in reported confirmed human cases of *E. multilocularis* in the EU/EEA, by month, 2008–2015

Thirteen MS provided information on hospitalisation, covering 20.5% of all confirmed cases of echinococcosis in the EU in 2015. The overall hospitalisation proportion has decreased during the last 4 years from 80% to 59.8%. In 2015, the highest proportions of hospitalised cases (80–100%) were reported in the Czech Republic, Greece, Poland, Romania and Slovakia. The proportion of hospitalised *E. multilocularis* cases was 74.4%, and the proportion of hospitalised *E. granulosus* cases was 71.0% based on reporting by four and eight MS, respectively.

Thirteen MS provided information on the outcome of the cases. One fatal case (species not specified) was reported in Germany. This resulted to an EU case fatality of 0.49% among the 203 cases for which this information was reported (23.5% of all confirmed cases).

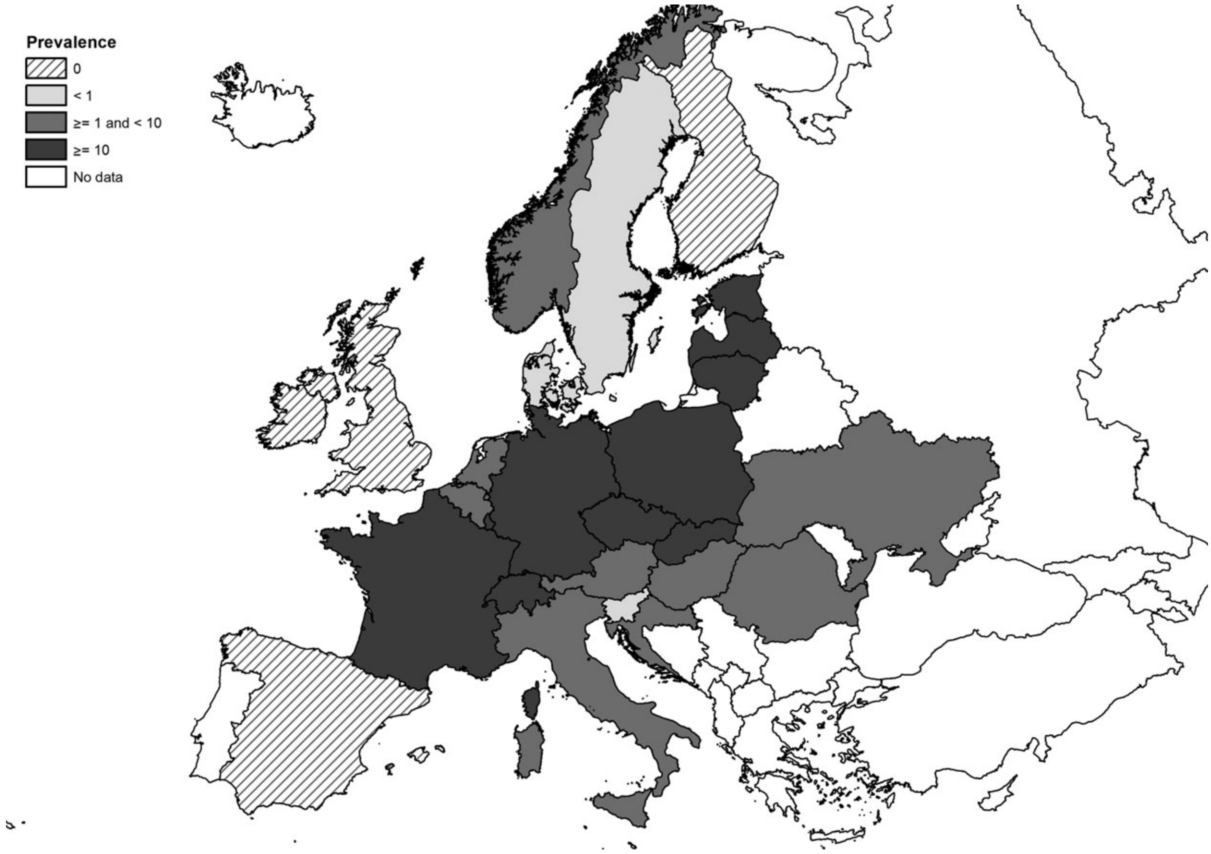
3.9.2. *Echinococcus multilocularis* and *Echinococcus granulosus* s.l. in animals: an overview in the EU

Surveillance for *E. multilocularis* is usually carried out on the main European definitive host (DH), the red fox (*Vulpes vulpes*), using mainly parasitological (sedimentation and counting technique, SCT) or molecular PCR-based methods for the identification of adult worms.

Four MS (Finland, Ireland, Malta and the United Kingdom) are considered free from *E. multilocularis*, and according to Regulation (EU) No 1152/2011[17], these MS require an annual surveillance programme in place to monitor the absence of *E. multilocularis*. One EEA State, mainland Norway (Svalbard excluded), has also claimed freedom from EM and implements a surveillance programme in line with Regulation (EU) No 1152/2011[18].

In all other MS, data on *E. multilocularis* rely on whether findings are notifiable and if monitoring is in place or if studies on *E. multilocularis* are performed. As data on *E. multilocularis* in animals vary geographically (also within countries) and timely, reported cases of *E. multilocularis* are difficult to compare within and between countries. According to a recent meta-analysis, based on studies published between 1900 and 2015, *E. multilocularis* has been documented in red foxes from 21 countries (Oksanen et al., 2016). Pooled prevalences were calculated by aggregating multiple prevalence estimates from different studies within one country. According to Oksanen et al. (2016), the following pooled prevalences within the EU were noted: low (≤ 1%; Denmark, Slovenia and Sweden); medium (> 1% to < 10%; Austria, Belgium, Croatia, Hungary, Italy, the Netherlands, Romania and Ukraine); and high (> 10%; the Czech Republic, Estonia, France, Germany, Latvia, Lithuania, Poland, Slovakia, Liechtenstein and Switzerland). Studies from Finland, Ireland, the United Kingdom and Norway reported the absence of *E. multilocularis* in red foxes. However, *E. multilocularis* was detected in Arctic foxes from the Arctic Archipelago of Svalbard in Norway.

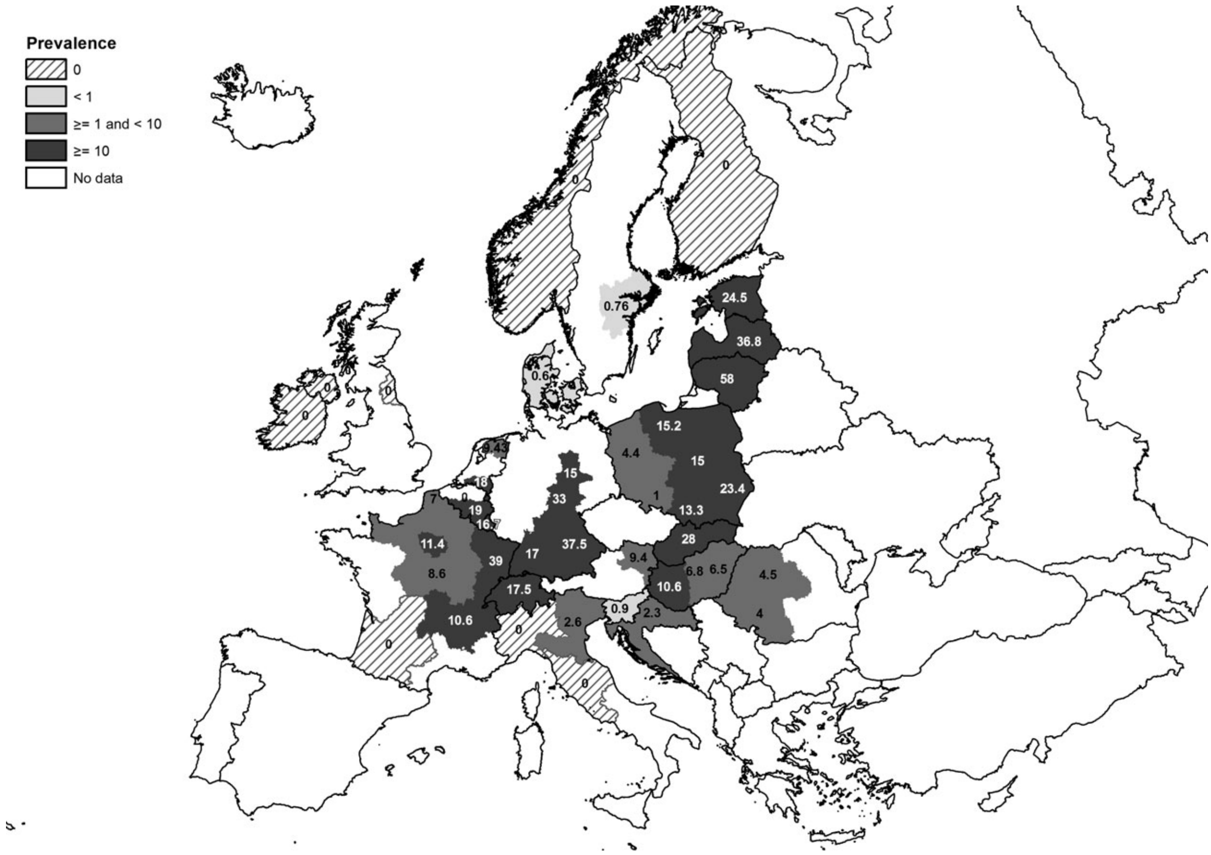
Pooled prevalence of *E. multilocularis* in red foxes within the EU and adjacent countries at national and NUTS 1 level are shown in Figures 58 and 59, respectively. Pooled prevalences from Figure 58 give an overview of countries highly endemic, while Figure 59 is useful to detail the presence or not of the parasite within single countries.



Source: Meta-analysed data from Oksanen et al. (2016); data were obtained from studies performed after 2000. The pooled prevalence data for Norway originated only from Arctic foxes on the Svalbard islands (no presence of the parasite documented in the mainland); prevalence data from Spain originated from single studies.

Figure 58: Pooled prevalence of *Echinococcus multilocularis* in red and Arctic foxes within the European Union and adjacent countries at national level

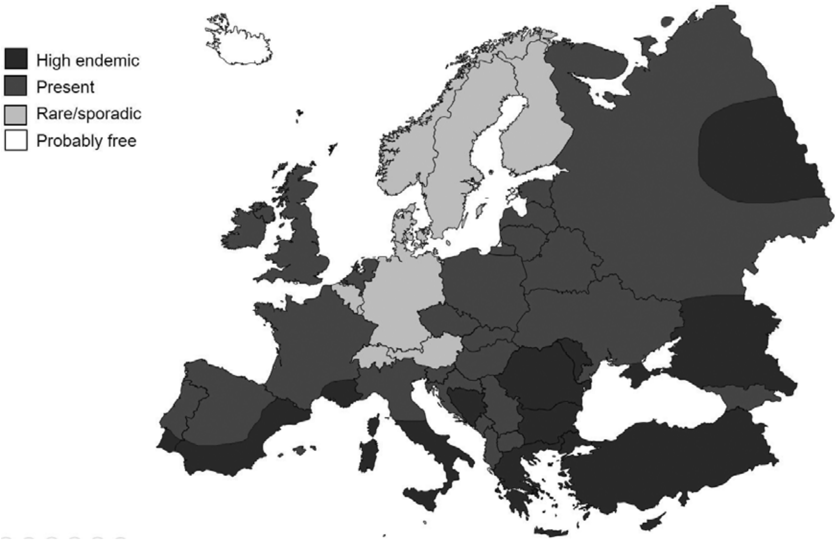
Echinococcus granulosus, formerly regarded as a single species, is now recognised as a complex of cryptic species. Based on phenotypic characters and gene sequences, *E. granulosus* s.l. circulating in Europe has by now been subdivided into *E. granulosus sensu stricto* (the 'sheep strain' and 'buffalo strain', genotypes G1 and G3), *Echinococcus equinus* (the 'horse strain', G4), *Echinococcus ortleppi* (the 'cattle strain', G5) and *Echinococcus canadensis*. (the 'camel strain', G6; the 'pig strain', G7; two 'cervid strains', G8 and G10) (Romig et al., 2015).



Data were obtained from studies after 2000; prevalence data from NL1 (the Netherlands) and SE1 (Sweden) originated from single studies; only studies reporting NUTS information were taken into account. Meta-analysed data from Oksanen et al. (2016).

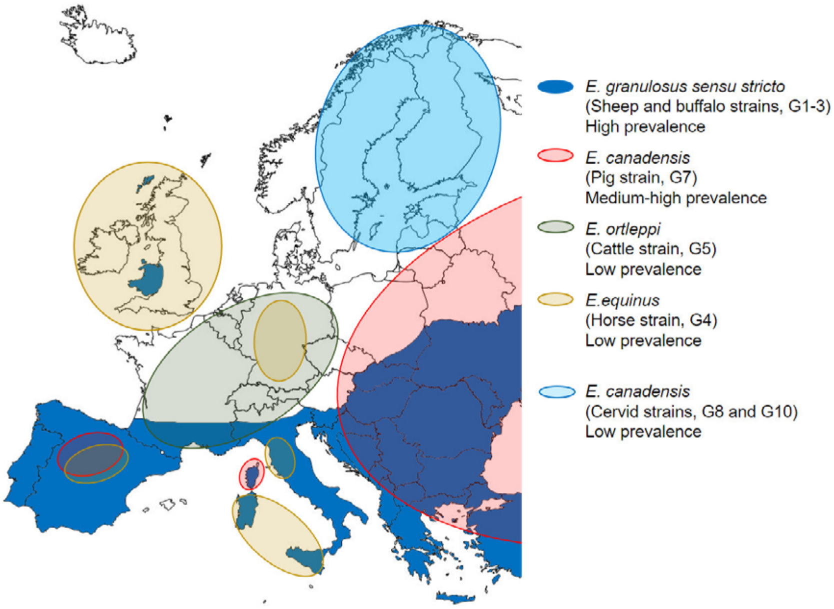
Figure 59: Pooled prevalence of *Echinococcus multilocularis* in red foxes within the European Union and adjacent countries at NUTS 1 level (http://ec.europa.eu/eurostat/web/nuts/overview)

E. granulosus sensu stricto and secondarily *E. canadensis* (G7) are the most frequent agent of human cystic echinococcosis in Europe. Because the presence of most of the *Echinococcus* strains depends on specific intermediate livestock species, it should be stressed that the distribution of *E. granulosus* s.l. in Europe is strongly influenced by animal husbandry and animal trade. Approximate distribution of *E. granulosus* s.l. and *Echinococcus* species/genotypes in Europe are reported in Figures 60 and 61, respectively.



Sources: World Health Organization, Department of Control of Neglected Tropical Diseases (http://www.who.int/echinococcosis/Global_distribution_of_cystic_echinococcosis_2011.pdf). WHO (online), Jenkins et al. (2005), Dakkak (2010).

Figure 60: Approximate distribution of *Echinococcus granulosus* s.l. in Europe



Sources: Cardona and Carmena (2013); Carmena and Cardona (2014); Oksanen and Lavikainen (2015); Romig et al. (2015).

Figure 61: Approximate geographical distribution of strains/genotypes belonging to *Echinococcus granulosus* s.l. in Europe

3.9.3. *Echinococcus multilocularis* and *Echinococcus granulosus* s.l. in animals reported in 2015

3.9.3.1. *E. multilocularis* in animals in 2015

Finland, Ireland, Malta, Norway and the United Kingdom, considered free of *E. multilocularis* (Regulation (EU) No 1152/2011), did not report any case to European Commission during 2015. According to Regulation 1152/2011, in 2015, the United Kingdom, Ireland and Norway tested 614, 398 and 523 foxes, respectively. In addition, Finland tested 273 foxes and 338 raccoon dogs and Malta tested 335 stray dogs. All of the tested samples were negative for *E. multilocularis*.

In 2015, 11 MS reported data on 5,720 foxes (Table 2015_ECHINOFOX) examined for *E. multilocularis,* and eight MS and one non-MS reported positive findings with a total prevalence of 10%. Luxembourg (26.9%), Switzerland (28.6%), Germany (23.6%), France (21.5%) and Slovakia (21.5%) reported the highest proportion of positive samples. Denmark (8.06%), Hungary (5.5%) and Sweden (0,1%) were reporting lower prevalences in foxes. It is also important to stress that some MS, such as France, were not providing data from the country as a whole but from some regions. These findings are similar to those of the last years. Interestingly for the first time, *E. multilocularis* was detected in red foxes of Croatia with a prevalence of 3.3%.

Findings from most of the countries fluctuated between years, but in most years, they reported positive findings. Fluctuations in reported cases probably are driven by efforts done in a particular year, than reflecting a true change in the prevalence.

In addition to foxes, *E. multilocularis* has been documented in France in 4 out of 239 tested cats and in 7 out of 26 dogs, in 1 out of 2 beavers, and in one hare. Moreover, the Netherlands reported one positive dog with *Echinococcus* spp. out of 1,495 tested, while Austria reported two positive pigs with *Echinococcus* spp. out of 5,381,689 tested. In both positive cases, it was not possible to confirm the *Echinococcus* species since in these countries, the IHs potentially can harbour both *E. multilocularis* and *E. granulosus* s.l.

In Europe, it has been noted that high *E. multilocularis* pooled prevalences in raccoon dogs and golden jackals correlated with high pooled prevalences in foxes (Oksanen et al., 2016). In fact, in areas with low pooled prevalences in foxes, no other DH was found infected with *E. multilocularis*. Moreover, when a fox *E. multilocularis* pooled prevalence was > 3%, this parasite can be detected also in raccoon dogs and golden jackals. In areas with a high *E. multilocularis* fox pooled prevalences, the wolf emerges as a potentially important DH. Dogs in Europe could be important for parasite introduction into non-endemic areas. Muskrats and arvicolids are important IHs (Oksanen et al., 2016).

Table 27 summarises the most relevant definitive and intermediate host species tested for *E. multilocularis*, such as foxes, raccoon dogs, dogs, wolves, rodents, cats, beaver, hare, voles and pigs by the MS and adjacent countries in 2015.

Table 27: *Echinococcus multilocularis* positive/tested (%) animals in 2015

Country	**Foxes**	**Raccoon dogs**	**Dogs**	**Wolves**	**Cats**	**Rodents**	**Beaver**	**Hare**	**Voles**	**Pigs$^{(c)}$**
Austria$^{(a)}$										
Croatia	5/150 (3.3%)									
Denmark	5/62 (8.06%)	0/122								0/18,164,000
Estonia										0/527,076
Finland	0/273	0/338							0/1,100	0/2,068,664
France	68/316 (21.5%)		0/61		4/239 (1.7%)	0/19				
Germany	434/1,839 (23.6%)	0/2	0/46		0/8					2/123 (1.6%)
Hungary	11/200 (5.5%)									
Ireland	0/398									
Latvia										0/407,228

Country	Foxes	Raccoon dogs	Dogs	Wolves	Cats	Rodents	Beaver	Hare	Voles	Pigs(c)
Luxembourg	7/26 (26.9%)									0/163,234
Netherlands(b)										
Sweden	2/1,570 (0.13%)	0/11	0/3	0/73						
United Kingdom	0/691									
Slovakia	42/195 (21,5%)		0/1,486		0/519					0/529,871
EU Total	574/5,720 (10%)	0/473	7/1,596 (0.43%)	0/73	4/766 (0.5%)	0/19	1/2	1/1	0/1,100	2/21,860,196 (< 0.01%)
Norway	0/523			0/4						
Switzerland	2/7 (28.6%)		7/24 (29.2%)				1/2	1/1		

(a): In Austria, two (< 0.01%) out of 5,381,689 domestic pigs tested positive for *Echinococcus* spp.

(b): In the Netherlands, one (0.07%) out of 1,495 dogs tested positive for *Echinococcus* spp.

(c): Pigs for which the species level of *Echinococcus* was not specified were allocated in this table for those MS for which is known there is circulation of *E. multilocularis*.

(d): Slaughter batch data and animals from zoo were not included in the table.

3.9.3.2. *Echinococcus granulosus* s.l. in animals in 2015

In total, 24 countries (23 MS and one non-MS) reported data from more than 78 million domestic and wild animals tested for *E. granulosus* s.l of which 99% are domestic animals (sheep, cattle, goats, pigs, horses and dogs). These data were obtained mainly from the meat inspection performed at slaughterhouse. Moreover, more than 475,000 wild animals (mouflons, reindeers, deer, wild boar, moose, wolves, water buffalos and foxes) were tested (Table 28).

Twelve MS reported a total of 113,517 positive samples of which 113,237 were domestic animals and 280 were wild animals. Positive animals were mainly sheep and goats (N = 59,287; 52%), pigs (N = 46,285; 41%) and cattle (N = 7,650; 6.7%).

Cyprus, Finland, Italy and Spain reported findings of *E. granulosus* s.l. in mouflons, reindeers, deer, wild boar, moose and wolves. Moreover, the Netherlands reported one positive dog with *Echinococcus* spp. out of 1,495 tested, while Austria reported two positive pigs with *Echinococcus* spp. out of 5,381,689 tested.

Table 28 summarises the most relevant domestic and wild definitive and intermediate host species tested for *E. granulosus* s.l., such as sheep, goats, cattle, pigs, mouflons, reindeers, solipeds, domestic deer, water buffalos, wild boar, moose, wolves and dogs.

Table 28: *Echinococcus granulosus* s.l. positive/tested (%) animals in 2015

Country	Sheep	Goats	Sheep and goats	Cattle	Pigs[b]	Mouflons	Reindeer	Solipeds, domestic	Deer	Water buffalos	Wild boars	Moose	Wolves	Dogs	Foxes
Austria	212/136,256 (0.16%)	0/7,763		117/695,174 (0.02%)	[a]										
Belgium				0/874,948											
Bulgaria	548/5,298 (10.34%)			1561/13,541 (11.53%)	48/17,945 (0.27%)										
Croatia					1/1										
Cyprus						1/23 (4.35%)									
Denmark				0/512,600	0/18,164,000										
Estonia	0/6,540	0/74		0/41,380	0/527,076			0/17				0/3,820			
Finland	0/57,572	0/238		0/277,427	0/2,068,664		4/69,801 (< 0.01%)	1/1,630 (0.06%)[c]	0/288		0/381	0/177	10/41 (24.39%)		
France														0/61	
Germany														0/23	
Greece	9,662/ 1,872,922 (0.52%)	1,661/ 505,787 (0.33%)		894/100,992 (0.89%)	3/747,208 (< 0.01%)						0/969				
Italy	3,975/ 335,860 (1.18%)	63/57,249 (0.11%)		1,189/ 285,492 (0.42%)	38/1,560,291 (< 0.01%)			0/2,478	0/153	28/27,022 (0.10%)	127/24,917 (0.51%)			3/15	
Latvia	0/17,076	0/67		0/91,816	0/407,228			0/274							
Luxembourg				0/24,831	0/163,234										
Malta														2/335 (0.60%)	
Netherlands				40/42 (95,24%)[c]										(0,07%)[b]	
Poland			193/3,922 (0.49%)	6/1,875,761 (< 0.01%)	4,4981/ 21,973,398 (0.20%)										
Romania	0/14	0/2		147/305 (48.20%)	2/7 (28.57%)									0/59	

Country	Sheep	Goats	Sheep and goats	Cattle	Pigs[(b)]	Mouflons	Reindeer	Solipeds, domestic	Deer	Water buffalos	Wild boars	Moose	Wolves	Dogs	Foxes
Slovakia	0/82,714			0/36,652	0/529,871									0/1,486	
Slovenia	0/9,712	0/718		0/111,468	0/242,497			0/1,966							
Spain[(e)]	24,014/ 3,282,503 (1.65%)	18959/ 546,460 (3.47%)	0/1172	3696/809,321 (0.45%)	1210/ 7,906,665 (0.014%)			8/13,358 (0.06%)	26/173,709 (0.01%)		84/95,007 (0.09%)				
Sweden	0/289,390	0/1,174			0/2,560,450		0/56,333	0/3,050	0/6,664		0/12,634				
United Kingdom															0/691
EU Total	38,411/ 6,095,857 (0.63%)	20,683/ 1,119,532 (1.84%)	193/5,094 (3.8%)	7,650/ 5,751,750 (0.13%)	46,285/ 62,250,224 (0.07%)[(a)]	1/23 (4.35%)	4/126,134 (< 0.01%)	9/22,773 (0.04%)	26/180,814 (< 0.01%)	28/27,022 (0.10%)	211/ 133,908 (0.16%)	0/3,997	10/41 (24.39%)	6/3,474[(b)] (0.17%)	0/691
Norway	0/1,228,000	0/24,000		0/284,000	0/1,605,000			0/330							

(a): In Austria, two (< 0.01%) out of 5,381,689 domestic pigs tested positive for *Echinococcus* sp.; the species was not identified and cannot be assumed since both *E. multilocularis* and *E. granulosus* s.l. are circulating in Austria.
(b): In the Netherlands, one (0.07%) out of 1,495 dogs tested positive for *Echinococcus* sp.; the species was not identified and cannot be assumed since both *E. multilocularis* and *E. granulosus* s.l. are circulating in the Netherlands.
(c): Imported animals from Eastern Europe.
(d): Pigs for which the species level of *Echinococcus* was not specified were allocated in this table for those MS for which circulation of *E. multilocularis could* be excluded.
(e): Meat from Sheep, Bovine animals (Cattle) and Pigs (single food samples) were included.
Slaughter batch data and animals from zoo were not included in the table.

3.9.4. Discussion

The EU notification rate of confirmed human echinococcosis cases has been stable since 2011. The EU case definition does not differentiate between the two clinical forms of the diseases, cystic echinococcosis and alveolar echinococcosis, caused by *E. granulosus* and *E. multilocularis*, respectively. These two species can, however, be reported separately to the ECDC. Majority of the MS reported the species information. Since the beginning of the surveillance of human echinococcosis in the EU, *E. granulosus* has been five to six times more frequently reported than *E. multilocularis* but showed a decreasing 8-year trend.

In the Netherlands, echinococcosis cases decreased from 1997 to 2008 (Herremans et al., 2010) but increased back to the original level in the last few years. The awareness of the disease among clinicians and the migration (people from endemic countries) may have influenced on the number of diagnosed cases (Wilfrid van Pelt, RIVM, personal communication, August 2016). *E. granulosus* prevalence is high in northern Africa and Asia and importation from these regions might have an impact to the number of cases detected in the EU. There are preliminary results indicating notable geographical differences in human echinococcosis prevalence in the EU countries (HERACLES, http://www.heracles-fp7.eu).

The proportion of the reported alveolar echinococcosis has increased in the recent years. An increasing EU trend of *E. multilocularis* was particularly due to observed rise of confirmed cases in three MS, two of them reporting significant increasing national trends of echinococcosis. Increase in reporting of echinococcosis cases with species information may also explain the detected increase of *E. multilocularis*.

It should be stressed that human AE and CE cases notified by country to the ECDC do not reflect the real epidemiological situation in Europe. In fact, the true prevalence of these diseases is extremely difficult to estimate due to the long incubation period (AE and CE), the high proportion of asymptomatic or paucisymptomatic carriers who never seek medical attention (CE) and the underreporting/misdiagnosed cases (AE and CE), factors, which contribute to their neglected status. For these reasons, the patchy data on the number of people affected by ‘echinococcosis’ currently reported by the EU MS, represents the tip of the iceberg. The invisible portion includes asymptomatic carriers of CE and misdiagnosed cases of AE especially in recently discovered foci where physicians do not have any experience on these diseases. In contrast to AE, CE may be considered more as a chronic disabling condition rather than a lethal one (Possenti et al., 2016).

As an example for this underreporting, data recently published in peer review journals reported around 34,000 hospitalisations of CE from Italy, France and Spain in 12-, 16- and 12-year period, respectively (Brundu et al., 2014; van Cauteren et al., 2016; Herrador et al., 2016). It should be noted that these three studies were showing a negative trend in time in the number of hospitalisations. In particular, in 2012, these hospitalisations were estimated at 242 in France, 535 in Spain and 703 in Italy. Ultrasound surveys conducted in Romania during 2014/2015, screening 7,500 people in rural areas (Casulli, 2016), identified a double of the CE cases notified at national level in Romania during the same time period (Table 26). These data gives an idea of the real magnitude of human CE as a public health problem and related costs in Europe.

The EFSA Panel on Animal Health and Welfare have stated in a scientific opinion that in many human cases the diagnosis is established only as echinococcosis, and the aetiological agent of the disease, *E. multilocularis* or *E. granulosus*, is not determined (EFSA, 2007c). Distinction between infection with *E. granulosus* and *E. multilocularis* is needed because the two diseases require different management of prevention and treatment. Furthermore, the detection of CE or AE in EU citizens or immigrants is of great epidemiological importance. In this context, a reconsideration of ‘echinococcosis’ case definition in the current Commission Decision 2012/506/EU, differentiating alveolar from cystic echinococcosis, would be crucial to collect specific epidemiological and clinical data to manage and trace back these infections. Furthermore, making the notification of human AE and CE cases mandatory in all the MS would enable more effective and coherent monitoring of trends of AE and CE occurrence in humans.

In animals, in 2015, *E. granulosus*, aetiological agent of cystic echinococcosis, and *E. multilocularis*, aetiological agent of alveolar echinococcosis, have been documented in 24 and 17 MS, respectively. The highest number of animals infected with *E. granulosus* s.l. was reported in Bulgaria, Greece, Italy, Poland and Spain. The highest number of animals (mainly foxes) infected with *E. multilocularis* was noted in Germany followed by Slovakia, France and Hungary.

The surveillance of *E. multilocularis* in foxes is important in order to assess the prevalence in Europe, since the distribution of *E. multilocularis* seems to be enlarged in the last decades and the fox population is increasing in Europe (Casulli et al., 2015; Oksanen et al., 2016). Whether the increased range of distribution of *E. multilocularis* is due to range expansion or reflects an increased surveillance effort is difficult to be proven, since there is a general lack of baseline data. Possibly, the parasite had been present, but undetected, in small foci, which rapidly expanded in the wake of an increasing red fox population (EFSA AHAW Panel, 2015). An increased prevalence in foxes can also lead to *E. multilocularis* being isolated from unusual IHs including beavers due to the heavy environmental contamination with *E. multilocularis* eggs. Indeed, in 2015, in Switzerland, where the pooled prevalence of *E. multilocularis* in foxes is estimated as 26.8% for the period 1988–2000, this helminthic infection has been documented in a beaver, a hare and in dogs. In addition, the prevalence data of *E. multilocularis* must be interpreted with caution since many variables such as temperature, rainfall, humidity levels and soil have been identified as relevant factors that explain partially the distribution of the parasite. These factors may vary a lot leading to local foci within the MS reporting positive cases.

In 2013, EFSA carried out the assessment and found that under the assumption of unbiased representative sampling (in the case of Finland, Ireland and the United Kingdom) and unbiased risk-based sampling (in the case of Malta) and considering the sensitivity of the tests applied, all four MS have fulfilled the requirement of Regulation (EU) No 1152/2011 to the effect that the surveillance activities should detect a prevalence of *E. multilocularis* of 1% or less at a confidence level of at least 0.95 (EFSA, 2013b). It should, however, be noted that *E. multilocularis* can occur at lower prevalences as reported in Sweden where 0.1% of investigated foxes were infected. Information campaigns about *E. multilocularis* tend to focus on warnings against eating berries and mushrooms from areas where *E. multilocularis* has been detected in wildlife, while little consideration is given to ownership of dogs and contact with wild carnivores (Antolová et al., 2014). A case-control study showed that having a dog and contact with wild carnivores are important risk factors (Kern et al., 2004). In 2015, the Netherlands and Switzerland reported positive dogs for *E. multilocularis*. It should be also stressed that scientific literature on AE and CE reporting data on risk factors and pathways of transmission is limited and no global synthesis has been performed till now.

Regarding animal data, the quality of the data reported on *Echinococcus* spp. has improved in recent years, with more information being provided about the sampling context and more data reported at species level. In this context, a more accurate animal data collection is recommended by EFSA to the MS and adjacent countries. In fact, reporting more detailed information on demographic data such as livestock age class for *E. granulosus* s.l., and detection methods for *E. multilocularis,* will provide a more clearly epidemiological picture of these parasites in Europe. Moreover, there is a gap on the accuracy of diagnostic tests for the detection of *Echinococcus* spp. In fact, as suggested by the AHAW Panel, a study should be undertaken to estimate the probability of each relevant test to detect infection using an adequate sample of specimens from endemic areas where the entire range of different infection stages and intensities are represented (EFSA AHAW Panel, 2015). In addition, routine post-mortem examination at slaughterhouse is considered the standard approach for detecting the presence of *E. granulosus* s.l. However, the accuracy of this test may be affected by several drawbacks such as incorrect identification (false positives due to *Taenia* species or non-parasitic cyst lesions) accuracy of inspection (false negative due to raw visual estimation) or over/underestimation due to bias introduced with the age-class analysed (Cardona and Carmena, 2013; WHO, online).

