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Annual Report on Zoonoses in Denmark 2025

DTU National Food Institute

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This is an official publication from the
DTU National Food Institute, Technical
University of Denmark, the Danish
Veterinary, Food, Agriculture and Fisheries Agency, and
Statens Serum Institut.

Suggested citation:
Anonymous, 2026, Annual Report on Zoonoses
in Denmark 2025, DTU National Food Institute,
Technical University of Denmark.

Reprints can be ordered from:
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Layout: Camilla Thougaard Vester
Photos: Colourbox
Printing: Stibo Complete A/S

1. edition

ISBN: 978-87-7586-087-6

The report is also available at:
www.food.dtu.dk

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Introduction

For more than 30 years the Annual Report on Zoonoses in Denmark has provided highlights of the One Health collaboration on zoonoses and supported decision making for policymakers, public health, industry, and research. The report is produced annually in a collaboration between the National Food Institute at the Technical University of Denmark, Statens Serum Institut, and the Danish Veterinary, Food, Agriculture and Fisheries Agency, with contributions from relevant collaborators.

Food- and waterborne infections

Campylobacter continues to be the most common cause of foodborne illness in humans, with a total of 5,714 reported cases in 2025, higher than previous years (5,546 in 2024 and 5,186 in 2023). The number of reported *Salmonella* cases in 2025 was 1,051, which is lower than in 2024 (1,266 cases). A total of 84 cases of *Listeria monocytogenes* were reported in 2025, representing the highest number since 2022, an increase of almost 38% compared with 2024.

In 2025, 56 foodborne outbreaks were reported, resulting in 1,109 human infections. The number of reported foodborne outbreaks was similar to previous years, with 55 outbreaks reported in 2024. Outbreaks were caused by a range of foodborne pathogens, including *Campylobacter*, *Salmonella*, *Listeria monocytogenes*, Norovirus, pathogenic *E. coli*, spore-forming bacteria, *Cryptosporidium*, and Hepatitis A. Three local outbreaks were caused by lectins from improperly prepared beans.

Thirteen outbreaks of *Salmonella* were reported in 2025. One local outbreak caused by *Salmonella* Enteritidis was linked to improperly handled chicken meat. The remaining 12 outbreaks of *Salmonella* were national, with two large outbreaks linked to green produce. The first of these was part of a recuring international outbreak caused by *Salmonella* Strathcona in small tomatoes, and the later was caused by *Salmonella* Typhimurium. While its exact source could not be clearly identified, several types of imported lettuce were suspected.

Six Norovirus outbreaks were reported in 2025, a decrease from previous years, all point source outbreaks related to catering or restaurants.

A marked increase of reported *Campylobacter* cases was observed during summer and autumn, primarily driven by two large outbreaks from chicken meat. The number of *Campylobacter* outbreaks remained stable, with 11 outbreaks reported in 2025. Nine outbreaks were linked to chicken meat.

In 2025, six national outbreaks with *Listeria monocytogenes* were reported. The largest outbreak, with 11 reported cases, was caused by *Listeria* in ready-to-eat fish patties.

Surveillance and control of zoonoses in animals, food, and food production

Denmark continued to operate integrated, coordinated surveillance and control programmes for zoonotic pathogens in humans, animals, food, and feed. The surveillance covers both notifiable and non-notifiable zoonotic pathogens and is based on collaboration between authorities, laboratories, and industry.

In 2025, adjustments were introduced to the surveillance of *Salmonella* in pigs. Human salmonellosis attributable to Danish pork remains low. Herd-level surveillance of *Salmonella* in pigs was discontinued following a risk assessment and now focuses on surveillance of pork carcasses and prevalence-based monitoring of caecum samples at slaughter-level. This highlights that surveillance strategies can be adjusted when supported by robust evidence and continued monitoring and surveillance strategies. Monitoring at critical control points in the food chain remains central for early detection of unfavourable trends.

Zoonotic infections transmitted via non-food pathways remain epidemiologically relevant. In 2025, events included highly pathogenic avian influenza (HPAI) spillover to mammals, a *Brucella suis* biovar 2 outbreak in pigs, and continued detection of *Echinococcus multilocularis* in wildlife. Wildlife surveillance and national coordination support detection and management of these events.

The Annual Report on Zoonoses in Denmark 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 2025. 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

Surveillance of vector-borne zoonoses continued to contribute important contextual information on zoonotic risks. Climatic conditions influenced vector abundance in 2025, with a warm and dry spring resulting in low mosquito and biting midge abundance, the lowest number of mosquitoes recorded since 2011. No circulation of West Nile virus was detected in mosquitoes in 2025; however, serological evidence of prior West Nile virus infection was identified in horses in the southern part of Denmark for the first time in Denmark. Tick- and midge-borne risks remained spatially and environmentally driven, with no tick-borne encephalitis virus detected in ticks in 2025 and a substantial decline in bluetongue outbreaks compared with 2024.

Whole genome sequencing and cross-sectoral collaboration

The joint-authority sequence platform "national Sequence-based surveillance Of Foodborne Infections" (SOFI) was implemented as a tool for real-time whole genome sequencing (WGS) based surveillance of foodborne infections in Denmark on 1 January 2025. TThe platform is owned by Statens Serum Institut (SSI) and the Danish Veterinary, Food, Agriculture and Fisheries Agency (DVFAFA), and was developed by the two institutions together with the National Food Institute at the Technical University of Denmark (DTU National Food Institute) and an external IT partner. SOFI enables cross-sectoral data sharing as well as preparedness for timely outbreak detection and investigation. Legal, technical, and organisational frameworks were established to support this collaboration. SOFI represents a concrete operationalisation of WGS-based surveillance in a One Health approach on handling foodborne infections.

Shiga toxin-producing *E. coli* in beef and game meat

Shiga toxin-producing *E. coli* (STEC) remains a zoonotic pathogen of concern in ruminant-derived foods. An ongoing monitoring project by the DVFAFA focuses on detection of STEC in beef and game meat, as well as WGS supported risk assessment. Detection methods for STEC in food can be complex, as official sampling requires accredited standardized methods, including verification of cultivated isolates from STEC PCR-positive samples. Low prevalence was observed in beef, while higher prevalence was detected in game meat, including ready-to-eat products. Game meat represents a distinct risk profile that benefits from targeted surveillance, risk communication, and food safety controls.

International and European perspectives

In 2025, Denmark continued to actively contribute to international guideline development and European research partnerships, which support national surveillance and control strategies. As an example, several Danish research institutions are part of the joined European Partnership on Animal Health and Animal Welfare (EUPAHW). Activities cover zoonotic pathogens, antimicrobial resistance, as well as animal health and welfare surveillance.

The Codex Alimentarius guidelines on safe use and reuse of water in food production, control of *Campylobacter* and *Salmonella* in chicken meat, and food hygiene to control *Listeria monocytogenes,* were updated, providing strengthened guidance to support authorities and food business operators in mitigating microbiological risks.

A tightening of the process hygiene criteria for *Campylobacter* on broiler carcasses came into effect in the European Union on 1 January 2025, strengthening requirements on control measures at slaughterhouse level to reduce consumer exposure.

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 occurring in 2025. Household outbreaks and clusters that are not expected to have a common foodborne source are excluded. Outbreak investigation procedures in Denmark are described in Chapter 7.

In 2025, 56 foodborne outbreaks were reported in FUD (Figure 1.1, Table A3), resulting in 1,109 human infections, with an average of 20 registered human cases per outbreak (range: 2-148). Of the 56 outbreaks, 22 were local or regional outbreaks and 34 were national, two of which were part of international outbreaks. The number of registered foodborne outbreaks in 2025 was similar to that in 2024, when 55 outbreaks were registered. Figure 1.2 presents the number of foodborne outbreaks reported in Denmark over the past five years by pathogen.

1.1 Norovirus outbreaks

Norovirus (NoV) accounted for six foodborne outbreaks in 2025. The number of NoV outbreaks decreased compared with 2024, in which 16 NoV outbreaks were registered. In the largest outbreak in 2025, 148 persons fell ill from salad and pancakes served by a catering company. Kitchen staff had been ill while preparing the food, which was identified as the likely source of contamination (FUD2437). Four out of the six NoV outbreaks were related to ill kitchen staff or an asymptomatic virus carrier among the kitchen staff in catering establishments or restaurants (see Table 1.1 and Table A3).

1.2 *Salmonella* outbreaks

In 2025, 13 *Salmonella* outbreaks were registered in Denmark, which was slightly higher than in 2024, when ten *Salmonella* outbreaks were registered. The largest outbreak, with 49 registered cases in November-December 2025, was due to *Salmonella* Typhimurium sequence type (ST) 19. Despite intensive investigations, including a case-control study, analysis of consumer purchase data, and trace-back efforts, the source of the outbreak could not be identified (FUD2499). However, different types of imported lettuce were suspected.

An outbreak of *Salmonella* Enteritidis, with six registered cases, was found to be local and linked to a chicken

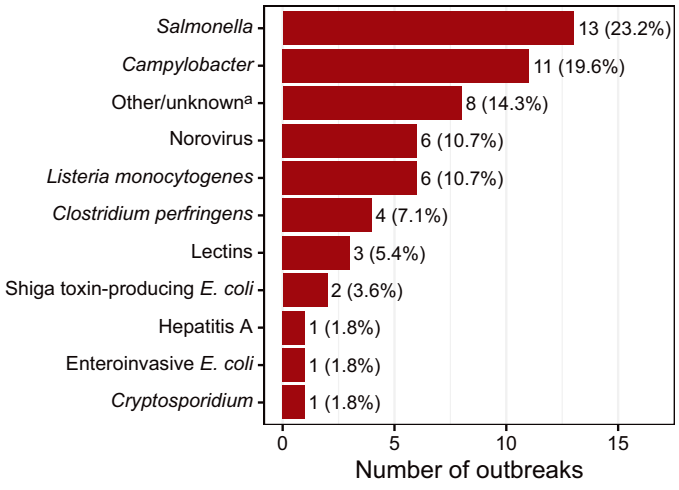

Figure 1.1 Aetiology of the 56 foodborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD), 2025. Percentage of total outbreaks indicated in brackets

a) Other/unknown: 3 outbreaks suspected to be spore-forming bacteria, 5 outbreaks with unknown pathogen

Source: Food- and waterborne Outbreak Database (FUD)

sandwich bar (FUD2432). DVFAFA conducted an inspection of the sandwich bar and identified a process deviation in the handling of chicken meat.

One outbreak caused by *Salmonella* Strathcona was part of a recurring international outbreak, in which small tomatoes from Italy were identified as the source (see box).

1.3 *Campylobacter* outbreaks

During summer and autumn, a marked increase in *Campylobacter* cases was observed compared with previous years. This increase was primarily driven by two large outbreaks caused by *Campylobacter jejuni* ST49 and ST52 (FUD2470 and FUD2462) (see box). A total of 11 *Campylobacter* outbreaks were registered in Denmark in 2025, which was at a similar level to 2024, when 10 outbreaks were registered. All outbreaks were national and caused by *Campylobacter jejuni*. For nine outbreaks, the source was identified as Danish chicken meat, based on whole genome sequencing (WGS) matches between human isolates and food isolates from the same time period.

1.4 *Listeria* outbreaks

Six national outbreaks of invasive *Listeria monocytogenes* were registered in 2025. Several outbreaks were prolonged genetic clusters, with additional cases detected in previous years (FUD2319, FUD2514, FUD2515). Between August and October 2025, 11 cases of invasive *L. monocytogenes* ST7 were identified in Denmark (FUD2467). The patients, were distributed across several regions, with a median age of 75 years (range 30-95 years). Ready-to-eat fish patties from a Danish producer were identified as the source of infection, with bacterial isolates from patients and products found to be genetically identical. The contaminated products were recalled in September 2025.

1.5 Other outbreaks of interest

In July 2025 SSI identified a cluster of *Cryptosporidium parvum* with a novel subtype: IIzeta (FUD2458). In total, 11 cases, aged 22-60 years, were registered between 1 June and 30 July 2025. The outbreak was linked to eating at different canteens within the same company. The source of the outbreak could not be established; however, imported

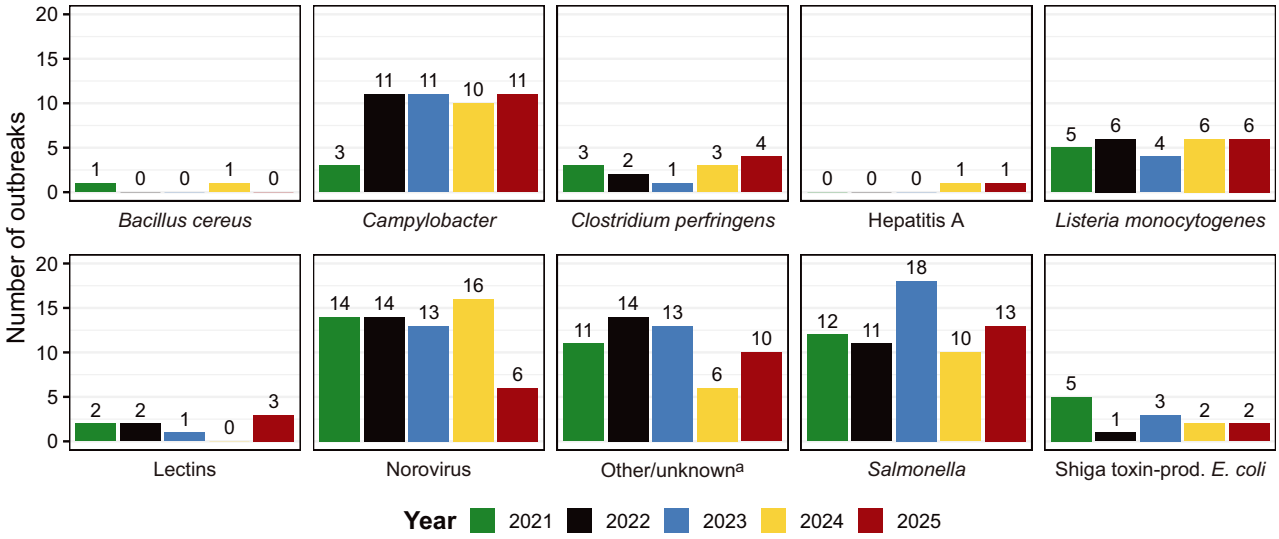

Figure 1.2 Foodborne outbreaks reported in Denmark 2021-2025 by the pathogens causing outbreaks in 2025. Please note that prolonged outbreaks with cases in different years are presented in all relevant years

a) Other/unknown in 2025 : 1 EIEC, 1 Cryptosporidium, *3 outbreaks suspected to be spore-forming bacteria either* Bacillus cereus *and/or* Clostridium perfringens, *5 outbreaks with unknown pathogen*

Source: Food- and waterborne Outbreak Database (FUD)

fresh flat-leafed parsley was identified as a possible source of infection.

An international outbreak of hepatitis A virus genotype 1A was detected in May 2025, with cases reported in nine European countries. In Denmark, seven cases were registered between January and July 2025 (FUD2439). Four cases occurred in children under 15 years of age and three in adult women. Interviews and trace-back investigations did not identify the source of the outbreak; however, fresh imported berries were suspected.

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Table 1.1 Norovirus outbreaks per route of transmission based on number of cases or number of outbreaks, 2023-2025

	2025		2024		2023	
Transmission route/source	No. of outbreaks	No. of persons ill	No. of outbreaks	No. of persons ill	No. of outbreaks	No. of persons ill
Ill kitchen staff or healthy carrier of virus among kitchen staff	4	235	3	57	8	320
Kitchen staff tending to ill persons at home before entering the kitchen	0	0	0	0	0	0
Ill persons/guests attending a buffet			0	0	0	0
Seafood (oysters)	0	0	1	14	5	142
Other route of transmission	0	0	1	15	0	0
Unknown route of transmission	2	71	12	335	0	0
Total	6	306	17	421	13	462

Source: Food- and waterborne Outbreak Database (FUD)

International outbreak of a *Salmonella* Strathcona linked to small tomatoes from Italy

Between November and December 2025, Denmark identified 29 cases of *Salmonella* Strathcona cluster type ST2559#1 (FUD2500). Cases were geographically widespread and affected all age groups, with a median age of 50 years (range 0-87 years). WGS confirmed that the cases belonged to a cluster with closely related isolates. This national outbreak was part of a prolonged multi-country outbreak in Europe, which has been ongoing since 2011.

In a joint rapid outbreak assessment published in October 2025 by the European Centre for Disease Prevention and Control and the European Food Safety Authority at least 437 confirmed cases were reported across 17 EU/EEA countries, as well as additional cases in the United Kingdom and North America, between January 2023 and September 2025 [1].

Epidemiological, microbiological, and traceability investigations conducted across multiple countries consistently identified small tomatoes—particularly originating from Sicily, Italy—as the primary source of infection. The Danish outbreak investigation in 2025 also pointed towards small tomatoes from Sicily, based on a case-control study and trace-back investigations using consumer purchase data. In Sicily, environmental investigations further supported this link, including detection of the outbreak strain in irrigation water at tomato production sites.

The outbreak strain has been associated with recurrent waves of cases for more than a decade, including outbreaks in Denmark in 2011 and 2020, highlighting a persistent contamination within the food chain [2].

Overall, this event illustrates an ongoing cross-border foodborne outbreak, driven by a likely common source, and emphasizes the need for coordinated surveillance, environmental investigations, and control measures at primary production level to prevent future outbreaks.

