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Annual Report on Zoonoses in Denmark 2024

DTU National Food Institute

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Contents

Introduction

The Annual Report on Zoonoses in Denmark represents one of the longest One Health collaborations in Denmark. The report is produced annually in a collaboration between the National Food Institute at the Technical University of Denmark, Statens Serum Institut, The Danish Veterinary and Food Administration and a network of partners. The chapters are discussing relevant events in the year 2024 and an in-depth analysis of zoonotic infections in humans, animals, the environment and the appendices compile as the occurrence of zoonotic agents in food and feeding stuffs in Denmark. The report has been created as a resource for policymakers, industry, researchers, public health officials, and the general public, offering insights into the efforts and effectiveness of the current control measures and highlighting areas that require further attention.

Food- and Waterborne Outbreaks

In 2024, 55 foodborne outbreaks were reported, resulting in 1,126 human infections. This represents a decrease from the previous year, when 64 outbreaks were registered. The reduction in outbreaks is primarily attributed to fewer *Salmonella* outbreaks.

Ten national *Salmonella* outbreaks were registered in 2024, with three being part of international outbreaks. Two significant outbreaks were linked to minced beef, with one caused by *Salmonella* Typhimurium and the other by *Salmonella* monophasic Typhimurium. In both outbreaks, a trend was noticed that several patients had consumed raw minced beef – either by tasting the raw minced beef before cooking it or eating it as steak tartare. This led to early warnings from the authorities with the public health message to cook minced beef properly before eating.

Norovirus was responsible for 16 foodborne outbreaks in 2024, an increase from 13 outbreaks in 2023. Eight point-source outbreaks related to restaurants and canteens were caused by the same genotype GII.17[P17]. Fresh produce was suspected as the common source.

The number of *Campylobacter* outbreaks remained stable, with ten outbreaks reported in 2024, similar to the 11 outbreaks in 2023. Seven outbreaks were linked to chicken meat.

Two prolonged *Listeria* outbreaks were linked to a Danish fish producer. Patients from Germany, Italy, and Sweden were also linked to these outbreaks and the same *Listeria* types were found in product samples from the Danish company. A regional outbreak of gastroenteritis among school children was associated with drinking milk and consuming silage. A small outbreak of hepatitis A was reported, with dried dates as the suspected.

Non-Foodborne Emerging Zoonoses and Threats

KOZO, the coordination group for zoonotic threats in Denmark, facilitated cross-sector collaboration to address zoonotic threats, including avian influenza, psittacosis, tick-borne encephalitis, and Usutu virus. The group also focused on preparedness plans for new threats such as West Nile Fever and mpox.

In 2024, KOZO focused on the H5N1 outbreak in cattle in the USA, prompting frequent meetings to evaluate information and establish comprehensive risk assessments.

KOZO addressed an outbreak of psittacosis in humans, the expansion of tick-borne encephalitis in new locations, and the first detection of Usutu virus in blackbirds.

Surveillance of Zoonotic *Echinococcus multilocularis* and *Trichinella* spp. in Red Foxes

A national study revealed a prevalence of 2.7% for *E. multilocularis*, with significant regional variations. Higher local prevalence was found in Tønder and Skive Municipalities.

Trichinella spp. was not detected in the sampled foxes, indicating a negligible risk of transmission to humans and domestic animals.

The Annual Report on Zoonoses presents a summary of the trends and sources of zoonotic infections in humans and animals, as well as the occurrence of zoonotic agents in food and feeding stuffs in Denmark in 2024. 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

Vectorborne Zoonoses

Usutu virus was detected in birds in Denmark for the first time in 2024. The virus was found in blackbirds from various locations, indicating local infection.

Targeted West Nile virus surveillance was conducted as part of the OH4Surveillance EU project. Denmark experienced its first outbreak of Bluetongue Virus serotype 3 (BTV-3) since 2008.

In 2024, 22 human Tick-Borne Encephalitis Virus cases were confirmed, with the majority of infections acquired in Denmark. Detailed tracking and flagging of areas with high tick density helped identify new infection sources.

The presence of exotic ticks like Hyalomma and Dermacentor reticulatus was noted. These ticks can carry and transmit dangerous pathogens, increasing the risk of disease spread.

Advances in *Campylobacter* Interventions and Surveillance in Denmark

Projects like OutCampy and SafeChicken focused on reducing *Campylobacter* in free-range and organic broiler flocks. The SafeChicken project investigated the effect of feed and water additives as potential on-farm intervention tools.

IceGun-technology, was assessed for its effectiveness in reducing *Campylobacter* load on broiler carcasses. The technology showed a significant reduction in *Campylobacter* on neck skins compared to conventional air-chilling.

Whole genome sequencing (WGS) was used to enhance *Campylobacter* control in broilers. The *Campylobacter* transmission dynamics project extended previous studies by further investigating transmission pathways and genomic stability. The PorA-method, a novel sequence-based typing method, was developed to improve detection and investigation of *Campylobacter* contamination in poultry production.

Listeria in ready-to-eat-foods

The new EU regulations on *Listeria monocytogenes* in ready-to-eat (RTE) foods, particularly sliced cold cuts, aim to reduce listeriosis in the population, which has been rising in the EU. From July 1, 2026, these regulations are in effect and require food business operators (FBOs) to ensure that *Listeria* levels do not exceed 100 CFU/g throughout the product's shelf-life or demonstrate its absence in 25 g samples. Denmark, despite stable listeriosis rates, has higher incidences compared to the EU average, primarily due to RTE foods.

To comply with the new rules, food business operators can carry out challenge tests or use predictive models to assess bacterial growth. Strategies to control *Listeria* include improving hygiene, shortening the shelf-life, modifying products, applying in-package treatments, or opting for frozen storage. Understanding product characteristics and learning from previous outbreak data is crucial for preventing future listeriosis cases.

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 2024. Household outbreaks and clusters not verified with a common source in foodborne outbreaks are excluded. Outbreak investigation procedures in Denmark are described in Chapter 7.

In 2024, 55 foodborne outbreaks were reported in FUD (Figure 1.1, Table A3) resulting in 1,126 human infections with an average of 20 infected persons per outbreak (range 2-95). Of the 55 outbreaks, 26 were local/regional and 29 were national outbreaks, of which five were part of international outbreaks. The number of registered foodborne outbreaks in 2024 has decreased from 2023, where in total 64 outbreaks were registered. The decrease was primarily due to fewer *Salmonella* outbreaks, as exceptionally many *Salmonella* Enteritidis outbreaks occurred in 2023 both in Denmark and other countries in Europe [1]. The number of foodborne outbreaks reported in Denmark caused by the pathogen over the last five years is illustrated in Figure 1.2.

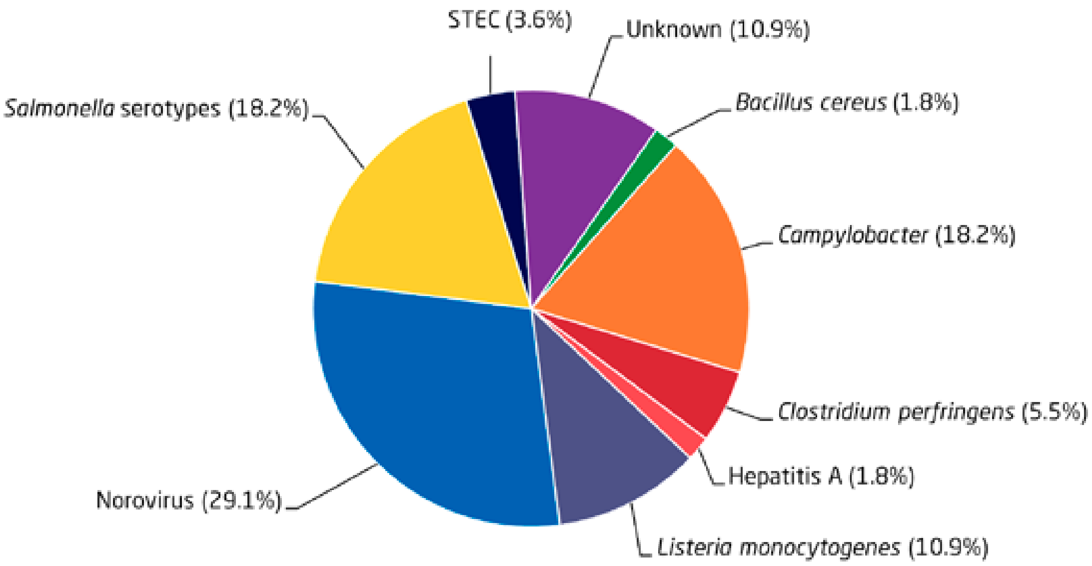
1.1 Norovirus outbreaks

Norovirus (NoV) accounted for 16 of the foodborne outbreaks in 2024. Additionally, both norovirus and rotavirus were detected in patients in another outbreak. The number of NoV outbreaks increased from 2023 where 13 NoV outbreaks were registered. The increase was primarily due to eight point-source outbreaks related to restaurants and canteens occurring between May to November 2024, that turned out to be caused by the same genotype GII.17[P17] with 100% identical sequence (FUD2330, FUD2350, FUD2353, FUD2362, FUD2370, FUD2373, FUD2384 and FUD2391). It was not possible to determine a common source for the eight outbreaks, but there was a suspicion towards fresh produce after comparing the invoices from some of the restaurants. Three outbreaks with 57 persons involved were related to ill kitchen staff or a healthy carrier of virus among the kitchen staff in restaurants (see Table 1.1 and Table A3). One single outbreak with 14 affected persons was related to the consumption of imported raw oysters served in restaurants. Another outbreak with 15 affected persons was related to the consumption of contaminated frozen blackberries. The route of transmission remained unknown for the remaining 12 NoV outbreaks that involved 335 cases.