Also in animals, notification is a requirement for reliable data and information on parasite speciation is very important for risk management efforts as *E. granulosus* and *E. multilocularis* have different epidemiology and pose different health risks to humans. For *E. granulosus*, notification requirement will ensure that comparable data between the MS will be obtained from meat inspection of food-producing animals. Concerning *E. multilocularis*, a general notification requirement for all the MS can be questioned but should be required in countries free from *Echinococcus*. In countries where the parasite is endemic, reporting each case gives no additional valuable information. Therefore, repeated surveys, as surveillance for *E. multilocularis*, can be a basis for follow up and monitoring (EFSA AHAW Panel, 2015).

Finally, it is noteworthy that in general reported data on animals and humans represents a raw underestimation of the real burden of these two diseases in Europe in which around two-hundred and in the range of thousand cases are annually expected for AE and CE, respectively (Conraths and Deplazes, 2015; Casulli, 2016).

3.10. *Toxoplasma*

The Appendix A lists all summaries made for the production of this section, for animals, including *Toxoplasma* summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.10.1. Toxoplasmosis in humans

Data on congenital toxoplasmosis in the EU in 2015 are available in the ECDC Surveillance Atlas of Infectious Diseases under the following link http://atlas.ecdc.europa.eu/public/index.aspx?Instance=GeneralAtlas. In 2015, in total 41 cases of congenital toxoplasmosis were reported in EU (in the Czech Republic, Germany, Hungary, Ireland, Lithuania, Poland, Slovenia and the United Kingdom). France reported data with 2-year delay, 216 confirmed congenital toxoplasmosis cases in 2014. National surveillance systems differ from each other and therefore also the case underascertainment between countries. Nine MS and Norway have no surveillance of congenital toxoplasmosis and surveillance systems in some countries focus only on severe cases in all age groups. Only three countries (the Czech Republic, France and Slovakia) have active surveillance of congenital cases.

3.10.2. *Toxoplasma* in animals

Toxoplasma gondii is a zoonotic protozoan parasite that may cause serious disease in humans, especially when primary infection is acquired during pregnancy. The detection of *Toxoplasma* in animals is variable in terms of the diagnostic methods used as well as to the different matrices analysed. The diagnostic methods reported for the detection of *Toxoplasma* in animals in 2015 were latex agglutination test (LAT), immunofluorescence antibody test (IFAT), ELISA and complement fixation test (CFT) as indirect (serological) methods while histology, real time PCR and IHC were used as direct methods. Indirect methods are used for the detection of *Toxoplasma*-specific antibodies in serum or meat juice samples taken at the slaughterhouse while the direct methods are applied to specific organs or tissues of the sampled animals. The results from different countries are not directly comparable owing to the use of different tests and analytical methods, as well as different sampling schemes. It should also be noted that both age of animals and production systems at farm level influence the level of *Toxoplasma* prevalence and data are therefore not always comparable.

In 2015, 13 MS and two non-MS (Switzerland, Norway) provided data on *Toxoplasma* in animals (Table 2015_TOXOOVERVIEW).

Eleven MS (Germany, Greece, Finland, Hungary, Ireland, Italy, Latvia, Romania, Slovakia, Spain and the United Kingdom) and two non-MS (Switzerland and Norway) reported information on *Toxoplasma* in small ruminants (Table 2015_TOXOOVINEGOAT). In contrast to pigs and cattle, positive sheep and goats were also detected using direct methods such as histology, PCR and immunohistochemistry. Overall, 39.4% of 3,058, animals tested in the reporting MS were positive for *Toxoplasma* mainly using indirect serological methods. Clinical investigations and sampling of suspect animals of sheep and goats in Greece, Romania, Spain and the United Kingdom resulted in a high proportion (> 50%) of positive animals. Only Italy reported results from investigations at herd level, with substantially higher seroprevalence in sheep herds (± 50%) compared to goat herds (30%).

Seven MS (Germany, Estonia, Ireland, Italy, the Netherlands, Slovakia and the United Kingdom) and two non-MS (Switzerland, Norway) reported data on *Toxoplasma* in cattle in 2015 (Table 2015_TOXOCATTLE). Overall, 5.9% of 847 tested animals and 2.8% of 1,265 cattle herds/holdings tested positive for *Toxoplasma*. All positive animals and herds were detected using indirect (serological) methods. Italy reported most of the samples, followed by the United Kingdom and Germany. In serological surveys (slaughterhouse sampling) performed in some countries, low prevalence (≤ 5%) was found in the United Kingdom, Italy and the Netherlands. No *Toxoplasma*-positive samples were reported by Germany during official sampling.

Three MS (Germany, Italy and the United Kingdom) and one non-MS (Switzerland) reported data on *Toxoplasma* in pigs (Table 2015_TOXOPIGS). Overall, 3.7% of 2,388 investigated animals were seropositive for *Toxoplasma*. None of the samples tested by Italy and the United Kingdom via direct methods (PCR) were positive for *Toxoplasma*. The United Kingdom accounted for the largest number of fattening pigs tested using a serological national survey at slaughterhouse. During a clinical investigation in Italy, 10 out of 30 pig herds tested positive by ELISA.

Seven MS (Germany, Estonia, Finland, Italy, Latvia, the Netherlands, Slovakia) and one non-MS (Switzerland) provided data on *Toxoplasma* in cats and dogs, mainly from clinical investigations. These samples were often found positive, mostly using serological tests (Table 2015_TOXOCATDOG). Overall, 15.5% of the 1,896 cats and 17.9% of 2,065 tested dogs were positive for *Toxoplasma*. Survey data (excluding clinical investigations) for cats and dogs from three MS (Germany, Italy and Slovakia) resulted in 6.6% of the 320 tested cats and 16.7% of 204 tested dogs positive for *Toxoplasma*. The type of cats and dogs (stray-type or not) was not specified. Only cats were found positive using direct diagnostic methods such as histology and PCR.

In addition, nine MS (Germany, Estonia, Finland, Greece, Italy, the Netherlands, Slovakia and the United Kingdom) and two non-MS (Switzerland and Norway) provided data on other animal species, reporting *Toxoplasma*-positive (via PCR and serological methods) samples from hares, Cantabrian chamois, red and roe deer, foxes, lamas, dolphin, wolves, alpacas, ducks, domestic fowl, and zoo animals (Table 2015_TOXOOTHERAN). Italy reported 420 PCR tests performed on hunted wild boar in which 10.3% of the animals were positive.

3.10.3. Discussion

Recently, the WHO reported the median rates per 100,000 of food-borne illnesses, Deaths and disability Adjusted Life Years (DALYs) in the defined EU region due to toxoplasmosis. Estimates were 2 (95% CI: 1–3) and 6 for (95% CI: 4–10) congenital *T. gondii* and acquired *T. gondii*, respectively (WHO, 2015). Food-borne toxoplasmosis is mainly spread through undercooked and raw meat and fresh produce.

The information reported by the MS in 2015 shows that *Toxoplasma* exposure occurs in most livestock species across the EU and supports the findings in recent publications on the high incidence of toxoplasmosis in sheep (Bacci et al., 2016), pigs (Djokic et al., 2016; Herrero et al., 2016; Wallander et al., 2016), goats (Deng et al., 2016), horses (Aroussi et al., 2015), small mammals including rodents (Machačová et al., 2016), pets (Cano-Terriza et al., 2016) and wild animals (Formenti et al., 2016; Reiterova et al., 2016). However, the high incidence of *Toxoplasma* in sheep and goats, detected by serological methods, may be partly due to vaccination in these species. In 2015, none of the reporting MS mentioned the vaccinations status of investigated animals. One MS reported that the vaccination status was unknown for the investigated animals.

It is clear that most MS use indirect methods to detect *Toxoplasma* instead of direct methods. In a recent published report, studying relationship between indirect and direct detection methods it was concluded that MAT based detection of antibodies, and possibly serological screening in general, are not recommended as an indicator of the presence of viable *T. gondii* in cattle and horses and in these species direct detection methods are preferred. For pigs, poultry and small ruminants serological methods could be useful for the detection of high-risk animals/herds but the correlation between direct and indirect methods was estimated to be low (Opsteegh et al., 2016) as confirmed by other recent studies as well (Aroussi et al., 2015; Djokic et al., 2016). Besides the low correlation there is also a problem with the interpretation of the serological methods as obtained negative results cannot be used to declare animals or products thereof (meat) as safe for human consumption. In addition, direct methods should be applied on matrices taken post-mortem as it was shown that the load of parasites in the different skeletal muscles in sheep and pigs do not vary much and that clear predilection sites are brain, heart and lung tissues.

Certain risk factors are associated with higher risk for transmission from animals to humans such as the presence of cats or rodents on farm and outdoor/backyard husbandry practises at farm level (EFSA BIOHAZ Panel, 2013b; Opsteegh et al., 2016). It appears that risk factor studies should be based on outcome obtained by direct methods rather than indirect methods. In order to manage the risk of *Toxoplasma* and propose intervention strategies in livestock (e.g. vaccination) it is important to collect and analyse information obtained from epidemiological investigations and surveys that standardise the sample matrix (brain, heart, lungs), the analytical method (direct methods preferentially) and the target population (species and risk categories). In addition, there is a lack of information on the contamination of vegetables and fruit and drinking water by *Toxoplasma* oocysts shed by cats (Dumetre and Darde, 2003; Lass et al., 2012). There is the need to investigate these transmission routes.

3.11. Rabies

The Appendix A lists all summaries made for the production of this section, for humans and animals, including rabies summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.11.1. Rabies in humans

Generally, very few cases of rabies in humans are reported in the EU, and most MS have not had any autochthonous cases for decades. In 2015, no case of rabies in humans was reported in the EU.

3.11.2. Rabies in animals

Rabies is a notifiable disease in all the MS and Switzerland. In 2015, 13 MS had their annual or multi-annual programmes for eradication of rabies cofinanced by the EU.[40] Eradication programmes include:

- oral vaccination of wild animals through baiting;
- assessment of rabies incidence (surveillance) by testing suspect animals[41]
- (wild or domestic) for rabies;
- monitoring of wild animals for vaccination effectiveness, based on the assessment of bait uptake and on the assessment of immunisation rates by testing for rabies antibodies in the target species (foxes and raccoon dogs) sampled in vaccinated areas.

Cofinanced oral vaccination campaigns were carried out in 2015 in 13 MS – Bulgaria, Croatia, Estonia, Finland, Greece, Hungary, Italy, Latvia, Lithuania, Poland, Romania, Slovakia and Slovenia. Some of these programmes included vaccination in buffer zones of neighbouring third countries to reduce the risk of rabies introduction via foxes or other potential carriers.

3.11.2.1. Bats

In total 17 MS and two non-MS reported *Lyssavirus* in bats. Bats infected with *Lyssavirus* were found in eight MS (the Czech Republic, France, Hungary, Germany, the Netherlands, Poland, Spain and the United Kingdom) and Norway. In these eight MS, 26 positive cases were found out of 1,391 examined (1.8%), the corresponding figures for 2014 being 27 and 1,636, respectively (1.7%) (Table 2015_RABIESBATS). Thus, the rate of positive cases per tested bats remained constant during 2015–2014. In addition, EBLV-type 2 was reported in France, the United Kingdom and Norway.

The apparent prevalence varies from 15% (5 out of 33 tested in the Netherlands) to 1% (4 positive out of 402 tested in France); however, the numbers are probably too small to indicate clear differences between the MS.

The geographical distribution of *Lyssavirus* cases (including reported EBLV-type 2 cases) in bats in 2015 is shown in Figure 62.

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[40] More information on EU approved and cofinanced eradication programmes for rabies carried out by the MS is available online at: http://ec.europa.eu/dgs/health_food-safety/funding/cff/animal_health/vet_progs_en.htm.

[41] Suspect animals include autochthonous or imported animals (domestic or wild) showing clinical signs of rabies or abnormal behaviour suggestive of rabies, animals found dead, animals to which humans have been exposed (bites, scratches or licking of wounds, etc.) and roadkill (only for rabies-endemic countries). These animals are used for rabies surveillance. This definition concerns infected and rabies-free countries.

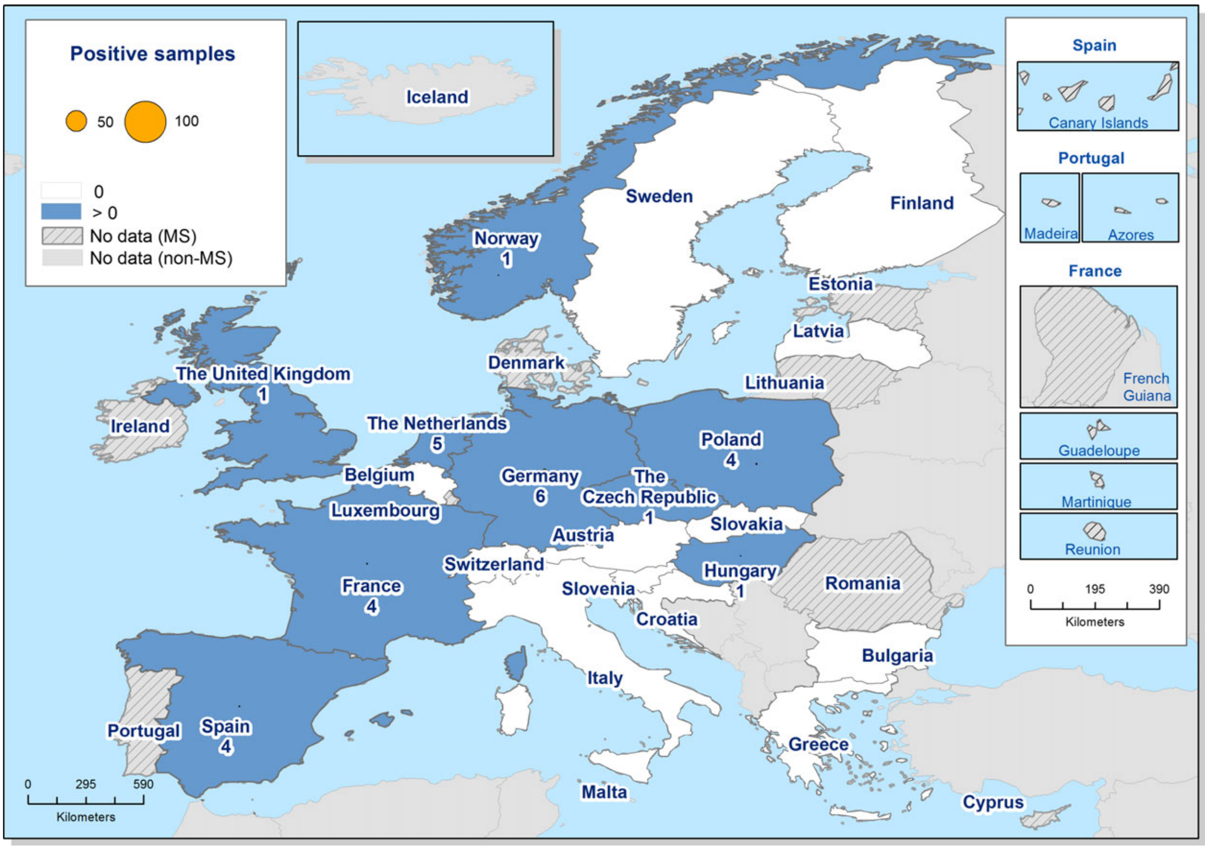


Figure 62: *Lyssavirus* cases (included reported EBLV-type 2) in bats, in the EU Member States and non-Member States, 2015

3.11.2.2. Wildlife animals and farmed domestic animals

Rabies in wildlife animals and farmed domestic animals has been completely eradicated from western and northern Europe and most countries in central Europe. However, residual risk for rabies and endemic foci still occurs in foxes and other wildlife species in certain eastern parts of the EU, in particular Romania and Poland, with sporadic spill-over to domestic animals, mainly dogs and cats (pet and stray) and ruminants.

In 2015, 22 MS and two non-MS reported data on foxes. In total, 99 rabies cases in foxes (0.2%) were reported out of the 46,588 tested. Only four MS reported these cases: Poland (68 cases), Romania (25 cases in 20 different regions tested), Slovakia (5 cases) and Lithuania (1 case in one region detected very near the border with Belarus). The total number of cases decreased by 69% compared to 2014, when 319 rabies cases in foxes were reported by six MS but mainly by Romania and Poland. This decrease in the number of cases in foxes from 2014 to 2015 is due to the reporting of no single case by the Eastern European MS, such as Hungary, Greece, Bulgaria and Croatia, and a reduction in case numbers reported by Poland and Romania (Table 2015_RABIESFOX).

The geographical distribution of reported cases in foxes in 2015 is shown in Figure 63.

Figure 63: Classical rabies or unspecified *Lyssavirus* cases in foxes, in the EU Member States and non-Member States, 2015

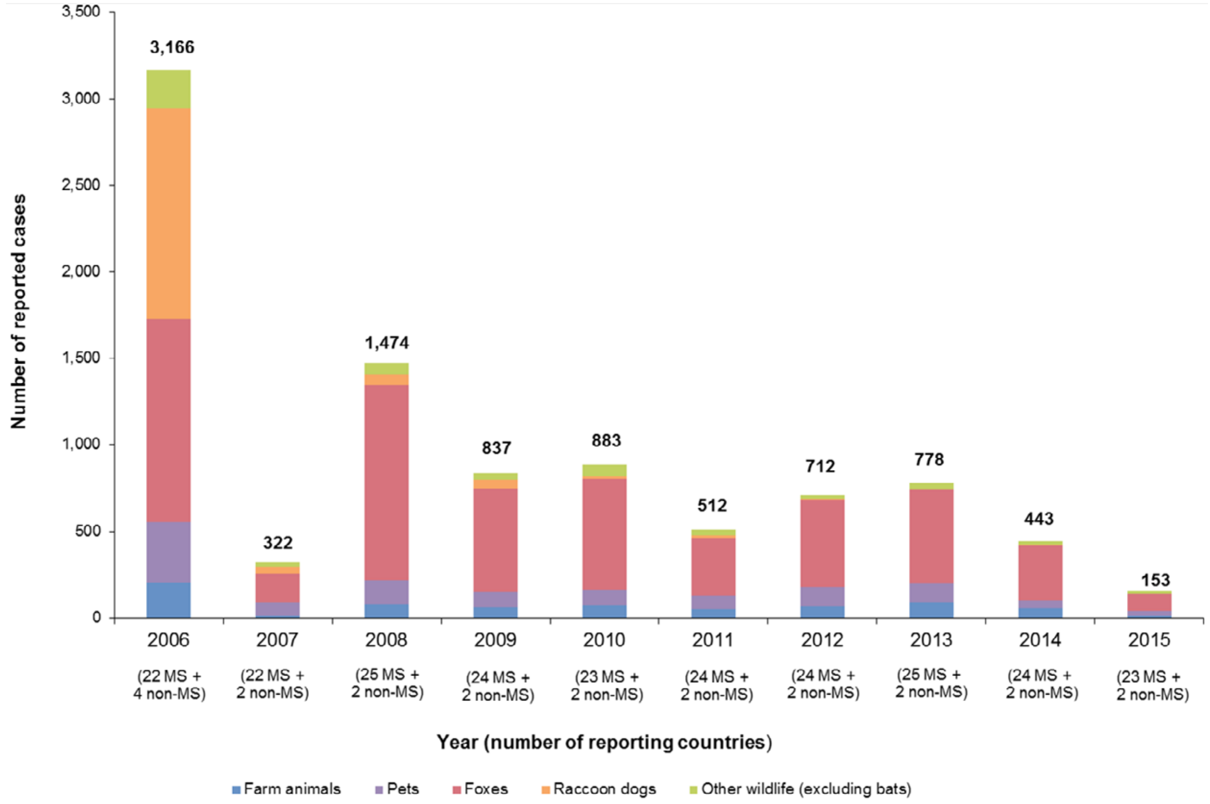
Other wildlife species in which rabies can be found are raccoon dogs (*Nyctereutes procyonoides*) and raccoons (*Procyon lotor*). Three rabies cases were reported in raccoon dogs in 2015 (2 by Poland and one by Lithuania) out of a total of 734 samples tested in EU. The majority of the samples was tested by Finland (262), Lithuania (108), Poland (89), Estonia (89) Germany (88), Latvia (66) and the Czech Republic (24). In Lithuania, the positive raccoon dog was hunted very close to the border with Belarus. Raccoon dogs are important rabies transmitters in northern and eastern Europe (1,215 cases reported in 2006), but the rabies incidence in this species was substantially reduced following oral vaccination programmes. Only 11 raccoons were tested in 2015 by Poland and the Czech Republic (Table 2015_RABIESRACCOON) and tested negative.

In 2015, 18 MS and two non-Ms reported approximately 3,600 samples tested in wildlife other than bats, foxes and raccoon dogs and raccoons (TABLE 2015_RABIESWILD). Only 13 animals tested positive for either classical rabies virus or unspecified *Lyssavirus* and were reported by Poland (1 badger and 4 martens) and Romania (4 bisons and 4 wolves).

In domestic farm animals, positive samples were reported in cattle by Poland (2 cases out of 28 suspected clinical diseased animals) and in cattle and solipeds by Romania (seven and two cases, respectively, collected during surveillance activities) (TABLE 2015_RABIESFARMED).

In 2015, two MS reported cases of rabies in pet animals: 12 infected cats (4 by Poland and 8 stray cats by Romania) and 16 infected dogs (2 imported cases by France, 2 by Romania and 12 by Poland) (Table 2015_RABIESCAT; Table 2015_RABIESDOG).

The reported cases of classical rabies or unspecified *Lyssavirus* cases in animals other than bats from 2006 until 2015 are shown in Figure 64. It is clear from the figure that the overall number of infected animals strongly decreased over the last year with a decrease from 443 infected animals in 2014 to 153 in 2015.



The number of reporting MS and non-MS is indicated at the bottom of each bar. The total number of rabies cases is reported at the top of each bar. Imported cases are not included. Source 2015: Austria, Belgium, Bulgaria, Croatia, Cyprus, the Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Italy, Latvia, Luxembourg, the Netherlands, Norway, Poland, Slovakia, Slovenia, Spain, Sweden, Switzerland and the United Kingdom.

Figure 64: Reported cases of classical rabies or unspecified *Lyssavirus* cases in animals other than bats, in the EU Member States and non-Member States, 2006–2015

3.11.3. Discussion

Human rabies claims more than 50,000 lives worldwide each year. It is an extremely rare zoonosis in Europe and is preventable by vaccination, but the disease is invariably fatal in infected humans once the first clinical symptoms have appeared. Usually, one or two human cases are annually reported in European citizens, with a majority of travel-related cases. In the EU no case of rabies in human was reported in 2015 in contrast with 2014 when three cases in patients were reported who travelled to a non-EU/EEA country endemic for rabies. It remains important to inform the public about the risk of contracting rabies if bitten by animals (especially dogs) while travelling to rabies-endemic countries or in the MS which have not eradicated the disease in their animal population.

In the EU the incidence of rabies in both domestic and wild animals, particularly in foxes and raccoon dogs, has been substantially reduced over the past decades, following systematic oral vaccination campaigns, and rabies cases have disappeared in western and most of central Europe. Thanks to the EU cofinanced eradication programmes, eastern European countries have also observed a rapid decline in the number of reported rabies cases in animals following their entry into the EU in 2004. About 23 million € was allocated in 2015 for rabies programmes (mainly vaccination programmes in the MS and bordering areas of neighbouring third countries, as the vast majority of sylvatic rabies cases in the EU occur in those areas.[42] The main expectation of the European Commission with relation to the national rabies programmes for 2015 was to achieve a decrease in the number of cases in wild animals in the EU. Figure 64 clear show a decreasing trend in the number of

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[42] Commission Implementing Decision (EC) No 2014/7437/F1 of 16 October 2014 on the adoption of the financing decision for the year 2015 for the implementation of Union cofunded programmes for the eradication, control and surveillance of animal diseases and zoonoses. http://ec.europa.eu/food/animals/docs/diseases_7437-2015_en.pdf

cases of rabies in wildlife animals. The endemicity of sylvatic rabies in neighbouring third countries is probably the reason for reintroduction and/or recurrence of rabies into certain border areas of the EU.

The recurrence of rabies in some countries highlights the fragility of the rabies-free status and the need for continuous surveillance. Mass vaccination of pets provides a first line of defence to prevent rabies in humans whereas oral vaccination of foxes and raccoon dogs has proved efficient for the long-term control and elimination of terrestrial sylvatic rabies. Rabies control programmes for foxes and raccoon dogs should be complemented by appropriate management measures in stray dogs and cat population (population registry, control and vaccination). It was shown that the successful elimination of fox rabies is a result of interaction of different key components during oral rabies vaccination campaigns such as vaccine strain, vaccine bait and strategy of distribution on a temporal and spatial scale (Müller et al., 2015). Rabies in pets imported from endemic countries is regularly reported in Europe, highlighting the need for continued vigilance concerning pet movements and campaigns to raise awareness among pet owners (Ribadeau-Dumas et al., 2016).

3.12. Q fever

The Appendix A lists all summaries made for the production of this section, for humans and animals, including Q fever summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.12.1. Q fever in humans

In 2015, 25 EU MS, Iceland and Norway provided information on Q fever in humans. Overall, 833 confirmed cases of Q fever were reported in the EU, one case was reported by Norway and 40 cases were reported by Switzerland (Table 29). The EU notification rate was 0.16 per 100,000 population, which is stable since 2011. The highest notification rate (0.54 cases per 100,000 population) was observed in Spain, followed by Croatia (0.49), Cyprus (0.47), France and Germany (both 0.38), and Hungary (0.35). As in most previous years, the highest numbers of confirmed cases were reported by Germany and France (311 and 250, respectively). Six countries (Estonia, Iceland, Lithuania, Malta, Poland and Slovakia) reported no human cases. A large majority (69.0%) of Q fever cases in the EU were domestically acquired. Only Germany, the Netherlands and Sweden reported travel-associated cases. Of the 16 travel-associated cases reported in total, seven were acquired within other EU countries, including six in Spain and one in Austria.

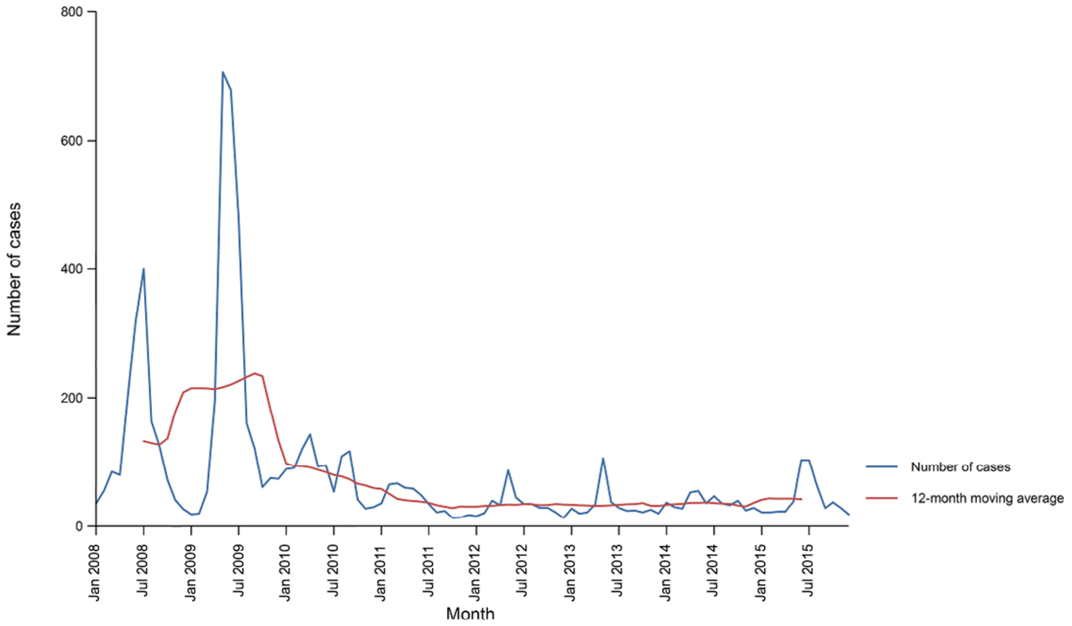
Table 29: Reported human cases of Q fever and notification rates per 100,000 in the EU/EEA, by country and year, 2011–2015

Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria(b)	–	–	–	–	–	–	–	–	–	–	–	–	–
Belgium(c)	N	A	20	8	–	0	–	6	–	18	–	6	–
Bulgaria	Y	A	18	15	0.21	15	0.21	23	0.32	29	0.4	12	0.16
Croatia	Y	A	14	14	0.49	21	0.49	–	–	43	1.02	–	–
Cyprus	Y	C	4	4	0.47	1	0.12	3	0.35	4	0.46	5	0.6
Czech Republic	Y	C	1	1	0	0	0	0	0	1	0.01	1	0.01
Denmark(b)	–	–	–	–	–	–	–	–	–	–	–	–	–
Estonia	Y	C	0	0	0	0	0	0	0	0	0	0	0
Finland	Y	C	3	3	0.05	0	0	5	0.09	0	0	4	0.07
France	Y	C	260	260	0.38	209	0.32	158	0.24	168	0.26	228	0.35
Germany	Y	C	322	311	0.38	238	0.3	114	0.14	198	0.24	287	0.35
Greece	Y	C	11	10	0.09	15	0.14	11	0.1	11	0.1	3	0.03
Hungary	Y	C	35	35	0.35	59	0.6	135	1.37	36	0.36	36	0.37

Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Ireland	Y	C	4	4	0.09	0	0	0	0	5	0.11	4	0.09
Italy(b)	–	–	–	–	–	–	–	–	–	–	–	–	–
Latvia	Y	C	1	1	0.05	3	0.15	1	0.05	1	0.05	1	0.05
Lithuania	Y	C	0	0	0	0	0	0	0	0	0	0	0
Luxembourg	Y	C	1	1	0.18	0	0	0	0	0	0	0	0
Malta	Y	C	0	0	0	0	0	2	0.48	0	0	0	0
Netherlands	Y	C	20	20	0.12	26	0.15	20	0.12	63	0.38	80	0.48
Poland	Y	C	0	0	0	1	0	0	0	0	0	0	0
Portugal	Y	C	20	20	0.19	25	0.24	21	0.2	26	0.25	5	0.05
Romania	Y	C	3	3	0.01	21	0.11	24	0.12	16	0.08	6	0.03
Slovakia	Y	C	0	0	0.02	1	0.02	0	0	0	0	0	0
Slovenia	Y	C	1	1	0.15	3	0.15	1	0.05	1	0.05	0	0
Spain(d)	N	C	97	97	0.54	77	0.54	75	0.54	58	–	33	–
Sweden	Y	C	4	4	0.04	2	0.02	3	0.03	2	0.02	5	0.05
United Kingdom	Y	C	21	21	0.03	60	0.09	46	0.07	12	0.02	43	0.07
EU Total	–	–	**833**	**833**	**0.16**	**777**	**0.18**	**648**	**0.17**	**692**	**0.16**	**759**	**0.2**
Iceland	Y	C	0	0	0	0	0	0	0	0	0	0	0
Norway	Y	C	1	1	0.02	1	0.02	4	0.08	0	0	0	0
Switzerland(e)	Y	C	–	–	–	44	0.54	27	0.33	–	–	–	–

(a): Y: yes; N: no; A: aggregated data report; C: case-based data report; –: no report.
(b): Not notifiable, no surveillance system exists.
(c): Sentinel surveillance; no information on estimated coverage; thus, notification rate cannot be estimated.
(d): Sentinel surveillance; notification rates calculated with estimated coverage of 30%.
(e): Switzerland provided data directly to EFSA. The human data for Switzerland also include the ones from Liechtenstein.

Overall, a decreasing trend in confirmed Q fever cases was observed over the period 2008–2015 in the EU/EEA (Figure 65). The peaks reported in 2008 and 2009 were due to a large outbreak occurring in the Netherlands between 2007 and 2010 and involving more than 4,000 human cases (van der Hoek et al., 2012). Q fever cases show a seasonal variation peaking mostly between April and August.



Source: Cyprus, the Czech Republic, Finland, Germany, Greece, Hungary, Ireland, Latvia, Malta, the Netherlands, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden. Estonia, Iceland, Lithuania and Luxembourg reported zero cases throughout the period. Austria, Belgium, Bulgaria, Croatia, Denmark, France, Italy, Switzerland and the United Kingdom did not report to the level of detail required for the analyses.

Figure 65: Trend in reported confirmed human cases of Q fever in the EU/EEA, by month, 2008–2015

Three deaths due to Q fever were reported in 2015 in the EU (one case in the Netherlands and two cases in Hungary), resulting in an EU case fatality of 0.36% among the 398 confirmed cases with reported outcome.

3.12.2. *Coxiella burnetii* in animals

The EU MS can report animal cases of Q fever to the European Commission under Directive 2003/99/EC on the monitoring of zoonoses and zoonotic agents. This directive states that, in addition to a number of zoonoses and zoonotic agents, for which monitoring is mandatory, others shall also be monitored where the epidemiological situation so warrants. Because of the use of different tests and analytical methods, as well as different sampling schemes, the results from different countries are not directly comparable. Proposals for harmonised schemes for the monitoring and reporting of Q fever in animals can be found in an External Scientific Report submitted to EFSA (Sidi-Boumedine et al., 2010).

Nineteen MS and three non-MS provided data on Q fever (*Coxiella burnetii*) for 2015, the same number of countries as in the previous year. All countries reported positive findings except for Finland, Romania, Slovenia, Sweden, Iceland, and Norway.