Two severe *Campylobacter* outbreaks traced to Danish chicken meat

From July to December 2025, Denmark experienced two unusually large, concurrent outbreaks caused by *Campylobacter jejuni* ST49 and ST52 (FUD2470 and FUD2462) (Figure 1.3). In the two outbreaks, 89 and 31 cases were identified, respectively. Under the current national surveillance system, only 10-15% of positive *Campylobacter* samples are sequenced. Using a probability-based approach, the true number of laboratory-confirmed outbreak cases was therefore estimated to be approximately 900 cases in total.

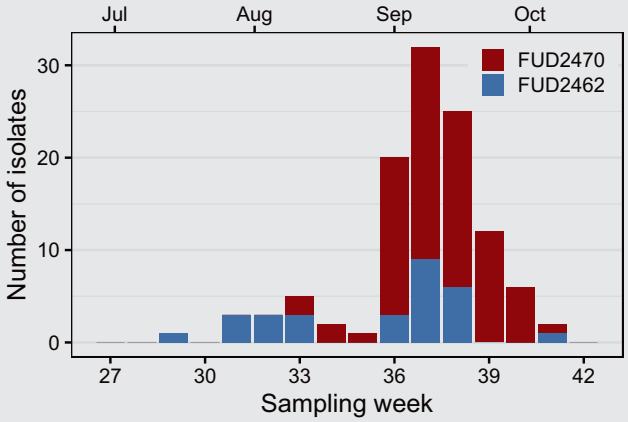

Figure 1.3 Number of Campylobacter jejuni *isolates in FUD2470 and FUD2462 in Denmark by week of sampling, July 1st - October 15th, 2025*

The outbreaks affected people across the country and were associated with more severe clinical outcomes than typically observed for *Campylobacter* infections. Overall, 45 cases (40%) required hospitalisation and 16 cases (14%) had a positive blood culture [3]. Possible contributing factors to the increased severity include higher exposure doses from contaminated products, clone-specific virulence, and/or wider dissemination within the food chain, as multiple slaughterhouses and farms were implicated.

WGS-based matching between human isolates and isolates from Danish chicken meat, identified through the DVFAFA monitoring, established Danish chicken meat as the source of both outbreaks. Control measures included increased focus on slaughter hygiene among broiler producers and at slaughter, follow-up testing of implicated farms to ensure that the specific *Campylobacter* types did not persist, and several consumer-targeted social media campaigns emphasising safe handling and thorough cooking of chicken meat.

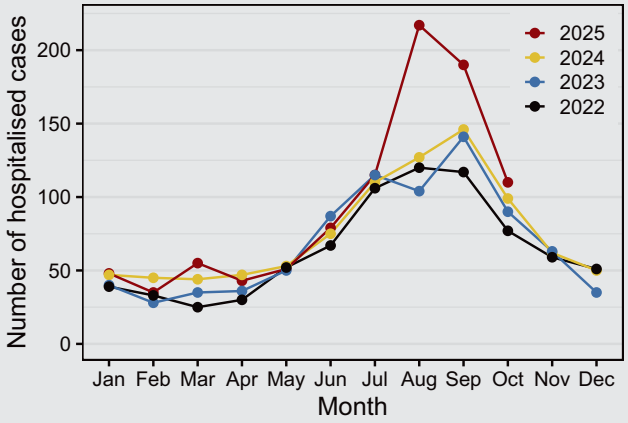

Figure 1.4 Total number of hospitalised Campylobacter *cases by month of sampling, 2022-October 2025*

Multi-country foodborne event caused by cereulide in infant formula products

A multi-country foodborne event was linked to infant formula contaminated with cereulide, a toxin produced by *Bacillus cereus*, prompting widespread product recalls from December 2025 [4]. Cases of gastrointestinal illness in infants were reported in several European countries. The majority of infants experienced mild symptoms; however, some required hospitalisation for management of dehydration.

In Denmark, the disease is not notifiable, and there is no routine diagnostic test for investigating the presence of cereulide in human samples. Consequently, no confirmed cases have been registered. However, DVFAFA received reports from parents of infants who developed gastrointestinal symptoms after consuming infant formula, following the recall initiated in December 2025.

The contamination was traced to a single producer supplying arachidonic acid oil, an ingredient used in infant formula production and distributed across multiple countries and brands. A new supplier has since been introduced. The investigation was challenging due to the non-specific nature of the symptoms, overlap with the winter virus season, and the limited capacity of European laboratories to detect cereulide in clinical samples. Following extensive product recalls and risk assessments, the overall likelihood of infant formula-related exposure to cereulide was assessed as low.

2. Other zoonotic outbreaks in animals

By Heidi Huus Petersen (hepet@fvst.dk)

Zoonoses transmitted via non-food pathways represent an important component of Denmark's national zoonosis surveillance. These infections are transmitted through diverse pathways, including direct or indirect contact with animals, vector-borne exposure, or environmental sources, rather than via contaminated food or drinking water. Although such outbreaks typically occur sporadically and involve relatively few cases, they remain epidemiologically significant due to changing ecological conditions, animal population dynamics, and human behaviour that may influence transmission patterns. This section provides an overview of some of the non-food- and non-waterborne zoonoses relevant for Denmark during the reporting year.

2.1 Highly pathogenic avian influenza (HPAI) in mammals

In 2025, a single case of highly pathogenic avian influenza (HPAI) H5N1 was detected in a red fox (*Vulpes vulpes*) in Denmark, marking a spillover event from birds to mammals. This occurred against the backdrop of numerous HPAI outbreaks in wild and domestic birds across the country, reflecting the continued high viral pressure in avian populations.

HPAI viruses are known to infect both wild and domestic mammalian species. In Denmark, HPAI has not been detected in companion animals, but infections have previously been identified in seals [1] and foxes [2] from Denmark.

Although mammalian infections occur infrequently in Denmark, they are epidemiologically important due to the potential for viral adaptation in new hosts. Avian influenza viruses are now detected year-round in wild birds in Denmark, and are increasingly also detected in mammals, highlighting the relevance of a One Health approach to surveillance.

Continuous surveillance in wildlife is therefore conducted to identify mammalian HPAI cases. This is important to assess any shifts in epidemiological patterns or pathogenicity, and to improve understanding of which mammalian wildlife species may contribute to transmission between environments, including introduction into poultry flocks.

As shown in tables A20 and A21, several animals were examined for HPAI in Denmark in 2025, including domestic and wild mammals.

2.2 Brucella suis outbreak

For the first time in more than 25 years, Denmark experienced an outbreak of brucellosis in domestic pigs. Brucellosis is a zoonotic disease caused by bacteria of the genus *Brucella*, which comprises several species with varying host preferences, but capable of infecting multiple animal species including humans.

In animals, brucellosis is primarily characterized by abortions or other reproductive failure. In humans, symptoms include intermittent or irregular fever, headache, weakness, profuse sweating, chills, weight loss and general aching. Veterinarians, farmers, and abattoir workers are at increased risk of infection due to their contact with infected animals, aborted foetuses or placentas. No transmission to humans was detected in connection with the outbreak.

The outbreak in Denmark was caused by *Brucella suis* biovar 2, which primarily affects members of the *Suidae* family. Biovar 2 is also naturally present in wild European hares (*Lepus europaeus*). While humans can be infected with *B. suis* biovar 2, it is rarely pathogenic for humans compared with biovars 1 and 3, which are highly pathogenic to humans.

In total, the Danish outbreak involved six establishments: one establishment where late-term abortions were observed, and five establishments that received pigs from the affected establishment. The sows involved in the outbreak were housed on paddocks. Although the exact transmission route could not be determined, contact with infected wildlife was considered a likely source of infection. The outbreak was resolved in November 2025, and no further suspected or confirmed cases have been detected since. However, the prevalence of *B. suis* in Danish wildlife remains uncertain, and consequently the risk of transmission from wildlife to pigs cannot be fully assessed.

2.3 Echinococcus multilocularis

Echinococcus multilocularis remains a relevant parasitic zoonosis in Denmark, with a persistent hyperendemic focus in the Højer area in southwestern Denmark. In recent years, the parasite has also been detected at three separate locations in northern Jutland, indicating a gradual geographic expansion. Despite this wider distribution in wildlife, no infections have been detected in humans or domestic dogs.

As a severe zoonotic disease in humans characterized by an exceptionally long incubation period—often taking many years before clinical signs appear—its presence in wildlife continues to warrant close monitoring and sustained surveillance efforts.

In 2025, *Echinococcus multilocularis* was detected in four red foxes in Denmark, supporting evidence of its continued circulation in wildlife populations.

2.4 Rabies

Rabies is a viral disease affecting the central nervous system of mammals, and among the most severe zoonotic diseases. Rabies virus is present in high concentrations in saliva and brain tissue of infected animals and is most commonly transmitted by bites from infected dogs. Dogs are the primary source of human infections globally, but bats also represent an important reservoir in certain regions. Rabies infected wildlife species can create multiple opportunities for cross species transmission, primarily affecting domestic animals and humans [3].

In Denmark, rabies is monitored through passive surveillance in all animal species, and by active surveillance in bats.

The genus Lyssavirus comprises genetic lineages, including classical rabies virus and European bat lyssavirus (EBLV). Carnivores, particularly species within the *Canidae* family, are the principal reservoir hosts for the classical rabies virus, whereas bats are the principal reservoir host for EBLV.

In recent years, no cases of rabies have been detected in either domestic or wild animals in Denmark. The latest outbreak of classical rabies in domestic animals in Denmark occurred in 1982, and in wild animals in 1981 [4]. Denmark has been officially free from infection with classical rabies virus since 2021. EBLV occurred in Denmark for a longer period. The most recent case of EBLV in domestic animals was diagnosed in 2002, and the latest cases of EBLV in Danish bats were diagnosed in 2009 and 2015, respectively [5].

2.5 Other zoonoses

Tularemia is a zoonosis caused by the bacteria *Francisella tularensis*. The infection occurs naturally in wildlife, mainly in lagomorphs and rodents, but has also been reported in other mammalian species. Transmission occurs mainly through vectors or direct contact with infected animals [6].

Tularemia is a well recognised zoonosis in Denmark, and cases in hares are detected intermittently through the national wildlife surveillance system. Historical findings in Danish hares demonstrate that *F. tularensis* circulates endemically in wildlife reservoirs, with sporadic detections reported over time. Consistent with this pattern, tularemia was also identified in two hares in 2025. The recurrent, but irregular occurrence highlights the continued need for surveillance, given the potential zoonotic risk to humans.

Ornithosis (psittacosis), caused by the bacteria *Chlamydia psittaci*, remains an important zoonotic infection due to its ability to transmit from birds to humans, typically associated with exposure to infected captive birds. Although ornithosis is a well-recognised zoonotic risk in Denmark, no outbreaks were detected in animals in 2025. The absence of documented animal cases underscores the effectiveness of ongoing surveillance, but continued vigilance is essential, as infections in birds may be subclinical and human cases can occur sporadically without clear epidemiological links.

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The national coordination structure for zoonotic diseases, KOZO, highlighted as an example of good practice

By the National Coordination Structure for Zoonotic Diseases Core Group (KOZO)

The national coordination structure for zoonotic diseases (KOZO) continues to support cross-sector collaboration between key actors. The KOZO core group includes expertise in human health, animal health, wildlife health and the environment, with permanent representatives from the Danish Veterinary, Food, Agriculture and Fisheries Agency, Statens Serum Institut, Danish Health Authority, Danish Patient Safety Authority, Agency for Green Transition and Aquatic Environment, Danish Medicines Agency and the University of Copenhagen.

The KOZO core group meets monthly, and ad hoc as needed, to discuss emerging signals, risk assessments, outbreak management, scenarios, and communication. A steering committee at director level meets twice a year to address overall and strategic matters. As a coordinating forum, KOZO ensures access to updated information and perspectives across sectors, supporting a shared understanding of the risk picture and coordination of responses.

KOZO was active throughout 2025, with information shared on several zoonotic diseases, including zoonotic influenza, brucellosis, rabies and mpox. The themes of KOZO workshops of 2025 were One Health surveillance of zoonotic pathogens with focus on wildlife, and West Nile virus.

KOZO work has been highlighted as an example of good practice, for example in the Copenhagen Recommendations from the One Health Conference, which was hosted by the Danish Minister for Food, Agriculture and Fisheries in collaboration with the WHO Regional Office for Europe, under Denmark's Presidency of the Council of the European Union [1].

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3. Shiga toxin-producing *E. coli* (STEC) in beef and game meat: Methods, findings, and interpretation

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3.1 Characteristics and natural reservoirs

Escherichia coli are Gram-negative bacteria known to inhabit the intestinal tract of warm-blooded animals. Although the majority of *E. coli* strains behave as harmless commensals, the species also includes a diverse array of variants with distinct pathogenic properties.

Among the pathogenic strains, Shiga toxin-producing *E. coli* (STEC)—historically also referred to as VTEC (verotoxin-producing *E. coli*)—represents the most virulent group. STEC are important zoonotic pathogens associated with food- and waterborne infections worldwide. These strains are characterized by the production of Shiga toxins, encoded by the *stx1* and *stx2* genes, which are typically acquired via lysogenic bacteriophages. Shiga toxins function as potent virulence factors that damage intestinal epithelial cells and can result in severe gastrointestinal illness. The characteristic clinical symptom of STEC infection is diarrhoea, often developing to bloody diarhhoea, and in rare cases, the infection may progress to the potentially life-threatening complication haemolytic uraemic syndrome (HUS). HUS occurs most frequently in young children and is associated with significant morbidity.

Ruminants are generally recognised as the principal natural reservoirs of STEC, with cattle traditionally identified as the primary source of human infections and outbreaks. However, in recent years, additional sources of infection have been identified or suspected within ruminants. A focus on animals such as sheep, goats and wildlife including deer could be beneficial for a better understanding of their roles in the epidemiology, transmission dynamics, and environmental distribution of STEC. As an illustrative example, a Swedish study from 2024 reported a markedly higher prevalence of STEC in Swedish lamb meat (57%) compared with Swedish beef (2%) [1]. These findings indicate that alternative animal sources may constitute substantial reservoirs for STEC and potentially play a more significant role in transmission to humans. In this context, DVFAFA has likewise examined the occurrence of STEC in game meat, as such data are relevant both for risk assessment, possible risk management options and for understanding potential sources in future outbreak investigations.

3.2 Methods for detection and isolation of STEC

Several PCR-based methods for the detection of STEC in food, feed and environmental samples are available, ranging from commercial systems to international standards such as ISO 13136:2012.

The initial step involves enrichment of the sample material in a general growth medium that supports the proliferation of STEC, allowing the detection of low numbers of STEC. However, this enrichment step also promotes the growth of a substantial portion of the background flora, which is a disadvantage as it can complicate subsequent detection and isolation of the bacterial strain of interest. STEC detection is then based on the amplification of the genes encoding the Shiga toxins 1 and 2, followed by visualization through gel electrophoresis or emission of fluorescence in the case of real-time PCR. For samples that test positive, isolation of the bacterial strain may be attempted by plating the enrichment culture onto a variety of different selective and non-selective media. Most commercial systems, however, focus on detection only and do not include a procedure for performing the isolation procedure.

Control sampling projects carried out between 2015 and 2018 at DVFAFA were based on a commercial BAX® Real-Time (RT) -PCR system. Because this method was not accredited, it prompted considerations regarding the adoption of an accredited alternative. Accreditation of methods used for official controls is a requirement according to EU regulation 2017/625, which ensures standardized and reliable results.

Furthermore, selecting a method that includes an isolation procedure is essential during disease outbreaks and for the risk assessment of food products, as only PCR results confirmed from viable STEC isolates can be considered as verified. When isolation is successful, the analytical result is reported as "detected". Conversely, PCR detection of the *stx* genes in the absence of an isolate is reported as "presumptive".

Obtaining an isolate also enables further characterisation, including the detection of additional virulence genes, thereby providing detailed information on the virulence profile.

Although the BAX® Real-Time (RT) -PCR system offered operational benefits—such as a simplified workflow and reduced hands-on time—it also had notable limitations. As a proprietary platform, it restricted methodological flexibility, relied on relatively expensive commercial consumables, and offered limited transparency regarding assay design.

ISO 13136:2012, developed by the European Reference Laboratory for *E. coli* [2], was selected as the replacement method. It is the standard method used among European Food and Feed National Reference Laboratories (NRLs), which facilitates comparability of results within the food side, essential in coordinated surveillance efforts. The method is also under continuous development, for example through incorporation of additional *stx* subtypes.

Compared with commercial systems like BAX® Real-Time (RT) -PCR system, ISO 13136:2012 is internationally recognized as the reference standard for STEC detection and isolation, and provides full transparency regarding primers, targets, and analytical steps. It allows laboratories to select and validate DNA extraction and PCR procedures according to local requirements. This flexibility supports adaptation to new scientific developments and facilitates harmonization across NRLs. However, the method also has drawbacks. The workflow is more labor-intensive and requires considerable technical expertise, resulting in a higher workload compared with integrated commercial platforms.

Isolation of the STEC strain remains a critical part of the analytical process. A description of the isolation procedure is included in ISO 13136:2012, but laboratories must further optimize and refine the procedure to ensure efficient recovery of STEC from different sample matrices. When using ISO 13136:2012, the detection step provides quantitative information about the signal strength of the *stx1* and *stx2* genes. These signal intensities can help decide which dilutions are most appropriate before plating the sample on selective media. In simple terms: the stronger the signal, the more you typically need to dilute the sample to obtain clear and defined STEC colonies on the plates. This approach enhances the likelihood of successful isolation.