1.2 *Salmonella* outbreaks

In 2024, ten national *Salmonella* outbreaks were registered in Denmark, and three of these were part of international outbreaks. Two large outbreaks where the

Figure 1.1 Aetiology of the 55 foodborne disease outbreaks reported with a causative agent in the Food- and waterborne Outbreak Database (FUD), 2024. Percentage of total outbreaks indicated in parenthesis.



Source: Food- and waterborne Outbreak Database (FUD)

investigation pointed to minced beef as the source started in the spring. The first outbreak was caused by *Salmonella* Typhimurium with 70 cases registered from March to August 2024 (FUD2325). The cases were 32 females and 38 males, aged 0-82 years. Twenty-four of the cases were hospitalised (34%). Cases with the same outbreak strain were identified from four countries via an international inquiry. The traceback investigation of the minced beef using consumer purchase data pointed to a meat processor in the United Kingdom. Upon further investigation, the meat processor found a matching outbreak strain in beef samples from the production site. The Danish supplier recalled the minced beef from the market in May 2024.

The other minced beef outbreak was due to *Salmonella* monophasic Typhimurium with registered 66 cases – this time only in Denmark (FUD2328). Cases were registered from April to September 2024, peaking in May. The cases were 27 females and 39 males with a median age of 51 years, of which 20 were hospitalised (30%). The outbreak strain was detected in samples from minced beef from Denmark. In both outbreaks, a trend was noticed that several patients had consumed raw minced beef– either by tasting the raw minced beef before cooking it or eating it as steak tartare. This led to early warnings from the authorities with the public health message to cook minced beef properly before eating.

An international outbreak of a rare serotype of *Salmonella* named *Salmonella* Umbilo occurred in late summer and was caused by fresh produce [2]. This outbreak is described in the box on page 9.

1.3 *Campylobacter* outbreaks

The number of registered *Campylobacter* outbreaks in 2024 was 10, which was the same level as in 2023 where 11 outbreaks were registered. Ten of the outbreaks were national outbreaks caused by *Campylobacter jejuni* except for one caused by *Campylobacter coli*. For seven outbreaks the source was identified as chicken meat, based on a whole genome sequencing (WGS) match between human samples and food isolates – one of which was from imported chicken.

1.4 Other outbreaks of interest

In 2024, two prolonged outbreaks of *Listeria* spanning seven years could be linked to the same Danish fish producer. The largest outbreak was due to *L. monocytogenes* ST1607 (FUD1969/FUD2262). The outbreak started in 2019 with dropwise cases throughout the period summing up to 20 cases, five of which were registered in 2024. The outbreak strain has been found in a salmon product and a sample taken from the environment of the Danish fish producer in 2023 and 2024. During control visits at the fish producer in December 2024 another *Listeria* type was found - *L. monocytogenes* ST8 – that matched another outbreak cluster with four cases in 2024, and additional three cases from 2018 and 2022 (FUD2339). Patients from Germany, Italy, and Sweden were also linked to these outbreaks and the same *Listeria* types were found in product samples from the Danish company [3]. Based on an inspection by the Danish Veterinary and Food Administration in the beginning of 2025 at the Danish fish producer, the company was reported to the police for not removing ready-to-eat food contaminated with *Listeria* identified in their own-control checks in 2023 and 2024 from the supply chain or informing the authorities.

A regional outbreak of gastroenteritis (GI) among a 5th-grade school class following a farm visit took place in September 2024 (FUD2377). A retrospective cohort study was undertaken to explore the association between gastrointestinal symptoms and exposures among the pupils. The findings indicated that drinking milk and consuming silage during the farm visit were significantly associated with an increased risk of developing GI symptoms. Laboratory analyses of a hospitalized patient revealed positive results for *Campylobacter* species and STEC, while an additional case also tested positive for *Campylobacter* species.

A small outbreak of hepatitis A occurred from March to May 2024 (FUD2331). Five cases with genetically matching genotype 3A were detected, and all were hospitalised. Interviews and the traceback investigation could not determine the source of the outbreak, however, dried dates were suspected as the outbreaks strain was similar to a large outbreak with 31 cases in 2018 (FUD1636), where dried dates from Iran was established as the source and recalled from the market.

1.5 References

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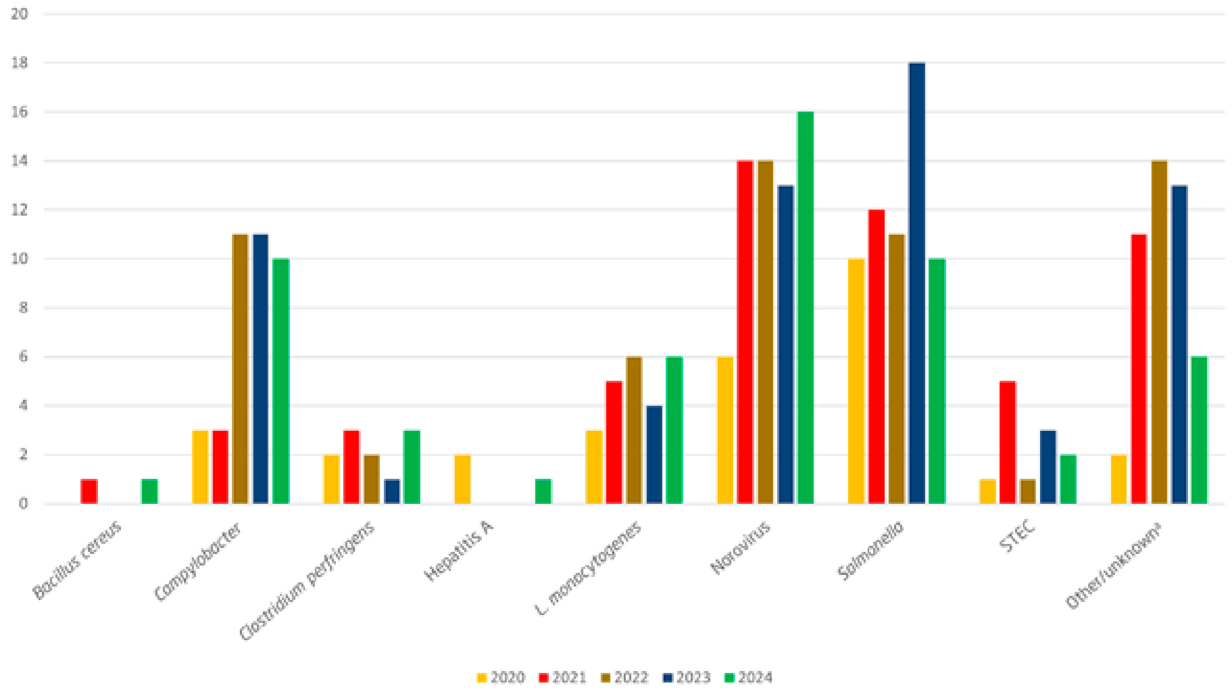
3. European Centre for Disease Prevention and Control, European Food Safety Authority. 2024. Prolonged multi-country outbreak of *Listeria monocytogenes* ST1607 linked to smoked salmon products – 25 April 2024. ISBN 978-92-9498-716-7; doi: 10.2900/061379; Catalogue number TQ-02-24-480-EN-N

Figure 1.2. Foodborne outbreaks reported in Denmark 2020-2024 by the pathogens causing outbreaks in 2024. Please note that prolonged outbreaks with cases in different years are presented in all relevant years.



a) Other/unknown in 2024: 2 outbreaks with multiple pathogens (*Campylobacter* & STEC, Norovirus & Rotavirus), 4 outbreaks with unknown pathogen

Source: Food- and waterborne Outbreak Database (FUD)

Table 1.1. Norovirus outbreaks per route of transmission based on number of cases or number of outbreaks, 2022-2024

	2024		2023		2022	
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	3	57	8	320	8	367
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	0	0
Seafood (oysters)	1	14	5	142	4	126
Other route of transmission	1	15	0	0	0	0
Unknown route of transmission	12	335	0	0	2	121
Total	17	421	13	462	14	614

Source: Food- and waterborne Outbreak Database (FUD)

In August 2024, Statens Serum Institut was notified by the national public health institute in Germany about an outbreak of *Salmonella* Umbilo. This serotype had not been registered in Denmark since 2017. However, in August three cases were identified in Denmark and since Austria also reported cases, a multinational investigation was initiated to identify the source and stop the outbreak (FUD2345).