Seventeen MS and three non-MS (Iceland, Norway and Switzerland) provided data on cattle (Table 2015_COXCATTLE). The majority of samples were collected in Germany and Belgium. Overall, 47,757 individual animals were tested in these countries and out of these 4,913 (10.3%) animals were positive for *C. burnetii*. When taking account of only reported investigations providing also the test method, either by direct methods (e.g. PCR) or indirect methods (e.g. serological testing), 1,724 (6.3%) of the 27,283 animals tested were positive. In addition, 366 (11.5%) positive herds were detected out of the 3,193 herds tested. Considering only investigations providing also the test method, 326 (15.6%) of the 2,088 herds tested positive. Finland, Iceland, Norway, Romania, Slovenia and Sweden did not report any positive results for *C. burnetii* in cattle samples.

Seventeen MS and one non-MS (Switzerland) provided data on sheep and goats for 2015 (Table 2015_COXOVINEGOAT). The majority of samples were collected in Germany, Poland and Italy. In total, 9,935 individual animals were tested in these countries, of which 1,041 (10.5%) tested positive for *C. burnetii*. When taking account only of reported investigations providing also the test method, 410 (14.1%) of the 2,917 animals tested were positive. Furthermore, 5,609 flocks/herds and four holdings were tested and, out of these, 182 (3.2%) and 0 tested positive, respectively. When taking account of the test methods specified, 95 (2.3%) of the 4,064 herds tested positive. The Czech Republic, Denmark, Finland, Ireland, Romania, Slovakia, Slovenia did not detect *C. burnetii* in either sheep or goat samples.

In 2015, six MS and two non-MS (Norway and Switzerland) sampled a range of other domesticated, captive or wild animals (Table 2015_COXOTHERAN). The majority of sampling was conducted in Italy. In total, 866 sampling units were tested and all countries reported negative findings apart from Italy, Cyprus and Switzerland. Italy reported 11 positive single animal tests out of 551 samples tested; six positive results from pet dogs and five from farmed water buffaloes. Switzerland found one positive among six pigs tested, and Cyprus reported one positive out of 30 herds/flocks tested of farmed animals.

3.12.3. Discussion

In 2015, the notification rate of confirmed human cases of Q fever in the EU/EEA decreased slightly compared to 2014. If the overall trend has significantly decreased from 2008 to 2015, we can also notice that the average trend between 2012 and 2015 has been quite stable. France and Germany accounted for the vast majority of confirmed cases reported since 2010.

The 2015 results reported from animals demonstrate that the *C. burnetii* is found in cattle, sheep, goats, pigs, farmed water buffaloes, and pet dogs. Although no other animal species were reported to be positive, and although Finland, Romania, Slovenia, Sweden, Iceland, and Norway reported no *C. burnetii*-positive animals, the pathogen is known to be widely distributed in the EU and infecting a large number of domesticated and wild mammals, birds and ticks (EFSA AHAW Panel, 2010). In these species, variation in surveillance strategies for detection of Q fever within the different MS (survey, passive surveillance, clinical detection, abortion testing, etc.) as well as the different tests and analytical methods used, does not allow comparing the reported prevalences. Harmonised schemes for the monitoring and reporting of Q fever in animals are proposed in an External Scientific Report submitted to EFSA (Sidi-Boumedine et al., 2010).

3.13. West Nile virus

The Appendix A lists all summaries made for the production of this section, for humans and animals, including West Nile virus (WNV)/West Nile fever (WNF) summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.13.1. West Nile fever in humans

West Nile fever is caused by a virus transmitted by mosquitoes and whose reservoir includes wild birds and mosquitoes. For 2015, information on WNF in humans was provided by 25 EU MS, Norway and Switzerland. Seven EU MS (Austria, Bulgaria, France, Hungary, Italy, Portugal and Romania) reported human cases. In total, 127 human cases of WNF, including 104 confirmed cases, were reported in the EU in 2015. The EU notification rate was 0.02 cases per 100,000 population (Table 30), the same as in 2014.

The highest numbers of cases were reported by Italy, where highly populated provinces were affected, particularly the city of Milano in Lombardy that had no previous history of local transmission. In Hungary and Romania the surveillance data of the 2015 transmission season were rather similar to the 2014 season. The capitals of both countries were affected, but compared with 2014, more cases were detected in Hungary and fewer counties were affected in Romania. For the second consecutive year, cases were reported in Austria (Vienna area) where mandatory reporting of WNF cases was implemented in 2015. In Bulgaria, cases were detected in the Sofia area; in 2012, cases had been reported in Burgas, along the Black sea coast. Greece reported zero cases.

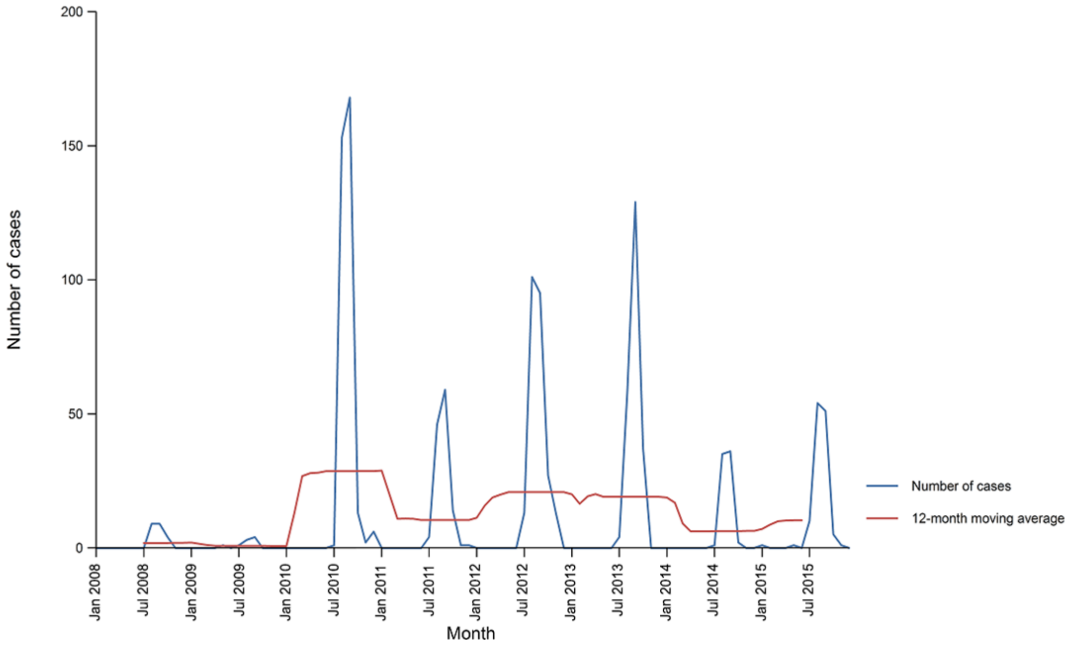
All the cases reported in Austria, Bulgaria, France, Italy, Portugal and Romania were domestically acquired. Hungary reported locally acquired cases as well as four travel-associated cases: one was acquired in Italy and the three other cases contracted the infection outside the EU.

Table 30: Reported human cases of West Nile fever and notification rates per 100,000 population in the EU/EEA, by country and year, 2011–2015

Country	2015					2014		2013		2012		2011	
	National data	Report type(a)	Confirmed cases	Total		Total		Total		Total		Total	
				Cases & rates		Cases & rates		Cases & rates		Cases & rates		Cases &rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	7	7	0.08	1	0.01	–	–	0	0	0	0
Belgium(c)	N	C	0	0	–	0	–	0	–	2	–	0	–
Bulgaria	Y	C	0	3	0.04	0	0	0	0	4	0.06	–	–
Croatia	–	–	–	–	–	–	–	20	0.48	6	0.14	–	–
Cyprus	Y	C	0	0	0	0	0	0	0	0	0	0	0
Czech Republic	Y	C	0	0	0	0	0	1	0.01	0	0	0	0
Denmark(b)	–	–	–	–	–	–	–	–	–	–	–	–	–
Estonia	Y	C	0	0	0	0	0	0	0	0	0	0	0
Finland	Y	C	0	0	0	0	0	0	0	0	0	0	0
France(c)	N	C	1	1	–	0	0	1	–	3	–	1	–
Germany(b)	–	–	–	–	–	–	–	–	–	–	–	–	–
Greece	Y	C	0	0	0	15	0.14	86	0.78	162	1.46	100	0.9
Hungary	Y	C	15	22	0.22	11	0.11	36	0.37	17	0.17	4	0.04
Ireland	Y	C	0	0	0	0	0	1	0.02	0	0	1	0.02
Italy(d)	N	C	61	61	–	24	–	79	0.13	28	0.05	14	0.02
Latvia	Y	C	0	0	0	0	0	0	0	0	0	0	0
Lithuania	Y	C	0	0	0	0	0	0	0	0	0	0	0
Luxembourg	Y	C	0	0	0	0	0	0	0	0	0	0	0
Malta	Y	C	0	0	0	0	0	0	0	0	0	0	0
Netherlands	Y	C	0	0	0	0	0	0	0	0	0	1	0.01
Poland	Y	C	0	0	0	0	0	0	0	0	0	0	0
Portugal	Y	C	1	1	0.01	–	–	–	–	–	–	–	–
Romania	Y	C	19	32	0.16	24	0.12	24	0.12	15	0.08	11	0.06
Slovakia	Y	C	0	0	0	0	0	0	0	0	0	0	0
Slovenia	Y	C	0	0	0	0	0	1	0.05	0	0	0	0
Spain	Y	C	0	0	0	0	0	0	0	0	0	0	0
Sweden	Y	C	0	0	0	0	0	1	0.01	1	0.01	0	0
United Kingdom	Y	C	0	0	0	2	0	0	0	0	0	0	0
EU Total	–	–	**104**	**127**	**0.02**	**77**	**0.02**	**250**	**0.08**	**238**	**0.07**	**132**	**0.04**
Iceland	–	–	–	–	–	–	–	–	–	–	–	–	–
Switzerland	Y	C	0	1	0.01	0	0	1	0.01	1	0.01	0	0

(a): Y: yes; N: no; A: aggregated data report; C: case-based data report; –: no report.
(b): No surveillance system.
(c): Sentinel surveillance; coverage unknown, hence notification rate cannot be estimated.
(d): No national coverage in 2015, hence notification rate not calculated.

WNF has been notifiable at the EU level since 2008. The number of cases varied from year to year (Figure 66). There was strong seasonality in the number of WNF cases reported in the EU in 2011–2015, with most cases being reported between July and September. The number of reported cases usually peaked in August, apart from in 2014 when the peak was recorded in September.



Source: Austria, Bulgaria, the Czech Republic, Greece, Hungary, Italy, Norway, Romania, Slovenia, Spain and the United Kingdom. Belgium, Cyprus, Estonia, Finland, France, Ireland, Latvia, Lithuania, Luxembourg, Malta, the Netherlands, Norway, Poland, Portugal, Slovakia, Sweden and Switzerland reported zero cases throughout the period. Croatia did not report data. Denmark and Germany do not have a surveillance system for this disease.

Figure 66: Trend in reported total cases of human West Nile fever in the EU/EEA, by month, 2008–2015

Hospitalisation status was reported for 51.2% of cases and 83.07% of these cases were reported as having been hospitalised.

In 2015, a total of 92 neuroinvasive, 15 non-neuroinvasive and 20 infections of unknown neuroinvasiveness were reported by the affected MS. The overall case fatality in the EU for neuroinvasive illness cases was very low (0.7%, n = 1, reported by Romania) among the 127 total documented cases, but 62 cases reported had an unknown outcome. Another death was reported by Bulgaria but the clinical manifestation was unknown.

An interactive overview map for both the EU and neighbouring countries is published on the ECDC website (ECDC, 2016) with an epidemiological update summarising the WNF season, the weekly updates of the ECDC West Nile risk map and historical maps (Figure 67).

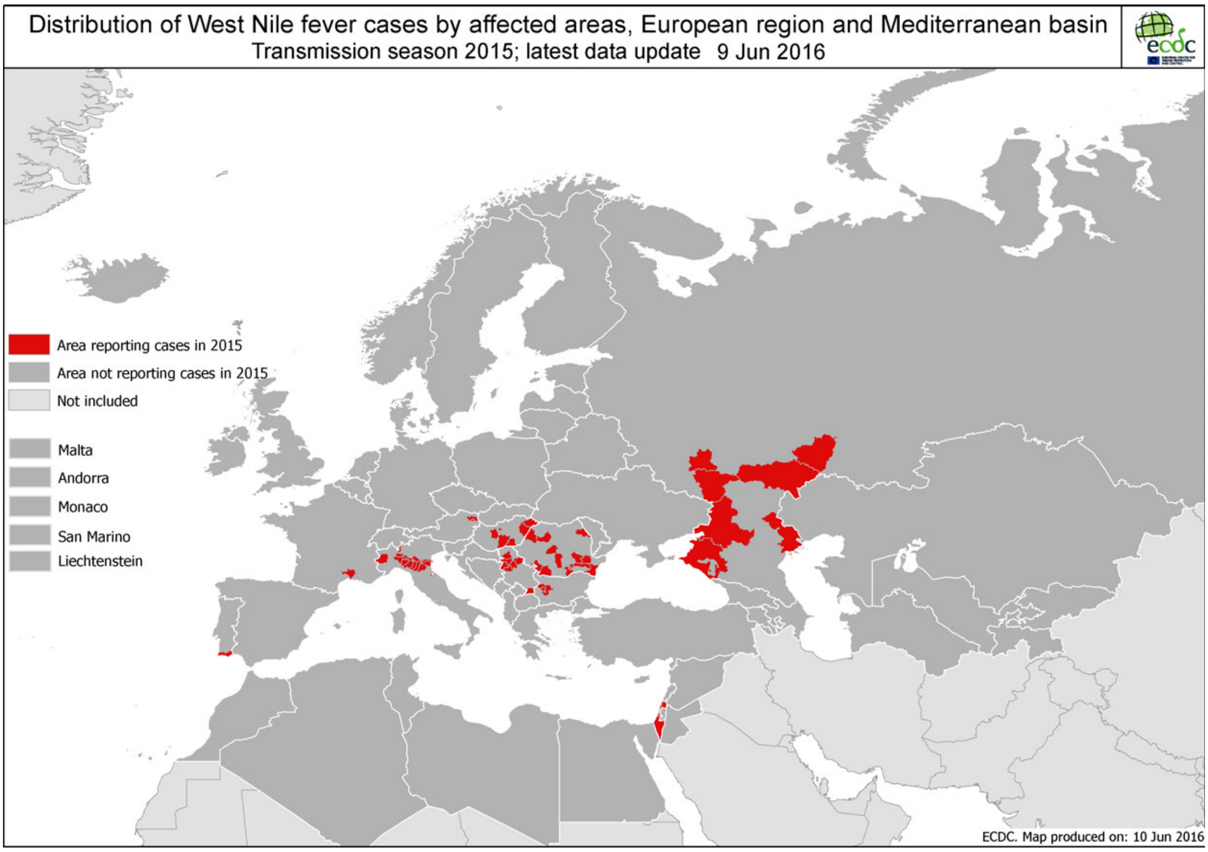


Figure 67: Distribution of West Nile fever human cases, the EU and neighbouring countries, transmission season 2015

3.13.2. West Nile virus in animals

Although the reporting of WNV infections in animals is not mandatory, the MS can report WNV infections in animals to the European Commission in accordance with the Zoonoses Directive 2003/99/EC. The directive specifies that, in addition to the number of zoonoses and zoonotic agents, for which monitoring is mandatory, others shall also be monitored when the epidemiological situation so warrants.

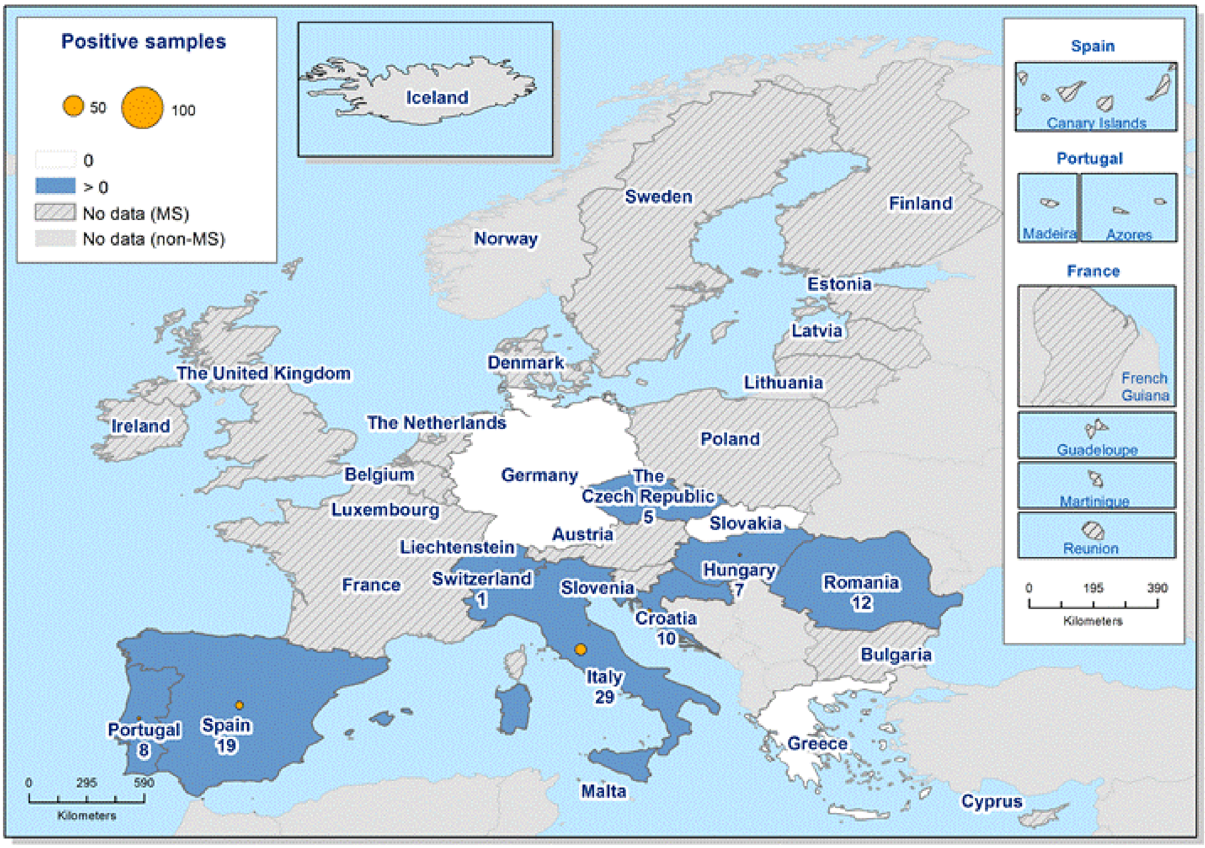
Owing to heterogeneity in study design and the variety of analytical methods used, the reported WNV prevalence in birds and solipeds from different countries is not directly comparable. Proposals for harmonised schemes for the monitoring and reporting of WNV in animals can be found in an External Scientific Report submitted to EFSA (Mannelli et al., 2012).

In 2015, a total of 22,337 animals (solipeds, birds and a hamster) were reported to be tested for WNV, which is slightly less than in 2014 when 23,629 animals were tested. In 2015, 9,582 birds, mostly wild birds but also fowl on farms, have been sampled for WNV in seven MS and one non-MS; Croatia (131), Italy (4,128), Spain (2,803), Switzerland (988), Belgium (933), the United Kingdom (336), Germany (206) and Hungary (57). A total of 177 positive bird samples were reported by Spain (101), Italy (72), Croatia (3) and Hungary (1) (Table 2015_WNVBIRDS). Italy, Hungary and Spain reported the bird samples to be positive to the polymerase chain reaction (PCR) test, which detects viral genetic material, whereas Croatia reported positivity to an IgG antibody ELISA (serological) test (Figure 68).

Positive test results were based on the polymerase chain reaction (PCR) as reported by Italy, Hungary and Spain and on the IgG antibody ELISA as reported by Croatia.

Figure 68: Findings of West Nile virus in birds in the EU, in 2015

Furthermore, in 2015, 12,754 solipeds were tested in 11 MS and one non-MS (Croatia, the Czech Republic, Germany, Greece, Hungary, Italy, Portugal, Romania, Slovakia, Spain, the United Kingdom and Switzerland) (Table 2015_WNVSOLIP). Eight of the reporting countries detected 91 test-positive animals: Croatia (10), the Czech Republic (5), Italy (29), Spain (19), Romania (12), Portugal (8), Hungary (7) and Switzerland (1) (Figure 69). Countries reported the horses (and in case of Italy one donkey) to be confirmatory test-positive specifically to the IgM-capture ELISA (MAC-ELISA), except for the Czech Republic and Switzerland reporting confirmatory test-positivity to neutralising antibody testing. Portugal did not report any analytical method information. Moreover, Croatia, the Czech Republic and Romania reported the confirmed positive horses to be unvaccinated, whereas the confirmed positive domestic horse in Switzerland was vaccinated against WNV. The other four countries reported an unknown WNV vaccination history (Italy and Spain) for their confirmed positive Solipeds, or did not report information regarding the vaccination status (Hungary and Portugal). Hungary reported one test-negative hamster.



Positive test results were based on the IgM-capture ELISA (MAC-ELISA) as reported by Croatia, Hungary, Italy, Romania, Spain, on the seroneutralisation test as reported by the Czech Republic and Switzerland, whereas Portugal did not report analytical method information. The reported WNV vaccination status of test-positive solipeds was; vaccinated (Switzerland), unvaccinated (Croatia, the Czech Republic and Romania), unknown (Italy and Spain) and missing (Hungary and Portugal).

Figure 69: Findings of West Nile virus in domestic solipeds in the EU, in 2015

3.13.3. Discussion

Variations and differences in WNF case numbers in humans are partly due to variations and differences in surveillance systems. It is difficult to compare case numbers and notification rates between countries, because some report all cases, including asymptomatic and mild cases, while others report only neuroinvasive cases. Variations in case reporting can also be partly explained by the substantial efforts made to strengthen the level of detection in the affected countries or in newly affected countries as soon as the first cases are identified. Health professionals (including blood transfusion safety authorities) are alerted at the beginning of the season, as are the stakeholders involved in animal and entomological surveillance. Some countries (e.g. Italy, Greece or Portugal) implemented a mosquito surveillance scheme to see if increased mosquito activity and/or early detection of the virus circulation mosquitoes could be used as an early warning system (Osório et al., 2014).

The MS report WNV monitoring data in animals to the EFSA under Directive 2003/99/EC. Reporting is focused on birds (prime reservoir hosts) and other species, such as horses, that can be infected incidentally.

Test-positive birds and solipeds were reported by Croatia, Italy, Hungary and Spain. Additionally positive solipeds were reported by the Czech Republic, Romania and Portugal. Switzerland reported one domestic, confirmed-positive horse, which was vaccinated against WNV.

France notified WNV data in animals to ADNS[43] but did not yet report them to EFSA. Published French surveillance data describe an equine WNV epizootics in the year 2015 in the Hérault,

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[43] ADNS, the EU Animal Disease Notification System, see http://ec.europa.eu/food/animals/animal-diseases/not-system_en

Bouches-du-Rhône and Gard departments (Bournez et al., 2015) while the public health authorities reported one human case in 2015 in the Gard department to the ECDC.

WNV monitoring data in animals provided by the MS to EFSA are generated by non-harmonised monitoring schemes for which no mandatory reporting requirements exist. These data are therefore not comparable between the MS and the reported findings must therefore be interpreted with extreme caution, and preclude subsequent data analysis like assessing temporal and spatial trends at the EU level.

3.14. Tularaemia

The Appendix A lists all summaries made for the production of this section, for humans and animals, including tularaemia summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

3.14.1. Tularaemia in humans

In 2015, 25 EU MS, Iceland and Norway provided information on tularaemia in humans. A total of 1,079 confirmed cases of tularaemia in humans were reported in 16 EU MS. The highest case numbers were reported from Sweden and Finland, 722 and 104 confirmed cases, respectively (Table 31). Eight EU MS (Cyprus, Estonia, Greece, Ireland, Latvia, Luxembourg, Portugal and Slovenia) and Iceland reported no human cases. The EU notification rate in 2015 was 0.21 cases per 100,000 population, considerably higher than in 2014 and 2013 but similar to rate in 2012. As in the previous 4 years, the notification rate was highest in Sweden (7.41 per 100,000), exceeding the rate in 2014 more than sixfold (1.13 per 100,000) as the country experienced an outbreak.

Less than 1% of tularaemia cases in Europe were reported to be travel-related (information available for 16.1% of the confirmed cases). Austria, Germany, Hungary, Spain and the United Kingdom reported nine travel-associated cases, with six of them acquired within another EU country.

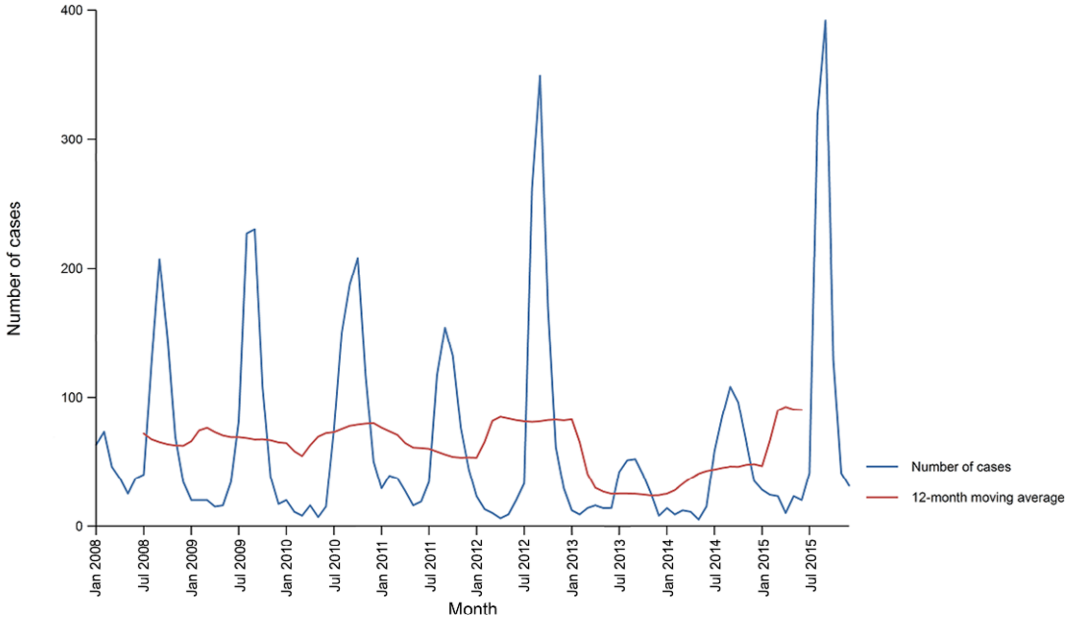
Table 31: Reported human cases of tularaemia and notification rates per 100,000 population in the EU/EEA, by country and year, 2011–2015

Country	2015					2014		2013		2012		2011	
	National coverage[(a)]	Data format[(a)]	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Austria	Y	C	4	4	0.04	0	0	2	0.02	2	0.02	0	0
Belgium	Y	C	1	0	0	0	0	1	0.01	0	0	0	0
Bulgaria	Y	A	22	17	0.23	1	0.01	1	0.01	0	0	0	0
Croatia	Y	A	13	13	0.3	2	0.05	2	0.05	1	0.02	–	–
Cyprus	Y	C	0	0	0	0	0	0	0	0	0	0	0
Czech Republic	Y	C	56	56	0.53	48	0.46	36	0.34	42	0.4	57	0.54
Denmark[(b)]	–	–	–	–	–	–	–	–	–	–	–	–	–
Estonia	Y	C	0	0	0	1	0.08	1	0.08	0	0	2	0.15
Finland	Y	C	104	104	1.9	9	0.17	15	0.28	233	4.31	75	1.4
France	Y	C	87	28	0.04	19	0.03	21	0.03	5	0.01	16	0.03
Germany	Y	C	34	34	0.04	21	0.03	20	0.02	21	0.03	17	0.02
Greece	Y	C	0	0	0	0	0	0	0	0	0	0	0
Hungary	Y	C	36	35	0.35	140	1.42	48	0.48	18	0.18	15	0.15
Ireland	Y	C	0	0	0	0	0	0	0	0	0	0	0
Italy	Y	C	–	–	–	0	0	1	0	2	0	0	0
Latvia	Y	C	0	0	0	0	0	0	0	6	0.29	0	0
Lithuania	Y	C	4	4	0.13	4	0.14	4	0.14	3	0.1	0	0
Luxembourg	Y	C	0	0	0	0	0	0	0	0	0	0	0

Country	2015					2014		2013		2012		2011	
	National coverage(a)	Data format(a)	Total cases	Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates		Confirmed cases & rates	
				Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate	Cases	Rate
Malta	Y	C	–	–	–	0	0	0	0	0	0	0	0
Netherlands	Y	C	1	1	0	5	0.03	1	0.01	–	–	1	0
Poland	Y	C	9	9	0.02	11	0.03	8	0.02	6	0.02	6	0.02
Portugal(b)	–	–	0	0	0	–	–	–	–	–	–	–	–
Romania	Y	C	1	1	0	0	0	1	0.01	0	0	0	0
Slovakia	Y	C	28	28	0.52	6	0.11	9	0.17	8	0.15	5	0.09
Slovenia	Y	C	0	0	0	1	0.05	2	0.1	4	0.2	0	0
Spain	Y	C	25	22	0.04	62	0.13	0	0	1	0	1	0
Sweden	Y	C	859	722	7.41	150	1.56	108	1.13	590	6.22	350	3.72
United Kingdom	Y	C	1	1	0	0	0	0	0	0	0	0	0
EU Total	–	–	**1285**	**1079**	**0.21**	**480**	**0.1**	**279**	**0.07**	**942**	**0.2**	**545**	**0.12**
Iceland	Y	C	0	0	0	0	0	0	0	0	0	0	0
Norway	Y	C	42	42	0.81	46	0.9	28	0.55	50	1	180	3.66
Switzerland(b)	Y	C	–	–	–	38	0.46	29	0.35	40	0.5	15	0.19

(a): Y: yes; N: no; A: aggregated data; C: case-based data.
(b): Not notifiable, no surveillance system exists.
(c): Switzerland provided data directly to EFSA. Liechtenstein has no surveillance system.

There was an increasing trend of confirmed tularaemia cases in 2008–2015 (Figure 70) with two peaks (2012 and 2015). These two peaks were both due to high case numbers in Finland and Sweden. The number of tularaemia cases varied seasonally peaking mostly between July and October.



Source: Austria, the Czech Republic, Finland, France, Germany, Hungary, Lithuania, the Netherlands, Norway, Poland, Romania, Slovakia, Spain, Sweden and the United Kingdom. Cyprus, Estonia, Greece, Iceland, Ireland, Italy, Latvia, Luxembourg, Malta and Slovenia reported zero cases throughout the period. Belgium, Bulgaria and Croatia did not report data to the level of detail required for the analysis. Denmark, Portugal and Liechtenstein do not have a surveillance system for this disease.

Figure 70: Trend in reported confirmed human cases of tularaemia in the EU/EEA, by month, 2008–2015

Nine MS provided data on hospitalisation status of their cases, and 55.6% of these cases were reported to have been hospitalised. Eleven MS provided information on the outcome of their cases accounting for 18% of all confirmed cases. No deaths due to tularaemia were reported in 2015.

3.14.2. *Francisella tularensis* in animals

In 2015, only one MS, Sweden, and Switzerland reported on the occurrence of *Francisella tularensis* in animals (Table 2015_FRANCISELLAANI). Sweden investigated, as part of their official monitoring, 65 wild hares and found 31 positives (47.7%, 5 out of 11 were detected using immunohistochemistry and 26 out of 54 were positive using PCR) which is much higher than in 2014 and 2013 (6.5% and 29.7%, respectively). Switzerland tested 3 beavers, 20 wild hares and 3 monkeys (zoo) and 6 hares tested positive. One case of *F. tularensis* in European brown hare was reported to OIE by Denmark in December 2015.

3.14.3. Discussion

Notification rates for tularaemia vary considerably among the MS. Two outbreaks occurred in Sweden, one in 2012 and one in 2015 (66.9% of the total of confirmed cases) with a notification rate of 7.41 per 100,000 population, exceeding the notification rate reported during the 2012 outbreak. The notification rate also increased in Finland in 2015 but far lower than in 2012. Slovakia also reported a notification rate increase in comparison with the previous years.

F. tularensis has many animal reservoirs in vertebrates and invertebrates. However, small rodents (mice, rats, voles, beavers) and lagomorphs (genus *Lepus*) are considered as possible key reservoirs in wild animals and potential dangerous for transmission to human (Hestvik et al., 2015). Occasionally, tularaemia is reported in non-human primates (Maurin and Gyuranecz, 2016). In 2015, a remarkably higher prevalence compared to previous years in wild hares was observed in Sweden, the only reporting MS in the EU. This confirms the fact that tularaemia is still highly prevalent in Sweden, probably via vector-borne transmission and therefore stresses the importance to assess the reservoir competence of different vectors in the transmission of *F. tularensis* (Desvars et al., 2015).