3.3 STEC in the food production chain: Insights from previous investigations

The occurrence of STEC in meat, cattle hides and carcasses has been investigated by DVFAFA. Official control sampling projects conducted between 2015 and 2018 examined the prevalence along the food production chain, from slaughter to raw meat, and were published in the Annual Report on Zoonoses in Denmark 2018 [3]. The study reported that 11% of swab samples collected from cattle hides tested positive for STEC, whereas only 0.35% of carcass swab samples tested positive.

In addition, the prevalence of STEC in beef was 0.75% both before and after the cutting process. For minced meat, a noticeably higher prevalence of 9.4% was observed, highlighting the risk of contamination and potential growth of STEC. These findings indicate that STEC can be substantially reduced through adequate slaughter hygiene. However, subsequent processing steps, such as mincing, may increase the risk of contamination or cross contamination of STEC within the product. This underscores the importance of effective microbial risk management throughout the slaughtering and meat-processing chain, and to cook minced meat thoroughly when preparing meals.

3.4 Screening of beef and game meat in Denmark

A screening study by DVFAFA has been focused on game meat, since a higher prevalence of STEC has been demonstrated in game meat compared with beef. A survey of game meat from different European countries showed notably high detection rates of Shiga toxin genes, with detection rates reaching up to 84% of the samples tested [4].

This increased prevalence in game meat is likely related to differences in animal handling and a higher risk of contamination during the slaughtering process. Game animals are often field dressed, which may involve less standardized hygiene procedures compared with those implemented in conventional cattle slaughterhouses.

Consequently, an ongoing screening study was initiated in 2024 with a particular focus on game meat, especially ready-to-eat (RTE) fermented sausages containing game meat, to further investigate prevalence of STEC in these products. At present, a total of 48 samples have been analysed in the project. Of these, 11 (23%) tested positive for the presence of genes encoding Shiga toxins. Isolates were obtained for 8 out of the 11 positive samples and could thus be reported as "STEC detected". Twenty-three of the 48 samples analysed contained game meat, and 10 out of the 11 positive samples were derived from this food category, corresponding to a prevalence of 44% in game meat (Figure 3.1).

3.5 Understanding game meat risks: Subtypes and their virulence

The intended preparation and handling of the food product, including whether it is heat treated or not, also determines

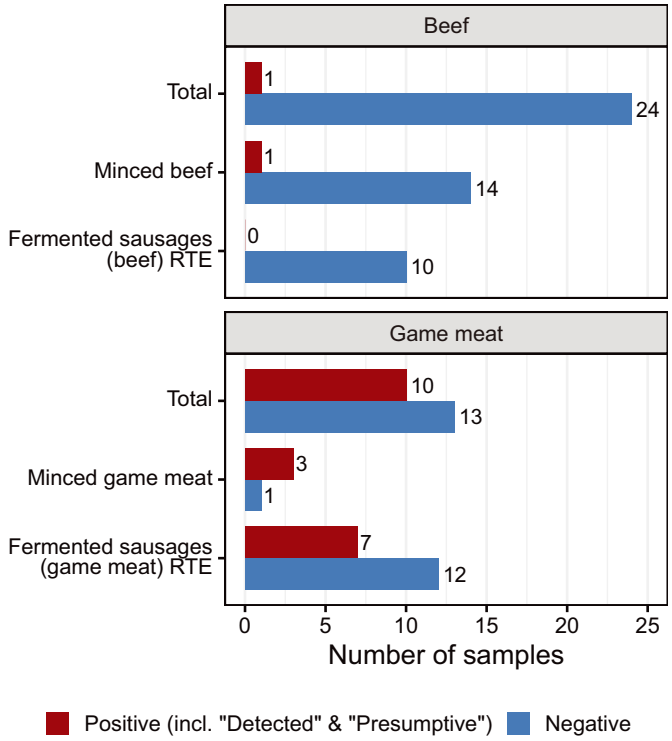

Figure 3.1 Number of samples testing positive for STEC (includes "Detected" and "Presumptive") in beef and game meat, further subdivided into minced meat and ready-to-eat (RTE) fermented sausages. Samples were collected in Denmark in 2024 to 2026

Table 3.1 Description of samples testing positive for stx1 *and/or* stx2*. For samples with successful bacterial isolation of STEC, the identified serotype and* stx *subtype are reported, together with information on the presence or absence of the* eae *gene*

Food item	PCR result	Isolate (Yes/No)	Serotype	*Stx* gene (subtype)	*eae* gene (Yes/No)
Fermented sausage (venison)	*stx2*	Yes	O2:H29	*stx2b*	No
Fermented sausage (venison)	*stx2*	No			
Fermented sausage (venison)	*stx1, stx2*	Yes	O146:H28	*stx1, stx2b*	No
Fermented sausage (venison)	*stx1, stx2*	Yes	O146:H28	*stx1, stx2b*	No
Red deer minced meat	*stx1, stx2*	Yes	O146:H28	*stx1, stx2b*	No
Fermented sausage (game meat)	*stx2*	No			
Fermented sausage (venison)	*stx2*	Yes	O27:H30	*stx2b*	No
Minced beef	*stx1, stx2*	No			
Fermented sausage (venison)	*stx2*	Yes	O146:H28	*stx2b*	No
Fermented sausage (venison)	*stx2*	Yes	O27:H30	*stx2b*	No
Fermented sausage (venison)	*stx1, stx2*	Yes	O130:H11	*stx1, stx2d*	No

the outcome of the risk management. All cases with STEC "detected" in RTE products are regarded as rendering the product unsafe and unfit for human consumption. To further investigate the potential risks associated with the detection of STEC in these products, WGS was performed for the isolates to determine both the serotypes and the specific *stx* subtypes present. This genomic information provides a more robust basis for evaluating the virulence potential of the isolates, as the *stx* subtype is linked to their ability to cause human disease.

Particularly important are the *stx2a* and *stx2d* subtypes, which have repeatedly been associated with the development of severe clinical outcomes, including HUS. Because these subtypes are known to exhibit higher virulence and are disproportionately represented among isolates from HUS patients, their presence in food products is of special concern. Consequently, isolates harbouring *stx2a* or *stx2d* lead to increased attention, as they represent a greater likelihood of leading to serious illness in consumers [5].

According to Table 3.1, a broad range of serotypes was identified among the isolates, whereas the *stx* profiles were dominated by the subtype *stx2b*. Notably, one isolate harboured the *stx2d* subtype, which is recognised as being associated with an increased risk of severe clinical outcomes, including HUS. The detection of *stx2d* is therefore of particular concern from a public health perspective, as this subtype is considered one of the more virulent variants within the *stx2* family.

However, this isolate—along with all other isolates included in the analysis—lacked the *eae* gene, which encodes the adhesion protein intimin. The absence of *eae* is an important factor to consider when assessing virulence potential, as intimin-mediated attachment is a key mechanism in the pathogenesis of typical HUS-associated STEC strains. While *stx2d* increases the risk of severe disease, the lack of *eae* may reduce the overall virulence potential of these strains.

3.6 Perspectives

Growing interest in sustainable diets has increased the awareness of game meat, which is often viewed as a sustainable and natural protein source. Understanding the occurrence of STEC in game meat is therefore essential. Clarifying these risks supports safer integration of game meat into modern diets - especially in RTE foods - and highlights the importance of slaughter hygiene and quality of the raw material for these products, and helps broaden food choices for consumers seeking variety and local products. Game meat is an interesting alternative to conventional livestock, but vulnerable groups, such as young children, may require tailored guidance to minimize exposure to foodborne hazards, especially with regard to RTE foods, as this screening study has demonstrated a high prevalence of STEC in these products.

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4. Vectorborne zoonoses

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The Danish Veterinary Consortium (DK-VET) monitors vectors at the University of Copenhagen (UCPH) on behalf of DVFAFA and contributes to the surveillance of vector-borne diseases in Denmark. The surveillance focuses on endemic vectors but also screens for exotic vectors. Mosquitoes and biting midges have been monitored weekly during the vector season since 2011 and 2012, respectively. Tick vectors have been monitored regularly since 2017. Surveillance data are continuously updated at www.myggetal.dk.

4.1 Endemic vector surveillance and research

The vector season in 2025 was affected by a dry and warm spring, resulting in low mosquito and biting midge abundance. The national surveillance program reported the lowest number of mosquitoes since 2011.

In 2025, DK-VET continued the active surveillance of mosquitoes for the second year in a row as a part of the OH4Surveillance project. The EU(HaDEA)-funded project focuses on the surveillance of West Nile virus (WNV) in mosquitoes collected in the southern parts of Denmark. Mosquitoes were collected using suction traps (BG-Pro and Mosquito Magnets) from May to September at four locations on Zealand, one location on the island of Møn, one location on the island of Falster, and three locations in southern Jutland. A total of 13,429 mosquitoes were caught in 2025, with a majority belonging to the genus *Aedes* (*Ae.*) (Figure 4.1a). During 2025, all mosquitoes from both 2024 and 2025 were identified to species-level. The most abundant mosquito species for both years combined were *Ae. detritus* and *Ae. caspius*, two of the most common species in coastal areas in Europe and considered as biting nuisances during the high season (Figure 4.1b). The West Nile fever mosquito, *Culex modestus*, which in previous years has been found in peri-urban areas close to Copenhagen, was found in two new locations in 2025. Both sites are located south of Zealand on the islands of Møn and Falster.

Mosquitoes collected in 2024 and 2025 were tested for WNV at SSI following pooling of the mosquitoes according to location, species, and collection week number. All mosquito pools tested negative for WNV. The pools were subsequently tested for Usutu virus (USUV), and three pools from southern Jutland collected in 2024 tested positive for this virus. USUV was first discovered in Denmark in 2024 in blackbirds (*Turdus merula*), however, this marks the first time USUV has been detected in mosquitoes in Denmark. All mosquitoes in the positive pools were morphologically identified as either of the two species *Culex pipiens* s.s./*torrentium*, both well-known vectors of USUV and WNV.

In 2025, a veterinary medicine master's thesis project conducted at UCPH and SSI screened 822 horses across 22 veterinary practices around Denmark for the presence of WNV antibodies. Sera from four horses were found positive, which was further confirmed with a WNV-specific neutralization test at the European reference laboratory. The horses had no history of travel or WNV vaccination. The four horses all originated from the southern part of Denmark. This is the first time that signs of prior infection with WNV in horses within Denmark was reported. The finding of WNV antibodies in horses highlights the need for increased awareness and surveillance of WNV in veterinary practices. In addition, since horses serve as a sentinel species for human WNV infections, WNV should be considered as a differential diagnosis for humans in Denmark.

SSI in collaboration with DK-VET is continuing the tick-borne encephalitis virus (TBEV) monitoring, mainly focusing on known TBEV hot spots. In Denmark, most domestic TBE cases can be linked to Bornholm and northern Zealand [1]. Throughout 2024, TBEV was detected and later confirmed in ticks collected from a new site located in Jonstrup Vang (northern Zealand). Follow-up collections were conducted in 2025 in Jonstrup Vang as well as Tisvilde Hegn, another previously confirmed hotspot in northern Zealand, but no ticks tested positive for TBEV. All adult ticks were morphologically typed as *Ixodes ricinus*.

Since 2017, DK-VET has conducted bi-weekly collections of *Ixodes ricinus* at six sites in northern Zealand. In 2025, DK-VET explored integrating tick monitoring combining field-based tick surveillance, weather-based tick activity models, Google search trends, and national Lyme neuroborreliosis (LNB) records in Denmark from 2017–2024 [2]. A strong correlation between predicted tick activity and Google search results for "ticks" (DA: "flåt" and "tæge") and "borrelia" was found with a one-month lag and no lag, respectively. This suggests that online search engine behaviour may be useful to predict public exposure to the *Ixodes ricinus* tick. Additionally, predicted tick activity closely matched seasonal patterns in LNB incidence and typically preceded reported cases by about one month, reflecting delays between exposure, symptom onset, and diagnosis. Together, these findings indicate that integrating environmental data, digital behaviour, and health records can provide a cost-effective early warning system for tick-

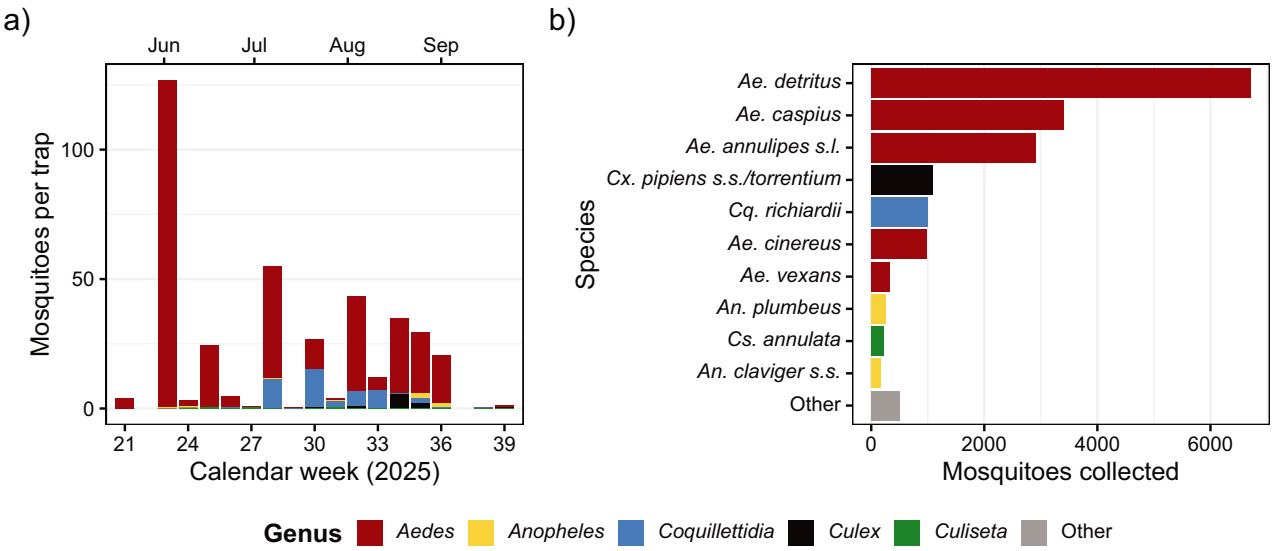

Figure 4.1 a) Number of mosquitoes by genus and per trap, collected in 2025. Only mosquitoes collected by BG-traps are included. Data displayed per week. b) Mosquito species abundance in 2024 and 2025 combined. All trap types included. Total number of mosquitoes = 17,557. Ae.: Aedes, An.: Anopheles, Cq.: Coquillettidia, Cs.: Culiseta, Cx.: Culex, s.l.: sensu lato, s.s.: sensu stricto

borne disease risk and support more timely public health responses. This study was published in early 2026 [2].

Alpha-gal syndrome (AGS) is a food allergy to galactose-alpha-1,3-galactose which is found in mammalian meat and other animal-based products. AGS was first recognized in 2008 and has for the past decades become more prevalent in the general adult population in Denmark. Tick bites have consistently been linked to the development of AGS, and in 2024, DK-VET in a project led by Frederiksberg Hospital investigated this presumed link in Danish suburban areas [3]. The study utilized health examination studies conducted in 2011–2017, covering a total of 8,742 participants, to investigate alpha-gal sensitization in relation to participants' homes' proximity to forests and predicted tick nymph abundance. Participants all lived in suburban areas west of Copenhagen, and of the 8,742 participants, 344 were found to exhibit alpha-gal sensitivity. The study found no relationship between AGS and predicted tick nymph abundance. However, it was found that participants living in suburban areas had higher odds (9%) of having alpha-gal sensitivity the closer they lived to forests, indicating that tick exposure is a possible risk factor for AGS.

Following the Bluetongue virus (BTV) outbreak in 2024, DK-VET has been monitoring outbreaks in Danish livestock herds. Although BTV is not a zoonosis and therefore not infectious to humans, it is spread by *Culicoides* midges whose weekly abundance in May-November has been monitored by DK-VET since 2012. Similarly to mosquitoes, the abundance of biting midges was low in 2025 due to the dry and warm spring. This is reflected in the dwindling number of BTV cases, as only a total of nine outbreaks were confirmed nationwide in 2025 compared to 1,300 in 2024. It should be noted that BTV vaccinations had also been initiated on voluntary basis since the end of August 2024. Due to low numbers of new cases, DVFAFA lessened their restrictions for livestock herds in late 2025.

4.2 Surveillance of exotic vectors

No exotic mosquitoes were recorded in 2025. A single meadow tick (*Dermacentor reticulatus*) was sent to the vector surveillance unit at UCPH, after being removed from a dog visiting a summer house rental area near Hvide Sande in February. The tick was likely introduced to the area by other visitors and their pets, e.g. from Germany, and the finding does therefore not indicate that the species is established.

An *Ixodes ricinus* tick was found for the first time in Greenland. The tick nymph was found attached to a housecat in Nuuk in May 2025 and was sent to the Institute of Animal Health and Welfare at UCPH for genetic testing. We believe the tick has likely been transported to Greenland via plane and should be considered an isolated find.

Disclaimer:
OH4Surveillance is co-funded by the European Union (Grant Agreement No. 101132473). Views and opinions expressed are those of the author(s) only and do not necessarily reflect those of the European Union or HaDEA. Neither the European Union nor the granting authority can be held responsible for them.

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5. SOFI - A joint platform for whole genome sequencing surveillance of foodborne infections in Denmark

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5.1 Background and establishment of the national Sequence-based surveillance Of Foodborne Infections (SOFI) platform

Since 1998, two Danish institutions have been collaborating on their authority task of monitoring human foodborne infections: SSI, responsible for the surveillance of foodborne illness in humans, and DVFAFA, responsible for surveillance of infectious agents in livestock, food and food production environments. This collaboration takes place through the Central Outbreak Management Group (COMG).

