

Annual Report on Zoonoses in Denmark 2021





Annual Report on Zoonoses in Denmark 2021

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Introduction

Campylobacter was the most common bacterial foodborne illness, with 3,740 confirmed human cases in 2021. Three *Campylobacter* outbreaks were investigated and they were all related to consumption of chicken meat. *Salmonella* resulted in 692 laboratory-confirmed human infections, the numbers being slightly higher compared to 2020 (n=614).

Foodborne outbreaks

In total, 63 foodborne outbreaks with 1,257 patients were reported in 2021. This is an increase compared to 2020, where 35 outbreaks were reported. The number of foodborne outbreaks registered in 2021 has increased again after an exceptional COVID-19 pandemic year of 2020.

Norovirus was the most common cause of foodborne outbreaks, mainly resulting from contamination from symptomatic or healthy carriers among kitchen staff. The number of norovirus outbreaks increased to 14 in 2021 from six registered outbreaks in 2020.

The number of *Salmonella* outbreaks in 2021 were at the same level as 2020. A large national outbreak of *Salmonella* Typhimurium with 54 cases was registered. During the outbreak, 59% of the cases were hospitalized, and three cases died within 30 days after testing positive. Through a case-control investigation and exchange of information between Staten Serum institute, the Veterinary and Food Administration and the Danish Medicines Agency, psyllium seed husks consumed as herbal medicine were identified as the source of infection. This investigation led to a product recall.

Influenza A in birds and pigs in Denmark

In 2021, passive surveillance in Danish swine herds found at least one positive sample for influenza A in 377 different herds. Virus with an HA gene, a major surface glycoprotein, of pandemic H1N1pdm09 origin was detected in 164 of these herds and accounted for 42% of all influenza A virus positive submissions.

Passive surveillance of highly pathogenic avian influ-

enza virus during the 2020/2021 season, detected 337 positive wild birds. Additionally, in the 2020/21 season, 16 outbreaks of highly pathogenic avian influenza H5 were detected in Danish poultry herds. In addition, outbreaks have been confirmed in 11 poultry herds in the current season. These outbreaks were detected in both closed herds, freerange and hobby flocks.

In 2021, highly pathogenic avian influenza was detected in a dead Danish harbour seal. This was the first detection of highly pathogenic avian influenza virus in mammals in Denmark. Detection of avian influenza viruses in non-human mammals indicate that potential further adaptation to mammals, including humans, can occur. In 2021 also the first case of human infection with influenza A (H1N1) virus containing a non-structural gene highly similar to Eurasian avian-like swine influenza virus was detected in a patient living near a pig farm.

Burden of disease of COVID-19 in Denmark

COVID-19 resulted in public health crisis and public health burden worldwide.

During the period the 26th of February 2020 to the 25th of February 2021, 211,823 individuals tested positive for SARS-CoV-2 by RT-PCR in Denmark, and 59% of the test positive had at least one disease symptom. Around 7% of symptomatic cases exhibited severe symptoms, 1% critical symptoms, and 2% died within 30 days of testing positive.

The overall burden of COVID-19 can be assessed using Disability-adjusted life years (DALYs). These can be calculated by adding the number of years of life lost due to premature mortality and the number of years lived with disability adjusted for severity. Calculating the DALYs for the COVID-19 gives a more comprehensive picture of the public health impact and allows for comparison with other diseases. The total estimated disease burden of COVID-19 was 30,181 DALYs equivalent to 520 DALYs/100,000. The DALYs were higher in the age groups above 70 years of age, particularly in men. To capture the full impact of

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 2021. 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.

the pandemic, these estimates need to be complemented with indirect impact measurements. These could be mental health issues due to national lockdowns or delay in medical treatment (including surgery), follow-up and delay in diagnoses through restrictions of vital healthcare services as well as post-acute consequences of COVID-19 ("long COVID").

Vectorborne zoonoses

Vectorborne infections of both veterinary and zoonotic importance are continuously introduced to Europe and endemic vectors and vector borne diseases expand their geographical range. In an attempt to identify future sources of large zoonotic epidemics, nine known pathogens were identified in 2021 and classified as pathogens with high epidemic potential. Five of these nine pathogens are vectorborne. (1) Tularemia in Sweden has recently changed in epidemiology and is now mainly a zoonotic mosquito-borne infection. (2) West Nile virus was recently established in northern Germany. This virus is transmitted between wild birds and from birds to humans by Culex mosquitoes. The vectors are able to spread the virus between birds and are abundant all over Denmark. (3) Equine encephalitis is caused by a group of zoonotic viruses in the Americas, some of which have a large epidemic potential. Just as West Nile virus was introduced from Africa or from Europe to North America in 1999, there is a risk of introduction of one of the epidemic Equine encephalitis viruses. (4) Rift Valley fever is a viral disease in African ruminants from south of Sahara. The infection is predicted to be able to cause high mortality in European cattle breeds and some virus strains may cause relatively high mortality rates in humans mostly due to kidney and liver failure. (5) Japanese encephalitis virus is endemic in some temperate areas in Asia and is now expanding geographically. Although the virus has a reservoir in wild water birds, pigs are very efficient amplifying hosts for the virus.

Toxoplasma gondii - an important food-borne parasite, also in Denmark

In Europe, *Toxoplasma gondii* is ranked as the second most important foodborne parasite. The parasite poses a risk to public health, as toxoplasmosis in humans can cause substantial disease burden.

European Food Safety Authority (EFSA) recommends mitigation of risk of toxoplasmosis in humans from meat consumption. And since undercooked pork is considered a potential source, EFSA recommends surveillance of pigs with outdoor access and those from farms that do not meet the controlled housing conditions. Between 2017-2018, serological screening of commercial finishers and sows, originating from indoor and outdoor production systems was carried out in Denmark. In total 447 plasma samples were analysed for antibodies against *T. gondii* parasite. Investigation revealed a lower apparent prevalence (2%) in indoor-raised finishers, but a moderate to a high apparent seroprevalence in outdoor-raised finishers (11%) and sows (up to 60% in outdoor-raised), respectively. As there is a strong correlation between seropositivity and presence of infectious tissue cysts in pork, the risk of becoming infected from consuming pork in Denmark is not a negligible one.

Toxoplasma gondii infection in humans can result in ocular disease also referred to as ocular toxoplasmosis. Recently, it was concluded that ocular toxoplasmosis contributes to the disease burden caused by *T. gondii* in Denmark, but uncertainty about the incidence and severity precluded estimation of its importance.

1. 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). Appendix Table A3 lists the outbreaks that occurred in 2021. Household outbreaks and clusters not verified as common source foodborne outbreaks are excluded. Outbreak investigation procedures in Denmark are described in Chapter 6.

In 2021, 63 foodborne outbreaks were reported in FUD and the total number of persons affected by foodborne outbreaks was 1,257 with an average of 20 persons per outbreak (range 2-85). Of the 63 outbreaks, 34 were local/ regional and 29 were national outbreaks, of which 6 were part of international outbreaks. The number of foodborne outbreaks in 2021 increased from 2020, where 35 outbreaks were registered. The number of foodborne outbreaks registered in 2021 has increased again after an exceptional COVID-19 pandemic year of 2020. The pandemic in 2020 led to general restrictions on gatherings, closed restaurants, and increased hygiene focus, which are considered to have influenced the number of local point-source outbreaks, whereas it does not seem to have affected the number of national outbreaks to the same degree. The number of norovirus outbreaks increased to 14 in 2021 from six registered outbreaks in 2020. In comparison, the number of *Salmonella* outbreaks were quite stable with 12 *Salmonella* outbreaks in 2021 and ten *Salmonella* outbreaks in 2020.

1.1 Norovirus outbreaks

Norovirus (NoV) was the most frequent cause of foodborne outbreaks in 2021 (14 outbreaks), and in total 493 persons were affected. The transmission routes for NoV causing foodborne outbreaks were multiple. The most common way of infection with NoV in 2021 was contamination from symptomatic or healthy carriers among kitchen staff. Four NoV outbreaks (207 persons affected) was related to canteen or workplace catering with a majority of outbreaks (10 outbreaks and 286 persons affected) related to restaurants, cafe or catering services.

1.2 Salmonella outbreaks

In 2021, 12 Salmonella outbreaks were identified as genetically closely related by whole genome sequencing

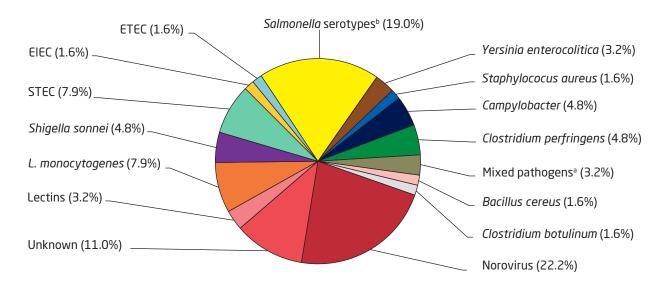


Figure 1.1. Aetiology of the 63 foodborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD), 2021. Percentage of total outbreaks indicated in brackets

a) One outbreak with *Cryptosporidium* and STEC. One outbreak with EIEC and *Shigella*. b) One outbreak with multiple serotypes

Source: Food- and waterborne Outbreak Database (FUD)

(WGS). Half of the *Salmonella* outbreaks registered in 2021 were part of international outbreaks. One international outbreak was caused by *Salmonella* Braenderup (*S.* Braenderup) and the cases were registered in 13 EU/ EEA countries and United Kingdom. In Denmark, 41 cases related to the outbreak were registered from March to July (FUD1954). A cross-border investigation was initiated, and case-control studies were conducted in Denmark and United Kingdom. The international investigation suggested small sugar melons (in particular Galia melons) from Honduras as the possible vehicle of infection (1).

A long-lasting international outbreak of multiple Salmonella enterica serotypes with cases registered from January 2019 and onwards were in 2021 linked to sesame-based products such as tahini from Syria (2). The serotypes were S. Amsterdam, S. Havana, S. Kintambo, S. Mbandaka, S. Orion, and S. Senftenberg. In Denmark, twelve cases were registered (FUD1988).

Another multi-country outbreak of *S*. Enteritidis infections was in 2021 linked to foreign eggs and egg products (3). In Denmark, seven cases were linked to this outbreak (FUD2019). Interviewed cases had been travelling to Spain and France.

In 2021, an outbreak due to Danish eggs was registered (FUD2009). From September 15 to December 2021, a total of 26 cases were registered. Interviews pointed out Danish eggs as the possible source and this was confirmed by the finding of the same strain of *Salmonella* in eggs and patients. The eggs were recalled from the market on October 30, 2021.

The largest national outbreak of 54 *Salmonella* cases in 2020-2021 was due to *S.* Typhimurium (FUD1917). Further description of this outbreak can be found in the text box.

1.3 Campylobacter outbreaks

Three outbreaks of *Campylobacter jejuni* were registered in Denmark in 2021. A long-lasting outbreak with 19 *Campylobacter jejuni* ST21#7 took place from March to October, and with historic human cases dating back to 2020 and 2019 (FUD1971). The second outbreak was caused by two different sequence types of *Campylobacter jejuni*, ST52#4 and ST52#5 (1974). The outbreak comprised 28 cases registered from April 1, 2021 to January 18, 2022. The last outbreak was from August to November with 16 cases of *Campylobacter jejuni* ST50#18 (FUD1999). The source for all three outbreaks were revealed by comparison of recent findings in the *Campylobacter* control programme (see chapter 6), where the same outbreak strain of *Campylobacter* was detected in Danish broiler meat.

1.4 Other outbreaks of interest

In November 2021, the first national outbreak of Enteroinvasive *Escherichia coli* (EIEC) was detected in Denmark (FUD2030). A total of 88 cases were registered from November 2021 to February 2022. The cases were 58 (66%) females and 30 (34%) males, aged 0-91 years old, with a median age of 52 years. Symptoms were reported by 41 cases, of whom 40 suffered from diarrhoea, and 10 also had bloody diarrhoea. Twenty-six cases were hospitalised, and three cases died within 30 days after the positive test

	2021		2020		2019	
Transmission route/source	No. of outbreaks	No. of persons ill	No. of outbreaks	No. of persons ill	No. of outbreaks	No. of persons ill
III kitchen staff or healthy carrier of virus among kitchen staff	9	307	2	109	12	691
Kitchen staff tending to ill persons at home before entering the kitchen	3	116	2	158	2	80
III persons/guests attending a buffet	0	0	0	0	2	89
Seafood (oysters)	0	0	2	122ª	З	72
Unknown route of transmission	2	70	0	0	0	0
Total	14	493	6	267	19	932

Table 1.1. Norovirus outbreaks per route of transmission based on number of cases or number of outbreaks, 2019-2021

a) One of the two outbreaks in 2020 (FUD1838) consisted of 286 cases of which 271 cases were additionally registered in 2019.

Source: Food- and waterborne Outbreak Database (FUD)

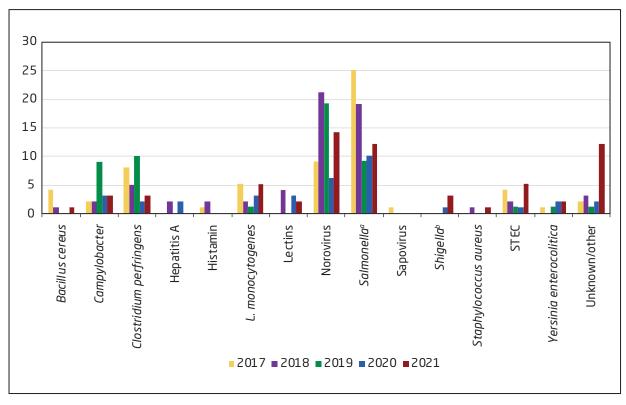


Figure 1.2. Number of foodborne outbreaks reported in Denmark by pathogen, 2017-2021

a) Note for *Salmonella* that travel-related outbreaks were not included in 2019 and 2020. b) One was found together with Enteroinvasive *Escherichia coli* (EIEC)

Source: Food- and waterborne Outbreak Database (FUD)

for EIEC. The investigation showed that cases had bought different ready-to-eat fresh cabbage salads from Danish supermarkets. Spring onions were the only common ingredient in the concerned salads and trace-back investigation showed that the spring onions originated from Egypt. The outbreak investigation highlights the importance of early communication of signals, rapid access to data and confirmation of cases by fast typing.

Three *Listeria* outbreaks of unknown source accumulated five or more new cases during 2021 and reached a total of 10-14 cases: One *Listeria* outbreak had started in October 2020 (FUD1939) and two had been ongoing since 2014 (FUD1525) and 2018 (FUD1941) respectively.