A total of 159 cases were reported in the three countries (118 in Germany, 22 in Denmark, 19 in Austria) between July and September 2024 [2]. Additionally, seven other European countries reported cases in the same period. Collaborative work between outbreak teams in Germany, Austria and Denmark, including epidemiological and microbiological investigations, as well as efforts by the food safety authorities to trace the possible source, enabled a rapid identification of rocket salad as the likely infection vehicle. *Salmonella* Umbilo was detected in rocket salad in Austria, and later also in baby spinach in Germany. The food isolates and clinical outbreak strain were genetically closely related. Both food items originated from the same company in Italy.

2. KOZO was highly active in 2024

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The coordination group for zoonotic threats in Denmark, KOZO (Myndighedsgruppen til KOordinering af ZOonoser), is a One Health forum that builds on regular contact to share information and risk assessments across sectors. KOZO was highly active throughout 2024, discussing signals and responses related to zoonotic threats and facilitating cross-sector collaboration.

KOZO welcomed the Danish Medicines Agency as a new member, strengthening its expertise in pharmaceutical preparedness for zoonotic diseases. Meanwhile, the Danish Environmental Protection Agency transferred responsibility for wildlife diseases to the Agency for Green Transition and Aquatic Environment; the representation in KOZO core group remained unchanged [1].

In 2024, the KOZO core group primarily focused on the ongoing challenges posed by avian influenza, particularly in light of the H5N1 outbreak in cattle in the USA, which significantly influenced the risk landscape. This situation prompted frequent KOZO meetings to evaluate the available information, identify knowledge gaps, and exchange views on the situation. The group continuously exchanged information to establish a comprehensive and unified risk understanding as the situation evolved. The information shared in KOZO meetings contributed significantly to establishing a knowledge base for relevant actions taken in the individual authorities and organisations to enhance preparedness and risk management. For example, Statens Serum Institut established testing protocols for milk samples based on the expanding host range and growing concerns regarding viral shedding in milk. The Danish Veterinary and Food Administration strengthened surveillance for subclinical mastitis in cattle, generated awareness and enforced notification obligation among practicing veterinarians. Furthermore, the Danish Veterinary and Food Administration instigated that the EU obtained guarantees from the USA that bull semen for export originate only from closed, high biosecurity units. Discussions and perspectives from KOZO fed into the update of guidelines on prevention and management of zoonotic influenza among humans that the Danish Health Authority had already initiated. Additionally, the authorities and organisations represented in KOZO created awareness among relevant stakeholders by presentations, articles and information sheets about the threat. The common risk picture was a useful foundation to ensure harmonised messages.

Changes to several other zoonotic risks in Denmark were also discussed during the year. These included the outbreak of psittacosis in humans in early 2024, expansion of tick-borne encephalitis in new locations, and the first detection of Usutu virus in blackbirds. KOZO also shared information on preparedness plans in the different sectors for new threats, such as West Nile fever and mpox Clade Ib, and coordinated collaborations and cross-sector input where needed.

KOZO also discussed and addressed existing cross-sector challenges in regards to zoonotic threats. Some were coordinated and solved in the relevant ministries, whilst others, such as some questions regarding the control of rodents and insects as vectors in a zoonotic epidemic, warrant further discussions.

Throughout the year, KOZO ensured coordination, information sharing and timely discussions, reinforcing its role as a well-established key One Health collaboration platform in Denmark. The work of KOZO was also highlighted at multiple fora, both nationally and internationally.

References

1. Vestergaard et al. 2024. 2. KOZO - the coordination group for zoonotic threats in Denmark In: Annual Report on Zoonoses in Denmark 2023, National Food Institute, Technical University of Denmark.

3. Surveillance of the zoonotic *Echinococcus multilocularis* and *Trichinella* spp. in red foxes

By Heidi Huus Petersen (hepet@fvst.dk)

Echinococcus multilocularis, is a zoonotic tapeworm, belonging to the family Taeniidae. In Europe, the parasite follows a sylvatic life cycle, with red foxes (*Vulpes vulpes*) serving as the primary definitive host, and rodents serving as intermediate hosts. Other carnivore species, including domestic dogs, can also serve as definitive host. Humans can become infected by inadvertently ingesting the eggs excreted by the definitive hosts.

Trichinella spp. is a parasitic nematode, infectious to almost all vertebrates, with many species being zoonotic. Infected animals pose a transmission risk to humans, as the parasite is transmitted exclusively through the consumption of undercooked meat containing live *Trichinella larvae*.

In Denmark, the detection of *E. multilocularis* in all animals is notifiable. Further, the Danish Veterinary and Food Administration (DVFA) is obligated to report the occurrence to both parasites to the EU Commission and the World Animal Health Organization (WOAH).

In 2022, at the request of DVFA, a surveillance study was launched to monitor the prevalence of *E. multilocularis* and *Trichinella* spp. through the Danish Veterinary Consortium. The study aimed at assessing the prevalence and distribution of these parasites in wild animals, to evaluate the risk of transmission to humans and domestic animals in Denmark. We sought to examine 800 red foxes found either dead, road-killed or shot during the hunting season.

So far, the results from 2022 to 2024, resulted in a national prevalence of *E. multilocularis* of 2.7%. However, a significant regional variation was observed, with a higher local prevalence of 15.5% in Tønder Municipality, and 25.0% in Skive Municipality. A previous surveillance study collected samples between 2012 and 2015 and found a national prevalence of 1.8% - also with a higher local prevalence of 28.5% in Tønder Municipality. *Echinococcus multilocularis*-positive foxes had not previously been detected near Skive, which is located approx. 180 km north of Tønder. This might mean that the parasite is spreading out of the endemic area in Tønder Municipality. All red foxes tested negative for *Trichinella* spp.

The most recent large-scale surveillance program for *Trichinella* spp. in red foxes was conducted between 2011 and 2012. Since then, only sporadic studies on the occurrence of *Trichinella* spp. have been carried out, including investigations in marine mammals, raccoon dogs, and wild-living mink. All of which were negative for *Trichinella* spp.

The surveillance results indicate a potential transmission risk of *Echinococcus multilocularis* to domestic animals and humans in Denmark, particularly in the endemic area of Southern Denmark. In contrast, *Trichinella* spp. currently poses a negligible risk, as no infections have been detected in recent or previous studies.

4. Vectorborne zoonoses

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The Danish Veterinary Consortium (DK-VET) monitors vectors at the University of Copenhagen (UCPH) on behalf of the Danish Veterinary and Food Administration (DVFA) 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 in Denmark 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 2024 was characterized by fairly normal weather conditions resulting in a low to average number of all five mosquito genera present in Denmark. However, we did see a higher-than-normal number of Culex mosquitoes between July and August 2024.