In 2013, SSI started the implementation of WGS for typing and surveillance. DVFAFA began the same transformation in 2016, enabling the comparison of bacterial genomic data from human and food origin in response to signals identified through surveillance and outbreak investigations. Initially, such comparisons were labor-intensive and required technical solutions for data exchange across institutions, which highlighted the need for a more structured, real-time cross-sectoral approach.

Therefore, it was decided in 2018 to establish a joint-authority sequence platform, the "national Sequence-based surveillance Of Foodborne Infections" (SOFI). SOFI should strengthen the national surveillance of foodborne infections and infectious agents in livestock, food and food production environments, as well as the work in the COMG. The platform would allow this by supporting real-time WGS-based surveillance of foodborne pathogens, enabling timely outbreak detection, facilitating outbreak management, and supporting source identification through cross-sectoral comparison. In other words, by putting One Health into practice.

As the first system of its kind, the development of SOFI required substantial preparatory work to define its scope, as well as to identify user needs, technical requirements, and the applicable legal framework. Therefore, a multidisciplinary working group was established in 2019, bringing together technical expertise, end-user perspectives and project management competences from SSI, DVFAFA and DTU National Food Institute, the latter acting in an advisory capacity to DVFAFA. An external IT partner was contracted to develop the front-end of the platform. During development, a steering committee with representatives from the same institutions oversaw financial, organizational and selected technical decisions. Following the launch of SOFI on 1 January 2025, the steering committee was replaced by a joint monitoring group consisting of DVFAFA and SSI.

The establishment of SOFI required a substantial legal framework to ensure data protection and secure partitioning of institute-specific data. A collaboration agreement was adopted between SSI, DVFAFA and DTU National Food Institute to regulate the development during the project and establishment of SOFI as well as use, operation, further development, and management hereafter. An agreement on joint controllership was adopted between SSI and DVFAFA, alongside data processing agreements between SSI and DTU National Food Institute, and both a data processing agreement and a confidentiality declaration with the external IT partner. In addition, a risk assessment describing technical and organizational security measures as well as IT security requirements for measures of risks was also developed.

Following the implementation of SOFI on 1 January 2025, the comparison of bacterial genomic data from human and food origin in response to signals identified through surveillance and outbreak investigations has transitioned from manual, case-by-case data exchange to a rapid and systematic approach. This enables immediate cross-sectoral comparison and early assessment of whether specific outbreak types observed in human surveillance are genetically linked to isolates from food or production environment.

5.2 Technical overview

SOFI is hosted at the Danish supercomputer DTU Computerome and is designed to handle bacterial sequence data. The platform is integrated into laboratory systems at SSI and DVFAFA, receiving uploaded encrypted metadata for each sample and matching it to the corresponding sequence data

(Figure 5.1). Each such upload initiates a series of analyses, including sequence quality control, genome assembly, genotypic antimicrobial resistance prediction, 7-locus and core genome Multilocus Sequence Typing (MLST), as well as in-silico serotyping and toxin gene identification. The results are stored in a database, and a web front-end allows both inspection and manual curation of data.

Integration with laboratory systems at SSI and DVFAFA facilitates the use of curated results within existing lab workflows. The comparison module, Microreact [1], a visualization tool for genomic epidemiology, enables cross-sectoral analysis, allowing genomic data to be compared and relations to be identified through phylogenetic analysis and cluster determination (core genome MLST and soon single-nucleotide polymorphisms).

Access is managed according to a role-based model which provides a high degree of granularity: only personnel involved in outbreak management have access to data across institutions, while all other users are restricted to data from their own institution. Data access can be limited both in terms of which sequences and what data fields on a sequence can be accessed.

5.3 Lessons learned

When the project began in 2019, an IT consultant was contracted to help draft the public procurement tender for the IT development contract. As no similar project had been developed before, the project group found it difficult to describe the technical requirements before the system was even built. Thus, the tender material took time to develop and needed to be adjusted based on a dialogue with potential bidders. As a result, the process of finding a suitable IT development contractor was long. It was also complex to settle on a financial model that allowed sufficient flexibility and agility in the development process but still ensured that the project could be accomplished within the agreed budget.

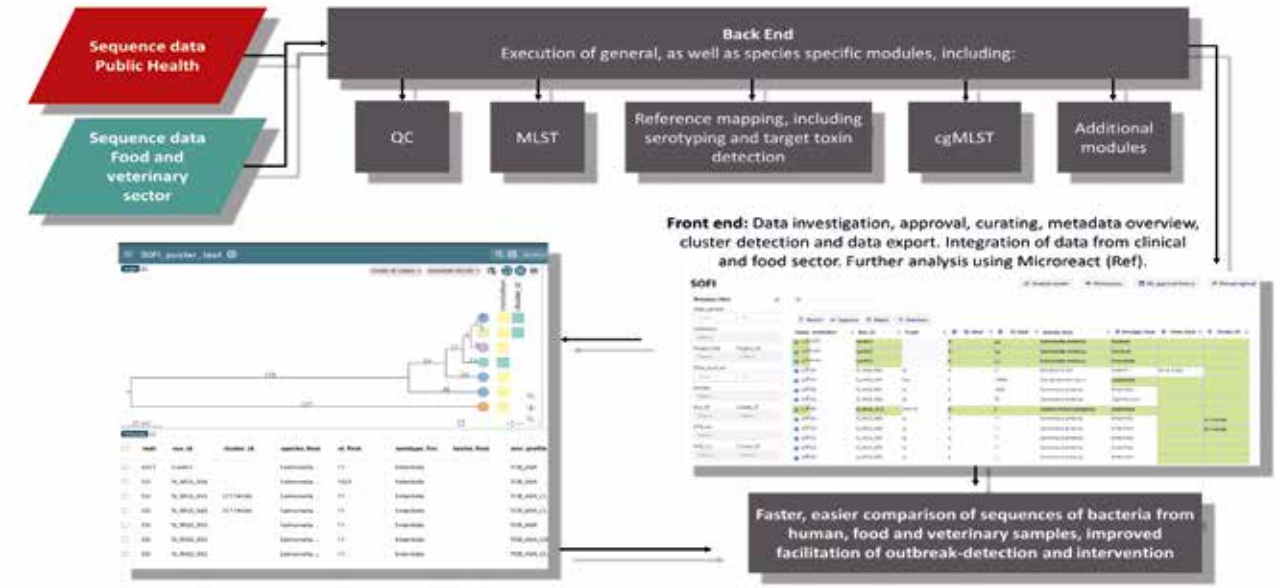

Figure 5.1 Dataflow in national Sequence-based surveillance Of Foodborne Infections (SOFI)

Project ownership is shared between DVFAFA and SSI, which also means that the economy is shared equally. There has been a great concordance in the working group in prioritizing what needs to be done, even though priorities have changed along the way. One of the biggest challenges has without a doubt been the length of the project. The long process affected the development, as some of the selected solutions and systems changed over time, and the integrations needed to be updated or adapted to changes in IT development. The project was also influenced by the COVID-19 pandemic, as 1) SSI being a public health institute had the pandemic as a primary focus in all regards, putting a strain on resources and 2) social distancing restricted the possibility of in-person meetings and required the partners meet and coordinate virtually instead.

As described previously, the legal framework was complex and was not something the project group had previous experience in. This required new competences for the project team members as well as the inclusion of legal advisors.

Looking back, the development of the platform could likely have been smoother, and many lessons were learned along the way. Nevertheless, the process was characterized by strong collaboration, engagement, and a positive working spirit within the working group. Over the years, trust between the institutions involved has been a key foundation for success and a recurring element throughout the project.

5.4 Future perspective

SOFI went live in January 2025; however, this was not without minor setbacks. There are still further development and optimization that needs to be done; thus, the working group is continuing the collaboration with the IT developing company. There is great potential for the platform, as it is developed with the possibility to be upscaled. For future development there have been discussions to integrate SOFI with other systems that are used for outbreak management or include data that originates from surveillance programs that are not analyzed in the laboratories that are currently included in the project.

From the beginning it was the plan to start with a few bacterial species - *Salmonella*, *Listeria*, *Campylobacter* and pathogenic *E. coli*, and include others along the way. In the future, it could also be relevant to include other agents such as viruses and parasites, making SOFI the primary platform for whole genome sequences of zoonotic agents. The system will also need to adapt to major new sequencing technologies as well as evolving analysis methods, ensuring its relevance with future developments in bioinformatics.

A future goal is to integrate data sharing functionalities within the SOFI platform in order to enable the timely upload of genomic data and metadata to the European Food Safety Authority and the European Centre for Disease Prevention and Control joint surveillance systems as well as to the European Nucleotide Archive, in line with relevant data standards and supporting cross-border outbreak detection and risk assessment.

To sum up, the SOFI platform is now the primary analysis platform for all partner institutions, allowing for real-time sharing and analysis of previously separated datasets. The platform allows for unique cross-referencing of previously isolated surveillance systems. This allows more efficient identification of potential clusters and outbreaks of foodborne bacterial infections in Denmark and links to possible sources, while also enhancing surveillance and outbreak investigation related to foodborne infections in Denmark.

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6. *Salmonella* surveillance in pigs in Denmark, 2025

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Denmark has implemented coordinated control measures against *Salmonella* in pig production since 1995. These measures resulted in a substantial reduction in *Salmonella* in Danish pork. After several years of stable and low prevalence in fresh pork and a low incidence of human salmonellosis attributable to Danish pork, it was decided to discontinue herd-level surveillance of *Salmonella* in pigs in 2025. Surveillance of fresh pork at slaughterhouses is maintained, and a new prevalence-based monitoring using caecum samples has been established to follow trends.

6.1 Introduction

The Danish *Salmonella* action plans in pig production were introduced in 1995 in response to a marked increase in human salmonellosis associated with pork. The plans were developed following a farm-to-fork approach and implemented through collaboration between DVFAFA, the Danish Agriculture and Food Council, the Danish Butchers Association FoodDenmark, and DTU National Food Institute.

In the following decades, the prevalence of *Salmonella* in fresh pork was reduced to a low and stable level. At the same time, the incidence of human salmonellosis attributed to pork decreased from approximately 15-20 cases per 100,000 inhabitants per year in the mid-1990s to 1-3 cases per 100,000 inhabitants per year during the last decade [1].

The most recent action plan expired in 2017 and was replaced by an operational plan focusing on maintaining the achieved low prevalence in Danish pork. In recent years, the proportionality and relevance of herd-level surveillance have been reassessed.

6.2 Surveillance and control measures

Control of *Salmonella* in Danish pig production has been based on integrated measures from primary production to slaughter. An overview of the former and present *Salmonella* surveillance programme for the Danish pig production can be found in Table 6.1.

At slaughterhouses processing more than 30,000 pigs annually, the prevalence of *Salmonella* in fresh pork (on carcasses) is monitored by daily sampling of five carcasses. The results are assessed using a rolling 11-day window to ensure a rapid detection of sudden increases in prevalence. A rolling 12-month weighted average (Table A11 and Table A33) is used to assess long term increasing trends in prevalence.

Since 2011, the target has been to maintain a maximum of 1% *Salmonella*-positive carcasses. If the 12-months prevalence at a slaughterhouse exceeds 2%, intensified sampling and control measures are implemented.

6.3 Changes in surveillance of *Salmonella* in pigs

During the last five years, the future design of the surveillance programme has been discussed. In 2024, the steering committee of the operational plan evaluated the resources used for herd-level surveillance in relation to the public health impact.

Given the current presence of *Salmonella* in the pig production, where almost all pig herds are infected with *Salmonella*, analyses conducted by the working group identified slaughterhouses as the most critical control point for ensuring food safety in the chain from farm-to-fork.

Based on these findings, and in view of the consistently low prevalence in fresh pork and the low incidence of human salmonellosis attributed to Danish pork, the steering committee decided to discontinue herd-level surveillance as of 2025. The committee assessed that this change would not have a negative impact on food safety.

6.4 Ongoing and supplementary surveillance

A monitoring programme for the occurrence of *Salmonella* in the population of slaughter pigs has been established, based on caecum samples collected for EU antimicrobial resistance surveillance [2] supplemented by samples from a centrally coordinated study (see Table A24 and section 7.4 for description). These samples are randomly collected at the slaughterhouses.

To assess the occurrence of *Salmonella* in slaughter pigs during the period with herd-level surveillance, the *Salmonella* cultivation results from 772 caecum samples collected in 2023 were used to estimate the prevalence of *Salmonella*-positive caecum samples. The corresponding estimate for the period following the discontinuation of

Table 6.1 Changes in Salmonella *surveillance programme[a] for the pig production, 2024-2025*

Time		Samples taken	Purpose/Comment
Breeding and multiplier herds	Discontinued from 1 January 2025		
Every month		10 blood samples per epidemiological unit	Calculation of *Salmonella*-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 *Salmonella*-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 *S.* Typhimurium, *S.* Infantis, *S.* Derby and *S.* Choleraesuis are considered positive for the following 5 years[d]		No samples are collected from the herd during the 5-year period when the herd is considered positive, unless the herd is proven negative	Reduce repeated sampling in positive herds infected with a persistent serotype
Slaughter pigs, herds (Discontinued from 1 January 2025)			
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 samples from the last three months with most weight to the result from the most recent month (1:1:5). Assigning herds to level 1-3 and assigning herds to risk-based surveillance (RBOV)[e]
Slaughter pigs, animals	Still in force		
At slaughter[f]		Caecum samples, avg. 25 samples per month, 12 months per year	Random collection of samples for monitoring of the distribution of serotypes and antimicrobial resistance
Pork carcasses at the slaughterhouse			
5 samples daily, pooled into one analysis[g,h]		Swab samples from 4 designated 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 designated 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 designated 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 1.000 pigs per year

a) Sampling requirements set out by Danish Order no. 597 of 29/05/2023 and Danish Order no. 1226 of 25/11/2024
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:i:-
e) RBOV: risk-based surveillance in herds with a slaughter pig index of zero (no positive samples in the previous three months) the sample size is reduced to one sample per month
f) Centrally coordinated study (Table A24)
g) If a slaughterhouse detects more than one positive sample in a rolling window of 11 slaughter days, the slaughterhouse must follow up according to Danish Order no. 1226 of 25/11/2024
h) If a slaughterhouse, within the last month, detects Salmonella and at the same time has a Salmonella prevalence above or equal to 2% (12 month average), the sampling frequency doubles to 10 samples daily, pooled into two analysis with 5 samples in each. If the 12-month average continues to be above or equal to 2% 4 times within a 6-month period, the slaughterhouse must follow up according to Danish Order no. 1226 of 25/11/2024

herd-level surveillance was based on 888 caecum samples collected in 2025. In 2023, *Salmonella* was cultivated in 11% of the samples (85 samples). In 2025, *Salmonella* was cultivated in 13% of the samples (116 samples).

The result of a statistical analysis comparing the data collected in 2023 and 2025 indicates that the observed increase may not be fully explained by random sampling variation (one-sided test, p = 0.08). This suggests a possible increase in the occurrence of *Salmonella* in slaughter pigs following the discontinuation of herd-level surveillance.

The newly established monitoring of the *Salmonella* occurrence in cecum samples from slaughter pigs will continue in the coming years, together with surveillance of *Salmonella* in fresh pork at slaughterhouses. The results of surveillance for *Salmonella* in Danish pork are summarised in Table A11 and Figure A1.

The target of a maximum prevalence of 1% *Salmonella*-positive carcasses is maintained, and the number of human salmonellosis cases and the *Salmonella* source attribution will continue to be closely monitored. If unfavourable trends are observed, the steering committee will be informed.

References

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7. 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 7.1. An overview of the notifiable and non-notifiable human and animal diseases, presented in this report, is provided in Table A26 and Table A27, respectively, including references to the relevant legislation.

7.1 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 SSI through different channels depending on the disease:

- Notifiable through the laboratory surveillance system: *Salmonella spp.*, *Campylobacter spp.*, pathogenic *Yersinia*, Shiga toxin-producing *E. coli* (STEC), *Shigella*/Enteroinvasive *E. coli* (EIEC) (ipaH positive), *Brucella* and *Listeria*.
- Individually notifiable zoonotic pathogens: *Chlamydia psittaci* (ornithosis), *Leptospira* (Weils disease), *Mycobacterium bovis*, Var. Creutzfeldt-Jakob Disease, haemolytic uraemic syndrome (HUS), HUS-inducing STEC, *Shigella*/EIEC, and Lyssavirus (rabies).

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 laboratories is transmitted to MiBa. All cases of infections with laboratory notifiable pathogens are registered in the Register of Enteric Pathogens maintained by SSI. *Campylobacter*, *Salmonella*, *Shigella*/EIEC and *Yersinia* cases are extracted from MiBa and STEC and *Listeria* are reported to SSI directly from the clinical microbiology laboratories.

