



## The burden of disease caused by botulism

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# Annual Report on Zoonoses in Denmark 2015



## **Annual Report on Zoonoses in Denmark 2015**

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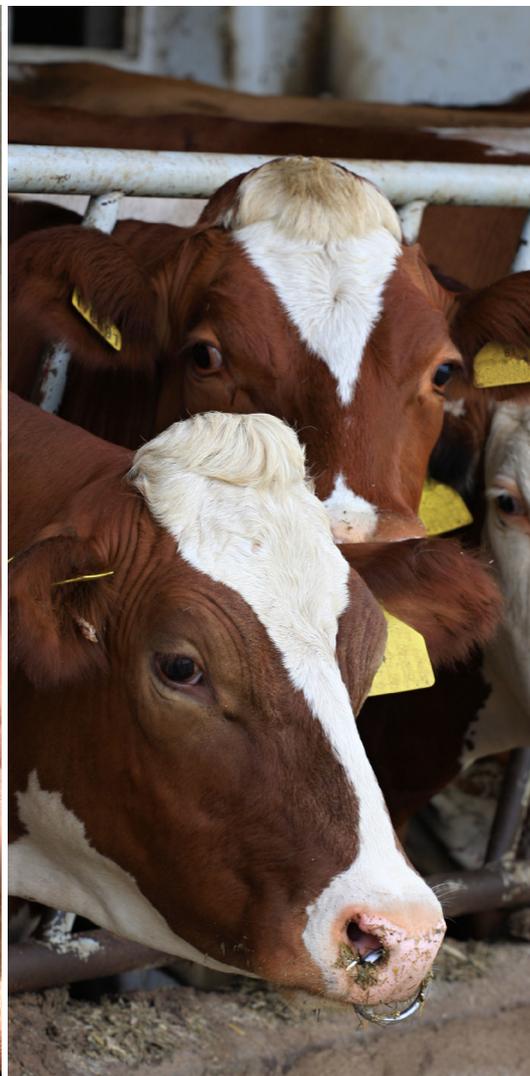
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The Annual Report on Zoonoses presents a summary of the trends and sources of zoonotic infections in humans and animals, as well as the occurrence of zoonotic agents in food and feeding stuffs in Denmark in 2015. Greenland and the Faroe Islands are not represented. The report is based on data collected according to the Zoonoses Directive 2003/99/EC, supplemented by data obtained from national surveillance and control programmes as well as data from relevant research projects. Corrections to the data may occur after publication resulting in minor changes in the presentation of historical data in the following year's report. The report is also available at [www.food.dtu.dk](http://www.food.dtu.dk).



# Introduction

For the first time in the history of the Danish *Salmonella* source account, i.e. since 1988, no cases were attributed to domestic table eggs, and for the fourth time in five years no cases were attributed to domestic broilers. For cases attributed to domestic pork, a noteworthy reduction from 15.4% of cases in 2014 to 3.7% of cases in 2015 was observed. This decrease can partly be explained by the absence of outbreaks related to domestic pork in 2015 for the first time since 2009. In contrast to the past three years, where Danish produced pork has been assessed to be the most important food source of human salmonellosis in Denmark, imported pork took the lead in 2015, estimated to account for 6.6% of the total number of cases.

A total of 925 human cases of salmonellosis were reported in 2015, which is the lowest number of cases since the beginning of the 1980'ies. *S. Enteritidis*, *S. Typhimurium* including monophasic strains continue to be the most common serovars found humans with an incidence of 4./100,000 inhabitants and 4.1/100,000, respectively. In animals, *S. Enteritidis* was only reported from imported broiler meat. Monophasic *S. Typhimurium* was more common than genuine *S. Typhimurium* in domestic pigs and pork, beef and broiler flocks.

Only 39 foodborne outbreaks were registered in 2015, with a total of 1,233 cases registered of which 63 were confirmed in the laboratory. In addition, three *Listeria* outbreaks reported in 2014 had an additional 8 cases in 2015. This is the lowest number of outbreaks since the introduction of the central registration of outbreaks in the Food- and Waterborne Outbreak Database (FUD) in the end of 2005. As in previous years Norovirus was the most frequent cause of foodborne outbreaks (16 outbreaks), and in total, 530 persons were affected by Norovirus outbreaks. One of the outbreaks was waterborne and involved 142 persons attending a concert. Heavy rain the night before the event had resulted in a flooding of sewage water and it is likely that this contaminated the water supply for a specific drink stand at the concert. A large outbreak due to *Campylobacter* caused by a lunch catering company involved 110 persons. The source was never identified, but a questionnaire study pointed out leafy green as the probable source. However it cannot be concluded whether the greens were the original source of *Campylobacter* or the vehicle due to cross contamination from other food items in the kitchen.

The highest level of human infections with *Campylobacter* was recorded in 2015 (4,348 cases), but it is not possible to determine if the reason for this increase was

due to changes in the reporting system as data are now extracted directly from the Danish Microbiology Database (MiBa), changes in the diagnostic practice as diagnostic PCR directly on faeces samples was being introduced, or if it represented a true increase in number of cases.

## Estimating the true burden of foodborne disease in Denmark

*Campylobacter*, *Salmonella* and vero-toxin producing *E. coli* (VTEC) have been amongst the leading causes of foodborne disease in Denmark in the last decades. Public health surveillance data allow us to identify food safety problems and the need for interventions in the food chain, but we know that they represent only the tip of the iceberg, and that the real number of cases in the population is largely unknown. The true burden of diseases caused by these pathogens in the period between 2013 and 2015 was estimated by accounting for the level of under-reporting and underdiagnoses of these diseases, and by estimating their overall health impact. For each reported human infection of *Salmonella*, *Campylobacter* and VTEC approximately 7, 12 and 19 people were estimated to be infected and ill, respectively. This led to an estimate of a total of between 7,800-9,600 cases of salmonellosis, 45,500-52,600 cases of campylobacteriosis, and 2,800-3,900 of VTEC infections annually in the time period.

## Vector-borne zoonoses

Cities in Denmark are changing and urban planning increasingly includes recycling and storage of water for environmental and recreational purposes. In 2015, a pilot study examining the impact of urban water projects was therefore conducted in Copenhagen City comparing green backyards with water project with traditional backyards. On average four times more mosquitoes of *Culex pipiens/torrentium* were collected in the green backyards than in the traditional backyards. This suggests that future urban development projects in Denmark should consider the potential for inadvertently creating a mosquito nuisance or even a health risk.

In another project, tick nymphs of *Ixodes ricinus* collected during 2013 were screened for bacteria and parasites. In total, 12 different pathogens were identified; the most common was *Borrelia* with 14% being positive for one or more of the 7 species of *Borrelia* identified. *Rickettsia helvetica* was the second most prevalent followed by *Anaplasma phagocytophilum*, *Neoehrlichia mikurensis* and two species of *Babesia* parasites.

# 1. Trends and sources in human salmonellosis

By Nanna Sophia Mucha Munck (nsmm@food.dtu.dk), Leonardo de Knegt, Birgitte Helwich and Tine Hald

*Salmonella enterica* causes salmonellosis and remains an important cause of foodborne disease throughout the world. Salmonellosis is a significant cause of morbidity, mortality and economic loss worldwide.

In 2015, a total of 925 human cases of salmonellosis were reported in Denmark, corresponding to an incidence of 16.3 cases per 100,000 inhabitants, which is the lowest number of cases since the beginning of the 1980'ies (Fig 1.1). The incidence of *S. Enteritidis* was 4.6/100,000 in habitants, continuing the decreasing trend seen from both 2014 (4.8/100,000) and 2013 (6.2/100,000). The incidence of *S. Typhimurium* was 4.1/100,000 in 2015 which was a decrease from 7.6/100,000 in 2014. There were almost identical number of cases with classical and monophasic *S. Typhimurium* strains (2.0/100,000 and 2.1/100,000, respectively) in 2015.

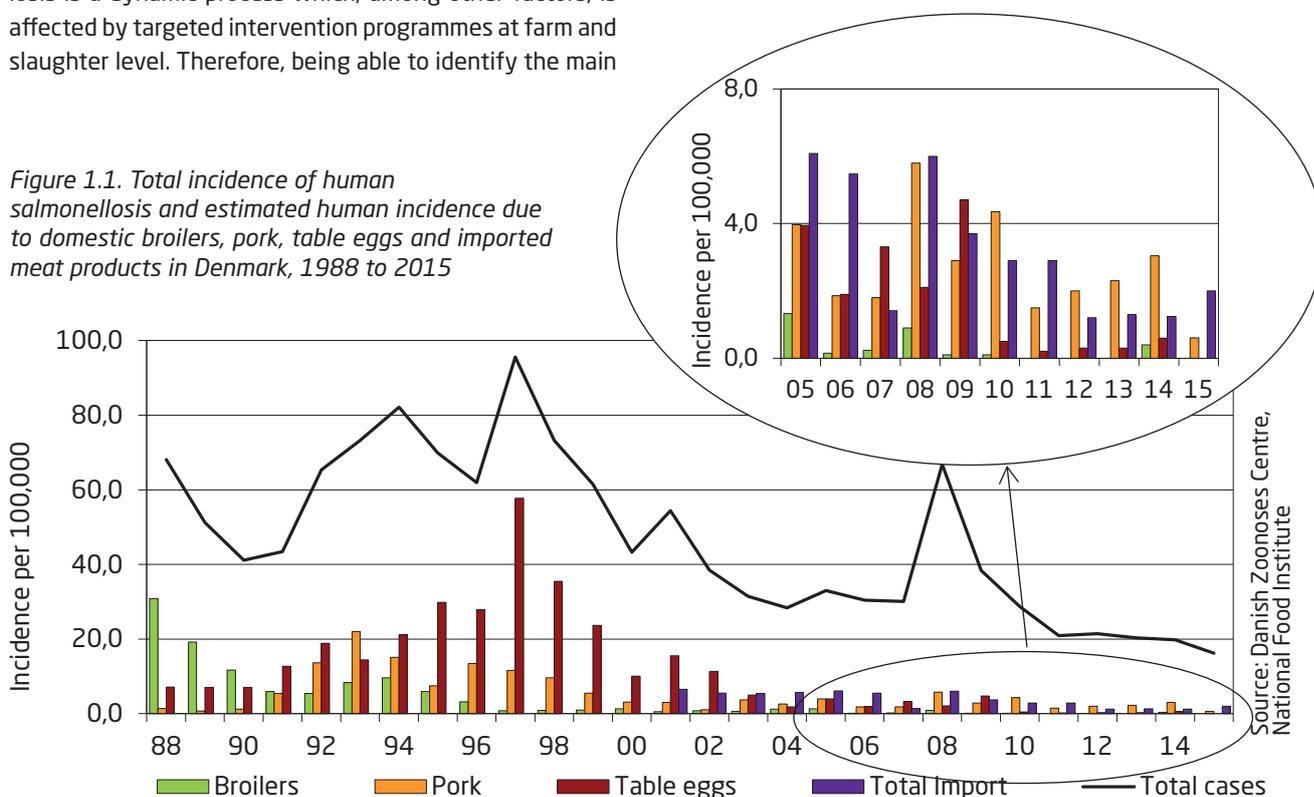
The contribution of different animal reservoirs and food sources to the total number of human cases of salmonellosis is a dynamic process which, among other factors, is affected by targeted intervention programmes at farm and slaughter level. Therefore, being able to identify the main

causative food sources of *Salmonella* is a solid support to risk management decisions, allowing for the evaluation of implemented interventions, as well as for the need of new ones. For that purpose, the Danish Zoonosis Centre, National Food Institute, uses a source attribution model to obtain yearly estimates of the contribution of the major animal-food sources to human infections of *Salmonella*. The principle of the method is to compare the number of human cases caused by different *Salmonella* subtypes with the distribution of the same subtypes isolated from various animal-food sources.

*Salmonella* subtypes are defined by serotyping (all isolates), Multiple Locus Variable Number Tandem Repeat Analysis, MLVA-typing (*S. Enteritidis* and *S. Typhimurium* including the monophasic variants) and resistance profiling (*S. Typhimurium* including monophasic variants).

MLVA profiles for *Salmonella* are defined by the number

Figure 1.1. Total incidence of human salmonellosis and estimated human incidence due to domestic broilers, pork, table eggs and imported meat products in Denmark, 1988 to 2015



Source: Danish Zoonosis Centre, National Food Institute.

of repetitions observed in five independent loci, namely SE1, SE5, SE2, SE9, and SE3 for *S. Enteritidis*, and STTR9, STTR5, STTR6, STTR10, and STTR3 for *S. Typhimurium*. For source attribution purposes, the level of discrimination of the original schemes was reduced for *S. Typhimurium* to include information on only three loci (STTR9|STTR10|STTR3), whereas the complete scheme was used for *S. Enteritidis*, as described by de Knecht et al. [1]. MLVA typing results of *S. Dublin* were not included in the source account in 2015 as isolates from human cases were not subjected to this analysis. The potential impact of that decision on the source account results is discussed below. In the source account model, monophasic strains of *S. Typhimurium* [4,12:i:- and 4,5,12:i:-] were separated from classical *S. Typhimurium*, to better identify any epidemiological shifts by those types.

### Salmonella source account 2015

The overall trend in human salmonellosis cases attributable to the major food-animal sources is presented in Figure 1.1. For the first time in the history of the Danish *Salmonella* source account, i.e. since 1988, no cases were attributed to domestic table eggs.

In contrast to the past three years, where Danish produced pork has been assessed to be the most important food source of human salmonellosis in the country, imported pork took the lead in 2015 (Figure 1.2, appendix A1), constituting 6.6% of the total number of cases.

For cases attributed to domestic pork, a noteworthy reduction from 15.4% of cases in 2014 to 3.7% of cases in 2015 was observed. This decrease can partly be explained by the absence of outbreaks related to domestic pork in 2015 (4.6% of cases attributed to domestic pork in 2014), for the first time since 2009. A minor reduction was seen for cases attributed to domestically produced beef when compared with 2014 (from 2.2% of cases in 2014 to 1.4% in 2015). However, this reduction may in fact be larger,

but due to the lack of MLVA-typing of *S. Dublin*, further discrimination between subtypes of this serovar was not possible, resulting in the attribution of the majority of all non-travel related *S. Dublin* cases to this source.

No cases were attributed to domestically produced table eggs and broilers in 2015. There were no monitoring samples available from Danish produced ducks in 2015, so the impact of this source could not be estimated.

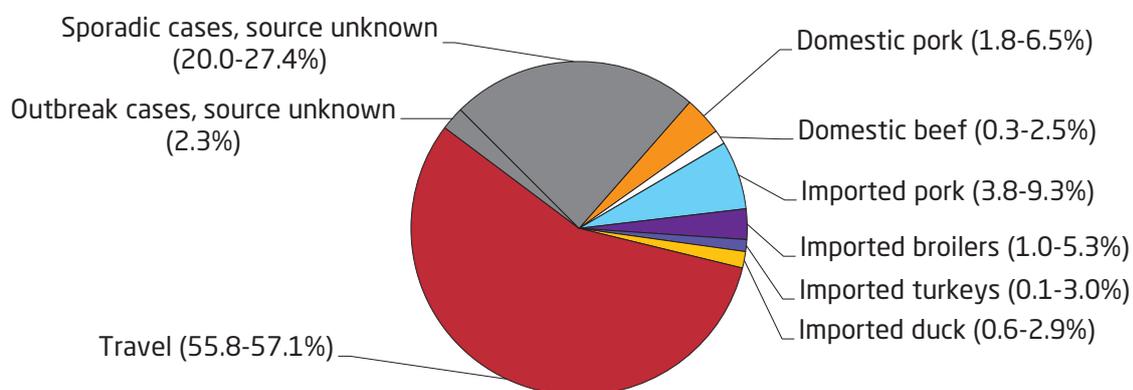
As for imported food, broilers, turkey and ducks were responsible for 2.9%, 1.2% and 1.6% of cases, respectively. No cases were attributed to imported beef, as the only serovar identified in this food source was *S. Indiana*, which was not reported as a cause of human salmonellosis in 2015.

A total of 56.5% of all cases was estimated to be travel-related, meaning that they reported travelling abroad within seven days prior to onset of disease symptoms. This is a relative increase compared to last year (48% in 2014), although the actual number of cases represent a small decrease. Of the 258 reported *S. Enteritidis* cases, 78.0% was estimated to be travel-related, which is consistent with the share for 2014 (77.9%). A total of 233 *S. Typhimurium* cases were reported in 2015, including 116 cases of classical *S. Typhimurium* and 117 cases of two monophasic strains [4,12:i:- and 4,5,12:i:-]. Of the 233 *S. Typhimurium* cases, a third (33.8%) was related to travel.

A total of 23.8% of *Salmonella* cases could not be associated to any of the sources included in the attribution model. This is in line with previous years. Cases allocated to unknown source may be associated with exposure to foods not included in the national surveillance programs, or by non-food sources such as direct contact with pet animals or person-to-person transmission.

Three *Salmonella* outbreaks causing 24 cases were reported in 2015. No source was identified for any of the outbreaks, which were caused by monophasic *S. Typhimurium* (6 cases), *S. Newport* (6 cases) and *S. Oranienburg* (12 cases).

Figure 1.2. Estimated sources of 925 cases of human salmonellosis in Denmark, 2015. (See also Appendix Table A1)



### Antibiotic resistance in *S. Typhimurium*

The panel of antibacterial agents used to compose the resistance profiles for this year changed a little, when compared to the previous years as Cefotaxime and Ceftazidime were included, replacing Ceftiofur.

Resistance information was available for 14 of the *S. Typhimurium* cases attributed to domestic food products. The majority (13 cases) was caused by resistant strains, while a single case was caused by a susceptible strain (Figure 1.3).

This year, resistant *S. Typhimurium* strains (52 cases) dominated among cases attributed to imported food sources with a resistance profile, which is an increase compared to the previous three years, when between 10 to 14 cases had resistant strains. In contrast, a reduction in cases caused by susceptible strains was seen. Thus, annual variations in the relative distribution of resistance patterns observed in previous years for *S. Typhimurium*

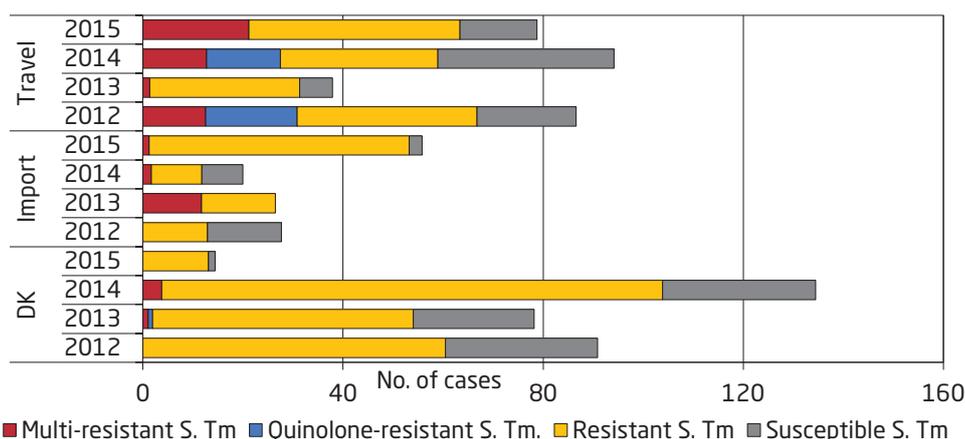
cases attributed to imported food sources continued (Figure 1.3).

Of the 79 *S. Typhimurium* cases estimated to be travel-related, for which resistance information was available, 27% was caused by multi-resistant types, 54% was caused by resistant types and 19% was caused by types susceptible to all tested antimicrobial agents. No quinolone resistant strains were observed among cases related to domestic food, imported food or travel (Figure 1.3).

### References

1. de Knecht LV, Pires SM, Löfström C, Sørensen G, Pedersen K, Torpdahl M, Nielsen EM & Hald T. (2016). Application of Molecular Typing Results in Source Attribution Models: The Case of Multiple Locus Variable Number Tandem Repeat Analysis (MLVA) of *Salmonella* Isolates Obtained from Integrated Surveillance in Denmark. *Risk Anal.* 36(3): 571-588.

Figure 1.3. Distribution of antimicrobial resistance<sup>a</sup> in *S. Typhimurium*, including *S. 1,4,[5],12:i:-*, from human infections attributed to domestic or imported food sources, or travel in the *Salmonella* source account, 2012-2015



a) Resistant: Resistant towards one to three antimicrobial agents; Multi-resistant: Resistant towards four or more antimicrobial agents. Antimicrobials in the resistance profile for the *Salmonella* source account were: ampicillin, ceftiofur or cefotaxime/ceftazidime, chloramphenicol, ciprofloxacin, gentamicin, nalidixic acid, sulphamethoxazole, tetracycline and trimethoprim.

Source: Danish Zoonosis Centre, National Food Institute.

## Where do we acquire *Salmonella* infections?

By Luise Müller (lum@ssi.dk)

In 2015, as in the previous years, Statens Serum Institut attempted to interview all registered *Salmonella* cases where no travel information was reported by the general practitioner. The patients were asked about the date of disease onset and whether they had travelled abroad within a seven-day period prior to disease onset. This information was complemented with information from general practitioners' reports. Travel information was obtained from a total of 82.7% of the *Salmonella* cases in 2015. Among the cases with known travel history, 56.6% were infected abroad (Table 1.1). However, the proportion of travel-related cases varied greatly between the different serotypes, hence 78.2% of the *S. Enteritidis* cases, 32.7% of the *S. Typhimurium* cases, 34.3% of the monophasic *S. 1,4,[5],12:i:-* cases and 55.7% of cases with other serotypes were infected abroad. In 2015, the majority of travel-related cases travelled to Turkey (18.9%), Thailand (15.7%), and Spain (7.9%). No travel-related outbreaks due to salmonella were registered in 2015 (Figure 1.4).