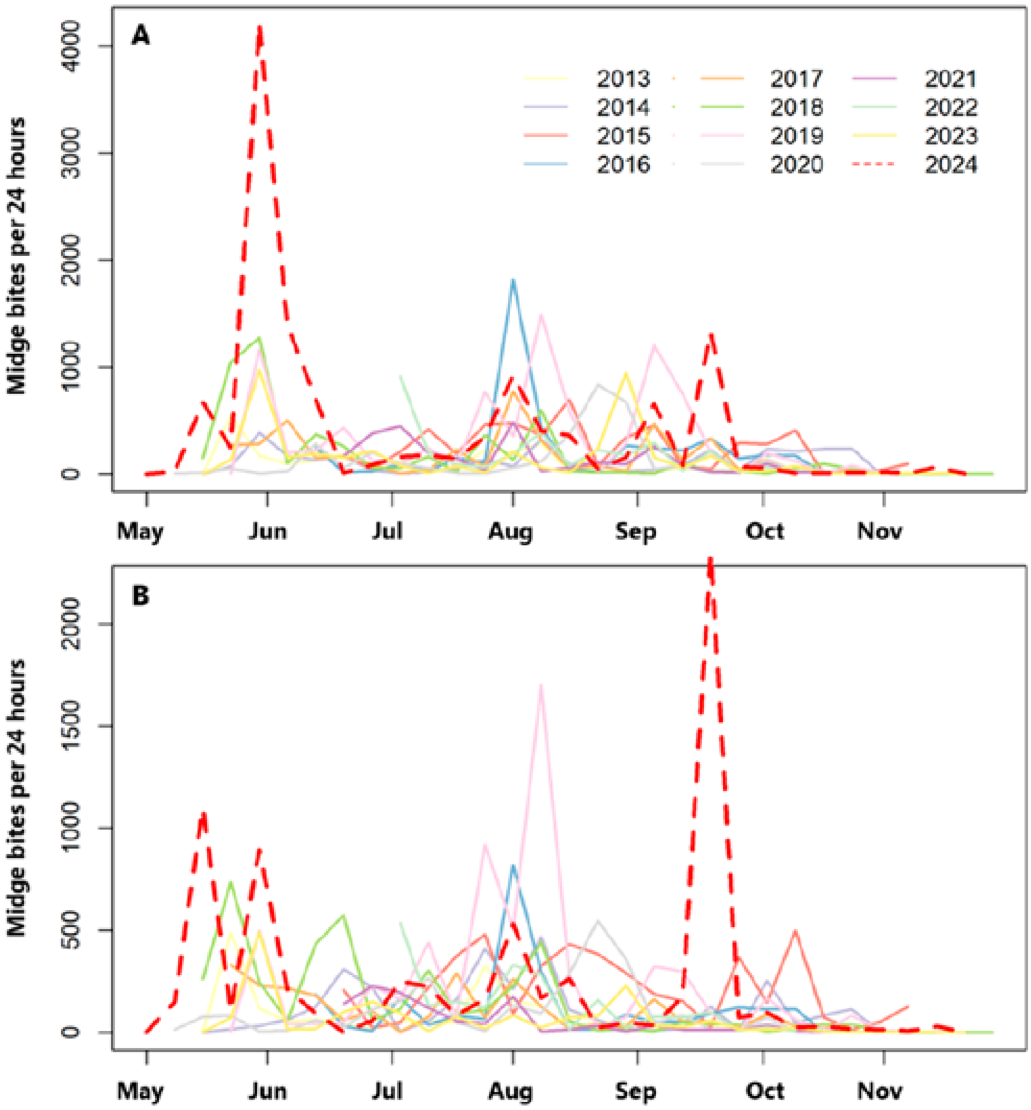
In September 2024, DK-VET detected Usutu virus (USUV) in birds in Denmark for the first time. Three blackbirds—two adults and one juvenile—tested positive for the virus. The birds were found in southern Jutland (Aabenraa), Zealand (Hundested), and the island of Bogø. Weak and dead blackbirds have been observed across the country throughout the summer, including young birds hatched in Denmark this year. It is likely that these birds were infected locally. Within 2024, the virus was detected in 56 blackbirds from different parts of Denmark. In recent years, USUV has spread from Africa to Europe, initially affecting southern and central regions before reaching northern Europe. During the first recorded outbreaks in Germany (2011–2012), authorities estimated that 200,000–400,000 blackbirds died. In 2019, the virus was detected in a single blackbird on the island of Öland in Sweden. In Northern Europe, the primary mosquito vectors for USUV are species within the Culex genus such as *Culex pipiens*, *Culex torrentium*, and *Culex modestus* which are known to feed on birds and serve as key transmission vectors.

As a part of the One health for Surveillance (OH4Surveillance) EU (HaDEA) funded project in collaboration with 10 other partners in Europe, DK-VET is running a targeted West Nile virus surveillance program in Denmark and develops mechanistic virus transmission models to identify the optimal surveillance strategies (risk-based surveillance). In 2024, DK-VET collected 4,726 of mosquitoes at locations in the southern part of Denmark, namely Karlstrup, Vestamager and Dragør on Zealand, Ulvshale on the island of Møn, Årup on the island of Funen and Frøslev in southern Jutland close to the German border. The species of these mosquitoes are yet to be identified.

Although not a zoonosis, and thus not a disease infecting humans, DK-VET has been involved in the response to Denmark's first outbreak of Bluetongue Virus serotype 3 (BTV-3) since 2008, confirmed in August 2024. The outbreak began with a case in a sheep from Tønder Municipality, and by the end of the year, over 1,000 herds across multiple regions had been affected. BTV is spread by Culicoides midges and primarily impacts ruminants like sheep, cattle, and goats, causing symptoms in animals that range from mild to severe, including fever, swelling, oral ulcers, and nasal discharge. In Denmark, the two main midge groups responsible for BTV transmission – *Culicoides obsoletus* and *Culicoides pulicaris* – remain active until late October (Figure 4.1). This prolonged activity period underscores the risk of further transmission and highlights how vector-borne diseases can spread rapidly in Denmark, even in relatively cool summers.

Building on a prior study of neuroborreliosis (NB) on the Danish island of Funen [1], researcher Nina Król from Leipzig University, Odense University Hospital, and DK-VET are investigating the *Borrelia* genospecies and genotypes associated with NB. NB is the most severe form of Lyme borreliosis (LB) and is linked to two genospecies - *B. bavariensis* and *B. garinii*. However, it is uncertain if all *Borrelia* genotypes within these pathogenic genospecies can cause disease in humans. The aim is to determine whether the risk of NB is tied to specific genotypes of *B. burgdorferi* s.l. in ticks or stems from general human exposure to tick activity/density. This ongoing research aims to enhance our understanding and provide further insights to assist in public health risk assessment and management. Preliminary results show that *Borrelia* was present in 11.7% of 2,007 ticks collected from various risk areas on Funen, Denmark

Figure 4.1. Midge surveillance over the past several years shows clearly separated generations, with periods of very low midge densities in between (www.myggetal.dk). The timing of peak generations varies slightly from year to year, but when analysing surveillance data from a single year, it is often possible to predict whether the density will increase or decrease in the next two to three weeks. Note that the graph shows midge bites per 24 hours, for the A) Obsoletus *and B)* Pulicaris *groups.*



[1]. Six genospecies were identified, with *B. afzelii* and *B. garinii* being the most prevalent (Figure 4.2). Interestingly, the prevalence of *Borrelia* was slightly higher in medium NB risk areas compared to high and control areas, suggesting that tick density and exposure might play a role. Sequence types (STs) refer to the genetic variations within a genospecies, and the study revealed a high diversity of STs in ticks, including some novel combinations. The study identified also several STs with known pathogenic profiles, including ST84 of *B. bavariensis* associated with NB. It was found in both high and medium NB risk areas. However, no specific *Borrelia* genospecies or ST was uniquely associated with high NB risk areas, indicating that other factors may contribute to the risk of NB.

Tick-borne encephalitis virus (TBEV) is mainly transmitted to humans through the bite of infected ticks. The clinical course of infection varies from asymptomatic to symptomatic, depending on the age and immune status of the infected person. A proportion of symptomatic individuals will develop tick-borne encephalitis (TBE), i.e.

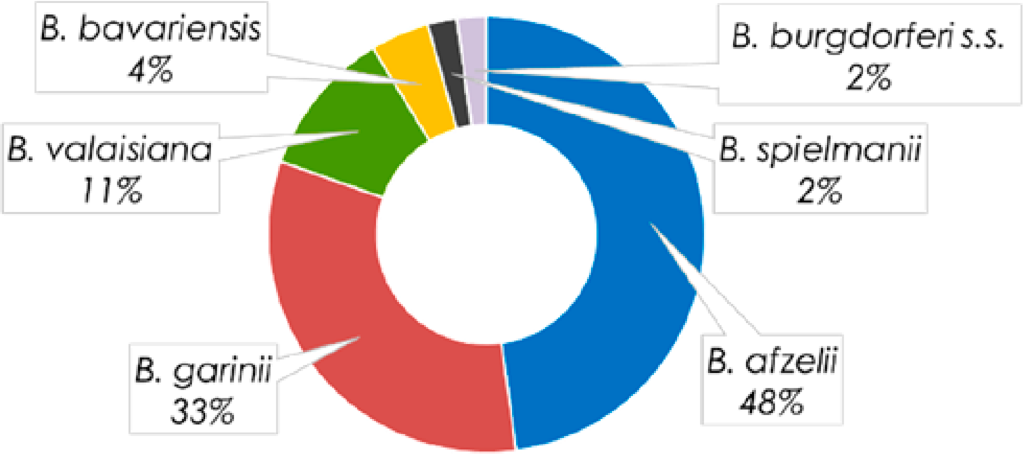
inflammation in the brain (encephalitis) and the surrounding membranes (meningitis). Prior 2008, TBEV infections in Denmark were limited to Bornholm. In 2008 and 2009, two TBE cases could be linked to an area in Northern Zealand (Tokkekøb Hegn), which was confirmed by detecting TBEV-positive ticks from flagging (dragging a white cloth over the vegetation, causing questing ticks to attach to the cloth) in the area. However, in 2019, a new infected area was discovered in Tisvilde Hegn, northern Zealand, with the number of reported cases increasing annually since then. The two sites harbour separate TBEV strains, hence originate from separate introductions. TBEV has been consistently detected in ticks from Tisvilde Hegn since 2019, and although the virus has only been found in ticks from small areas around the Tisvilde nature playground, new human TBE cases suggest it may have spread to surrounding areas over time. In 2024, 22 human TBE cases were confirmed in Denmark, with 17 believed to be domestic infections – 2 from Bornholm, 14 from Zealand (mainly northern Zealand), and one from Jutland. Two of the confirmed domestic human TBE cases, indicated a possible infection source in the forest Hareskoven, specifically the Jonstrup Vang forest area. Detailed tracking of one patient's movements in Jonstrup Vang via GPS prior to symptom onset enabled precise flagging of the area. Two regions within Jonstrup Vang (labelled JV1 and JV2) were flagged by DK-VET/SSI, and ticks from these areas were collected, pooled, and tested for TBEV in October 2024. Despite a high tick density in JV1, no ticks tested positive for TBEV. However, in JV2, which had less vegetation and a lower tick density, 0.86% (95% CI: 0.14-2.64) of ticks tested positive for TBEV. In a confirmatory follow-up flagging in November 2024, the area remained positive for TBEV, with a prevalence of 0.30% (95% CI: 0.02-1.24). Whole genome sequencing of the Jonstrup Vang samples revealed that this was a new introduction of TBEV, likely from Central Europe. Sequence comparisons showed the virus was closely related to strains previously found in southern Germany and Austria, suggesting that it did not spread from other established foci in Denmark. In contrast, new virus findings from the Tisvilde focus in 2023 were highly similar to earlier sequences from the same area, suggesting that the original introduction is still circulating in the region.