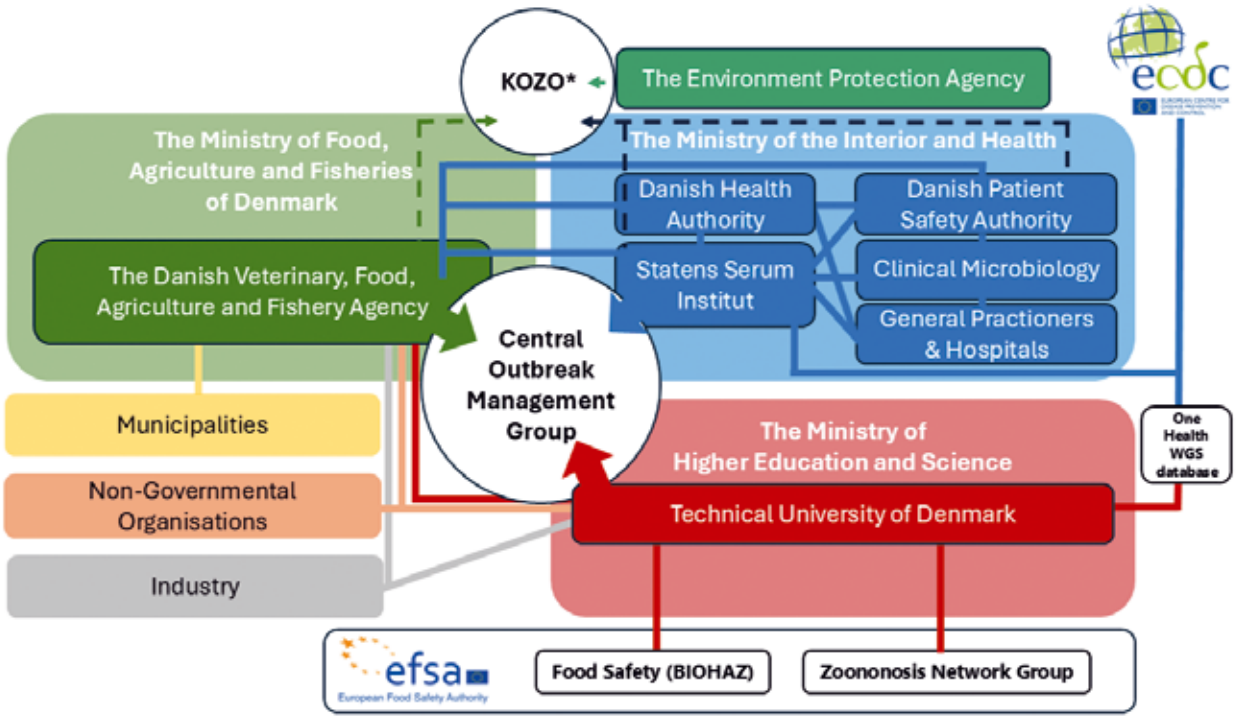

*Figure 7.1 Overview of the monitoring and outbreak investigation network for reporting infectious diseases in humans, animals, feed, and food in Denmark. *KOZO, "Myndighedsgruppen til KOordinering af ZOnoser" (The Group of Authorities for the Coordination of Zoonoses)*

Furthermore, all culturable *Salmonella* and *Listeria* as well as a subset of STEC, *Shigella*/EIEC, *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 Table A1.
- STEC O-group distribution in humans is presented in Table A2.
- The *Salmonella* serovar distribution is presented in Table A4.
- The *Salmonella* serovar distribution related to travel is presented in Table 7.1 and Figure 7.2.

7.2 Outbreaks of zoonotic gastrointestinal infections

In Denmark, local and regional foodborne outbreaks are typically investigated by the local 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 DTU National Food Institute, and DVFAFA 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 the Interior and 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, public swimming pools, etc.

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 business operators are obliged to contact the DVFAFA if the food they served or produced is 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 outbreaks 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 Table A3 and some of the outbreaks from 2025 are further described in Chapter 1.

7.3 Surveillance and control of animals and animal products

In Denmark, action plans and programmes on zoonoses have been in place for more than 30 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, chicken meat and the environment, as well as *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 of target statuses can be seen in Table A25.

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

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

- Results from the table egg production are presented in Tables A5-A6.
- Results from the broiler production are presented in Tables A4 and A7.
- Results from the duck and turkey productions are presented in Table A8.

- Results from the pig production are presented in Tables A4, A11 and Figures A1.
- Results from the cattle production are presented in Tables A4, A12-A13 and Figure A2.
- Results from the rendering plants are presented in Table A14.
- Results from the feed production are presented in Tables A15-A16.
- Results based on suspicion of diseases in domestic animals, zoo animals and wildlife are presented in Tables A20-A21.

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

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

Pig and cattle carcasses are screened for *Mycobacterium* and *Echinococcus* during meat inspection at the slaughterhouse. Although pigs kept under controlled housing conditions in Denmark are exempted from examination for *Trichinella* at slaughter, approximately 95% of 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 DVFAFA. Results are presented in Tables A11-A12.

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

7.4 Official testing of zoonotic pathogens in foodstuffs

In Denmark, control of zoonotic microorganisms in foodstuffs is mainly conducted through projects coordinated at the central level of DVFAFA. 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 2025.

For further information, consult the website of the DVFAFA, www.fvst.dk (in Danish).

Where do we acquire *Salmonella* infections?

In 2025, SSI extracted 1051 registered *Salmonella* cases including the available travel information from the Danish Microbiology Database (MiBa). MiBa receives copies of reports from all Danish Departments of Clinical Microbiology. Travel information was available from 88.6% of the *Salmonella* cases in 2025. The total number of *Salmonella* cases has decreased by 17% compared to 2024. However, the proportion of travel-related cases (45.7%) was similar to both 2024 (44.7%) and 2023 (46.0%) (Table 7.1). A similar number of *S.* Enteritidis cases was seen in 2025 (255 cases) and 2024 (274 cases) (Table A1) and just as in 2024, no larger outbreaks were caused by *S.* Enteritidis (Figure 7.2).

In 2025, the proportions of domestically acquired *S.* Typhimurium and *S.* 1,4,[5],12:i:- cases slightly decreased from 83.9% and 83.6% in 2024 to 79.1% and 79.9% in 2025 (Table 7.1), likely due to fewer major *Salmonella* outbreaks detected in 2025 (Chapter 1, Figure 7.2, and Table A3).

Table 7.1. Top 10 Salmonella *serotypes in humans and information about travel abroad, 2024-2025*

2025	Number of patients (%)	% of patients[a] infected Abroad[b]	Domestically	2024	Number of patients (%)	% of patients[a] infected Abroad[b]	Domestically
Enteritidis	255 (24.3)	56.3	43.8	Enteritidis	274 (21.6)	66.1	33.9
Typhimurium	142 (13.5)	20.9	79.1	Typhimurium	177 (14.0)	16.1	83.9
1,4,[5],12:i:-	81 (7.7)	26.1	79.9	1,4,[5],12:i:-	133 (10.5)	16.4	83.6
Strathcona	34 (3.1)	13.8	86.2	Stanley	33 (2.6)	64.3	35.7
Oranienburg	25 (2.4)	35.0	65.0	Paratyphi B var. Java	29 (2.3)	81.5	18.5
Stanley	22 (2.1)	66.7	33.3	Newport	28 (2.2)	56.5	43.5
Paratyphi B var. Java	21 (2.0)	94.7	5.3	Chester	26 (2.1)	57.1	42.9
Newport	19 (1.8)	52.9	47.1	Umbilo	24 (1.4)	0.0	100.0
Chester	18 (1.7)	62.5	37.5	Agona	18 (1.4)	64.3	35.7
Saintpaul	17 (1.6)	37.5	62.5	Infantis	17 (1.3)	78.6	21.4
Other serotypes	275 (26.1)	53.2	46.8	Other serotypes	295 (23.3)	51.7	48.3
Total	1051	45.7	54.3	Total	1266	44.7	55.3

a) Patients with unknown travel information (11.3% of all patients in 2025 and 16.7% of all patients in 2024) were excluded from the percent calculations
b) Infected abroad is defined as travel abroad prior to disease onset

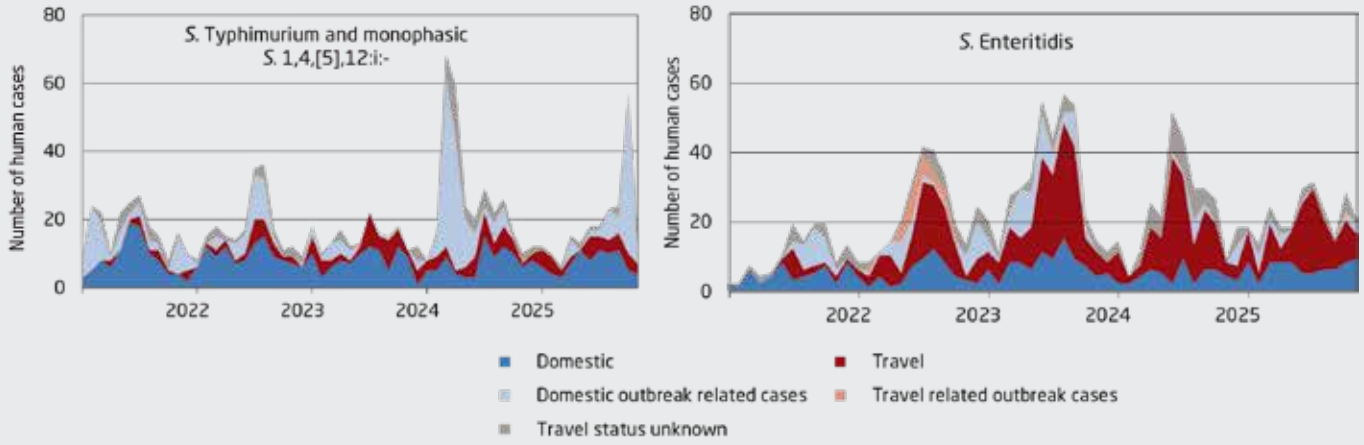

Figure 7.2 Monthly distribution of S. Enteriditis *and* S. Typhimurium *incl. monophasic S. 1,4,[5],12i- cases, 2021-2025*

Source: Statens Serum Institut

8. International Topics

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8.1 Codex Alimentarius

At the December 2025 meeting of the Codex Committee on Food Hygiene (CCFH55), several documents were finalized and forwarded for adoption at the upcoming meeting of the Codex Alimentarius Committee [1].

Annex II on Fish and fishery products and Annex IV on Water fit-for-purpose assessment, safety management, and technologies for recovery and treatment of water for reuse were completed [2]. With these additions, the Guidelines for the safe use and reuse of water in food production and processing (CXG 100-2023) [3] are now fully updated. The guidelines already include annexes on fresh produce, milk, and milk products.

The Guidelines for the control of *Campylobacter* and *Salmonella* in chicken meat were updated for the first time since 2011 [4]. The update incorporates new scientific recommendations from the Joint FAO/WHO Expert Meetings on Microbiological Risk Assessment (JEMRA) [5].

The Guidelines on the application of general principles of food hygiene to the control of *Listeria monocytogenes* in foods were also updated [6]. The revised version includes three annexes with recommendations for:

- Food business operators, on environmental monitoring programmes for *Listeria monocytogenes* in primary production and processing areas.
- Competent authorities, on the use of microbiological testing to verify the effectiveness of HACCP and prerequisite programmes for the control of *Listeria monocytogenes* in ready-to-eat foods.
- Competent authorities and food business operators, on developing and applying microbiological criteria for *Listeria monocytogenes* in ready-to-eat foods.

8.2 Process Hygiene Criteria for *Campylobacter* in carcasses from broilers

The process hygiene criteria for *Campylobacter* in carcasses from broilers entered into force on 1 January 2018 in the European regulation on microbiological criteria for foodstuffs [7]. The criteria require weekly sampling, with compliance assessed over a five-week rolling period (equivalent to fifty samples). At introduction, up to 20 of the 50 samples were allowed to exceed the limit of 1,000 CFU/g.

A stepwise tightening of the criteria for non-compliance was established in the regulation, and in 2020 the compliance threshold was reduced to 15 of 50 samples exceeding 1,000 CFU/g.

The final adjustment, as laid down in the regulation, took effect in January 2025. The criteria is now met only if no more than 10 out of 50 samples exceed 1,000 CFU/g.

8.3 The European Partnership for animal health and animal welfare EUPAHW

The European Partnership on Animal Health and Animal Welfare (EUPAHW) (2024 to 2030) has so far initiated two rounds of internal projects, into which European universities and research institutions were invited. The Partnership also issues open external calls on selected research topics. The Technical University of Denmark, UCPH, SSI, and Aarhus University participate in the projects – the latter also engages in the leadership of EUPAHW.

An example from the first round of internal projects (2024 to 2026/2027) is the "Set of Objective" (SOA) 8: Surveillance of pathogens of veterinary importance and their antimicrobial resistance profiles [8]. SOA8 will fill existing gaps in antimicrobial susceptibility testing for bacterial pathogens from terrestrial and aquatic food-producing animals. Furthermore, the project will boost the use of genomic methods for surveillance of veterinary pathogens and their antimicrobial resistance, by mapping genomic monitoring activities among project participants, developing harmonised tools for sharing and analysis of genomic monitoring data and evaluating the potential of metagenomics for surveillance. A comparative assessment of different approaches to surveillance of antimicrobial resistance (AMR) in animal populations will also be performed, including monitoring in pathogenic and indicator bacteria, active and passive surveillance, and diseased and healthy animals. The project will also assess the potential spread of antimicrobial resistance from farmed animals to the surrounding environment and identify the potential of terrestrial and aquatic wildlife as sentinels for environmental surveillance. A workshop for all partners was organised at DTU National Food Institute in May 2025.

Examples of SOAs in the second round of internal projects (2026 to 2028/2029) are mentioned in the following [9]. SOA27 aims to integrate genomic data into animal health and food safety risk assessment, as genomic approaches offer great potential to improve prediction, prevention, and control of infectious diseases. At present, widespread application across the EU is still limited by fragmented methodologies, lack of harmonized protocols, and challenges in data interoperability, and hence SOA27

will address these barriers. SOA28 aims at identifying the occurrence and genetic location of antimicrobial resistance genes (ARGs) in field isolates of veterinary pathogens from for example mastitis, diarrhoea, pneumonia or systemic infections. The general tool for this will be WGS, and subsequent bioinformatic analyses investigating the genetic location of the ARGs in relation to mobile elements. The project includes using existing WGS but will also generate new data through laboratory-based in-vitro studies to address the dynamics and risks of horizontal gene transfer between bacteria, and the maintenance and sustainment of AMR carried on mobile genetic elements. The knowledge generated in the project is essential for understanding the risk of dissemination and sustainment among and between livestock, and for performing accurate risk assessments. In SOA34 digitally assisted monitoring technologies will be developed and validated for on-farm precision management of animal health and welfare. The focus will be on visual surveillance technologies (e.g. cameras to analyse behavior) and auditory surveillance technologies (e.g. bioacoustics approaches to analyse vocalizations). For both types of technologies, the project focuses on several species, linking the species in question to the most suitable technology or combination of technologies. In SOA39, the focus will be on how complex decisions on animal health and welfare are made, based on multiple assessment outcomes. The project output will support animal health risk managers in developing control strategies for animal diseases, considering various dimensions. System thinking, burden of disease estimation, animal health/welfare economics and socioeconomics will be applied.

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Photo. Participants in the SPAMR-VET project at DTU building 101, May 2025

Human disease and outbreak data

Table A1 Zoonoses in humans, number of laboratory-confirmed cases, 2020-2025

	Incidence per 100,000 inhabitants	Reported no. of cases					
Zoonotic pathogen	2025	2025	2024	2023	2022	2021	2020
Bacteria							
Brucella abortus/melitensis[a,b]	0.0	2	1	1	1	1	1
Campylobacter	95.2	5,714	5,546	5,186	5,142	3,740	3,742
Chlamydia psittaci	0.3	16	35	17	16	25	27
Leptospira spp.	0.2	14	25	13	6	10	14
Listeria monocytogenes	1.4	84	61	54	86	62	43
Mycobacterium bovis	0.0	1	0	2	0	0	0
Salmonella total	17.5	1,051	1,266	1,207	899	692	614
S. Enteritidis	4.3	255	274	384	251	114	117
S. Typhimurium[c]	3.7	223	310	174	208	205	149
Other serotypes	7.1	427	470	649[d]	344	301	302
Shigella/EIEC[e]	13.4	803	728	709	-	-	-
Shigella[f]	2.2	134	140	139	-	-	-
EIEC	1.2	73	82	63	-	-	-
STEC total[g]	17.5	1,049	1,269	1,431	1,330	927	448
O157	0.5	30	32	38	47	32	39
Other O-groups or non-typeable	3.0	183	310	375	394	376	198
HUS cases[h]	0.0	3	13	18	11	12	10
Yersinia enterocolitica total[i]	21.1	1,269	1,296	1,199	747	454	413
Yersinia enterocolitica (Biotype 2, 3, 4 and 5)	1.6	95	99	118	174	137	106
Viruses							
Lyssavirus	0.0	0	0	0	0	0	0

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) Including the monophasic variant of *S.* Typhimurium (1,4,[5],12:i:-)
d) Other serotypes and isolates not available for typing
e) The diagnostic PCR assays target the IpaH-gene shared by both *Shigella* spp. and enteroinvasive *Escherichia coli (*EIEC) species
f) Includes *Shigella* spp., *S. boydii*, *S. flexneri* and *S. sonnei*
g) Shiga toxin-producing *Escherichia coli* (STEC)
h) Clinical reported cases of hemolytic uraemic syndrome
i) A subset of *Yersinia enterocolitica* (15.5%) was isolated and sent from the local clinical departments to SSI for surveillance. Characterisation disclosed 53.7% (115 isolates) being apathogenic biotype 1a, and these are excluded from the total number for 2025