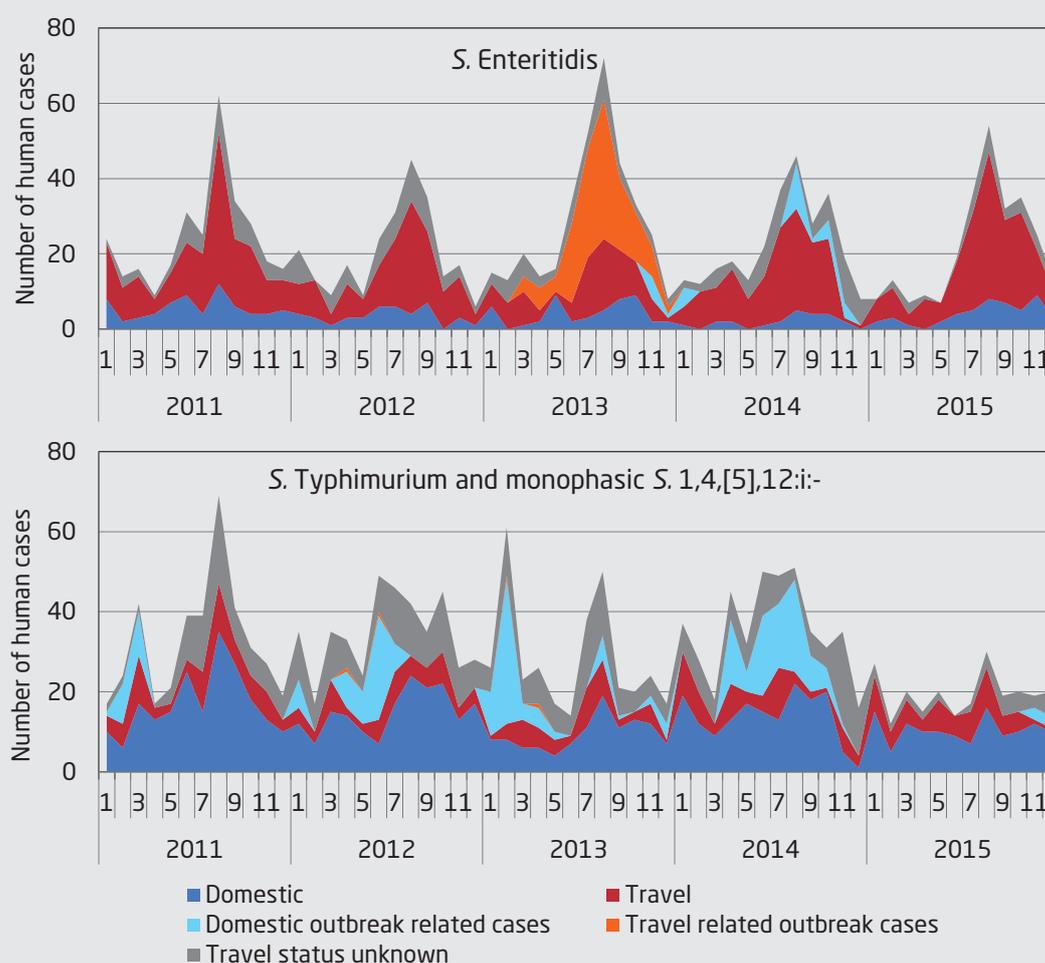
Table 1.1. Top 10 Salmonella serotypes in humans and information about travel abroad, 2014-2015

2015	Number of patients (%)	% of patients <sup>a</sup> infected Abroad <sup>b</sup>	% of patients <sup>a</sup> infected Domestically	2014	Number of patients (%)	% of patients <sup>a</sup> infected Abroad <sup>b</sup>	% of patients <sup>a</sup> infected Domestically
Enteritidis	258 (27.9)	78.2	21.8	Enteritidis	268 (23.9)	77.2	22.8
1,4,[5],12:i:-	117 (12.6)	34.3	65.7	1,4,[5],12:i:-	230 (20.5)	12.7	87.3
Typhimurium	116 (12.5)	32.7	67.3	Typhimurium	197 (17.6)	31.2	68.8
Newport	32 (3.5)	50.0	50.0	Infantis	38 (3.4)	26.1	73.9
Oranienburg	24 (2.6)	25.0	75.0	Dublin	21 (1.9)	0	100
Infantis	21 (2.3)	53.3	46.7	Stanley	21 (1.9)	81.3	18.8
Stanley	21 (2.3)	80.0	20.0	Newport	19 (1.7)	50.0	50.0
Dublin	19 (2.1)	30.0	70.0	Virchow	18 (1.6)	77.8	22.2
O:4,5,12; H:b:-	17 (1.8)	54.5	45.5	Agona	16 (1.4)	28.6	71.4
Java	16 (1.7)	71.4	28.6	Kentucky	16 (1.4)	58.3	41.7
Other serotypes	284 (30.7)	57.8	42.2	Other serotypes	278 (24.8)	59.0	41.0
Total	925 (100)	56.6	43.4	Total	1,122 (100)	46.4	53.6

a) Patients with unknown travel information (17.3 of all patients in 2014 and 28.8 of all patients in 2015) were excluded from the percent calculations.

b) Infected abroad is defined as travel abroad in a seven-day period prior to disease onset.

Source: Statens Serum Institut.

Figure 1.4. Monthly distribution of *S. Enteritidis* and *S. Typhimurium* incl. monophasic *S. 1,4,[5],12:i:-* cases, 2011-2015

Source: Statens Serum Institut.

## 2. Food- and waterborne outbreaks

### By the Central Outbreak Management Group

Food- and waterborne outbreaks in Denmark are reported in the Food- and waterborne Outbreak Database (FUD). Outbreaks that occurred in 2015 are presented in Appendix Table A4. Figure 2.1 shows the relative distribution of these outbreaks by the different causative agents. Household outbreaks and clusters that could not be verified as common source outbreaks are not included. The outbreak investigation procedures in Denmark are described in further details in Chapter 8.

In total, 39 foodborne outbreaks were reported to FUD in 2015 (Appendix Table A4). This is the lowest number of outbreaks since the introduction of the central registration of outbreaks in the Food- and waterborne Outbreak Database (FUD) in the end of 2005. There appear to be no single explanation to this. The decrease is mainly seen in outbreaks caused by Norovirus, *Salmonella* and *Listeria* while outbreaks caused by other agents are stable in numbers. Some of the decrease in *Listeria* outbreaks may be due to the intensive focus and efforts at the production sites investigating presence of *Listeria* in both products and environment (see also Annual report on Zoonoses in Denmark 2014). The decrease seen for Norovirus may be due to the focused campaigns on the issue towards restaurants and catering establishments especially at the times of seasonal festive events and holidays.

In total, the number of persons affected by foodborne outbreaks was 1,233, with a median of 21 persons per

outbreak (range 2 - 142). The outbreaks were mainly regional or local outbreaks (89%) and only two outbreaks were considered national outbreaks. The largest outbreak involving 142 persons was a waterborne outbreak caused by Norovirus (FUD1464), see description below in section 2.1. In 2015 as well as in 2014 a marked decrease in the number of outbreaks registered has been seen.

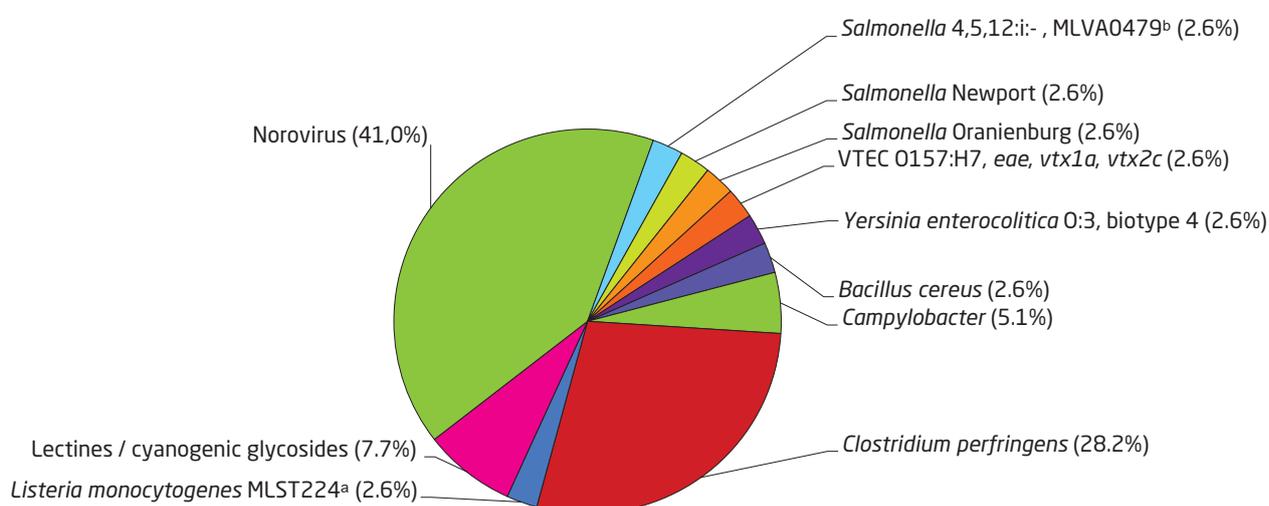
In 2015, *Clostridium perfringens* was associated with 11 foodborne outbreaks affecting a total of 423 people compared to 7, 16, and 8 outbreaks caused by this agent in 2014, 2013, and 2012 respectively.

When dividing the outbreaks into reported settings, the most frequent setting was restaurants (41%) with 16 outbreaks affecting 301 people (mean: 17 people per outbreak). Outbreaks taking place in workplace canteens and catering (10 outbreaks) also affected a high number of people (587 people) and affected on average 59 persons per outbreak. Composite meals (12 outbreaks) and buffet meals (12 outbreaks) were the most frequently reported sources of outbreaks in 2015 and most often these outbreaks were associated with NoV or *C. perfringens* (Appendix Table A4).

### 2.1 Norovirus outbreaks

As in previous years Norovirus was the most frequent cause of foodborne outbreaks (16 outbreaks), and in total, 530 persons were affected by Norovirus outbreaks. The transmission routes for Norovirus causing foodborne outbreaks

Figure 2.1. Aetiology of the 39 foodborne disease outbreaks reported with a causative agent in the Food- and waterborne Outbreak Database (FUD), 2015. Percentage of total outbreaks indicated in brackets



Source: Food- and waterborne Outbreak Database (FUD).

were multiple. In Table 2.1 a breakdown of the number of outbreaks and the number of people affected per route of transmission for 2014-15 are shown. The most common way of infection with Norovirus in 2015 was contamination from ill kitchen or healthy carrier among kitchen staff. In 2015, this way of infection constituted 56% of the Norovirus outbreaks. An increase in the number of outbreaks and persons affected caused by ill guest attending a buffet was seen in 2015 compared to 2014. This way of contamination deserves continued focus. Less often, the infection originated from contaminated ready-to-eat products like oysters and frozen berries.

## 2.2 Outbreaks with *Salmonella*

In 2015, three outbreaks of *Salmonella* with patients in two or more regions were reported in FUD. The first outbreak - caused by *S. Newport* with a specific PFGE type- occurred in March-April 2015, where six people got ill (FUD1453). Interviews with cases showed that four patients had visited the same café in Jutland and one had a non-ill girlfriend working in the same café. The last case was from Copenhagen and had not been to Jutland prior to disease onset. Trace-back investigations did not reveal any common ingredients from the café in Jutland and restaurants in the Copenhagen area where the last case had been. Even though the source was not found, the conclusion of the investigation was that it is likely that cross-contamination from poultry or meat to other dishes had happened at the café in Jutland.

The second *Salmonella* outbreak was due to *S. Oranienburg* (FUD1469). This was a long-lasting outbreak from July 2015 to January 2016 with 14 cases genetically clustering by whole-genome-sequencing. The patients were only adults, 30-86 years old and the majority were male (62%). The patients lived in Jutland, Zealand and Funen and one patient resided on the Faroe Islands. Despite in-depth interviews, no source of the outbreak was identified.

The third outbreak was caused by *S. 4,5,12:i:-*, with a specific MLVA type, with six patients from November 2015 to December 2015 and three from January 2016 (FUD1487). The patients lived in Jutland and Zealand, they were 9-93

years old and four were female (44%). The source was not identified for this outbreak.

## 2.3 Other outbreaks of interest

In September 2015, an increase of *Yersinia* biotype 4, serotype 3 in Mid Jutland was seen (FUD1468). Interviews revealed that a point source outbreak had occurred after a handball cup with boys and girls aged 13-14 years. This outbreak had not been reported to the local authorities. In all, 375 participated in the handball cup and approximately 60 got ill. The source was not identified. In September, fourteen patients with *Yersinia* biotype 4, serotype 3 were registered at the national laboratory notification system and of these, three were found to be a part of the handball cup outbreak. It was not possible to identify any food item served at the handball cup and eaten by the sporadic cases. *Yersinia* biotype 4, serotype 3 is common in Denmark and further subtyping was not performed.

In May, a large outbreak was seen caused by a national lunch catering company (FUD1455). During one week in May, the catering company had served food for approximately 700 persons and electronic questionnaire survey showed that 110 got ill with diarrhea, stomach pain and/or fever. The median age was 36 years and 69 (63%) were male. Laboratory tests of six persons showed that the outbreak was caused by *Campylobacter*. The questionnaire study pointed out leafy greens as the possible source. However it cannot be concluded whether the greens were the original source of *Campylobacter* or the vehicle due to cross contamination from other food items in the kitchen.

A waterborne outbreak occurred after a free concert event 15 August 2015 in Funen (FUD1464). Around 142 got ill with vomiting and diarrhea. A cohort study with 35 persons showed a higher risk of getting ill among persons who had consumed slush ice drinks from a specific drink stand at the concert. Heavy rain the night before the event had resulted in a flooding of sewage water and it is likely that this contaminated the water supply for a drink stand. Norovirus genogroup II was found in three patients and in the water supply.

Table 2.1. Norovirus outbreaks per route of transmission based on number of cases or number of outbreaks, 2014-2015

Transmission route/source	2015		2014	
	No. of outbreaks	No. of persons ill	No. of outbreaks	No. of persons ill
Ill kitchen staff or healthy carrier of virus among kitchen staff	5	153	11	507
Kitchen staff tending to ill persons at home before entering the kitchen	4	96	6	729
Ill person/guest attending a buffet	4	108	2	43
Seafood (oysters)	1	22	3	40
Frozen raspberries/strawberries	1	9	2	20
Water	1	142	0	0
Total	16	530	24	1,339

Source: Food- and waterborne Outbreak Database (FUD).

# 3. Estimating the true burden of foodborne diseases in Denmark

By Sara Monteiro Pires (smpi@food.dtu.dk)

Foodborne diseases cause substantial health and economic burden worldwide. Recent WHO estimates show that 1 in 10 people get ill from food contaminated with pathogens or chemicals annually, resulting in 600 million cases and 420,000 deaths worldwide<sup>1</sup>. This study showed that the most important causes of foodborne disease in Europe are norovirus, *Campylobacter* and *Salmonella*, causing over 20 million illnesses each year. While these estimates are crucial to raise awareness and guide policies, they are the product of an enormous research initiative that faced substantial data challenges. Precise national disease burden estimates are essential to inform policy-makers and allocate food safety resources.

Many foodborne diseases are notifiable in Denmark, and public health surveillance data allow us to identify food safety problems and highlight the need for interventions in the food chain. Still, we recognize that they represent only the tip of the iceberg, and that the real number of cases in the population is largely unknown.

The gap between the true number of cases caused by contaminated foods and what is captured by public health surveillance systems can be easily explained: for a case to be identified, the ill person must seek medical care; the doctor must request a sample; the causative pathogen must be identified at a laboratory; and the results must be reported to public health officials. Any failure in this process leads to under-diagnosis and under-reporting.

But even knowledge on the true incidence of different diseases (i.e. corrected for under-reporting) is insufficient to make conclusions about the overall health impact of each disease in the population. Even though the most common clinical presentation of foodborne bacterial infections takes the form of gastrointestinal symptoms, such infections can also lead to chronic, life-threatening symptoms including neurological, immunological disorders and death. These long term effects and sequelae may be difficult to account for and to link to earlier occurring foodborne infections, but they have an important impact on the overall disease burden.

Burden of disease studies have been recognized as a powerful tool to enable policy makers and other stakeholders to set appropriate, evidence-based priorities in the area of food safety. These use harmonized health metrics such as the disability adjusted life year (DALY), which translates the health impact of a disease in the population

by taking into account not only its frequency, but also the duration and severity of its symptoms, thus allowing for a comparison between different diseases and risk factors. At the National Food Institute and under the Metrix Project<sup>a</sup>, we are developing methods to estimate the burden of a range of foodborne diseases caused by microbial agents, chemical hazards and diet-associated risk factors. These estimates will then be used to rank diseases in Denmark according to their overall health impact in the population, and ultimately to inform risk management strategies in the area of food and health.

## 3.1 Burden of disease by *Campylobacter*, *Salmonella* and vero-toxin producing *E. coli* (VTEC) in Denmark, 2013-2015

*Campylobacter*, *Salmonella* and vero-toxin producing *E. coli* (VTEC) have been amongst the leading causes of foodborne disease in Denmark in the last decades. While food safety interventions implemented in animal and food production have been clearly successful and resulted in a notorious reduction in the incidence of human salmonellosis over the last years, infections caused by *Campylobacter* and VTEC have been either stable or increasing in the population.

We estimated the burden of diseases caused by these pathogens in Denmark in the period between 2013 and 2015 by estimating the level of under-reporting and under-diagnosis of these diseases, and by estimating their overall health impact in terms of DALYs. A detailed description of the methods has been published elsewhere<sup>2</sup>.

To estimate the total incidence of these diseases in Denmark, we have derived multiplication factors that translate the probability that a patient seeks care, is diagnosed with infection by a specific foodborne pathogen, and the case is reported, and applied it to surveillance data from 2013 to 2015. To account for differences in the incidence of disease in different strata of the population, we have categorized reported cases into six age categories and gender.

We assumed that the degree of underreporting of disease by each pathogen was constant over these years.

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a) The Metrix Project is funded by the National Veterinary and Food Authorities, Ministry of Environment and Food of Denmark and aims at performing integrated analyses of the health risks and benefits of food, nutrients, and food diets, as well as ranking foodborne diseases on the basis of their health and economic burden in Denmark.

We estimated that for each reported *Salmonella* infection, around seven (95% Confidence Interval, CI: 4.2-15.6) people were in fact infected and ill. This estimate was higher for *Campylobacter* (12 infections; 95% CI: 6.6- 20.8) and even higher for VTEC, for which we estimated that only 1 in 19 cases were captured by public health surveillance (95% CI:16.6-27).

These led to an estimate of a total of between 7,800-9,600 cases of salmonellosis, 45,500-52,600 cases of campylobacteriosis, and 2,800-3,900 of VTEC infections annually in the time period (Tables 3.1 to 3.3). While *Salmonella* and VTEC infections are more common among children under 5 years of age than in other age groups, age differences were less evident in campylobacteriosis (Figure 3.1). No gender differences were observed (results not shown).

The ranking of the three diseases in terms of DALYs followed the same as the estimated incidence. The pathogen causing the highest burden of disease from 2013-2015 was *Campylobacter* (1,542-1,886 DALYs), followed by *Salmonella* (348-401 DALY's) and VTEC (30-42 DALY's). The contribution of sequelae of the different infections for the burden of the diseased varied (Figure 3.2). The

largest contribution for disease burden of salmonellosis and campylobacteriosis came irritable bowel syndrome reactive arthritis. For VTEC cases, end-stage renal disease, although rare leads to a substantial burden of disease.

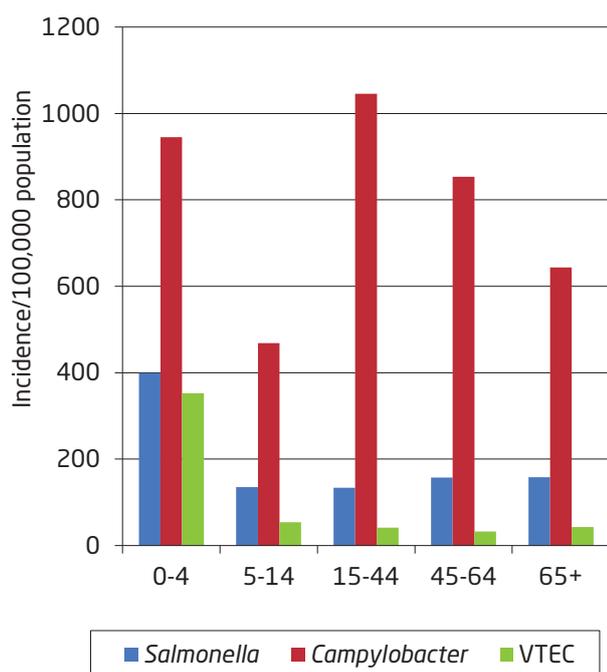
Our results show that, among the three studied food-borne pathogens, *Campylobacter* is the one causing the highest burden of disease in Denmark. These findings highlight the importance of intervention strategies in the food chain targeted at reducing this burden in the population.