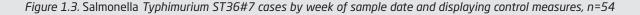
1.5 References

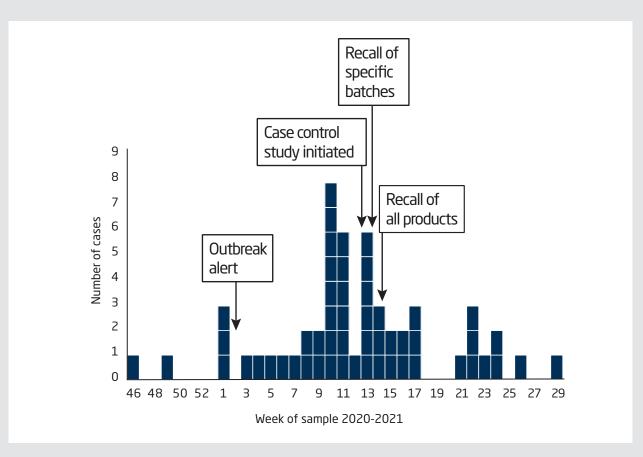
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- European Centre for Disease Prevention and Control, European Food Safety Authority, 2021. Multi-country outbreak of multiple Salmonella enterica serotypes linked to imported sesame-based products - 14 October 2021.
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By the Central Outbreak Management Group

In January 2021, a national outbreak of *Salmonella* Typhimurium defined by whole genome sequencing was identified through the surveillance system (FUD1917) (Figure 1.3). Epidemiological, microbiological and food investigations were initiated to confirm the outbreak, identify the vehicle of transmission and propose appropriate control measures. In total, 54 cases were identified, aged 2-92 years old, in the period from November 2020 to July 2021. Thirty-two cases (59%) were hospitalized and three cases died within 30 days after testing positive for *Salmonella*. Results from initial interviews indicated a vulnerable patient group with underlying illness and physical handicaps leading to the suspicion of food supplements. The case-control study showed that cases were more likely to consume herbal medicine psyllium seed husks than controls (matched OR=26, 95%CI [3.8-175]). Cases reported to have consumed a single brand of herbal medicine in capsules on a daily basis. The raw psyllium seeds were imported from India and used in food supplements. The herbal medicine and food supplements were recalled from the Danish market on April 9, 2021. The outbreak strain of *Salmonella* was identified in an open package from a patient's home and in a reference sample from the producer.

In conclusion, psyllium seed husks were identified as a new vehicle of *Salmonella* infection and this investigation illustrates the severity and risks when *Salmonella* contaminate herbal medicine, with an intended use for vulnerable patients suffering from for example gastrointestinal diseases, high blood cholesterol and diabetes. Interdisciplinary collaboration and exchange of information between Statens Serum institut, the Veterinary and Food Administration and the Danish Medicines Agency was crucial for the investigation of the outbreak and recall of the products. The identification of the cause of the outbreak following intervention and recall of the products are considered to have had a direct impact on mitigating the outbreak. The producer of the herbal medicine and food supplements implemented heat treatment of the raw psyllium seeds to prevent outbreaks from occurring in the future.





2. Influenza A virus in pigs and birds in Denmark

By Lars Erik Larsen (lael@sund.ku.dk), Charlotte Hjulsager (SSI), Pia Ryt-Hansen (KU), Klara Andersen (SSI) and Ramona Trebbien (SSI)

Influenza A virus (IAV) is an important pathogen of wild and domesticated birds as well as a range of mammalian species including pigs and humans. Generally, the virus strains circulating in the different species are host specific, but occasionally, the virus may jump from one species to another, including zoonotic events where a human is infected from an animal source.

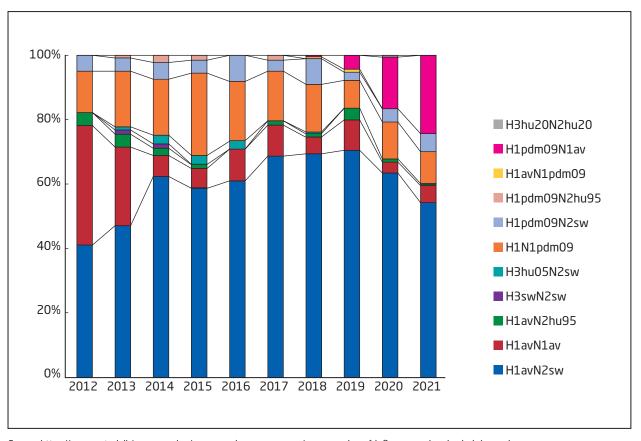
IAVs are named according to their possession of HA and NA glycoprotein subtypes. There are 16 different HA and 9 different NA subtypes known in birds – a subtype is defined as the combination of these genes e.g., H1N1, H5N2 etc. Avian influenza virus (AIV) of the H5 and H7 subtypes can evolve into highly pathogenic avian influenza (HPAI) viruses in poultry. HPAI virus detections are notifiable in Denmark and in most other countries. The Danish Veterinary Consortium are performing surveillance of IAV in wild birds, domesticated birds and pigs in Denmark on behalf of the Danish Veterinary and Food Administration. A summary of the findings in 2021 is described below, with focus on the zoonotic aspects.

2.1 Influenza A virus in pigs

A systematic, prospective, passive monitoring of circulating influenza virus subtypes in Danish pigs was carried out in 2021. The overall purpose of the monitoring was to identify which influenza virus subtypes and genotypes circulated among Danish pigs.

In 2021, a total of 2,895 influenza A virus tests were performed on 857 submissions to Danish veterinary laboratories from 647 herds registered with different CHR no. In total, 453 (53%) of the submissions from 377 different herds had at least one positive sample. Submissions were distributed across the country. There were a higher number of submissions during the winter. The proportion of positive

Figure 2.1. Distribution of the Influenza A virus (IAV) subtypes found in pigs from 2012-2021.



Source: https://www.vetssi.dk/overvaagning/overvaagningsprogrammer/overvaagning-af-influenza-a-virus-i-svin-i-danmark

samples ranged from 44-62%, with the highest proportion of positive submissions in September-December.

Virus with an HA gene of pandemic H1N1pdm09 origin (H1pdm09) was detected in 189 submissions from 164 herds registered with different CHR no. and thereby accounted for 42% of the influenza A virus positive submissions. The proportion of H1pdm09 is significantly higher than the 29% observed in 2020. In total, 312 IAV positive submissions were subtyped for both HA and NA. Together these analyses showed that the most common subtypes in Danish pigs in 2021 were H1avN2sw, H1pdm09N1av and H1N1pdm09. The prevalence of the H1pdm09N1av subtype increased further in 2021 and represented 24 % of all subtyped submissions. In the same period, the H1avN2sw subtype has decreased in prevalence, and is now constituting 54% of all subtyped submissions. The H1N1pmd09 and the Hpdm09N1av swine viruses share a HA protein similar to that of human seasonal influenza. However, phylogenetic analysis has revealed that genetically distinct swine-specific clusters of H1pdm have been generated over time in the Danish swine population (Figure 2.1) [3]. Updated figures on IAV detections in pigs are published online^a.

2.2 Influenza A virus in wild and domestic birds

In 2021, there has been an extensive number of detections of highly pathogenic avian influenza virus (HPAI) in Europe and Denmark was also heavily affected. Virtually all European countries have reported findings of HPAI in both wild birds and domestic poultry. Detections accumulated in the beginning and the end of 2021, with only few detections over the summer. Detections started in the autumn 2020, and have continued into 2022, and HPAI outbreaks are now assigned to seasons with starting and ending in October. In the 2020/2021 season, HPAI H5N8 virus was the subtype most frequently found, but additional HPAI H5Nx subtypes were also found. In the 2021/2022 season, detections have been mainly of the HPAI H5N1 subtype. In both seasons, the HPAI viruses contained H5 belonging to clade 2.3.4.4b, which is a classification of HPAI H5 viruses based on their genetic similarity of the HA gene segment.

In the 2021/2022 season, there have been significantly more registered HPAI outbreaks in poultry in France, Italy, Hungary, and Poland than in the other EU countries, some of which are suspected to be caused by transmission of virus between farms. Most findings of HPAI virus in wild birds have been in Germany, the Netherlands, Denmark, and Belgium. In the 2020/2021 season, HPAI viruses were detected in 337 wild birds found dead across Denmark. This corresponds to 40% of the dead wild birds that were tested throughout that season.

The first findings of an HPAI virus in Denmark in the

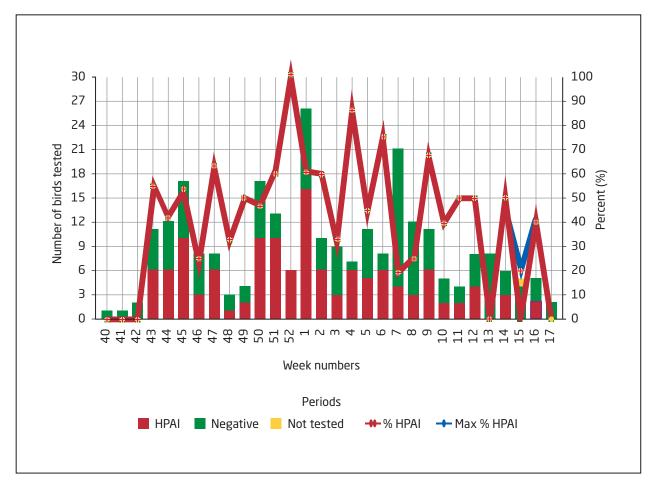
2021/2022 HPAI season, was in samples from apparently healthy wild birds collected at the end of October 2021 in the Danish part of the Wadden Sea area. Detection of HPAI in healthy wild birds have been rare, but the Danish detections are in line with contemporary detections in other European countries. From October 2021 through April 2022, HPAI H5 virus was detected in 120 wild birds found dead in nature (46% of the tested birds) across the country (Figure 2.2). The vast majority of the detected viruses were of the HPAI H5N1 subtype.

In the 2020/2021 season, there were 16 outbreaks in Danish poultry herds with HPAI H5 virus. In the current season, outbreaks of HPAI virus have been confirmed in 11 poultry herds. For both seasons, outbreaks were both in closed herds, free-range and hobby flocks. The herds were primarily located on Zealand and around Smålandsfarvandet, but there were also outbreaks in Central Jutland and on Bornholm. In the 2020/2021 season, the first outbreak was in a chicken flock near Randers on 16. November 2020 and was the first outbreak of HPAI in a commercial farm ever in Denmark. The season ended with an outbreak in a commercial chicken flock in Southern Jutland, that was confirmed on 5. July 2021. In the 2021/2022 season, the first poultry outbreak was confirmed on 1. November 2021 in a commercial turkey flock near Slagelse. The most recent outbreak was confirmed on 29. March 2022 in a hobby flock of chickens on Langeland. The Danish poultry outbreaks in both seasons were detected in the periods with the highest rate of detection of HPAI positive wild birds in Denmark. The viruses detected in poultry were genetically very closely related to viruses detected contemporary in wild birds, which underline the exchange of viruses between wild and domestic birds.

2.3 Avian influenza in mammals

During the recent European HPAI seasons with HPAI H5 clade 2.3.4.4b viruses in birds, viruses have also been detected sporadically in mammals, mainly red foxes, habour -and grey seals in European countries [1]. In Denmark, HPAI H5N8 clade 2.3.4.4b virus was detected in a harbor seal found dead in September 2021 at a beach of southwestern Funen. Genetic analyses showed that the virus was closely related to the HPAI H5N8 viruses detected in wild birds and poultry in the 2020/2021 season. This was the first detection of HPAI virus in mammals in Denmark. Detection of avian influenza viruses in non-human mammals is of great zoonotic concern because this indicate that potential further adaptation to mammals, including humans, can occur.

Human infection with clade H5N6 clade 2.3.4.4b viruses has been detected in a few cases in China, some of which had a fatal outcome. The HA gene of these viruses is related to the European H5 clade 2.3.4.4b viruses, while Figure 2.2. Detections of highly pathogenic avian influenza (HPAI) virus in wild birds found dead in Denmark in the season 2021/2022 (week 40, 2021 - week 17, 2022). There are still unfinished analyses of one bird found dead in week 15. The red line shows the proportion of HPAI positive, while the pink line shows the proportion of HPAI positive if birds still in test are HPAI positive.



Source: www.ai.fvst.dk

other parts of the genome is more distantly related to that of the European viruses. Human cases of HPAI have never been detected in Denmark.

2.4 Human infections with IAV from animal sources in Denmark

Until 2021, human infection with swine influenza A virus had not previously been detected in Denmark, but sporadic cases have been reported from other countries. In January 2021, the first case of human infection with influenza A (H1N1) pdm09 virus containing a non-structural gene highly similar to Eurasian avian-like H1Nx swine influenza virus was detected in Denmark [2]. The case was an elderly patient with underlying diseases, who was admitted to hospital with influenza like illness. The patient resided in the countryside, <2 km from a medium-sized farm with finisher pigs. There were only 46 confirmed seasonal influenza cases in Denmark during the 2020-2021 season, and transmission

of the variant virus was considered negligible. The Danish Patient Authority did not identify any person-to-person swine influenza transmission.

In November 2021, a second case of human infection with IAV of swine origin was identified in Denmark, less than one year after the very first case. The virus (H1pdm-09N1av) detected in this case was clearly different from the virus detected in the first case and showed a high level of identity with viruses detected in Danish swine. The patient had exposure to Danish swine related to work in a pig slaughterhouse. The patient was hospitalized for a short period with acute severe disease. The patient was previously healthy with no underlying disease. As in the previous case no other cases of influenza was detected in connection to the patient.

The detection of the first two cases in Denmark of swine influenza in humans, emphasizes the obvious zoonotic potential of some swine influenza viruses and highlight that more attention should be given to routine surveillance and control of swine influenza viruses.

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3. Burden of COVID-19 in the first full year of the pandemic in Denmark

By Sara M. Pires (smpi@food.dtu.dk) and Steen Ethelberg (SSI)

The COVID-19 pandemic has had an enormous public health impact. In Denmark, the first case of SARS-CoV-2 infection was diagnosed on 26 Febuary and during the following year, Denmark registered over 200,000 cases and 2,600 deaths, and implemented a range of public health measures to limit spread of infections. Statens Serum Institut (SSI) is responsible for surveillance of COVID-19 in humans, including case counts, admissions and deaths. In addition, national surveys of prevalence of antibodies to SARS-CoV-2 were carried out [1][2]. These metrics have been useful to monitor the evolution of the epidemic over time, the effects of measures to reduce transmission of infection, and guide options for introducing or lifting restrictions at different stages.

For assessing the health significance and severity of a disease on the society, tools that account for the overall health impact are needed. Burden of disease studies are useful to compare the public health impact of a disease across population groups, across diseases in a country, or of the same disease across countries.

3.1 The Disability Adjusted Life Year (DALY)

Incidence, prevalence and cause-specific mortality are all metrics commonly used to inform on the impact of diseases or the effect of interventions on public health. However, they are insufficient to provide a comprehensive picture of the public health impact of different diseases, and to allow for a comparison across diseases, because they do not integrate occurrence and severity of these diseases. Summary measures of population health, such as disabilityadjusted life years (DALYs), offer a more detailed estimation of the direct impact of the disease in a given population, and can provide future opportunities to assess the indirect impact of the pandemic as a result of preventive measures such as national lockdowns, or of disruption of vital health care services. The DALY is a health gap metric, measuring the healthy life-years lost due to diseases or risk factors [2]. DALYs are calculated by adding the number of years of life lost due to premature mortality (YLL) and the number of years lived with disability (YLD), adjusted for severity.