4.2 Surveillance of exotic vectors.

No exotic mosquitoes were recorded in Denmark in 2024. The first Hyalomma bite reported in Denmark happened in 2024 on Bornholm, where a woman was bitten while walking her dogs. Hyalomma ticks are a concern because they can carry and transmit dangerous pathogens such Crimean-Congo hemorrhagic fever (CCHF), not found in our native tick species *Ixodes ricinus*. CCHF is a viral disease transmitted by ticks, causing severe bleeding, organ failure, and high mortality in humans. It is primarily found in parts of Africa, Asia, and Southern Europe and is considered highly contagious.

The presence of Hyalomma ticks in new areas increases the risk disease spread. Additionally, a Dermacentor reticulatus tick was found on a dog in Western Jutland. This tick species has been expanding northward in Germany, now

Figure 4.2. Detected B. burgdorferi *genospecies from ticks collected a Funen, Denmark 2023-2024*



reaching Hamburg, and is increasingly observed in Denmark. Dogs that have never left Denmark are being diagnosed with the severe *Babesia canis* infection, which is spread by *D. reticulatus* [1], but not by the native *I. ricinus* tick.

Dermacentor ticks also carry zoonotic pathogens like *Rickettsia raoulti*, which has been found in introduced ticks in Denmark. We have however, not found any reason to believe that Hyalomma and Dermacentor ticks have established small, low-level populations in Denmark, and it seems more likely that the species are being repeatedly introduced by migrating birds or mammals.

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. Will new EU regulations on *Listeria monocytogenes* in ready-to-eat foods contribute to the prevention of listeriosis?

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As shown in Figure 5.1., an increasing trend in listeriosis cases is observed in EU member states, where rates of 0.40 cases per 100.000 people in 2010 have risen to 0.66 cases in 2023 [1]. This has led to the European commission approving tighter rules on the permissible levels of *Listeria monocytogenes* in ready-to-eat foods, where growth of *L. monocytogenes* is not inhibited during the storage of the food (so-called category 1.2 foods, [2]). Before going to the specifics of the new regulation, which will come into effect on July 1, 2026, the current *L. monocytogenes* situation in Denmark will be presented.

Contrary to the EU, Denmark has reported a relatively stable number of human listeriosis cases over the last 14 years with average of 57 (CI 95% 50-64) reported cases per year (Figure 5.1). This corresponds roughly to 1 person in 100.000 people contracting the disease every year, which is higher than the EU average of 0.5 per 100.000 people [1]. Epidemiological evidence shows that most cases are due to the consumption of ready-to-eat (RTE) foods, i.e., foods that are eaten as purchased without further heat treatment by the consumer [3]. Outbreak investigations using whole genome sequencing of *L. monocytogenes* isolates from human cases and suspected foods is a very efficient way to pinpoint, which RTE foods caused the listeriosis cases. Using this approach, rullepølse (spiced meat roll), and fiskefrikadeller (fish cakes/patties) were repeatedly identified as the culprit foods in recent outbreaks in Denmark in 2014 and 2022 [4,5]. Press releases following outbreaks, where the contaminated product has been identified, typically end with recommendations to improve sanitation in the processing facility, alerting consumers not to eat foods close to their best before date and that consumers belonging to high-risk groups should not consume certain foods, such as unpasteurized milk and soft cheese made from raw milk. However, since the same or similar RTE foods repeatedly cause listeriosis outbreaks, these recommendations are either not addressing the root cause of the outbreaks or not being implemented by the industry or consumers.

The aim of this article is to present the new EU rules on *L. monocytogenes* in category 1.2 RTE foods and options for the management of *L. monocytogenes* in these foods.

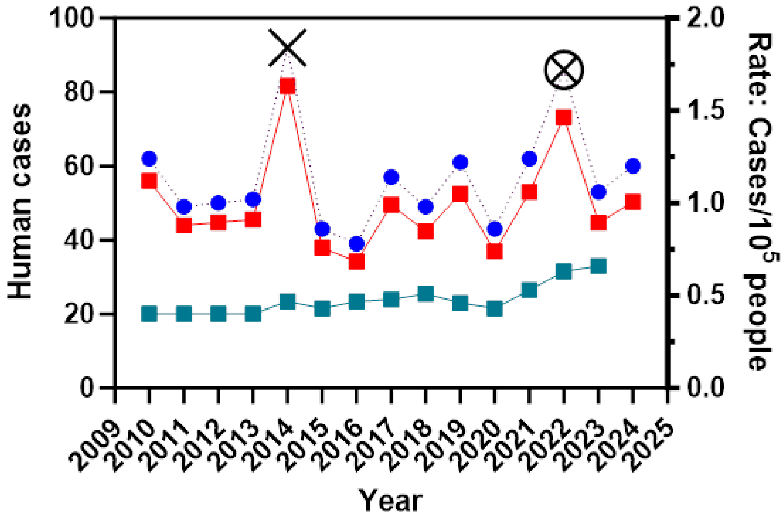

*Figure 5.1. Annual rates of human listeriosis (cases/105 people) in Denmark (■) and the EU (■). Also shown are the numbers of annual human listeriosis cases in Denmark (●) as reported during the period of 2010 to 2024 and amounting to a total of 857 cases. Major Danish outbreaks in 2014 (spiced meat roll/rullepølse, **X**) and 2022 (multiple products, ⊗) are also indicated. (Data extracted from Statens Serum Institut, ECDC, and EFSA, March 2025).*