The presented burden of disease estimates rely on a number of assumptions and on data collected from a variety of studies because of still existing knowledge gaps. We are currently conducting further epidemiological studies to address these gaps, and will use upcoming evidence to revise our current estimates in the future. At this point, the estimates represent the best available evidence of the burden of these foodborne diseases in Denmark.

### 3.2 How are these estimates useful?

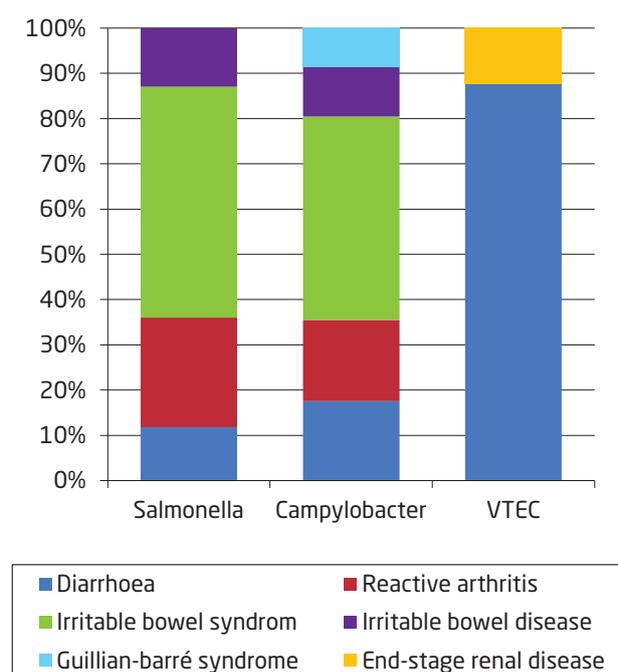
Because burden of disease studies quantify the health impact of diseases in a population by integrating information on the incidence, mortality and disability caused by all potential harmful health effects of these diseases, they

Figure 3.1. Estimated burden on disease distributed by agegroup, incidence/100,000 population, 2013-2015



Source: National Food Institute and Statens Serum Institut

Figure 3.2. Relative contribution of disease sequelae for total DALYs, 2013-2015



Source: National Food Institute and Statens Serum Institut

Table 3.1. Estimated burden of diseases caused by Salmonella, 2013-2015

	2013	2014	2015
	Mean 95% CI	Mean 95% CI	Mean 95% CI
Reported cases	1.132	1.123	925
Total cases	9,584 [4,106; 1,4512]	9,478 [4,144; 20,319]	7,807 [3,368; 17,072]
Deaths	13	13	11
DALY Total	401 [388; 415]	390 [377; 404]	348 [226; 360]
YLD	273 [259; 286]	271 [258; 285]	251 [240; 263]
YLL	129	119	97

Source: National Food Institute and Statens Serum Institut

Table 3.2. Estimated burden of diseases caused by Campylobacter, 2013-2015

	2013	2014	2015
	Mean 95% CI	Mean 95% CI	Mean 95% CI
Reported cases	3.779	3.780	4.364
Total cases	45,556 [22,772; 93,406]	45,698 [22,520; 92,966]	52,654 [26,067; 106,456]
Deaths	16	30	29
DALY Total	1,542 [1,475; 1,614]	1,663 [1,595; 1,735]	1,866 [1,786; 1,950]
YLD	1,304 [1,237; 1,376]	1,373 [1,305; 1,445]	1,567 [1,488; 1,651]
YLL	238 [235; 241]	290 [286; 293]	299 [295; 303]

Source: National Food Institute and Statens Serum Institut

Table 3.3. Estimated burden of diseases caused by VTEC, 2013-2015

	2013	2014	2015
	Mean 95% CI	Mean 95% CI	Mean 95% CI
Reported cases	192	256	196
Total cases	2,810 [2,437; 3,831]	3,886 [3,367; 5,287]	3,016 [2,612; 4,116]
Deaths	0	0	0
DALY Total	39 [32; 46]	42 [33; 51]	30 [24; 38]
YLD	20 [16; 26]	17 [12; 24]	11 [7; 16]
YLL	19 [14; 23]	25 [18; 31]	20 [14; 25]

Source: National Food Institute and Statens Serum Institut

provide the scientific evidence necessary to allow policy-makers to rank different foodborne diseases thus prioritise interventions to reduce their public health, as well as economic burden. We will expand our efforts to estimate the burden of other foodborne diseases in Denmark, thereby providing a more complete picture of the public health burden. The next step will be to integrate these estimates with economic analyses and calculate the total costs of foodborne illnesses in Denmark.

### 3.3 References

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## The burden of disease caused by botulism

By Janna Nissen (ioni@food.dtu.dk), Sara M. Pires and Andreas A. Pedersen

In Denmark, botulism is a rare disease. During the last 20 years, 15 cases of botulism have been registered, with 0-2 cases per year. The majority of both infant and adult botulism cases for which a causative source was identified were foodborne.

### Overall incidence of botulism

Most countries recognize that public health surveillance systems are able to capture only a fraction of all botulism cases. We corrected reported cases to under-diagnosis and under-reporting based on Danish data and international scientific literature and estimated that two cases (1.6, 95% CI 1.4-1.8) of botulism occur in Denmark, annually. In other words, we estimated that for each reported case of botulism, at least one other case could be expected to have occurred and go unreported. The likelihood of under-diagnosis and under-reporting depends on the severity of the symptoms and the botulism type; it is possible that other (milder) cases may occur in the population. As an illustration, no cases of wound botulism have been registered between 1995-2015. Whether this is because no episodes occurred in that time period or because cases are simply not reported is unknown.

### The disease burden of botulism

The annual disease burden of botulism was estimated to be 6 DALYs (See main text for explanation). Most of this burden is explained by an occasional fatal case. Infants under one year of age account for 80% of the cases, which means that a potential fatality case will result in large numbers of life lost.

### Cost of illness

Annually, the expenses related to botulism amount to 2 million DKK. Mild botulism costs 26,000 DKK per case, whereas severe cases cost 620,000 DKK. These costs include direct healthcare costs like medical visits, hospitalisations and treatment, direct non-healthcare costs like ambulance transportation, and non-healthcare costs like cost to absence of work<sup>1</sup>. The greatest contributors to the overall economic burden are the antitoxin (291,581 DKK per dose)<sup>2</sup> and respiratory aid during paralysis (205,111 DKK per case). Despite the low disease incidence in Denmark, we show that the overall burden of botulism per case is high, and that infants account for the larger proportion of the burden.

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2. May MLA, Corkeron M & Stretton M (2010). Infant botulism in Australia: availability of human botulinum antitoxin for treatment. Medical Journal of Australia 193(10):614-615.

## The Burden of diseases caused by congenital toxoplasmosis

By Janna Nissen (ioni@food.dtu.dk), Sara M. Pires and Henrik Vedel Nielsen

Toxoplasmosis is a zoonotic disease caused by the parasite *Toxoplasma gondii* that can be acquired through foodborne or environmental exposure. *T. gondii* has been ranked the third most important cause of foodborne disease in Europe by the World Health Organization (WHO), Foodborne Disease Burden Epidemiology Reference Group (FERG), which estimated that over one million cases of foodborne toxoplasmosis occur in the region annually<sup>1</sup>.

Toxoplasmosis can also occur following maternal transmission. Congenital toxoplasmosis (CT) can result in miscarriage or stillbirth, or lead to illness in live-born infants with symptoms such as chorioretinitis, intracranial calcification, hydrocephalus, and CNS abnormalities leading to neurological deficiencies (psychomotor or other neurological deficiencies, convulsions, and mental retardation)<sup>2,3</sup>. Many infants with CT appear asymptomatic at birth, but may later in life develop chorioretinitis.

Acquired toxoplasmosis is not included in any national surveillance programme and therefore the disease burden is unknown in Denmark. For CT, Denmark had an active surveillance programme from 1999–2007 that covered over 98% of all newborns in the country<sup>4</sup>. During that time period, between 6 and 19 cases of CT were diagnosed annually. In contrast, after the programme was terminated and during the last seven years (2008–2014), only 0–5 cases have been diagnosed each year (Table 3.4). These data suggest that CT is currently under-diagnosed and under-reported, and that consequently public health surveillance data do not provide a complete picture of the impact of the disease in the country.

A Toxoplasmosis Working Group, led by the National Food Institute, DTU in collaboration with Statens Serum Institut, is currently estimating the disease burden of CT in Denmark. The burden of CT will be expressed in terms of incidence, mortality, and disability-adjusted life years (DALYs) (See main text for explanation).

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## 4. Verocytotoxin-producing *E. coli* (VTEC)

By Flemming Scheutz (fsc@ssi.dk) and Charlotte Kjelsø

In 2015, 228 episodes of verocytotoxin-producing *Escherichia coli* (VTEC) were registered. VTEC isolates were obtained from 174 episodes, of which 33 (19%) were caused by O157 and 19 (11%) by O26 and 17 (10%) by O103 (Appendix Table A3). Twenty percent were infected abroad, mostly travelling as tourists. Seventy-six patients were 0 - 5 years old.

### 4.1 Outbreaks with Verocytotoxin-producing *E. coli*

Serotype, virulence profile and multi locus sequence type (MLST) were determined for all VTEC isolates in 2015 by whole genome sequencing (WGS) in real time. WGS allows for a more specific analysis and comparison of isolates than the previously used traditional combination of phenotypic and molecular typing followed by pulsed field gel electrophoresis (PFGE). Isolates that were identical or very similar by WGS were analysed for single nucleotide polymorphism (SNP) in the core genome. No major outbreaks were identified in 2015. Ten genomic clusters with two to three patients in each cluster were identified by these SNP analyses. All patients or parents from the ten genetic clusters were interviewed, which identified four institutionally and two family related clusters. Four clusters were geographically and temporally dispersed. No sources were indicated and secondary person-to-person infections were most often suspected. One isolate was identical to isolates from cases related to an outbreak in 2014 associated with the consumption of kebab. The serotypes in the ten genomic clusters were O157:H7 (5 clusters), O103:H2 and O26:H11 (two clusters each), and O128:H2 (one cluster).

### 4.2 Virulence factors and HUS

Nine patients developed haemolytic uraemic syndrome (HUS), but VTEC was only obtained from one case (O26:H11). No deaths were reported.

In 2015, The Danish National Board of Health launched new HUS guidelines recommending differentiated management of VTEC / HUS patients depending on VTEC virulence

profile and *vtx* subtyping. Primary detection of *vtx2*, regardless of other genes, indicates a **possible** association with HUS (HUSEC). Subsequent *vtx* subtyping defines which isolates are associated with HUS (HUSEC):

1. *vtx2a* regardless of other virulence genes
2. *vtx2d* regardless of other virulence genes

Patients who are positive for HUSEC (*vtx2a* and *vtx2d* subtypes) cannot attend child care centres or work in sensitive professions, such as food- or health care industry, before they have been tested negative for VTEC in two independent stool samples.

Using the above definition, 30 of the 174 (17%) VTEC isolates were HUSEC (26 *vtx2a* and 4 *vtx2d*) and 144 (83%) were VTEC with a low risk of association to HUS. Twenty-five of the *vtx2a* positive strains were also positive for the *eae* gene and other *vtx* genes: *vtx1a* (16), *vtx2c* (3), and *vtx1a* + *vtx2c* (1). Two *vtx2d* positive strains were also positive for the *eae* gene and other *vtx* genes: *vtx1a* (2) and *vtx1a* + *vtx2b* (1).

### 4.3 Comments

While no major outbreaks were seen in 2015, several genetic clusters were identified by WGS. Subsequent epidemiological investigations indicated person-to-person transmission as the most possible explanation in six of the ten genetic clusters. Thus, the most effective way of preventing disease spread seem to be the earliest possible diagnosis of primary cases followed by quarantine measures – especially for patients with HUSEC strains. Four out of five Danish patients were infected by VTEC, which are not associated with HUS. Twenty-two of the patients infected with HUSEC strains indicated that they had not been travelling abroad, two had travelled and data was not available for six patients. This indicates that HUSEC is primarily acquired in Denmark and more attention should be focused on identifying the sources of these HUSEC infections in order to reduce the risk for developing HUS in Denmark.

## 5. Vectorborne zoonoses

By René Bødker (reb@vet.dtu.dk), Cecilie Grønlund Clausen, Carsten Kirkeby, David Bille Byriel and Kirstine Klitgaard Schou

The National Veterinary Institute, Technical University of Denmark monitors vectors and vector borne diseases in Denmark on behalf of the Danish Veterinary and Food Administration. The Veterinary Institute is responsible for the national weekly surveillance of mosquito and *Culicoides* vectors and for quantifying and mapping ticks and tick borne pathogens. The surveillance is focused on endemic vectors but also screens for exotic vectors. For an overview of relevant diseases that can be transmitted by the vectors found in Denmark see Table 6.1 in Annual Report 2014.

The West Nile Fever mosquito *Culex modestus* was found in a residential area south of Copenhagen in high abundance in 2014. This important vector for transmission of West Nile virus from birds to humans has been spreading northwards in Europe in recent decades. To monitor this northernmost breeding site in Europe surveillance was continued in 2015 at the same site as in 2014 using a CO<sub>2</sub> and octonol baited Mosquito Magnet suction trap. Only a single individual of *Cx. modestus* was collected all summer in 2015, suggesting the only known breeding site in Denmark was either no longer able to sustain development of the larvae or that the mosquito locally had died out during the preceding winter (Fig 5.1). In 2014 almost all *Culex* sp. recorded from that breeding site were *Cx. modestus* the remaining being *Cx. pipiens/torrentium*. Transmission of West Nile virus has never been detected in Denmark.

No exotic mosquitoes were discovered in any of the eight weekly surveillance sites in Denmark in 2015. But the exotic species *Aedes japonicus* established in Northern Germany (Hanover) still remains a threat.

The native *Anopheles maculipennis* complex of malaria mosquitoes consists of several species with very different capacities to transmit human malaria parasites. Despite the differences in vector competence, they can only be identified to species level by molecular methods. In Germany, four species have been identified including the two vector species *An. messeae* and the salt tolerant *An. atroparvus*. It was therefore decided to identify individual *An. maculipennis* complex mosquitoes collected annually in the Danish surveillance programme since 2011. A total of 444 individuals were analyzed. All were identified as *An. messeae* except a single individual of *An. maculipennis* s.s. Unexpectedly, *An. atroparvus* which is thought to be responsible for the large malaria outbreaks in rural

Southern Denmark following episodes of flooding in the 19<sup>th</sup> century<sup>1</sup> and recently recorded as common in north-western Germany<sup>2</sup> was completely absent from the collections. Interestingly it was found that in some years *An. messeae* now breeds in small pockets in Copenhagen City and also in suburban residential areas without livestock while it is now very scarce in rural areas.

Cities in Denmark are changing and urban planning increasingly includes recycling and storage of water for environmental and recreational purposes. In 2015, a pilot study examining the impact of urban water projects was therefore conducted in Copenhagen City. In a matched case control study four backyards with water projects ("Green") was compared with four nearby traditional backyards ("Traditional") from the 7<sup>th</sup> July until 7<sup>th</sup> August. The mosquitoes were collected by two CDC light traps in each backyard. In each geographically matched pair, more mosquitoes of *Culex pipiens/torrentium* were collected in the green backyards than in the traditional backyards. On average four times more *Culex* vectors were collected in backyards with water projects despite these four projects being very modest in size (figure 5.2). This suggests that future urban development projects in Denmark should consider the potential for inadvertently creating a mosquito nuisance or even a health risk.

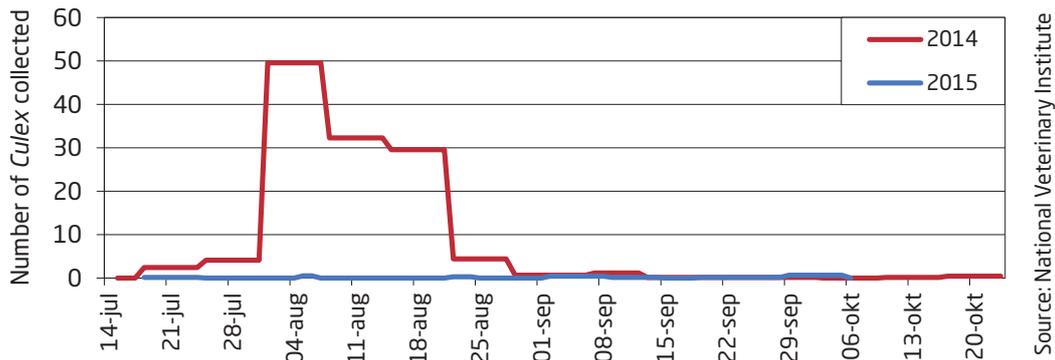
In 2015, a total of 5,000 tick nymphs were collected from six selected locations on Zealand and in Jutland by flagging. All of these were identified as *Ixodes ricinus*. So far no invasive ticks have been collected despite *Ixodes persulcatus*, *Haemaphysalis punctata* and in 2010 also *Dermacentor reticulatus* being recorded in Sweden and despite *Dermacentor reticulatus* spreading in Germany and recently also in the Netherlands and in the UK<sup>3,4</sup>.

In another project, *I. ricinus* nymphs collected from 24 different sites during 2013 from all regions of Denmark were screened for bacteria and parasites. For each of the 24 sites 225 ticks were analyzed with PCR using a Fluidigm DNA chip. From these 5,400 ticks, 12 different pathogens were identified (figure 5.3). The most common was *Borrelia*, with 14% of tick nymphs being positive for one or more of the 7 species of *Borrelia* identified. *Rickettsia helvetica* was the second most prevalent followed by *Anaplasma phagocytophilum*, *Neoehrlichia mikurensis* and two species of *Babesia* parasites.

## 5.1 References

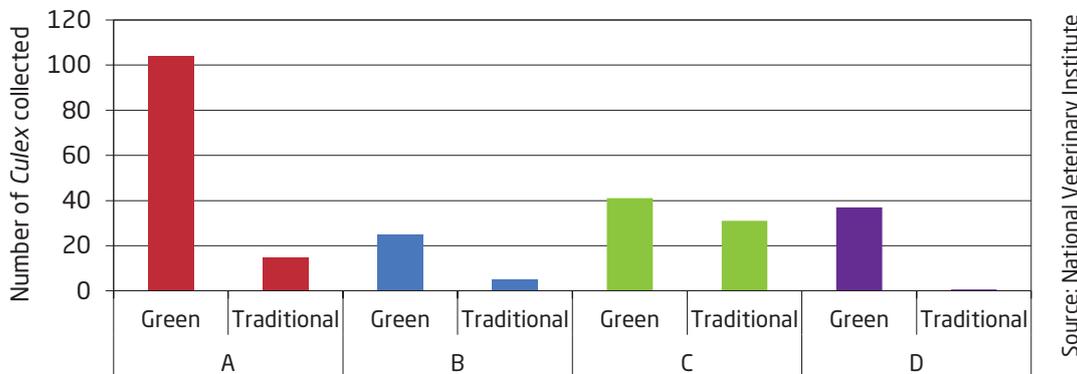
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Figure 5.1. The daily number of *Culex* mosquitoes, 2014-2015



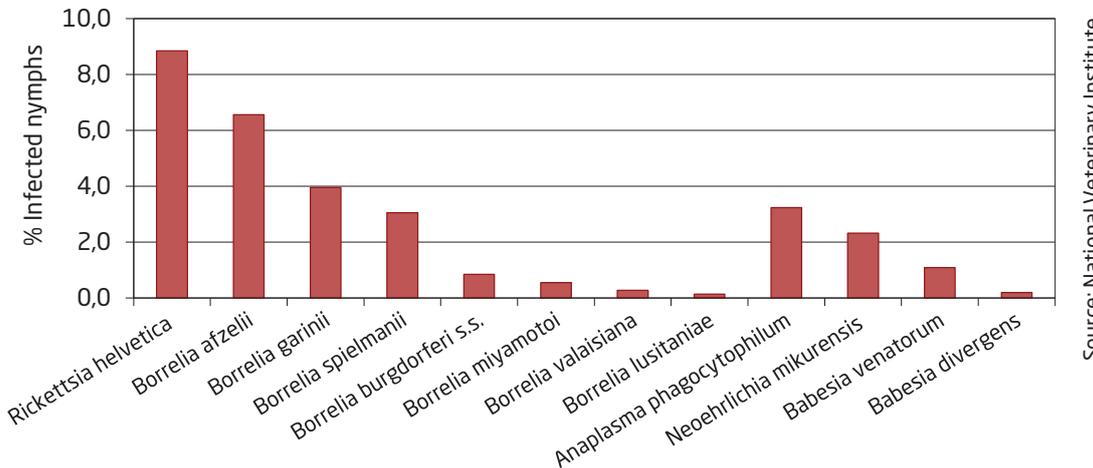
Source: National Veterinary Institute

Figure 5.2. Four matched pairs of backyards with ('Green') and without ('Traditional') a modest recreational water project, 2015



Source: National Veterinary Institute

Figure 5.3. The average national prevalence of 12 tick borne pathogens in 5,400 *Ixodes ricinus* nymphs collected by flagging at 24 geographically stratified sites in Denmark, 2013



Source: National Veterinary Institute

## 6. Status on national and EU targets

By Gudrun Sandø (gus@fvst.dk) and Pernille C.S. Tillisch (pes@fvst.dk)

In Denmark, action plans and programs on zoonoses have been in place for more than 25 years. The first plan targeted *Salmonella* in the broiler production and was developed as a response to an increase in the number of human cases related to eating chicken meat. Since then, plans have been developed for *Salmonella* in pigs and pork, *Salmonella* in layers (eggs), *Campylobacter* in broilers and *S. Dublin* in cattle and beef.