3.15. Other zoonoses and zoonotic agents

In 2015, data on *Anisakis*, *Chlamydia*, *Cysticercus*, *Bacillus* and *Sarcocystis* were reported to EFSA.

3.15.1. *Anisakis*

In 2015, one MS (Malta) reported data on *Anisakis* spp. in unspecified wild fish samples at retail. Fifty-nine out of the 104 samples tested were positive (56.7%). This positive proportion of *Anisakis* spp. in fresh fish is lower than the prevalence of 66% in commercial fish from northern Sardinia reported by Piras et al. (2014), but higher than the prevalences found in other studies in fish caught in the Mediterranean Sea, 31% and 21.5% (Serracca et al., 2013; Madrid et al., 2016).

3.15.2. *Chlamydia*

In 2015, as in the previous year, Germany was the only MS which submitted data on *Chlamydia* spp., *Chlamydia abortus* and *Chlamydia psittaci* in various animals – cattle, pigs, sheep, goats, poultry, pigeons, domestic solipeds, cats and dogs, among others.

C. abortus was detected in 1,415 (9.5%) of the 14,856 bovine animals tested. Compared to 2014, the prevalence of *C. abortus* in bovine animals was 16.3% and among them 0.24% of the examined dairy cows were positive.

In sheep, 220 (17.0%) out of the 1,296 samples tested were positive for *C. abortus*, which is comparable with the prevalence observed in 2014 (16.6%).

C. psittaci was detected in 1.3% of the duck and *G. gallus* (fowl) samples tested and in 9.8% of the pigeon samples tested in 2015. In comparison, in 2014, the prevalence of *C. psittaci* in pigeons was reported to be 21.4%.

3.15.3. *Cysticercus*

In 2015, three MS; Belgium, Slovenia and Sweden, provided information on bovine and porcine cysticercosis caused by, respectively, *Taenia saginata* and *Taenia solium*.

Belgium tested 874,948 cattle carcases based on official meat inspection at slaughter and detected *T. saginata* in 1,253 (0.14%) cases. Of these, 11 carcases were reported to be heavily infested. This proportion is similar to the data provided by Belgium in 2014.

Slovenia and Sweden submitted information on both bovine and porcine cysticercosis. Slovenia reported data on a considerably higher number of samples in 2015 compared with 2014. Specifically, 111,468 bovine samples were tested for *T. saginata* and 242,497 porcine samples for *T. solium*, of which none were detected as positive. Sweden tested 2,560,450 porcine and 428,220 bovine organ/tissue samples for *T. solium* and *T. saginata*, respectively, and found no positive samples, as in 2014. According to Devleesschauwer et al. (2015), Slovakia reported one porcine cysticercosis case to the World Organisation for Animal Health (OIE) in 2014, while no cases were submitted to OIE in 2015.

3.15.4. *Bacillus*

Bulgaria submitted data on *Bacillus* prevalence in foods in 2015. Seven suspected bakery products (desserts) taken from a processing plant investigation were tested for *Bacillus cereus* contamination. None of them were positive.

3.15.5. *Sarcocystis*

In 2015, as in the previous 2 years, Belgium was the only MS which provided information on *Sarcocystis* in cattle. Of the 874,948 cattle samples tested at slaughter (meat inspection), 107 (0.012%) were positive, which is comparable with a prevalence of 0.010% reported in 2014, and 0.007% in 2013.

Reports on *Sarcocystis* prevalence in cattle are lacking in most of the European countries. In contrast to the very low prevalence of *Sarcocystis* in the Belgian cattle, a countrywide survey performed in Hungary by conventional PCR and sequencing found 66% *Sarcocystis*-positive cattle samples at slaughter (Hornok et al., 2015). High *Sarcocystis* prevalence was also reported in Italy by Domenis et al. (2011), where *Sarcocystis* by histological examination were found in 78.1% of the tested bovine animals.

3.16. Food-borne outbreaks

The Appendix A lists all summaries made for the production of this section, for food-borne outbreaks, including also all summary tables and figures that were not included in this section because they did not trigger any marked observation. All tables and figures are available in downloadable files attached to this report.

>It is important to note that food-borne outbreak investigation systems at the national level are not harmonised among the MS. Therefore, the differences in the number and type of reported outbreaks, as well as in the causative agents, may not necessarily reflect the level of food safety among the MS; rather they may indicate differences in the sensitivity and representativeness of the surveillance systems for food-borne outbreaks in the different MS. In addition, some MS have implemented changes in national systems over time, which may have had an impact on the number of outbreaks reported by the same MS in different years.

3.16.1. General overview

The reporting of investigated food-borne outbreaks has been mandatory for the EU MS since 2003. Starting in 2007, harmonised specifications on the reporting of food-borne outbreaks at the EU level have been increasingly applied in the EU. The current system for reporting food-borne outbreak is known as European Union Food-borne reporting System (EU-FORS) and was implemented for the first time in the reporting of data from 2010 and subsequent years. Since then, the outbreaks reported have been categorised as having 'strong evidence' or 'weak evidence' based on the strength of evidence implicating a suspected food vehicle as the cause of the outbreak (EFSA, 2014a).

The evaluation of the strength of evidence implicating a suspected food vehicle in food-borne outbreaks as being strong or weak is based on the assessment of all available types of evidence (i.e. microbiological, epidemiological, descriptive environmental, based on tracing-back of the investigated foodstuffs) and according to the EU-FORS guidance and the last published manual for reporting on food-borne outbreaks (EFSA, 2014a, 2016a).

In 2015, 26 MS and two non-MS provided data on food-borne outbreaks, whereas no outbreak data were reported by Spain and Malta. In the present chapter, data on reported food-borne outbreaks in the EU MS and non-MS are presented separately for 'strong-evidence' or 'weak-evidence' outbreaks, since a detailed data set for strong-evidence outbreaks has to be specified by the reporting countries. Notably, since 2014, the MS also have the possibility to report detailed information on the suspected vehicle in weak-evidence outbreaks (EFSA, 2014a). The types of evidence reported for the strong-evidence outbreaks, including waterborne outbreaks, are presented in Table 2015_FBOEVID.

Data for 2015 provide information on the total number of reported food-borne outbreaks attributed to different causative agents, including food-borne outbreaks for which the causative agent was unknown. In this general overview, all reported food-borne outbreaks including waterborne outbreaks are summarised in the tables and figures. Outbreak data are mainly aggregated by causative agent, implicated food vehicle and place of exposure. Section 3.16.2 aims to analyse data from strong-evidence food-borne outbreaks to provide information useful to characterise the risk profile of the different types of food vehicles and settings associated with outbreaks. In Section 3.16.3, more details on food-borne outbreaks by causative agent, excluding waterborne outbreaks, are provided. All waterborne outbreaks with strong-evidence are addressed separately in Section 3.16.4.

Categorisation of causative agents has been changed in the present report, compared with previous years, to better fit the need to represent the epidemiological picture at the EU level according to the rationale for the prioritisation of causative agents in Directive 2003/99/EC. All the causative agents associated with food-borne outbreaks and listed in Directive 2003/99/EC under annex IA (zoonoses and zoonotic agents to be included in monitoring) and IB (list of zoonoses and zoonotic agents to be monitored according to the epidemiological situation) have been described as single entities. The single causative agents are then grouped into larger macro-categories, by type of agent, i.e. bacteria, bacterial toxins, viruses, parasites and other causative agents. All the causative agents not explicitly mentioned in the directive annexes have been reported as 'other agents' and grouped according to their nature within the macro-categories. Compared with previous years, this new approach results in outbreaks caused by *Brucella*, *Listeria*, Shiga toxin-producing *E. coli* (STEC) and *Vibrio* being described as single causative agents for 2015, while they were previously classified as 'other bacterial agents'. Similarly, calicivirus and hepatitis A virus which were previously categorised into the 'viruses' group, *Trichinella* and *Cryptosporidium* which were previously categorised into the group 'parasites', and *C. botulinum* which was previously categorised into the 'bacterial toxins' group, are described individually.

The burden of food-borne outbreaks (including waterborne outbreaks) in the EU, 2015: number of outbreak and human cases

In 2015, a total of 4,362 food-borne outbreaks including both strong-evidence (N = 422) and weak-evidence outbreaks (N = 3,940) were reported by 26 MS (Table 32). Compared with data reported in 2014 (N = 5,251) this corresponds to a 17% decrease. A similar difference (18%) also applies to the comparison with the mean annual number of outbreaks reported for the whole 2010–2014 period (N = 5,349) when the trend was quite stable (Figure 71). In 2015, another 50 outbreaks were reported by two non-MS (Norway and Switzerland). France reported the largest number of outbreaks (N = 1,429) and accounted for 32.8% of all reported outbreaks, followed by Slovakia (N = 425), with 9.7% of total outbreaks reported.

In 2015, 422 strong-evidence outbreaks were reported by 21 MS, accounting for 9.7% of the total food-borne outbreaks recorded in 2015 (Table 32). This was 28.7% less than the number of strong-evidence outbreaks in 2014 (592 outbreaks, accounting for the 11.3% of total outbreaks). The highest number of strong-evidence outbreaks were reported by France, followed by Poland, Germany and Lithuania and accounted altogether for the 61.1% of total strong-evidence outbreaks reported in the EU in 2015 (Table 32).

Overall in the EU MS, the reporting rate of food-borne outbreaks (including waterborne outbreaks) per 100,000 was 0.95 (Table 32) which represents a 14.4% reduction compared with the mean reporting rate observed in the previous 5 years (2010–2014) for which the mean value was 1.11 outbreaks per 100,000 population. Reporting rates varied importantly among the MS, ranging from 0.06 (Italy) to 7.84 (Slovakia) outbreaks per 100,000 population (median of the reporting MS: 0.50 outbreaks per 100,000). Outbreak reporting rates in the different MS and non-MS in 2015 are shown in Figure 72. Compared with the five previous years (2010–2014), for seven MS a decrease in the annual reporting rate over 50% was observed (Austria, Estonia, Hungary, Italy, Latvia, Lithuania and Luxembourg) while an increase of over 50% in Portugal and the Netherlands was reported (Table 32).

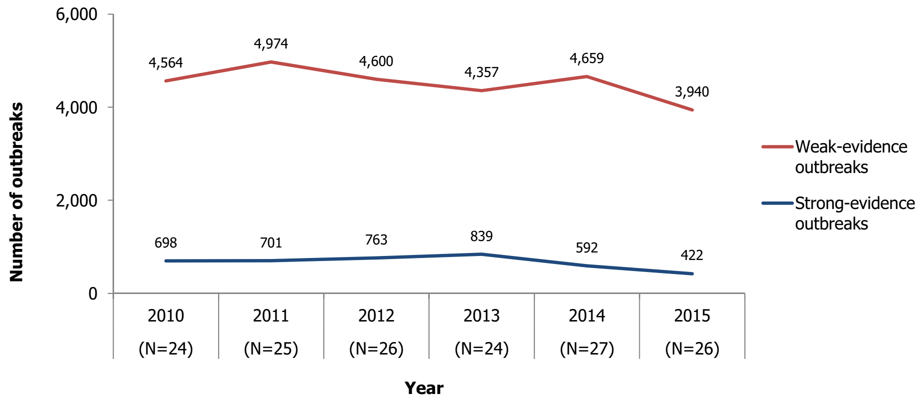
Overall in 2015, food-borne outbreaks (including waterborne) caused 45,874 cases of illness (209 more than in 2014), 3,892 hospitalisations (2,546 less than in 2014) and 17 deaths (10 less than in 2014) in 26 MS. A total of 1,853 cases and 7 hospitalisations were reported in Norway and Switzerland. More details on hospitalisation and deaths by causative agents are described in Table 33. Similarly to the outbreak reporting rate, a wide range of variation in the rate of human cases involved in food-borne outbreaks, among countries, was observed (Figure 73). This ranged from 0.21 (Italy) to 57.1 (the Czech Republic) cases per 100.000 (median among the 26 reporting MS: 7.28 cases per 100,000).

Table 32: Number of food-borne outbreaks (including waterborne outbreaks) and human cases, hospitalisations and deaths, reported by the EU Member States and non-Member States, 2015

Country	Strong-evidence outbreaks				Weak-evidence outbreaks				Total outbreaks	Reporting Rate per 100,000	
	N	Cases	Hospitalised	Deaths	N	Cases	Hospitalised	Deaths		2015	2010–2014 (mean)
Austria	6	155	51	0	72	178	35	0	78	0.91	1.85
Belgium	14	237	10	0	338	1,978	31	1	352	3.13	2.51
Bulgaria	0	0	0	0	6	61	12	0	6	0.08	0.13
Croatia	27	446	31	1	29	713	14	0	56	1.33	1.22
Cyprus	2	15	0	0	1	2	1	0	3	0.35	–
Czech Republic	0	0	0	0	28	6,016	160	0	28	0.27	0.21
Denmark	0	0	0	0	37	1,206	9	0	37	0.65	1.26
Estonia	0	0	0	0	6	15	12	0	6	0.46	1.21
Finland	16	1,104	13	0	27	326	6	0	43	0.79	0.83
France	135	2,073	135	2	1,294	10,119	587	3	1,429	2.15	1.86
Germany	28	619	53	0	356	1,453	171	0	384	0.47	0.51
Greece	4	478	3	0	5	47	10	2	9	0.08	0.13
Hungary	14	654	54	0	38	761	44	1	52	0.53	1.49
Ireland	2	7	0	0	27	125	7	0	29	0.63	0.50
Italy	3	16	16	2	34	109	8	0	37	0.06	0.49
Latvia	5	178	29	0	93	493	139	0	98	4.93	20.74
Lithuania	28	202	103	1	0	0	0	0	28	0.96	5.17
Luxembourg	1	43	0	0	0	0	0	0	1	0.18	0.73
Malta	0	0	0	0	0	0	0	0	0	0.00	8.30
Netherlands	6	92	17	0	400	1,758	9	0	406	2.40	1.48
Poland	67	959	236	0	356	5,187	1,136	2	423	1.11	1.19
Portugal	8	112	71	0	12	309	26	0	20	0.19	0.12
Romania	18	350	255	0	3	47	15	0	21	0.11	0.09
Slovakia	13	209	21	1	412	2,102	286	0	425	7.84	9.90
Slovenia	0	0	0	0	5	69	2	0	5	0.24	0.33
Spain	0	0	0	0	0	0	0	0	0	0.00	0.92
Sweden	8	1,476	5	0	325	2,173	22	0	333	3.42	2.93

Country	Strong-evidence outbreaks				Weak-evidence outbreaks				Total outbreaks	Reporting Rate per 100,000	
	N	Cases	Hospitalised	Deaths	N	Cases	Hospitalised	Deaths		2015	2010–2014 (mean)
United Kingdom	17	412	17	0	36	790	30	1	53	0.08	0.12
Norway	1	18	0	0	40	467	0	0	41	0.79	1.23
Switzerland	5	1,348	5	0	4	20	2	0	9	0.11	0.11
EU Total	**422**	**9,837**	**1,120**	**7**	**3,940**	**36,037**	**2,772**	**10**	**4,362**	**0.95**	**1.11**

Outbreak reporting rate for 2015 and mean value for the five previous years (2010–2014) is also provided in this table.



N. of Member States with data on food-borne outbreaks reported, by year, are in brackets.

Figure 71: Number of food-borne and waterborne outbreaks reported in the EU Member States, from 2010 to 2015

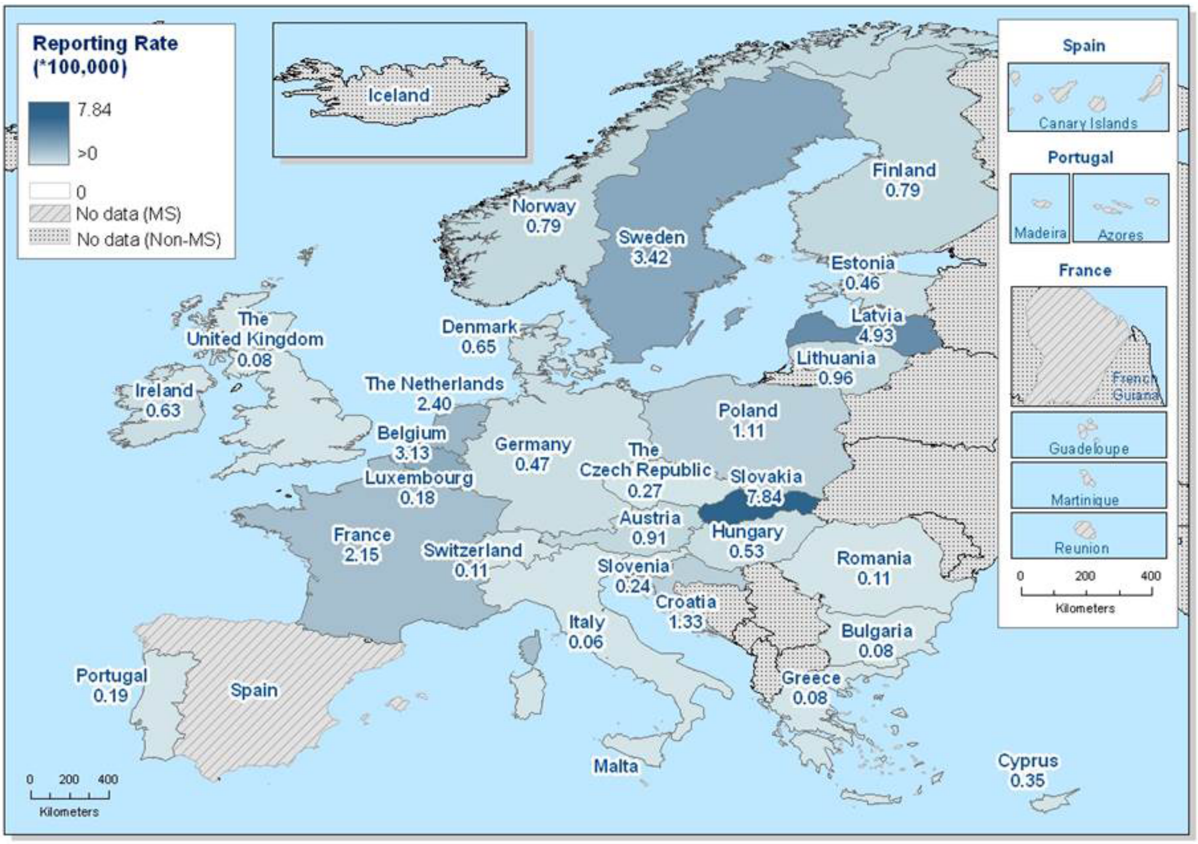


Figure 72: Distribution of reporting rate of food-borne and waterborne outbreaks per 100,000 population, in the EU Member States and non-Member States, 2015

In the MS, food-borne outbreaks involving cases from a single household numbered 887 (20.3% of total outbreaks) in 2015, while those with cases from multiple households or residential institutions were 1,586 (36.4% of total outbreaks). For 1,889 outbreaks (43.3% of total outbreaks), this information was not available.

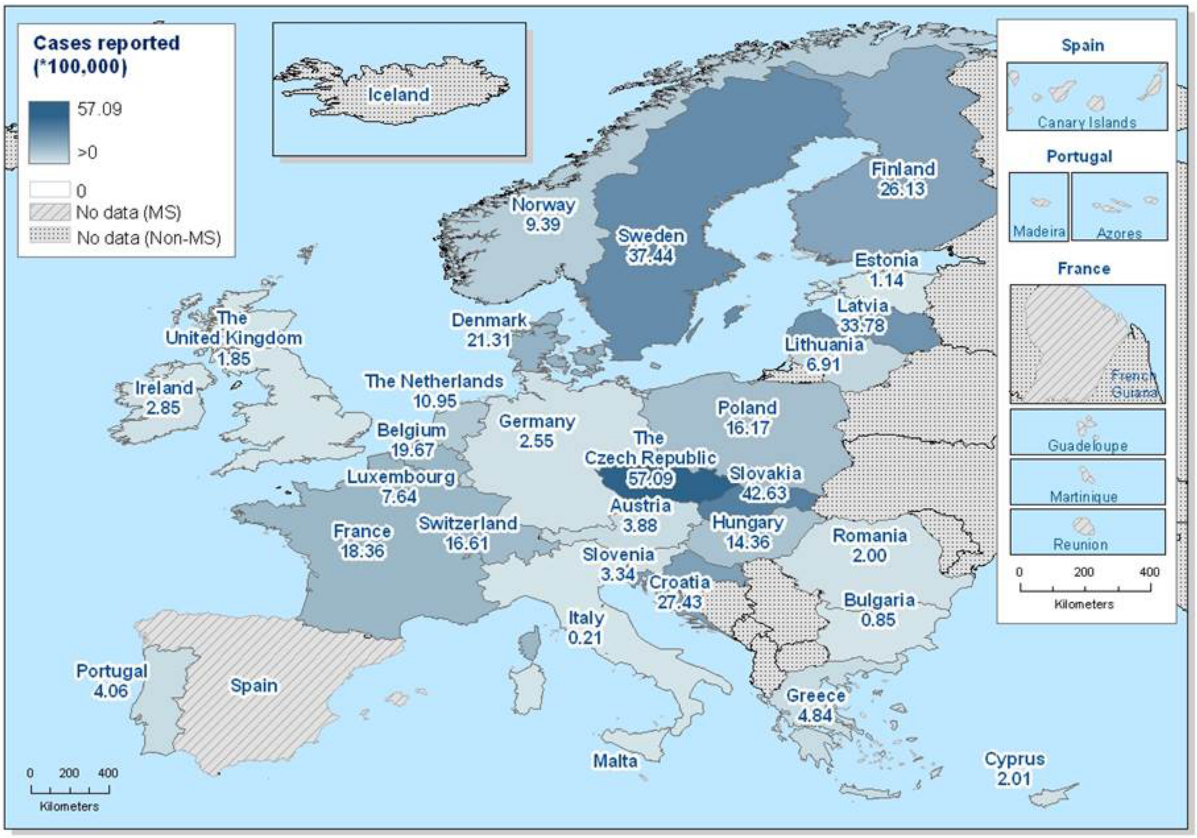


Figure 73: Distribution of human cases involved in food-borne and waterborne outbreaks per 100,000 population, in the EU Member States and non-Member States, 2015

Causative agents

Within the EU, the causative agent was known for 66.5% of all reported outbreaks (Table 33). In contrast it was unknown in 3.3% of strong-evidence outbreaks and in 36.8% of weak-evidence outbreaks. Details on food-borne outbreaks reported, including waterborne outbreaks, by causative agents are shown in Table 33.

Most of the outbreaks reported in 2015 were caused by bacterial agents (33.7% of all outbreaks), in particular *Salmonella* (21.8% of all outbreaks) and *Campylobacter* (8.9% of all outbreaks), even though the reporting of outbreaks by both these agents has declined over recent years. Bacterial toxins ranked second among the causative agents in food- and waterborne outbreaks and were reported in 19.5% of the total outbreaks, while viruses, which were the agents most frequently reported in 2014, accounted for just the 9.2% of total outbreaks in 2015. Parasites and other causative agents, in particular histamine, were reported in less than 3% of the outbreaks. As for bacterial toxins, and other causative agents it should be highlighted that the vast majority of the outbreaks (87.2% and 81.1%, respectively) were reported from a single MS. These findings clearly show how the estimates are to be interpreted with caution as they cannot be considered representative of the whole EU. For a third of the reported outbreaks (33.5%), the causative agent remained unknown.

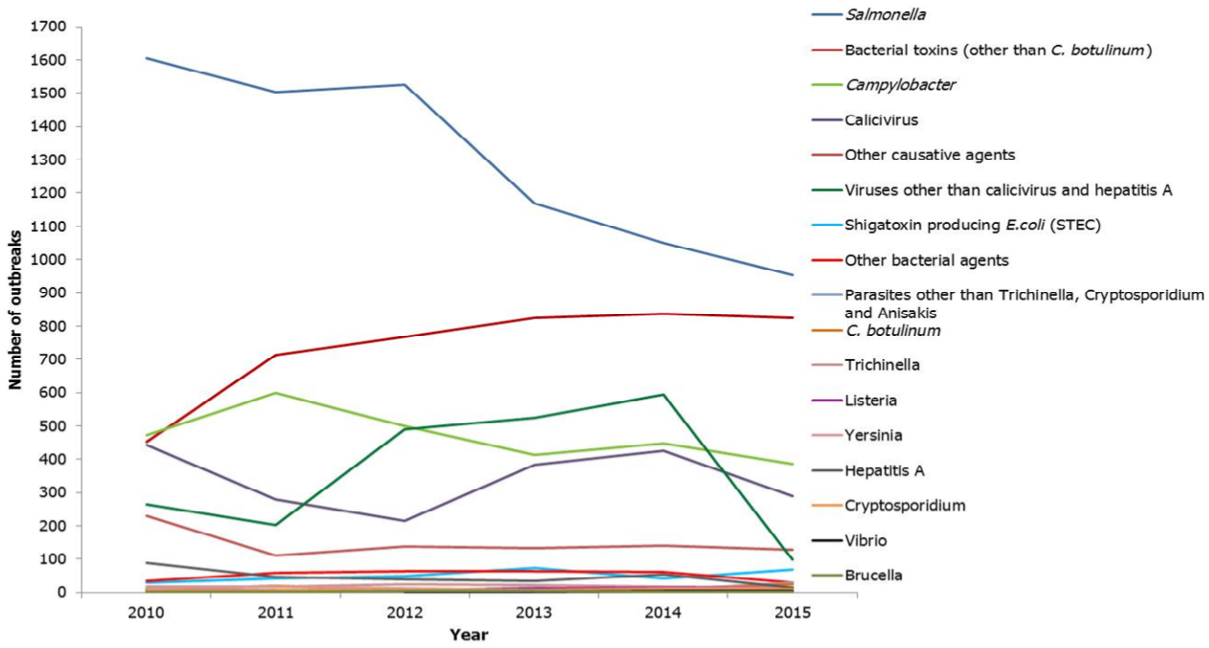
In 2015, reporting rates of food-borne outbreaks caused by *Salmonella* and bacterial toxins (other than those produced by *C. botulinum*) were, by far, the highest in the EU, with 0.21 and 0.18 outbreaks per 100,000 population, respectively. Outbreaks by *Campylobacter* and calicivirus including Norwalk-like virus (norovirus) were reported at similar rates, 0.08 and 0.06 per 100,000 population, respectively. For all the other causative agents, the reporting rates did not exceed a rate of 0.03 outbreaks per 100,000 (Table 33).

Figure 74 shows the temporal trend in the number of food-borne outbreaks reported by the MS and non-MS in the EU in the period 2010 to 2015, by causative agent. Although *Salmonella* continues to represent the most frequently reported causative agent in food-borne outbreaks, a marked progressive decreasing trend over time can be observed, with a 40.6% reduction in the number of outbreaks reported in 2015 (N = 953) compared with 2010 (N = 1,604). In the same period, outbreaks caused by bacterial toxins (other than *C. botulinum*) were increasingly reported. In 2015 (N = 825) they were almost twice those reported in 2010 (N = 453). This finding, however, should be interpreted with caution at the EU level, taking into account that most of the outbreaks by bacterial toxins (other than *C. botulinum*) were reported, from a single MS (France).

No clear trends could be observed in the occurrence of outbreaks caused by pathogens less frequently reported in food-borne outbreaks, except for *Listeria* which increased consistently from 2010 (N = 5) to 2014 (N = 15) and 2015 (N = 14).

Outbreaks caused by *Salmonella* and bacterial toxins (other than *C. botulinum)* presented the biggest health impact in the EU MS and non-MS, in terms of total number of hospitalisations and deaths. Calicivirus including Norwalk-like virus (norovirus) caused the highest number of cases with 13,536 cases (29.5% of all cases of illness caused by outbreaks). This pathogen was also the causative agent associated with the largest outbreaks in terms of overall human cases involved and the highest mean number of cases per outbreak (Table 33). In Switzerland, 1,194 cases were reported in a single outbreak. In the Czech Republic, three outbreaks of norovirus caused a total of 5,344 cases of illness. Next to calicivirus including Norwalk-like virus (norovirus), outbreaks by bacterial toxins (other than *C. botulinum)* and by *Salmonella* resulted in the highest number of cases (19.2% and 14.4% of all cases, respectively).

In 2015, outbreaks caused by *C. botulinum* and hepatitis A had the highest proportion of cases hospitalised (71.7% and 62.8%, respectively), and those caused by *Listeria* and Hepatitis A resulted in the highest proportion of fatal cases (1.7% and 1.3%, respectively).



Outbreaks by unknown causative agents are not included. Other bacterial agents include *Francisella*, *Shigella*, pathogenic *E. coli* other than Shiga toxin-producing *E. coli*, and other unspecified bacteria. Other bacterial toxins include toxins produced by *Bacillus*, *Clostridium* other than *Clostridium botulinum* and *Staphylococcus* and other unspecified bacterial toxins. Other viruses include adenovirus, flavivirus, rotavirus and other unspecified viruses. Other causative agents include chemical agents, histamine, marine biotoxins, mushroom toxins and scrombotoxin. Other parasites include *Giardia* and other unspecified parasites. Outbreaks caused by *Anisakis* were not reported in 2015.

Figure 74: Number of food-borne and waterborne outbreaks reported by causative agent in the EU Member States from 2010 to 2015

Table 33: Number of food-borne outbreaks (including waterborne outbreaks), human cases, hospitalisations and deaths per causative agent in the EU Member States (including waterborne outbreaks), 2015

Type of agent		Outbreaks				Cases					
		Strong-evidence outbreaks	Weak-evidence outbreaks	Total outbreaks	Reporting rate per 100,000	Human cases	Mean number per outbreak	Hospitalised		Deaths	
		N	N	N	N	N		% of cases	N	% of cases	
Bacteria	*Salmonella*	184	769	953	0.21	6,616	6.9	1,719	26.0	3	0.0
	Campylobacter	25	362	387	0.08	1,440	3.7	129	9.0	1	0.1
	Shiga toxin-producing *E. coli* (STEC)	6	63	69	0.01	674	9.8	62	9.2	0	0.0
	Listeria	5	9	14	< 0.01	230	16.4	25	10.9	4	1.7
	Yersinia	1	12	13	< 0.01	54	4.2	9	16.7	0	0.0
	Vibrio	0	4	4	< 0.01	29	7.3	0	0.0	0	0.0
	Brucella	0	1	1	< 0.01	2	2.0	1	50.0	0	0.0
	Other bacterial agents	3	26	29	0.01	337	11.6	23	6.8	0	0.0
	Subtotal	**224**	**1,246**	**1,470**	**0.32**	**9,382**	**6.4**	**1,968**	**21.0**	**8**	**0.1**
Bacterial toxins	*C. botulinum*	15	9	24	0.01	60	2.5	43	71.7	0	0.0
	Other bacterial toxins	87	738	825	0.18	8,787	10.7	454	5.2	3	0.1
	Subtotal	**102**	**747**	**849**	**0.18**	**8,847**	**10.4**	**497**	**5.6**	**3**	**0.1**
Viruses	Calicivirus including norovirus (Norwalk-like virus)	38	251	289	0.06	13,536	46.8	352	2.6	1	0.0
	Hepatitis A	2	11	13	< 0.01	78	6.0	49	62.8	1	1.3
	Other viruses/unspecified	5	94	99	0.02	1,140	11.5	130	11.4	3	0.3
	Subtotal	**45**	**356**	**401**	**0.09**	**14,754**	**36.8**	**531**	**3.6**	**5**	**0.0**
Parasites	*Cryptosporidium*	0	9	9	< 0.01	120	13.3	3	2.5	0	0.0
	Trichinella	12	3	15	< 0.01	119	7.9	34	28.6	0	0.0
	Other parasites/unspecified	0	28	28	0.01	63	2.3	7	11.1	0	0.0
	Subtotal	**12**	**40**	**52**	**0.01**	**302**	**5.8**	**44**	**14.6**	**0**	**0.0**

Type of agent		Outbreaks				Cases					
		Strong-evidence outbreaks	Weak-evidence outbreaks	Total outbreaks	Reporting rate per 100,000	Human cases	Mean number per outbreak	Hospitalised		Deaths	
		N	N	N	N	N		% of cases	N	% of cases	
Other causative agents	Other causative agents	25	102	127	0.05	648	5.1	64	9.9	0	0.0
	Subtotal	**25**	**102**	**127**	**0.05**	**648**	**5.1**	**64**	**9.9**	**0**	**0.0**
Unknown	Unknown	14	1,449	1,463	0.32	11,941	8.2	788	6.6	1	0.0
	Subtotal	**14**	**1,449**	**1,463**	**0.32**	**11,941**	**8.2**	**788**	**6.6**	**1**	**0.0**
EU Total		**422**	**3,940**	**4,362**	**0.95**	**45,874**	**10.5**	**3,892**	**89.2**	**17**	**0.1**

Other bacterial agents include *Francisella*, *Shigella*, pathogenic *E. coli* other than Shiga toxin-producing *E. coli*, and other unspecified bacteria. Other bacterial toxins include toxins produced by *Bacillus*, *Clostridium* other than *Clostridium botulinum* and *Staphylococcus* and other unspecified bacterial toxins. Other viruses include adenovirus, flavivirus, rotavirus and other unspecified viruses. Other causative agents include chemical agents, histamine, marine biotoxins, mushroom toxins, and scrombotoxin. Other parasites include *Giardia* and other unspecified parasites.