3.2 DALYs associated with COVID-19 in Denmark

We quantified the direct burden of COVID-19 in the first 12 months of the epidemic in Denmark. We obtained

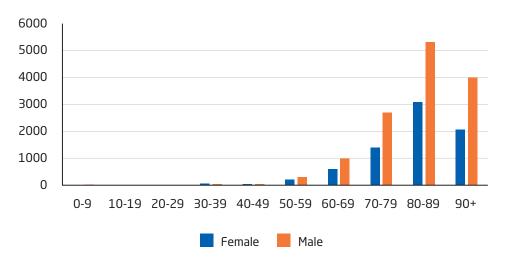
information on all individuals that tested positive for SARS-CoV-2 with RT-PCR in the period between the 26th of February, 2020 to the 25th of February, 2021 from The Danish Microbiological Database (MiBa), which contains all microbiological test results from the national TestCenter Denmark and all clinical microbiological departments in Denmark [3, 4]. Data on dates of admission and discharge from hospitals for stays longer than 12 hours, including intensive care units (ICU), were obtained by linkage to the National Patient Registry [5]. We defined an admission as 'COVID-19-related' if the patient had confirmed SARS-CoV-2 and the first positive test was performed in the time window from 14 days prior to admission date and until the date of discharge. We defined intensive care treatment as 'COVID-19-related' if the intensive care was provided during a COVID-19-related admission. Information about vital status within 60 days was obtained from the Danish Civil Registration System and The National Cause of Death Register [6]. We defined death as 'COVID-19-related' if it occurred within 30 days from the first positive SARS-CoV-2 test.

The severity of symptoms in COVID-19 patients varied from mild to critical, and not all individuals that tested positive to the virus had symptoms. To estimate the number of symptomatic cases among all registered PCR-positive individuals, we obtained estimates of the proportion of symptomatic SARS-CoV-2 infections from the Danish National Seroprevalence Survey of SARS-CoV-2 infection (DSS) [1]. We defined cases that had been hospitalized as "severe", and cases that had been in ICU as "critical".

We applied the consensus disease model defined by the European Burden of Disease Network [7] To calculate DALYs, we assumed that mild to moderate symptoms lasted 10 days, and that severe and critical health states had the duration of the individuals' stay at those units at the hospital. The disability weights that defined severities were extracted from the Global Burden of Disease study [8]

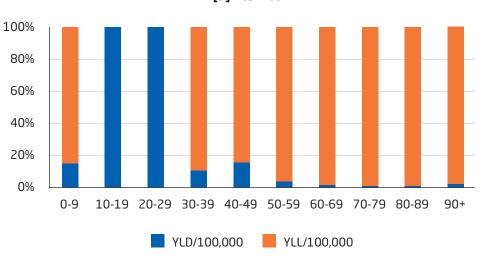
3.3 Results

We estimated that of the 211,823 individuals who tested positive to SARS-CoV-2 by RT-PCR in the oneyear period, 124,163 (59%; 95% uncertainty interval (UI) 112,782-133,857), corresponding to 59% (95% UI 53 – 63%), had at least one disease symptom. Around 7% of Figure 3.1. Disability adjusted life years (DALYs) associated with COVID-19 in Denmark in the first year of the pandemic, by age group and sex (per 100,000 individuals).



[A] DALY/100,000

Figure 3.1. Relative contribution of years of life lost to disability (YLD) and years of life lost due to premature mortality (YLL) for total DALYs associated with COVID-19 in Denmark, by age group.



[B] YLD/YLL

symptomatic cases exhibited severe symptoms, 1% critical symptoms, and 2% had died within 30 days.

The total estimated disease burden was 30,181 DALYs due to COVID-19 (95% UI 30,126; 30,242), or 520 DALYs/100,000. The DALY was higher in the age groups above 70 years of age, particularly in men (Figure 3.1.A & B). A total of 232 years of life were lost due to disability (YLD) in the one-year period, overall equal to around 1% of total DALY. Mild cases contributed overall with 35% of YLD, severe with 5%, and critical cases with 60%. The 2,383 deaths registered in the one-year period resulted in the loss of 29,689 years of life lost due to premature mortality (YLL). The total YLL was larger in males than in females, and larger in the age group 70-79 years old. Except in females aged 0-29 and males aged 10-19, YLL contributed with more than 99% of total DALY.

3.4 Impact

COVID-19 has had an unquestionable impact on societies globally. In Denmark, we estimated that 30,181 life years were lost in the first full year of the epidemic. Over 99% of DALYs were associated with the premature death of nearly 2,400 individuals. On average, fatal cases lost 13 years due to premature death. To capture the full impact of the pandemic, these estimates will need to be complemented with indirect impact measurements, from for example increases in mental health issues due to national lockdowns or delay in medical treatment (including surgery), follow-up and delay in diagnoses through restrictions of vital healthcare services. This indirect impact is expected to be large and to expand beyond the termination of the epidemic. Furthermore, several patients report post-acute consequences of COVID-19 ("long COVID"), which is still to be measured [9-11]. Such data, along with data distinguishing between all-cause and COVID-19 specific hospitalisation and death may be included in future analyses.

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4. Vectorborne zoonoses

By René Bødker (rebo@sund.ku.dk), Masja Reipurth (KU), Anne Sofie V. Hammer (KU), Louise Lohse (SSI) and Lene J. Kjær. (KU)

The Danish Veterinary Consortium at the University of Copenhagen monitor vectors and vector-borne diseases in Denmark on behalf of the Danish Veterinary and Food Administration. This surveillance has taken place since 2011 and data are continuously updated on www.myggetal.dk.

3.1 Monitoring of endemic vectors

The vector season 2021 was characterized by normal weather conditions resulting in an average number of all five mosquito genuses present in Denmark. In the previous year 2020, the West Nile fever mosquito *Culex modestus* was almost absent, probably due to an unusual cold July. In 2021, July was warm and the number of *Cx. modestus* returned in high numbers. At West Amager near Copenhagen airport, the mosquito attack rate on a single human was 406 in just 70 minutes on July 23rd around 3pm. Cx. modestus was first reported in Denmark in 2013 (Bødker et al, 2014). Surveillance of this species since then, strongly suggests that it is sensitive to low temperatures during midsummer and that a future warmer climate is likely to increase its abundance in Denmark. All Cx. modestus collected in West Amager were tested for West Nile virus and for Usutu virus and all were found negative, despite both viruses circulating in Holland and Northern Germany since the warm summer in 2018, and despite Usutu virus was identified in a single Black bird (Turdus merula) in Sweden in 2019.

3.2 Passive surveillance of exotic vectors

No exotic mosquitoes were recorded in 2021. The exotic Hyalomma tick was first reported in large numbers in Northern Europe shortly after the summer in 2018. Here two adult Hyalomma ticks were reported from Denmark and another overwintering adult was reported in the spring of 2019. Hyalomma ticks are introduced annually with migrating birds arriving from Africa and the Middle East and they may carry both the severe zoonotic Crimean Congo Hemorrhagic Fever virus and the Alkhurma hemorrhagic fever virus (Hoffman et al 2018). However, in colder climates, Hyalomma ticks may be unable to mature to their adult stage. The record-warm summer in 2018 apparently offered temperatures sufficiently high to permit maturation. However, in 2021 the surveillance program received a fourth adult Hyalomma specimen removed mid-July from a Danish horse, despite a summer of only average temperatures. This suggests that adult Hyalomma ticks in Northern

Europe may not be as rare as previously thought and that specimens simply may have been unnoticed or unreported until the media attention and increased awareness, following the large number of Hyalomma ticks observed in 2018.

3.3 Surveillance at emerging TBE hot spot

In 2019, a new hotspot with Ixodes ricinus ticks carrying Tick Borne Encephalitis virus (TBE) was identified in a public forest on the coast of North Zeeland after three visitors developed clinical TBE. Infected ticks were found to be limited to two coherent small areas on one side of a playground just inside the Tisvilde forest, but with high TBE prevalence reaching 10% or more (Anonymous, 2019). Ticks from this site have been collected regularly since then, and ticks collected in the spring of 2021 and tested in pools for virus, confirmed the continuous presence of TBE virus at both sites and with a high pool prevalence. So far, TBE-positive ticks have only been reported from this small area, but new human clinical cases were reported in 2021, and some of these cases must have been infected at other locations in Northern Zealand. This suggests that TBE is now emerging and spreading in the northern part of the densely populated island of Zealand and possibly also in other regions in Denmark.

3.4 Identifying risks of large outbreaks of zoonotic vector-borne diseases

After the COVID-19 outbreak, Danish veterinary authorities in 2021 requested the Danish Veterinary Consortium to identify new zoonotic disease threats with a considerable epidemic potential in Denmark, both in the present and in a future warmer climate. Of the so far nine specific diseases identified, five are vector-borne: Tularemia, West Nile virus, Equine encephalitis, Rift Valley fever and Japanese encephalitis (www.dkvet.dk; Danish only). The main reasons for including the five vector-borne pathogens as present or future threats in Denmark are briefly described below and summarized in Table 1.

Tularemia (*Francisella tularensis*) is a bacteria that is low endemic in Scandinavia. In Denmark, human cases are mainly associated with hunters handling dead hares. However, in Sweden the epidemiology of tularemia has recently changed, and it is now mainly a mosquito-borne infection that is moving south. Large outbreaks in humans with locally high incidence rates have been observed in

	West Nile Virus	Rift Valley Virus	Japanese encephalitis	Equine encephalitis (Western, Eastern & Venezuelan)	Tularemia
Pathogen	Flavivirus	Phlebovirus	Flavivirus	Alpha virus	Intra-cellular bacteria
Risk of introduction to Denmark	Very high	Low	Low	Very low	Mild strain endemic in Denmark
Zoonotic animal reservoir	Wild birds	Ruminants + camelids and also Aedes mosquito eggs	Wild birds. Pigs are important amplifying hosts	Large range of mostly birds and rodents. But epidemic strains depends on mutations	Rodents and hares
Vectors	Culex mosquitoes, common in DK	Culex pipiens and Aedes detritus + Ae. vexans and Ae. caspius both common in DK after flooding	Culex species, Aedes detritus and the invasive Ae. japonicus (the closest population is in Hanover)	Primarily mosquitoes especially Aedes, Anopheles and Mansonia species	<i>Aedes cinereus</i> common in Denmark after flooding
Potential impact on human health (incidence and severity of infection)	Low and with little mortality	Large and with medium mortality	Large and with medium mortality, potentially permanent brain damage	Large and with low mortality, but potentially permanent brain damage	Large but low mortality
Impact on production animals (economic)	Minor	Large on cattle production	Very large on swine production	Small on horses	Only horses affected
Humane vaccine/ treatment	No vaccine or treatment	No approved vaccine, no treatment	Approved efficient vaccine available	No approved vaccine, no treatment	No vaccine but treatable with fluoroquinolones

Table 4.1 Five vector-borne infections have so far been identified as potential emerging diseases in Denmark (www.dkvet.dk).

Continued on next page

Table 4.1. Five vector-borne infections have so far been identified as potential emerging diseases in Denmark (www.dkvet.dk) continued from previous page.

	West Nile Virus	Rift Valley Virus	Japanese encephalitis	Equine encephalitis (Western, Eastern & Venezuelan)	Tularemia
Climate change sensitive in Denmark	Very temperature sensitive	Aedes vectors sensitive to severe rainfall and flooding	Increasing temperatures expected to facilitate transmission in Denmark	Endemic in temperate North America	Vector sensitive to severe rainfall and flooding
Diagnostic tools available	PCR established in DK, but virus may be difficult to detect in blood	PCR and serology available	Yes	Neither serology or PCR are simple and may require spinal samples	PCR and serology established in Denmark
Persistence of pathogen in the Danish environment	Several years	Many years (survives in Aedes eggs)	Few years	Several years	Permanent

Central Sweden. The reason for this development is not understood, but mosquitoes appear to become infected orally from the water they live as larvae, and subsequently emerge as infectious adult mosquitoes. The vector is often *Aedes cinereus*, a common mosquito in Denmark. The national mosquito surveillance program has shown that the abundance of *Aedes cinereus* may rise dramatically following extreme rainfall events – events that are expected to increase in a warmer climate (Table 4.1).

West Nile virus is transmitted by Culex mosquitoes between wild birds and between wild birds and humans. West Nile virus in humans is often a mild infection with subclinical or influenza-like disease course, but it may develop into a potentially fatal encephalitis. There is no vaccine for humans. The virus has been spreading north in Europe during the last two decades and arrived in northern Germany during the record warm summer of 2018. The two main Culex species in Denmark probably rarely bite humans, but the new species *Culex modestus* will both bite humans and wild birds. This mosquito species is common in warmer parts of Europe where it has been involved in large outbreaks of West Nile virus in humans. The vector is now established in the Køge Bugt area, where the Danish vector surveillance program shows it is locally abundant in warm summers. The potential for transmission of West Nile virus in Denmark is expected to increase with warmer temperatures that both increase the *Culex modestus* density and speeds up virus development in the vector (Table 4.1).

Equine encephalitis is a group of zoonotic viruses in the Americas, some of which are epidemic. They are transmitted by a wide range of mosquito species. Some of these viruses may produce large outbreaks in humans and horses. They have reservoirs in wild rodents and birds. However, some epidemic types do not seem to have a reservoir. They instead appear to be spontaneous mutations from non-epidemic types and die out when herd immunity is reached. West Nile virus was absent in the Americas until 1999, but spread rapidly, also in temperate areas, after being accidentally introduced to New York. Likewise for equine encephalitis, there is a potential risk of introduction to Europe. The large number of natural reservoir host species in South- and North America and the large number of natural mosquito species acting as vectors in the Americas indicate a real risk of the virus finding a suitable vector in Europe. The relatively closely related Sindbis virus is an endemic mosquito-borne zoonosis in northern Scandinavia further suggesting that the European absence of equine encephalitis may simply be because the virus so far has not been introduced (Table 4.1).

Rift Valley fever is a viral disease in African ruminants south of Sahara. The disease is often ranked high on international lists of emerging diseases because of its recently expanding geographical area, its high zoonotic potential and because once introduced, it may survive for years in the environment protected inside dormant eggs of Aedes mosquitoes. The infection is predicted to cause high mortality in European cattle breeds and some virus strains may also cause relatively high mortality rates in humans mostly due to kidney and liver failure. At least four vector species are common in Denmark. The Danish mosquito surveillance program has found both Aedes caspius and Ae. vexans to be highly abundant after flooding in Denmark. Climate change is expected to increase the frequency of extreme rain in Denmark, and climate warming itself is also expected to increase the transmission potential in Northern Europe. Direct air traffic with endemic African countries is assumed to constitute the major risk for introduction of virus to Europe via infected mosquitoes (Table 4.1).

Japanese encephalitis virus is also frequently ranked high on lists of emerging epidemic threats. It has been con-

fined to Asia including some temperate areas, but is now expanding geographically. Virus that is genetically similar to Japanese encephalitis virus has twice been reported from birds and mosquitoes in northern Italy, but these findings remain unconfirmed. Outbreaks in humans are often in the form of large epidemics. Although the virus has a reservoir in wild water birds, pigs are important and very efficient amplifying hosts for the virus. The virus may spread directly between pigs in close contact. Denmark has at least three species of mosquitoes that are known to be able to act as vectors, but they are either not common in the Danish mosquito surveillance or they rarely bite humans. However, if virus spreads within Denmark's large pig population, it may result in a very large infectious reservoir, that even at low vector abundance will be able to spill over to humans. Additionally, increasing temperatures are expected to facilitate transmission in Europe if the virus is introduced (Table 4.1).