All plans have been outlined in cooperation between industry, research institutes and authorities, and are followed by a technical working group and a steering committee. This ensures progress, that new knowledge is incorporated in the plans, and an assessment of achievement of targets.

At EU level, harmonized surveillance programs and common targets have been set for the broiler and laying egg production.

An overview on the status on the targets can be seen in Table 6.1.

### 6.1 National targets

The first action plan for *Campylobacter* was initiated in 2008 and followed by the second plan in 2013 that covers the period until the end of 2016. The plan is targeting *Campylobacter* in broilers and chicken meat as well as other sources and food. Targets have been set for the reduction of the prevalence of *Campylobacter* positive flocks and of the relative risk related to eating chicken meat. At flock level the target is a 20% sum of reduction in 2011-2013 and 2014 - 2016. A reduction of 9.4% was obtained from 2011 to 2013, and from 2014 to 2015 a further reduction of 29% was obtained. At slaughterhouse level the target is a reduction of the relative risk by 25% in 2014 and by 50% by 2016 compared to 2013. A reduction of 28% was obtained in 2014 compared to 2013, and in 2015 a reduction of 36% was obtained, compared to 2013.

The first action plan for reduction of *Salmonella* in the broiler production was developed by the industry in 1988. An official plan of action was adopted in 1996 and included the table-egg production as well. Both action plans have been adjusted several times over the years. The target was from the beginning an eradication of *Salmonella* from the broiler production. Today there is a zero-tolerance of *Salmonella* in Danish produced broiler meat. Meat from *Salmonella* positive flocks must be heat treated, and broiler meat tested positive for *Salmonella* after slaughter cannot be marketed as fresh meat. In the table-egg production, Denmark has achieved special guarantees for *Salmonella*

in the EU (for further information see Annual Report 2012, Chapter 7). Both plans are now focused on maintaining the low prevalence.

In the pig production, the 5<sup>th</sup> *Salmonella* action plan was adopted at the end of 2013 and runs until the end of 2017. It continues the measures from former plans and points at new measures as well (See Annual Report 2013 for more information). The target is set for the prevalence of *Salmonella* positive carcasses at the slaughterhouse level and is a maximum of 1% positive carcasses. The target had to be achieved in 2014 and maintained throughout the period. At the end of 2014 the prevalence was just below 1%, however in 2015 the prevalence was 1.2% (Table A15).

The first action plan for eradication of *S. Dublin* in cattle and beef was adopted in 2008 and has been changed several times since then. In recent years, the programme has been tightened as the number of positive herds has been declining (for further information see infobox page 25 and Annual Report 2013, Chapter 5). The target is to eradicate *S. Dublin* in cattle herds by the end of 2016. By December 2015, 7.1% of milk-producing herds and 2.1% of non-milk producing herds were in level 2 or 3 (Table A17).

### 6.2 EU targets

Harmonised regulation on targets and surveillance in the poultry production has been laid down by the Commission.

According to Regulation (EC) No 1190/2012, the EU target for *Salmonella* in breeding and fattening turkey flocks is 1% positive for *S. Typhimurium* or *S. Enteritidis*. In Denmark, no turkey flocks were positive with *S. Typhimurium* or *S. Enteritidis* in 2015 (Appendix Table A12).

In breeding flocks of *Gallus gallus*, Regulation (EC) No 200/2010 lays down a target of maximum 1% adult flocks positive for *S. Typhimurium* including the monophasic *S. 1,4,[5],12:i:-* strains, *S. Enteritidis*, *S. Hadar*, *S. Infantis* and *S. Virchow*. In the legislation no distinction is made between breeding flocks from the table egg and broiler production lines. In Denmark, one breeding flock from the broiler production was positive with *S. Typhimurium* DT12 in 2015 (Appendix Table A9 and A11).

Regulation (EC) No 517/2011 lays down targets for the reduction of *Salmonella* in laying flocks. The targets are Member States specific and are set either as an annual 10-40% reduction of positive adult flocks dependent on the prevalence of adult flocks in the Member State the previous year or a maximum of 2% adult flocks positive. For Denmark, the target is a maximum of 2% adult flocks positive for *S.*

Typhimurium (including the monophasic S. 1,4,[5],12:i:- strains) and S. Enteritidis. The prevalence in Denmark has been below 2% since 2004. In 2015, no flocks were positive for the target serotypes (Appendix table A9).

In broiler flocks of *Gallus gallus*, Regulation (EC) No 200/2012 lays down a target at a maximum of 1% flocks

positive for S. Enteritidis and S. Typhimurium including the monophasic S. 1,4,[5],12:i:- strains. Denmark has had intensive *Salmonella* control programmes since the 90's and the target of 1% was reached in 2000. In 2015, 0.2% of broiler flocks was positive with S. Typhimurium including the monophasic S. 1,4,[5],12:i:- strains (Appendix Table A11).

Table 6.1. Status on targets for *Campylobacter* and *Salmonella*, 2015

National Action Plans	Target	Status
<i>Campylobacter</i> in broilers 2013-2016		
Flocks at farm	20% reduction in prevalence of positive flocks in 2016 compared to 2012	A reduction of 9.4% was obtained for the period 2011-2013 <sup>a</sup> A reduction of 29% was obtained for the period 2014-2015 <sup>a</sup>
Fresh meat at slaughterhouse	Reduction of the relative human risk (RR) compared to the level in 2013 <sup>a</sup> 2014: RR reduced by 25% 2016: RR reduced by 50%	A reduction of 28% was obtained in 2014 compared with 2013 <sup>b</sup> A reduction of 36% was obtained in 2015 compared to 2013 <sup>b</sup>
<i>Salmonella</i> in poultry <sup>c</sup>		
Laying hen flocks of <i>Gallus gallus</i>	Initially eradication, later a reduction strategy in the table egg production	No positive flocks (Table A9-A10) Eggs from positive flocks are destroyed or heat treated
Carcasses at slaughterhouse	Initially eradication, later a reduction strategy in the broiler production Zero-tolerance in Danish broiler meat.	No positive batches (Table A11) Positive batches are heat treated
<i>Salmonella</i> in pigs 2014-2017		
Carcasses at slaughterhouse	Max. 1% <i>Salmonella</i> at carcass level in 2014-2017	1.2% (Table A15)
Estimated human cases from pigs	No considerable increase in the number of estimated human cases from pigs in the Danish <i>Salmonella</i> source account	In total 35 cases were attributed to Danish pork in 2015 (CI95%: 16-60) vs. 172 cases in 2014 (CI95%: 126-214). (Chapter 1 and Table A1)
<i>Salmonella</i> Dublin in cattle 2012-2016		
Herds at farm	Eradication of S. Dublin in all herds by 2016., i.e. all herds in level 1 <sup>d</sup> by the end of 2016	7.1% of milk-producing herds and 2.1% of non-milk producing herds are in level 2 or 3 (December 2015)(Table A17)
EU Regulations		
Regulation (EC) No. 1190/2012		
Breeding and fattening turkey flocks	Max. 1% positive for S. Enteritidis and S. Typhimurium <sup>e</sup>	No fattening flocks positive with target serovars (N=15). (Table A12)
Regulation (EC) No. 200/2010		
Breeding flocks of <i>Gallus gallus</i>	Max. 1% adult flocks positive for S. Typhimurium <sup>e</sup> , S. Enteritidis, S. Hadar, S. Infantis and S. Virchow	0.3% (1 flock) (Table A9 and A11)
Regulation (EC) No. 1168/2006		
Laying hen flocks of <i>Gallus gallus</i>	MS specific targets, for Denmark: Max. 2% adult flocks positive for S. Typhimurium <sup>e</sup> and S. Enteritidis	0% (Table A9)
Regulation (EC) No. 646/2007		
Broiler flocks of <i>Gallus gallus</i>	Max. 1% positive S. Typhimurium <sup>e</sup> and S. Enteritidis	0.2% (8 flocks) positive with target serovars (Table A11)

a) As a consequence of a change in sampling from AM testing 7-10 days before slaughter to cloacal swabs at the point of slaughter, 2013 and 2014 data cannot be compared. The target has therefore been changed to cover firstly the period 2011-2013 and secondly the period 2014-2016. For the two periods as a whole, the target is 20%.

b) 2013 is agreed as the baseline since 2012 data are not comparable with data from 2013 and onwards due to a necessary improvement in the data collection

c) Supplementary to EU-regulations.

d) See Table A36 for explanation of the herd levels

e) Including the monophasic strains S. 1,4,[5],12:i:-.

Source: Danish Veterinary and Food Administration.

# 7. International topics

By Gudrun Sandø (gus@fvst.dk)

## 7.1 Antimicrobial resistance

The Commission has implemented a harmonised monitoring of antimicrobial resistance within the EU from 2014. The decision is based on a recommendation from the European Food Safety Authority (EFSA). The harmonized monitoring of antimicrobial resistance is implemented for poultry, pigs and calves (under 1 year) and meat of broilers, pigs and cattle. The monitoring includes antimicrobial resistance in *Salmonella*, *Campylobacter jejuni*, *Escherichia coli* and ESBL in *Salmonella* and *E. coli*. It is optional for Member States to monitor antimicrobial resistance in enterococci and *Campylobacter coli*. The samples will be collected during a two-year rotation period. In the years 2014, 2016, 2018 and 2019 poultry will be sampled and in 2015, 2017 and 2019 pigs and calves will be sampled. The sampling strategy is harmonised to ensure comparable results between Member States. The idea is that the knowledge gained from the monitoring will raise awareness of the potential antimicrobial resistance problems in the individual Member States and thus lead to increased problem solving. Results from the EU monitoring will be published in The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2015.

## 7.2 Regulation on official supervision of the process hygiene criterion for *Salmonella* on pig carcasses.

Regulation 854/2004 regarding official controls of products of animal origin is amended and now includes provisions for official supervision of the correct implementation by food business operators of the process hygiene criterion for *Salmonella* on pig carcasses. The supervision of actions taken by the food business operator in case of non-compliance is integrated in the pig meat inspection, and all results from the monitoring of *Salmonella* are registered and reported to EFSA.

## 7.3 Codex Alimentarius; Guideline for the control of *Salmonella* in pork and beef.

In November 2013 work on "Codex Guidelines for the Control of Nontyphoidal *Salmonella* spp. in Pork and Beef Meat" was initiated with the establishment of a working group led by the USA and co-chaired by Denmark. The document was finalized in November 2015 at the Codex Alimentarius plenary meeting in Boston, USA. The guidelines apply to control of all nontyphoidal *Salmonella* that may contaminate beef and pork meat and cause foodborne disease. The primary focus is to provide information on best practices that may be used to prevent, eliminate, or reduce levels of *Salmonella* on pork and beef.

## 8. Surveillance and control programmes

The collaboration on zoonoses between national and regional authorities, the industry and non-governmental organizations in Denmark is presented in Figure 8.1. According to the Danish legislation, 41 infectious diseases are notifiable in Denmark. An overview of the notifiable and non-notifiable human and animal diseases, presented in this report, is provided in Appendix Table A30 and Table A31, respectively, including reference to the relevant legislation.

### 8.1 Surveillance of human disease

Information on human cases due to zoonotic pathogens presented in this report is reported to Statens Serum Institut through different channels depending on the disease:

- Notifiable through the laboratory surveillance system: *Salmonella*, *Campylobacter*, *Yersinia*, Verotoxin-producing *E. coli* (VTEC) and *Listeria*.
- Individually notifiable zoonotic pathogens: *Chlamydia psittacci* (ornithosis), *Leptospira* (Weils disease), *Mycobacterium*, Bovine Spongiform Encephalopathy (BSE) prions (var. Creutzfeldt-Jakob Disease), Verotoxin-producing *E. coli* (VTEC) and Lyssavirus (rabies).
- Non-notifiable zoonotic pathogens: *Brucella*.

In Denmark, the physicians report individually notifiable zoonotic diseases to the Danish Health Authority (previous Danish Health and Medicines Authority) and the Department of Infectious Disease Epidemiology at Statens Serum Institut. Physicians send specimens from suspected cases to one of the clinical microbiology laboratories depending on the geographical region. Positive cases diagnosed by a clinical microbiological laboratory are reported through the laboratory surveillance system to the Unit of Gastrointestinal Infections at Statens Serum Institut. The laboratories must report positive results to Statens Serum Institut within one week. Furthermore, all *Salmonella* and VTEC isolates are sent to the reference laboratory at Statens Serum Institut for further sero- and genotyping. The results are recorded in the Register of Enteric Pathogens maintained by Statens Serum Institut. Cases are reported as episodes, i.e. each patient-infectious agent combination is only recorded once in any six-month period. Overviews of results from the Register of Enteric Pathogens are presented as follows:

- All laboratory confirmed human cases are presented in Appendix Table A2.
- VTEC O-group distribution in humans is presented in Appendix Table A3.
- The *Salmonella* serovar and MLVA distribution is presented in Appendix Table A6-A8.

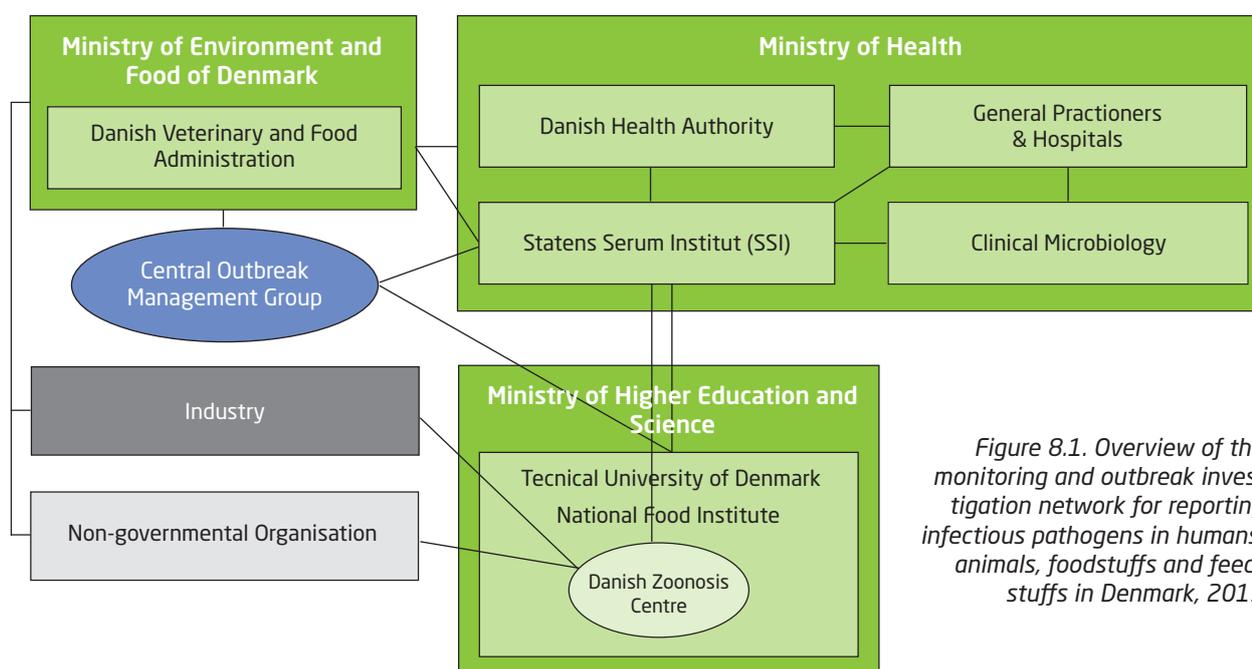


Figure 8.1. Overview of the monitoring and outbreak investigation network for reporting infectious pathogens in humans, animals, foodstuffs and feedstuffs in Denmark, 2015

## 8.2 Outbreaks of zoonotic gastrointestinal infections

In Denmark, local and regional foodborne outbreaks are typically investigated by the Food Control Offices<sup>a</sup> in collaboration with the Public Health Medical Officers at the Danish Patient Safety Authority, and the regional clinical microbiology laboratories. Larger regional and national outbreaks are investigated by Statens Serum Institut, the National Food Institute, Technical University of Denmark and the Danish Veterinary and Food Administration in collaboration. These institutions may also aid in the investigation of local outbreaks. Representatives from these institutions meet regularly in the Central Outbreak Management Group to discuss surveillance results, compare the reported occurrence of zoonotic agents in animals, food and feedstuffs with that in humans, and coordinate the investigation of outbreaks. The formal responsibility of investigating food- or waterborne outbreaks is currently divided between two ministries based on the outbreak source: the Ministry of Health for infectious diseases; the Ministry of Environment and Food for foodborne and animal related diseases, and for waterborne diseases. The latter are investigated in collaboration with the municipalities.

Outbreaks may be detected in various ways. Individuals who experience illness related to food intake in settings such as restaurants or work place cafeterias may report these incidents directly to the Food Control Office. General practitioners and hospitals are obliged to report all suspected water- and foodborne infections to the Danish Patient Safety Authority and to Statens Serum Institut. Clusters of cases may also be noted in the laboratory or identified at Statens Serum Institut through the laboratory surveillance system of gastrointestinal bacterial infections or through subtyping of bacterial isolates from patients.

A list of verified outbreaks (not including household outbreaks) reported to the Food- and waterborne Outbreak Database (FUD) are presented in Appendix Table A4 and some of the outbreaks from 2015 are outlined in Chapter 2.

## 8.3 Surveillance and control of animals and animal products

*Salmonella* surveillance and control programmes for poultry, pigs and cattle are presented in Appendix Tables A32-A37. Sample analysis is performed at authorised private laboratories, the Danish Food and Veterinary Administrations laboratory, the National Food Institute and the National Veterinary Institute at the Technical University of Denmark. *Salmonella* isolates are forwarded to the National Food Institute for serotyping, some isolates are also phage- and

genotyped as well as tested for antimicrobial resistance. An overview of the methods used for subtyping is presented in Appendix Table A38.

Overviews of results from surveillance and control of *Salmonella* are presented as follows:

- Results from the table egg production are presented in Appendix Tables A9-A10.
- Results from the broiler production are presented in Appendix Tables A6-A7, A11 and A18.
- Results from the duck and turkey productions are presented in Appendix Tables A6 and A12.
- Results from the pig production are presented in Appendix Tables A6-A7, A15, A18 and Figures A1-A3.
- Results from the cattle production are presented in Appendix Tables A6, A16-A17 and Figure A4.
- Results from the feeding stuff production are presented in Appendix Tables A19-A20.
- Results from the rendering plants are presented in Appendix Table A21.
- Results based on suspicion of diseases in pets, zoo animals and wild life are presented in Appendix Tables A23-A24.

Overviews of results from monitoring and control of *Campylobacter* are presented as follows:

- Results from the broiler production are presented in Appendix Tables A13-A14 and A18.
- Results based on suspicion of diseases in pets, zoo animals and wild life are presented in Appendix Table A24.

Pig and cattle carcasses are screened for *Mycobacterium* and *Echinococcus* during meat inspection at the slaughterhouse. Although Denmark is assigned as a region where the risk of *Trichinella* in domestic swine is negligible, all slaughter pigs are still examined for *Trichinella* at slaughter as well as wild boars, and horses slaughtered for human consumption. In addition, boars and bulls are tested for *Brucella* and bulls are tested for *Mycobacterium* at semen collection centres. All positive results for notifiable infectious diseases are reported to the Danish Veterinary and Food Administration. Results are presented in Appendix Table A15-A16.

Results from the surveillance for Bovine Spongiform Encephalopathy (BSE) in cattle, and Transmissible Spongiform Encephalopathy (TSE) in sheep/goat are presented in Appendix Tables A25-A27.

Results from the monitoring of *Coxiella burnetii* (Q fever) in cattle are presented in Appendix Table A16.

Results based on suspicion of diseases with *Chlamydia psittacci*, *Cryptosporidium*, *Trichinella*, classical rabies and

a) The Danish Veterinary and Food Administration (DVFA) is one authority but operates from more locations throughout the country. To be able to distinguish the locations the terms DVFA is used synonymous with the location in Glostrup and Food Control Office followed by the location synonymous with the location in question.

European Bat *Lyssavirus* in zoo animals, pets and wild life are presented in Appendix Table A23-A24.

#### 8.4 Official testing of zoonotic pathogens in foodstuffs

In Denmark, control of zoonotic microorganisms in foodstuffs is mainly carried out as projects which are coordinated at the central level of the Danish Veterinary and Food Administration. Sampling and testing are carried out with the following purposes:

- To verify that food business operators comply with microbiological criteria laid down in the legislation
- To verify the microbiological safety of food for which no

microbiological criteria are laid down at EU Community level.

- To monitor the effect of established risk management procedures in order to evaluate if these provide the desired results or need to be reconsidered.
- To generate data for the preparation of risk profiles and risk assessments to support microbial risk management
- To discover emerging problems with microbiological contaminants.

Appendix Table A28 provides information on the centrally coordinated studies conducted in 2015.

For further information consult the website of the Danish Veterinary and Food Administration, [www.fvst.dk](http://www.fvst.dk).