3.16.2. Overview by food vehicle and place of exposure in the EU, 2015

This section aims at better describing the causative agents associated with the different food vehicles and settings and the connected health burden, in order to provide information to characterise the risk profiling of food vehicles and settings associated with outbreaks. Indeed, although surveillance of food-borne diseases in public health and monitoring of causative agents along the food chain is carried out by type of agent, according to Directive 2003/99/EC, hygienic measures and food-borne hazard control policies are targeted to the different points of the food production/preparation, rather than to single causative agents and should be based on the evaluation of the risks arising from multiple hazards. Consumers may also be interested in acquiring knowledge of the most frequent risks connected with the different places of exposure (either in household settings or elsewhere) and type of foodstuffs.

Food vehicle

In 2015, information on food vehicles associated with strong-evidence food-borne outbreaks (including waterborne outbreaks) reported by the MS was available for all 422 strong-evidence outbreaks (Table 34), even though for 51 of these the food vehicle was reported to be ‘unknown’ (N = 6) or ‘other foods’ (N = 45).

Reported strong-evidence outbreaks were predominantly associated with food of animal origin (61.4% of all strong-evidence outbreaks); in particular meat from various animal species and products thereof (28.9%), milk, cheese and dairy products (13.0%), ‘eggs and egg products’ (10.0%), and fish, shellfish, molluscs, crustaceans and products thereof (9.5%). Both eggs and egg products and ‘pig meat and products thereof’ were the single food items most frequently reported in strong-evidence food-borne outbreaks (N = 42). Foods of non-animal origin accounted for 6.6% of all strong-evidence outbreaks, and included vegetables, fruits, cereals, sprouts, herbs and spices and products thereof (4.5%), drinks and water (2.1%). Mixed food and buffet meals, as well as other foods including unspecified foods were reported in almost a third of all strong-evidence outbreaks (13.0% and 17.5%, respectively). It is important to note that no detailed information was provided on the food vehicles (reported as ‘other foods’) that were associated with the highest number of cases reported in strong-evidence outbreaks (N = 1,275). Compared with previous years, no significant trends for any of the food items implicated in strong-evidence food-borne outbreaks were observed, except for ‘eggs and egg products’.

Information on factors suspected to have contributed to the occurrence of the outbreaks was reported in almost half of the strong-evidence outbreaks (N = 199). Contamination of the implicated food vehicle by the use of unprocessed contaminated ingredients, and by cross-contamination was reported in 84 (42.2% of the outbreaks with information available) and 20 outbreaks (10.1%), respectively. For 65 outbreaks (32.7%), storage/time temperature abuse as well as inadequate heat treatment or chilling were reported. Manipulation of the implicated food vehicle by an infected food handler was reported in 36 outbreaks (18.1%). Moreover, in three outbreaks (1.5%), failure in the treatment of water or use of untreated water was reported. Contributory factors categorised as ‘other’ with no further detail were reported for nine outbreaks (4.5%).

Information on the suspected food vehicle was also provided for 1,799 weak-evidence outbreaks reported by the EU MS. The reporting of this information, however, is not mandatory and the possibility for the reporting countries to also provide such details for weak-evidence outbreaks has only been available since 2014. Vehicles most frequently suspected to be implicated in these outbreaks were reported as ‘other foods’ (no additional detailed information provided) and ‘mixed food’ (N = 652 and N = 374, respectively), followed by meat from various animal species and products thereof (N = 328), ‘fish, shellfish, molluscs, crustaceans and products thereof’ (N = 179), vegetables, fruits, cereals, sprouts, herbs and spices and products thereof (N = 75), eggs and egg products (N = 70), milk cheese and dairy (N = 40).

Table 34: Frequency distribution of strong-evidence food-borne and waterborne outbreaks, by implicated food vehicle, reported by the EU Member States, 2015

Type of vehicle		**Strong-evidence outbreaks**				**Reporting Rate per 100,000**	
		N of outbreaks	**% of total outbreaks**	**N of cases**	**% of total cases**	**2015**	**2010–2014 (mean)**
Meat and product thereof	Pig meat and products thereof	42	10.0	623	6.3	0.009	0.009
	Broiler meat and products thereof	37	8.8	596	6.1	0.008	0.009
	Bovine meat and products thereof	18	4.3	205	2.1	0.004	0.004
	Meat and meat products	12	2.8	139	1.4	0.003	0.003
	Sheep meat and products thereof	1	0.2	10	0.1	< 0.001	< 0.001
	Turkey meat and products thereof	3	0.7	215	2.2	0.001	0.001
	Other or mixed red meat and products thereof	9	2.1	187	1.9	0.002	0.004
	Subtotal	**122**	**28.9**	**1,975**	**20.1**	**0.026**	**0.030**
Mixed food and buffet meals	Mixed food	47	11.1	978	9.9	0.010	0.019
	Buffet meals	8	1.9	888	9.0	0.002	0.005
	Subtotal	**55**	**13.0**	**1,866**	**19.0**	**0.012**	**0.024**
Milk cheese and dairy	Cheese	33	7.8	380	3.9	0.007	0.003
	Dairy products (other than cheeses)	1	0.2	8	0.1	< 0.001	0.001
	Milk	21	5.0	229	2.3	0.005	0.002
	Subtotal	**55**	**13.0**	**617**	**6.3**	**0.012**	**0.006**
Eggs and egg products	Eggs and egg products	42	10.0	370	3.8	0.009	0.030
	Subtotal	**42**	**10.0**	**370**	**3.8**	**0.009**	**0.030**
Fish, shellfish, molluscs and crustaceans and products thereof	Crustaceans, shellfish, molluscs and products thereof	11	2.6	207	2.1	0.002	0.010
	Fish and fishery products	29	6.9	367	3.7	0.006	0.012
	Subtotal	**40**	**9.5**	**574**	**5.8**	**0.009**	**0.022**
Vegetables, fruits, cereals, sprouts, herbs and spices and products thereof	Vegetables and juices and other products thereof	12	2.8	299	3.0	0.003	0.009
	Cereal products including rice and seeds/pulses (nuts, almonds)	4	0.9	99	1.0	0.001	0.002
	Fruit, berries and juices and other products thereof	2	0.5	138	1.4	< 0.001	0.002
	Herbs and spices	1	0.2	184	1.9	< 0.001	< 0.001
	Subtotal	**19**	**4.5**	**720**	**7.3**	**0.004**	**0.013**
Drinks, water	Tap water, including well water	8	1.9	1,798	18.3	0.002	0.002
	Drinks, including bottled water	1	0.2	3	0.0	< 0.001	< 0.001
	Subtotal	**9**	**2.1**	**1,801**	**18.3**	**0.002**	**0.003**
Other foods	Bakery products	23	5.5	356	3.6	0.005	0.006
	Sweets and chocolate	3	0.7	36	0.4	0.001	0.003
	Canned food products	3	0.7	6	0.1	0.001	< 0.001
	Other foods	45	10.7	1,275	13.0	0.010	0.009
	Subtotal	74	17.5	1,673	17.0	0.016	0.019
Unknown	Unknown	6	1.4	241	2.4	0.001	–
	Subtotal	**6**	**1.4**	**241**	**2.4**	**0.001**	–
EU Total		**422**	**100**	**9,837**	**100**	**0.091**	**0.151**

Outbreak reporting rate for 2015 and for the five previous years (2010–2014) is also provided in this table.

Top-5 combinations of causative agents and food vehicles associated with the highest health burden in strong-evidence food-borne outbreaks (including waterborne outbreaks)

This newly introduced section aims to provide a concise insight into the combinations of the causative agents and the food vehicles that in 2015 were associated with the highest health burden in the EU, in terms of total outbreaks reported (Table 35), overall numbers of human cases involved (Table 36), hospitalisations (Table 37), and deaths (Table 38). The five causative agent/food combinations with the highest impact are progressively ranked in each table according to their frequency. Rank position occupied by the same combination in the five previous years, is also reported to provide rapid information on its trend of occurrence, over time. Rank for the period 2010–2014 was estimated based on the mean annual number of strong-evidence outbreaks, human cases, hospitalisation and deaths reported by the MS in this period for the given combination.

As in previous years, *Salmonella* in eggs continues to represent the most high-risk agent/food combination being represented among the top-5 combinations for number of outbreaks, cases involved and hospitalisations. Similar to the previous 5 years, this combination ranked first in 2015 for the number of strong-evidence outbreaks. Two other combinations among the top-5 pairs causing the highest number of outbreaks, also involved *Salmonella* (in pig meat and products thereof, and bakery products), both of which were reported with an increased frequency in 2015 compared with previous years. In 2015, bacterial toxins other than *C. botulinum* (mainly caused by *C. perfringens* and *B. cerus* followed by staphylococcal enterotoxins) in 'other foods' was third most common combination of strong-evidence outbreaks, while in the period 2010–2014 this combination was the 14th. No further details on the implicated food vehicles were available. Histamine was the causative agent involved in quite all the strong-evidence outbreaks (20 out of 21) caused by 'other causative agents' in fish and fishery products. Although very frequently reported, the trend in occurrence of outbreaks involving this combination was slightly decreased compared with previous years.

Calicivirus, including norovirus, was the causative agent associated with the largest outbreaks in terms of number of human cases involved, despite the low number of implicated outbreaks. This agent was involved in three of the five top-combinations causing the highest number of human cases in strong-evidence outbreaks, in combination with tap water, buffet meals and other foods (no other details available). Outbreaks by bacterial toxins other than *C. botulinum* (mainly *B. cereus* and staphylococcal enterotoxins) in mixed food ranked third in 2015 for the number of human cases involved, although the outbreak reporting rate for this combination more than halved in 2015 compared with previous years.

In 2015, the top-5 combinations associated with the highest number of hospitalisations always included *Salmonella* as causative agent, in combination with buffet meal, eggs and eggs products, bakery products, mixed foods and other foods.

Agent/food combinations implicated in strong-evidence outbreaks causing the highest number of deaths in 2015, included a wide variety of causative agents and food vehicles. It is worth mentioning that none of these combinations were reported to be associated with any deaths in the 2010–2014 period. In 2015, two deaths were reported among cases involved in strong-evidence outbreaks caused by *Listeria* in pig meat and products thereof, viruses other than calicivirus and hepatitis A virus in milk and bacterial toxins (other than *C. botulinum*) in broiler meat and products thereof, respectively. In Italy, a severe general outbreak of listeriosis associated with the consumption of 'pig meat and products thereof' caused two deaths among the 12 patients involved. One case of death in two different household outbreaks caused by flavivirus (in one case it was specified as tick-borne encephalitis virus) in raw goat milk was reported by Slovakia and Lithuania. In both circumstances, inadequate heat treatment of milk was reported as the critical contributory factor. In France, two patients died in an outbreak caused by *C. perfringens* toxins associated with broiler meat that involved 38 people in a residential institution. One death connected with a strong-evidence outbreak caused by calicivirus in broiler meat and products thereof that involved nine patients in a residential institution was reported by Croatia.

Table 35: Top-5 combinations (agent/food vehicle) causing the highest number of strong-evidence outbreaks, reported by the EU Member States, 2015

Causative agent	Food vehicle	2015						2010–2014		
		Rank	Number of outbreaks	Cases			Reporting rate per 100,000	Rank	N of outbreaks (mean)	Reporting rate per 100,000 (mean)
				N	Hospitalised	Deaths				
Salmonella	Eggs and egg products	1	39	319	92	0	0.008	1	139.2	0.029
Salmonella	Pig meat and products thereof	2	24	290	30	0	0.005	10	20.0	0.004
Bacterial toxins other than *C. botulinum*	Other foods	3	22	619	13	0	0.005	7	14.8	0.003
Other causative agents	Fish and fishery products	4	21	172	11	0	0.005	3	42.0	0.009
Salmonella	Bakery products	5	21	306	87	0	0.005	6	22.6	0.005

Other causative agents include chemical agents, histamine, marine biotoxins, mushroom toxins, and scrombotoxin.
Bacterial toxins other than *C. botulinum* include toxins produced by *Bacillus*, *Clostridium* other than *C. botulinum* and *Staphylococcus* and other unspecified bacterial toxins.
The category 'other foods' includes unspecified foods reported as 'other foods'.
The rank for the period 2010–2014 has been calculated based on the mean annual number of strong-evidence outbreaks reported during 2010–2014 as associated with the top-5 combinations included in this table.

Table 36: Top-5 combinations (agent/food vehicle) causing the highest number of cases in strong-evidence outbreaks, reported by the EU Member States, 2015

Causative agent	Food vehicle	2015						2010–2014		
		Rank	Number of outbreaks	Cases			Reporting rate per 100,000	Rank	N of outbreaks (mean)	Reporting rate per 100,000 (mean)
				N	Hospitalised	Deaths				
Calicivirus	Tap water, including well water	1	2	780	3	0	< 0.001	5	1,822.4	0.001
Calicivirus	Buffet meals	2	3	624	0	0	0.001	10	529.8	0.002
Bacterial toxins other than *C. botulinum*	Mixed food	3	16	619	63	0	0.003	6	1,540.4	0.008
Calicivirus	Other foods	4	5	417	4	0	0.001	32	299.2	0.001
Salmonella	Eggs and egg products	5	39	319	92	0	0.008	3	2,978.2	0.029

Bacterial toxins other than *C. botulinum* include toxins produced by *Bacillus*, *Clostridium* other than *C. botulinum* and *Staphylococcus* and other unspecified bacterial toxins.
The category 'other foods' includes unspecified foods reported as 'other foods'.
The rank for the period 2010–2014 has been calculated based on the mean annual number of cases reported during 2010–1014 as associated with the top-5 combinations included in this table.

Table 37: Top-5 combinations (agent/food vehicle) causing the highest number of hospitalised cases in strong-evidence outbreaks, reported by the EU Member States, 2015

Causative agent	Food vehicle	2015						2010–2014		
		Rank	Number of outbreaks	Cases			Reporting rate per 100,000	Rank	N of outbreaks (mean)	Reporting rate per 100,000 (mean)
				N	Hospitalised	Deaths				
Salmonella	Buffet meals	1	3	210	179	0	0.001	9	54.8	0.001
Salmonella	Eggs and egg products	2	39	319	92	0	0.008	1	349	0.029
Salmonella	Bakery products	3	21	306	87	0	0.005	4	63.6	0.005
Salmonella	Mixed food	4	20	149	79	0	0.004	5	94.2	0.008
Salmonella	Other foods	5	11	155	70	0	0.002	7	45.8	0.003

The category ‘other foods’ includes unspecified foods reported as ‘other foods’.
The rank for the period 2010–2014 has been calculated based on the mean annual number of hospitalised cases reported during 2010–1014 as associated with the top-5 combinations included in this table.

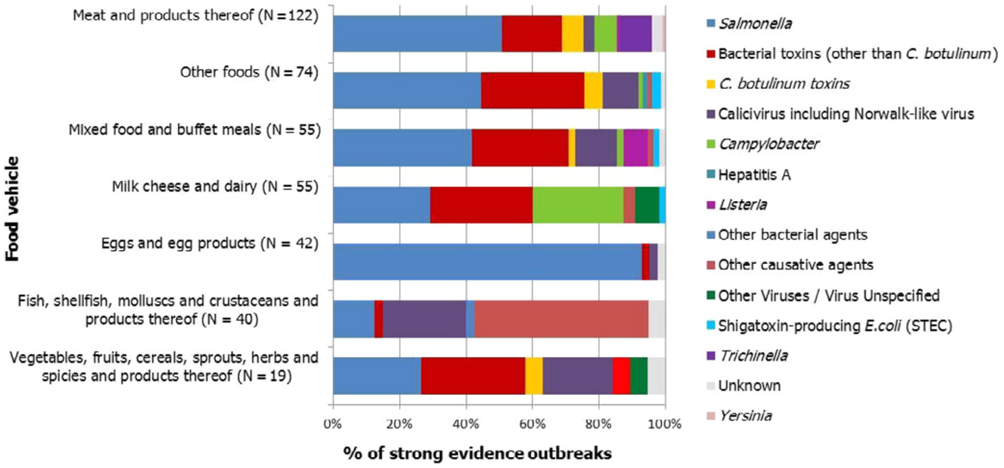
Table 38: Top combinations (agent/food vehicle) causing the highest number of deaths in strong-evidence outbreaks, reported by the EU Member States, 2015

Causative agent	Food vehicle	2015						2010–2014		
		Rank	Number of outbreaks	Cases			Reporting rate per 100,000	Rank	N of outbreaks (mean)	Reporting rate per 100,000 (mean)
				N	Hospitalised	Deaths				
Listeria	Pig meat and products thereof	1	1	12	12	2	< 0.001	–	–	–
Viruses other than calicivirus and hepatitis A	Milk	2	4	14	13	2	0.001	–	–	–
Bacterial toxins other than *C. botulinum*	Broiler meat and products thereof	3	8	248	6	2	0.002	–	–	–
Calicivirus	Broiler meat and products thereof	4	2	57	2	1	< 0.001	–	–	–

‘Bacterial toxins other than *C. botulinum*’ include toxins produced by *Bacillus*, *Clostridium* other than *Clostridium botulinum* and *Staphylococcus* and other unspecified bacterial toxins.
The category ‘other foods’ includes unspecified foods reported as ‘other foods’. No deaths were reported during the period 2010–2014 for the top-5 combinations therefore the rank for this period was not calculated.

Causative agent of food-borne outbreaks by food vehicle

The distribution of causative agents by type of food is shown in Figure 75. The pattern was roughly similar for 'meat and products thereof' (n = 122), 'mixed food and buffet meals' (N = 55), 'milk, cheese and dairy products' (N = 55), and 'other foods' (N = 74), with bacterial agents accounting for most of the outbreaks. *Salmonella* ranked first among bacteria, and bacterial toxins, viruses and others causative agents were reported in lower proportions. Outbreaks caused by parasites (i.e. *Trichinella*) were only associated with meat and products thereof. A non-negligible proportion of outbreaks associated with the consumption of 'milk, cheese and dairy products' was caused by *Campylobacter* (27.3%), which was reported in this food category at a higher frequency than in any other. In 'fish, shellfish, molluscs, crustaceans and products thereof', histamine was the leading cause of strong-evidence outbreaks (52.5%) followed by calicivirus including Norwalk-like virus (norovirus) (25.0%) and *Salmonella* (12.5%). In the egg-associated outbreaks *Salmonella* predominated (92.9%). In 'vegetables, fruits, cereals, sprouts, herbs and spices', bacterial toxins (other than *C. botulinum*) (31.6%) ranked first, compared with *Salmonella* (26.3%) and calicivirus including Norwalk-like virus (norovirus) (21.1%), respectively.



A single strong-evidence outbreak by bacterial toxins other than *C. botulinum* in drinks and water and six strong-evidence outbreaks with food vehicle 'unknown' are not shown in the figure. 'Other bacterial agents' include *Francisella*, *Shigella*, pathogenic *E. coli* other than Shiga toxin-producing *E. coli*, and other unspecified bacteria. 'Other bacterial toxins' include toxins produced by *Bacillus*, *Clostridium* other than *C. botulinum*, staphylococcal toxins and other unspecified bacterial toxins. 'Other viruses' include adenovirus, flavivirus, rotavirus and other unspecified viruses. 'Other causative' agents include chemical agents, histamine, marine biotoxins, mushroom toxins, and scrombotoxin. Other parasites include *Giardia* and other unspecified parasites.

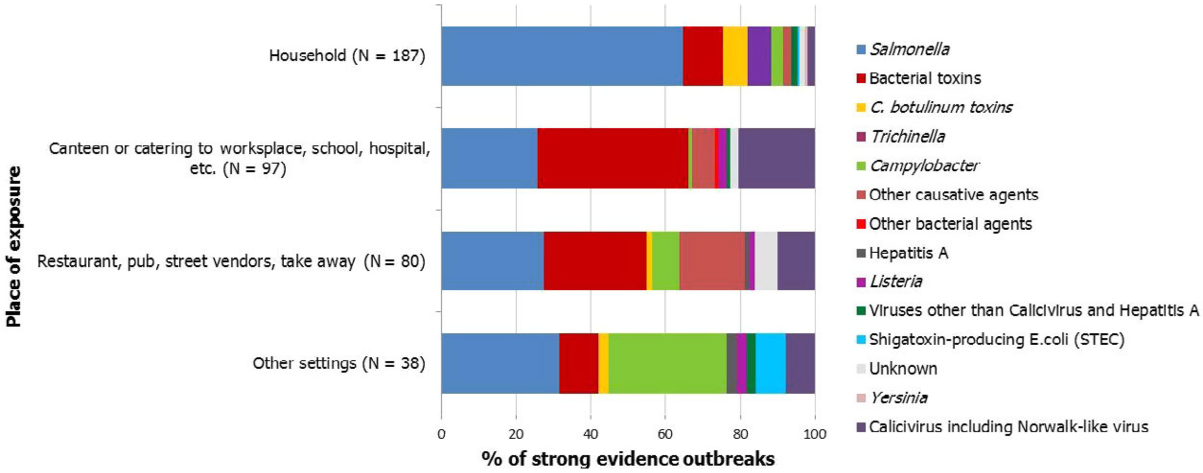
Figure 75: Frequency distribution of causative agents associated with strong-evidence food-borne and waterborne outbreaks by implicated food vehicle reported in the EU Member States, 2015

Place of exposure

Information on the place of exposure was provided in 2015 for 409 strong-evidence outbreaks. Household was by far the most frequent place of exposure of cases to the implicated food vehicle, followed by canteens and other settings where food was prepared and/or served by catering services. Restaurants, pubs, street vendors and take-away establishments were reported with a frequency similar to canteen and other catering services. Other settings such as farms, fairs and festivals, and other undefined places were reported less frequently. No significant trends over years in the reporting rates of outbreaks associated with these settings was observed, even though a slight decrease was reported for households and restaurants, pubs, street vendors and take-away establishments, in 2015.

Causative agent of food-borne outbreaks by place of exposure

Analysis of causative agents and food vehicles associated with strong-evidence food-borne outbreaks by the place of exposure to the implicated foodstuffs (Figure 76) indicate important differences. *Salmonella* was strongly associated with households. Compared with the other places of exposure, the outbreak reporting rate for household outbreaks caused by *Salmonella* was more than four-times higher. In contrast, outbreaks caused by bacterial toxins (other than *C. botulinum*) and calicivirus including Norwalk-like virus (norovirus) were much more frequently reported in settings served by catering services and in restaurants, pubs etc. than in households. Outbreaks caused by *C. botulinum* toxins and *Trichinella*, which surprisingly ranked third and fifth among food-borne agents in household settings in 2015, were also associated with food consumed at home. Among outbreaks associated with other places of exposure, it is important to highlight that *Campylobacter* outbreaks, which ranked second in this group, were mostly linked to 'farm' as place of exposure.



Other setting include: 'camp or picnic', farm, multiple places of exposure in more than one country, multiple places of exposure in one country, temporary mass catering (fairs or festivals), other unspecified settings. Strong-evidence food-borne outbreaks (N=12) with no information on the place of exposure or with place of exposure categorised as 'Unknown' are not shown.

Figure 76: Frequency distribution of strong-evidence food-borne and waterborne outbreaks reported in the EU Member States in the different places of exposure, by causative agent, 2015

Food vehicle in strong-evidence food-borne outbreaks by place of exposure

The distribution of food vehicles implicated in strong-evidence food-borne outbreaks by place of exposure also reflects important differences between outbreaks linked to households and those associated with other settings. While 'meat and products thereof' were the food vehicles most frequently reported in all the settings except restaurant, 'eggs and egg products' were predominantly associated with households. 'Fish, shellfish, molluscs and crustaceans' were mainly associated with restaurant, pubs, street vendors etc. where they were found to cause one in every four strong-evidence outbreaks reported in these places of exposure.

3.16.3. Overview by causative agents in the EU, 2015

Agent-specific information on the reported food-borne outbreaks can be found in this section. The figures of outbreaks presented here do not include waterborne outbreaks, which are addressed separately in Section 3.16.4.

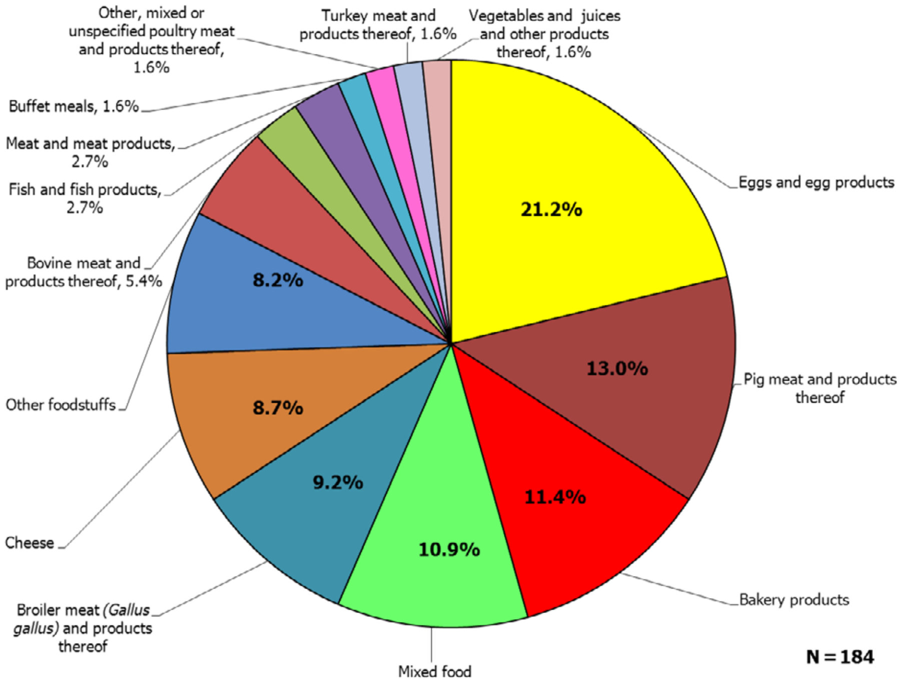
3.16.3.1. Bacteria

Salmonella

In 2015, 23 MS reported a total of 953 food-borne outbreaks caused by *Salmonella* (Table 2015_FBOSALM), representing 21.8% of all outbreaks. The total number of *Salmonella* outbreaks within the EU decreased by 40.6% between 2010 (1,604 food-borne outbreaks) and 2015 (953 outbreaks). In 2015, the reporting rate for the *Salmonella* outbreaks in the EU was 0.21 per 100,000 population. Overall, the outbreaks involved 6,616 cases, 1,719 hospitalisations and 3 deaths. As in 2014, Slovakia reported the highest number of outbreaks (N = 232) followed by France and Poland (198 and 180 outbreaks, respectively). In total, 18 MS reported 184 *Salmonella* outbreaks with strong evidence (19.3%). France, Poland and Lithuania together reported 71.7% of the strong-evidence outbreaks. Only one outbreak was reported by a non-MS (Norway).

In total, three fatal *Salmonella* cases were reported for three different *Salmonella* outbreaks, all reported as weak-evidence outbreaks. Two outbreaks were due to *S*. Enteritidis and one was reported as due to 'unspecified' *Salmonella*.

'Eggs and egg products' were the most frequently identified food vehicles, associated with 21.2% (N = 39) of the reported strong-evidence *Salmonella* outbreaks. However, the number of strong-evidence outbreaks associated with this food vehicle decreased by 60.6% if compared with 2014 data (N = 99, 44%). Poland, Slovakia and France, together reported 82.3% of these outbreaks. 'Pig meat and products thereof' accounted for 13% of the outbreaks (9.3% in 2014) and 'bakery products' for 11.4% of the outbreaks (12.9% in 2014). Figure 77 shows the distribution of the most common food vehicles implicated in the strong-evidence *Salmonella* outbreaks in 2015. Also in weak-evidence outbreaks, 'eggs and egg products', were the most common food vehicles, accounting for 31.2% of the 112 weak-evidence outbreaks for which information on food vehicle was provided. No further details were available on food vehicles associated with most of the weak-evidence *Salmonella* outbreaks, which were reported as either 'unknown' or 'other foods'.



Data from 184 outbreaks are included: Austria (2), Belgium (2), Croatia (15), Finland (1), France (57), Germany (3), Greece (1), Hungary (2), Italy (1) Latvia (4), Lithuania (21), the Netherlands (2), Poland (54), Portugal (1), Romania (6), Slovakia (9), Sweden (1) and the United Kingdom (2). Other foodstuffs (n = 15) include: cereal products including rice and seeds/pulses (nuts, almonds) (1), herbs and spices (1), sweets and chocolate (1) unknown (1) and other foods (11).

Figure 77: Distribution food vehicles in strong-evidence outbreaks caused by *Salmonella* (excluding waterborne outbreaks) in the EU, 2015

The most frequent reported place of exposure to foods implicated in *Salmonella* strong-evidence outbreaks was 'household' (121 outbreaks), followed by 'restaurant, cafè, pub, bar, hotel' (21 outbreaks), 'school and kindergarten' (9 outbreaks) and 'catering on aircraft or ship' (8 outbreaks). In nine strong-evidence outbreaks, information on the place of exposure was either not provided (1) or reported as 'unknown' (3) or 'others' (5).

Unprocessed contaminated ingredients (43 outbreaks) represented the most frequently reported factor implicated in the strong-evidence *Salmonella* outbreaks, followed by inadequate heat treatment

(13 outbreaks). In 115 strong-evidence outbreaks, information on the contributory factors was either not provided (86) or reported as ‘unknown’ (28) or ‘other contributory factor’ (1).

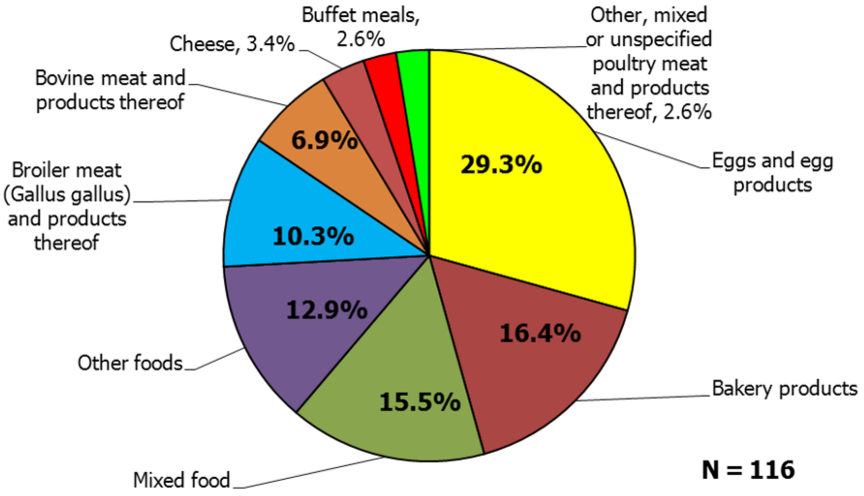
In 2015, *S.* Enteritidis was implicated in 63.0% of the *Salmonella* strong-evidence outbreaks (116 outbreaks), which is a decrease of 18.3%, compared with 2014. As in previous years, ‘eggs and egg products’ were the food vehicles most frequently associated with *S.* Enteritidis outbreaks. However, this proportion decreased from 46.1% in 2014 to 29.3% in 2015.

S. Typhimurium (including *S.* Typhimurium monophasic) was implicated in 16.3% of the strong-evidence outbreaks (30 outbreaks). ‘Pig meat and products thereof’ (12 outbreaks) was the most common food vehicle category associated with *S.* Typhimurium outbreaks as in 2014. The second most common food vehicle was ‘cheese’ (9 outbreaks, all reported by France), while in 2014 it was ‘eggs and egg products’.

The distribution of food vehicles in strong-evidence outbreaks caused by *S.* Enteritidis and *S.* Typhimurium is shown in Figures 78 and 79.

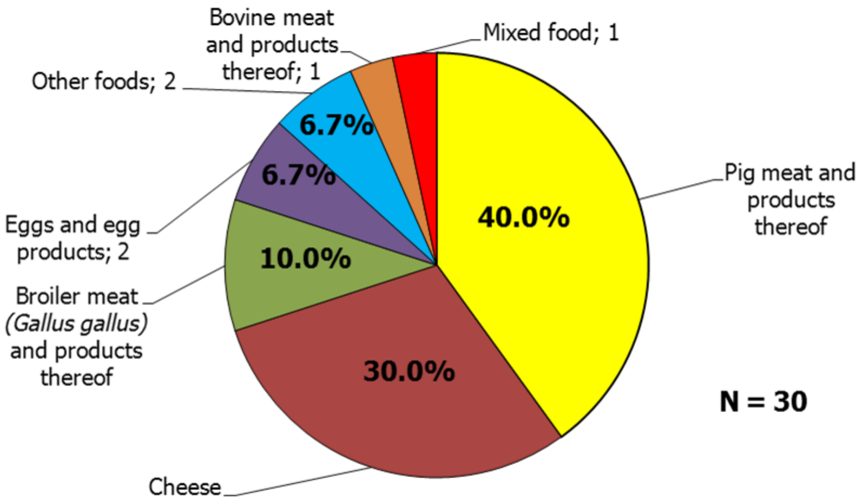
S. Bovismorbificans was reported as the causative agent in three strong-evidence outbreaks associated with the consumption of ‘fish and fish products’. All were reported by Latvia, with ‘restaurant’ as place of exposure.