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5. *Toxoplasma gondii* – an important foodborne parasite, also in Denmark

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In Europe, *Toxoplasma gondii* has been ranked as the second most important foodborne parasite [1]. The protozoan parasite is prevalent worldwide and has been found in a wide range of warm-blooded animals. Only felids can serve as definitive hosts and shed *T. gondii* oocysts in their feces. In all other infected hosts, the parasite lives within tissue cysts localized in various organs and can be transmitted if the host or its tissues are eaten. In most host species, the majority of *T. gondii* infections are subclinical. However, the parasite can cause clinical disease, toxoplasmosis, in both humans and animals, and it causes a substantial disease burden [2].

Humans can become infected with *T. gondii* by ingesting oocysts or tissue cysts of the parasite. From a farm-to-fork perspective, consumption of undercooked meat of animals infected with *T. gondii* and consumption of food or water contaminated with *T. gondii* oocysts are potential pathways of *T. gondii* infection for humans [2,3]. An ongoing large European multidisciplinary research project One Health EJP TOXOSOURCES, led by Statens Serum Institut, investigates the relative importance of these two pathways [4].

At present there is no national surveillance program for *T. gondii* in Denmark. There is no monitoring of *T. gondii* in farmed animals, and human toxoplasmosis is not a notifiable disease. Data on seroprevalence in animals have been mainly available from research projects.

European Food Safety Authority has identified *T. gondii* as a public health hazard and recommends addressing this, following a risk-based approach [5]. However, for example, the current meat inspection does not even attempt to detect *T. gondii* infections. If meat of infected animals is eaten without heat-treating it to 67° C, tissue cysts may remain viable and pose a risk to the consumer. Fresh meat products that are undercooked accidentally or intentionally could thus pose a risk to the consumers, while processed products that are sufficiently treated (heat, and/or $\ge 3.3\%$ NaCl) are regarded safe for consumption [2].

Among meat products, pork is consumed by many in Denmark, and thus, the risk of exposure from eating undercooked pork may not be negligible [2]. An initial exploratory investigation of *T. gondii* seroprevalence in pigs in Denmark, conducted in 2016, found higher seroprevalences in outdoor-raised finishers and indoor-raised sows in comparison with indoor-raised finishers [6] (Table 1). A larger-scale follow-up screening of pigs originating from commercial farms was carried out at Danish slaughterhouses in 2017-2018 and indicated a lower seroprevalence in indoor finishers compared with outdoor-raised finishers, and in indoor-raised sows compared to outdoor-raised sows. A separate investigation of *T. gondii* seroprevalence in farmed wild boars, sampled in 2016-2018, revealed a high seroprevalence (27.7%, 95% confidence interval

Indoor-raised		Outdo	or-raised	Reference
Finishers	Sows	Finishers	Sows	
3% (0-2%)	34%(26-54%)	11% (0-26%)	N.A ^b	Kofoed et al., 2017 [6]
2% (0.1-5%)	19% (2-26%)	11%(0.3-14%)	60% (43-70%)	Olsen et al., 2020 [7]

Table 5.1 Estimates of apparent Toxoplasma gondii seroprevalence (95% credible interval for true prevalence)^a in pigs in Denmark

a = true prevalence estimated by correcting for sensitivity and specificity of the diagnostic test

b = not available

19.7–37.1%) [8]. For other livestock species such as cattle and sheep, *T. gondii* seroprevalence is yet to be estimated in Denmark. However, the present evidence from pigs and wild boars collectively suggests that *T. gondii* has opportunities to infect farmed animals in Denmark.

Recently, it was concluded that ocular toxoplasmosis contributes to the disease burden caused by *T. gondii* in Denmark, but uncertainty about the incidence and severity precludes estimation of its importance. Previous estimates of disease burden have focused on congenital toxoplasmosis, and an overall estimate of the burden the parasite causes remains to be estimated [9, 10].

In a Danish study, it has been estimated that out of the 10 [95% CI 8-12] cases on congenital toxoplasmosis, in 61% of the cases, the mothers may have become infected from a foodborne source. This highlights that there is a need to identify the potential sources of *T. gondii* infections in Denmark [11].

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6. Surveillance and control programmes

The collaboration on zoonoses between national and regional authorities, the industry and non-governmental organisations in Denmark is presented in Figure 6.1. An overview of the notifiable and non-notifiable human and animal diseases, presented in this report, is provided in Appendix Table A26 and Table A27, respectively, including reference to the relevant legislation.

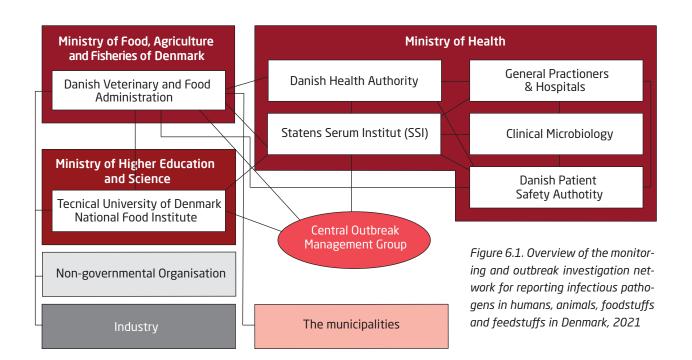
6.1 Surveillance of human disease

Information on human cases due to zoonotic pathogens presented in this report is extracted from the Danish Microbiology Database (MiBa) or reported to Statens Serum Institut (SSI) through different channels depending on the disease:

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

In Denmark, the physicians report individually notifiable zoonotic diseases to the Danish Patient Safety Authority and SSI. Physicians send specimens from suspected cases to one of the clinical microbiology laboratories depending on the geographical region. A copy of the results of the diagnostic analysis from regional clinical microbiology laboratory is transmitted to MiBa. All cases of infections with laboratory notifiable pathogens are collected in the Register of Enteric Pathogens maintained by SSI. Campylobacter, Salmonella and Yersinia cases are extracted from MiBa and STEC and Listeria are reported to SSI directly from the clinical microbiology laboratories. Furthermore, all culturable Salmonella and STEC and a subset of Yersinia and Campylobacter isolates are sent to SSI for further characterisation and the results are recorded in the Register of Enteric Pathogens. 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 A1.
- STEC O-group distribution in humans is presented in Appendix Table A2.
- The Salmonella serovar distribution is presented in Appendix Table A4.



6.2 Outbreaks of zoonotic gastrointestinal infections

In Denmark, local and regional foodborne outbreaks are typically investigated by the Food Inspection Unit in collaboration with the Public Health Medical Officers at the Danish Patient Safety Authority, and the regional clinical microbiology laboratories. National outbreaks are investigated by SSI, the National Food Institute at the Technical University of Denmark (DTU Food) and the Danish Veterinary and Food Administration (DVFA) in collaboration. These institutions may also aid in the investigation of regional or 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 three ministries based on the outbreak source: the Ministry of Health for infectious diseases; the Ministry of Food, Agriculture and Fisheries for foodborne and animal related diseases, and the Ministry of Environment for outbreaks of diseases related to supply of tap water.

Outbreaks may be detected in various ways. Clusters of cases may be noted in the local clinical laboratory or identified at SSI through the laboratory surveillance of gastrointestinal bacterial infections by subtyping of bacterial isolates from patients. Food handlers are obliged to contact the DVFA if the food they served are suspected to have caused illness. Individuals who experience illness related to food intake in settings such as restaurants or workplace cafeterias may report these incidents directly to the Food Inspection Unit. General practitioners and hospitals are obliged to report all suspected food- and waterborne infections to the Danish Patient Safety Authority and to SSI.

A list of verified outbreaks (not including household outbreaks) reported to the Food- and waterborne Outbreak Database are presented in Appendix Table A3 and some of the outbreaks from 2021 are outlined in Chapter 1.

6.3 Surveillance and control of animals and animal products

In Denmark, action plans and programmes 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 broiler 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, harmonised surveillance programmes 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 A25.

Salmonella surveillance and control programmes for poultry including table eggs, pigs and cattle are presented in Appendix Tables A30-33. Sample analysis, including serotyping and testing of antimicrobial resistance is performed at official laboratories designated by the DVFA. An overview of the methods used for subtyping is presented in Appendix Table A34.

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

- Results from the table egg production are presented in Appendix Tables A5-A6.
- Results from the broiler production are presented in Appendix Tables A4 and A7.
- Results from the duck and turkey productions are presented in Appendix Tables A4 and A8.
- Results from the pig production are presented in Appendix Tables A4, A11 and Figures A1-A3.
- Results from the cattle production are presented in Appendix Tables A4, A12-A13 and Figure A4.
- Results from the rendering plants are presented in Appendix Table A14.
- Results from the feed production are presented in Appendix Tables A15-A16.
- Results based on suspicion of diseases in pets, zoo animals and wild life are presented in Appendix Tables A20-A21.

a) The Danish Veterinary and Food Administration (DVFA) is one authority that 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 Inspection Unit followed by the location synonymous with the location in question.

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

Results from the broiler production are presented in Appendix Tables A9-A10.

Pig and cattle carcases are screened for *Mycobacterium* and *Echinococcus* during meat inspection at the slaughterhouse. Although swine kept under controlled housing conditions in Denmark are exempted from examination for *Trichinella* at slaughter, all slaughter pigs, sows and boars are still examined at slaughter. Free range pigs, horses, wild game (e.g., wild boar) and other species susceptible to *Trichinella* must still be tested. 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 DVFA. Results are presented in Appendix Table A11-A12.

Results from the surveillance for Bovine Spongiform Encephalopathy (BSE) in cattle, and Transmissible Spongiform Encephalopathy (TSE) in sheep/goat are presented in Appendix Tables A22-A23.

6.4 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 DVFA. 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 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 A24 provides information on the centrally coordinated studies conducted in 2021.

For further information, consult the website of the DVFA, <u>www.foedevarestyrelsen.dk</u> (in Danish).

The Danish Veterinary Consortium at the University of Copenhagen is involved in the technical working group reporting to the Steering Committee under the Danish Veterinary and Food Administration in the *Salmonella* Dublin (*S.* Dublin) surveillance and control programme. The technical working group members mainly provide technical answers to questions regarding changes in the legislation that would be likely to reduce the spread of *S*. Dublin between and within cattle properties. This includes movement restrictions and other control measures as well as herd and animal testing schemes and procedures.

S. Dublin is a bacterium, which is host-adapted to cattle. However, it can also infect other animal species and humans. According to Statens Serum Institute (SSI), *S.* Dublin infections are more serious for humans than infections caused by other non-typhoidal *Salmonella* serotypes [1]. SSI has reported *S.* Dublin zoonotic infections as rare, but serious, and stated that it should be surveyed and targeted similarly to other serious foodborne infections such as listeriosis, considering the incidence rate of 0.5–1.1 cases/100,000 Danish inhabitants per year and a high case fatality risk [2].

The surveillance programme for *S*. Dublin

A national surveillance programme targeting *S*. Dublin in the Danish cattle population was initiated in October 2002 [3]. The initial aim of the surveillance programme was to identify properties with cattle that were most likely free from *S*. Dublin infection to provide a pool of low-risk source herds for trade of cattle. All cattle properties were placed into one of three levels: Level 1 (most likely not infected with *S*. Dublin) and Level 2 (may be infected with *S*. Dublin) based on serological testing of bulk tank milk (BTM) and blood samples, combined with other knowledge about the properties. Level 3 was assigned to herds with clinical signs and bacteriological confirmation of *S*. Dublin infection. The samples are tested by an indirect ELISA method, developed in Denmark [4], which is directed against O-antigens in lipopolysaccharides of *S*. Dublin (0:1,9,12).

Dairy herds in Level 1 continuously have to live up to two test-criteria: 1) the average antibody value (called ODC%) measured across the last four quarterly collected BTMs should be below 25 ODC%, and 2) the last BTM sample should not have jumped to more than 20 ODC% higher than the average of the previous three BTM-samples. Non-dairy herds are placed in Level 1, if none of the last eight blood samples collected from slaughtered cattle from the property are equal to or higher than 50 ODC%, unless they are coming from Level 2. Then in such a case more testing is today required to be moved to Level 1, as described below.

The initiation of the programme dramatically changed the cattle trade behaviour to less risky over the first 3-6 months, and a fast drop in the prevalence of test-positive dairy properties followed, from 25-26% in 2002 to 16-18% 3 years later [5]. However, the prevalence-reducing effect of the surveillance programme waned around 2006.

Efforts to eradicate S. Dublin

New initiatives to further control the spread of *S*. Dublin were implemented. First as voluntary efforts in the cattle sector, e.g., projects and communication campaigns from 2007-2009. In 2010 new legislation introduced more consequences for cattle properties with signs of spread of *S*. Dublin (Order no. 1723 22/12/2010). Since then, the legislation has been changed and tightened several times. A major initiative included regionalisation of Denmark with a ban of movements of cattle for live use from the high prevalence to the low prevalence regions. However, this approach was abandoned during 2017 due to unsatisfactory effects and too high administrative burden. Since then, an increasing proportion of the Level 2 properties have been placed under Official Veterinary Supervision (OVS) under different sets of regulations.

A large change of the surveillance and control programme was implemented in July 2021 (Order no. 1055 31/05/2021). This includes changes in the blood sampling requirements on properties in Level 2 to improve detection of within-herd spread of *S*. Dublin and thereby increasing the certainity of a property being free of *S*. Dublin before being placed in Level 1 again. The required sample size was made dependent on the size of the group of animals to be tested on a given cattle property in Level 2.

When a property moves to Level 2, the herd owner is required to make an agreement with a veterinarian to make an action plan that should be implemented, re-evaluated and updated every 6 months and be available for checking by the veterinary authorities at any time. These measures in the tightened legislation are expected to increase the farmers' and veterinarians' focus on controlling the spread of *S*. Dublin through effective on-farm biosecurity and disease management.

The changes include:

• The number of calves and heifers to be tested has been made dependent on the number of animals in the respective groups on each property. The lowest number would be 8 blood samples (or all animals if there are fewer than 8 animals present) and the highest number is 25 blood samples.

• Heifer rasing properties must perform blood testing 1-2 times per year (depending on the number and ownership of source herds). If they do not perform the required testing they are placed in Level 2.

• Level 2 properties are visited every 6 months by the veterinary authorities for check of action plans and testing procedures, and the visits will be paid by the herd owner.

• Removal of the prior requirements for bacteriological testing of faecal and slurry samples in Level 2 farms with test-positive blood samples from the calves.

Hence, today only properties with clinical salmonellosis are required to collect samples to confirm, whether *Salmonella* is the likely cause of the observed disease. Cattle going to slaughter from properties under OVS for clinical salmonellosis still need to go for special hygienic slaughter and need to be tested and the meat heat-treated if found positive.

The effect of these changes are closely followed by the Steering Committee and the technical working group for the *S*. Dublin programme.