Source: Statens Serum Institut

Table A2 STEC[a] O-group distribution in humans, 2025

O-group[b]	Number of episodes	Proportion of total (%)	O-group	Number of episodes	Proportion of total (%)
O157	30	2.9	O128	10	1.0
O146	20	1.9	O91	6	0.6
O103	19	1.8	O71	5	0.5
O26	19	1.8	Other O groups	78	7.4
O145	11	1.0	Isolate not available	840	80.1
O63	11	1.0	Total	1049	
Continued in the next column					

a) Shiga toxin-producing *Escherichia coli* (STEC)
b) Top nine O-groups are listed

Source: Statens Serum Institut

Table A3 Food- and waterborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD) (N = 56), 2025

Pathogen[a]	No. of patients[b]	Patients laboratory confirmed[b]	Setting	Source	FUD no.
Campylobacter jejuni ST14804	5	5	National	Chicken meat	2494
Campylobacter jejuni ST21	5	5	National	Chicken meat	2482
Campylobacter jejuni ST21	5	5	National	Unknown	2487
Campylobacter jejuni ST22	11	11	National	Chicken meat	2502
Campylobacter jejuni ST257	5	5	National	Unknown	2481
Campylobacter jejuni ST257	6	6	National	Chicken meat	2483
Campylobacter jejuni ST475	7	7	National	Chicken meat	2486
Campylobacter jejuni ST48	9	9	National	Chicken meat	2425
Campylobacter jejuni ST49	89	89	National	Chicken meat	2470
Campylobacter jejuni ST52	31	31	National	Chicken meat	2462
Campylobacter jejuni ST8549	7	7	National	Chicken meat	2480
Clostridium perfringens	24	0	Restaurant	Mixed food	2406
Clostridium perfringens	17	0	Restaurant	Ready-to-eat chicken meat	2423
Clostridium perfringens	12	0	Catering	Burgers	2454
Clostridium perfringens	30	0	Catering	Pork stew	2466
Cryptosporidium parvum ST IIzeta A12	11	11	National	Unknown	2458
EIEC O110:H30 ST6	6	6	National	Unknown	2429
Hepatitis A, 1A	7	7	International	Unknown	2439
Continued on the next page					

Table A3 Food- and waterborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD) (N = 56), 2025 (Continued from previous page)

Pathogen[a]	No. of patients[b]	Patients laboratory confirmed[b]	Setting	Source	FUD no.
Lectins	60	0	Canteen	Black bean patties	2409
Lectins	33	0	Canteen	Bean spread	2445
Lectins	28	0	Canteen	Chilli sin carne	2450
Listeria monocytogenes ST1	7	7	National	Unknown	2319
Listeria monocytogenes ST321	4	4	National	Unknown	2464
Listeria monocytogenes ST403	7	7	National	Unknown	2465
Listeria monocytogenes ST6	2	2	National	Unknown	2514
Listeria monocytogenes ST7	11	11	National	Fish patties	2467
Listeria monocytogenes ST7	2	2	National	Unknown	2515
Norovirus	148	4	Catering	Pancakes and salad	2437
Norovirus	28	6	Catering	Cocktails	2441
Norovirus	52	0	Workplace catering	Mixed food	2469
Norovirus	43	1	Restaurant	Buffet meals	2491
Norovirus	15	0	Catering	Sandwiches	2495
Norovirus	20	0	Restaurant	Unknown	2498
Salmonella Agona ST13	4	4	National	Unknown	2501
Salmonella Enteritidis ST11	2	2	National	Unknown	2411
Salmonella Enteritidis ST11	4	4	National	Unknown	2413
Salmonella Enteritidis ST11	6	6	Restaurant	Unknown	2432
Salmonella Enteritidis ST11	5	5	National	Unknown	2456
Salmonella Enteritidis ST11	7	7	National	Unknown	2506
Salmonella Oranienburg ST174	9	9	National	Unknown	2434
Salmonella Saintpaul ST50	7	7	National	Unknown	2453
Salmonella Strathcona ST2559	29	29	International	Tomatoes (imp)	2500
Salmonella Typhimurium ST19	49	49	National	Unknown	2499
Salmonella Typhimurium ST36	7	7	National	Unknown	2448
Salmonella Typhimurium, monophasic ST19	9	9	National	Unknown	2472
Salmonella Typhimurium, monophasic ST34	11	11	National	Unknown	2473
STEC O145:H28 ST32 *(stx2a)*	4	4	National	Unknown	2484
STEC O26:H11 ST21 *(stx1a)*	4	4	National	Unknown	2457
Unknown	15	0	Restaurant	Oysters (imp)	2420
Unknown	24	0	Restaurant	Buffet meals	2485
Unknown	47	0	Restaurant	Cake and bread	2493
Unknown	27	0	Restaurant	Oysters	2510
Unknown	18	0	Restaurant	Soup	2492

Continued on the next page

Table A3 Food- and waterborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD) (N = 56), 2025 (Continued from previous page)

Pathogen[a]	No. of patients[b]	Patients laboratory confirmed[b]	Setting	Source	FUD no.
Other[c]	47	0	Restaurant	Buffet meals	2424
Other[c]	20	0	Canteen	Unknown	2444
Other[c]	7	0	Street food	Rice dish	2460
Total	1,109	405			

a) ST = Sequence Type
STEC = Shigatoxin-producing *Escherichia coli*
EIEC= Enteroinvasive *Escherichia coli*
b) Data only include outbreak cases from 2025
c) Spore-forming bacteria either *Bacillus cereus* and/or *Clostridium perfringens* suspected
Note: (imp) = imported product

Source: Food- and waterborne Outbreak Database (FUD)

Monitoring and surveillance data

Table A4 Top 15 (humans) serotype distribution (%) of Salmonella *from humans, animals, carcases, Danish and imported meat, 2025. N=number of culture positive units[a]*

	Human cases N=1,051	Pork[b] batches N=86	Beef[c] batches N=4	Broiler[d] flocks N=12	Layer[d] flocks N=4
Agona	1.3	-	-	-	-
Bareilly	1.0	-	-	-	-
Chester	1.8	-	-	-	-
Dublin	1.0	-	75.0	-	-
Enteritidis	24.3	2.3	-	25.0	-
Infantis	1.3	3.5	-	8.3	-
Muenster	1.0	-	-	-	-
Newport	1.8	-	-	-	-
Oranienburg	2.4	-	-	-	-
Paratyphi B var Java	2.0	-	-	-	-
Saintpaul	1.6	-	-	-	-
Stanley	2.0	-	-	-	-
Strathcona	3.2	-	-	-	-
Typhimurium	13.5	8.1	-	8.3	75.0
4,5,12:i:- & 4,(5),12:i:-	7.7	24.4	-	8.3	-
Other	20.4	52.3[e]	25.0[f]	50.0[g]	25.0[h]
Unknown	13.5	9.3	-	-	-

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 A30)
e) 9,12:lv:- (n=2), Derby (n=35), Give (n=5), Livingstone (n=3)
f) 9,12:-:- (n=1)
g) Coeln (n=4), Goettingen (n=1), Isangi (n=1)
h) Senftenberg (n=1)

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency and Statens Serum Institut

Table A5 Occurrence of Salmonella *in the table egg production[a], 2015-2025*

	Rearing period[b] (parent flocks)		Adult period[c] (parent flocks)		Pullet-rearing flocks		Table egg layer flocks	
	N	Positive	N	Positive	N	Positive	N	Positive
2015	15	0	8	0	123	0	344	0
2016	15	0	10	0	132	0	426	3
2017	7	0	8	1	138	1	446	3
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
2022	4	0	8	1	90	0	418	1
2023	5	0	11	0	124	0	378	7
2024	4	0	12	0	119	1	364	2
2025	6	0	10	0	105	0	387	5[d]

a) See Tables A28 and A30 for description of the surveillance programmes
b) *Salmonella* was not detected in grandparent flocks (0) during rearing period
c) *Salmonella* was not detected in grandparent flocks during adult (0) period
d) *S.* Typhimurium (4), *S.* Senftenberg (1)

Source: Danish Agriculture and Food Council, and Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A6 Occurrence of Salmonella *in the table egg layer flocks sorted by type of production, 2015-2025*

	Deep litter		Free range		Organic		Cage	
	N	Positive	N	Positive	N	Positive	N	Positive
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	2	44	1	213	1	21	0
2022	90	0	24	0	127	1	13	0
2023	95	3	21	1	109	0	11	0
2024	136	0	36	0	171	2	21	0
2025	153	2[a]	44	0	172	3[b]	18	0

a) *S.* Typhimurium (2)
b) *S.* Typhimurium (2), *S.* Senftenberg (1)

Source: Danish Agriculture and Food Council, and Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A7 Occurrence of Salmonella *in the broiler production[a], 2015-2025*

	Rearing period[b] (parent flocks)		Adult period[c] (parent flocks)		Broiler flocks		Slaughterhouse[d] (flocks/batches)	
	N	Positive	N	Positive	N	Positive	N	Positive
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	263	0
2022	166	0	267	2	3,680	6	230	2
2023	199	2	136	0	3,966	15	240	0
2024	163	0	107	0	4,239	12	233	0
2025	108	0	160	1[e]	4,531	12[f]	248	0

a) See Tables A28-A30 for a description of the surveillance programmes
b) *Salmonella* was not detected in grandparent flocks during rearing period (2 flocks)
c) *Salmonella* was detected in 1 grandparent (*S.* Typhimurium) flock during adult period (9 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.* Coeln (1)
f) *S.* 4,5,12:i:- (1), *S.* Coeln (4), *S.* Enteritidis (3), *S.* Goettingen (1), *S. I*nfantis (1), *S.* Isangi (1), *S.* Typhimurium (1)

Source: Danish Agriculture and Food Council and Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A8 Occurrence of Salmonella *in turkey flocks, 2015-2025*

	Turkey flocks[a]	
	N	Positive
2015	80	1
2016	76	0
2017	24	1
2018	13	0
2019	85[b]	0
2020	19[8]	0
2021	115	0
2022	132	3
2023	151	1
2024	109	1[c]
2025	155	2[d]

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.
c) *S.* Newport
d) *S.* Newport (1), *S.* Schleis (1)

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A9 Occurrence of Campylobacter *in broiler flocks, 2015-2025*[a]

	Cloacal swabs at slaughter		Neck skin samples at slaughter[b]	
	N (Flocks)	% pos	N (Batches)	% pos[c]
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	19.1[d]	1,150	14.3
2022	2,990	18.6	1,090	10.5
2023	3,364	22.6	1,065	8.8
2024	3,694	28.2	1,065	9.4
2025	3,701	28.3	1,140	12.5

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 >1,000 cfu/g
d) Corrected from 2022 report

Source: Danish Agriculture and Food Council and Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A10 Occurrence of Campylobacter *in non-heat treated chilled broiler meat samples at slaughter and retail*[a]*, 2019-2025*

		At slaughter[b]		At retail			
		Denmark		Denmark		Import	
		N (samples)	% pos	N (samples)	% pos[c]	N (samples)	% pos[c]
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
2022	Conventional	1,205	26.1	774	9.8	24	41.7
	Organic/free-range	98	40.8	107	25.2	43	60.5
2023	Conventional	1,232	28.6	798	14.3	32	46.9
	Organic/free-range	96	21.9	115	29.6	47	74.5
2024	Conventional	1,233	30.4	762	11.0	33	63.6
	Organic/free-range	97	50.5	143	23.1	33	75.8
2025	Conventional	1233	28.4	772	13.5[d]	30	40.0[f]
	Organic/free-range	97	49.5	92	27.2[e]	25	72.0[g]

a) Centrally coordinated studies (see Table A24 and section 7.4 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 resluts
d) *C. jejuni* (78.8%), *C. coli* (10.6%), *C.* sp. (10.6%)
e) *C. jejuni* (68.0%), *C. coli* (28.0%), *C.* sp. (4.0%)
f) *C. jejuni* (58.3%), *C. coli* (41.7%)
g) *C. jejuni* (38.9%), *C. coli* (55.6%), C. sp. (5.6%)

Source: National Food Institute and Danish Veterinary, Food, Agriculture and Fisheries Agency

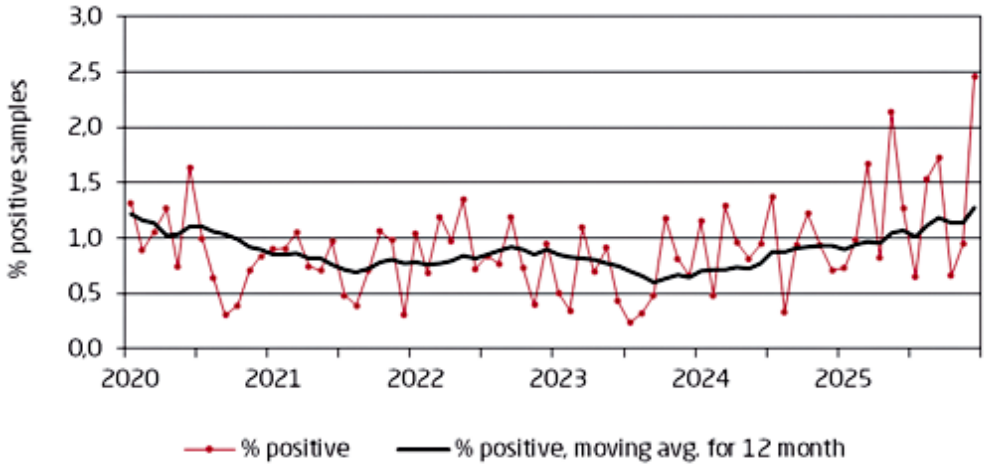
Table A11 Occurrence of zoonotic pathogens in pigs and pork in Denmark, 2025

	Herds		Animals/Samples		
Zoonotic pathogen	N	Pos	N	Pos	% pos
At slaughterhouse (slaughter pigs)					
Salmonella spp.[a,b]	-	-[g]	-	-	-
Salmonella spp.[a,c] (slaughtering >30,000 pigs/year)	-	-	14,935	-	0.95[h]
Salmonella spp.[a,c] (slaughtering 1,000 or more and less than 30,000 pigs/year)	-	-	89	-	0
Salmonella spp.[a,d]	-	-	888	116	13.1
Trichinella spp.[e]	-	-	14,897,963	0	-
Mycobacterium spp.[f]	-	-	15,570,862	0	-
Echinococcus granulosis/multilocularis[f]			15,570,862	0	-

a) See Table A33 for description of the *Salmonella* surveillance programme
b) Slaughter pig herds monitored using serological testing of meat juice samples collected at slaughter was discontinued from 1 January 2025 according to Danish Order no. 1226 of 25/11/2024
c) Swab samples from 4 designated areas after 12 hours chilling (4x100cm2)
d) Caecum samples are randomly collected from slaughter pigs at slaughter. Samples are collected according to EU Regulation (EC) 2020/1729 supplemented by samples from a centrally coordinated study (see Table A24 and section 7.4 for description)
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 extempted testing for *Trichinella*. Free range pigs must be tested for *Trichinella*
f) Slaughter pigs were examined by meat inspectors at slaughter
g) Sampling of herds discontinued from 1 January 2025 according to Danish Order no. 1226 of 25/11/2024
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 compatative studies, as described in Annual Report 2021. Furtermore, the prevalence has been adjustet for doublesampling carried out in slaughterhouses with a prevalence of 2% or above (12month average)

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency, and National Food Institute, Technical University of Denmark

Figure A1 Salmonella *in pork, monitored at slaughterhouses[a,b], 2020-2025*



a) For more information about the surveillance programme, see Table A33
b) Prevalence in graph is not adjusted for double sampling carried out in slaughterhouses with a prevalence of 2% or above

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

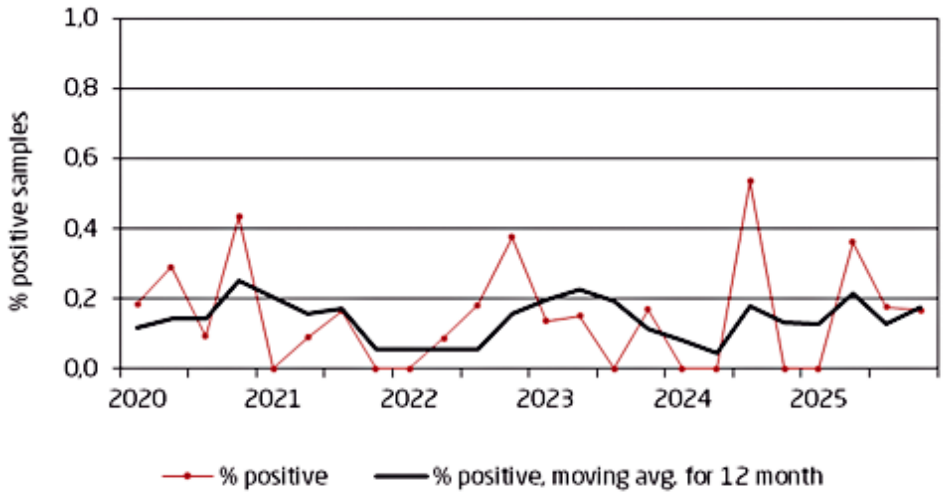
Table A12 Occurrence of zoonotic pathogens in cattle and beef in Denmark, 2025