S. Stanley was responsible for three strong-evidence outbreaks associated with the consumption of turkey meat reported by Austria, Belgium and Croatia, which involved a total of 215 cases with 46 being hospitalised.



Data from 116 outbreaks included: Austria (1), Belgium (1), Croatia (12), France (17), Germany (2), Greece (1), Hungary (1), Latvia (1), Lithuania (20), Poland (48), Portugal (1), Romania (2), Slovakia (7), Sweden (1) and the United Kingdom (1). Other foods (N = 15) include: other foods (5), vegetables and juices and other products thereof (2), Pig meat and products thereof (2), Meat and meat products (2), Fish and fish products (2), herbs and spices (1) and sweets and chocolate (1).

Figure 78: Distribution of food vehicles in strong-evidence outbreaks caused by *S.* Enteritidis (excluding waterborne outbreaks) in the EU, 2015

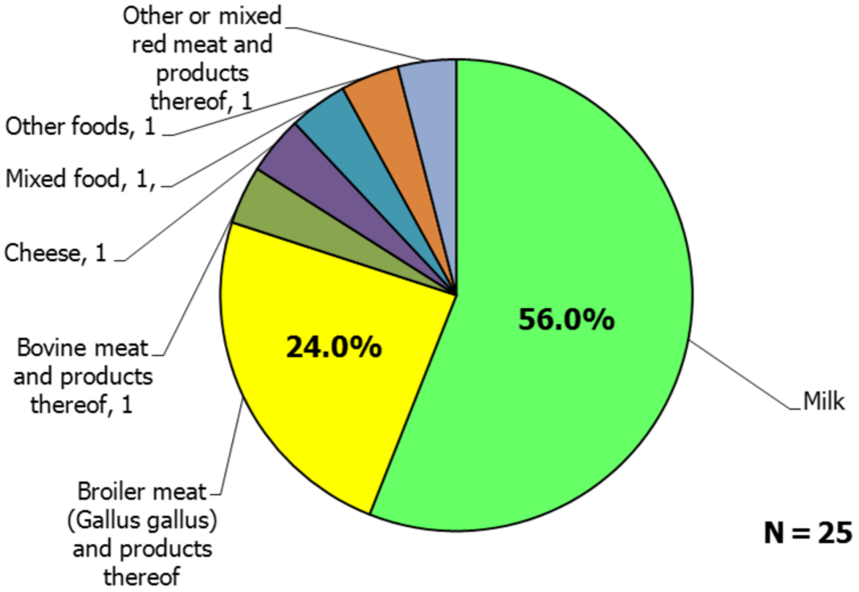


Data from 30 outbreaks are included: France (23), Germany (1), Hungary (1), Italy (1), Lithuania (1), the Netherlands (1), Romania (1) and the United Kingdom (1).

Figure 79: Distribution of food vehicles in strong-evidence outbreaks caused by *S*. Thyphimurium (excluding waterborne outbreaks) in the EU, 2015

Campylobacter

In 2015, 17 MS reported a total of 385 food-borne *Campylobacter* outbreaks (excluding two waterborne outbreaks), representing 8.8% of all outbreaks reported in the EU (Table 2015_FBOCAMP). This is a decrease compared with 2014, when 444 outbreaks were reported. The reporting rate for the annual total number of *Campylobacter* outbreaks was 0.08 per 100,000, slightly lower than in the five previous years (0.11 per 100,000). *Campylobacter* outbreaks accounted for 8.9% of the total food-borne outbreaks reported in the EU. In total, the outbreaks caused 1,421 cases of which 129 were hospitalised and one died. Germany reported the highest number of outbreaks (N = 182) followed by Slovakia and France (103 and 32, respectively). In addition, Norway and Switzerland reported one weak-evidence outbreak each, involving three and two cases, respectively.



Data from 25 outbreaks are included: Austria (1), Finland (1), France (3), Germany (12), the Netherlands (3) and the United Kingdom (5). Number after the label refers to the number of outbreaks.

Figure 80: Distribution of food vehicles in strong-evidence outbreaks caused by *Campylobacter* (excluding waterborne outbreaks) in the EU, 2015

In total, six MS reported 25 *Campylobacter* outbreaks with strong-evidence (6.5%). Differently from 2014 when broiler meat was the most common food vehicle implicated in strong-evidence outbreaks caused by *Campylobacter*, in 2015 the most frequently reported food vehicle was raw milk (14 outbreaks), followed by broiler meat and products thereof (6 outbreaks). All other food vehicles were associated with one outbreak each. The distribution of the most common food vehicles implicated in strong-evidence *Campylobacter* outbreaks is represented in Figure 80.

Among strong-evidence outbreaks, information on *Campylobacter* species was reported in 16 outbreaks only: 15 outbreaks were caused by *C. jejuni* and one caused by *C. fetus.* This outbreak occurred in the Netherlands, involved five cases (all hospitalised), and was associated with the consumption of sheep cheese.

Seventeen outbreaks were reported as general outbreaks and four as household outbreaks (four outbreaks were reported as unknown). The most frequently reported place of exposure was 'farm' (10 outbreaks all associated with raw milk and one with cheese), followed by 'household' (6 outbreaks) and 'restaurant or cafe or pub or bar or hotel' or 'catering service' (4 outbreaks).

Inadequate heat treatment was reported as the most probable contributory factor in 12 strong-evidence *Campylobacter* outbreaks.

Information on food vehicle was also provided for 49 of the 360 weak-evidence outbreaks: 'broiler meat and products thereof' was the food vehicle most frequently reported (11 outbreaks), followed by 'mixed foods' (5 outbreaks), 'eggs and eggs products', 'other or mixed red meat and products thereof', and 'pig meat and products thereof' (3 outbreaks each), 'milk', 'bovine meat and products thereof' 'other, mixed or unspecified poultry meat and products thereof' and 'vegetables and juices and other products thereof' (2 outbreaks each), 'sweets and chocolate' and 'cereal products including rice and seeds/pulses (nuts, almonds)' (1 outbreak each). Interestingly, a food item classified as 'vegetables and juices and other products thereof' reported by Denmark was associated with a general outbreak, with 110 human cases involved and originating from a contamination of a processing plant.

Shiga toxin-producing Escherichia coli (STEC)

In 2015, 10 MS reported a total of 50 food-borne outbreaks caused by STEC (excluding 19 waterborne outbreaks) representing 1.6% of the reported food-borne outbreaks in the EU (Table 2015_FBOSTEC). In total, 572 people were affected of which 52 were hospitalised, no deaths were reported. There was a 32% increase in the number of outbreaks compared with 2014, when 38 outbreaks were reported involving 270 cases and 34 hospitalisations.

Four strong-evidence STEC outbreaks were reported; three of them were caused by STEC O157 and were reported by the United Kingdom. The food vehicles implicated in these three strong-evidence outbreaks were 'mixed leaf lettuce and raw minced lamb' (1 outbreak), 'chicken burgers and beef burgers' (1 outbreak) and 'various meat products' (1 outbreak). All were general outbreaks with 'multiple places of exposure in one country' (2 outbreaks), and 'temporary mass catering (fairs or festivals)' as the outbreak setting. No information on the serogroup was available for the remaining STEC strong-evidence household outbreak reported by Ireland, which was associated with cheese consumption.

No information on food vehicle implicated in weak-evidence STEC outbreaks was provided for 31 out of 46 outbreaks (reported as 'other foods' or 'unknown'). Meat and products thereof was reported as implicated food vehicle in seven weak-evidence outbreaks, out of which three were associated with the consumption of bovine meat and products thereof. A large outbreak, involving 120 people in a University school, was reported by Portugal as caused by non-O157 STEC and associated with 'mixed food' (cooked hamburger and cooked onions). Single outbreaks were reported associated with 'raw milk', 'eggs and egg products', 'mixed food', 'vegetables, juices and other products thereof'.

Listeria

In 2015, a total of 14 *Listeria* outbreaks (11 due to *Listeria monocytogenes* and three due to unspecified *Listeria* species) were reported by nine MS (Table 2015_FBOLISTERIA). Overall, the MS reported 230 cases, of which 25 were hospitalised and 4 died. Compared with previous years a persistent increasing trend was observed since 2010. The number of outbreaks was stable compared with 2014 (N = 15), whereas an increase was reported for both the number of cases involved and hospitalised. Despite the low reporting rate (< 0.001 outbreaks per 100,000 population), outbreaks involving *Listeria* had a high health burden. Regarding the fatal cases, two occurred in a single strong-evidence general outbreak reported by Italy involving 12 human cases (all hospitalised) and associated with the consumption of 'pig meat and products thereof'. The other two fatal cases occurred in a weak-evidence outbreak caused by serovar 1/2a in a hospital setting, involving only two people reported by Greece, for which no other information is available. Information regarding serovar was available for only six outbreaks; serovar 4b was associated with four outbreaks and serovar 1/2a with two outbreaks.

Four of the five strong-evidence outbreaks were reported as general outbreaks. Three strong-evidence outbreaks were linked to the consumption of 'mixed foods', while the remaining two strong-evidence outbreaks were associated with the consumption of 'buffet meals' and 'pig meat and products thereof', respectively.

Germany reported the largest *L. monocytogenes* (serovar 4b) outbreak affecting 159 cases, of which only two were hospitalised. This was a strong-evidence outbreak associated with the consumption of mixed food (rice pudding) and occurred in a school or kindergarten.

Yersinia

In 2015, 13 outbreaks caused by *Yersinia enterocolitica* (one strong-evidence outbreak and 12 weak-evidence outbreaks) were reported by seven MS (Table 2015_FBOYERS). In addition, one weak-evidence outbreak was reported by Norway.

Even though the number of outbreaks and hospitalisations was stable compared with 2014 (11 outbreaks and 9 hospitalised cases), a decrease was registered in the number of cases: 54 cases in 2015 compared with 2008 in 2014. The only strong-evidence food-borne outbreak was reported by Lithuania and was associated with the consumption of 'pig meat and products thereof'. Two weak-evidence outbreaks associated with the consumption of 'pig meat and products thereof' were reported by France and Lithuania (one outbreak each). One weak-evidence outbreak reported by Belgium was associated with the consumption of 'turkey meat and products thereof'. The food vehicle was reported to be 'unknown' (9 outbreaks) or 'other foods' (1 outbreaks) for the remaining outbreaks.

Vibrio

Four outbreaks due to *Vibrio parahaemolyticus* were reported by France in 2015, involving 29 cases (Table 2015_FBOVIBRIO). The data for 2015 are similar to 2014 (five outbreaks, with 28 cases and one hospitalised). None of these outbreaks were supported by strong evidence. In two outbreaks the consumption of 'crustaceans, shellfish, molluscs and products thereof' was suspected, while the remaining outbreaks were associated with 'other foods' without additional details.

Brucella

Only one *Brucella* outbreak was reported in 2015 affecting two cases in Germany, of which one was hospitalised (Table 2015_FBOBRUCELLA). This was a weak-evidence outbreak for which no information on the implicated food vehicle was provided. In 2014, two outbreaks, with seven cases, of which five hospitalised, were reported by Germany, with no reports from other MS.

Other bacterial agents

Under the category 'other bacterial agents', outbreaks due to *Shigella*, pathogenic *Escherichia coli* (other than STEC), and *Francisella* are reported (Tables: 2015_FBOOTHERBACT; 2015_FBOSTROTHBACT).

In 2015, a total of 22 outbreaks caused by *Shigella* were reported by 11 MS and affected 134 people, of which 20 were hospitalised. Four cases were also reported from a single outbreak by Norway. These data are similar to 2014 (21 outbreaks reported by nine MS, affecting 104 cases of which 22 were hospitalised). Information on the *Shigella* species involved was reported for 16 of the 22 *Shigella* outbreaks and from the Norwegian outbreak: overall, 13 outbreaks were caused by *Shigella*. *sonnei* and three were due to *Shigella flexneri*. Only two outbreaks were supported by strong evidence and one of these was associated with the consumption of coriander, while for the others, the food vehicle was reported to be 'unknown'. Information on food vehicle was provided for five of the 20 weak-evidence *Shigella* outbreaks, two of which were linked to the consumption of 'mixed food', one to 'meat and meat products', one to 'cheese' and one was associated with 'fruit, berries and juices and other products thereof'.

One household weak-evidence outbreak caused by *Francisella tularensis* and involving five human cases (of which three hospitalised) was reported by Croatia (weak-evidence outbreak) but no information on the food vehicle was provided. In 2014, only one weak-evidence outbreak caused by *F. tularensis* was reported by Norway.

One general strong-evidence outbreak caused by 'pathogenic *Escherichia coli* other than STEC' and involving 43 human cases was reported by Luxembourg as linked to the consumption of 'fish and fishery products'.

In addition, five weak-evidence outbreaks due to other (unspecified) bacteria involving 155 cases were reported by the United Kingdom (4 outbreaks, 132 cases) and Hungary (1 outbreak, 23 cases). Information on food vehicle was provided for three of these outbreaks: 'dairy products (other than cheeses)', hog roast and lamb dish.

3.16.3.2. Bacterial toxins

In this report, food-borne outbreaks caused by 'bacterial toxins' includes outbreaks associated with toxins produced by *Bacillus*, *Clostridium* and *Staphylococcus*.

In 2015, 20 MS reported a total of 849 food-borne outbreaks caused by bacterial toxins (19.5% of the total outbreaks), which caused 8,847 cases of illness, 497 hospitalisations and 3 deaths. These findings are similar to 2014, when 840 food-borne outbreaks caused by bacterial toxins were reported by 18 MS. As in 2014, France reported the majority (88.5%) of these outbreaks, which included 6,869 human cases, 2 hospitalisations and 3 reported deaths. In addition, one strong-evidence and seven weak-evidence outbreaks caused by bacterial toxins have been reported by Norway.

The reporting rate for food-borne outbreaks caused by bacterial toxins (0.18 outbreaks per 100,000 population) was only slightly higher than in 2014 (0.09) and the five previous years (0.15). In the EU, the health burden of food-borne outbreaks caused by bacterial toxins was important, with 19.5% of total outbreak cases, 12.8% of hospitalisations and 17.6% of deaths caused by these agents.

Bacillus cereus toxins

In 2015, a total of 291 outbreaks caused by *Bacillus cereus* toxins were reported by nine MS (Table 2015_FBOBACIL) and involved 3,131 cases, of which 101 were hospitalised. In addition, Norway reported four outbreaks, which affected 17 human cases. Two-hundred and seventy-seven out of the 291 outbreaks (including 15 strong-evidence outbreaks and 262 weak-evidence outbreaks) were reported by France. A slight decrease was observed in the number of outbreaks reported in 2015. In 2014, 287 outbreaks caused by *Bacillus* toxins involving 3,073 cases, of which 257 hospitalised, were reported by the MS. All these outbreaks, except one, were caused by *B. cereus.*

In the 24 strong-evidence outbreaks caused by *B. cereus* toxins, 'mixed food' was the most commonly implicated food vehicle (8 outbreaks), followed by 'cereal products including rice and seeds/pulses (nuts, almonds)' (2 outbreaks). No specific food category (other food) was provided for eight outbreaks. The distribution of the food vehicles in strong-evidence outbreaks caused by *B. cereus* toxins is presented in Figure 2015_FBOBACILLUSVEHIC. Detailed information of the implicated food vehicle was also provided for 264 of the 271 weak-evidence outbreaks, which were mostly associated with the consumption of 'mixed food', similar to strong-evidence outbreaks.

Information on the type of outbreak was available for all the strong-evidence *B. cereus* outbreaks: 18 were general outbreaks and 6 were household outbreaks. The most frequently reported place of exposure was 'restaurant, cafe, pub, bar, hotel' (7 outbreaks), followed by 'household' (5 outbreaks), 'school and kindergarten' (4 outbreaks) and 'residential institution (nursing home or prison or boarding school)' (3 outbreaks), 'canteen or workplace catering' (2 outbreaks), 'catering on aircraft or ship or train' (2 outbreaks) and 'hospital or medical care facility' (1 outbreak). The most common places of exposure reported for weak-evidence outbreaks were, as for strong-evidence outbreaks, 'restaurant, cafe, pub, bar, hotel' (109 outbreaks) and 'household' (50 outbreaks), followed by 'catering on aircraft or ship or train' (45 outbreaks) and 'school and kindergarten' (28 outbreaks).

No outbreaks caused by *Bacillus* toxins other than *B. cereus* toxins were reported in the EU and non-MS.

Clostridium botulinum toxins

In 2015, 24 outbreaks caused by *C. botulinum* toxins with 60 cases involved, of which 43 hospitalised, were reported by 10 MS (Table: 2015_FBOBOT). Although the reporting rate of outbreaks by *C. botulinum* toxins was low and fell within the same range of previous years, *C. botulinum* toxins was the causative agent associated with the highest proportion of cases hospitalised (71.7%). The number of outbreaks reported in 2015 represents an increase compared with 2014, when nine outbreaks were reported.

Information on the type of outbreak was known for 23 outbreaks, of which 20 were household and 3 were general outbreaks. Fifteen outbreaks were reported to be supported by strong evidence, these were associated with the consumption of different foods, including 'pig meat and product thereof' (4 outbreaks, 2 of which associated with smoked ham), unspecified 'meat and meat products' (3 outbreaks, including smoked meat) and 'canned food products' (3 outbreaks including mushrooms in oil). Other food vehicles (including 'mixed food', 'cereal products including rice and seeds/pulses' and 'other or mixed red meat and products thereof') were associated with one outbreak each. No detailed information on the implicated food was provided for two outbreaks, for which the food vehicle was either reported as 'other food' or 'unknown'. The distribution of the food vehicles in strong-evidence food-borne outbreaks caused by *C. botulinum* is presented in Figure 2015 FBOCLOSTRBOTVEHIC.

For two outbreaks, the contamination of the implicated food (smoked sausage and chickpea spread) with *C. botulinum* took place at processing plants. Botulinum toxin B was specified for five outbreaks.

Clostridium perfringens toxins

In 2015, a total of 96 food-borne outbreaks caused by *C. perfringens* toxins were reported by seven MS and involved 2,014 cases, of which 25 were hospitalised and 3 died (2015_FBOCLOSTOX). One additional strong-evidence outbreak that involved 18 cases was reported by Norway. Compared with 2014 (124 outbreaks), the number of outbreaks reported in 2015 was 22% less. Outbreaks were mostly general outbreaks (91), followed by household outbreaks (4), while in one case this information was not provided.

Sixty-six of the 96 outbreaks (15 strong-evidence outbreaks and 51 weak-evidence outbreaks) were reported by France.

Twelve of the 24 strong-evidence outbreaks caused by *C. perfringens* toxins were associated with the consumption of different types of meat and products thereof, especially 'bovine meat and products thereof' (5 outbreaks), followed by 'pig meat and product thereof' (3 outbreaks), 'broiler meat and products thereof' (2 outbreaks), 'other, mixed or unspecified poultry meat and products thereof' and 'sheep meat and products thereof' (one outbreak each). Two outbreaks were associated with 'mixed food', one with 'vegetables and juices and other products thereof', while the food category was not specified (reported as 'other food') for the remaining nine outbreaks.

Information of the implicated food vehicle was also known for 69 of the 72 weak-evidence outbreaks, which were mostly associated with the consumption of 'mixed food' (14 outbreaks) and several types of meat and products thereof (accounting altogether for 14 outbreaks), followed by 'buffet meals' (3 outbreaks). In 38 weak-evidence outbreaks 'other food' was reported as the implicated food vehicle without further specification. The distribution of the food vehicles in strong-evidence food-borne outbreaks caused by *C. perfringens* is presented in Figure 2015_FBOCLOSTRPERFRVEHIC.

The most frequently reported place of exposure in strong-evidence outbreaks was 'residential institution' (5 outbreaks) followed by 'restaurant or cafe or pub or bar or hotel', 'catering on aircraft or ship or train' and 'canteen or workplace catering' (4 outbreaks each).

The food vehicle implicated in the strong-evidence outbreaks reported by Norway was bovine meat.

Other Clostridia

In 2015, three weak-evidence outbreaks caused by *C. difficile* were reported by Slovakia. The outbreaks involved nine cases, all hospitalised, and no information on food vehicle (reported as 'unknown') was provided.

An additional weak-evidence outbreak was reported by Poland as due to unspecified *Clostridium* species.

Staphylococcal toxins

In 2015, 16 MS reported 434 food-borne outbreaks caused by staphylococcal toxins. This represents 9.9% of all outbreaks, a small increase compared with 2014 when 12 MS reported 393 outbreaks caused by staphylococcal toxins. The overall reporting rate in the EU was 0.15 per 100,000. As in 2014, France reported the vast majority (91.7%) of these outbreaks. Details on the number of food-borne outbreaks and human cases caused by staphylococcal enterotoxins in 2015 are summarised by reporting country in Table 2015_FBOSTAPH. In addition, Norway reported 3 weak-evidence outbreaks, involving a total of 10 cases.

In the 39 strong-evidence outbreaks caused by staphylococcal toxins, 'cheese' was the most commonly implicated food vehicle (13 outbreaks), followed by 'mixed food' (6 outbreaks). No specific food category (reported as 'other food') was provided for five outbreaks. The distribution of the food vehicles in strong-evidence outbreaks caused by staphylococcal toxins is presented in Figure 2015_FBOSTAPHYLVEHIC.

The most frequently reported place of exposure in the 39 strong-evidence outbreaks was 'household' (14 outbreaks), followed by 'restaurant, cafe, pub, bar, hotel, catering service' (9 outbreaks).

Detailed information of the implicated food vehicle was also provided for 245 of the 295 weak-evidence outbreaks, which were mostly associated with the consumption of 'mixed food' (75 outbreaks), different types of meat and meat products (accounting for 85 outbreaks), and various types of food vehicles: 'fish and fish products' (18 outbreaks), 'vegetables and juices and other products thereof' (16 outbreaks), 'eggs and egg products' (14 outbreaks), 'crustaceans, shellfish, molluscs and products thereof' (12 outbreaks), 'cheese' (10 outbreaks), etc. Specific information on the food vehicle was not provided for 150 outbreaks which were associated with the consumption of either 'other foods' (142 outbreaks) or 'unknown' food vehicle (8 outbreaks).

The most commonly reported place of exposure for the weak-evidence outbreaks was 'restaurant, cafe, pub, bar, hotel, catering service' (174 outbreaks), followed by 'household' (109 outbreaks), 'school or kindergarten' (42 outbreaks) and 'catering on aircraft or ship or train' (35 outbreaks).

In 95 outbreaks (6 strong-evidence and 89 weak-evidence outbreaks) an 'infected food handler' was reported as a contributory factor.

3.16.3.3. Other causative agents

In this report the category 'other causative agents' includes chemical agents, histamine, marine biotoxins, mushroom toxins, and scrombotoxin.

In 2015, nine MS reported a total of 127 food-borne outbreaks due to other causative agents involving 648 cases, of which 64 were hospitalised. This represents the 2.9% of all outbreaks reported at the EU level, a small decrease compared with 2014, when 140 outbreaks were reported. The reporting rate was 0.05 outbreaks per 100,000 population. Two strong-evidence outbreaks with 24 cases were also reported by Switzerland, both caused by histamine.

The majority (63.0%) of outbreaks due to 'other causative agents' were caused by histamine (23 strong- and 57 weak-evidence outbreaks), which accounted for 67.4% of human cases and 67.2% of hospitalisations reported in these outbreaks. This is a slight increase compared with 2014 when outbreaks caused by histamine represented 53.2% of total outbreaks. Forty-four of 127 outbreaks (34.6%) due to 'other causative agents' were caused by marine biotoxins, while chemical agents, mushroom toxins and scrombotoxins were associated with one outbreak each.

Information on the type of outbreak was available for 116 out of 127 outbreaks caused by other agents: 79 were general outbreaks, while 37 were household outbreaks. For 11 outbreaks this information was either 'unknown' (3 outbreaks) or not reported (8 outbreaks).

In total, 25 strong-evidence outbreaks were reported by six MS, mainly by France (11 strong-evidence outbreaks). France reported the highest number of outbreaks (103 outbreaks, including both strong- and weak-evidence outbreaks) due to other causative agents (Tables 2015_FBOOTHER and 2015_FBOSTROTHER).

Most of the strong-evidence outbreaks caused by other causative agents were associated with the consumption of 'fish and fishery products' (21 out of 25 strong-evidence outbreaks), mostly containing tuna. In addition, 'cheese' was reported as food vehicle in two strong-evidence outbreaks, while 'mixed food' (plain yogurt with banana) and 'other foods' were associated with one strong-evidence outbreak each. Histamine was responsible of most of the strong-evidence outbreaks associated with the consumption of 'fish and fishery products' (20 out of 21). Histamine was also the causative agent in the two strong-evidence outbreaks associated with 'cheese' and in one outbreak associated with 'mixed food'. The other two strong-evidence outbreaks associated with the consumption of 'fish and fish products' and 'other foods' were caused by marine biotoxin (ciguatoxin) and mushroom toxins, respectively.

The place of exposure most frequently reported in strong-evidence outbreaks was 'restaurant or cafe or pub or bar or hotel or catering service' (14 outbreaks), followed by 'household' and 'school or kindergarten' (4 outbreaks each) and 'canteen or workplace catering' (2 outbreaks). Information on the place of exposure was not reported for one outbreak.

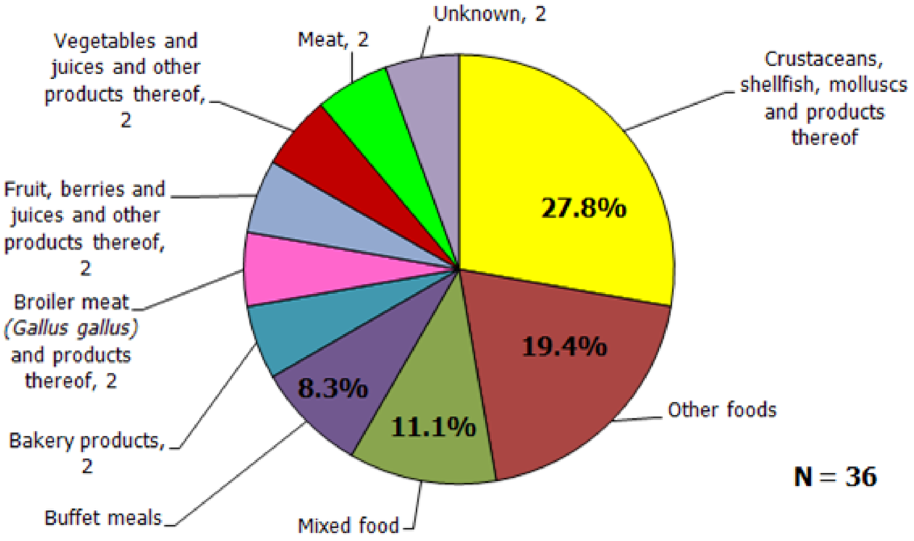
3.16.3.4. Viruses

Overall, 16 MS reported a total of 396 food-borne outbreaks caused by viruses (excluding three strong and five weak-evidence waterborne outbreaks); this represents a 63% decrease compared with 2014, when 1,070 food-borne outbreaks (excluding waterborne outbreaks) were reported. In 2015, only 43 (10.9%) of the reported food-borne outbreaks caused by viruses in the EU were supported by strong-evidence, and these were reported by 10 MS. Overall, the outbreaks implicated 13,453 cases, 526 hospitalisations and 5 deaths. In 2015 the overall reporting rate for outbreaks by any viruses was 0.08 outbreaks per 100,000 population, which is a decrease compared with 2014 (0.27 per 100,000 population). In addition, Norway reported 13 weak-evidence outbreaks implicating 320 cases.

Calicivirus

In 2015, 15 MS reported 285 outbreaks (36 strong evidence and 249 weak evidence) caused by calicivirus including norovirus (Table 2015_FBOCALICIV). All calicivirus outbreaks were caused by norovirus, except for four weak-evidence outbreaks due to calicivirus. Norovirus was the most commonly reported virus implicated in the strong-evidence outbreaks (36 norovirus outbreaks out of 43 strong-evidence outbreaks caused by virus). In 2015, the overall reporting rate for calicivirus including norovirus in the EU was 0.07 outbreaks per 100,000 population, as in the previous 5 years. Overall, the outbreaks implicated 12,591 cases, 349 hospitalisations and one death. France reported the highest number of outbreaks (22.4% of all reported food-borne outbreaks caused by calicivirus including norovirus), followed by Poland (14.7%) and Latvia (13%). France and Hungary reported the highest number of strong-evidence outbreaks due to calicivirus including norovirus (11 and 7 outbreaks, respectively). In addition, Norway reported 13 outbreaks.

In the 36 strong-evidence outbreaks caused by norovirus, 'crustaceans, shellfish, molluscs and products thereof' was the most commonly implicated food vehicle (27.8% of outbreaks), followed by 'other foods' (19.4% of outbreaks), 'mixed food' (11.1%) and 'buffet meals' (8.3%) (Figure 81).



Data from 36 outbreaks are included: Croatia (3), Finland (6), France (11), Germany (1), Hungary (7), Poland (4), Sweden (2), the United Kingdom (2). Other foods (N = 7): other foods (5), Eggs and egg products (1), Sweets and chocolate (1). Meat (N = 2) include: Meat and meat products (1) and Pig meat and products thereof (1).

Figure 81: Distribution of food vehicles in strong-evidence outbreaks caused by norovirus (excluding waterborne outbreaks) in the EU, 2015

Information on the type of outbreak was reported for 34 out of the 36 strong-evidence outbreaks: 30 were general outbreaks, and 4 occurred within the household. The place of exposure most frequently reported was 'restaurant or cafe or pub or bar or hotel or catering service' (8 outbreaks), followed by 'school or kindergarten' (6 outbreaks).

The two most often reported contributory factors for the strong-evidence norovirus outbreak were 'infected food handler', 'cross-contamination' in 11 outbreaks and 'unprocessed contaminated ingredient' in 9 of the 22 strong-evidence outbreaks where the information was available.

Hepatitis A

A total of 13 outbreaks (2 strong-evidence outbreak and 11 weak-evidence outbreak) with 78 human cases, 49 hospitalisations and one death were reported from five countries (Finland, Germany, Greece, Hungary, Poland) (Table 2015_FBOHEPA).

Food vehicle was reported in only one weak-evidence outbreak (crustaceans, shellfish, molluscs and products thereof). The place of exposure was 'restaurant or cafe or pub or bar or hotel or catering service' (3) 'household' (3) 'multiple place of exposure' (1).

Other Viruses (including adenovirus, flavivirus and unspecified viruses)

A total of 98 outbreaks were reported (5 strong-evidence outbreaks and 93 weak-evidence outbreaks) by nine MS (Tables 2015_FBOOTHVIRUS and 2015_FBOSTROTHVIRUS). Rotavirus was the most commonly reported virus implicated in this group (45 out of 98 outbreaks), accounting for 79% of cases (619 cases out of 784). Most of these were reported by Poland (78.4%). It is important to underline that 46 outbreaks were caused by viruses unspecified. Four of the five strong-evidence outbreaks involving viruses other than calicivirus and hepatitis A were caused by flavivirus and associated with the consumption of 'milk' (raw goat milk was reported in three outbreaks). These outbreaks were characterised by the high severity of clinical illness with 13 hospitalisations and 2 deaths among the 14 cases involved. The other strong-evidence outbreak was caused by rotavirus and associated with the consumption of 'vegetables and juices and other products thereof'. Regarding the 93 weak-evidence outbreaks, information on food vehicle was available for 53 outbreaks: the main vehicles identified were 'other food' (15), followed by 'mixed food' (14), 'crustaceans, shellfish, molluscs and products thereof' (8) and 'fish and fish products' (4).

Information on the type of outbreak was reported in 88 outbreaks: 62 were general outbreaks and 26 household. The place of exposure most frequently reported was 'household' (31 outbreaks) followed by 'restaurant or cafe or pub or bar or hotel or catering service' (8 outbreaks).

The three most frequently reported contributory factors were 'infected food handler' in 7 outbreaks, 'unprocessed contaminated ingredient' in 3 outbreaks, 'inadequate heat treatment' in 3 outbreaks. For 38 outbreaks, the information was not reported.

3.16.3.5. Parasites

In 2015, 12 MS reported a total of 45 food-borne outbreaks caused by parasites. Overall this represents 1% of all food-borne outbreaks reported in the EU. This represents an increase if compared with 2014, when a total of 33 outbreaks were reported.

Trichinella

In 2015, 15 *Trichinella* outbreaks were reported by eight MS (reporting rate < 0.01 outbreaks per 100,000 population) (Table 2015_FBOTRICH). In particular 4 MS (Lithuania, Romania, Poland, Croatia) reported more than one outbreak each In total 119 people were involved, 34 of which were hospitalised. The trend of occurrence of outbreaks is quite stable if compared with 2014 (17 outbreaks in 2014) whereas the overall number of cases and hospitalisations decreased (187 and 84 in 2014, respectively). Twelve outbreaks were reported as strong-evidence outbreaks: five of these were associated with 'pig meat and products thereof', five with 'other or mixed red meat and products thereof' (including four outbreaks involving wild boar meat) and two with 'meat and meat products'.