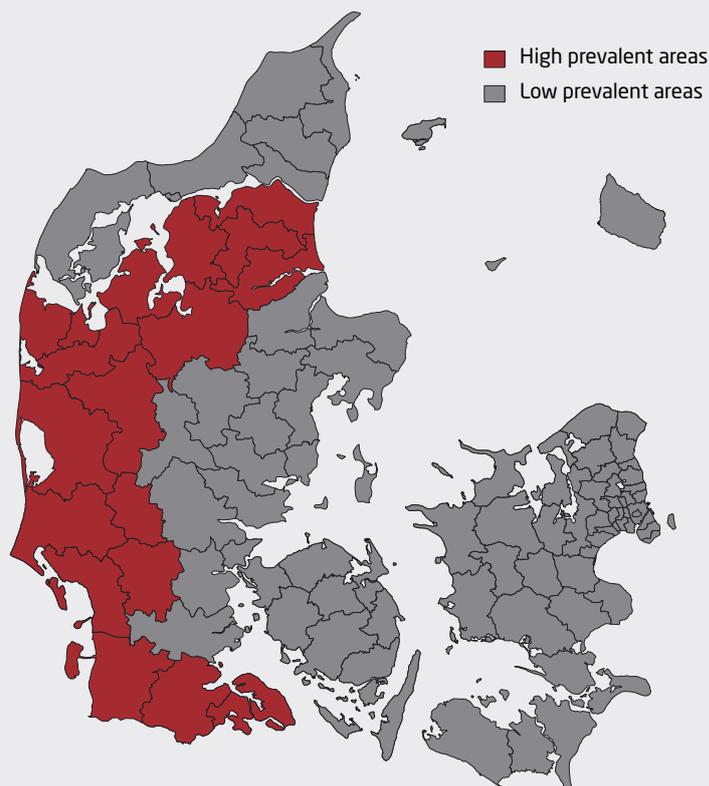
### Salmonella Dublin in cattle

By Gudrun Sandø ([gus@fvst.dk](mailto:gus@fvst.dk)) and Erik Rattenborg

The national control programme on *Salmonella* Dublin is described in Annual Report 2013. The overall aim of the programme is an eradication of *S. Dublin* in the Danish cattle production.

The programme is mandatory according to order no 537 of 1<sup>st</sup> June 2016. In October 2015 the programme was changed, the most important change being the enlargement of the low prevalence region. Since 2013 the low prevalence region was Zealand and Funen, but from October 2015 North of Jutland and East Jutland belongs to the low prevalence region as well (Fig. 8.2). Furthermore, adjustments were made, i.e. the possibility for dairy herds to shift from level 2 (positive) to level 1 based on blood samples is no longer an option and heifer herds in the high prevalence region are obliged to take blood samples once or twice a year depending on whether they are rearing heifers for one or several dairy herds. Movement of live cattle from positive herds as well as from high to low prevalence regions is generally prohibited. Positive herds in the low prevalence region are placed under official restrictions.

Figure 8.2. Overview of the high and low prevalence regions in the *Salmonella* Dublin control programme in cattle, 2015



Source: Seges, Cattle

***Campylobacter* - state of play and new initiatives**

By Gudrun Sandø (gus@fvst.dk)

The action plan for *Campylobacter* was adopted in 2013. It is the second plan on *Campylobacter* and it targets *Campylobacter* in broilers and chicken meat as well as other sources and food. It runs until the end of 2017 (initially 2016). Targets have been set for the reduction of the prevalence of positive *Campylobacter* flocks and of the relative risk related to eating chicken meat.

According to the action plan it is an objective to obtain new knowledge on other sources and routes of transmission of *Campylobacter* to humans, than broilers and chicken meat, and in 2015 several projects were initiated. The source account on *Campylobacter*, developed by National Food Institute, Technical University of Denmark is being further developed and combined with an exposure model. Samples from the most relevant sources (pigs, cattle, poultry, dogs, vegetables, bathing water, meat of different kind, unpasteurized milk etc.) as well as from humans with campylobacteriosis are analysed and isolates are typed (WGS) to feed into the new and updated source account model. This project runs from autumn 2015 to spring 2017.

In 2016 a case-control study is undertaken by the Statens Serum Institut to establish risk factors of acquiring campylobacteriosis. As opposed to previous case-control studies, this case-control study will also focus on environmental exposure and is targeting younger age groups to reduce the risk of acquired immunity.

Finally a retrospective analysis of human cases will be carried out by Statens Serum Institut, looking at the distribution of age, gender, season and geography and variations over time.

The initiatives are financed by The Ministry of Environment and Food.

**Changes undergoing the surveillance of human campylobacter cases**

By Steen Ethelberg (set@ssi.dk)

In 2015, the Danish surveillance of human *Campylobacter* cases underwent changes affecting the surveillance statistics. Data on diagnosis of first-positive cases have traditionally been sent from each clinical microbiological laboratory to the Statens Serum Institute and then entered into the surveillance database, the Register of Enteric Pathogens. Beginning late 2014, data were drawn directly from the Danish Microbiology Database (MiBa) and only supplementary data were entered from submissions from the clinical laboratories. MiBa is a national database capturing and collecting all diagnostic results sent from Danish clinical microbiological laboratories to the requesting physicians. *Campylobacter* is among the first infectious disease agents for which automatic data capture has been put into place. Other agents are expected to follow in coming years. It is anticipated that this will lead to an improvement in disease surveillance in terms of obtaining more complete data (more cases), more timely data, more information on each case and an overall reduced workload. A comparative analysis of the number of patients with campylobacteriosis reported via the traditional method and patients available via MiBa in the 2011-14 period suggested that underreporting did occur, at the level of 5-20%.

Changes to diagnostic practice is also believed to have influence on surveillance data and is expected to do so even more in coming years. One such is the gradual introduction of diagnostic PCR directly on faeces sample material which has now begun in Danish laboratories. This method is more sensitive than traditional culture and depending on how it is being used, may therefore lead to more cases being found.

Because of these changes, it is not possible to determine if the fact that the number of registered cases has increased in 2015 reflects a real increase, an unchanged number of cases or a decrease with respect to 2014.



## Trends and sources in human salmonellosis

Table A1. Estimated no. of reported human cases and percentage of cases per major food source, travel or outbreaks, 2013-2015

Source	2015		2014		2013	
	Estimated no. of reported cases (95% credibility interval <sup>a</sup> )	Percentage of reported cases	Estimated no. of reported cases (95% credibility interval <sup>a</sup> )	Percentage of reported cases	Estimated no. of reported cases (95% credibility interval <sup>a</sup> )	Percentage of reported cases
Domestic pork	35 (16-60)	3,7	172 (126-214)	15.4	128 (86-163)	11.3
Domestic beef	13 (3-23)	1,4	25 (20-31)	2.2	21 (4-58)	1.9
Domestic table eggs	0 <sup>b</sup>	0	33 (22-47)	3.0	17 (7-31)	1.5
Domestic broilers	0 <sup>c</sup>	0	22 (1-69)	2.0	0 <sup>c</sup>	0
Domestic ducks	No data	-	No data	-	9 (0-21)	0.8
Imported pork	61 (35-86)	6,6	13 (0-44)	1.1	30 (15-50)	2.6
Imported beef	0 <sup>b</sup>	0	3 (0-7)	0.2	22 (13-33) <sup>d</sup>	2.0
Imported broilers	27 (9-49)	2,9	33 (14-53)	2,9	12 (2-26)	1.1
Imported turkey	11 (1-28)	1,2	0 <sup>e</sup>	0	7 (0-18)	0.6
Imported duck	15 (5-27)	1,6	22 (11-34)	2.0	No data	-
Travels	522 (516-528)	56,5	538 (528-549)	48.0	458 (445-471)	40.3
Unknown source	220 (185-254)	23,8	216 (178-252)	19.2	228 (191-264)	20.1
Outbreaks, unknown source	21	2,3	45	4.0	204	18.0
<b>Total</b>	<b>925</b>		<b>1,122</b>		<b>1,136</b>	

a) The model is based on a Bayesian framework which gives 95% credibility intervals.

b) No samples from domestic table egg layers and imported beef were found positive for *Salmonella* in 2015

c) No samples from domestic broiler meat were found positive for *Salmonella* in 2013 and 2015.

d) No data from imported beef in 2013. The number of cases attributed to this source was modelled from previous years' data.

e) No samples from imported turkey meat were found positive for *Salmonella* in 2014.

Source: Danish Zoonosis Centre, National Food Institute.

## Human disease and outbreak data

Table A2. Zoonoses in humans, number of laboratory-confirmed cases, 2010-2015

Zoonotic pathogen	Incidence per 100,000 inhabitants	Reported no. of cases					
	2015	2015	2014	2013	2012	2011	2010
<b>Bacteria</b>							
<i>Brucella abortus/melitensis</i> <sup>a,d</sup>	-	6	4	4	2	7	6
<i>Campylobacter coli/jejuni</i> <sup>b</sup>	76,6	4.348	3,782	3,766	3,728	4,068	4,035
<i>Chlamydia psittaci</i> <sup>b</sup>	0,4	25	16	12	12	7	9
<i>Leptospira</i> spp. <sup>b</sup>	0,1	5	10	3	7	11	10
<i>Listeria monocytogenes</i> <sup>b</sup>	0,8	43	92	50	50	49	62
<i>Mycobacterium bovis</i> <sup>b</sup>	0,02	1	1	0	0	1	2
<i>Salmonella</i> total <sup>b</sup>	16,3	925	1,122	1,136	1,198	1,166	1,598
<i>S. Enteritidis</i> <sup>b</sup>	4,6	258	268	346	242	293	388
<i>S. Typhimurium</i> <sup>b,c</sup>	4,1	233	427	337	415	386	521
Other serotypes <sup>b</sup>	7,6	434	427	453	541	487	689
VTEC total <sup>b</sup>	4,0	228	248 <sup>e</sup>	186	190	224	184
O157	0,6	33	37	23	36	27	25
Other O-groups or non-typeable	3,4	195	192	163	154	197	159
<i>Yersinia enterocolitica</i> <sup>b</sup>	9,5	539	432	345	291	224	192
<b>Viruses</b>							
<i>Lyssavirus</i> <sup>b</sup>	0	0	0	0	0	0	0

a) Not notifiable, hence the incidence cannot be calculated.

b) Notifiable.

c) *S. Typhimurium* and the monophasic *S. 1,4,[5],12:i:-* strains.

d) Data presented are from one laboratory (Statens Serum Institut) only, representing a proportion of the Danish population. The proportion of the population represented varies from year to year, thus results from different years are not comparable. Testing for these pathogens is carried out only if specifically requested on the submission form.

e) Includes 19 cases verified by PCR only (see Table A3).

Source: Statens Serum Institut.

Table A3. VTEC O-group distribution in humans<sup>a</sup>, 2015

O-group	Number of episodes	O-group	Number of episodes
0157	33	0146	7
026	19	08	5
0103	17	O-rough	3
027	12	Notification <sup>b</sup>	51
091	10	Other O-groups or not-typed	51
0117	9	Isolate not available but presence of vtx genes confirmed by PCR	3
0128	8		
Continued in the next column		Total	228

a) All O-groups that resulted in five or more episodes are listed.

b) The cases are reported through the notification system, isolates or DNA not available for verification.

Source: Statens Serum Institut.

Table A4. Food- and waterborne disease outbreaks<sup>a</sup> reported in the Food- and waterborne Outbreak Database (FUD) (n=39), 2015

Pathogen	No. of patients	Patients laboratory confirmed	Setting	Source	FUD no.
<i>Bacillus cereus</i>	6	-	Restaurant	Buffet meal	1424
<i>Campylobacter</i>	110	6	Catering	Composite meal	1455
<i>Campylobacter</i>	25	4	Scouts event	Chicken	1466
<i>Clostridium perfringens</i>	8	-	Restaurant	Composite meal	1492
<i>Clostridium perfringens</i>	15	-	Restaurant	Buffet meal	1447
<i>Clostridium perfringens</i>	60	-	Catering	Buffet meal	1490
<i>Clostridium perfringens</i>	80	-	Catering	Composite meal	1493
<i>Clostridium perfringens</i>	44	-	Catering	Composite meal	1461
<i>Clostridium perfringens</i>	40	-	Catering	Composite meal	1488
<i>Clostridium perfringens</i>	24	-	Restaurant	Buffet meal	1495
<i>Clostridium perfringens</i>	42	-	Catering	Composite meal	1471
<i>Clostridium perfringens</i>	50	-	Catering	Composite meal	1496
<i>Clostridium perfringens</i>	40	-	Restaurant	Buffet meal	1473
<i>Clostridium perfringens</i>	20	-	Restaurant	Composite meal	1472
<i>L. monocytogenes</i> MLST224 <sup>a</sup>	2	2	Unknown	Unknown	1452
Lectines / cyanogenic glycosides	70	-	Canteen	Elderberries (raw)	1491
Lectines / cyanogenic glycosides	12	-	Restaurant	Elderberries (raw)	1494
Lectines / cyanogenic glycosides	12	-	Hotel	Elderberries (raw)	1467
Norovirus	22	-	Restaurant	Oysters (imp)	1422
Norovirus	10	-	Restaurant	Buffet meal	1414
Norovirus	21	-	Restaurant	Composite meal	1415
Norovirus	13	-	Canteen	Buffet meal	1413
Norovirus	28	-	Restaurant	Buffet meal	1425
Norovirus	31	-	Restaurant	Composite meal	1442
Norovirus	78	-	Canteen	Buffet meal	1429
Norovirus	48	-	Restaurant	Buffet meal	1444
Norovirus	11	-	Private party	Composite meal	1445
Norovirus	9	-	Private party	Raspberries (imp)	1450
Norovirus	38	1	Shop	Open sandwiches	1489
Norovirus	142	3	Music event	Water	1464
Norovirus	11	-	Shop	Open sandwiches	1481
Norovirus	21	-	Hotel	Buffet meal	1479
Norovirus	40	3	Private party	Cake	1474
Norovirus	7	2	Restaurant	Composite meal	1505
<i>Salmonella</i> 4,5,12:i:-, MLVA0479 <sup>b</sup>	6	6	National	Unknown	1487
<i>Salmonella</i> Newport	6	5	Restaurant	Composite meal	1453
<i>Salmonella</i> Oranienburg <sup>c</sup>	14	14	National	Unknown	1469
VTEC O157:H7, <i>eae</i> , <i>vtx1a</i> , <i>vtx2c</i>	3	3	Restaurant	Kebab <sup>d</sup>	1463
<i>Yersinia enterocolitica</i> O:3, biotype 4	14	14	Unknown	Unknown	1468
<b>Total</b>	<b>1,233</b>	<b>63</b>			

Note: (imp)= imported product.

a) MLST = Multi-Locus Sequence Type

b) MLVA profiles for the most common human MLVA-types can be found in tables A6, A7 and A8

c) One case was from Faroe Islands and one case is diagnosed in January 2016 but is expected to have been infected in December 2015

d) The suspected kebab was produced in Denmark with raw material of multiple origins

Source: Food- and waterborne Outbreak Database (FUD).

Table A5. Outbreaks reported in 2014 but where additional patients were reported in 2015

Pathogen	No. of patients	Patients laboratory confirmed	Setting	Source	FUD no.
<i>L. monocytogenes</i> MLST391	2	2	National	Fish <sup>a</sup>	1376
<i>L. monocytogenes</i> MLST399	2	2	National	Composite meal	1384
<i>L. monocytogenes</i> MLST6	4	4	National	Fish <sup>a</sup>	1385
<b>Total</b>	<b>8</b>	<b>8</b>			

a) Cold smoked fish

Source: Food- and waterborne Outbreak Database (FUD).

## Monitoring and surveillance data

Table A6. Top 15 (humans) serotype distribution (%) of *Salmonella* from humans, animals, carcasses and imported meat, 2015. N=number of culture positive units<sup>a</sup>

Serotype	Human	Pig <sup>b</sup>	Pork <sup>c</sup>	Beef <sup>d</sup>	Broiler <sup>e</sup>	Turkey <sup>f</sup>	Imported meat (batches)				
	cases N=925	animals N=144	batches N=118	batches N=4	flocks N=23	flocks N=1	Pork <sup>g</sup> N=11	Beef <sup>h</sup> N=1	Broiler <sup>g</sup> N=20	Ducks <sup>h</sup> N=10	Turkey <sup>g</sup> N=6
Enteritidis	27.9	0	0	0	0	0	0	0	40.0	0	0
1,4,[5],12:i:-	12.6	27.8	28.8	25.0	25.0	0	36.4	0	0	10.0	0
Typhimurium	12.5	11.1	12.6	0	8.3	0	36.4	0	0	30.0	0
Newport	3.5	0.7	0	0	8.3	100	0	0	0	20.0	16.7
Oranienburg	2.6	0	0	0	0	0	0	0	0	0	0
Infantis	2.3	3.5	3.4	0	25.0	0	0	0	35.0	0	0
Stanley	2.3	0	0	0	0	0	0	0	0	0	0
Dublin	2.1	0	0.8	25.0	0	0	0	0	0	0	0
O:4,5,12; H:b:-	1.8	0	0	0	0	0	0	0	0	0	0
Java	1.7	0	0	0	0	0	0	0	5.0	0	0
Virchow	1.6	0	0	0	0	0	0	0	0	0	0
Kentucky	1.5	0	0	0	0	0	0	0	0	0	16.7
Derby	1.4	54.2	35.6	0	8.3	0	9.1	0	0	0	0
Agona	1.3	0	0.8	0	0	0	0	0	5.0	0	33.3
Saintpaul	1.2	0	0	0	0	0	0	0	0	0	33.3
Others	22.5	2.7	5.1	0	25.0	0	18.1	100	15.0	40.0	0
Unknown	2.4	0	12.7	50.0	0	0	0	0	0	0	0
Total	100	100	100	100	100	100	100	100	100	100	100

a) One isolate per serotype per unit is included, thus the number of isolates may exceed the number of units. Thus, in 2015 more isolates were included from broiler flocks.

b) Isolates collected from coecum samples taken randomly at slaughter. Where more than one *Salmonella* positive pig with different serotypes was randomly selected from a herd, one pig per serotype was included.

c) Sampling of pork carcasses at slaughterhouses according to the surveillance programme (Table A37).

d) Sampling of beef carcasses at slaughterhouses according to the surveillance programme (Table A36).

e) Sampling of production flocks prior to slaughter according to surveillance programmes (Tables A33). One flock with two serotypes: S:Infantis and S:Gottengen.

f) Sampling of production flocks prior to slaughter according to surveillance programmes (Tables A35).

g) Case-by-case control of imported meat. For further information regarding case-by-case control programme see Annual Report on Zoonoses in Denmark, 2007.

h) Centrally coordinated study (see section 8.4 and Table A28 for description).

Source: Danish Veterinary and Food Administration, Statens Serum Institut, and National Food Institute

Table A7. Top 10 (humans) MLVA<sup>i</sup> distribution (%) of *Salmonella Typhimurium* including the monophasic S. 1,4,[5],12:i:- from humans, animals, carcasses and imported meat, 2015. N= number of isolates

MLVA type <sup>i</sup>	Human cases	Pork <sup>c</sup> batches	Beef <sup>d</sup> batch	Broiler <sup>e</sup> flocks	Imported meat (batches)	
					Pork <sup>g</sup>	Ducks <sup>h</sup>
STTR 9 5 6 10 3 Danish	N=231	N=49	N=1	N=6	N=14	N=4
3 12 10 NA 211 0005	7.8	6.1	0	0	0	0
3 13 10 NA 211 0192	3.9	6.1	0	0	0	0
3 14 9 NA 211 0201	3.9	0	0	0	0	0
3 13 9 NA 211 0008	3.5	6.1	0	16.7	0	0
3 11 9 NA 211 0006	2.6	2.0	0	16.7	0	0
3 13 8 NA 211 0479	2.6	0	0	0	0	0
3 14 11 NA 311 0251	2.2	0	0	0	0	0
3 12 9 NA 211 0007	2.2	14.3	0	0	0	0
3 12 8 NA 211 0338	2.2	0	0	0	0	0
3 11 8 NA 211 0378	1.7	0	0	0	0	0
Other	67.5	65.3	100	66.7	100	100
Total	100	100	100	100	100	100

For footnotes a-h see Table A5.

i) The isolates are analysed for the following loci: STTR9|STTR5|STTR6|STTR10|STTR3 and the results are reported in the same order in the table. "Danish" is the Danish MLVA-number for the MLVA profile. "NA"= locus missing.

Source: Danish Veterinary and Food Administration, Statens Serum Institut, and National Food Institute.

Table A8. Top 10 (humans) MLVA<sup>i</sup> distribution (%) of *Salmonella Enteritidis* from humans and imported meat, 2015. N= number of isolates

MLVA type <sup>i</sup>	Human cases	Imported broiler meat (batch) <sup>g</sup>	
		Danish	N=7
SE 1 5 2 9 3	N=253 <sup>j</sup>		
3 10 7 2 2 0004	21,7		0
4 10 5 3 1 0019	7,9		0
3 11 7 2 2 0029	7,9		0
4 9 5 3 1 0017	7,5		0
4 11 5 3 1 0020	5,9		0
4 10 4 3 1 0035	4,3		0
3 10 8 2 2 0005	3,2		0
4 12 5 3 1 0031	2,4		0
5 10 10 2 2 0006	2,4		0
3 13 9 2 2 0022	2,4		0
Other	34,4		100
Total	100		100

For footnotes a-h see Table A5.

i) The isolates are analysed for the following loci: SE1|SE5|SE2|SE9|SE3 and the results are reported in the same order in the table. "Danish" is the Danish MLVA-number for the MLVA profile.

j) In total, 259 human cases of *S. Enteritidis* was reported in 2015 (Table A2), only 253 isolates were analysed for MLVA type

Source: Danish Veterinary and Food Administration, Statens Serum Institut, and National Food Institute.