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In 2021, Statens Serum Institut (SSI) extracted 692 registered *Salmonella* cases including the available travel information from the Danish Microbiology Database (MiBa) that receives copies of reports from all Danish departments of clinical microbiology. This information was complemented with information from interviews performed by SSI of some of the *Salmonella* cases. Travel information was available from 80.5% of the *Salmonella* cases in 2021. A significant decrease was seen in cases with travel reported less than 7 days before onset of disease from 28.1% in 2020 to 11.0% in 2021 (Table 6.1). This was probably caused by less travel due to covid-19, see also Annual Report on Zoonoses in Denmark 2020. This also affected the proportion of travel-related cases of *Salmonella* Typhimurium (*S*. Typhimurium) and monophasic *S*. 1,4,[5],12:i:- (both below 10%) and *Salmonella* Enteritidis (*S*. Enteritidis) (below 20%) in 2021 and significantly lower than previous years (Figure 6.2). Especially, a significant decrease of travel related *S*. Enteritidis cases was seen from 51.1% in 2020 to 18.3% in 2021, even though the number of cases was at the same level, with 118 in 2020 and 114 in 2021. The decrease was caused by firstly; the percentage of travel related cases being high in the beginning of 2020 in contrast to 2021. Secondly, the number of domestic number cases were higher in the second half of 2021 due to especially one domestic outbreak (Figure 6.2).

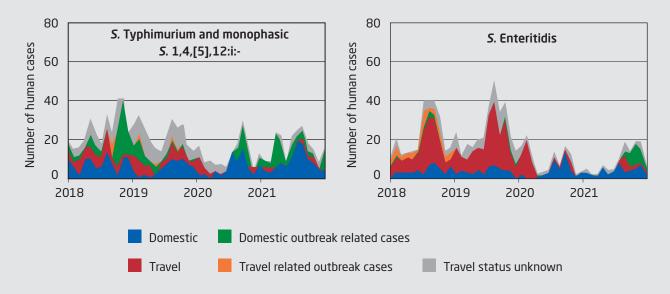
2021	Number of patients (%)		ntsª infected Domestically	2020	Number of patients (%)	% of patio Abroad ^b	entsª infected Domestically
Typhimurium	117 (16.9)	5.6	94.4	Enteritidis	118 (19.2)	51.1	48.9
Enteritidis	114 (16.5)	18.3	81.7	1,4,[5],12:i:-	86 (14.0)	9.4	90.6
1,4,[5],12:i:-	88 (12.7)	6.9	93.1	Typhimurium	63 (10.3)	19.1	46.6
Braenderup	42 (6.1)	2.4	97.6	Dublin	33 (5.4)	0.0	100.0
Newport	27 (3.9)	15.0	85.0	Strathcona	27 (4.4)	0.0	100.0
Dublin	25 (3.6)	0.0	100.0	Kottbus	24 (3.9)	15,8	84.2
Montevideo	17 (2.5)	0.0	100.0	Coeln	17 (2.8)	7.7	92.3
Chester	14 (2.0)	0.0	100.0	Newport	17 (2.8)	30.8	69.2
Bovismorbificans	11 (1.6)	9.0	91.0	Stanley	16 (2.6)	66.7	33.3
Oranienburg	10 (1.4)	14.3	15.7	Kasenyi	12 (2.0)	0.0	100.0
Other serotypes	227 (32.8)	15.7	84.3	Other serotypes	201 (32.7)	33.8	66.2
Total	692	11.0	89.0	Total	614	28.1	71.9

Table 6.1. Top 10 Salmonella serotypes in humans and information about travel abroad, 2020-2021

a) Patients with unknown travel information (19.5% of all patients in 2021 and 28.2% in 2020) 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 6.2. Monthly distribution of S. Enteritidis and S. Typhimurium incl. the monophasic variant 1,4,[5],12:i:- cases, 2018-2021



7. International topics

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7.1 EU targets

Harmonised regulation on targets and surveillance in the poultry production has been laid down by the Commission. An overview is presented in Appendix Table A25.

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 2021 (Appendix Table A8).

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:-, *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 was positive for target serovars in 2021 with *S*. 4.5.12:i:- (Appendix Table A5 and A7). Thereby, 0.3% of the breeding flocks of *G. gallus* in Denmark were positive for target serovars.

Regulation (EC) No 517/2011 lays down targets for the reduction of *Salmonella* in laying flocks. The targets are Member State 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 monophasic S. 1,4,[5],12:i:- and *S*. Enteritidis. The prevalence in Denmark has been below 2% since 2004, except for 2018, where 2.2% of flocks were found positive with target serovars. In 2021 the prevalence was 0.5, as two flocks were positive with target serovars (Appendix Table A5).

In broiler flocks of *G. 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:- variant. Denmark has had intensive *Salmonella* control programmes since the 90's and the target of 1% was reached in 2000. In 2021, 0.1% of broiler flocks were positive with target serovars (Appendix Table A7).



Human disease and outbreak data

	Incidence per 100,000 inhabitants	Reported r	no. of cases				
Zoonotic pathogen	2021	2021	2020	2019	2018	2017	2016
Bacteria							
Brucella abortus/melitensisª,b	-	1	1	7	З	З	З
Campylobacter coli/jejuni ^{c,e}	63.9	3,740	3,742	5,389	4,546	4,257	4,677
Chlamydia psittaci ^c	0.4	25	27	32	16	14	24
<i>Leptospira</i> spp. ^c	0.2	10	14	14	19	22	10
Listeria monocytogenes ^c	1.1	62	43	62	47	58	39
Mycobacterium bovis ^c	0.0	0	0	0	1	2	2
Salmonella total ^{c,e}	11.8	692	614	1,120	1,168	1,067	1,074
S. Enteritidis ^{c,e}	1.9	114	117	310	268	226	246
S. Typhimurium ^{c,d}	3.5	205	149	272	306	290	320
Other serotypes ^c	5.1	301	302	449	594	551	508
STEC total ^{c,e}	15.8	927	448	630	495	346	269
0157	0.5	32	39	60	43	50	37
Other O-groups or non-typeable	6.4	376	198	359	259	215	204
Yersinia enterocolitica total ^{c,e,f}	7.8	453	413	374	366	354	573
Yersinia enterocolitica (Biotype 2,3 and 4)	2.3	139	106	139	-	-	-
Viruses							
Lyssavirus ^c	0	0	0	0	0	0	0

Table A1. Zoonoses in humans, number of laboratory-confirmed cases, 2016-2021

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

b) 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.

c) Notifiable.

d) Including the monophasic variant of S. Typhimurium (S. 1,4,[5],12:i:-).

e) Includes also only notified cases.

f) A subset, of *Yersinia enterocolitica* (46.8%) was isolated and sent from the local clinical departments to SSI for surveillance. Characterisation disclosed 49.6% (137 isolates) being apathogenic biotype 1a, and these are excluded from the total number for 2021.

Source: Statens Serum Institut

0-group	Number of episodes	Proportion of total (%)	0-group	Number of episodes	Proportion of total (%)
0146	45	4.9	027	18	1.9
0103	42	4.5	0125	17	1.8
0157	32	3.5	0128	16	1.7
063	29	3.1	0111	12	1.3
026	28	3.0	Other	127	13.7
091	22	2.4	Notification ^{b,c}	519	56.0
0145	20	2.2			
Continued in t	Continued in the next column		Total	927	

Table A2. STEC O-group distribution in humans^a, 2021

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

b) Including isolates sent for verification at SSI, but not possible determine O-group.

c) Cases not sent for verification at SSI and/or only notified through the clinical notification system.

Source: Statens Serum Institut

Table A3. Food- and waterborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD)
(n=63), 2021	

Pathogen ^a	No. of patients	Patients labora- tory confirmed	Setting	Source	FUD no.º
Bacillus cereus	3	-	Private party	Mixed food	2045
Campylobacter jenuni, ST50#18	16	16	National	Chicken meat	1999
<i>Campylobacter jejuni</i> , ST52#4 and ST252#5	27	27	National	Chicken meat	1974 ^b
Campylobacter jejuni, ST21#7	19	19	National	Chicken meat	1971 ^c
Clostridium botulinum	5	3	Private party	Roe	1944
Clostridium perfringens	33	-	Catering	Pulled pork	2043
Clostridium perfringens	21	3	Restaurant	Lamb chop	2018
Clostridium perfringens	6	1	Take-away	Tartlets with chicken and asparagus	1993
<i>Cryptosporidium</i> and STEC 0145: H28 ST32#4	14	9	School	Unknown	1982
EIEC 0136 ST270#1 and 096 ST99#1	85	32	National	Spring onions	2030 ^d
EIEC and Shigella	48	3	Residential insti- tution	Unknown	1962
EIEC 06 ST4#1	16	З	Catering	Mixed food	2040
Lectins	2	-	Restaurant	Fried beans	1998
Lectins	6	-	National	Elderberry smoothie	1945
Listeria monocytogenes, ST398#1	З	3	National	Unknown	2005
Listeria monocytogenes, ST7#4	9	9	National	Unknown	1970
Listeria monocytogenes, ST7#6	5	5	National	Unknown	1966
Listeria monocytogenes, ST5#1	10	10	National	Unknown	1941
		Continue	d on the next page		

Pathogen ^a	No. of patients	Patients labora- tory confirmed	Setting	Source	FUD no.º
Listeria monocytogenes, ST11#1	11	11	National	Unknown	1939
Norovirus	20	4	Restaurant	Mixed food	2029
Norovirus	57	2	Restaurant	Mixed food	2002
Norovirus	25	4	Catering	Open sandwhich	2001
Norovirus	16	7	Restaurant	Mixed food	1997
Norovirus	15	7	Restaurant	Mixed food	1996
Norovirus	41	1	Canteen	Ready-to-eat salads	1994
Norovirus	75	7	Canteen or workplace	Mixed food	1987
Norovirus	55	5	Hotel	lce-cream cake	1983
Norovirus	25	5	Restaurant	Mixed food	1980
Norovirus	46	4	Canteen	Buffet meals	1967
Norovirus	40	4	Catering	Mixed food	1965
Norovirus	14	8	Restaurant	Sushi	1958
Norovirus	45	З	Canteen	Buffet meals	1956
Norovirus	19	2	Catering	Mixed food	1947
S <i>almonella</i> Bovismorbificans, ST1499#4	8	8	Take-away	Chicken meat	2008
Salmonella Braenderup, ST22#2	41	41	International	Sugar melons	1954
Salmonella Chester, ST1954#6	8	8	International	Unknown	1989
Salmonella Enteritidis, ST11#117	З	З	International	Eggs	2019°
Salmonella Enteritidis, ST11#142	26	26	National	Eggs	2009
Salmonella Litchfield, ST214#1	7	7	International	Unknown	1991
S <i>almonella</i> Mikawasima, ST1815#13	4	4	National	Unknown	1981
Salmonella Montevideo, ST2327#1	11	11	National	Unknown	1964 ^f
Salmonella 4,[5],12:i, ST34#146	11	11	National	Unknown	2039 ^g
Salmonella Typhimurium, ST36#9	9	9	National	Unknown	1992
Salmonella Typhimurium, ST36#7	52	52	International	Dietary supplement, psyllium	1917 ^h
Salmonella multiple serotypes	6	6	International	Tahini	1988 ⁱ
Shigella sonnei, ST152#4	9	5	Canteen	Buffet meals	2031
Shigella sonnei, ST152#3	З	3	National	Unknown	1948 ^j
Shigella sonnei, ST152#2	12	4	Canteen	Ready-to-eat salads	1940
Staphylococcus aureus	11	-	Restaurant	Truffle puree	2012
Jnknown	16	-	Canteen	Chilli con carne	2042
Jnknown	4	-	Take-away	Pasta dishes	2041
Jnknown	15	-	Restaurant	Unknown	2014
Unknown	20	-	Restaurant	Stew	2010
Unknown	82	-	Hotel	Mixed food	2003

Table A3. Food- and waterborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD) (n=63), 2021 (Continued from previous page)

Pathogenª	No. of patients	Patients labora- tory confirmed	Setting	Source	FUD no.º
Unknown	2	-	Take-away	Mixed food	1942
Unknown	5	-	Restaurant	Slow cooked pork jowls	1905
STEC 012:H6, ST583#10	9	9	National	Unknown	2033
STEC 0157:H7, ST11#19	12	11	National	Unknown	2032 ^ĸ
STEC 0103:H2, ST12#22	5	5	National	Unknown	1973
STEC 0103:H2, ST17#23	7	7	National	Unknown	1972
STEC 026:H11, ST21#14	4	4	National	Unknown	1959
Yersinia enterocolitica, ST18#3	15	15	National	Unknown	2021'
Yersinia enterocolitica, ST18#2	8	8	National	Unknown	1943
Total	1,257	474			

Table A3. Food- and waterborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD) (n=63), 2021 (Continued from previous page)

a) ST = Sequence Type

STEC = Shigatoxin-producing Escherichia coli

EIEC = Enteroinvasive *Escherichia coli*

ETEC = Enterotoxigenic Escherichia coli

b) FUD1974: One additional case in 2022

c) FUD1971: One additional case in 2019 and five in 2020

d) FUD2030: Three cases registered in 2022

e) FUD2019: Three additional cases in 2020 and 1 case in 2022 $\,$

f) FUD1964: One additional case in 2022

g) FUD2039: Five additional cases in 2022

h) FUD1917: Two additional cases in 2020

i) FUD1988: Two additional cases in 2019, two in 2020, two in 2022

j) FUD1948: Two additional cases in 2020

k) FUD2032: Two additional cases in 2022

I) FUD2021: One additional case in 2022

Source: Food- and waterborne Outbreak Database (FUD)

Monitoring and surveillance data

	Human	Pork⁵	Beef ^c	Broilerd	Layer ^d	Duck ^e	Imported r (batches)	neat
	cases	batches	batches	flocks	flocks	batches	Pork ^e	Duck ^e
	N=692	N=88	N=3	N=6	N=4	N=2	N=13	N=18
Typhimurium	16.9	18.2	-	33.2	-	50.0	15.4	17.0
Enteritidis	16.5	-	-	-	50.0	-	-	28.0
4,5,12:i:-	12.7	26.1	-	16.7	-	-	69.2	-
Braenderup	6.1	-	-	-	-	-	-	-
Newport	3.9	-	-	16.7	-	50.0	-	6.0
Dublin	3.6	-	100	-	-	-	-	-
Montevideo	2.5	-	-	-	-	-	-	-
Chester	2.0	-	-	-	-	-	-	-
Bovismorbificans	1.6	-	-	-	-	-	-	-
Oranienburg	1.4	-	-	-	-	-	-	-
Stanley	1.4	-	-	-	-		-	-
Infantis	1.4	4.5	-	-	-	-	-	-
Derby	1.2	38.6	-	16.7	-		7.7	6.0
Coeln	1.2	-	-	-	25.0	-	-	-
Litchfield	1.0	-	-	-	-		-	-
Other	16.2	9.1 ^f	-	16.7	25.0	-	7.7 ^g	43.0 ^h
Unknown	10.4	3.4	-	-	-		-	-
Total	100	100	100	100	100	100	100	100

Table A4. Top 15 (humans) serotype distribution (%) of Salmonella from humans, animals, carcases, Danish and imported meat, 2021. N=number of culture positive units^a

a) One isolate per serotype per unit is included, thus the number of isolates may exceed the number of units.

b) Sampling of pork carcases at slaughterhouses according to the surveillance programme (Table A33).

c) Sampling of beef carcases at slaughterhouses according to the surveillance programme (Table A32).

d) Sampling of production flocks prior to slaughter according to surveillance programmes (Tables A29).

e) Centrally coordinated study (see section 6.4 and Table A24 for more information).

f) S. Brandenburg (1); S. London (2); S. Livingstone (1); 4.5.12 (1); 4.12 (1); 1.4.5.12.:-- (1); S. Senftenberg (1)

g) One serotype of S. Hadar.

h) Of the 43% positive with "Other" serotypes, 33% were positive for S. Hadar.