	Animals/Samples		
Zoonotic pathogen	N	Pos	% Pos
At farm			
Brucella spp.[a]	942	0	0
Mycobacterium Tuberculosis Complex (MTBC)[b,c]	575	0	0
Coxiella burnetii[d]	3	2	67
At slaughterhouse			-
Salmonella spp.[e,f](slaughtering ≥7,500 cattle/year)	3,660	4	0.2[g]
Salmonella spp.[e,f](slaughtering ≥250 and <7,500 cattle/year)	94	0	0
Mycobacterium bovis[b]	426,268	0	-
Echinococcus granulosis/multilocularis	426,268	0	-

a) Samples are collected from bulls at semen collection centres, samples collected in connection with export and aborted fetus (n=39)
b) Analysed using the intradermal tuberculin test, testing for the MTBC, which includes *Mycobacterium bovis*, *Mycobacterium tuberculosis* and *Mycobacterium caprae*
c) Samples are collected from bulls at semen collection centres and samples collected in connection with export
d) Samples are collected from bulls at semen collection centres (n=86) and bulk milk samples (n=2). The positive sample was from a bulk milk sample
e) Swab samples from 4 designated areas after 12 hours chilling (4x100 cm²)
f) See Table A32 for description of the surveillance programme
g) 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 compatative studies, as described in Annual Report 2001

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency, Danish Veterinary Consortium, and National Food Institute, Technical University of Denmark, and SEGES Innovation P/S

Figure A2 Salmonella *in beef, monitored at slaughterhouses[a], 2020-2025*



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

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A13 Cattle herds in the Salmonella *Dublin surveillance programme[a], December 2025*

Salmonella Dublin level			Non-milk producing herds N	Non-milk producing herds %	Milk producing herds N	Milk producing herds %
Level 1		On the basis of milk samples	-	-	1,718	85.6
		On the basis of blood samples	10,561	96.7	-	-
	Total	Probably *S.* Dublin free	10,561	96.7	1,718	85.6
Level 2		Titer high in blood- or milk samples	170	1.6	236	11.8
		Contact with herds in level 2	135	1.2	29	1.4
		Other causes	61	0.6	23	1.1
	Total	Non *S.* Dublin free	366	3.3	288	14.4
Total number of herds			10,927	100	2,006	100

a) See Table A32 for description of the surveillance programme

Source: SEGES Innovation

Table A14 Salmonella *in three categories of meat and bone meal by-products not intended for human consumption[a,d], 2025*

Category of processing plant	Own-check samples N	Own-check samples Positive	Product samples N	Product samples Positive
1+2: By-products of this material cannot be used for feeding purposes	-	-	-	-
2: By-product of this material may be used for feed for fur animals[b]	-	-	-	-
3: By-products from healthy animals slaughtered in a slaughter-house. Products of these may be used for pet food[c] and for feed for fur animals	-	-	-	-
Total				

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
d) No data available for 2025

Source: Daka Denmark A/S

Table A15 Control of Salmonella *in feed processing and feed material (batch-based data), 2023-2025*

	2025[d] N	2025[d] Positive	2024 N	2024 Positive	2023 N	2023 Positive
Feed materials, farm animals[a]	-	-	61	0	69	0
Feed processing plants (process control)[b]:						
Ordinary inspections[c]	-	-	281	7	282	11

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) No samples were collected in 2025

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A16 Feed business operators own sampling of Salmonella *in compound feeds, feed processing and feed material (batch-based data), 2023-2025*

	2025		2024		2023	
	N	Positive	N	Positive	N	Positive
Compound feed, farm animals	2,934	6[d]	3,305	6	2,504	1
Feed materials, farm animals[a]	3,390	29[e]	1,908	30	1,837	36
Feed processing plants (process control):						
Ordinary inspections - clean zone[b]	8,594	5[f]	7,564	13	6,197	26
Ordinary inspections - unclean zone[b]	896	132[g]	705	65	563	32
Transport vehicles, clean zone/hygiene samples[c]	885	0	867	0	1,176	1
Transport vehicles, unclean zone/hygiene samples[c]	82	3[h]	107	16	108	15

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), fish meal, 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. Falkensee (1), S. Lille (5)
e) S. Corvallis (1), S. Cubana (2), S. enterica subspecies enterica (I)4:d:- *(1), S. Gaminara (1), S. Kentucky (1), S. Livingstone (1), S. Matadi (1), S. Mbandaka (4), S. Molade (4), S. Putten (1), S. Quakam (1), S. Rissen (1), S. Senftenberg (6), S. Soerenga (2), S. Yarrabah (1), S. Yoruba (1)
f) S. Lille (2), S. Derby (1), S. Havana (1), S. Schleissheim (1)
g) S. Agona (4), S. Falkensee (2), S. Idikan, (1) S. Infantis (2), S. Poona (1), S. Putten (59), S. Rissen (25), S. Schleissheim (38)
h) S. Infantis (2), S. Leeuwarden (1)

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency, Danish Grain & Feed Trade Association and the feed business operators

Table A17 Listeria monocytogenes *in Danish and non-Danish produced ready-to-eat (RTE) foods[a], 2025*

			Samples analysed by a qualitative method[b]		Samples analysed by a quantitative method	
			Batches		Batches	
	Food category	Sampling place	N	Positive	N	Positive[c]
Danish	Fish and fishery products, RTE	Wholesale	5	1	21	0
	Products made from beef, RTE	Wholesale	2	0	3	0
	Products made from pork, RTE	Wholesale	13	1	19	0
	Products made from chicken, RTE	Wholesale	0	0	1	0
	Other meats, RTE	Wholesale	1	0	5	0
	Other, RTE[d]	Wholesale	7	1	27	0
Non-Danish[e]	Crustaceans, RTE	Border inspection	0	0	10	0
	Crustaceans, RTE	Processing plant	0	0	15	0
	Molluscan Shellfish, RTE	Border inspection	0	0	5	0
	Surimi, RTE	Border inspection	0	0	2	0
	Duck meat, RTE	Border inspection	0	0	1	0
	Total		28	3	109	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 10 or 25 g sample of the product
c) Levels > 10 cfu/g
d) The positive sample batch is classified as "Ready-to-eat salads - containing mayonnaise"
e) Samples from Canada, Chile, China, Greenland, United States, Vietnam

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A18 Histamine in batches of Danish and non-Danish fish products[a,b], 2025

		Danish		Non-Danish[c]	
Food category	Sampling place	N	Positive	N	Positive
Fish sauce	Border inspection	-	-	27	18
Fish, unspecified, canned	Border inspection	-	-	171	0
Fish, unspecified, raw	Border inspection	-	-	45	0
Total		-	-	243	18

a) Samples are collected by the local food control offices according to EU Regulation (EC) No 2073/2005
b) The findings of histamine did not exceed the limits according to EU Regulation (EC) No 2073/2005
c) Samples from Ecuador, El Salvador, Ghana, Indonesia, Mauritius, Philippines, Thailand, United Kingdom, Vietnam

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A19 Salmonella *in Danish and non-Danish produced food items[a], 2025*

Food category	Sampling place	N	Positive	N	Positive
Products made from poultry, intended to be cooked	At border inspection	-	-	35	0
Products made from beef, RTE[c]	At processing	5	0	-	-
Products made from pork, RTE[c]	At processing	60	0	-	-
Products made from other animal species, RTE[c]	At processing	5	0	-	-
Crustaceans, RTEc	At border inspection	-	-	50	0
	At processing	-	-	75	0
Molluscan shellfish, RTE[c]	At border inspection	-	-	25	0
Seeds, sprouted, RTE[c]	At processing	10	0	-	-
Other products of animal origin	At border inspection	-	-	15	0
Total		80	0	200	0

a) Samples are collected by the local food control offices according to EU Regulation (EC) No 2073/2005
b) Samples are from Brazil, Canada, Chile, China, Greenland, Thailand, United States and Vietnam
c) Ready-to-eat

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A20 Occurrence of zoonotic pathogens in pets and zoo animals in Denmark[a], 2025

	Pet animals								Zoo animals			
	Dogs		Cats		Pigs		Others[c]		Mammals & reptiles		Birds	
Zoonotic pathogen	N	Pos	N	Pos	N	Pos	N	Pos	N	Pos	N	Pos
Chlamydia psittaci[b]	0	0	0	0	0	0	15	7	0	0	0	0
Echinococcus spp.	0	0	0	0	0	0	0	0	0	0	-	-
Lyssavirus (classical)[d]	1	0	3	0	0	0	0	0	3	0	-	-
European Bat Lyssavirus	0	0	0	0	0	0	0	0	0	0	0	0
West Nile virus[c]	0	0	0	0	0	0	5	0	0	0	0	0
Highly pathogenic avian influenza	4	0	3	0	0	0	41	0	0	0	57[e]	0
Swine influenza virus[f]	0	0	0	0	400	254	0	0	0	0	0	0

a) Samples does not reflect the country prevalence, as most samples are analysed based on suspicion of disease
b) A bird can have been examined multiple times using different sample materials. Therefore, the numbers N and Pos represent the samples analysed and the samples that tested positive
c) In the case of *Chlamydia psittaci*, others refer to captive birds. In the case of West Nile virus, others refer to horses. In the case of Highly pathogenic avian influenza, others refer to pools from pigs (n=4), individual sheep (n=6), pools from sheep (n=3), individual cattle (n=27) and pools from cattle (n=1)
d) The zoo animals are bats
e) Several different bird species kept in zoo
f) Tested in the national passive surveillance of influenza A virus in pigs

Source: Danish Veterinary Consortium and the Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A21 Occurrence of zoonotic pathogens in wild and farmed wildlife in Denmark[a], 2025

	Farmed wildlife						Wildlife			
	Wild boar		Mink & chinchillas		Birds		Mammals		Birds	
Zoonotic pathogen	N	Pos	N	Pos	N	Pos	N	Pos	N	Pos
Echinococcus multilocularis	-	-	-	-	-	-	188	4	N.R.	-
Lyssavirus (classical)[b]	-	-	-	-	-	-	2	0	0	0
European Bat Lyssavirus[c]	-	-	-	-	-	-	105	0	0	0
West Nile virus[d,e]	-	-	-	-	-	-	19	0	462	0
Highly pathogenic avian influenza[f]	-	-	0	0	30[g]	0	56[h]	1	627[i]	161

a) All samples are analysed based on suspicion of disease or risk based surveillance, and does not reflect the country prevalence
b) The mammals are red foxes
c) The mammals are bats. These samples originate from both dead bats (brain material, n=28) and living bats (saliva, n=77)
d) The mammals are bats
e) Samples originate from dead wild birds (brain material, n =126) and living migratory wild birds (serum, n=336). No samples were positive for West Nile Virus, while approx. 4% of analysed serum samles (13/336) tested positive or inconclusive for antibodies against flaviviruses
f) The positive wild mammal was a red fox with H5N1. Data for HPAI surveillance in wild birds can also be seen at https://ai.fvst.dk/. Samples were collected and tested under OH4Surveillance, which is co-funded by the European Union (Grant Agreement No 101132473)
g) The samples are pools of up to 10 birds of mallard ducks (n=29) and pheasants (n=1)
h) Four samples were collected and tested under OH4Surveillance, which is co-funded by the European Union (Grant Agreement No 101132473)
i) These samples are both pools of up to 5 birds (n=289) and samples from individual birds (n=338). Data for HPAI passive surveillance in wild birds can also be seen at https://ai.fvst.dk/

Source: Danish Veterinary Consortium and Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A22 The Bovine Spongiform Encephalopathy (BSE) surveillance programme[a] for cattle, 2025

Type of surveillance	N[b]	Positive
Active surveillance		
Slaughtered animals	0	0
Risk categories:		
Emergency slaughters	1,407	0
Slaughterhouse antemortem inspection revealed suspicion or signs of disease	0	0
Fallen stock (>48 months)	19,254	
Animals from herds under restriction	0	0
Passive surveillance		
Animals suspected of having clinical BSE	0	0
Total	20,661	0

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 an IDEXX technique or Bio-Rad. Confirmatory testing is carried out using western blotting, histopathology, or immunohistochemistry. Further confirmation on autolysed material is performed at the European Union TSE reference laboratory

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency, data extraction from the EFSA database, 31 March 2026

Table A23 The Transmissible Spongiform Encephalopathy (TSE) surveillance programmea for sheep and goats, 2025

Type of surveillance	N[b] goats	Positive	N[b] sheep	Positive
Active surveillance				
Animals from herds under restriction	0	0	0	0
Fallen stock (>18 months)	115	0	485	1
Slaughtered for human consumption	0	0	0	0
Passive surveillance				
Animals suspected of having clinical TSE	0	0	0	0
Total	115	0	485	1

a) According to the EU Regulation (EC) 999/2001 as amended and Danish Order no. 1491 of 12/12/2019 as amended
b) Samples (brain stem material) are tested using a Bio Rad . Confirmatory testing is carried out using histopathology or immunohistochemistry. Further confirmation on autolysed material is performed at the European Union TSE reference laboratory
c) Denmark do not test slaughter animals

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency, data extraction from the EFSA database, 31 March 2026

Table A24 Examples of centrally coordinated studies planned for 2025

Title of project	No. of planned samples	Pathogen surveyed	Further information[a]
BU microbiology - slaughterhouses	120	various	Not published
Campylobacter spp. in fresh, chilled Danish broiler meat at slaughterhouses (conventional)	1,250	*Campylobacter* spp.	To be published
Campylobacter spp. in fresh, chilled Danish broiler meat at slaughterhouses (organic)	100	*Campylobacter* spp.	To be published
Campylobacter spp. in fresh, chilled Danish broiler meat	800	*Campylobacter* spp.	Appendix Table A10
Campylobacter spp. in imported broiler meat	40	*Campylobacter* spp.	Appendix Table A10
Campylobacter spp. in imported and intratraded poultry meat	130	*Campylobacter* spp.	To be published[a]
DANMAP - Antibiotic resistance in poultry, pork and cattle	165	AMR	To be published
DANMAP and EU surveillance Surveillance of antibiotic resistance at slaughterhouses	730	AMR	To be published
EU surveillance of antibiotic resistance in retail	630	AMR	To be published
EU MRSA-surveillance at slaughterhouses	460	*E. coli,* MRSA	Not published
Export - USA - environmental samples	100	*Listeria monocytogenes*	Not published
Export - USA swab	420	*Salmonella* spp.	Not published
IMPORT - Intensified control of Brazilian beef and poultry meat	10	*Salmonella* spp, *Listeria monocytogenes*	To be published
IMPORT - Microbiologic control of fish, fish products and bivale molluscan shellfish from 3rd.countries	110	*Listeria monoctogenes, Salmonella* spp.	To be published
IMPORT - Microbiological control of food of animal origin, excluding fish	30	*Listeria monoctogenes, Salmonella* spp.	To be published
IMPORT - Special control microbiology - not animal Reg.(669/2009)	100	*Various*	To be published
Listeria monocytogenes, Salmonella spp., Escherichia coli and staphylococci in fish producs from Greenland	105	*Listeria monocytogenes,* S*almonella* spp., *Escherichia coli*, staphylococci	To be published
Microbiological classification of mussel production areas in Denmark	60	*Salmonella* spp., *Escherichia coli*	To be published
Fish and fish products	165	*Listeria monocytogenes*	To be published
Listeria monocytogenes in other RTE products - wholesale	240	*Listeria monocytogenes*	To be published
Meat products	240	*Listeria monocytogenes*	To be published
Listeria in the production environment	400	*Listeria monocytogenes*	To be published
Plant-based replacements for meat & dairy prodcts	100	Various	To be published
Salmonella in pet feed materials	120	*Salmonella* spp.	To be published

Continued on the next page

Table A24 Examples of centrally coordinated studies planned for 2025 (Continued from previous page)

Title of project	No. of planned samples	Pathogen surveyed	Further information
Salmonella in fresh poultry meat	600	*Salmonella* spp.	To be published
Salmonella & AMR in pig carcasses	500		To be published
STEC in leafy green	25	STEC	To be published
Norovirus in soft berries & leafy green	50	Norovirus	To be published

a) Results will be published on the DVFAFA website www.fvst.dk (in Danish)

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A25 Status on targets for Campylobacter *and* Salmonella, *2025*

National Action Plans	Target	Status
Campylobacter in broilers 2022-2026		
Flocks at farm	Maintaining low prevalence in flocks of 15% for conventional and 65% for organic/free-range flocks	The prevalance in flocks in 2025 was 24.7% for conventional flocks and 57.7% for organic/free-range flocks
Fresh meat at slaughterhouse[a]	In 2023 individual targets per slaughterhouse was decided. 1) A target on prevalence 2) A target on proportion of positive samples >1000 cfu/g in the summer period (june-october) and winter period (november-may)	1) None of the four slaughterhouses met their targets on prevalence in 2025 2) Three out of the four slaughterhouses met their targets on proportion of positive samples >1,000cfu/g in the winter period 2024-2025 and three out of four met their targets in the summer period 2025
Salmonella in poultry[b]		
Laying hen flocks of *Gallus gallus*	Initially eradication, later a reduction strategy in the table egg production	5 positive flocks (1.3%) (Table A5-A6) Eggs from positive flocks are destroyed or heat treated
Carcases at slaughterhouse	Initially eradication, later a reduction strategy in the broiler production	0 positive batches (Table A7) Positive batches are heat treated
Salmonella in pigs 2014-2017		
Carcases at slaughterhouse	Max. 1% *Salmonella* at carcass level	0.95% (Table A11)
Salmonella Dublin in cattle 2021-2025		
Herds at farm	Eradication of *S.* Dublin in all herds, i.e. all herds in level 1[c]	14.4% of milk-producing herds and 3.3% 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 *S.* Enteritidis and *S.* Typhimurium[d]	No fattening flocks positive with target serovars (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	No flocks flocks positive with target serovars (Table A5 and A7)
Regulation (EC) No. 1168/2006		
Laying hen flocks of *Gallus gallus*	MS specific targets, for Denmark: Max. 2% adult flocks positive for *S.* Typhimurium[d] and *S.* Enteritidis	1% (4 flocks) positive with target serovars (Table A5)
Regulation (EC) No. 646/2007		
Broiler flocks of *Gallus gallus*	Max. 1% positive *S.* Typhimurium[d] and *S.* Enteritidis	0.1% (6 flocks) positive with target serovars (Table A7)

a) Targets on prevalence were set as a reduction on the 3-year average from 2019-2021
b) Supplementary to EU-regulations
c) See Table A32 for an explanation of the herd levels
d) Including the monophasic variant of *S.* Typhimurium (S. 1,4,[5],12:i:-)