Table A9. Occurrence of *Salmonella* in the table egg production<sup>a</sup>, 2005-2015

	Rearing period <sup>b</sup> (parent flocks)		Adult period <sup>c</sup> (parent flocks)		Pullet-rearing flocks		Table egg layer flocks	
	N	Positive	N	Positive	N	Positive	N	Positive
2005	16	0	9	0	355	6	655	7
2006	17	0	11	0	289	2	565	2
2007	11	0	12	0	326	0	510	5
2008	10	0	6	0	258	1	508	4
2009	13	0	6	0	253	0	454	8
2010	15	0	9	0	225	0	455	8
2011	8	0	9	0	195	0	410	2
2012	9	0	8	0	197	1	359	3
2013	10	0	7	0	173	0	373	4
2014	22	0	8	0	150	0	347	2
2015	15	0	8	0	123	0	344	0

a) See Tables A32 and A34 for description of the surveillance programmes.

b) *Salmonella* was not detected in grandparent flocks during rearing period (2 flocks).

c) *Salmonella* was not detected in grandparent flocks during adult period (7 flocks).

Source: Danish Agriculture and Food Council, and Danish Veterinary and Food Administration.

Table A10. Occurrence of *Salmonella* in the table egg layer flocks sorted by type of production, 2005-2015

	Deep litter		Free range		Organic		Battery	
	N	Positive	N	Positive	N	Positive	N	Positive
2005	217	3	70	0	178	0	175	4
2006	185	0	62	0	164	2	148	0
2007	155	2	56	0	146	2	146	1
2008	151	0	61	2	145	1	135	1
2009	133	1	78	0	130	4	110	3
2010	117	0	45	2	136	1	157	5
2011	109	0	40	0	130	1	131	1
2012	101	0	37	1	136	1	131	1
2013	108	0	37	1	137	3	94	0
2014	97	0	30	0	125	1	95	1
2015	108	0	29	0	172	0	86	0

Source: Danish Agriculture and Food Council, and Danish Veterinary and Food Administration.

Table A11. Occurrence of *Salmonella* in the broiler production<sup>a</sup>, 2005-2015

	Rearing period <sup>f</sup> (parent flocks)		Adult period <sup>g</sup> (parent flocks)		Broiler flocks		Slaughterhouse (flocks/batches)	
	N	Positive	N	Positive	N	Positive	N	Positive
2005	214	0	185 <sup>b</sup>	0	4,034	87	1,174	27
2006	190	0	282	5	3,621	71	875 <sup>c</sup>	17
2007	152	0	258	3	3,703	60	884	10
2008	146	0	293	2	3,845	43	518 <sup>d</sup>	3
2009	140	0	225	4	3,767	35	375	3
2010	126	0	200	5	3,773	43	346	1
2011	114	0	213	0	3,795	47	306	0
2012	123	0	183	0	3,448	27	368	0
2013	128	0	152	1	3,498	34	288	0
2014	121	2	131	3	3,470	26	277	4
2015	91	0	289	1 <sup>e</sup>	3,631	23	148	0

a) See Tables A32-A33 for description of the surveillance programmes.

b) In 2005, only one flock per house was registered per year although there may have been more than one flock in the house, however all flocks were sampled according to the surveillance programme.

c) From 2006, data cover only samples taken following the *Salmonella* programme. Verification samples taken once a week by producers of poultry meat approved to market *Salmonella*-free poultry meat are not included. Collection of verification samples started in the middle of 2005.

d) From 2008, all AM positive flocks are heat treated at slaughter. Sampling is now carried out as verification of the AM results of the negative flocks.

e) *S. Give*

f) *Salmonella* was not detected in grandparent flocks during rearing period (12 flocks).

g) *Salmonella* was not detected in grandparent flocks during adult period (4 flocks).

Source: Danish Agriculture and Food Council, and Danish Veterinary and Food Administration.

Table A12. Occurrence of *Salmonella* in turkey and duck flocks, 2006-2015

	Duck flocks		Turkey flocks <sup>a</sup>	
	N	% pos	N	% pos
2006	266	80.5	11	0
2007	-	-	13	0
2008	68	64.7	10	10.0
2009	85	63.5	15	0
2010	108	56.5	24	4.2
2011	95	58.1	38	2.6
2012	96	49.0	23	0
2013	64 <sup>b</sup>	20.3	56	3.6
2014	0 <sup>b</sup>	-	10	0
2015	0	-	80	1.3 <sup>c</sup>

a) See Table A35 for description of the surveillance programme for turkey flocks. The two major turkey and duck slaughterhouses in Denmark closed down in 2004 and 2007, respectively. Therefore, most commercially reared duck and turkey flocks are transported abroad for slaughter.

b) Since 20/09/2013 samples from ducks were no more taken.

c) One flock positive with *S. Newport*

Source: Danish Agriculture and Food Council.

Table A13. Occurrence of *Campylobacter* in broiler flocks, 2006-2015<sup>a</sup>

	Cloacal swabs at slaughter		Sock samples at farm	
	N (Flocks)	% pos	N (Flocks)	% pos
2006	4,522	30.8	-	-
2007	4,527	26.8	-	-
2008	4,950	26.3	-	-
2009	4,591	29.4	-	-
2010	-	-	3,132	16.5
2011	-	-	3,379	14.4
2012	-	-	3,376	11.6
2013	-	-	3,508	13.1
2014	3,474	27.7	-	-
2015	3,274	19.6	-	-

a) See Tables A33 for description of the surveillance programmes. In 2014 the sampling method changed back from boot swabs collected in the stable 7-10 days before slaughter to cloacal swabs at slaughter according to Regulation no. 1512 of 13/12/2013.

Source: Danish Agriculture and Food Council and National Veterinary Institute (until 2009).

Table A14. Occurrence of *Campylobacter* in non-heat treated broiler meat at slaughter and retail<sup>a</sup>, 2012-2015

		Chilled broiler meat (samples)					
		At slaughter		At retail			
		Denmark		Denmark		Import	
		N	% pos	N	% pos <sup>b</sup>	N	% pos <sup>b</sup>
2012	Conventional	1,044 <sup>c</sup>	21.5	-	-	-	-
	Organic/free-range	-	-	-	-	-	-
	In total	-	-	521	9.7	154	28.2
2013	Conventional	870 <sup>d</sup>	28.2	849	12.1	170	12.8
	Organic-free-range	93 <sup>d</sup>	90.3	35	42.9	38	71.1
	In total	-	-	884	17.8	208	31.9
2014	Conventional	927	25.7	-	-	-	-
	Organic/free-range	108	75.0	-	-	-	-
2015	Conventional	960	20.1	-	-	-	-
	Organic/free-range	115	78.2	-	-	-	-

a) Centrally coordinated studies (see Table A28 and section 9.4 for description). Limit of quantification: 10 cfu/g.

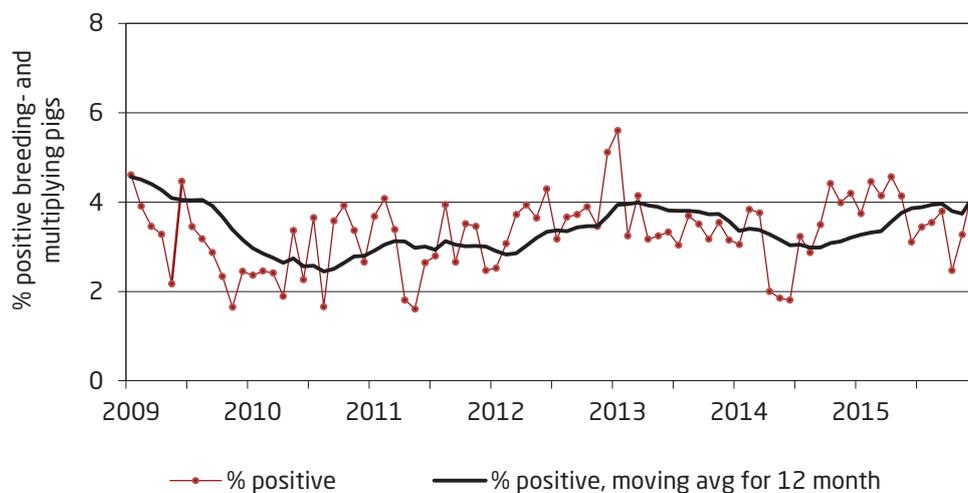
b) The prevalence is calculated as a mean of quarterly prevalences, except organic/free-range results.

c) Included are 238 leg-skin samples, prevalence = 24.4%.

d) Leg-skin samples only.

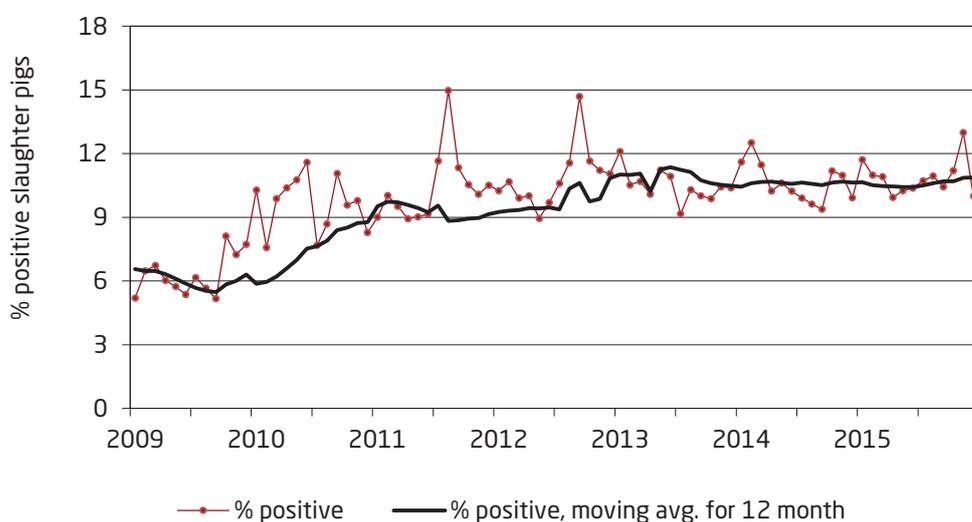
Source: National Food Institute.

Figure A1. Serological surveillance of Salmonella in breeding and multiplying pigs<sup>a</sup> based on monthly testing of blood samples, 2009-2015



a) For more information about the surveillance programme, see Table A37.  
Source: Danish Agriculture and Food Council.

Figure A2. Serological surveillance of Salmonella in slaughter pigs<sup>a</sup>, 2009-2015. Percentage of seropositive meat juice samples (first sample per herd per month)<sup>b</sup>



a) For more information about the surveillance programme, see Table A37.  
b) The peaks in January 2010 and August 2011 were due to data transfer problems. The reason for the increase in late summer 2012 is unknown.  
Source: Danish Agriculture and Food Council.

Table A15. Occurrence of zoonotic pathogens in pigs and pork in Denmark, 2015

Zoonotic pathogen	Herds		Animals/Samples		
	N	Pos	N	Pos	% pos
<b>At farm</b>					
<i>Brucella abortus</i> <sup>a</sup>	-	-	21,870	0	-
<i>Leptospira</i> <sup>b</sup>	119	1	133	1	-
<b>At slaughterhouse (slaughter pigs)</b>					
<i>Salmonella</i> spp. <sup>c,d</sup>	6,559	348 <sup>e</sup>	-	-	-
<i>Salmonella</i> spp. <sup>c,f</sup> (slaughtering >30.000 pigs/year)	-	-	15,905	-	1.2 <sup>g</sup>
<i>Salmonella</i> spp. <sup>c,f</sup> (slaughtering 1.000 or more and less than 30.000 pigs/year)	-	-	678	-	1.2
<i>Salmonella</i> spp. <sup>c,h</sup>	-	-	803	144	17.8
<i>Trichinella</i> spp. <sup>i</sup>	-	-	18,176,109	0	0
<i>Mycobacterium bovis</i> <sup>j</sup>	-	-	18,293,442	0	0
<i>Echinococcus granulosus/multilocularis</i> <sup>j</sup>	-	-	18,293,442	0	0

a) Including samples from boars (examined at pre-entry, every 18 month, and prior to release from semen collection centres) (18,259 samples), samples collected in connection with export (3,559), import (no samples this year) and diagnostic samples (52 samples). 5-8 ml blood samples were analysed using either the SAT, RBT, CFT or ELISA methods.

b) Sampling is based on suspicion of leptospirosis due to increased abortions or other reproductive problems in a herd. Samples are investigated using immunofluorescence techniques.

c) See Table A37 for description of the *Salmonella* surveillance programme.

d) Data are from December 2015. Slaughter pig herds monitored using serological testing of meatjuice samples collected at slaughter.

e) Includes herds belonging to *Salmonella* level 2 and 3 only (See Table A37).

f) Swab samples from four designated areas of the half-carcass were collected at the slaughterhouse after min. 12 h chilling. Sample size is 4x100 cm<sup>2</sup>. Samples from five animals were pooled, at slaughterhouses where 30.000 pigs or more were slaughtered per month. In slaughterhouses slaughtering 30.000 pigs or less per year, samples were analysed individually.

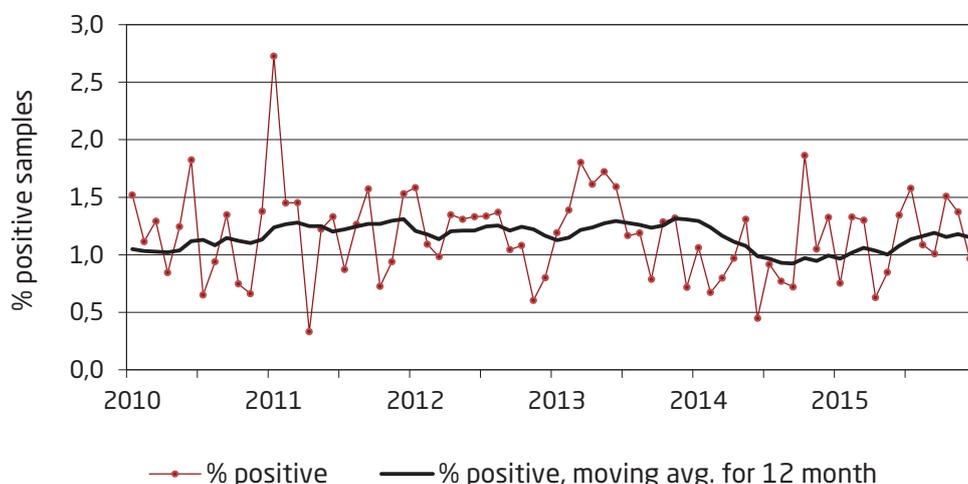
g) When estimating the prevalence of *Salmonella*, both the loss of sensitivity and the probability of more than one sample being positive in each pool are taken into consideration. A conversion factor has been determined on the basis of comparative studies, as described in Annual Report 2001.

h) Coecum samples are randomly collected from slaughter pigs at slaughter.

i) Samples collected from slaughter pigs at slaughter were examined using the method described in Directive 2075/2005/EEC. In 2014, an amendment to EU regulation (EC) No 2075/2005 came into force stating that slaughter pigs, sows and boars kept under "controlled housing conditions" in Denmark are exempted testing for *Trichinella*. Free range pigs, horses and wild game and other species susceptible to *Trichinella* must be tested

j) Slaughter pigs were examined by meat inspectors at slaughter.

Source: Danish Veterinary and Food Administration, National Veterinary Institute and National Food Institute, Technical University of Denmark.

Figure A3. *Salmonella* in pork, monitored at slaughterhouses<sup>a</sup>, 2009-2015

a) For more information about the surveillance programme, see Table A37.

Source: Danish Veterinary and Food Administration.

Table A16. Occurrence of zoonotic pathogens in cattle and beef in Denmark, 2015

Zoonotic pathogen	Herds		Animals/Samples		
	N	Pos	N	Pos	% pos
<b>At farm</b>					
<i>Brucella abortus</i> <sup>a</sup>	-	-	1,650	0	-
<i>Mycobacterium bovis</i> <sup>b, c</sup>	-	-	1,680	0	-
<i>Coxiella burnetii</i>	95 <sup>d</sup>	10	207 <sup>e</sup>	7	-
<b>At slaughterhouse</b>					
<i>Salmonella</i> spp. <sup>f</sup> (slaughtering >=7.500 cattle/year)	-	-	5,935	-	0.08 <sup>g</sup>
<i>Salmonella</i> spp. <sup>f</sup> (slaughtering 250 or more and 7.500 or less cattle/year)	-	-	285	1	0.35
<i>Mycobacterium bovis</i> <sup>b, h</sup>	-	-	512,600	0	0
VTEC	-	-	92	10 <sup>i</sup>	
<i>Echinococcus granulosus/multilocularis</i> <sup>h</sup>	-	-	512,600	0	0

a) Denmark has been declared officially brucellosis free since 1979. The last outbreak was recorded in 1962. Including samples from bulls (examined at pre-entry, every year, and prior to release from semen collection centres) (1,102 samples), samples collected in connection with export (219), import (1) and diagnostic samples (160). 5-8 ml blood samples were analysed using either the SAT, RBT, CFT or ELISA methods.

b) Denmark has been declared officially tuberculosis free since 1980. The last case of TB in cattle was diagnosed in 1988.

c) Analysis using the interdermal tuberculin test. Including samples from bulls (examined at pre-entry, every year, and prior to release from semen collection centres) and samples collected in connection with export.

d) Bulk tank milk samples taken for diagnostic testing and analysed using an ELISA method.

e) Serum samples taken for diagnostic testing (27 samples, 2 pos), export (103 samples, 4 pos), breeding (77 samples, 1 pos) and analysed using an ELISA method.

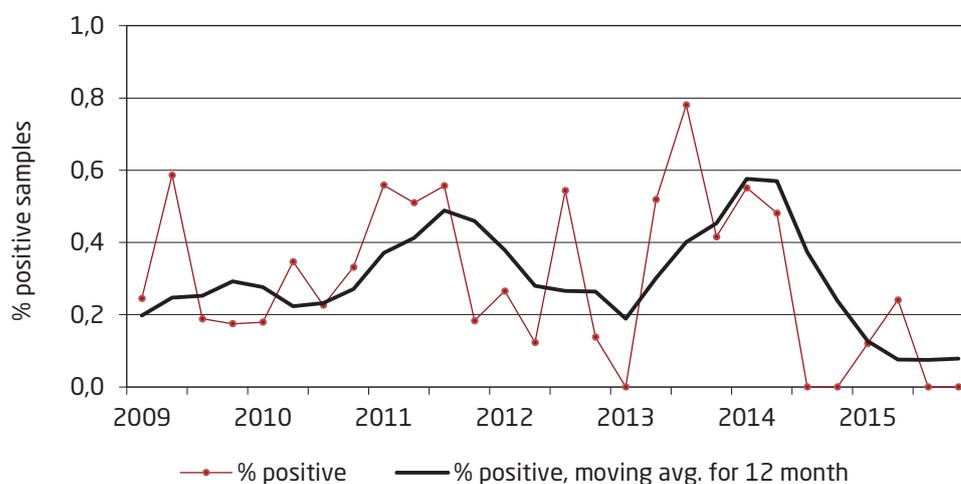
f) See Table A36 for description of the surveillance programme. Swab samples from four designated areas of the half-carcass were collected at the slaughterhouse after min. 12 h chilling. Sample size is 4x100 cm<sup>2</sup>. Samples from five animals were pooled at slaughterhouses slaughtering 7,500 or more cattle per year. At slaughterhouses slaughtering 250 or more and less than 7,500 cattle per year, samples were analysed individually.

g) When estimating the prevalence of *Salmonella*, both the loss of sensitivity and the probability of more than one sample being positive in each pool are taken into consideration. A conversion factor has been determined on the basis of comparative studies, as described in Annual Report 2001.

h) Slaughtered cattle were examined by the meat inspectors at slaughter.

i) 2 samples had triple infection with O121+O157:H7+O103, 2 samples had double infection with O121+O157:H7, 4 samples was positive with O121, 1 sample was positive with O157:H7+O103, and 1 sample was positive with O157:H7.

Source: Danish Veterinary and Food Administration, Danish Agriculture and Food Council, National Veterinary Institute, and National Food Institute, Technical University of Denmark.

Figure A4. *Salmonella* in beef, monitored at slaughterhouses<sup>a</sup>, 2009-2015

a) For more information about the surveillance programme, see Table A36.

Source: Danish Veterinary and Food Administration.

Table A17 Cattle herds in the *S. Dublin* surveillance programme<sup>a</sup>, December 2015

<i>Salmonella</i> Dublin level		Non-milk producing herds		Milk producing herds	
		N	%	N	%
Level 1	On the basis of milk samples	-	-	3,056	92.9
	On the basis of blood samples	13,915	97.9		
Total	Probably <i>Salmonella</i> Dublin free	13,915	97.9	3,056	92.9
Level 2	Titer high in blood- or milk samples	96	0.7	177	5.4
	Contact with herds in level 2 or 3	131	0.9	25	0.8
	Other causes	63	0.4	22	0.7
Level 3	Salmonellosis, official supervision	12	0.1	10	0.3
	Total	Non <i>Salmonella</i> Dublin free	302	2.1	234
Total number of herds		14,217	100	3,290	100

a) See Table A36 for description of the surveillance programme.