Source: Danish Veterinary and Food Administration and Statens Serum Institut

	Rearing period ^b (parent flocks)		Adult period ^c (parent flocks)		Pullet-rearing flocks		Table egg layer flocks	
	Ν	Positive	Ν	Positive	Ν	Positive	Ν	Positive
2011	8	0	9	0	195	0	410	2
2012	9	0	8	0	197	1	359	З
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
2016	15	0	10	0	132	0	426	З
2017	7	0	8	1	138	1	446	З
2018	7	0	6	0	124	1	454	12
2019	7	0	6	0	101	0	411	8
2020	8	0	9	0	134	0	432	8
2021	6	0	9	0	112	0	429	4 ^d

Table A5. Occurrence of Salmonella in the table egg production^a, 2011-2021

a) See Tables A28 and A30 for description of the surveillance programmes.

b) Salmonella was not detected in grandparent flocks during rearing period (1 flocks).

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

d) S. Coeln (1) S. Enteritidis (2), S. Anatum. (1)

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

	Deep litter		Free range		Organic		Cage	
	Ν	Positive	Ν	Positive	Ν	Positive	Ν	Positive
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
2016	125	1	31	0	196	1	74	1
2017	126	0	42	1	217	2	61	0
2018	139	4	46	1	227	4	42	3
2019	135	1	34	2	220	5	22	0
2020	151	3	40	1	216	4	25	0
2021	151	2ª	44	1 ^b	213	1 ^c	21	0

Table A6. Occurrence of Salmonella in the table egg layer flocks sorted by type of production, 2011-2021

a) S. Coeln (1), S. Enteritidis (1).

b) S. Anatum.

c) S. Enteritidis (1).

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

	Rearing period ^b (parent flocks)		Adult period ^c (parent flocks)		Broiler flocks	r flocks Slaughterhoused (flocks/batches)		
	Ν	Positive	Ν	Positive	Ν	Positive	Ν	Positive
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	3,631	23	148	0
2016	184	0	182	3	3,606	21	203	1
2017	170	2	250	1	4,290	25	259	0
2018	184	1	149	1	4,245	35	249	1
2019	210	0	137	1	4,012	12	254	0
2020	357	0	217	2	3,604	13	231	0
2021	154	0	290	1°	3,758	6 ^f	263	0

Table A7. Occurrence of Salmonella in the broiler production^a, 2011-2021

a) See Tables A28-A29 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 (8 flocks).

d) From 2008, meat from 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. 4,5,12:i:-

f) S. Newport (1), S. Derby (1), S. 4,5,12:i:- (1), S. 4:12:-I (1), S. Typhimurium (2).

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

Table A8. Occurrence of Salmonella in turkey flocks, 2011-2021

	Turkey flocks ^a	
	Ν	Positive
2011	38	1
2012	23	0
2013	56	З
2014	10	0
2015	80	1
2016	76	0
2017	24	1
2018	13	0
2019	85⁵	0
2020	198	0
2021	115	0

a) See Table A31 for description of the surveillance programme for turkey flocks. The major turkey slaughterhouse in Denmark closed down in 2004. Therefore, most commercially reared turkey flocks are transported abroad for slaughter.

b) The increase in number of tested flocks is primarily based on a change of registration.

	Sock samples at	farm	Cloacal swabs at	slaughter	Neck skin sample:	s at slaughter⁵
	N (Flocks)	% pos	N (Flocks)	% pos	N (Batches)	% pos⁰
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	-	-
2016	-	-	3,184	20.8	-	-
2017	-	-	3,316	16.6	-	-
2018	-	-	3,411	24.6	1,120	9.7
2019	-	-	3,327	22.7	1,063	7.4
2020	-	-	3,189	20.2	985	7.0
2021	-	-	3,332	19,5	1,150	7.5

Table A9. Occurrence of Campylobacter in broiler flocks, 2011-2021^a

a) See Table A29 for description of the surveillance programmes. In 2014 the sampling method changed from boot swabs collected in the stable 7-10 days before slaughter to cloacal swabs at slaughter according to Danish Order no. 1512 of 13/12/2013.

b) In 2018, additional sampling of neck skin began at the slaughterhouses according to Regulation (EC) 2073/2005, see Table A29 for further description. c) Percent positive samples >1000 cfu/g.

Source: Danish Agriculture and Food Council

Table A10. Occurrence of Campylobacter in non-heat-treated chilled broiler meat samples at slaughter and retail[®], 2015-2021

		At alau abtaub		At			
		At slaughter ^b		At retail			
		Denmark		Denmark		Import	
		N (samples)	% pos	N (samples)	% pos⁰	N (samples)	% pos ^c
2015	Conventional	960	20.1	-	-	-	-
	Organic/free-range	115	78.2	-	-	-	-
2016	Conventional	999	21.3	1,339	12.8	232	37.9
	Organic/free-range	117	87.2	93	71.0	245	78.8
2017	Conventional	1,258	25.0	-	-	-	-
	Organic/free-range	203	79.0	-	-	-	-
2018	Conventional	1,250	31.0	-	-	-	-
	Organic/free-range	199	91.0	-	-	-	-
2019	Conventional	1,248	32.6	697	12.4	28	36.1
	Organic/free-range	123	68.3	155	31.6	28	82.1
2020	Conventional	1,224	25.8	436	15.2	64	67.3
	Organic/free-range	95	49.5	192	34.4	-	-
2021	Conventional	1,232	22.2	623	11.9	14	64.3
	Organic/free-range	96	36.5	158	30.4	62	69.4

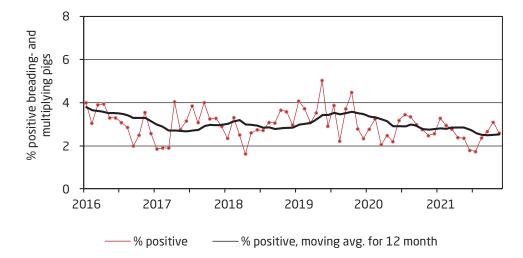
a) Centrally coordinated studies (see Table A24 and section 6.4 for description). Limit of quantification: 10 cfu/g.

b) Leg-skin samples.

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

Source: National Food Institute and Danish Veterinary and Food Administration

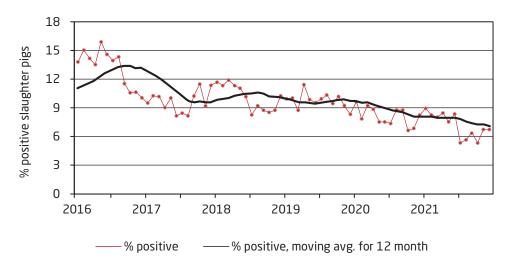
Figure A1. Serological surveillance of Salmonella in breeding and multiplying pigs^a based on monthly testing of blood samples, 2016-2021^b



a) For more information about the surveillance programme, see Table A33.b) Monthly data for the month of December 2021 not available

Source: Danish Agriculture and Food Council

Figure A2. Serological surveillance of Salmonella in slaughter pigs^a, 2016-2021. Percentage of seropositive meat juice samples (first sample per herd per month)



a) For more information about the surveillance programme, see Table A33.

Source: Danish Agriculture and Food Council

	Herds		Animals/Samp	es	
Zoonotic pathogen	Ν	Pos	N	Pos	% pos
At slaughterhouse (slaughter pigs)					
Salmonella spp. ^{a,b}	5,465	152 ^g	-	-	-
Salmonella spp. ^{a,c} (slaughtering >30,000 pigs/year)	-	-	17,955	-	0.7 ^t
<i>Salmonella</i> spp. ^{a.c} (slaughtering 1,000 or more and less than 30,000 pigs/year)	-	-	134	-	-
Salmonella spp.ª,d	-	-	483	59	12.2
Trichinella spp. ^e	-	-	17,946,611	0	-
Mycobacterium spp. ^f	-	-	18,592,853 ⁱ	0	-
Echinococcus granulosis/multilocularis ^t			18,592,853 ⁱ	0	-

Table A11. Occurrence of zoonotic pathogens in pigs and pork in Denmark, 2021

a) See Table A33 for description of the Salmonella surveillance programme.

b) Data are from December 2021. Slaughter pig herds monitored using serological testing of meat juice samples collected at slaughter.

c) Swab samples from 4 designated areas after 12 hours chilling (4x100cm²).

d) Caecum samples are randomly collected from slaughter pigs at slaughter.

e) Samples collected from slaughter pigs at slaughter were examined using the method described in Regulation (EU) 2015/1375. 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 must be tested for *Trichinella*.

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

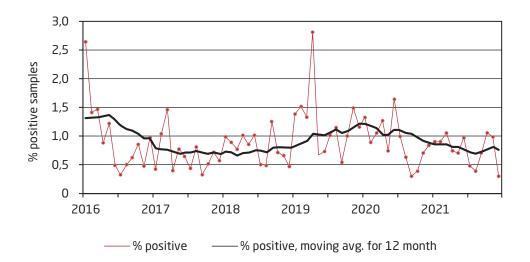
g) Includes herds belonging to Salmonella level 2 and 3 only (See Table A33).

h) When estimating the prevalence of Salmonella, both the loss of sensitivity and probability of more than one sample beinge positive in a pool are taken into consideration. A conversion factor has been determined on the basis of comparative studies, as described in Annual Report 2021. Furthermore, the prevalence has been adjusted for double sampling carried out in slaughterhouses with a prevalence of 2% or above (12month average).

i) Includes sows and boars slaughtered.

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

Figure A3. Salmonella in pork, monitored at slaughterhouses^a, 2016-2021



a) For more information about the surveillance programme, see Table A33.

Table A12. Occurrence of zoonotic pathogens in cattle and beef in Denmark, 2021

	Animals/Samp	les	
Zoonotic pathogen	Ν	Pos	% pos
At farm			
Brucella spp.ª	303	0	-
Mycobacterium bovis ^{b, c}	350	0	-
Coxiella burnetiiª	43	0	-
At slaughterhouse			-
Salmonella spp. ^{e,f} (slaughtering >=7,500 cattle/year)	8,285	З	0.1 ^h
Salmonella spp. ^{e,f} (slaughtering 250 or more and 7,500 or less cattle/year)	309	0	-
Mycobacterium spp. ^{b, g}	452,600	0	-
Echinococcus granulosis/multilocularis ^g	452,600	0	-

a) Denmark has been declared officially brucellosis free since 1979. The last outbreak was recorded in 1962. 5-8 ml blood samples were analysed using either the SAT or CFT methods. In addition 34 aborted foetuses were tested, none were positive.

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 intradermal 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) One positive sample was seen - it came from a herd that also tested positive in 2020 hence is not reported again.

e) Swab samples from 4 designated areas after 12 hours chilling (4x100cm²)

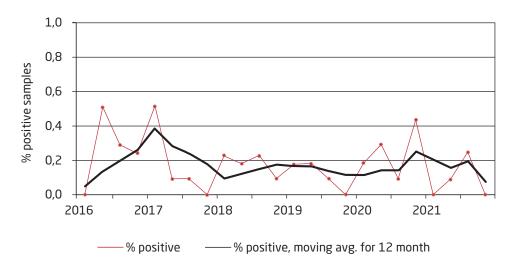
f) See Table A32 for description of the surveillance programme.

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

h) When estimating the prevalence of *Salmonella*, both the loss of sensitivity and probability of more than one sample being positive in a pool are taken into consideration. A conversion factor has been determined on the basis of comparative studies, as described in Annual Report 2021.

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

Figure A4. Salmonella in beef, monitored at slaughterhouses^a, 2016-2021



a) For more information about the surveillance programme, see Table A32.

			Non-milk producing h	erds	Milk produci herds	ng
Salmonel	<i>lla</i> Dublin le	evel	Ν	%	Ν	%
Level 1		On the basis of milk samples	-	-	2,173	88.8
		On the basis of blood samples	12,285	95.4		
	Total	Probably S. Dublin free	12,285	95.4	2,173	88.8
Level 2		Titre high in blood- or milk samples	145	1.1	219	8
		Contact with herds in level 2	102	0.8	28	1
		Other causes	48	0.4	27	1
	Total	Non S. Dublin free	295	2.3	274	10.1
Total nun	nber of her	ds	12,875		2,447	

Table A13. Cattle herds in the Salmonella Dublin surveillance programme^o, December 2021

a) See Table A32 for description of the surveillance programme.

Source: SEGES

Table A14. Salmonella in three categories of meat and bone meal by-products not intended for human consumption^o, 2021

Category of processing plant	Own-check	samples	Product samples	
	Ν	Positive	Ν	Positive
1+2: By-products of this material cannot be used for feeding purposes	480	3	320	0
2: By-product of this material may be used for feed for fur animals $^{\scriptscriptstyle \mathrm{b}}$	0	0	0	0
3: By-products from healthy animals slaughtered in a slaughter- house. Products of these may be used for petfood ^c and for feed for fur animals	1,513	0	33	0
Total	1,993	3	353	0

a) Regulation (EC) No 1774 of 03/10/2002 as amended.

b) No production.

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

Source: Daka Denmark A/S

Table A15. Control of Salmonella in feed processing and feed material (batch-based data), 2019-2021

	2021		2020		2019	
	Ν	Positive	Ν	Positive	Ν	Positive
Feed materials, farm animals ^a	60	2 ^d	17	0	61	0
Feed processing plants (process control) ^b :						
Ordinary inspections ^c	285	0	132	4	289	0

a) Predominantly products of soybean, fish meal and rapeseed cake.

b) 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.

c) Primarily findings of Salmonella in the unclean zone.

d) S. Agona (1), S. Livingstone (1)

	2021		2020		2019	
	Ν	Positive	Ν	Positive	Ν	Positive
Compound feed, farm animals	2,263	0	2,253	9	1,918	1
Feed materials, farm animals ^a	2,148	27 ^d	2,300	32	2,432	31
Feed processing plants (process control):						
Ordinary inspections - clean zone ^b	8,344	7 ^e	8,252	31	7,531	4
Ordinary inspections - unclean zone ^b	1,222	40 ^f	1,239	34	1,257	25
Transport vehicles, clean zone/hygiene samples ^c	1,110	0	1,082	1	1,121	1
Transport vehicles, unclean zone/hygiene samples ^c	245	10 ^g	219	4	346	З

Table A16. Feed business operators own sampling of Salmonella in compound feeds, feed processing and feed material (batch-based data), 2019-2021

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

a) Predominantly products of soy (e.g. soybean meal) but also products of rape (e.g. rapeseed cake) and sunflower (e.g. sunflower meal).

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

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

d) S. 42:r:1,5 (1), S. Aarhus (2), S. Agona (2), S. Cubana (2), S. Havana (1), S. Livingstone (3), S. Mbandaka (4), S. Pomona (1), S. Rissen (1), Salmonella spp. (4), S. Seftenberg (4), S. Soegenra (1), S. Tennesee (1).

e) S. Falkensee (1), S. Idikan (1), S. Mbandaka (1), Salmonella spp. (1), S. Tennesee (1), S. Typhimurium (2).

f) S. Ajiobo (1), S. Derby (1), S. Enterica 23:-- (1), S. Enterica 4b (1), S. Enterica subspecies diarizonae (IIIb) (1), S. Idikan (1), S. Livingstone (2), S. London (1), S. Mbandaka (2), S. Newport (1), S. Ouagadougou (1), S. Putten (6), S. Rideau (1), S. Rissen (18) Salmonella spp. (1), S. Typhimurium (1).

g) S. Enterica 23:-:- (1), S. Putten (1), S. Rissen (8).