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Monitoring and surveillance programmes

Table A26 Overview of referral of isolates, individual and laboratory notifiable human diseases presented in this report, 2025

Microorganism	Notification type[a,b,c]	Referral of isolates or biological material to SSI[a]	Portion (%) of cases received as isolates or biological material
Bacteria			
Brucella spp.	Laboratory	Mandatory[d]	NA[f]
Campylobacter spp.	Laboratory	Voluntary[d]	12.1
Chlamydophila psittaci (Ornithosis)	Laboratory and clinical notification	Mandatory	NA
Listeria monocytogenes	Laboratory	Mandatory[d]	96.4
Leptospira spp.	Laboratory and clinical notification	No	-
Mycobacterium bovis/tuberculosis	Laboratory and clinical notification	No[e]	-
Coxiella burnetii	Laboratory	No	-
Salmonella spp.	Laboratory	Mandatory[d]	86.3
Shigella spp. and EIEC[g]	Laboratory and clinical notification	Voluntary[d]	23.3
STEC[h]	Laboratory and clinical notification	Mandatory from patients with HUS, all other voluntary[d]	20.6
Yersinia enterocolitica	Laboratory	Voluntary[d]	15.5
Parasites			
Cryptosporidium spp.	Laboratory	Mandatory when outb-reak suspected	NA
Echinococcus multilocularis	Laboratory	Mandatory	NA
Echinococcus granulosus	Laboratory	Mandatory	NA
Trichinella spp.	Laboratory	No	-
Viruses			
Lyssavirus (Rabies)	Laboratory and clinical notification	No[e]	-
Prions			
BSE/ variant Creutzfeld Jacob	Laboratory and clinical notification	No	-

a) According to the Danish Order no. 260 of 27/10/2023
b) The regional microbiological laboratories report confirmed cases
c) The physician report individually notifiable infections
d) Only isolates
e) All diagnostics are carried out at SSI, therefore there is no requirement for further submission
f) Not applicable, implemented by November 1, 2023
g) The diagnostic PCR assays target the IpaH-gene shared by both *Shigella* spp. and enteroinvasive *Escherichia coli* (EIEC) species
h) Shiga toxin-producing *Escherichia coli* (STEC)

Source: Statens Serum Institut

Table A27 Overview of notifiable and non-notifiable animal diseases presented in this report, 2025

Pathogen	Notifiable	EU legislation	Danish legislation
Bacteria			
Brucella spp.	1920[a]		
Cattle	OBF in 1979[b]	Regulation (EU) 2021/620	Order no 542 of 22/05/2025
Sheep and goats	ObmF in 1995[c]	Regulation (EU) 2021/620	Order no 542 of 22/05/2025
Pigs	Outbreak of B*rucella suis* in 2025[d]	Regulation (EU) 2016/429	-
Campylobacter spp.	No	-	-
Chlamydophila psittaci			
Birds and poultry	1920	-	-
Listeria monocytogenes	No	-	-
Leptospira spp. (only in production animals)	2003	Decision 1999/22/EC	Order no. 1246 of 20/11/2024
Mycobacterium bovis/ tuberculosis	1920[a]		
Cattle	OTF in 1980[e]	Decision 2003/467/EC	Order no. 1290 of 10/11/2023
Coxiella burnetii	2005	-	Order no. 1246 of 20/11/2024
Salmonella spp.	1993[f]	-	-
Cattle	-	-	Order no. 777 of 18/06/2025
Swine	-	-	Order no. 1226 af 25/11/2024
Eggs for consumption	-	-	Order no. 524 of 22/05/2025
Hatching eggs	-	-	Order no. 1247 of 23/10/2023
Poultry for slaugther	-	-	Order no. 525 of 22/05/2025
STEC	No	-	-
Yersinia enterocolitica	No	-	-
Parasites			
Cryptosporidium spp.	No	-	-
Echinococcus multilocularis	2004	Regulation (EU) 2016/429	Order no. 1246 of 20/11/2024
Echinococcus granulosus	1993	Regulation (EU) 2016/429	Order no. 1246 of 20/11/2024
Trichinella spp.	1920[a]	Regulation (EU) 2015/1375	Order no. 1714 of 15/12/2015
Viruses			
Lyssavirus (Rabies)	1920	Regulation (EU) 2021/620	-
Prions			
TSE			
Sheep and goats	Yes	Regulation 999/2001/EC (as amended)	Order no. 1491 of 12/12/2019
BSE			
Cattle	Yes[g]	Regulation 999/2001/EC (as amended)	Order no. 1442 of 11/12/2019

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 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) Last case was in 1999
e) 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
f) Only clinical cases notifiable
g) Denmark was recognized as a country with negligible risk for BSE at World Organisation for Animal Health (OIE) general session in May 2011

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

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, 2025*

Time	Samples taken	Material	Material
Rearing flocks		*Grandparent generation*	*Parent generation*
Day-old[a,b,c]	Per delivery	5 transport crates from one delivery: crate liners (>1 m2 in total) or swab samples (>1 m2 in total). Analysed as one pool	5 transport crates from one delivery: crate liners (>1 m2 in total) or swab samples (>1 m2 in total). Analysed as one pool
1st & 2nd week[b, c]	Per unit	-	2 pairs of boot swabs (analysed as one pooled sample) or 1 faecal sample of 60 g
4th week[a,b,c]	Per unit	5 pairs of boot swabs (analysed as two pooled samples), or 1 faecal sample consisting of 2x150 g	2 pairs of boot swabs (analysed as one pooled sample) or 1 faecal sample of 60 g
8th week[b,c]	Per unit	2 pairs of boot swabs (analysed as one pooled sample) or 1 faecal sample of 60 g	2 pairs of boot swabs (analysed as one pooled sample) 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 pooled samples), or 1 faecal sample consisting of 2x150 g	2 pairs of boot swabs (analysed as one pooled sample) or 1 faecal sample of 60 g
Adult flocks		*Grandparent generation*	*Parent generation*
After each hatch[b,c,e]	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,f]	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[f]	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 after moving, 8-0 weeks before slaughter	Per unit	5 pairs of boot swabs (analysed as two pooled samples), or 1 faecal sample consisting of 2x150 g	5 pairs of boot swabs (analysed as two pooled samples), or 1 faecal sample consisting of 2x150 g
22-24 weeks after moving[f]	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,g]	Per unit	5 pairs of boot swabs (analysed as two pools), 2 dust samples (250 ml) and 5 birds (analysed for antimicrobial substances)	5 pairs of boot swabs (analysed as two pools), 2 dust samples (250 ml) and 5 birds (analysed for antimicrobial substances)

a) Sampling requirements set out by Regulation (EC) No 200/2010
b) Samples collected by the food business operator
c) Sampling requirements set out by Danish Order no. 1247 of 23/10/2023
d) Samples collected by the Danish Veterinary, Food, Agriculture and Fisheries Agency
e) Sampling requirements set out by Danish Order no. 1247 of 23/10/2023
f) If samples are negative, sampling is repeated 14 days later

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A29 Salmonella *and* Campylobacter *surveillance programme for the broiler flocks, 2025*

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 samples can be pooled into 2 pools
7 - 10 days before slaughter[d,e]	Per flock	5 pairs of boot swabs. Herds up to 500 animals: the 5 samples can be pooled into 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 g, pooled into subsamples of 60 g from one batch per week. From slaughterhouses slaughtering less than 1,000 chickens or hens per day: 15 neck skin samples of approx. 10 g pooled into 5 subsamples of 25 g 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[g,h]
After slaughter[b,d,f]	Per batch	From slaughterhouses slaughtering 1,000,000 chickens or more per year: 15 neck skin samples of approx. 10 g, pooled into five subsamples of 25 g from one batch per week. From slaughterhouses slaughtering less than 1,000,000 chickens per year and more than 10,000: 15 neck skin samples of approx. 10 g pooled into 5 subsamples of 25 g from one batch every tenth day of slaughter

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, Food, Agriculture and Fisheries Agency
d) Sampling requirements set out by Danish Order no. 1819 of 02/12/2020 replaced by Danish Order no. 525 of 22/05/2025
e) Samples are collected by a representative of the slaughterhouse, laboratory or the Danish Veterinary, Food, Agriculture and Fisheries Agency
f) Sampling requirements set out by Regulation (EC) 2073/2005
g) For flocks to be slaughtered outside Denmark, 1 pair of boot swabs is collected by the owner 10 days before slaughter at the latest
h) If the flock is slaughtered over several days, the last batch is sampled

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A30 Salmonella *surveillance programme for the pullet-rearing, table egg layer and barnyard/hobby flocks in the table egg production, 2025*

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 pooled sample)
4, 8, and 10 weeks old and 1 week before moving[a,b]	Per flock	5 pairs of boot swabs (analysed as two pooled samples) or 5 faeces samples of 60 g
2 weeks before moving[a,c]	Per flock	5 pairs of boot swabs (analysed as two pooled samples) or 5 faeces samples of 60 g
Table egg layers (Production for certified packing stations)		
24 weeks old[a,c]	Per flock	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample consisting of 2x150 g. 250 ml (100 g) dust or a dust sample by a cloth of min. 900 cm^2
Every 2 weeks from age 20 weeks[a,b,d,]	Per flock	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample consisting of 2x150 g
After positive serological findings[c]	Per flock	5 pairs of boot swabs (analysed as two pooled samples) or 5 faecal samples consisting of 60 g each
After positive findings of other serotypes than *S.* Enteritidis, *S.* Hadar, *S.* Infantis, *S.* Virchow or *S.* Typhimurium including the monophasic variant S. 1,4,[5],12:i:-c	Per flock	5 pairs of boot swabs (analysed as two pooled samples) or 5 faeces samples consisting of 60 g 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 g each (analysed as one pooled sample)

a) Sampling requirements set out by Danish Order no. 524 of 22/05/2025
b) Samples collected by the food business operator
c) Samples collected by the Danish Veterinary, Food, Agriculture and Fisheries Agency
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

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A31 Salmonella *surveillance programme for the turkey flocks, 2025*

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.525 of 22/05/2025
b) Samples collected by the food business operator or the local food control offices

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A32 Salmonella *surveillance programme[a] for the cattle production, 2025*

No. of samples	Samples taken	Purpose/Comment
Milk producing herds		
4 samples distributed over a maximum of 18 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 at non-milk producing farms, depending on whether the heifers are owned by a single or several owners	Blood samples	Calculation of herd level[b,d]
Beef carcases at the slaughterhouse		
5 samples daily, pooled into one analysis	Swab samples from 4 designated areas after 12 hours chilling (4x100 cm^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 (4x100 cm^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 (4x100 cm^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. 777 of 18/06/2025. It is compulsory to have an action plan to eradicate *Salmonella* Dublin in Level 2 herds. Prior to 1st of July 2021, sampling of heifer herds was not 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

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency and SEGES

Table A33 Salmonella *surveillance programme[a] for the pig production, 2025*

Time	Samples taken	Purpose/Comment
Slaughter pigs, animals		
At slaughter[f]	Caecum samples, avg. 25 samples per month, 12 months per year	Random collection of samples for monitoring of the distribution of serotypes and antimicrobial resistance.
Pork carcases at the slaughterhouse		
5 samples daily, pooled into one analysis[g]	Swab samples from 4 designated areas after 12 hours chilling (4x100cm2)	Slaughterhouses slaughtering more than 30,000 pigs per year
5 samples every second month	Swab samples from 4 designated areas after 12 hours chilling (4x100cm2)	Slaughterhouses slaughtering 10,000 or more pigs and less than 30,000 pigs per year
10 samples per year, 5 each 6 month	Swab samples from 4 designated areas after 12 hours chilling (4x100cm2)	Slaughterhouses slaughtering 1,000 or more pigs and less than 10,000 pigs per year
No sampling	-	Slaughterhouses slaughtering less than 1,000 pigs per year

a) Sampling requirements set out by Danish Order no. 1226 of 25/11/2024.
b) Centrally coordinated study (Table A24)
c) If a slaughterhouse detects more than one positive sample in a rolling window of 11 slaughter days, the slaughterhouse must follow up according to Danish Order no. 1226 of 25/11/2024
d) If a slaughterhouse, within the last month, detects *Salmonella* and at the same time has a *Salmonella* prevalence above or equal to 2% (12 month average), the sampling frequency doubles to 10 samples daily, pooled into two analysis with 5 samples in each. If the 12 month averrage continues to be above or equal to 2% 4 times within a 6 month period, the slaughterhouse must follow up according to Danish Order no. 1226 of 25/11/2024

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency

Table A34 Typing methods used in the surveillance of foodborne pathogens in Denmark, 2025

Methods	Human[a]	Food	Animal
Salmonella enterica			
Serotyping	All isolates by WGS and a subset phenotypically tested	All isolates (by WGS)[b]	All isolates (by WGS)[b]
Antimicrobial resistance	All isolates by WGS and most phenotypically tested	Almost all isolates	Isolates for DANMAP and EFSA
WGS (ST and cluster analysis)	All isolates	All isolates[b]	All isolates[b]
Campylobacter coli/jejuni			
Antimicrobial resistance	All isolates by WGS and phenotypically tested	Isolates for DANMAP and EFSA surveillance of antimicrobial resistance	Isolates for DANMAP and EFSA surveillance of antimicrobial resistance
WGS (ST and cluster analysis)	All isolates	40 - 100% of positive isolates (varies between studies. Isolates primarily from chilled chicken meat)[b]	Isolates for DANMAP and EFSA surveillance of antimicrobial resistance
STEC[c]			
Serotyping	All isolates by WGS and a subset phenotypically tested	All isolates (WGS)	None
Virulence profile	All isolates by WGS and a subset by PCR	All isolates (by PCR & WGS)	None
Antimicrobial resistance	All isolates by WGS	None	None
WGS (ST and cluster analysis)	All isolates	All isolates	None
Listeria			
WGS (ST and cluster analysis)	All isolates	Selected isolates	None
Yersinia enterocolitica			
Serotyping	All isolates	None	None
WGS (ST and cluster analysis)	Outbreaks investigations, research	None	None
Shigella/EIEC[d]			
Biochemical separation of *Shigella* spp. and EIEC	All isolates	None	None
Species designation and serotyping	All isolates	None	None
Antimicrobial resistance (*Shigella* spp. only)	All isolates phenotypically tested	None	None
WGS (ST and cluster analysis)	Outbreaks investigations, research	None	None

a) All isolates include the isolates referred to SSI for surveillance as outlined in Table A26
b) Other commercial laboratories have been used for some centrally coordinated studies. Alternative methods (not listed here) may have been used for these samples
c) Shiga toxin-producing *Escherichia coli* (STEC)
d) The PCR assays target the *IpaH*-gene shared by both *Shigella* spp. and enteroinvasive *Escherichia coli* (EIEC) species

Source: Statens Serum Institute and Danish Veterinary, Food, Agriculture and Fisheries Agency, Laboratory

Population and slaughter data

Table A35 Human population, 2025

Age groups (years)	Males	Females	Total
0-4	155,208	146,308	301,516
5-14	321,628	305,313	626,941
15-24	371,207	354,616	725,823
25-44	780,801	755,860	1,536,661
45-64	772,862	777,469	1,550,331
65+	582,679	678,469	1,261,148
Total	2,984,385	3,018,035	6,002,420

Source: Statistics Denmark, 1 July 2025

Table A36 Number of livestock establishments, livestock and animals slaughtered, 2025

	No. of establishments	Livestock (capacity)	Number slaughtered
Slaughter pigs	6,109	12,659,424	15,570,862
Cattle	12,944	1,399,423	426,268
Broilers	318	21,890,778	106,336,645
Layers (excl. barnyard)	414	5,740,451	-
Turkeys	24	311,996	4,876
Sheep & lambs	5,200	126,821	61,501[a]
Goats	3,014	17,539	-
Horses	20,938	25,775	452

a) Number of sheep, lamb and goats slaughtered

Source: Statistics Denmark and Danish Veterinary, Food, Agriculture and Fisheries Agency - the Central Husbandry Register, May 2026

Table A37 Number of establishments, flocks and livestock capacity in the broiler production, 2025

	No. of establishments	No. of flocks	Livestock (capacity)
Rearing period (grandparent)	1	2	50,000
Adult period (grandparent)	3	8	81,500
Rearing period (parent)	19	85	680,300
Adult period (parent)	46	127	1,015,200
Hatcheries	5	0	0
Broilers	318	683	21,890,778

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency, April 2026

Table A38 Number of establishments, flocks and livestock capacity in the table egg production, 2025

	No. of establishments	No. of flocks	Livestock (capacity)
Rearing period (grandparent)	0	0	0
Adult period (grandparent)	0	0	0
Rearing period (parent)	4	4	28,800
Adult period (parent)	8	8	53,500
Hatcheries	5	0	0
Pullet-rearing	33	53	1,288,300
Layers (excl. barnyard)	139	232	4,613,084

Source: Danish Veterinary, Food, Agriculture and Fisheries Agency, April 2026

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ISBN: 978-87-7586-087-6