Cryptosporidium

Five outbreaks caused by *Cryptosporidium* were reported by three MS (Germany, Sweden and United Kingdom) as weak-evidence outbreaks (reporting rate < 0.01 outbreak per 100,000 population) (Table 2015_FBOCRYPT). No information on the implicated food vehicle was provided. The number of outbreaks is similar to 2014 (seven outbreaks in two MS). Sweden reported a large outbreak (82 cases) occurring during a national meeting; eating at any of the lunches during the meeting days was identified as the main risk factor; however, no specific food vehicle was identified.

Other parasites

In 2015, 25 weak-evidence outbreaks, all caused by *Giardia*, were reported by three MS (Poland, Latvia and Germany) (Table 2015_FBOOTHPAR). In particular Poland reported 16 out of 25 outbreaks (64%). The reporting rate was 0.01 per 100,000 population, this represents an increase compared with the number of *Giardia* outbreaks reported in 2014 (six weak-evidence outbreaks reported by six MS). No information on food vehicles involved was provided.

3.16.3.6. Unknown agents

In 2015, 17 MS reported 1,458 outbreaks with causative agent 'unknown' (33% of all outbreaks). These outbreaks caused 10,930 cases of illness, 783 hospitalisations and one death. In addition, two non-MS (Norway and Switzerland) reported 20 outbreaks with 250 cases of illness and 2 hospitalisations.

Twelve outbreaks (excluding four waterborne outbreaks) were supported by strong evidence (2.8% of all strong-evidence outbreaks, excluding waterborne outbreaks). No prevalent food category was associated with these outbreaks.

3.16.4. Waterborne outbreaks

In 2015, six MS reported 38 waterborne outbreaks and 8 of these were reported as strong-evidence outbreaks by six MS. The outbreaks involved 2,458 cases of which 22 were hospitalised. In addition, one non-MS, Switzerland, reported one large strong-evidence outbreak.

Two different agents were detected in the eight strong-evidence outbreaks: Shiga toxin-producing *E. coli* (STEC O157 and unspecified serogroup) and norovirus. For four outbreaks, the causative agents remained unknown.

Six MS reported 30 weak-evidence outbreaks caused by calicivirus (Norwalk-like virus) (2 outbreaks), *Campylobacter* (2 outbreaks), *Cryptosporidium* (4 outbreaks), *Giardia* (4 outbreaks), rotavirus (1 outbreak), and STEC (STEC O157, O145, O26, unspecified) (17 outbreaks). In the EU the largest waterborne outbreak was caused by an unknown agent and caused 726 cases. In Switzerland a single outbreak due to contamination by norovirus in the water distribution system caused 1,194 cases. Further details on the number of strong-evidence outbreaks and human cases, including information on the causative agents, reporting countries and settings can be found in Table 39.

Table 39: List of strong-evidence waterborne outbreaks reported in the EU, 2015

Causative agent	Country	Setting	Additional information	Strong-evidence outbreaks			
				N	Human cases	Hospitalised	Deaths
Shiga toxin-producing *E. coli* (STEC)	Ireland	Household		1	5	0	0
	United Kingdom	Others	Private Water Supply – Spring Water. VTEC O157 PT 21 ∣ 28, VT 2. MLVA and Whole Genome Sequencing results confirmed close genetic relatedness of outbreak isolates.	1	22	5	0
Norovirus	Greece	Others	Community waterborne outbreak	1	230	0	0
	Sweden	Unknown		1	550	3	
	Switzerland	Others	Drinking Water; Water distribution system	1	1,194	5	0
Unknown	Belgium	Camp or picnic		1	12	5	0
		Household		1	40	0	0
	Finland	Household		1	726	0	0
	Greece	Restaurant or Cafe or Pub or Bar or Hotel or Catering service	Water supply from a private well	1	213	0	0
EU Total				**8**	**1,798**	**13**	**0**

3.16.5. Discussion

In 2015, 26 MS reported a total of 4,362 food-borne outbreaks, including waterborne outbreaks. Overall, these outbreaks caused 45,874 cases of illness (209 more than 2014), 3,892 hospitalisations (2,546 less than 2014) and 17 deaths (10 less than 2014). In addition, two non-MS reported data on 50 food-borne outbreaks involving 1,853 cases and 7 hospitalisations. The overall reporting rate of food-borne outbreaks in the EU was 0.95 outbreaks per 100,000 population, which represents a slight decrease, compared with data for both 2014 (1.04 outbreaks per 100,000) and the previous 5 years (1.11 outbreaks per 100,000). Important differences in the reporting rates among the MS were observed. It is important to highlight that they may not only reflect true epidemiological differences among the MS in the rate of occurrence of outbreaks as well as in the causative agents and food vehicles involved but also the different systems, components (e.g. case definition, diagnostic procedures), and sensitivity of surveillance programmes for food-borne outbreaks in place in the various EU countries. As a consequence of this, the estimates presented in this report should be carefully interpreted when they refer to the EU level. As an example, the vast majority of the outbreaks caused by bacterial toxins (751 out of 849 outbreaks) were reported by a single MS only. In this case, general findings such as the temporal trends of occurrence or sources at the EU level, is likely to be critically affected by the trend within this country.

In 2015, bacteria, in particular *Salmonella*, were the most commonly detected causative agents in food-borne outbreaks (33.7% of all outbreaks; reported by 26 MS), followed by bacterial toxins (19.4% of all outbreaks; reported by 20 MS), viruses (9.2% of all outbreaks; reported by 17 MS), other causative agents (2.9% of all outbreaks; reported by 9 MS), and parasites (1.2% of all outbreaks; reported by 12 MS). A major limitation is that in a large proportion of the reported outbreaks (33.5%) the causative agent could not be identified. Many of these outbreaks also lacked of information on the suspected food vehicle and the place of exposure.

The implicated food vehicles identified in strong-evidence outbreaks were mostly of animal origin, in particular 'eggs and egg products' and pig meat (both accounting for 10% of all strong-evidence outbreaks), broiler meat (9%) and cheese (8%) followed by fish and fish products (7%), milk and dairy products (5%), bovine meat (4%) and crustaceans (3%). Compared with previous years, a marked reduction in the occurrence of strong-evidence outbreaks associated with the consumption of eggs and egg products was observed. A decrease was also reported for outbreaks associated with 'fish and fish products' and 'crustaceans'. Conversely, reporting rates of strong-evidence outbreaks associated with the consumption of cheese, milk and dairy products increased. The reporting of 'other food vehicle of animal origin' was stable compared with the previous years. Foods of non-animal origin, mainly vegetables, juices and other products thereof, accounted for 6.6% of all strong-evidence outbreaks. Mixed food and buffet meals, as well as other unspecified foods were reported in almost a third of all strong-evidence outbreaks (13% and 18%, respectively). These items were also the foods causing the highest number of illnesses reported in strong-evidence outbreaks.

These findings, however, should be interpreted with caution as they only refer to strong-evidence outbreaks which represent a minority of all reported outbreaks (422 outbreaks out of 4,362; 9.7%). Biases connected with the ease/difficulty in investigating the different causative agents and types of vehicle and depending from the overall epidemiological context in which the implicated food is investigated should be considered, as they may influence the likelihood that strong evidence is obtained or not. As an example, although *Campylobacter* represents the main food-borne causative agent in sporadic cases in the EU, the proportion of strong-evidence outbreaks caused by this agent was lower than *Salmonella* (6% *Campylobacter* vs 19% *Salmonella*) probably due to the poor persistence of the organism in food, making its detection in residual food samples from outbreaks (microbiological evidence) more difficult. The long incubation period may also affect epidemiological investigations.

Information on place of exposure highlights that household was by far the most frequent place of exposure of cases to the implicated food vehicle. It is important also to note that the causative agents identified in household and the food vehicle were often different from those reported in other settings (i.e. canteen, catering services, restaurants, pubs, street vendors and take away). Such findings clearly indicate the important differences between household outbreaks and those from other places of exposure. Consequently, attention should be paid to deliver different and specific recommendations for control policies (i.e. general populations vs food business operators) to the relevant stakeholders.

The analysis of associations between causative agent and food vehicle confirms the same epidemiological trends described in previous years (e.g. *S.* Enteritidis in eggs and *C. perfringens* in meat). Analysing the combinations between causative agents and food vehicles is important to monitor the trend of occurrence of food-borne pathogens subjected to control plans in specific reservoirs (e.g. *Salmonella* in poultry) as well as for those hazards with safety criteria established for a specific food chain point. In 2015, as in previous years, a reduction was observed in the number of reported outbreaks caused by *Salmonella*. *Salmonella* outbreaks in the EU have steadily and progressively decreased since 2010 (41% from 2010 to 2015). The implementation of the National Control Programmes for *Salmonella* in laying hens, as well as the restrictions on sale of fresh eggs from infected flocks, are likely to have contributed to the decline of *Salmonella* strong-evidence outbreaks associated with 'eggs and egg product'. Furthermore, the analysis of the association between causative agent and food vehicle facilitates identification of the emergence of new/unfrequent combinations.

Beside the approach to food-borne outbreak data analysis based primarily on causative agents, in agreement with the principles of Directive 2003/99/EC, in the present report the relationship between causative agents, food vehicles and place of exposure have been more deeply analysed. This aimed at more comprehensively investigating the different contexts and mechanisms underlying the occurrence of food-borne outbreaks in the EU and their impact on public health. Important differences emerged in the main epidemiological features of food-borne outbreaks; primarily in the place of exposure.

Highlighting these differences is important to properly support the targeting of control policies and risk communication to consumers and the relevant stakeholders. Surveillance of food-borne outbreaks including analyses by the food vehicle and place of exposure also allows provision of information on the risk association with multiple hazards.

3.17. Microbiological contaminants (for which food safety criteria are laid down in EU legislation)

This chapter summarises the information provided to the zoonoses database at EFSA in 2015 on the non-zoonotic microbiological contaminants (histamine, *Cronobacter sakazakii* and staphylococcal enterotoxins and for which EU Regulation (EC) No 2073/2005 lays down food safety criteria) in food.

3.17.1. Histamine

Presence of histamine in fish and fishery products was reported by 17 MS (Austria, Belgium, Bulgaria, Croatia, Cyprus, the Czech Republic, Estonia, France, Ireland, Italy, Latvia, Poland, Portugal, Romania, Slovakia, Slovenia and Spain) and two non-MS (Iceland and Norway) in samples taken from border inspection activities, retail, processing plant and unspecified sampling stages. In total, 127 samples were analysed from border inspection activities by seven MS. None of them were positive. At retail, 102 out of 2,743 (3.7%) samples were histamine-positive. The majority of them were reported by Italy and Spain with, respectively, 75 out of 1,602 (4.7%) and 7 out of 408 (1.7%) samples found positive. At processing plant level, 12 MS and two non-MS submitted data on histamine in fish and fishery products. In total, 368 were positive out of the 1,180 (31.2%) samples tested. Poland reported the majority of the positive samples (95%). One MS (Ireland) submitted data from unspecified sampling stages and out of the 161 tested samples, eight were positive (5%).

Only Spain reported data on the fishery products which have undergone enzyme ripening treatment in brine at retail. One sample out of seven tested positive with a value of 400 mg/kg (Table 2015_HISTAMINEFISH).

Histamine in other food was reported by three MS (Austria, Italy and Ireland) from border inspection activities, retail and unspecified sampling stages. Overall, 26 (22.4%) out of 116 samples were positive. Of these, 16 (61.5%) were reported by Ireland in sauce and dressings taken at unspecified sampling stages (Table 2015_HISTAMINEOTHER).

3.17.2. Staphylococcal enterotoxins

In 2015, 12 MS (Belgium, Bulgaria, Croatia, Cyprus, the Czech Republic, Germany, Greece, Italy, Portugal, Romania, Slovakia and Spain) and one non-MS (Switzerland) reported data on staphylococcal enterotoxins in milk and dairy products. Out of the 2,309 samples tested, 19 (0.8%) were positive and were mostly reported by Italy at processing plant level: reports comprised hard cheese made from sheep’s milk (5 out 5 tested), soft and semisoft cheese from unspecified milk (2 out of 55 tested) and cheeses made from unspecified milk (4 out of 704 tested). At retail, positive samples were found in hard cheese made from sheep’s milk (1 out of 1 tested), cheeses made from unspecified milk (3 out of 365) and in raw cow’s milk (2 out of 31). Belgium and Portugal reported one positive sample each out of one sample of dairy products (excluding cheeses) and 50 samples of cheeses made from sheep’s milk, respectively (Table 2015_STAPHENTERCHEESE).

Data on staphylococcal enterotoxins in other food were submitted by eight MS (Belgium, Bulgaria, Cyprus, the Czech Republic, Germany, Italy, Slovakia and Spain). In total, 871 samples were tested, of which 21 (2.4%) were found positive. Positive samples were reported by Spain (14), Italy (4), Belgium (1) and Slovakia (1), taken either at retail or processing plant level (Table 2015_STAPHENTEROTHER).

3.17.3. *Cronobacter sakazakii*

In 2015, 12 MS (Austria, Belgium, Cyprus, the Czech Republic, Estonia, Germany, Ireland, Italy, Portugal, Slovakia, Slovenia and Spain) provided data on *Cronobacter* in infant formula and dietary foods for special medical purposes. In total, 1,591 samples were examined. Belgium and Slovakia each reported one positive sample for *Cronobacter sakazakii* out of 297 and 16 samples tested, respectively. Both samples were taken at retail (Table 2015_CRONOBINFDIE).

In addition, three MS (the Czech Republic, Italy and Slovakia) submitted data on *Cronobacter* in other foods. Overall, 600 samples were tested at processing plant and retail level. The Czech Republic reported two positive samples out of 41 (4.9%) dairy products (milk powder and whey powder) tested (Table 2015_CRONOBOTHER).

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Abbreviations

AE	alveolar echinococcosis
AHAW	EFSA Panel on Animal Health and Welfare
BIOHAZ	EFSA Panel on Biological Hazards

CE	cystic echinococcosis
CFT	complement fixation test
CFU	colony-forming unit
CONTAM	EFSA Panel on Contaminants in the Food Chain
DCF	Data Collection Framework
EBLV	European bat lyssavirus
ECDC	European Centre for Disease Prevention and Control
EEA	European Economic Area
ELISA	Enzyme-linked immunosorbent assay
ESRI	Economic and Social Research Institute
EURL	European Union Reference Laboratory
FAT	fluorescent antibody test
HACCP	hazard analysis and critical control point
HAV	hepatitis A virus
HUS	haemolytic-uraemic syndrome
i-ELISA	indirect enzyme-linked immunosorbent assay
IFA	immunofluorescence assay
IHC	immunohistochemistry
ISO	International Organization for Standardization
LHT	low heat-treated
MLST	multi locus sequence typing
MRSA	meticillin-resistant *Staphylococcus aureus*
MS	Member State
NMKL	Nordic Committee on Food Analysis
NT	not typable
OBF	official brucellosis-free in cattle
ObmF	official *Brucella melitensis*-free in sheep and goats
OIE	World Organisation for Animal Health
OTF	official tuberculosis-free in cattle
PCR	polymerase chain reaction
PFGE	pulsed field gel electrophoresis
PHC	process hygiene criteria
RTE	ready-to-eat
RT-PCR	reverse transcriptase-polymerase chain reaction
STEC	Shiga toxin-producing *Escherichia coli*
TESSy	The European Surveillance System
VTEC	verocytotoxigenic *Escherichia coli*
WNF	West Nile fever
WNV	West Nile virus
WAHID	World Animal Health Information Database
WHO	World Health Organization

Country codes

Austria	AT
Belgium	BE
Bulgaria	BG
Croatia	HR
Cyprus	CY
Czech Republic	CZ
Denmark	DK
Estonia	EE
Finland	FI
France	FR
Germany	DE
Greece	GR
Hungary	HU
Iceland	IS

Ireland	IE
Italy	IT
Latvia	LV
Liechtenstein	LI
Lithuania	LT
Luxembourg	LU
Malta	MT
Netherlands	NL
Norway	NO
Poland	PL
Portugal	PT
Romania	RO
Slovakia	SK
Slovenia	SI
Spain	ES
Sweden	SE
Switzerland	CH
United Kingdom	UK

Appendix A – List of usable data

The numbering in the Appendix A corresponds to the section numbers.

Summary

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_summary.zip

Table abbreviation	Table name
2015_ZOONHOSPITRATES	Reported notification rates of zoonoses in confirmed human cases in the EU, 2015

Figure abbreviation	Figure name
2015_ZOONHUMRATES	Reported hospitalisation and case fatality due to zoonoses in confirmed human cases in the EU, 2015
2015_FBOAGENTNUMOUT	Distribution of food-borne and water-borne outbreaks per causative agent in the EU Member States, 2015

A.3.1. *Salmonella*

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_salmonella.zip

Table abbreviation	Table name
2015_SALMOVERVIEW	Overview of countries reporting data for *Salmonella*, 2015

A.3.1.1. Salmonellosis in humans

	Table abbreviation	Table name
Humans	2015_SALMHUMRATES	Reported human cases of salmonellosis and notification rates per 100,000 in the EU/EEA, by country and year, 2011–2015
	2015_SALMHUMSEROVARS	Distribution of reported confirmed cases of human salmonellosis in the EU/EEA, 2013–2015, by the 20 most frequent serovars in 2015

	Figure abbreviation	Figure name
Humans	2015_SALMHUMTREND	Trend in reported confirmed cases of human salmonellosis in the EU/EEA, by month, 2008–2015

A.3.1.2. *Salmonella* in food, animals and feed

	Table abbreviation	Table name
Food	2015_SALMCOMPL	Compliance with the food safety *Salmonella* criteria laid down by the EU Regulations 2073/2005 and 1441/2007 and 1086/2011, 2015
	2015_SALMBROILMEAT	*Salmonella* in fresh broiler meat at slaughter, processing/cutting level and retail, 2015
	2015_SALMRTEBROIL	*Salmonella* in RTE products from broiler meat, 2015
	2015_SALMTURKMEAT	*Salmonella* in fresh turkey meat at slaughter, processing/cutting level and retail, 2015
	2015_SALMRTETURK	*Salmonella* in RTE products from turkey meat, 2015
	2015_SALMPIGMEAT	*Salmonella* in fresh pig meat, at slaughter, cutting/processing level and retail, 2015
	2015_SALMRTEPIG	*Salmonella* in RTE products from minced meat, meat preparation and meat products from pig meat, 2015

	Table abbreviation	**Table name**
Food	2015_SALMBOVINEMEAT	*Salmonella* in fresh bovine meat, at slaughter, cutting/processing level and retail, 2015
	2015_SALMRTEBOVINE	*Salmonella* in RTE products minced meat, meat preparations and meat products from bovine animals, 2015
	2015_SALMEGGS	*Salmonella* in table egg samples, 2015
	2015_SALMBIVMOLLUSC	*Salmonella* in live bivalve molluscs, 2015
	2015_SALMFRUIT	*Salmonella* in fruit, 2015
	2015_SALMFRUITVEG	*Salmonella* in fruit and vegetable, 2015
	2015_SALMVEGET	*Salmonella* in vegetables, 2015
	2015_SALMHERBS	*Salmonella* in spices and herbs, 2015
	2015_SALMSPRSEED	*Salmonella* in seeds, sprouted, 2015
	2015_SALMPIGCARCAS	*Salmonella* in pig carcases, at slaughter, 2015 (based on R 854/2004)
	2015_SALMPIGCARCASHACCP	*Salmonella* in pig carcases, at slaughter, HACCP, 2015
	2015_SALMDRIEDSEED	*Salmonella* in seeds, dried, 2015
Animals	2015_SALMBREEDPROD	*Salmonella* in breeding flocks of *Gallus gallus* during the production period (all types of breeding flocks, flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2015
	2015_SALMLAYPROD	*Salmonella* in laying hen flocks of *Gallus gallus* during the production period (flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2015
	2015_SALMBROIBS	*Salmonella* in broiler flocks of *Gallus gallus* before slaughter (flock-based data) in countries running control programmes, 2015
	2015_SALMBREEDTURK	*Salmonella* in breeding flocks of turkeys (adults, flock-based data) in countries running control programmes, 2015
	2015_SALMFATTURKBS	*Salmonella* in fattening flocks of turkeys before slaughter (flock-based data) in countries running control programmes, 2015
	2015_SALMAPBREEDEGGLINE	*Salmonella* in adult parent breeding flocks for the egg production line during the production period (*Gallus gallus*, flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2015
	2015_SALMAPBREEDMEAT	*Salmonella* in adult parent breeding flocks in the broiler meat production line (*Gallus gallus*, flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2015
	2015_SALMGPBREEDPROD	*Salmonella* in elite and grandparent breeding flocks of *Gallus gallus* during the production period (flock-based data) in countries running control programmes in accordance with Regulation (EC) No 2160/2003, 2015
	2015_SALMDUCKGEESE	*Salmonella* in flocks of ducks and geese (flock-based data), 2015
	2015_SALMPIGSBACT	*Salmonella* in pigs from bacteriological monitoring programmes, 2015
	2015_SALMCATBACT	*Salmonella* in cattle from bacteriological monitoring programmes, 2015
	2015_OUTCTRENDANAL	Outcome of the statistical trend analysis using the EU *Salmonella* target serovar flock prevalence poultry data, 2007–2015
Feed	2015_SALMDERIVEDFEED	*Salmonella* in feedingstuffs, in the EU, 2015
	2015_SALMCOMPFEEDCATTLE	*Salmonella* in compound feedingstuffs for cattle, in the EU, 2015
	2015_SALMCOMPFEEDPIGS	*Salmonella* in compound feedingstuffs for pigs, in the EU, 2015
	2015_SALMCOMPFEEDPOULTRY	*Salmonella* in compound feedingstuffs for poultry, in the EU, 2015

	Table abbreviation	Table name
Serovars	2015_SERALLMATRIX	Reported *Salmonella* serovar isolates, in different animal species and meat sectors, EU, 2015
	2015_SERBROMEAT	Distribution of the ten most common reported *Salmonella* serovars in broiler meat, at the EU level, 2015
	2015_SERTURKMEAT	Distribution of the ten most common reported *Salmonella* serovars in turkey meat, at the EU level, 2015
	2015_SERMONTMEATPOU	Distribution of *S*. Typhimurium-like strains and monophasic *S*. Typhimurium detected in poultry meat, 2015
	2015_SERPIGMEAT	Distribution of the ten most common reported *Salmonella* serovars in pig meat, at the EU level, 2015
	2015_SERMONTMEATPIG	Distribution of *S*. Typhimurium-like strains and monophasic *S*. Typhimurium detected in meat from pigs, 2015
	2015_SERBOVMEAT	Distribution of the ten most common reported *Salmonella* serovars in bovine meat, at the EU level, 2015
	2015_SERMONTMEATBOV	Distribution of *S*. Typhimurium-like strains and monophasic *S*. Typhimurium detected in meat from bovine animals, 2015
	2015_SERGAL	Distribution of the ten most common reported *Salmonella* serovars in *Gallus gallus*, at the EU level, 2015
	2015_SERLAY	Distribution of the ten most common reported *Salmonella* serovars in laying hens, at the EU level, 2015
	2015_SEREGGS	Distribution of the ten most common reported Salmonella serovars in table egg samples, from all monitoring activities, at EU-level, 2015
	2015_SERBRO	Distribution of the ten most common reported *Salmonella* serovars in broilers, at the EU level, 2015
	2015_SERTURK	Distribution of the ten most common *Salmonella* serovars in turkeys, 2015
	2015_SERMONTPOU	Distribution of *S*. Typhimurium-like strains and monophasic *S*. Typhimurium detected in poultry flocks, 2015
	2015_SERPIGS	Distribution of the ten most common *Salmonella* serovars in pigs, 2015
	2015_SERMONTPIG	Distribution of *S*. Typhimurium-like strains and monophasic *S*. Typhimurium detected in pigs, 2015
	2015_SERBOV	Distribution of the ten most common *Salmonella* serovars in cattle, 2015
	2015_SERMONTBOV	Distribution of *S*. Typhimurium-like strains and monophasic *S*. Typhimurium detected in bovine animals, 2015
	2015_SERGALFEED	Distribution of the ten most common *Salmonella* serovars in compound feed for *Gallus gallus*, 2015
	2015_SERPIGSFEED	Distribution of the ten most common *Salmonella* serovars in compound feed for pigs, 2015
	2015_SERBOVFEED	Distribution of the ten most common *Salmonella* serovars in compound feed for cattle, 2015

	Figure abbreviation	Figure name
Food	2015_SALMCOMPLCRITERIA	Proportion of units not complying with the EU *Salmonella* criteria, 2011–2015
	2015_SERBROMEATTREND	*Salmonella* regulated and non-regulated serovars (percentage of isolates of regulated and non-regulated serovars out of the total number of isolates serotyped per year) from broiler meat, EU, 2010–2015
	2015_SERPIGMEATTREND	The three most frequent *Salmonella* serovars (number of isolates of each serovar per year out of the total number of isolates serotyped per year) from pig meat, EU, 2010–2015
	2015_SALMTRENDPOULTRY	Prevalence of *S*. Enteritidis, *S*. Typhimurium, *S*. Infantis, *S*. Virchow and/or *S*. Hadar-positive breeding flocks of *Gallus gallus* during production in the EU, 2007–2015; of *S*. Enteritidis and/or *S*. Typhimurium-positive laying hen flocks, broiler flocks, flocks of breeding and fattening turkeys, during the production period in the EU, 2008–2015

	Figure abbreviation	**Figure name**
Animals	2015_SALMTARGETBREED	Prevalence of *S*. Enteritidis, *S*. Typhimurium, *S*. Infantis, *S*. Virchow and/or *S*. Hadar-positive breeding flocks of *Gallus gallus* during the production period and target for the Member States, Iceland, Norway and Switzerland, 2015
	2015_SALMMAPBREED	Prevalence of the five target serovars (*S*. Enteritidis, *S*. Typhimurium, *S*. Infantis, *S*. Virchow and/or *S*. Hadar)-positive breeding flocks of *Gallus gallus* during the production period, 2015
	2015_SALMBREEDTRENDMS	Country-specific temporal trends in prevalence of *Salmonella* five target serovars (*S*. Enteritidis, *S*. Typhimurium, *S*. Infantis, *S*. Virchow and/or *S*. Hadar)-positive breeding flocks of *Gallus gallus* during the production period, 2007–2015
	2015_SALMTARGETLAY	Prevalence of *S*. Enteritidis and/or *S*. Typhimurium-positive laying hen flocks of *Gallus gallus* during the production period and targets for the Member States, Norway and Switzerland, 2015
	2015_SALMMAPLAY	Prevalence of the two target serovars (*S*. Enteritidis and/or *S*. Typhimurium)-positive laying hen flocks of *Gallus gallus* during the production period, 2015
	2015_SALMLAYTRENDMS	Country-specific temporal trends in prevalence of *Salmonella* two target serovars (*S*. Enteritidis and/or *S*. Typhimurium)-positive laying hen flocks of *Gallus gallus* during the production period, 2008–2015
	2015_SALMTARGETBROIBS	Prevalence of *S*. Enteritidis and/or *S*. Typhimurium-positive broiler flocks of *Gallus gallus* before slaughter and target for the Member States, Iceland, Norway and Switzerland, 2015
	2015_SALMMAPBROIBS	Prevalence of the two target serovars (*S*. Enteritidis and/or *S*. Typhimurium)-positive broiler flocks of *Gallus gallus* before slaughter, 2015
	2015_SALMBROIBSTRENDMS	Country-specific temporal trends in prevalence of *Salmonella* two target serovars (*S*. Enteritidis and/or *S*. Typhimurium)-positive broiler flocks of *Gallus gallus* before slaughter, 2009–2015
	2015_SALMTARGETBREEDTURK	Prevalence of *S*. Enteritidis and/or *S*. Typhimurium-positive breeding flocks of turkeys during the production period and target for the Member States, Iceland, and Norway, 2015
	2015_SALMMAPBREEDTURK	Prevalence of the two target serovars (*S*. Enteritidis and/or *S*. Typhimurium)-positive breeding flocks of turkeys during the production period, 2015
	2015_SALMBREEDTURKTRENDMS	Country-specific temporal trends in prevalence of *Salmonella* two target serovars (*S*. Enteritidis and/or *S*. Typhimurium)-positive breeding flocks of turkeys during the production period, 2010–2015
	2015_SALMTARGETFATTURKBS	Prevalence of *S*. Enteritidis and/or *S*. Typhimurium-positive fattening flocks of turkeys and target for the Member States, Iceland, Norway and Switzerland, 2015
	2015_SALMMAPFATTURKBS	Prevalence of the two target serovars (*S*. Enteritidis and/or *S*. Typhimurium)-positive fattening flocks of turkeys, 2015
	2015_SALMFATTURKTRENDMS	Country-specific temporal trends in prevalence of *Salmonella* two target serovars (*S*. Enteritidis and/or *S*. Typhimurium)-positive fattening flocks of turkeys, 2010–2015

	Figure abbreviation	Figure name
Serovars	2015_SERLAYTREND	*Salmonella* regulated and non-regulated serovars (percentage of isolates per serovar out of the total number of isolates serotyped each year) from laying hens, EU, 2010–2015
	2015_SERBROTREND	*Salmonella* regulated and non-regulated serovars (percentage of isolates of regulated and non-regulated serovars out of the total number of isolates serotyped per year) from broilers, EU, 2010–2015
	2015_SERENTBROTRENDMAP	Distribution of *S.* Enteritidis (percentage out of the total number of serotyped isolates per year) reported from broilers, Europe, 2010–2015
	2015_SERBROPYRAM	Pyramid plot showing the distribution of the most common *Salmonella* serovars between broilers and broiler meat, EU, 2015
	2015_SERTURKTREND	*Salmonella* regulated and non-regulated serovars (percentage of isolates of regulated and non-regulated serovars out of the total number of isolates serotyped per year) from turkey flocks, EU, 2010–2015
	2015_SERTURKPYRAM	Pyramid plot showing the distribution of the most common *Salmonella* serovars between turkeys and turkey meat, EU, 2015
	2015_SERPIGSTREND	The most frequent *Salmonella* serovars (percentage of isolates of each serovar out of the total number of isolates serotyped per year) from pigs, EU, 2010–2015
	2015_SERPIGPYRAM	Pyramid plot showing the distribution of the most common *Salmonella* serovars between pigs and pig meat, EU, 2015
	2015_SERBOVTREND	The most frequent *Salmonella* serovars (percentage of isolates of each serovar out of the total number of isolates serotyped per year) from cattle, EU, 2010–2015
	2015_SERBOVPYRAM	Pyramid plot showing the distribution of the most common *Salmonella* serovars between cattle and bovine meat, EU, 2015
	2015_SERSANKEY	Sankey diagram of the 17 most reported *Salmonella* serovars, in animal species and foods of animal origin, by source, EU, 2015

A.3.2. *Campylobacter*

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_campylobacter.zip

Table abbreviation	Table name
2015_CAMPOVERVIEW	Overview of countries reporting data for *Campylobacter*, 2015

A.3.2.1. Campylobacteriosis in humans

	Table abbreviation	Table name
Humans	2015_CAMPHUMRATES	Reported human cases of campylobacteriosis and notification rates per 100,000 in the EU/EEA, by country and year, 2011–2015

	Figure abbreviation	Figure name
Humans	2015_CAMPHUMTREND	Trend in reported confirmed cases of human campylobacteriosis in the EU/EEA, by month, 2008–2015

A.3.2.2. *Campylobacter* in food and animals

	Table abbreviation	Table name
Food	2015_CAMPBOVMEAT	*Campylobacter* in fresh bovine meat, 2015
	2015_CAMPBOVPROD	*Campylobacter* in ready-to-eat bovine meat products, 2015
	2015_CAMPBROILMEAT	*Campylobacter* in fresh broiler meat, 2015
	2015_CAMPBROILPROD	*Campylobacter* in ready-to-eat broiler meat products, 2015
	2015_CAMPCHEESE	*Campylobacter* in cheeses, 2015
	2015_CAMPMILK	*Campylobacter* in milk, 2015
	2015_CAMPOTHERPOULMEAT	*Campylobacter* in fresh poultry meat other than broiler meat 2015
	2015_CAMPPIGMEAT	*Campylobacter* in fresh pig meat, 2015
	2015_CAMPPIGPROD	*Campylobacter* in ready-to-eat pig meat products, 2015
	2015_CAMPTURKMEAT	*Campylobacter* in fresh turkey meat, 2015
	2015_CAMPTURKPROD	*Campylobacter* in ready-to-eat turkey meat products, 2015
	2015_CAMPUNSPPROD	*Campylobacter* in ready-to-eat unspecified meat products, 2015
Animals	2015_CAMPBROILERS	*Campylobacter* in broilers, 2015
	2015_CAMPCATDOG	*Campylobacter* in cats and dogs, 2015
	2015_CAMPCATTLE	*Campylobacter* in cattle, 2015
	2015_CAMPOTHERAN	*Campylobacter* in other animals, 2015
	2015_CAMPPIGS	*Campylobacter* in pigs, 2015
	2015_CAMPTURKEYS	*Campylobacter* in turkeys, 2015