Source: Seges, Cattle.

Table A18 Results from the intensified control of *Salmonella* and *Campylobacter* in fresh meat based on case-by-case risk assessments, 2015

		Batches tested	No. of batches positive	No. of batches deemed unsafe based on a risk assessment	Batches deemed unsafe based on other criteria <sup>a</sup>	Mean prevalence in batches <sup>b,c</sup>	Mean relative human risk in batches <sup>c,d</sup>
<b>Campylobacter</b>							
Danish	Broiler	121	51	3	-	40.8	3.4
Imported	Broiler	148	72	8	-	38.1	3.6
<b>Salmonella</b>							
Danish	Pork	149	12	1	-	7.9	3.7
	Broiler	101	0	0	0	-	-
Imported	Pork	150	11	1	-	13.2	6.7
	Broiler	180	18	3	6	18.8	14.6
	Turkey	25	4	3	0	11.6	61.8

a) Microbiological criteria specified in regulation (EC) No 2073/2005 as amended. For Danish broiler meat there is a zero-tolerance for *Salmonella* and all positive batches must be heat treated before being put on the market (Order no. 1512 of 13/12/2013).

b) The *Salmonella* prevalence in each batch is based on the proportion of positive pooled samples (12 pools per batch) and number of subsamples per pool.

c) For *Salmonella*, only results for batches subjected to risk assessment have been included. For *Campylobacter* all positive batches have been included.

d) Calculated as the risk relative to a batch of the same size with a mean prevalence (weighted average in Danish and imported meat) of *Campylobacter* or of a *Salmonella* type with an average impact to cause human infection.

Source: Danish Veterinary and Food Administration, and National Food Institute.

Table A19. Feed business operators own sampling of *Salmonella* in compound feeds, feed processing and feed material (batch-based data), 2013-2015

	2015		2014		2013	
	N	Positive	N	Positive	N	Positive
Feed processing plants (process control) <sup>a</sup> :						
Ordinary inspections - clean zone	7,307	6 <sup>d</sup>	7,557	17	7,132	2
Ordinary inspections - unclean zone	602	29 <sup>e</sup>	456	63	577	88
Compound feed, farm animals	1,148	1 <sup>f</sup>	858	0	375	0
Feed materials, farm animals <sup>b</sup>	1,416	17 <sup>g</sup>	1,656	28	1,295	11
Transport vehicles, clean zone/hygiene samples <sup>c</sup>	1,190	5 <sup>h</sup>	1,143	1	973	4
Transport vehicles, unclean zone/hygiene samples <sup>c</sup>	63	10 <sup>i</sup>	235	7	255	0

Note: Data are from one feed and grain trade organisation only, representing a proportion of feed at the Danish market.

a) Presence of *Salmonella* in compound feed is indirectly monitored by environmental samples collected during feed processing.

b) Predominantly soy bean meal but also sunflower products and rapeseed cake.

c) Samples from transport vehicles (hygiene samples) prior to loading of feed compounds.

d) S. Derby, S. Havana, S. Seftenberg, S. Falkensee

e) S. Orion var. 15,34, S. Indika, S. Rissen, S. Putten, S. Tennessee, S. Falkensee

f) S. Havana

g) S. Orion var. 15,34, S. Rissen, S. Quakam, S. Liverpool, S. Amsterdam, S. Havana, S. Tennessee, S. Senftenberg, S. Mbandaka

h) S. 4.5.12i, S. Derby

i) S. Putten, S. Rissen, S. Kralingen

Source: Danish Veterinary and Food Administration and the feed business operators.

Table A20. Control of *Salmonella* in compound feeds, feed processing and feed material (batch-based data), 2012-2015

	2015		2014		2013		2012	
	N	Positive	N	Positive	N	Positive	N	Positive
Feed processing plants (process control) <sup>a</sup> :								
Ordinary inspections <sup>b</sup>	319	17 <sup>d</sup>	402	10 <sup>d</sup>	333	7	311	11
Feed materials, farm animals <sup>c</sup>	71	3 <sup>e</sup>	90	4 <sup>e</sup>	99	2	99	4

a) Presence of *Salmonella* in compound feed is indirectly monitored by environmental samples collected during feed processing. Companies are sampled one to four times per year.

b) Primarily findings of *Salmonella* in the dirty zone.

c) Predominantly soy bean meal, and rapeseed cake and fish meal.

d) S. Putten, S. Falkensee, S. Idikan, S. Meleagridis, S. Nyborg, S. Infantis, S. Rissen, S. Seftenberg

e) S. Infantis, S. Havana

Source: Danish Veterinary and Food Administration.

Table A21. *Salmonella* in three categories of meat and bone meal by-products not intended for human consumption<sup>a</sup>, 2015

Category of processing plant		Own-check samples		Product samples	
		N	Positive	N	Positive
1+2	By-products of this material cannot be used for feeding purposes	259	17	51	2
2	By-product of this material may be used for feed for fur animals	85	0	24	0
3	By-products from healthy animals slaughtered in a slaughterhouse. Products of these may be used for petfood <sup>b</sup> and for feed for fur animals	545	2	1,115	0
Total		889	19	1,190	2

a) Regulation No. 1774 of 03/10/2002.

b) For cats and dogs. Only by-products from pigs are used in this pet food.

Source: Daka Denmark A/S.

Table A22. Pathogens in batches<sup>a</sup> of ready-to-eat vegetables, herbs and fruits<sup>b</sup>, 2015

Type of sample	<i>Salmonella</i>		<i>Campylobacter</i>		<i>E. coli</i>	
	N	Pos	N	Pos	N	>100 cfu/g <sup>g</sup>
<b>Vegetables</b>						
Baby corn	1	0	1	0	1	0
Cucumber	4	0	4	0	4	0
Pepper	3	0	3	0	3	0
Salad/leafy green	23	0	23	0	23	0
Sprouts <sup>c</sup>	4	0	4	0	4	0
Sugar peas	3	0	3	0	3	0
Tomato	6	0	6	0	6	0
Other vegetables <sup>d</sup>	13	0	13	0	13	0
<b>Herbs</b>						
Parsley	3	0	3	0	3	0
Spearmint	1	0	1	0	1	0
Spring onions	1	0	1	1 <sup>h</sup>	1	0
Other herbs <sup>e</sup>	2	0	2	0	2	0
<b>Fruit and berries</b>						
Grapes	1	0	1	0	1	0
Cherries	2	0	2	0	2	0
Raspberries	3	0	3	0	3	0
Strawberries	10	0	10	0	10	0
Blueberries	4	0	4	0	4	0
Other berries <sup>f</sup>	3	0	3	0	3	0
<b>Total</b>	<b>87</b>	<b>0</b>	<b>87</b>	<b>1</b>	<b>87</b>	<b>0</b>

a) Five samples per batch.

b) Centrally coordinated study (See section 8.4 for description) to control and investigate *Salmonella*, *Campylobacter* and *E. coli* in Danish and imported ready-to-eat vegetables, sprouts and herbs.

c) Additionally tested for *Listeria monocytogenes*, not detected.

d) Including cucumber, broccoli, cauliflower, mushrooms, brussels sprouts, green beans, celery, cabbage.

e) Unspecified

f) Including blackcurrant, blackberries

g) Batches with >100 cfu/g in one or more samples.

h) 1 batch of spring onions from Egypt.

Source: Danish Veterinary and Food Administration.

Table A23. Occurrence of zoonotic pathogens in pets and zoo animals in Denmark<sup>a</sup>, 2015

Zoonotic pathogen	Pet animals						Zoo animals			
	Dogs		Cats		Others		Mammals & reptiles		Birds	
	N	Pos	N	Pos	N	Pos	N	Pos	N	Pos
<i>Salmonella</i> spp.	0	-	0	-	0	-	5 <sup>b</sup>	2 <sup>c</sup>	4 <sup>d</sup>	0
<i>Chlamydia psittaci</i>	0	-	0	-	0	-	0	-	730 <sup>e</sup>	50 <sup>f</sup>
<i>Cryptosporidium</i> spp.	3	-	0	-	0	-	0	-	0	-
Lyssavirus (classical)	0	-	0	-	3 <sup>g</sup>	0	0	-	0	-
European Bat Lyssavirus	0	-	0	-	3 <sup>g</sup>	0	0	-	0	-

a) All samples are analysed based on suspicion of disease, and does not reflect the country prevalence.

b) 1 camel, 2 lizard Ameiva, 2 Chestnut-sided forest turtle.

c) *S. Abaetetuba* (1), *S. IV-45:g,z51:-* (1).

d) 2 dove, 2 red-tailed kakadu.

e) 1 ara, 168 homing pigeon, 210 dove, 13 lovebird, 8 finches, 162 parrots, 1 gray parrot, 5 canary, 4 cockatiel, 16 parrots, 16 parakeet, 125 budgerigar, 1 quail.

f) Homing pigeon (2), dove (28), parrots (3), canary (1), parrots (1), parakeet (4), budgerigar (11).

g) 2 cattles, 1 sheep.

Source: National Veterinary Institute, Technical University of Denmark, and Danish Veterinary and Food Administration.

Table A24. Occurrence of zoonotic pathogens in wild and farmed wildlife in Denmark<sup>a</sup>, 2015

Zoonotic pathogen	Farmed wildlife				Wildlife			
	Wild boar		Minks & chinchillas		Mammals		Birds	
	N	Pos	N	Pos	N	Pos	N	Pos
<i>Salmonella</i> spp.	60	0	20	0	6 <sup>b</sup>	2 <sup>c</sup>	6 <sup>d</sup>	0
<i>Campylobacter</i> spp.	0	-	2	0	0	-	0	-
<i>Chlamydia psittaci</i>	0	-	0	-	0	-	7 <sup>e</sup>	0
<i>Cryptosporidium</i> spp.	0	-	0	-	34 <sup>f</sup>	1 <sup>g</sup>	0	-
<i>Echinococcus multilocularis</i>	0	-	0	-	187 <sup>h</sup>	5 <sup>i</sup>	0	-
<i>Trichinella</i> spp <sup>j</sup>	414	0	0	-	62 <sup>l</sup>	0	0	-
Lyssavirus (classical)	0	-	0	-	13 <sup>m</sup>	0	0	-
European Bat Lyssavirus	0	-	0	-	13 <sup>m</sup>	0	0	-

a) All samples are analysed based on suspicion of disease or risk based and does not reflect the country prevalence, except for animals analysed for *Echinococcus multilocularis*. These animals are collected as part of a survey.

b) 5 badger, 1 hedgehog.

c) *S. Enteritidis* (1), not serotyped (1).

d) 1 hooded crow, 5 common starlings.

e) 5 dove, 2 mallards.

f) 1 red deer, 7 raccoon dogs, 2 hedgehog, 24 deer.

g) 1 hedgehog.

h) 1 badger, 122 raccoon dogs, 62 foxes, 2 raccoons.

i) Foxes (5)

j) In 2014, an amendment of EU regulation (EC) No 2075/2005 came into force stating that slaughter pigs, sows and boars kept under "controlled housing conditions" in Denmark are exempted testing for *Trichinella*. Free range pigs, horses and wild game and other species susceptible to *Trichinella* must be tested

l) 1 dolphin, 1 pilot whale, 7 gray seal, 4 harbour porpoise, 29 mink, 20 harbor seal.

m) 13 bats

Source: National Veterinary Institute, Technical University of Denmark, and Danish Veterinary and Food Administration.

Table A25. The Bovine Spongiform Encephalopathy (BSE) surveillance programme<sup>a</sup> for cattle, 2015

Type of surveillance	N <sup>b</sup>	Positive
Active surveillance		
Healthy slaughtered animals	33	0
Risk categories:		
Emergency slaughters	1,112	0
Slaughterhouse antemortem inspection revealed suspicion or signs of disease	0	-
Fallen stock	18,366	0
Animals from herds under restriction	0	-
Passive surveillance		
Animals suspected of having clinical BSE	3	0
<b>Total</b>	<b>19,514</b>	<b>0</b>

a) According to the EU Regulation (EC) 999/2001 as amended, Commission Decision 2009/719/EC as amended and Danish Order no. 878 of 01/07/2013 as amended.

b) Samples (brain stem material) are tested using a IDEXX technique. Confirmatory testing is carried out using histopathology or immunohistochemistry. Further confirmation on autolysed material is performed at the European Union TSE reference laboratory.

Source: National Veterinary Institute, Technical University of Denmark, and Danish Veterinary and Food Administration.

Table A26. The Transmissible Spongiform Encephalopathy (TSE) surveillance programme<sup>a</sup> for sheep and goats, 2015

Type of surveillance	N <sup>b</sup>	Positive
Active surveillance		
Fallen stock (>18 months)	770	0
Animals from herds under restriction	0	-
Passive surveillance		
Animals suspected of having clinical TSE	2 <sup>c</sup>	0
<b>Total</b>	<b>772</b>	<b>0</b>

a) According to the EU Regulation (EC) 999/2001 as amended, Commission Decision 2009/719/EC as amended and Danish Order no. 1288 of 20/12/2011 as amended.

b) Samples (brain stem material) are tested using a IDEXX technique. Confirmatory testing is carried out using histopathology or immunohistochemistry. Further confirmation on autolysed material is performed at the European Union TSE reference laboratory.

c) One of the clinical suspects was rejected without testing according to TSE Regulation 999/2001 as later amended, Article 12(1).

Source: National Veterinary Institute, Technical University of Denmark, and Danish Veterinary and Food Administration.

Table A27. Distribution<sup>a</sup> (%) of prion protein genotype of sheep randomly selected, 2015

	Genotype	Sheep n=100
NSP 1	ARR/ARR	24.0
NSP 2	ARR/AHQ, ARR/ARH, ARR/ARQ	20.0
NSP 3 (ARQ/ARQ)	ARQ/ARQ	37.0
NSP 3 (Other)	AHQ/AHQ, AHQ/ARH, AHQ/ARQ, ARH/ARQ, ARH/ARH, ARQ/ARH, ARH/AHQ, ARQ/AHQ	14.0
NSP 4	ARR/VRQ	3.0
NSP 5	ARH/VRQ, ARQ/VRQ, VRQ/VRQ, AHQ/VRQ	2.0
<b>Total</b>		<b>100.0</b>

a) The genotypes were grouped in the NSP classification system according to their different susceptibility:

NSP 1: Genetically most resistant, NSP 2: Genetically resistant, NSP 3: Genetically little resistance,

NSP 4: Genetically susceptible, and NSP 5: Genetically highly susceptible.

Source: National Veterinary Institute, Technical University of Denmark, and Danish Veterinary and Food Administration.

Table A28. Centrally coordinated studies conducted in 2015

Title of project	No. of samples	Pathogen surveyed	Further information
<i>Campylobacter</i> spp. in fresh, chilled Danish broiler meat (conventional)	950	<i>Campylobacter</i> spp.	Appendix Table A14
<i>Campylobacter</i> spp. in fresh, chilled Danish broiler meat (organic)	115	<i>Campylobacter</i> spp.	Appendix Table A14
<i>Campylobacter</i> spp. in fresh, chilled Danish and imported broiler meat (processed meat)	205	<i>Campylobacter</i> spp.	Data are being processed <sup>a</sup>
<i>Campylobacter</i> spp. in poultry at slaughter	96	<i>Campylobacter</i> spp.	Data are being processed <sup>a</sup>
Official verification of microbiological criteria	2,260	<i>Listeria monocytogenes</i> , <i>Salmonella</i> spp., staphylococci, <i>Escherichia coli</i> , aerobic plate count, <i>Enterobacteriaceae</i> .	Results are published on the DVFA website <a href="http://www.fvst.dk">www.fvst.dk</a> (In Danish)
Pathogens in Danish and imported ready-to-eat vegetables	435	<i>Salmonella</i> spp., <i>Campylobacter</i> spp., <i>Escherichia coli</i>	Appendix Table A22
ESBL in Danish poultry production	147	ESBL	Results are presented in the 2015 DANMAP report and
DANMAP - Antibiotic resistance in poultry, pigs and cattle, and in Danish and imported broiler, beef and pork meat	599	<i>Campylobacter</i> spp., <i>Enterococcus faecium</i> , <i>E. faecalis</i> , ESC <i>Escherichia coli</i>	Results are presented in the 2015 DANMAP report
Surveillance of antibiotic resistance in beef and pork meat at retail (DANMAP and EU surveillance)	604	<i>Escherichia coli</i> , enterococci, ESBL, AmpC, carbapenemase-producing <i>E. coli</i>	Results are presented in the 2015 DANMAP report
Surveillance of antibiotic resistance in poultry, pig and cattle (DANMAP and EU surveillance)	593	<i>Escherichia coli</i> , ESBL, AmpC, carbapenemase-producing <i>E. coli</i>	Results are presented in the 2015 DANMAP report and
Antibiotic resistance in pigs at slaughter	270	<i>Escherichia coli</i> , <i>Enterobacteriaceae</i> , enterococci, ESBL	Results are presented in the 2015 DANMAP report and
Salmonella in pigs at slaughter	509	<i>Salmonella</i> spp.	Appendix Tables A5 and A15
<i>Salmonella</i> spp. antibiotic resistance in fresh, chilled and frozen imported beef and duck meat incl. ESBL in duck meat	307	<i>Salmonella</i> spp., ESC <i>Escherichia coli</i>	Results are presented in the 2015 DANMAP report
<i>Salmonella</i> in intratraded shell eggs	10	<i>Salmonella</i> spp.	Data are being processed <sup>a</sup>
Import control - fish, fish products and bivalve molluscan shellfish	110	<i>Listeria monocytogenes</i> , <i>Salmonella</i> spp., <i>Escherichia coli</i> , staphylococci	Data are being processed <sup>a</sup>
<i>Listeria monocytogenes</i> , <i>Salmonella</i> spp., <i>Escherichia coli</i> and staphylococci in fish and fish products from Greenland	100	<i>Listeria monocytogenes</i> , <i>Salmonella</i> spp., <i>Escherichia coli</i> , staphylococci	Results are published on the DVFA website <a href="http://www.fvst.dk">www.fvst.dk</a> (In Danish)
<i>Salmonella</i> spp. and <i>Escherichia coli</i> in raw frozen scallops from Greenland	35	<i>Salmonella</i> spp., <i>Escherichia coli</i>	Data are being processed <sup>a</sup>
<i>Salmonella</i> Dublin and STEC in beef	375	<i>Salmonella</i> spp., <i>Escherichia coli</i> , enterobacteriaceae, enterococci	Data are being processed <sup>a</sup>
Import control - food of non animal origin	40	<i>Salmonella</i> spp. (sesame seeds)	Data are being processed <sup>a</sup>
<i>Salmonella</i> in animal feed	390	<i>Salmonella</i> spp.	Results are published on the DVFA website <a href="http://www.fvst.dk">www.fvst.dk</a> (In Danish)
Intensified control for <i>Salmonella</i> spp. and <i>Campylobacter</i> in fresh Danish and imported meat (poultry and pig)	647 partier	<i>Campylobacter</i> spp., <i>Salmonella</i> spp.	Appendix Table A18

a) Results will be published on the DVFA website [www.fvst.dk](http://www.fvst.dk) (in Danish).

Source: Danish Veterinary and Food Administration.

Table A29. *Listeria monocytogenes* in Danish produced ready-to-eat (RTE) foods<sup>a</sup>, 2015

Food category	Sampling place	Samples analysed by a qualitative method <sup>b</sup>				Samples analysed by a quantitative method			
		Batches <sup>c</sup>		Single samples		Batches <sup>c</sup>		Single samples	
		N	Pos	N	Pos	N	Pos	N	Pos
Bakery products	At processing	1	0	5	0	-	-	-	-
Egg and egg products	At processing	2	0	10	0	4	0	20	0
Cheese, RTE	At processing	19	0	95	0	10	0	50	0
Milk and dairy products excluding cheeses), RTE	At processing	35	1	170	1	9	0	45	0
Products made from broiler meat, RTE	At processing	1	0	5	0	1	0	5	0
Products made from turkey meat, RTE	At processing	2	0	10	0	-	-	-	-
Products made from pork, RTE	At processing	39	1	190	2	16	0	80	0
Products made from beef, RTE	At processing	5	0	25	0	4	0	20	0
Fruit, RTE	At processing	2	0	10	0	2	0	10	0
Vegetables, RTE	At processing	20	1	95	1	12	0	60	0
Fish and Fishery products, RTE	At processing	28	1	140	5	13	0	65	0
Shellfish and products thereof, RTE	At processing	3	0	15	0	8	0	40	0
Other RTE products	At processing	49	1	240	1	19	0	95	0

a) Samples are collected by the local food control offices according to EU Regulation (EC) No 2073/2005.

b) *Listeria monocytogenes* present in a 25 g sample of the product.

c) Five samples from each batch, analysed individually.

Source: Danish Veterinary and Food Administration.