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

Table A17. Listeria monocytogenes in Danish and non-Danish produced ready-to-eat (RTE) foods^a, 2021

				nalysed by a ve method⁵		nalysed by a tive method
			Ba	tches	Ba	tches
	Food category	Sampling place	Ν	Positive	N	Positive
Danish	Fish and fishery products, RTE ^d	Processing plant	60	4	60	0
	Infant formula, RTE ^d	Processing plant	0	0	0	0
	Products made from pork, RTE ^d	Processing plant	75	1	75	0
	Vegetables, RTE ^d	Processing plant	0	0	0	0
Non-Danish	Crustaceans, RTE ^d	Border inspection	7	0	7	0
		Processing plant	13	0	13	0
	Fish and fishery products, RTE ^d	Border inspection	2	0	2	0
	Molluscan shellfish, RTE ^d	Border inspection	З	0	З	0
	Total		160	5	160	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 25g sample of the product.

c) Levels > 10 cfu/g.

d) Ready-to-eat.

e) Samples from Greenland, Canada, USA China, Chile, Vietnam.

		Danish		Non-Dani	sh⁵
Food category	Sampling place	Ν	Positive	Ν	Positive
Escolar	Border inspection				
Herring in dressing	Processing plant				
Herring	Border inspection				
	Processing plant				
Mackerel	Border inspection				
	Processing plant			63	0
Sardines	Border inspection				
Tuna	Border inspection			216	0
Total				279	0

Table A18. Histamine in batches of Danish and non-Danish fish products^a, 2021

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

b) Samples from Greenland, Columbia, El Salvador, Ghana, Mauritius, Phlippines, Senegal, Seychelles, Thailand, Vietnam

c) The findings of histamine did not exceed the limits according to EU Regulation (EC) No 2073/2005.

Source: Danish Veterinary and Food Administration

Table A19. Salmonella in Danish and non-Danish produced food items^a, 2021

		Danish		Non-Da	nish⁵
Food category	Sampling place	Ν	Positive	Ν	Positive
Molluscan shellfish, intended to be cooked	Processing plant	-	-	15	0
Products made from beef, intended to be cooked	Border inspection	-	-	-	-
	Processing plant	125	0	-	-
Products made from pork, intended to be cooked	Border inspection	-	-	-	-
	Processing plant	215	Зq	-	-
Products made from poultry, intended to be cooked	Processing plant	256	0	-	-
Products made from turkey, intended to be cooked	Processing plant	-	-	-	-
Crustaceans, RTE ^c	Border inspection	-	-	-	-
	Processing plant	-	-	65	-
Molluscan shellfish, RTE ^c	Border inspection	-	-	-	-
Products made from poultry, RTE ^c	Processing plant	-	-	-	-
Infant formula, dried	Border inspection	-	-	-	-
Total		596	3	75	

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

b) Brazil, Greenland, and Vietnam.

c) Ready-to-eat.

d) Three positive samples were from the same batch.

Zoo animals				Pet animals ^c		
	Mammali	ans & reptiles	Birds			
Zoonotic pathogen	Ν	Pos	Ν	Pos	Ν	Pos
Chlamydia psittaci ^ь	-	-	106	26	-	-
Echinococcus spp.	-	-	-	-	-	-
Lyssavirus (classical)	-	-	-	-	-	-
European Bat Lyssavirus	-	-	-	-	-	-

Table A20. Occurrence of zoonotic pathogens in zoo and pet animals in Denmark^a, 2021

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

b) The number N and Pos represents cases. One case may contain more birds sampled at the same location /address.

c) No samples were analysed for cats, dogs, and other pet animals

Source: Statens Serum Institut and Danish Veterinary and Food Administration

Table A21. Occurrence of zoonotic pathogens in wild and farmed wildlife in Denmark^a, 2021

	Farmed w	ildlife⁵		Wildlife		
	Birds		Mammals	;	Birds	
Zoonotic pathogen	Ν	Pos	Ν	Pos	Ν	Pos
Echinococcus multilocularis	-	-	-	-	-	-
Lyssavirus (classical)º	-	-	25	0	-	-
European Bat Lyssavirus ^c	-	-	25	0	-	-
West Nile virus ^d	560	0	-	-	331	0

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

b) Under farmed wildlife, no samples were analysed for wild boar, minks and chinchillas

c) Samples are analysed using PCR. The results are not specified concerning the Lyssa virus types. Hence the 25 samples from Danish bats are mentioned for both Lyssa virus types.

d) No samples were positive for West Nile Virus. But two samples (one wild bird and one farmed bird) were positive for WNV antibodies.

Source: Statens Serum Institut and Danish Veterinary and Food Administration

Type of surveillance	N ^b	Positive
Active surveillance	-	-
Slaughtered animals	-	-
Risk categories:	-	-
Animals from herds under restriction	-	-
Emergency slaugther	1,336	0
Fallen stock	21,534	0
Slaughterhouse antemortem inspection revealed suspicion or signs of disease	-	-
Passive surveillance	-	-
Animals suspected of having clinical BSE	-	-
Total	22,870	0

Table A22. The Bovine Spongiform Encephalopathy (BSE) surveillance programme^a for cattle, 2021

a) According to the EU Regulation (EC) 999/2001 as amended, Commission Decision 2009/719/EC as amended and Danish Order no. 1442 of 11/12/2019 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: Danish Veterinary and Food Administration, data extraction from the EFSA database, April 2022

Type of surveillance	N ^b	Positive
Active surveillance	-	-
Animals from herds under restriction	-	-
Fallen stock (>18 months)	-	-
Not slaughtered for human comsumption	562	0
Slaughtered for human consumption	30	0
Passive surveillance	-	-
Animals suspected of having clinical TSE	-	-
Total	592	0

Table A23. The Transmissible Spongiform Encephalopathy (TSE) surveillance programme^a for sheep and goats, 2021

a) According to the EU Regulation (EC) 999/2001 as amended, Commission Decision 2009/719/EC as amended and Danish Order no. 1491 of 12/12/2019 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: Danish Veterinary and Food Administration, data extraction from the EFSA database, April 2022

Table A24. Centrally coordinated studies conducted in 2021

Title of project	No. of planned samples	Pathogen surveyed	Further information
Norovirus in samples of oysters from Danish production sites	60	Norovirus, <i>E. coli</i>	Not published
BU microbiology - slaughterhouses	50	Various	Not published
Campylobacter spp. in fresh, chilled Danish broiler meat at slaughterhouses (conventional)	1,250	Campylobacter spp.	To be published ^a
Campylobacter spp. in fresh, chilled Danish broiler meat at slaughterhouses (organic)	100	Campylobacter spp.	To be published ^a
Campylobacter spp. in fresh, chilled Danish and imported broiler meat	800	Campylobacter spp.	Appendix Table 10ª
<i>Campylobacter</i> spp. in imported and 200 intra-traded poultry meat	500	Campylobacter spp.	Appendix Table 10ª
Campylobacter spp. on cattle carcasses	300	Campylobacter spp.	To be published ^a
Campylobacter spp. contamination in poultry slaughterhouses	500	Campylobacter spp.	Appendix Table 9ª
DANMAP - Antibiotic resistance in poultry, pork and cattle	165	AMR	To be published ^a
DANMAP and EU surveillance of antibiotic resistance in broiler, pork and cattle meat at retail (appendicitis samples)	630	AMR	To be published ^a
EU surveillance of antibiotic resistance in retail	630	AMR.	To be published ^a
Export -USA- environmental samples	50	Listeria monocytogenes	Not published
Export- USA swab	468	Salmonella	Not published
Import - Intensified control of Brazilian beef and poultry meat	50	Listeria monoctogenes, Salmo- nella	To be published
Import - Microbiologic control of fish, fish products and bivalve molluscan shellfish from 3rd.countries	110	Listeria monoctogenes, Salmo- nella	To be published
Import - Microbiological control of food of animal origin, excluding fish	50	Listeria monoctogenes, Salmo- nella	To be published ^a
Import - Special control microbiology - not animal Reg.(669/2009)	100	Various	To be published ^a
<i>Listeria monocytogenes, Salmonella</i> spp, <i>Escherichia coli</i> and <i>Staphylococci</i> in fish products from Greenland	10	Listeria monocytogenes, Sal- monella spp., Escherichia coli, staphylococci	To be published ^a
Microbiologic classification of mussel produc- tion areas in Denmark	60	Salmonella spp., Escherichia coli	To be published ^a
Part 1: Minced meat - wholesale	300	According to Reg. 2073/2005	To be published ^a
Part 2: Prepared meat - wholesale	300	According to Reg. 2073/2005	To be published ^a
Part 3: Ready-to-eat meat products - whole- sale	300	According to Reg. 2073/2005	To be published ^a
Part 7: Fruit and vegetables	300	According to Reg. 2073/2005	To be published ^a
Part 6: Fish and fish products - wholesale	300	According to Reg. 2073/2005	To be published ^a
	Conti	nued on the next page	

Title of project	No. of planned samples	Pathogen surveyed	Further information
Part 8: <i>Listeria monocytogenes</i> in other RTE products - wholesale	300	Listeria monocytogenes	To be published ^a
Salmonella in imported pork and beef and in duck meat	700	Salmonella spp.	To be published ^a
Salmonella and resistance in pig/pork - surveillance	500	Salmonella spp.	To be published ^a
Salmonella in feed materials from feed companies	60	Salmonella spp.	Appendix Table A15
Salmonella in intratraded shell eggs - retail	25	Salmonella spp.	To be published ^a
Salmonella in intratraded shell eggs whole-sale	25	Salmonella spp.	To be published ^a
Salmonella process samples from feed companies	280	Salmonella spp.	Appendix Table A15
<i>Salmonella</i> spp. and <i>Escherichia coli</i> in raw frozen scallops from Greenland	25	Salmonella spp., Escherichia coli	To be published ^a
Salmonella in fresh poultry meat	200	Salmonella spp.	To be published ^a
Hygiene quality of minced meat	750	Various	To be published ^a

Table A24. Centrally coordinated studies conducted in 2021 (Continued from previous page)

a) Results will be published on the DVFA website www.foedevarestyrelsen.dk (in Danish).

National Action Plans	Target	Status
Campylobacter in broilers 2018-20	21	
Flocks at farm	Maintaining low prevalence in flocks of 17.3%	The prevalance in flocks in 2021 was 19.1% (Table A9)
Fresh meat at slaughterhouse	Reduction of the relative human risk (RR) by 50% compared to the level in 2013ª	A reduction in relative risk (RR) compared to the level in 2013 was reduced by 47%
Salmonella in poultry ^b		
Laying hen flocks of Gallus gallus	Initially eradication, later a reduction strategy in the table egg production	4 positive flocks (0.9%) (Table A5-A6) Eggs from positive flocks are destroy- ed or heat treated
Carcases at slaughterhouse	Initially eradication, later a reduction strategy in the broiler production Zero-tolerance in Danish broiler meat.	0 positive batches (Table A7) Positive batches are heat treated
Salmonella in pigs 2014-2017		
Carcases at slaughterhouse	Max. 1% Salmonella at carcase level	0.7% (Table A11)
Salmonella Dublin in cattle 2021-2	025	
Herds at farm	Eradication of S. Dublin in all herds, i.e. all herds in level 1°	10.1% of milk-producing herds and 2.3% of non-milk producing herds are in level 2 (Table A13)
EU Regulations		
Regulation (EC) No. 1190/2012		
Breeding and fattening turkey flocks	Max. 1% positive for <i>S</i> . Enteritidis and <i>S</i> . Typhimurium ^d	No fattening flocks positive with tar- get serovars (N=106) (Table A8)
Regulation (EC) No. 200/2010		
Breeding flocks of Gallus gallus	Max. 1% adult flocks positive for S. Typhimurium ^d , S. Enteritidis, S. Hadar, S. Infantis and S. Virchow	0.3% (1 flock) (Table A5 and A7)
Regulation (EC) No. 1168/2006		
Laying hen flocks of <i>Gallus</i> gallus	MS specific targets, for Denmark: Max. 2% adult flocks positive for <i>S.</i> Typhimurium ^d and <i>S.</i> Enteritidis	0.5% (2 flocks) positive with target serovars (Table A5)
Regulation (EC) No. 646/2007		
Broiler flocks of Gallus gallus	Max. 1% positive <i>S.</i> Typhimurium ^d and <i>S.</i> Enteritidis	0.1% (4 flocks) positive with target serovars (Table A7)

Table A25. Status on targets for Campylobacter and Salmonella, 2021

a) 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.

b) Supplementary to EU-regulations.

c) See Table A32 for explanation of the herd levels.

d) Including the monophasic variant of S. Typhimurium (S. 1,4,[5],12:i:-).

Monitoring and surveillance programmes

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

Table A26. Overview of notifiable and non-notifiable human diseases presented in this report, 2021

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

Pathogen	Notifiable	EU legislation	Danish legislation
Bacteria			
Brucella spp.	1920ª		
Cattle	0BF in 1979 ^b	Regulation (EU) 2021/620	Order no 1485 of 12/12/2019
Sheep and goats	ObmF in 1995 ^c	Regulation (EU) 2021/620	Order no 1486 of 12/12/2019
Pigs	No cases since 1999	Regulation (EU) 2021/620	Order no 1392 of 12/12/2019
Campylobacter spp.	no	-	-
Chlamydophila psittaci	-	-	-
Birds and poultry	1920	-	Order no 1385 of 12/12/2019
Listeria monocytogenes	no	-	-
<i>Leptospira</i> spp. (only in production animals)	2003	-	Order no. 1171 of 17/7/2020
Mycobacterium bovis/tu- berculosis	1920ª		-
Cattle	0TF in 1980 ^d	Decision 2003/467/EC	Order no. 1447 of 12/12/2019
Coxiella burnetii	2005	-	Order no. 1171 of 17/7/2020
Salmonella spp.	1993º		
Cattle		-	Order no. 1055 of 31/05/2021
Swine		-	Order no. 1079 of 1/6/2021
Eggs for consumption		-	Order no. 499 of 23/3/2021
Hatching eggs		-	Order no. 782 of 2/6/2020
Poultry for slaugther		-	Order no. 1819 of 2/12/2020
STEC	no	-	-
Yersinia enterocolitica	no	-	-
Parasites			
Cryptosporidium spp.	no	-	-
Echinococcus multilocularis	2004	Regulation (EU) 2016/429	Order no. 1171 of 17/7/2020
Echinococcus granulosus	1993	Regulation (EU) 2016/429	Order no. 1171 of 17/7/2020
Trichinella spp.	1920ª	Regulation (EU) 2015/1375	Order no. 1714 of 15/12/2015
Viruses			
Lyssavirus (Rabies)	1920	-	Order no. 1454 of 12/12/2019
Prions			
TSE			
Sheep and goats	yes	Regulation 999/2001/EC (as amended)	Order no. 1491 of 12/12/2019
BSE			
Cattle	yes ^f	Regulation 999/2001/EC (as amended)	Order no. 1442 of 11/12/2019

Table A27. Overview of notifiable and non-notifiable animal diseases presented in this report, 2021

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 Commission implementing regulation (EU) 2021/620. The disease has never been detected in sheep or goat.

d) Officially Tuberculosis Free (OTF) implementing regulation (EU) 2021/620, 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.