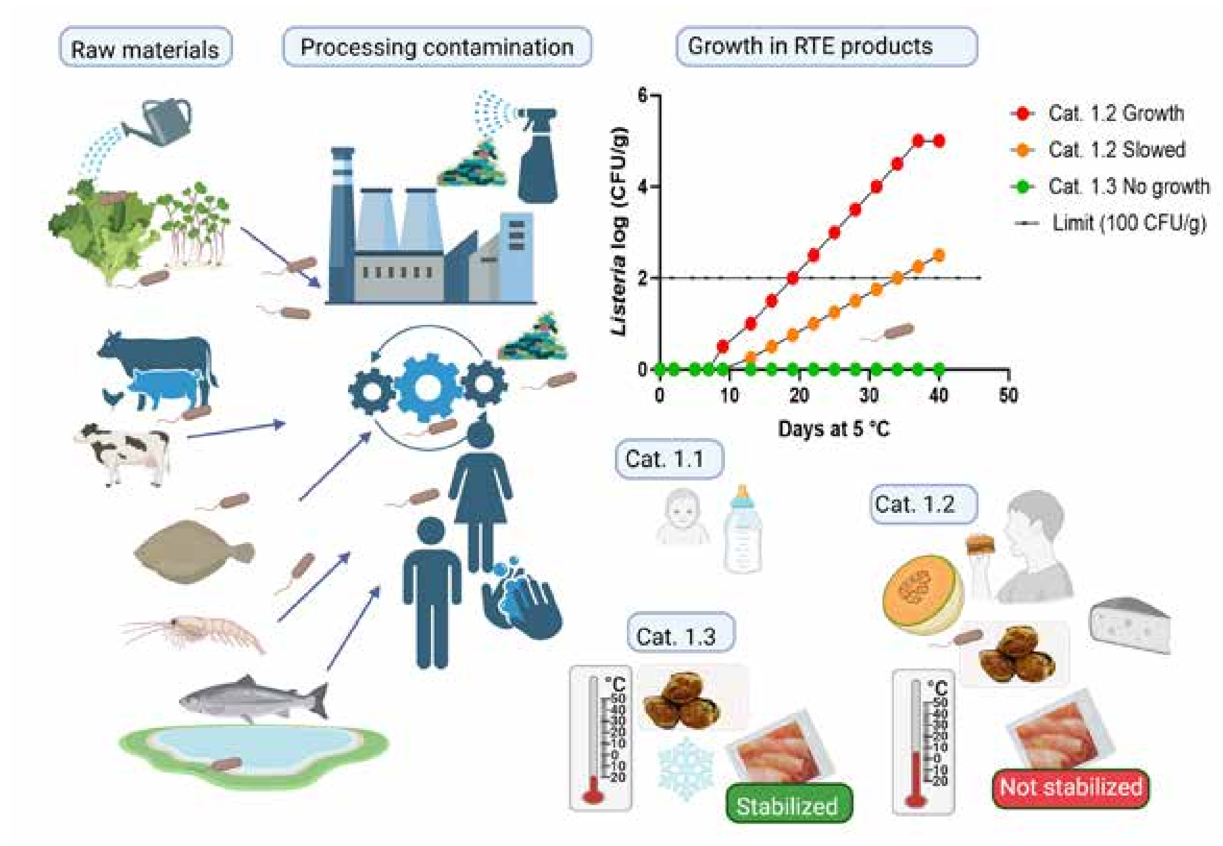

Figure 5.2. Transmission of the environmental foodborne pathogen, Listeria monocytogenes, *through the food production chain. Contaminated ready-to-eat (RTE) foods can, based on their characteristics and storage conditions, support growth of* L. monocytogenes *above the critical limit of 100 CFU/g (Cat 1.2) unless the RTE product has been stabilized by preservation or freezing to prevent growth (Cat. 1.3). (Created in Biorender).*

5.1 What is the problem with *L. monocytogenes* in RTE foods?

L. monocytogenes is an environmental bacterium that is found in water, soils, plants and animals. This means that raw materials entering the food producing facilities regularly contain *L. monocytogenes* [6]. The bacterium grows at temperatures between 0 and 40 °C. This ability to grow at low temperatures is central for the listeria problem as it allows the bacterium to survive and grow in food processing environments and in the RTE food during refrigerated storage (Figure 5.2). Indeed, genetically similar subtypes of *L. monocytogenes* have been shown to be repeatedly isolated from the same production sites over several years, testifying to the difficulty in eradicating the pathogen by sanitation [7].

Since the infectious dose of *L. monocytogenes* is estimated to be high (>104 bacteria) and the "natural" contamination level in foods is low (~0.1-1 colony forming unit (CFU)/g in e.g., raw salmon [6], outbreaks are always associated with growth of the bacteria in the RTE food prior to its consumption.

It should be noted that the infectious dose depends on the health and age of the consumer, with epidemiological evidence pointing to individuals who are younger (<4 years), older (>65 year), pregnant or immune-compromised (YOPIs) being more susceptible and presumably need to consume fewer bacteria to get ill compared to the general population [8].

5.2 What do the current EU rules say about *L. monocytogenes* in RTE foods?

EU's microbiological criteria [9] divide RTE foods into three categories. The first category (1.1) is comprised of foods intended for infants and special medical purposes, where there is a requirement for the absence of *L. monocytogenes* in 10 samples of 25 g of food throughout the product shelf-life.

All other RTEs are divided into two categories depending on whether *L. monocytogenes* is able (1.2) or unable (1.3) to grow in the food under normal storage conditions for the specific product. To belong to category 1.3, the food producer must document that *L. monocytogenes* cannot grow in the product. EU 2073/2005 (Chapter 1, footnote 8) specifies that RTE foods with shelf-life of ≤4 days or product pH ≤4.4, water activity ≤0.92 or a combined product pH ≤5.0 and water activity ≤0.94 automatically belong to category 1.3 products [9]. Other products belong to the category pending scientific justification, which can convince the competent authority (CA) that the product has been stabilized and will not exceed the legal limit for *L. monocytogenes* levels of 100 CFU/g throughout the marketed shelf-life of the product.

For category 1.2 foods, which support growth of the bacterium, the current EU regulation (EU 2073/2005) stipulates that producers must show that the bacterium is not detected in 125 g (5 portions of 25 g each) at the time of the product leaving their control or that it will never reach levels higher than 100 CFU/g for the duration of the product shelf-life.

5.3 New EU rules on management of *L. monocytogenes* in category 1.2 RTE foods

Rising numbers of human listeriosis cases in the EU and the fact that EU 2073/2005 did not provide a criterion, which could be applied to foods leaving the immediate control of the producing food business operator (FBO) with no evidence that the limit of 100 CFU/g will not be exceeded during their shelf-life, has led to the new revised rules for *L. monocytogenes* in category 1.2 RTE foods.

The new regulation (EU 2895/2024) gives the FBO and the competent authority CA a new criterion by which to determine whether a 1.2 RTE product must stay at or below 100 CFU/g or obey the stricter limit of "not detected in 25 g" for the duration of the shelf-life [2]. According to the new regulation, the responsibility is on the FBO to provide satisfactory evidence to the CA to determine which limit their category 1.2 RTE product falls under (Table 5.1). To note, the new regulation applies to all FBOs involved in the production, distribution and/or sales of the RTE foods.

5.4 Options for controlling *L. monocytogenes* in category 1.2 RTE foods

Firstly, it is the responsibility of the FBO to document whether their product(s) belong(s) to category 1.2. Secondly, the FBO needs to know how long it will take *L. monocytogenes* to reach the legal level of 100 CFU/g during storage according to prescribed conditions (on the label). If the FBO does not have this information, their products will automatically be placed under the stricter requirement for absence in 25 g throughout the shelf-life (Table 5.1).

To find out if or when *L. monocytogenes* reaches the 100 CFU/g limit, the FBOs could conduct a challenge test where the RTE food is inoculated with the bacterium followed by storage and measurements of growth. This can be expensive and would have to be performed for each RTE food prior to establishing the shelf-life and satisfy the requirement for documentation to the CA. Guidance on how to conduct challenge tests is described in a document from the European Union Reference Laboratory for *L. monocytogenes* [10]. However, to help the FBOs, researchers have integrated results from challenge tests into mathematical models, which use characteristics of the foods to predict growth of *L. monocytogenes*. Examples include FSSP, DMRI Predict, Sikre fødevarer and ComBase [11,12,13,14,15]. Use of predictive modelling tools to demonstrate the 100 CFU/g limit is not reached, is accepted by the Danish CA. Prior to using the models, the FBO will need to characterize their RTE product in terms of its content of salt, pH and other factors that limit growth of *L. monocytogenes*.

By making use of challenge tests or computer based predictive modelling tools for foods, where suitable models are available, the FBO now has the following options to comply with EU 2895/2024:

1. Reduce initial levels of *L. monocytogenes* by optimizing processing plant hygiene. To note, this cannot stand alone and must be combined with one of the other options.
2. Set the shelf-life sufficiently short to make sure it can be demonstrated that *L. monocytogenes* will not be able to reach 100 CFU/g during the shelf-life.
3. Obtain desired shelf-life by modifying the product so it can be demonstrated to the CA that *L. monocytogenes* cannot reach levels of 100 CFU/g during the shelf-life.
4. Apply in-package treatment (e.g., heat, high pressure processing) to inactivate *L. monocytogenes* in the product without chance of recontamination.
5. Obtain desired shelf-life by moving the RTE product to category 1.3. This can be obtained by altering the product or the storage conditions such that *L. monocytogenes* cannot grow in the product during its shelf-life.

The FBO must include safety margins in the setting of the shelf-life or modification of products to allow for product variability.

5.5 Outbreak Category 1.2 RTE foods and food safety design by predictive models

To prevent future outbreaks of listeriosis it is essential to evaluate information from previous and on-going outbreaks. This should include information about product characteristics (i.e., salt, pH, food preservatives) and product shelf-life as these factors determine the growth of *L. monocytogenes* in RTE food prior to their consumption – a key aspect associated with listeriosis.

"Rullepølse" (spiced meat roll) is an example of a category 1.2 product, which has caused repeated outbreaks in Denmark [4,5]. Despite heat treatment, the product is at risk of recontamination during the subsequent slicing, handling and packaging of the product prior to refrigerated storage.