## Monitoring and surveillance programmes

Table A30. Overview of notifiable and non-notifiable human diseases presented in this report, 2015

Patogen	Notifiable	Notification route
<b>Bacteria</b>		
<i>Brucella</i> spp.	no	-
<i>Campylobacter</i> spp.	1979 <sup>a</sup>	Laboratory <sup>b</sup>
<i>Chlamydophila psittaci</i> (Ornithosis)	1980 <sup>a</sup>	Physician <sup>c</sup>
<i>Listeria monocytogenes</i>	1993 <sup>a</sup>	Physician
<i>Leptospira</i> spp.	1980 <sup>a</sup>	Physician
<i>Mycobacterium bovis/ tuberculosis</i>	1905 <sup>a</sup>	Physician (and laboratory <sup>d</sup> )
<i>Coxiella burnetii</i>	no	-
<i>Salmonella</i> spp.	1979 <sup>a</sup>	Laboratory
VTEC	2000 <sup>a</sup>	Physician and laboratory
<i>Yersinia enterocolitica</i>	1979 <sup>a</sup>	Laboratory
<b>Parasites</b>		
<i>Cryptosporidium</i> spp.	no	-
<i>Echinococcus multilocularis</i>	no	-
<i>Echinococcus granulosus</i>	no	-
<i>Trichinella</i> spp.	no	-
<b>Viruses</b>		
<i>Lyssavirus</i> (Rabies)	1964 <sup>a</sup>	Physician (via telephone)
<b>Prions</b>		
BSE/Creutzfeldt Jacob	1997 <sup>a</sup>	Physician

a) Danish order no. 277 of 14/04/2000. Cases must be notified to Statens Serum Institut.

b) The regional microbiological laboratories report confirmed cases.

c) The physician report individually notifiable infections.

d) The laboratories voluntarily report confirmed cases.

Source: Statens Serum Institut.

Table A31. Overview of notifiable and non-notifiable animal diseases presented in this report, 2015

Patogen	Notifiable	EU legislation	Danish legislation
<b>Bacteria</b>			
<i>Brucella</i> spp.	1920 <sup>a</sup>		
Cattle	Obf in 1979 <sup>b</sup>	Decision 2003/467/EC	Order no 305 of 3/5 2000
Sheep and goats	ObmF in 1995 <sup>c</sup>	Decision 2003/467/EC	Order no. 739 of 21/8 2001
Pigs	No cases since 1999	Directive 2003/99/EC	Order no. 205 of 28/3 2008
<i>Campylobacter</i> spp.	no	-	-
<i>Chlamydophila psittaci</i>	1920	-	
Birds and poultry			Order no. 871 of 25/8 2011
<i>Listeria monocytogenes</i>	no	-	-
<i>Leptospira</i> spp. (only in production animals)	2003	-	Act no. 466 of 15/05/2014
<i>Mycobacterium bovis/tuberculosis</i>	1920 <sup>a</sup>		
Cattle	OTF in 1980 <sup>d</sup>	Decision 2003/467/EC	Order no. 1417 of 11/12 2007
<i>Coxiella burnetii</i>	2005	-	Act no. 466 of 15/05/2014
<i>Salmonella</i> spp.	1993 <sup>e</sup>	-	
Cattle			Order no.1192 of 20/10/2015
Swine			Order no. 1280 of 04/12/2014
Poultry			Order no. 1512 of 13/12/2013
VTEC	no	-	-
<i>Yersinia enterocolitica</i>	no	-	-
<b>Parasites</b>			
<i>Cryptosporidium</i> spp.	no	-	-
<i>Echinococcus multilocularis</i>	2004	Council Directive 64/433/EC	Act no. 466 of 15/05/2014
<i>Echinococcus granulosus</i>	1993	Council Directive 64/433/EC	Act no. 466 of 15/05/2014
<i>Trichinella</i> spp.	1920 <sup>a</sup>	Regulation 2075/2005/EC (as amended)	Order no. 544 of 28/05/2014
<b>Viruses</b>			
<i>Lyssavirus</i> (Rabies)	1920	-	Order no. 330 of 14/04/2011
<b>Prions</b>			
TSE			
Sheep and goats	yes	Regulation 999/2001/EC (as amended)	Order no. 1288 of 20/12/2011
BSE			
Cattle	yes <sup>f</sup>	Regulation 999/2001/EC (as amended)	Order no. 1326 of 26/11/2015

a) Clinical cases, observations during the meat inspection at the slaughterhouse, positive blood samples or finding of agents are notifiable.

b) Officially Brucellosis Free (Obf) according to Council Directive 64/432/EC as amended and Commission Decision 2003/467/EC. No cases in since 1962.

c) Officially *Brucella melitensis* Free (ObmF) according to Council Directive 91/68/EC and Commission Decision 2003/467/EC. the disease has never been detected in sheep or goat.

d) Officially Tuberculosis Free (OTF) according to Council Directive 64/432/EC as amended and Regulation (EC) No 1226/2002, and Commission Decision 2003/467/EC. No cases in since 1988 or in deer since 1994.

e) Only clinical cases notifiable.

f) Denmark was recognized as a country with negligible risk for BSE at World Organisation for Animal Health (OIE) general session in May 2011.

Source: Danish Veterinary and Food Administration.

Table A32. Salmonella surveillance programme for the rearing flocks and adult flocks of the grandparent and parent generation of the broiler and table egg production, 2015

Time	Samples taken	Material	Material
Rearing flocks		<i>Grandparent generation</i>	<i>Parent generation</i>
Day-old <sup>a,b,c</sup>	Per delivery	5 transport crates from one delivery: crate liners (>1 m <sup>2</sup> in total) or swab samples (>1 m <sup>2</sup> in total). Analysed as one pool	5 transport crates from one delivery: crate liners (>1 m <sup>2</sup> in total) or swab samples (>1m <sup>2</sup> in total). Analysed as one pool
1st & 2nd week <sup>b,c</sup>	Per unit	-	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g
4th week <sup>a,b,c</sup>	Per unit	5 pairs of boot swabs (analysed as two pooled samples), or 1 faeces sample consisting of 2x150 g	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g
8th week <sup>b,c</sup>	Per unit	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g
2 weeks prior to moving <sup>a,c,d</sup>	Per unit	5 pairs of boot swabs (analysed as two pooled samples), or 1 faeces sample consisting of 2x150 g	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g
Adult flocks		<i>Grandparent generation</i>	<i>Parent generation</i>
Every two weeks <sup>a,b,c,e</sup> (Every 16th week) <sup>d</sup>	Per flock	Hatcher basket liners from 5 baskets (>1 m <sup>2</sup> in total) or 10 g of broken eggshells from each of 25 hatcher baskets (reduced to 25 g sub-sample). Analysed as one pool	Hatcher basket liners from 5 baskets (>1 m <sup>2</sup> in total) or 10 g of broken eggshells from each of 25 hatcher baskets (reduced to 25 g sub-sample). Analysed as one pool
After each hatch <sup>b,c</sup>	Per hatch	Wet dust samples. Up to four hatchers of the same flock can be pooled	Wet dust samples. Up to four hatchers of the same flock can be pooled
Every week <sup>b,c</sup>	Per unit	-	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g
0-4 weeks after moving, 8-0 weeks before slaughter	Per unit	5 pairs of boot swabs (analysed as two pooled samples), or 1 faeces sample consisting of 2x150 g	5 pairs of boot swabs (analysed as two pooled samples), or 1 faeces sample consisting of 2x150 g
After positive findings <sup>c,d,f</sup>	Per unit	5 pairs of boot swabs (analysed as two pooled samples), 2 dust samples (250 ml) and 5 birds (analysed for antimicrobial substances)	5 pairs of boot swabs (analysed as two pooled samples), 2 dust samples (250 ml) and 5 birds (analysed for antimicrobial substances)

a) Sampling requirements set out by Regulation (EC) No 200/2010

b) Samples collected by the food business operator.

c) Sampling requirements set out by Order no 952 of 10/07/2013.

d) Samples collected by the Danish Veterinary and Food Administration.

e) When eggs from a flock exceed the capacity of one incubator, each incubator should be sampled as described.

f) If samples are negative, sampling is repeated 14 days later.

Source: Danish Veterinary and Food Administration.

Table A33. Salmonella and Campylobacter surveillance programme for the broiler flocks, 2015

Time	Samples taken	Material
<i>Salmonella</i>		
15 - 21 days before slaughter <sup>a,c,d</sup>	Per flock	5 pairs of boot swabs. Analysed individually
7 - 10 days before slaughter <sup>b,e</sup>	Per flock	5 pairs of boot swabs. Analysed individually
After slaughter <sup>b,c,f</sup>	Per batch	300x1 g neck skin, analysed in pools of max. 60 grams. Sampling size depends on whether the slaughterhouse slaughters only AM-negative flocks or AM-negative as well as AM-positive flocks
<i>Campylobacter</i> <sup>g</sup>		
After slaughter	Per flock	12 cloacal swabs from 24 animals, analysed in one pool <sup>h</sup>

a) Sampling requirements set out by Regulation (EC) 200/2012

b) Sampling requirements set out by Order no. 1512 of 13/12/2013 replacing 1105 of 18/09/2013 replacing 1462 of 16/12/2009.

c) Samples collected by the food business operator.

d) Once a year, one pair of socks is collected by the Danish Veterinary and Food Administration.

e) Samples are collected by a representative of the slaughterhouse, laboratorium or the Danish Veterinary and Food Administration.

f) sampling requirements set out by Regulation (EC) 2073/2005

g) For flocks to be slaughtered outside Denmark, 1 pair of boot swabs is collected by the owner 10 days before slaughter at the latest.

h) If the flock is slaughtered over several days, the last batch is sampled.

Source: Danish Veterinary and Food Administration.

Table A34. Salmonella surveillance programme for the pullet-rearing, table egg layer and barnyard/hobby flocks in the table egg production, 2015<sup>a</sup>

Time	Samples taken	Material
Pullet-rearing		
Day-old <sup>a,c</sup>	Per delivery	5 transport crates from one delivery: Crate liner (> 1 m <sup>2</sup> in total) or swab samples (> 1 m <sup>2</sup> in total) (Analysed as one pooled sample)
4 weeks old <sup>a,c</sup>	Per flock	5 pairs of boot swabs (analysed as two pooled samples) or 5 faeces samples of 60 gram
2 weeks before moving <sup>a,b</sup>	Per flock	5 pairs of boot swabs (analysed as two pooled samples) or 5 faeces samples of 60 gram. 60 blood samples (serology)
Table egg layers (Production for certified packing stations)		
24 weeks old <sup>a,b</sup>	Per flock	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample consisting of 2x150 g, 250 ml (100 g) dust or a dust sample by a cloth of min. 900 cm <sup>2</sup>
Every 2 weeks from age 20 weeks <sup>a,c,d</sup>	Per flock	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample consisting of 2x150 g.
After positive serological findings <sup>b</sup>	Per flock	5 pairs of boot swabs (analysed as two pooled samples) or 5 faecal samples consisting of 60 gram each
After positive findings of other serotypes than <i>S. Enteritidis</i> , <i>S. Hadar</i> , <i>S. Infantis</i> , <i>S. Virchow</i> or <i>S. Typhimurium</i> including the monophasic strains <i>S. 1,4,[5],12:i:-</i> <sup>b</sup>	Per flock	5 pairs of boot swabs (analysed as two pooled samples) or 5 faeces samples consisting of 60 gram each, 2 dust samples (250 ml) and 5 birds (analysed for antimicrobial substances)
Barnyard and hobby flocks <sup>e</sup>		
Every 18 weeks <sup>a,c,f</sup>	Per flock	Egg samples (serology)

a) Sampling requirements set out by Order no 517/2011, replaced by Order no. 227 of 02/03/2015

b) Samples collected by the Danish Veterinary and Food Administration.

c) Samples collected by the food business operator.

d) According to Regulation (EC) 2160/2003 sample collection must be carried out every 15 weeks as a minimum.

e) Voluntary for hobby flocks.

f) For flocks with 30 birds or less: No testing if only delivered to a well-known circle of users.

Source: Danish Veterinary and Food Administration.

Table A35. Salmonella surveillance programmes for turkey flocks, 2015

Time	Samples taken	Material
Turkey production		
Max. 21 days before slaughter <sup>a,b</sup>	Per flock	2 pairs of boot swabs. Analysed individually

a) Sampling requirements set out by Regulation (EC) 584/2008 and Order no. 1512 of 13/12/2013.

b) Samples collected by the food business operator or the Danish Veterinary and Food Administration

Source: Danish Veterinary and Food Administration.

Table A36. Salmonella surveillance programme<sup>a</sup> for the cattle production, 2015

No. of samples	Samples taken	Purpose/Comment
Milk producing herds		
4 samples distributed over 18 months	Bulk tank samples	Calculation of herd level <sup>b</sup>
Non-milk producing herds		
1 sample every 180 days at slaughter <sup>c</sup>	Blood samples	Calculation of herd level <sup>b</sup>
4-8 samples depending on herd size	Blood samples	Consecutive negative samples required for level 1 <sup>d</sup>
Beef carcasses at the slaughterhouse		
5 samples daily, pooled into one analysis	Swab samples from 4 designated areas after 12 hours chilling (4x100cm <sup>2</sup> )	Slaughterhouses slaughtering 7.500 or more cattle per year
Samples from 5 carcasses every second month	Swab samples from 4 designated areas after 12 hours chilling (4x100cm <sup>2</sup> )	Slaughterhouses slaughtering 2.500 or more and less than 7.500 cattle per year
Samples from 10 carcasses per year, 5 each 6 month	Swab samples from 4 designated areas after 12 hours chilling (4x100cm <sup>2</sup> )	Slaughterhouses slaughtering 250 or more and less than 2.500 cattle per year
No sampling		Slaughterhouses slaughtering less than 250 cattle per year

a) Order no. 886 of 02/07/2014 as amended. In 2013 and 2014, the programme for eradication of *Salmonella* Dublin from the Danish cattle production was intensified. This implies regionalisation of the country according to prevalence and compulsory eradication plans in Level 2 herds.

b) Herd levels based on serological testing (blood and milk):

Level 1: Herd assumed free of infection based on bulk milk samples (milk producing herd) or blood samples (non-milk producing herd),

Level 2: Herd not assumed free of infection,

Level 3: Herd infected based on culture and clinical signs or bacteriological findings in the intensified sampling.

c) No samples are taken, if the herd has been tested for *S. Dublin* within the last 180 days or 8 samples have been tested within the last 24 months.

d) Number of samples equals total number of animals in the herd minus 2 (max. 8 animals, min. 4 animals).

Source: Danish Agriculture and Food Council, and Danish Veterinary and Food Administration.

Table A37. *Salmonella* surveillance programme<sup>a</sup> for the pig production, 2015

Time	Samples taken	Purpose/Comment
<b>Breeding and multiplier herds</b>		
Every month	10 blood samples per epidemiological unit	Calculation of <i>Salmonella</i> -index based on the mean seroreaction from the last three months with more weight to the results from the more recent months (1:3:6) <sup>b</sup>
Max. twice per year	Herds with <i>Salmonella</i> -index 5 or above: Pen-faecal samples	Clarify distribution and type of infection in the herd <sup>c</sup>
<b>Sow herds</b>		
When purchaser of piglets is assigned to level 2 or 3, max. twice per year	Pen-faecal samples	Clarify distribution and type of infection in the herd, and possible transmission from sow herds to slaughter pig herds
Herds positive with <i>S. Typhimurium</i> , <i>S. Infantis</i> , <i>S. Derby</i> and <i>S. Choleraesuis</i> are considered positive for the following 5 years <sup>d</sup>	No samples are collected from the herd during the 5 year period when the herd is considered positive, unless the herd is proven negative	Reduce repeated sampling in positive herds infected with a persistent serotype
<b>Slaughter pigs, herds</b>		
At slaughter	Meat juice, 60-100 samples per herd per year. Herds in RBOV <sup>e</sup> : one meat juice sample per month	Calculation of slaughter pig index based on the mean proportion of positive samples from the last three months with most weight to the result from the most recent month (1:1:3) <sup>f</sup> . Assigning herds to level 1-3 and assigning herds to risk-based surveillance (RBOV) <sup>e, g</sup>
<b>Slaughter pigs, animals</b>		
At slaughter <sup>h</sup>	Coecum samples, avg. 57 samples per month, 9 months per year	Random collection of samples for monitoring of the distribution of serotypes and antimicrobial resistance.
<b>Pork carcasses at the slaughterhouse</b>		
5 samples daily, pooled into one analysis	Swab samples from 4 designated areas after 12 hours chilling (4x100cm <sup>2</sup> )	Slaughterhouses slaughtering more than 200 pigs per day
5 samples every second month	Swab samples from 4 designated areas after 12 hours chilling (4x100cm <sup>2</sup> )	Slaughterhouses slaughtering 10.000 or more pigs and less than 30.000 pigs per year
10 samples per year, 5 each 6 month	Swab samples from 4 designated areas after 12 hours chilling (4x100cm <sup>2</sup> )	Slaughterhouses slaughtering 1.000 or more pigs and less than 10.000 pigs per year
No sampling		Slaughterhouses slaughtering less than 50 pigs per month

a) Sampling requirements set out by Order no. 1280 of 4/12/2014.

b) Herds with index above 10 have to pay a penalty for each pig sold.

c) The herd owner must inform buyers of breeding animals about the infection level and type of *Salmonella*.

d) These serotypes are primarily spread by live trade, and are known to persist in herds. *S. Typhimurium* includes the monophasic *S. 1,4,[5],12:i:-*.

e) RBOV: risk-based surveillance in herds with a slaughter pig index of zero (no positive samples in the previous three months) the sample size is reduced to one sample per month. Increasing seroprevalence from level 1 to level 3.

f) Since November 2014: based on the proportion of seropositive samples from the last three months. Both the number of seropositive and total number of samples are weighted with most weight to samples from the most recent month (1:1:5).

g) Pigs from herds with highest level of infection (Level 3) must be slaughtered under special hygienic precautions.

h) Centrally coordinated study (Table A28)

Source: Danish Veterinary and Food Administration.

Table A38. Typing methods used in the surveillance of foodborne pathogens in Denmark, 2015

Methods	Human	Food	Animal
<i>Salmonella enterica</i>			
Serotype	All	All	All
Phage type	None	Few <i>S. Typhimurium</i> and <i>S. Enteritidis</i>	Few <i>S. Typhimurium</i> and <i>S. Enteritidis</i> , all isolates danish from poultry
Antimicrobial resistance	All <i>Salmonella</i> except <i>S. Enteritidis</i>	Almost all isolates	Almost all isolates
MLVA	<i>S. Typhimurium</i> <sup>a</sup> and <i>S. Enteritidis</i>	<i>S. Typhimurium</i> <sup>a</sup> and <i>S. Enteritidis</i> for the <i>Salmonella</i> source account, outbreak investigations and research	<i>S. Typhimurium</i> <sup>a</sup> and <i>S. Enteritidis</i> for the <i>Salmonella</i> source account, outbreak investigations and research
PFGE	Outbreak investigations	Outbreak investigations	Outbreak investigations
WGS	Outbreak investigations	Some for outbreak investigation and research	Some for outbreak investigation and research
<i>Campylobacter coli/jejuni</i>			
Antimicrobial resistance	Isolates from 3 districts for DANMAP surveillance	For DANMAP surveillance purposes and the case-by-case program	Only for DANMAP surveillance purposes
FlaA-SVR	None	Outbreak investigations	None
MLST, WGS	Outbreaks investigations, research	None	None
VTEC			
Serotype	Based on WGS	None	All (O157)
Virulence profile	Based on WGS	None	All (O157)
PFGE	Few	None	Outbreak investigations
WGS	All	None	None
<i>Listeria</i>			
Serogroup	All	None	None
PFGE	All	All	All
WGS	All	All	All
<i>Yersinia enterocolitica</i>			
O-group	All isolates send to SSI	None	None

a) Including the monophasic strains *S. 1,4,[5],12:i:-*.

Source: Statens Serum Institut, Danish Veterinary and Food Administration and Danish Zoonosis Laboratory, National Food Institute.

## Population and slaughter data

Table A39. Human population, 2015

Age groups (years)	Males	Females	Total
0-4	151,130	143,618	294,748
5-14	341,219	324,307	665,526
15-24	377,566	360,147	737,713
25-44	722,402	706,694	1,429,096
45-64	754,824	750,922	1,505,746
65+	490,746	583,676	1,074,422
<b>Total</b>	<b>2,837,887</b>	<b>2,869,364</b>	<b>5,707,251</b>

Source: Statistics Denmark, 1 January 2016.

Table A40. Number of herds/flocks, livestock and animals slaughtered, 2015

	Herds/flocks (capacity)	Livestock (capacity)	Number slaughtered
Slaughter pigs (>30 kg)	6,701	5,979,922	18,293,442
Cattle	18,435	1,559,377	512,600
Broilers	243	n/a	95,681,400
Layers (excl. barnyard)	225	3,250,000	-
Turkeys	35	351,31	6,700
Sheep & lambs	6,671	145,209	81,585
Goats	2,998	20,036	1,556
Horses	-	-	1,328

Source: The Central Husbandry Register and Danish Veterinary and Food Administration.

Table A41. Number of farms in the broiler production, 2015

	No. of holdings	No. of houses/flocks	Livestock (capacity)
Rearing period (grandparent)	3	13	50,000
Adult period (grandparent)	4	7	90,000
Rearing period (parent)	20	100	350,000
Adult period (parent)	40	144	720,000
Hatcheries	4	-	-
Broilers	241	3,631	n.a.

Source: Danish Veterinary and Food Administration, and Danish Agriculture and Food Council.

Table A42. Number of farms in the table egg production, 2015

	No. of holdings	No. of houses/flocks	Livestock (capacity)
Rearing period (grandparent)	2	2	50,000
Adult period (grandparent)	2	7	80,000
Rearing period (parent)	8	12	20,000
Adult period (parent)	8	9	50,000
Hatcheries	4	-	-
Pullet-rearing	44	80	720,000
Layers (excl. barnyard)	158	225	3,250,000

Source: Danish Veterinary and Food Administration, and Danish Agriculture and Food Council.

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