Time	Samples	Material	Material
	taken		
Rearing flocks		Grandparent generation	Parent generation
Day-old ^{a,b,c}	Per delivery	5 transport crates from one delivery: cra- te liners (>1 m ² in total) or swab samples (>1 m ² in total). Analysed as one pool	5 transport crates from one delivery: cra- te liners (>1 m ² in total) or swab samples (>1 m ² in total). Analysed as one pool
1st & 2nd week ^{b, c}	Per unit	-	2 pairs of boot swabs (analysed as one pool) or 1 faecal sample of 60 g
4th week ^{a,b,c}	Per unit	5 pairs of boot swabs (analysed as two pools), or 2 faecal samples consisting of 150 g each (no pooling)	2 pairs of boot swabs (analysed as one pool) or 1 faecal sample of 60 g
8th week ^{b,c}	Per unit	2 pairs of boot swabs (analysed as one pool) or 1 faecal sample of 60 g	2 pairs of boot swabs (analysed as one pool) or 1 faecal sample of 60 g
2 weeks prior to moving ^{a.c.d}	Per unit	5 pairs of boot swabs (analysed as two pools), or 2 faecal samples consisting of 150 g each (not pooled) or 2 pairs of boot swabs (analysed as one pool) and 1 dust sample	2 pairs of boot swabs (analysed as one pool) or 1 faecal sample of 60 g
Adult flocks		Grandparent generation	Parent generation
After each hatch ^{b,c,}	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 ^{b,c,e}	Per unit	-	5 pairs of boot swabs (analysed as two pools), or 2 faecal samples consisting of 150 g each (not pooled) or 2 pairs of boot swabs (analysed as one pool) and 1 dust sample
Every 2 weeks ^e	Per unit	5 pairs of boot swabs (analysed as two pools), or 2 faecal samples consisting of 150 g each (not pooled) or 2 pairs of boot swabs (analysed as one pool) and 1 dust sample	-
0-4 weeks af- ter moving, 8-0 weeks before slaughter	Per unit	5 pairs of boot swabs (analysed as two pools), or 1 faecal sample consisting of 2x150 g	5 pairs of boot swabs (analysed as two pools), or 1 faecal sample consisting of 2x150 g
22-24 weeks after moving ^e	Per unit	5 pairs of boot swabs (analysed as two pools), or 2 faecal samples consisting of 150 g each (not pooled) or 2 pairs of boot swabs (analysed as one pool) and 1 dust sample	5 pairs of boot swabs (analysed as two pools), or 2 faecal samples consisting of 150 g each (not pooled) or 2 pairs of boot swabs (analysed as one pool) and 1 dust sample
After positive findings ^{c,d,f}	Per unit	5 pairs of boot swabs (analysed as two pools), 2 dust samples (250 ml) and 5 birds (analysed for antimicrobial substan- ces)	5 pairs of boot swabs (analysed as two pools), 2 dust samples (250 ml) and 5 birds (analysed for antimicrobial substan- ces)

Table A28. Salmonella surveillance programme for the rearing flocks and adult flocks of the grandparent and parent generation of the broiler and table egg production, 2021

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 Danish Order no. 782 of 02/06/2020.

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

e) Sampling requirements set out by Danish Order no. 782 of 02/06/2020, changes in sampling requirements were in effect from July 2020. The first six months of 2020, samples were collected according to Danish Order no. 1423 of 30/11/2018.

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

Time	Samples taken	Material
Salmonella		
15 - 21 days before slaughter ^{a,b,c}	Per flock	5 pairs of boot swabs. Herds up to 500 animals: the 5 samp- les can be pooled in to 2 pools
7 - 10 days before slaughter ^{d,e}	Per flock	5 pairs of boot swabs. Herds up to 500 animals: the 5 samp- les can be pooled in to 2 pools
After slaughter ^{b,d,f}	Per batch	From slaughterhouses slaughtering 1,000 chickens or hens per day or more: 300 neck skin samples of 1 gram, pooled into subsamples of 60 gram from one batch per week. From slaughterhouses slaughtering less than 1,000 chickens or hens per day: 15 neck skin samples of approx. 10 gram pooled into 5 subsamples of 25 gram from one batch every fifth day of slaughter
Campylobacter		
After slaughter ^{b,d}	Per flock	12 cloacal swabs from 24 animals, analysed in one pool ^{gh}
After slaughter ^{ь,f}	Per batch	From slaughterhouses slaughtering 1,000,000 chickens or more per year: 15 neck skin samples of approx. 10 gram, poo- led into five subsamples of 25 gram from one batch per week. From slaughterhouses slaughtering less than 1,000,000 chickens per year and more than 10,000: 15 neck skin samp- les of approx. 10 gram pooled into 5 subsamples of 25 gram from one batch every tenth day of slaughter

Table A29. Salmonella and Campylobacter surveillance programme for the broiler flocks, 2021

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

b) Samples collected by the food business operator.

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

d) Sampling requirements set out by Danish Order no. 1819 of 02/12/2020.

e) Samples are collected by a representative of the slaughterhouse, laboratory 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.

Time	Samples taken	Material
Pullet-rearing		
Day-old ^{a,b}	Per delivery	5 transport crates from one delivery: Crate liner (> 1 m ² in total) or swab samples (> 1 m ² in total) (Analysed as one pool)
4, 8 and 10 weeks old and 1 week before moving ^{a,b}	Per flock	5 pairs of boot swabs (analysed as two pools) or 5 faecal samples of 60 gram
2 weeks before moving ^{a,c}	Per flock	5 pairs of boot swabs (analysed as two pooled samples) or 5 faecal samples of 60 gram.
Table egg layers (Production for certi	fied packing statio	ns)
24 weeks old ^{a,c}	Per flock	2 pairs of boot swabs (analysed as one pool) or 1 faecal sample consisting of $2x150$ g. 250 ml (100 g) dust or a dust sample by a cloth of min. 900 cm ²
Every 2 weeks from age 20 weeks ^{a,b,d,}	Per flock	2 pairs of boot swabs (analysed as one pool) or 1 faecal sample consisting of 2x150 g.
After positive serological findings ^c	Per flock	5 pairs of boot swabs (analysed as two pools) or 5 faecal samples consisting of 60 gram each
After positive findings of other serotypes than <i>S.</i> Enteritidis, <i>S.</i> Hadar, <i>S.</i> Infantis, <i>S.</i> Virchow or <i>S.</i> Typhimurium including the monop- hasic variant <i>S.</i> 1,4,[5],12:i:- ^c	Per flock	5 pairs of boot swabs (analysed as two pool) or 5 faecal samples consisting of 60 gram each, 2 dust samples (250 ml) and 5 birds (analysed for antimicrobial substances) ^g
Barnyard and hobby flocks ^e		
Every 9 weeks ^{a,b,f}	Per flock	2 pairs of boot swaps (analysed as one pooled sample) or 2 faeces samples consisting of 60 gram each (analysed as one pooled sample).

Table A30. Salmonella surveillance programme for the pullet-rearing, table egg layer and barnyard/hobby flocks in the table egg production, 2021

a) Sampling requirements set out by Danish Order no. 1818 of 02/12/2020 and no. 499 of 23/03/2021.

b) Samples collected by the food business operator.

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

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, who are informed about the fact that no Salmonella control was performed.

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

Table A31. Salmonella surveillance programme for the turkey flocks, 2021

Time	Samples taken	Material
Turkey production		
Max. 21 days before slaughter ^{a,b}	Per flock	2 pairs of boot swabs. Analysed individually

a) Sampling requirements set out by Regulation (EC) 1190/2012 and Danish Order no. 1819 of 02/12/2020. b) Samples collected by the food business operator or the local food control offices.

Source: Danish Veterinary and Food Administration

Table A32. Salmonella surveillance programme^a for the cattle production, 2021

No. of samples	Samples taken	Purpose/Comment
Milk producing herds		
4 samples distributed over 18 maximum months	Bulk tank samples	Calculation of herd level ^b
Non-milk producing herds		
1 sample every 3 months at slaughter ^c	Blood samples	Calculation of herd level ^b
Sampling once or twice a year in heifer herds on rearing farms, depending on whether the heifers originate from a single or several dairy herds	Blood samples	Calculation of herd level ^{b,d}
Beef carcases at the slaughterhou	se	
5 samples daily, pooled into one analysis	Swab samples from 4 designated areas after 12 hours chilling (4x100cm ²)	Slaughterhouses slaughtering 7.500 or more cattle per year
5 samples every second month, analysed individually	Swab samples from 4 designated areas after 12 hours chilling (4x100cm ²)	Slaughterhouses slaughtering 2.500 or more and less than 7.500 cattle per year
5 samples every 6th month, analysed individually	Swab samples from 4 designated areas after 12 hours chilling $(4x100cm^2)$	Slaughterhouses slaughtering 250 or more and less than 2.500 cattle per year
No sampling		Slaughterhouses slaughtering less than 250 cattle per year

a) Danish Order no. 1055 af 31/05/2021. It is compulsory to have an action plan to eradicate *Salmonella* Dublin in Level 2 herds. Before the 1st of July2021, the order no. 1791 af 02/12/2020 var applicable, in which sampling of heifer herds weren't mandatory.

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.

c) No samples are taken, if the herd has been tested for S. Dublin within the last 3 months.

d) The number of samples from heifers depend on herd size.

Time	Samples taken	Purpose/Comment
Breeding and multiplier herds		
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) ^b
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 ^c
Sow herds		
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.</i> Typhimu- rium, <i>S.</i> Infantis, <i>S.</i> Derby and <i>S.</i> Choleraesuis are considered posi- tive for the following 5 years ^d	No samples are collected from the herd during the 5-year period when the herd is considered po- sitive, unless the herd is proven negative	Reduce repeated sampling in positive herds infected with a persistent serotype
Slaughter pigs, herds		
At slaughter	Meat juice, 60-100 samples per herd per year. Herds in RBOV ^e : one meat juice sample per month	Calculation of slaughter pig index based on the mean proportion of positive samp- les from the last three months with most weight to the result from the most recent month (1:1:3) ^f . Assigning herds to level 1-3 and assigning herds to risk-based surveillance (RBOV) ^e
Slaughter pigs, animals		
At slaughter ^f	Caecum samples, avg. 25 samples per month, 12 months per year	Random collection of samples for monito- ring of the distribution of serotypes and antimicrobial resistance.
Pork carcases at the slaughterhouse		
5 samples daily, pooled into one analysis [®]	Swab samples from 4 designa- ted areas after 12 hours chilling (4x100cm ²)	Slaughterhouses slaughtering more than 30.000 pigs per year
5 samples every second month	Swab samples from 4 designa- ted areas after 12 hours chilling (4x100cm ²)	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 designa- ted areas after 12 hours chilling (4x100cm ²)	Slaughterhouses slaughtering 1.000 or more pigs and less than 10.000 pigs per year
No sampling		Slaughterhouses slaughtering less than 1000 pigs per year

Table A33. Salmonella surveillance programme^a for the pig production, 2021

a) Sampling requirements set out by Danish Order no. 1792 of 02/12/2020, replaced by Danish Order no. 1079 of 01/06/2021.

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 type of Salmonella.

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

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.

f) Centrally coordinated study (Table A24).

g) If a slaughterhouse, within the last month, finds a sample positive for Salmonella and at the same time has a Salmonella prevalence above or equal to 2% (12month average), the sampling frequency doubles to 10 samples daily, pooled into two analyses with 5 samples in each.

Methods	Human	Food	Animal
Salmonella enterica			
Serotyping	All isolates (mainly WGS)	All isolates (by WGS) ^a	All isolates (by WGS)
Antimicrobial resistance testing	All <i>Salmonella</i> except <i>S.</i> Enteritidis	Almost all isolates	Isolates for DANMAP and EFSA
MLVA	In relation to International outbreak	None	None
WGS	All isolates	All isolates ^a	All isolates
Campylobacter coli/jejuni			
Antimicrobial resistance testing	Isolates from 4 districts for DANMAP surveillance	Isolates for DANMAP and EFSA	Isolates for DANMAP and EFSA
WGS	Subset representing 10-15% of isolates	Few (isolates from chilled chicken meat) ^a	None
STEC			
Serotyping	All isolates (mainly WGS)	All isolates (by PCR & WGS)	All 0157 isolates
Virulence profile	All isolates (mainly WGS)	All isolates (by PCR & WGS)	All 0157 isolates
WGS	All isolates	All isolates	None
Listeria			
WGS	All isolates	Selected isolates (ST typing and outbreak investigations)	None
Yersinia enterocolitica			
Serotyping	All pathogenic isolates sent to SSI	None	None
WGS	Outbreaks investigations, research	None	None

Table A34 Tvn	ing methods used	in the surveillanc	a of foodborna	nathonens in	Denmark 2021
тиріе Аз4. тур	ing memous useu	III the surveinunc	e oj jooubonne	pulliogens in	Definition K, ZOZI

a) Other commercial laboratories have been used for some centrally coordinated studies. Alternative methods (not listed here) may have been used for these samples

Source: Statens Serum Institut and the Laboratory of the Danish Veterinary and Food Administration

Population and slaughter data

Table A35. Human population, 2021

Age groups (years)	Males	Females	Total
0-4	159,616	151,094	310,710
5-14	326,391	309,500	635,891
15-24	364,505	348,898	713,403
25-44	738,911	716,909	1,455,820
45-64	773,432	773,288	1,546,720
65+	547,750	639,895	1,187,645
Total	2,910,605	2,939,584	5,850,189

Source: Statistics Denmark, 1 July 2021

Table A36. Number of livestock establishmer	nts, livestock and animals slaughtered, 2021
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	No. of establishments	Livestock (capacity)	Number slaughtered
Slaughter pigs	7,814	13,629,282	18,592,853
Cattle	16,285	1,498,130	452,600
Broilers	274	19,601,167	102,212,100
Layers (excl. barnyard)	183	5,063,142	-
Turkeys	26	393,650	6,200
Sheep & lambs	6,298	131,614	64,000
Goats	3,197	18,698	-
Horses	-	-	761

Source: Statistics Denmark and Danish Veterinary and Food Administration - the Central Husbandry Register, May 2022

Table A37. Number of establishments,	flocks and livestock capaci	ity in the broiler production.	2021
Table (15), Namber of establishments,	JIOCKS and INCSTOCK Capaci	nty in the biolici production, i	LOLI

	No. of establishments	No. of flocks	Livestock (capacity)
Rearing period (grandparent)	2	10	50,000
Adult period (grandparent)	4	10	82,500
Rearing period (parent)	21	91	764,310
Adult period (parent)	47	138	1,115,600
Hatcheries	5	0	0
Broilers	274	653	19,601,167

Source: Danish Veterinary and Food Administration, March 2022

Table A38 Number of establishments, flocks and livestock capacity in the table egg production, 2021

	No. of establishments	No. of flocks	Livestock (capacity)
Rearing period (grandparent)	2	2	47,500
Adult period (grandparent)	2	7	75,000
Rearing period (parent)	4	4	30,800
Adult period (parent)	9	10	60,400
Hatcheries	8	0	0
Pullet-rearing	46	68	1,269,249
Layers (excl. barnyard)	183	294	5,063,142

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