Table 5.1. Comparison of the old versus the new rules for L. monocytogenes *in category 1.2 RTE foods, which support the growth of L. monocytogenes other than those intended for infants and for special medical purposes. EU 2895/2024 will come into effect on July 1, 2026.*

EU Regulation	Limits (in 5 samples)[a]	When	Scope of application
OLD: EU 2073/2005			
	100 CFU/g[b]	Products placed on the market during their shelf-life	Apply if FBO[d] **can** demonstrate to the CA[e] that 100 CFU/g will not be reached during the shelf-life of the product
	Not detected in 25 g[c]	When leaving the control of the food business operator, who has produced it	Apply if FBO **cannot** demonstrate to the CA that 100 CFU/g will not be reached during the shelf-life of the product
NEW: EU 2895/2024			
	100 CFU/g[b]	Products placed on the market during their shelf-life	Apply if FBO can demonstrate to the CA that 100 CFU/g will not be reached during the shelf-life of the product
	Not detected in 25 g[c]	Products placed on the market during their shelf-life	Apply if FBO cannot demonstrate to the CA that 100 CFU/g will not be reached during the shelf-life of the product

a) n = 5, c = 0, for 100 CFU/g limit m=M=100; b) Analytical method EN/ISO11290-2; c) Analytical method EN/ISO 11290-1; d) FBO is the food business operator (entity responsible for ensuring that food law requirements are met); e) CA is the competent authority.

The predictive modelling tool FSSP shows how low numbers (1 CFU in 25 g) of *L. monocytogenes* will grow to 100 CFU/g within 21 days at 5 °C in spiced meat roll products with low salt content (1.2-1.6%) and high pH levels (5.8-6). This makes a market shelf-life of 28 days at 5 °C dangerous and non-compliant with the new EU regulation. In the opinion of the authors, FBOs could consider using options 3 or 4 listed above to bring their product into compliance, e.g., by addition of an inhibitory acid such as acetic acid to the brine or apply in-package heat treatment.

Smoked salmon is a lightly preserved fish product, which has caused numerous outbreaks in Denmark and other countries, including on-going multi-year outbreak involving a Danish producer [16]. Traditionally this product is smoked at low temperatures (<30 °C) and contains wood smoke components and salt, which slows growth of *L. monocytogenes* but may not hinder the bacterium in reaching levels of 100 CFU/g after 20-25 days at 5 °C. Since the FBO declared shelf-life often is longer than this, e.g., 28-35 days at 5 °C, this is an example of a shelf-life not supported by scientific justification. Here predictive tools could be used to suggest modifications of the product recipe by e.g., addition of organic acids to slow the growth of the pathogen.

The last case focusses on fish cakes/patties (fiskefrikadeller), which are sold on the Danish market. Products from one FBO have in recent years caused outbreaks of listeriosis [5]. This is an interesting case, since the modified atmosphere packaged products were given a shelf-life of 35 days at 5 °C and labelled with instructions to heat the cakes before consumption. However, fish cakes/patties on the Danish market are often sold with labels stating the product is ready-to-eat, which would push the product to category 1.2. Since the fish cakes/patties have a pH of ~6.5 and low salt concentration of 1% it likely only takes 16 days for low levels of the bacterium (1 CFU in 25 g) to reach 100 CFU/g in the product, again rendering a declared shelf-life of 35 days illegal and dangerous. If the producers do not wish to change the shelf-life or alter the composition of their product, one solution is frozen distribution where *L. monocytogenes* cannot grow.

5.6 Is freezing of all category 1.2 RTE products a solution to the *L. monocytogenes* problem?

Like all other living organisms, *L. monocytogenes* requires liquid water to grow. This availability of liquid water is prevented by storing foods at low temperatures, e.g., -20 °C. Implementation of frozen storage will essentially move category 1.2 RTE foods to category 1.3., where growth of the pathogen is not supported during the shelf-life of the product. To note, however, is that freezing will not kill *L. monocytogenes*, meaning that thawed products should have a restricted shelf-life.

For some types of RTE products this solution should be attractive to the FBOs as it removes the burden of evidence from them, making it easier to comply with the new regulations. One could also speculate that freezing will spare many Danes from contracting listeriosis, a disease which comes with a lethality rate of 18-22% [1,8].

5.7 Conclusions

- *L. monocytogenes* continues to cause listeriosis cases from consumption of RTE foods.
- To counter this, the EU is implementing stricter rules for category 1.2 RTE foods that support growth of *L. monocytogenes*.
- The new rules come into effect on July 1, 2026 and mandate that the FBOs demonstrate absence in 5 x 25 g throughout the shelf-life of the RTE foods or present scientific justification to the CA that the bacterium cannot reach 100 CFU/g within the shelf-life.
- Challenge tests and/or predictive models can be used to document growth of *L. monocytogenes* in specific RTE foods.
- Mitigation options include shortening the shelf-life, redesigning products to manage *L. monocytogenes* growth, in-package inactivation treatments or implementing frozen storage of the RTE food.

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6. Advances in *Campylobacter* Interventions and Surveillance in Denmark

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Preventing campylobacteriosis has proven to be a difficult task, but in the last five years there have been a series of initiatives advancing our knowledge and opening new paths forward for finding ways to understand and prevent the spread of *Campylobacter*. Several of these have been initiatives originating from the current and previous National Action Plan against *Campylobacter* in broilers, food and the environment.

The issues assessed in the different projects cover a better understanding of the sources of *Campylobacter* introduction into the food chain, finding and implementing interventions that can prevent or reduce *Campylobacter* in production, improving existing tools used for estimating the impact of *Campylobacter* in production, and expanding on the know-how of how the increased sequencing of DNA from *Campylobacter* isolates can be used for understanding the epidemiology, the relevance of different *Campylobacter* species and subtypes and the tracing of the disease to its source.

6.1 Reduction opportunities for *Campylobacter* in primary production for free-range and organic broiler flocks (OutCampy) [1]

The OutCampy project focused on finding new opportunities to control *Campylobacter* in primary production by improving the understanding of the epidemiology, routes of infection and risk factors for free-range and organic flocks.

Based on historical data, it could be estimated that organic broiler production accounted for 4% of broiler chicken production in 2018 and contributed with 6-8% of the total amount of *Campylobacter* coming from Danish broilers.

An examination of the national surveillance data from 2018-2021 found that the production of free-range and organic flocks has, from 2019 been exclusively located in Jutland. Changes in the production types may have been driven by dynamics between abattoirs and producers of free-range and organic flocks. Following the change abattoirs accepting free-range and organic in 2019 there has been a decrease in the number of positive flocks annually (Appendix Table A10).

A literature review screened the scientific literature for applicable and ready-to-use interventions that had been tested in free-range and organic flocks [2]. The review found a lack of interventions that had been tested in a production environment, and particularly in free-range and organic productions. The interventions found with the highest potential were ferric tyrosine chelate, a prebiotic fermentation product of *Saccharomyces cerevisiae*, short-chain fatty acid butyrate added to feed, and product of organic acids that were added to drinking water.

Funding: The Ministry of Food, Agriculture and Fisheries of Denmark

6.2 Feed and water additives for reducing *Campylobacter* in free-range broilers (SafeChicken) [3]

On-farm interventions to reduce *Campylobacter* in the gut of broilers will subsequently reduce the contamination of poultry meat. The first part of the SafeChicken project, therefore, aimed to investigate the effect of feed/water additives as potential on-farm intervention tools under normal production conditions. *Campylobacter* prevalence in poultry flocks from free-range and organic production has been generally higher than in conventional production in Denmark. Thus, SafeChicken targeted applications in a free-range system and the feeding experiment was conducted in an operational Danish free-range farm.

This project investigated the *Campylobacter* reducing effect of four possible feed and water additives (biochar, yeast fermentate, oat hulls in feed and organic acids in water) based on products readily available and applicable for organic production. Each of the selected additives were provided to the experimental groups of broilers for their entire rearing period, and the experiment was repeated for three successive flocks.

The addition of organic acids into water reduced the *C. jejuni* level in caecum on day 36 by 0.62 $\log_{10}$ compared to the control group. Additionally, the group fed with biochar added feed had 0.7 $\log_{10}$ lower *C. jejuni* than the control group on day 59. According to the air samples analyses, all three flocks acquired *Campylobacter* before having access to outdoors on day 36. Whole-genome-sequencing (WGS) of the *Campylobacter* isolates collected from the broilers and the environment showed genetic similarities, suggesting carryover of *Campylobacter* strains from the preceding flocks and the outdoor environment may also have played a role in transmission. However, further testing is still needed to verify the observed effect since high variability was seen between the flocks.

Funding: Green Development and Demonstration Programme (GUDP)

6.3 IceGun technology effect on reducing *Campylobacter* in slaughterhouses (Chillbact & Safe-Chicken) [4,5]

A target for an acceptable level of contamination at slaughterhouses is set by the process hygiene criterion for *Campylobacter* spp. on broiler carcasses in the European Union. The industry is required to improve hygiene and process controls on farms and slaughter facilities in case of unsatisfactory results, but no effective control measures and strategies exist in practice.