A.3.3. *Listeria*

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_listeria.zip

Table abbreviation	Table name
2015_LISTERIAOVERVIEW	Overview of countries reporting data for *Listeria*, 2015

A.3.3.1. Listeriosis in humans

	Table abbreviation	Table name
Humans	2015_LISTHUMRATES	Reported cases and notification rates per 100,000 of human listeriosis in 2009–2015

	Figure abbreviation	Figure name
Humans	2015_LISTHUMTREND	Trend in reported confirmed cases of human listeriosis in the EU/EEA, by month, 2008–2015

A.3.3.2. Listeria in food and animals

	Table abbreviation	**Table name**
Food	2015_LISTERIABAKERY	*L. monocytogenes* in RTE bakery products, 2015
	2015_LISTERIACOMPL	Non-compliance with the L. monocytogenes criteria laid down by Regulation (EC) No 2073/2005 in food categories in the EU, 2015
	2015_LISTERIACONF	*L monocytogenes* in RTE confectionary products and pastes, 2015
	2015_LISTERIAEGGPR	*L. monocytogenes* in RTE egg products, 2015
	2015_LISTERIAFISHPR	*L. monocytogenes* in RTE fishery products, 2015
	2015_LISTERIAFISH	*L. monocytogenes* in fish, 2015
	2015_LISTERIAFRUITVEG	*L. monocytogenes* in RTE fruit and vegetables, 2015
	2015_LISTERIAHCCOWPM	*L. monocytogenes* in hard cheeses made from pasteurised milk from cows, 2015
	2015_LISTERIAHCCOWRM	*L. monocytogenes* in hard cheeses made from raw or low heat-treated milk from cows, 2015
	2015_LISTERIAHCGOATPM	*L. monocytogenes* in hard cheeses made from pasteurised milk from goats, 2015
	2015_LISTERIAHCGOATRM	*L. monocytogenes* in hard cheeses made from raw or low heat-treated milk from goats, 2015
	2015_LISTERIAHCMIXEDPM	*L. monocytogenes* in hard cheeses made from pasteurised milk from mixed, unspecified or other animal milk, 2015
	2015_LISTERIAHCMIXEDRM	*L. monocytogenes* in hard cheeses made from raw or low heat-treated milk from mixed, unspecified or other animal milk, 2015
	2015_LISTERIAHCSHEEPPM	*L. monocytogenes* in hard cheeses made from pasteurised milk from sheep, 2015
	2015_LISTERIAHCSHEEPRM	*L. monocytogenes* in hard cheeses made from raw or low heat-treated milk from sheep, 2015
	2015_LISTERIAMILK	*L. monocytogenes* in RTE milk, 2015
	2015_LISTERIAPREPDISH	*L. monocytogenes* in RTE other processed food products and prepared dishes, 2015
	2015_LISTERIARTEBOVINE	*L. monocytogenes* in RTE meat products from bovine animals, 2015
	2015_LISTERIARTEBROIL	*L. monocytogenes* in RTE meat products from broilers, 2015
	2015_LISTERIARTEPIG	*L. monocytogenes* in RTE meat products from pig, 2015
	2015_LISTERIARTETURK	*L. monocytogenes* in RTE meat products from turkey, 2015
	2015_LISTERIASALAD	*L. monocytogenes* in RTE salads, 2015
	2015_LISTERIASCCOWPM	*L. monocytogenes* in soft and semisoft cheeses made from pasteurised milk from cows, 2015
	2015_LISTERIASCCOWRM	*L. monocytogenes* in soft and semisoft cheeses made from raw or low heat-treated milk from cows, 2015
	2015_LISTERIASCGOATPM	*L. monocytogenes* in soft and semisoft cheeses made from pasteurised milk from goats, 2015
	2015_LISTERIASCGOATRM	*L. monocytogenes* in soft and semisoft cheeses made from raw or low heat-treated milk from goats, 2015
	2015_LISTERIASCSHEEPRM	*L. monocytogenes* in soft and semisoft cheeses made from raw or low heat-treated milk from sheep, 2015
	2015_LISTERIASCMIXEDPM	*L. monocytogenes* in soft and semisoft cheeses made from pasteurised milk from mixed, unspecified or other animal milk, 2015
	2015_LISTERIASCMIXEDRM	*L. monocytogenes* in soft and semisoft cheeses made from raw or low heat-treated milk from mixed, unspecified or other animal milk, 2015
	2015_LISTERIASCSHEEPPM	*L. monocytogenes* in soft and semisoft cheeses made from pasteurised milk from sheep, 2015
	2015_LISTERIASAUCE	*L. monocytogenes* in sauce and dressings RTE, 2015
	2015_LISTERIASPICES	*L. monocytogenes* in RTE spices and herbs, 2015

	Table abbreviation	Table name
Animals	2015_LISTERIAANIMALS	*Listeria monocytogenes* and other species in animals, 2015

	Figure abbreviation	Figure name
Food	2015_LISTERIACOMPLFIG	Proportion of single samples at processing and retail in non-compliance with the EU *L. monocytogenes* criteria, 2011–2015
	2015_LISTERIAMEAT	Proportion of *L. monocytogenes*-positive units in ready-to-eat meat categories in the EU, 2015
	2015_LISTERIACHEESE	Proportion of *L. monocytogenes*-positive units in soft and semi-soft cheeses, and hard cheeses made from raw or low heat-treated milk and pasteurised milk, 2015
	2015_LISTERIAFISHFIG	Proportion of *L. monocytogenes*-positive units in ready-to-eat fishery products categories in the EU, 2015

A.3.4. Shiga toxin-producing *Escherichia coli* (STEC)

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_stec.zip

Table abbreviation	Table name
2015_STECOVERVIEW	Overview of countries reporting data for STEC, 2015

A.3.4.1. STEC in humans

	Table abbreviation	Table name
Humans	2015_STECHUMRATES	Reported human cases of STEC infections and notification rates per 100,000 population in the EU/EEA, by country and year, 2011–2015
	2015_STECHUMSEROGROUP	Distribution of reported confirmed cases of human STEC infections in the EU/EEA, 2011–2013, by the 20 most frequent serogroups in 2015

	Figure abbreviation	Figure name
Humans	2015_STECHUMTREND	Trend in reported confirmed cases of human STEC infections in the EU/EEA, by month, 2008–2015

A.3.4.2. STEC in food and animals

	Table abbreviation	Table name
Food and Animals	2015_STECANMETH	Proportion of food and animal samples tested for the presence of STEC with the different analytical methods in the Member States and non-Member States, 2015

	Table abbreviation	Table name
Food	2015_STECBOVINEMEAT	STEC in fresh bovine meat, 2015
	2015_STECBROIMEAT	STEC in fresh broiler meat, 2015
	2015_STECDAIRY	STEC in milk and dairy products, excluding raw milk, 2015
	2015_STECFRUITS	STEC in fruits, 2015
	2015_STECGOATMEAT	STEC in fresh goat meat, 2015
	2015_STECOTHERFOOD	STEC in other food, 2015
	2015_STECOTHERMEAT	STEC in fresh meat from other animal species, 2015
	2015_STECOVINEMEAT	STEC in fresh ovine meat, 2015
	2015_STECPIGSMEAT	STEC in fresh pigs meat, 2015
	2015_STECRAWCOWMILK	STEC in raw cows' milk, 2015
	2015_STECRAWGOATSMILK	STEC in raw goats' milk, 2015
	2015_STECSEED	STEC in sprouted seed, 2015
	2015_STECTURKMEAT	STEC in fresh turkey meat, 2015
	2015_STECVEGETABLE	STEC in vegetables, 2015
	2015_STECTOP5GROUPFOOD	Proportion of positive samples for any STEC and STEC belonging to the 'top-5' serogroups in food categories in the Member States and non-Member States, 2015
	2015_STECNONO157FOOD	Frequency distribution of non-O157 STEC serogroups in food categories in the Member States, 2015
	2015_STECGROUPTRENDFOOD	Proportion of food samples positive for the most frequent STEC serogroups (per 1,000 samples tested), reported by the Member States and non-Member States between 2011 and 2015
	2015_STECFOODCOUNTRY	Proportion of samples tested in each food and animal category (sampling fraction) by reporting country, 2015
	2015_STECMETHCOUNTRYFOODTREND	Proportion of the Member States and non-Member States using the different analytical methods for testing food samples for STEC, between 2011 and 2015
	2015_STECMETHFOODTREND	Proportion of food samples tested for STEC per analytical method, reported by the Member States and non-Member States, 2011–2015
	2015_STECMETHANYO157FOODTREND	Proportion of food samples tested for STEC by the Member States and non-Member States between 2011 and 2015, by using analytical methods specifically aimed at detecting STEC O157 or any STEC, regardless the serotype

	Table abbreviation	Table name
Animals	2015_STECANYO157ANIM	Frequency distribution of STEC serogroups in animals in the Member States, 2015
	2015_STECNONO157ANIM	Frequency distribution of non-O157 STEC serogroups in animals in the Member States, 2015
	2015_STECCATTLE	STEC in cattle, 2015
	2015_STECOTHERANIMAL	STEC in other animals, 2015
	2015_STECOVINEGOAT	STEC in sheep and goats, 2015
	2015_STECPIGS	STEC in pigs, 2015
	2015_STECGROUPTRENDANIM	Proportion of animal samples positive for the most frequent STEC serogroups (per 1,000 samples tested), reported by the Member States between 2011 and 2015
	2015_STECMETHCOUNTRYANIMTREND	Proportion of the Member States and non-Member States using the different analytical methods for testing animal samples for STEC, between 2011 and 2015
	2015_STECMETHANIMTREND	Proportion of animal samples tested for STEC per analytical method, reported by the Member States and non-Member States, 2011–2015
	2015_STECMETHANYO157ANIMTREND	Proportion of animal samples tested for STEC by the Member States and non-Member States between 2011 and 2015, by using analytical methods specifically aimed at detecting STEC O157 or any STEC, regardless the serotype

	Figure abbreviation	Figure name
Food	2015_STECPROPORTIONFOOD	Proportion of STEC-positive samples in food categories in the reporting Member States, 2012–2015
	2015_STECGROUPTRENDFOODFIG	Proportion of food samples positive for the most frequent STEC serogroups (per 1,000 samples tested), reported by the Member States and non-Member States between 2011 and 2015
Animals	2015_STECPROPORTIONANIM	Proportion of STEC-positive samples in animals in the reporting Member States, 2012–2015
	2015_STECGROUPTRENDANIMFIG	Proportion of animal samples positive for the most frequent STEC serogroups (per 1,000 samples tested), reported by the Member States and non-Member States between 2011 and 2015
Food and animals	2015_STECATLASFOODANIM	Relative presence and absence of STEC serogroups in foods and animals, sampled in the EU in 2015
	2015_STECATLASGROUPCOUNTRY	Presence and absence of STEC serogroups in animals and food sampled in 21 Member States and Switzerland in 2015, by reporting country
	2015_STECGROUPATLASTREND	Trends in the presence of the different STEC serogroups in food and animals reported in the EU between 2011 and 2015

A.3.5. *Yersinia*

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_yersinia.zip

Table abbreviation	Table name
2015_YERSOVERVIEW	Overview of countries reporting *Yersinia* data, 2015

A.3.5.1. *Yersinia* in humans

	Table abbreviation	Table name
Humans	2015_YERSHUMRATES	Reported cases and notification rates per 100,000 of human yersiniosis in the EU, 2011–2015

	Figure abbreviation	Figure name
Humans	2015_YERSHUMTREND	Trend in reported confirmed cases of human yersiniosis in the EU/EEA, by month, 2008–2015

A.3.5.2. *Yersinia* in food and animals

	Table abbreviation	Table name
Food	2015_YERSPIGMEAT	*Yersinia* in pig meat and products thereof, 2015
	2015_YERSBOVINEMEAT	*Yersinia* in bovine meat and products thereof, 2015
	2015_YERSMILKDAIRY	*Yersinia* in milk and dairy products, 2015
Animals	2015_YERSPIGS	*Yersinia* in pigs, 2015
	2015_YERSDOMAN	*Yersinia* in domestic livestock other than pigs, 2015
	2015_YERSOTHERAN	*Yersinia* in other animal species, 2015

A.3.6. Tuberculosis due to *Mycobacterium bovis*

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_m.bovis.zip

Table abbreviation	Table name
2015_TUBOVERVIEW	Overview of countries reporting data for tuberculosis due to *M. bovis* for humans and for animals, 2015

A.3.6.1. *Mycobacterium bovis* in humans

	Table abbreviation	Table name
Humans	2015_MBOVHUMRATES	Reported human cases of tuberculosis due to *M. bovis* and notification rates per 100,000 population in the EU/EEA, by country and year, 2011–2015

A.3.6.2. Bovine tuberculosis in cattle

	Table abbreviation	Table name
Animals	2015_DSTUBCOF	Bovine tuberculosis in cattle herds in the cofinanced non-OTF Member States, 2015
	2015_DSTUBOFNCOFCAT	Bovine tuberculosis in cattle herds in the OTF or non-cofinanced non-OTF Member States, 2015
	2015_TUBALL	Complementary reporting on *M. bovis* and on mycobacteria other than *M. bovis*, 2015

	Figure abbreviation	Figure name
Animals	2015_DSTUBPROPINF_OTF	Proportion of cattle herds infected with or positive for bovine tuberculosis, in OTF regions, EU, 2010–2015
	2015_DSTUBPROPINF_nOTF	Proportion of cattle herds infected with or positive for bovine tuberculosis, in non-OTF regions, EU, 2010–2015
	2015_DSTUBMAP	Status of countries regarding bovine tuberculosis, 2015
	2015_DSTUBPROPMAP	Proportion of cattle herds infected with or positive for bovine tuberculosis, 2015
	2015_DSTUBTREND_nOTF	Prevalence of bovine tuberculosis test-positive cattle herds, in non-OTF regions of six non-OTF cofinanced Member States, 2004–2015

A.3.7. *Brucella*

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_brucella.zip

	Table abbreviation	Table name
	2015_BRUCOVERVIEW	Overview of countries reporting data for *Brucella*, 2015

A.3.7.1. Brucellosis in humans

	Table abbreviation	Table name
Humans	2015_BRUCHUMRATES	Reported human cases of brucellosis and notification rates per 100,000 in the EU/EEA, by country and year, 2011–2015

	Figure abbreviation	Figure name
Humans	2015_BRUCHUMTREND	Trend in reported confirmed cases of human brucellosis in the EU, by month, 2008–2015

A.3.7.2. *Brucella* in food and animals

	Table abbreviation	Table name
Food	2015_BRUCFOOD	*Brucella* in food, 2015
Animals	2015_DSBRUCOFCAT	*Brucella* in cattle herds in the cofinanced non-OBF Member States, 2015
	2015_DSBRUOFNCOFCAT	*Brucella* in cattle herds in the OBF or non-cofinanced non-OBF Member States, 2015
	2015_DSBRUCOFOV	*Brucella* in sheep and goat herds in the cofinanced non-ObmF Member States, 2015
	2015_DSBRUOFNCOFOV	*Brucella* in sheep and goat herds in the ObmF or non-cofinanced non-ObmF Member States, 2015
	2015_BRUCOTHERAN	*Brucella* in species other than cattle, sheep and goat, 2015

	Figure abbreviation	Figure name
Animals	2015_DSBRUCCATMAP	Status of countries regarding bovine brucellosis, 2015
	2015_DSBRUCCATPROPMAP	Proportion of existing cattle herds infected with or positive for *Brucella*, country-based data, 2015
	2015_DSBRUCCATPROPINF_nOBF	Proportion of *Brucella*–positive cattle herds, in non-OBF regions, EU, 2012–2015
	2015_DSBRUCCATTREND_nOBF	Prevalence of *Brucella* test-positive cattle herds, in non-OBF regions of four non-OBF cofinanced Member States, 2004–2015
	2015_DSBRUCOVCAPMAP	Status of countries regarding ovine and caprine brucellosis, 2015
	2015_DSBRUCOVCAPPROPMAP	Proportion of existing sheep and goats herds infected with or positive for *Brucella*, country-based data, 2015
	2015_DSBRUCOVPROPINF_nObmF	Proportion of sheep and goat herds infected with or positive for *B. melitensis*, in non-ObmF regions, EU, 2012–2015
	2015_DSBRUCOVCAPTREND_nObmF	Prevalence of *Brucella melitensis* test-positive sheep and goat herds, in non-ObmF regions of five non-ObmF cofinanced Member States, 2004–2015

A.3.8. *Trichinella*

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_trichinella.zip

Table abbreviation	Table name
2015_TRICHOVERVIEW	Overview of countries reporting data on *Trichinella* spp., 2015

A.3.8.1. Trichinellosis in humans

	Table abbreviation	Table name
Humans	2015_TRICHUMRATES	Reported cases and notification rates per 100,000 of human trichinellosis in 2011–2015

	Figure abbreviation	Figure name
Humans	2015_TRICHUMTREND	Trend in reported confirmed cases of human trichinellosis in the EU/EEA, by month, 2008–2015

A.3.8.2. *Trichinella* in animals

	Table abbreviation	Table name
Animals	2015_TRICHHORSE	Findings of *Trichinella* in domestic solipeds, 2015
	2015_TRICHWILDWILDBOAR	Findings of *Trichinella* in hunted wild boar, 2015
	2015_TRICHFOX	Findings of *Trichinella* in foxes, 2015
	2015_TRICHPIGS	Findings of *Trichinella* in pigs other than not raised under controlled housing conditions, 2015
	2015_TRICHPIGSNOT	Findings of *Trichinella* in pigs not raised under controlled housing conditions, 2015
	2015_TRICHFARMEDWILDBOAR	Findings of *Trichinella* in farmed wild boar, 2015

	Figure abbreviation	Figure name
Animals	2015_TRICHFIGUREDOMPIGS	*Trichinella* spp. in domestic pigs of 28 MS and 3 non-MS (IC, NO and CH) in the last 20 years and in 2015.
	2015_TRICHFIGUREWILD	Distribution of *Trichinella* spp. in wildlife of 28 MS and 3 non-MS (IC, NO and CH) in the last 20 years.

A.3.9. *Echinococcus*

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_echinococcus.zip

Table abbreviation	Table name
2015_ECHINOOVERVIEW	Overview of countries reporting data on *Echinococcus* spp., 2015

A.3.9.1. *Echinococcus* in humans

	Table abbreviation	Table name
Humans	2015_ECHINOHUMRATES	Reported cases and notification rates per 100,000 of human echinococcosis in the EU/EEA, 2011–2015

	Figure abbreviation	Figure name
Humans	2015_ECHINOHUMTREND	Reported confirmed cases by species in the selected MS, by month, 2008–2015

A.3.9.2. *Echinococcus* in animals

	Table abbreviation	Table name
Animals	2015_ECHINOFOX	*Echinococcus* findings in foxes, 2015
	2015_ECHINOOTHER	Other *Echinococcus* findings in animals, 2015

	Figure abbreviation	Figure name
Animals	2015_ECHINOFOX_FIGURE_NUTS0_	Pooled prevalence of *Echinococcus multilocularis* in red and Arctic foxes within the European Union and adjacent countries at national level.
	2015_ECHINOFOX_FIGURE_NUTS1_	Pooled prevalence of *Echinococcus multilocularis* in red foxes within the European Union and adjacent countries at NUTS 1 level.
	2015_ECHINOGRANSL_FIGURE	Approximate distribution of *Echinococcus granulosus* s.l. in Europe.
	2015_ECHINOGRANSTRAIN_FIGURE	Approximate geographical distribution of strains/genotypes belonging to *Echinococcus granulosus* s.l. in Europe.

A.3.10. *Toxoplasma*

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_toxoplasma.zip

Table abbreviation	Table name
2015_TOXOOVERVIEW	Overview of countries reporting data for *Toxoplasma*, 2015

A.3.10.1. Toxoplasma in animals

	Table abbreviation	Table name
Animals	2015_TOXOPIGS	*Toxoplasma* in pigs, 2015
	2015_TOXOCATTLE	*Toxoplasma* in cattle, 2015
	2015_TOXOOVINEGOAT	*Toxoplasma* in sheep and goats, 2015
	2015_TOXOCATDOG	*Toxoplasma* in cats and dogs, 2015
	2015_TOXOOTHERAN	*Toxoplasma* in other animal species, 2015

A.3.11. Rabies

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_rabies.zip

Table abbreviation	Table name
2015_RABIESOVERVIEW	Overview of countries reporting data on Lyssavirus, 2015

A.3.11.1. Rabies in animals

	Table abbreviation	Table name
Animals	2015_RABIESCAT	Rabies in cats, 2015
	2015_RABIESDOG	Rabies in dogs, 2015
	2015_RABIESBATS	Rabies in bats, 2015
	2015_RABIESRACCOON	Rabies in raccoon dogs, 2015
	2015_RABIESFARMED	Rabies in farmed animals, 2015
	2015_RABIESFOX	Rabies in foxes, 2015
	2015_RABIESWILD	Rabies in wildlife other than bats, foxes and raccoon dogs, 2015
	2015_RABIESOVERVIEW	Overview of countries reporting data on Lyssavirus, 2015

Figure abbreviation	Figure name
2015_RABIESMAPBATS	*Lyssavirus* cases (included reported EBLV-type 2) in bats, in the EU Member States and non-Member States, 2015
2015_RABIESMAPFOX	Classical rabies or unspecified *Lyssavirus* cases in foxes, in the EU Member States and non-Member States, 2015
2015_RABIESFIGUREANIM	Reported cases of classical rabies or unspecified *Lyssavirus* in animals other than bats, in the Member States and non-Member States, 2006–2015

A.3.12. Q fever

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_q_fever.zip

Table abbreviation	Table name
2015_COXOVERVIEW	Overview of countries reporting data for Q fever, 2015

A.3.12.1. Q fever in humans

	Table abbreviation	Table name
Humans	2015_COXHUMRATES	Reported human cases of Q Fever and notification rates per 100,000 in the EU/EEA, by country and year, 2011–2015

	Figure abbreviation	Figure name
Humans	2015_COXHUMTREND	Trend in reported confirmed cases of human Q fever in the EU/EEA, by month, 2008–2015

A.3.12.2. *Coxiella burnetii* in animals

	Table abbreviation	Table name
Animals	2015_COXCATTLE	Q fever in cattle, 2015
	2015_COXOVINEGOAT	Q fever in sheep and goats, 2015
	2015_COXOTHERAN	Q fever in other animals species, 2015

A.3.13. West Nile Virus

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_wnv.zip

Table abbreviation	Table name
2015_WNVOVERVIEW	Overview of countries reporting data for West Nile Virus, 2015

A.3.13.1. West Nile Virus in humans

	Table abbreviation	Table name
Humans	2015_WNFHUMRATES	Reported human cases of West Nile Fever and notification rates per 100,000 in the EU/EEA, by country and year, 2011–2015

	Figure abbreviation	Figure abbreviation
Humans	2015_WNFHUMTREND	Trend in reported confirmed cases of human West Nile fever in the EU/EEA, by month, 2008–2015

A.3.13.2. West Nile Virus in animals

	Table abbreviation	Table name
Animals	2015_WNVSOLIP	West Nile Virus in solipeds, 2015
	2015_WNVBIRDS	West Nile Virus in birds, 2015
	2015_WNVOTHERAN	West Nile Virus in other animal species, 2015

	Figure abbreviation	Figure abbreviation
Animals	2015_WNVBIRDSMAP	Findings of West Nile Virus in birds in the EU, 2015
	2015_WNVSOLIPMAP	Findings of West Nile Virus in solipeds in the EU, 2015

A.3.14. Tularaemia

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_tularaemia.zip

Table abbreviation	Table name
2015_FRANCISELLAOVERVIEW	Overview of countries reporting data for *Francisella*, 2015

A.3.14.1. Tularaemia in humans

	Table abbreviation	Table name
Humans	2015_TULARHUMRATES	Reported cases and notifciation rates per 100,000 of human tularaemia in the EU/EEA, 2011–2015

	Figure abbreviation	Figure name
Humans	2015_TULARHUMTREND	Trend in reported confirmed cases of human tularaemia in the EU/EEA, 2008–2015

A.3.14.2 *Francisella tularensis* in animals

	Table abbreviation	Table name
Animals	2015_FRANCISELLAANI	*Francisella tularensis* in animals, 2015

A.3.16. Food-borne outbreaks

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_fbo.zip

A.3.16.1. General overview

Table abbreviation	Table name
2015_FBOOVERVIEW	Overview of countries reporting data on food-borne outbreaks, 2015
2015_FBOEVID	Evidence in strong-evidence food-borne outbreaks (including strong-evidence waterborne outbreaks) in the EU, 2015
2015_NOOUTHUM	Number of food-borne outbreaks (including waterborne outbreaks) and human cases, hospitalisations and deaths, reported by the EU Member States and non-Member States, 2015
2015_NOFBOAGENT	Number of food-borne outbreaks (including waterborne outbreaks), human cases, hospitalisations and deaths per causative agent in the EU Member States (including waterborne outbreaks), 2015
2015_FBOVEHIC	Frequency distribution of strong-evidence food-borne and waterborne outbreaks, by implicated food vehicle, reported by the EU Member States, 2015
2015_FBOTOPCOMBOUT	Top-5 combinations (agent/food vehicle) causing the highest number of strong-evidence outbreaks, reported by the EU Member States, 2015
2015_FBOTOPCOMBCASES	Top-5 combinations (agent/food vehicle) causing the highest number of cases in strong-evidence outbreaks, reported by the EU Member States, 2015
2015_FBOTOPCOMBHOSP	Top-5 combinations (agent/food vehicle) causing the highest number of hospitalised cases in strong-evidence outbreaks, reported by the EU Member States, 2015
2015_FBOTOPCOMBDEATHS	Top combinations (agent/food vehicle) causing the highest number of deaths in strong-evidence outbreaks, reported by the EU Member States, 2015

Figure abbreviation	Figure name
2015_FBONUMTREND	Number of food-borne and waterborne outbreaks reported in the EU Member States, from 2010 to 2015
2015_FBOCOUNTRYRATEMAP	Distribution of reporting rate of food-borne and waterborne outbreaks per 100,000 population, in the EU Member States and non-Member States, 2015
2015_FBOCOUNTRYCASESMAP	Distribution of human cases involved in food-borne and waterborne outbreaks per 100,000 population, in the EU Member States and non-Member States, 2015.
2015_FBOAGENTNUMOUT	Distribution of food-borne and waterborne outbreaks per causative agent in the EU Member States, 2015
2015_FBOAGENTTREND	Number of food-borne and waterborne outbreaks reported by causative agent in the EU Member States from 2010 to 2015
2015_FBOVEHICAGENT	Frequency distribution of causative agents associated with strong-evidence food-borne and waterborne outbreaks by implicated food vehicle reported in the EU Member States, 2015
2015_FBOEXPAGENT	Frequency distribution of strong-evidence food-borne and waterborne outbreaks reported in the EU Member States in the different places of exposure, by causative agent, 2015

A.3.16.2. Agent-specific outbreaks

Table abbreviation	Table name
2015_FBOSALM	Strong- and weak-evidence food-borne outbreaks caused by *Salmonella* (excluding waterborne outbreaks), 2015
2015_FBOCAMP	Strong- and weak-evidence food-borne outbreaks caused by *Campylobacter* (excluding waterborne outbreaks), 2015
2015_FBOSTEC	Strong- and weak-evidence food-borne outbreaks caused by STEC (excluding waterborne outbreaks), 2015

Table abbreviation	**Table name**
2015_FBOLISTERIA	Strong- and weak-evidence food-borne outbreaks caused by *Listeria* (excluding waterborne outbreaks), 2015
2015_FBOYERS	Strong- and weak-evidence food-borne outbreaks caused by *Yersinia* (excluding waterborne outbreaks), 2015
2015_FBOVIBRIO	Strong- and weak-evidence food-borne outbreaks caused by *Vibrio* (excluding waterborne outbreaks), 2015
2015_FBOBRUCELLA	Strong- and weak-evidence food-borne outbreaks caused by *Brucella* (excluding waterborne outbreaks), 2015
2015_FBOOTHERBACT	Strong- and weak-evidence food-borne outbreaks caused by other bacterial agents (excluding waterborne outbreaks), 2015
2015_FBOSTROTHBACT	Strong-evidence food-borne outbreaks caused by other bacterial agents (excluding waterborne outbreaks), 2015
2015_FBOBACIL	Strong- and weak-evidence food-borne outbreaks caused by *Bacillus* toxins (excluding waterborne outbreaks), 2015
2015_FBOCLOSTOX	Strong- and weak-evidence food-borne outbreaks caused by *Clostridium* toxins other than C. botulinum (excluding waterborne outbreaks), 2015
2015_FBOBOT	Strong-evidence food-borne outbreaks caused by *Clostridium botulinum* toxins (excluding waterborne outbreaks), 2015
2015_FBOSTAPH	Strong- and weak-evidence food-borne outbreaks caused by staphylococcal (excluding waterborne outbreaks), 2015
2015_FBOVIRUS	Strong- and weak-evidence food-borne outbreaks caused by viruses (excluding waterborne outbreaks), 2015
2015_FBOOTHER	Strong- and weak-evidence food-borne outbreaks caused by other causative agents (excluding waterborne outbreaks), 2015
2015_FBOSTROTHER	Strong-evidence food-borne outbreaks caused by other causative agents (excluding waterborne outbreaks), 2015
2015_FBOCALICIV	Strong- and weak-evidence food-borne outbreaks caused by calicivirus (excluding waterborne outbreaks), 2015
2015_FBOHEPA	Strong- and weak-evidence food-borne outbreaks caused by hepatitis A virus (excluding waterborne outbreaks), 2015
2015_FBOOTHVIRUS	Strong-evidence food-borne outbreaks caused by other viruses (excluding waterborne outbreaks), 2015
2015_FBOSTROTHVIRUS	Strong-evidence and weak-evidence food-borne outbreaks caused by other viruses (excluding waterborne outbreaks), 2015
2015_FBOTRICH	Strong- and weak-evidence food-borne outbreaks caused by *Trichinella* (excluding waterborne outbreaks), 2015
2015_FBOCRYPT	Strong- and weak-evidence food-borne outbreaks caused by *Cryptosporidium* (excluding waterborne outbreaks), 2015
2015_FBOOTHPAR	Strong- and weak-evidence food-borne outbreaks caused by other parasites (excluding waterborne outbreaks), 2015

Figure abbreviation	**Figure name**
2015_FBOSALMVEHIC	Distribution of food vehicles in strong-evidence outbreaks caused by *Salmonella* (excluding waterborne outbreaks) in the EU, 2015
2015_FBOSALMENTVEHIC	Distribution of food vehicles in strong-evidence outbreaks caused by *S.* Enteritidis (excluding waterborne outbreaks) in the EU, 2015
2015_FBOSALMTYPVEHIC	Distribution of food vehicles in strong-evidence outbreaks caused by *S.* Typhimurium (excluding waterborne outbreaks) in the EU, 2015
2015_FBOCAMPVEHIC	Distribution of food vehicles in strong-evidence outbreaks caused by *Campylobacter* (excluding waterborne outbreaks) in the EU, 2015
2015_FBONOROVIRUSVEHIC	Distribution food vehicles in strong-evidence outbreaks caused by norovirus (excluding waterborne outbreaks) in the EU, 2015

Figure abbreviation	Figure name
2015_FBOBACILLUSVEHIC	Distribution of food vehicles in strong-evidence outbreaks caused by *Bacillus* toxins (excluding waterborne outbreaks) in the EU, 2015
2015_FBOCLOSTRBOTVEHIC	Distribution of food vehicles in strong-evidence outbreaks caused by *Clostridium botulinum* toxins (excluding waterborne outbreaks) in the EU, 2015
2015_FBOCLOSTRPERFRVEHIC	Distribution of food vehicles in strong-evidence outbreaks caused by *Clostridium perfringens* toxins (excluding waterborne outbreaks) in the EU, 2015
2015_FBOSTAPHYLVEHIC	Distribution of food vehicles in strong-evidence outbreaks caused by staphylococcal toxins in the EU (excluding waterborne outbreaks) in the EU, 2015

A.3.16.3. Waterborne outbreaks

Table abbreviation	Table name
2015_FBOWATER	List of strong-evidence waterborne outbreaks reported in the EU, 2015

A.3.17 Microbiological Contaminants

http://www.efsa.europa.eu/sites/default/files/scientific_output/documents/4634a_microbiological_contaminants.zip

A.3.17.1. Histamine

Table abbreviation	Table name
2015_HISTAMINEFISH	Histamine in fish and fishery products, 2015
2015_HISTAMINEOTHER	Histamine in other food, 2015

A.3.17.2. Staphylococcal enterotoxins

Table abbreviation	Table name
2015_STAPHENTERCHEESE	Staphylococcal enterotoxins in milk and dairy products, 2015
2015_STAPHENTEROTHER	Staphylococcal enterotoxins in other foods, 2015

A.3.17.3. *Enterobacter sakazakii* (*Cronobacter* spp.)

Table abbreviation	Table name
2015_CRONOBINFDIE	*Cronobacter* in infant formula and dietary foods for special medical purposes, 2015
2015_CRONOBOTHER	*Cronobacter* in other food, 2015