ThorIce Chilling Solutions (Reykjavik, Iceland) developed a technology called IceGun® to spray slurry ice on broiler carcasses to enhance chilling speed. Faster chilling means that the line speed can be increased, enabling increased production without expanding the existing air-chilling chamber. The company expected that IceGun® not only contributes to more efficient chilling but also helps to reduce bacteria, including *Campylobacter*, on the carcasses. We have therefore conducted two projects (in France and in Denmark) in collaboration with ThorIce Chilling Solutions to assess the effect of using IceGun® in reducing *Campylobacter* load on broiler carcasses.

Both projects showed a significant reduction of 0.44 $\log_{10}$ on the neck skins of poultry compared to carcasses chilled only by conventional air-chilling. The reduction was not seen on the leg skins. The IceGun® treated group maintained the product quality throughout the shelf-life period. Further studies need to establish whether the observed effect on neck skin was solely due to the IceGun® treatment, a possible washing effect, or a combination of both. The industry may benefit from the installation of IceGun® not only for increased production capacity but also as a

potential measure to reduce the load of *Campylobacter* on broiler carcasses.

Funding: EU Horizon 2020 Fast Track to Innovation Programme & Green Development and Demonstration Programme (GUDP)

6.4 *Campylobacter*-transfer from carcass to meat product in the relative risk model (CampTau) [6]

The risk of *Campylobacter* infection from ingestion of poultry meat can be estimated by a mathematical model called the Quantitative Microbial Risk Assessment (QMRA) model. QMRA is useful in, for example, establishing acceptable targets for the concentration of bacteria on products and assessing of the effect of potential control options implemented along the farm-to-fork chain.

One of the parameters used in the model, namely the transition factor (Tau) of *Campylobacter* from neck skin to meat on poultry carcasses, is currently set as 1 $\log_{10}$ based on an expert opinion rather than on empirical data because of a lack of field studies. CampTau project aimed to fill this data gap by taking samples in a Danish slaughterhouse to be able to make a more realistic estimate. In parallel, the project investigated the effect of modified atmosphere packaging (MAP) on *Campylobacter* present in fresh poultry products.

The difference between *Campylobacter* concentrations on the neck skin and breast fillet was 2.22 $\log_{10}$, which was higher than the previously estimated value of 1. The values were, however, highly variable depending on the sampled flocks. Additionally, 0.74 $\log_{10}$ lower *Campylobacter* concentration on neck skins was observed after 7 days of storage in MAP. The acquired data can help make more precise QMRA models and broaden our understanding of the extent of *Campylobacter* contamination in various poultry products and the impact of the packaging interventions.

Funding: Poultry Levy Fund (Denmark)

6.5 Multi-country model for *Campylobacter* source attribution [8]

As part of the Joint Research Project "Discovering the sources of *Salmonella*, *Campylobacter*, VTEC and antimicrobial resistance (DiSCoVer)" within the One Health European Joint Program (OHEJP), a source attribution study was conducted to predict the sources of human campylobacteriosis cases across multiple EU countries using available whole-genome sequencing (WGS) data [9]. By using genetic patterns, specifically k-mer frequency patterns, as input data, a machine-learning model was developed to estimate the likely sources of human cases and explore how differences in sample size and data availability across countries may affect the accuracy of the predictions. First, up-sampling was applied to balance the dataset by artificially increasing the number of samples in underrepresented source categories to match those with the largest number of samples. Next, down-sampling was performed by reducing the number of samples in sources exceeding 300 samples.

By using the up-sampled model, broilers from Denmark were found to be the most important infection source for Danish cases (199/232 cases, 86%), followed by cattle from Denmark (19/232 cases, 8%). Few Danish cases could be attributed to sources outside of Denmark, like imported broiler meat (6/232 cases, 3%), meat from broilers in Poland (2/232 cases, 1%) or The Netherlands (2/232 cases, 1%). The model predicted 9 non-Danish cases from other countries (Netherlands, Portugal, Ireland) to originate from Danish broilers (9/41, 22%).

Using the down-sampled data, cases from Denmark were mostly attributed to broilers from Denmark (226/365 cases, 62%), with some also attributed to cattle from Denmark (54/365 cases, 15%), as well as broilers from the Netherlands (22/365 cases, 6%). Denmark had a low proportion of cases attributed to non-domestic sources (75/365 cases, 21%). The down-sampled model predicted 50 non-Danish cases from other countries (Netherlands, Portugal, Ireland, Spain) to originate from Danish broilers (53/170, 31%).

The results suggested that more samples from a specific source like broilers not only introduces more genetic variation in the samples included in the model, but also – and maybe because of that - increases the probability that a random human case of campylobacteriosis is allocated to that source. Conversely, a source that is more sparsely sampled will show less genetic variation, which consequently will result in a lower probability of human cases being attributed to this source. The study highlights a key challenge in foodborne disease attribution: The quantity of samples and the diversity of sources from where they are collected play an important role, as unbalanced dataset may overestimate the importance of 'oversampled' sources, while underestimating sources with fewer samples. Future studies should aim for more balanced data collection to improve the accuracy of source attribution efforts and, thereby, provide better support for food-safety decision makers. Despite the uncertainties introduced by unbalanced datasets, the results still support that the broiler reservoir is most important single source of human campylobacteriosis in Denmark and other EU countries.

6.6 *Campylobacter* transmission in broilers investigated by whole-genome sequencing (WGS)

This study aimed to enhance *Campylobacter* control in broilers using WGS and transmission analysis, with the broader goal of contributing to a reduction in *Campylobacter*-positive broiler flocks and, over time, decreasing consumer infections from Danish chickens.

The project examined *Campylobacter* diversity and prevalence within houses, across houses, and between farms. Specifically, it examined (i) the diversity of *Campylobacter* within flocks, (ii) the persistence of specific types within the same house across rotations, (iii) transmission between houses on the same farm, (iv) occurrence of the same type across different farms, (v) potential relationships between transmission pathways and production conditions, and (vi) genomic stability during colonisation and persistence.

Cloacal swab samples were collected from broilers at three slaughterhouses: two conventional and one free-range. From each flock, ten samples were taken during slaughter and cultured for *Campylobacter*. Samples were collected from broilers across 18 farms between March and November 2020, covering 60 houses over 2–6 rotations. Farms were included based on previous *Campylobacter*-status. In total, 240 flocks were included yielding 2,820 samples from 282 slaughter events. Approximately 42% of the flocks and 34% of the samples tested positive for *Campylobacter*. A total of 940 isolates were identified, of which 86% were *C. jejuni*, 12% were *C. coli*, and 2% were *C. lari*. To investigate genetic relatedness, a selection of these isolates was subjected to WGS and analysed using core-genome multilocus-sequence typing (cgMLST).

The findings showed considerable diversity across flocks. Most flocks (70%) contained only a single *Campylobacter*-type based on cgMLST. Isolates of the same type often appeared across houses within the same farm during the same rotation, but also recurrent types appeared across rotations in some conventional farms and strongly indicated persistence. No clear evidence of transmission between farms was found. Correlations between transmission pathways and production conditions remained unclear, requiring further investigation by slaughterhouses as the information was anonymous. Genomic stability of the relatively few persistent strains detected over time in this study was generally high.

Funding: Fjerkræsafgiftsfonden, 2020 (Campylobacter *smittespredning i slagtekyllinger undersøgt ved genomsekventering*)

6.7 *Campylobacter* transmission dynamics in broiler chickens

This project extended the previous study (Fjerkræsafgiftsfonden, 2020 -*Campylobacter* transmission in broilers investigated by WGS) by further investigating *Campylobacter* transmission dynamics, focusing on the same conventional farms as included in 2020 over another peak season and tracing infection routes using WGS. The study was also expanded to include broilers from more free-range farms.

Cloacal swab samples were collected from broilers at slaughter at three slaughterhouses: two conventional and one free-range. Additionally, boot sock samples were collected 7-10 days before slaughter from inside and outside houses, along with samples from pigs, cattle, flies, and the environment. *Campylobacter* presence was determined through culture, and positive isolates underwent WGS and core-genome multilocus sequence typing (cgMLST).

Between April and November 2021, samples from broilers across 9 conventional farms (27 houses, 94 flocks) and 9 free-range farms (18 houses, 57 flocks) were collected. Of nearly 1,500 swab samples, 44% from conventional and 75% from free-range flocks tested positive. Of the approximately 200 sock samples, 24% from within-house conventional flocks were positive, while only 2% from exterior samples were positive. *Campylobacter* was also detected in samples from pigs and cattle.

A total of 798 *Campylobacter* isolates (81% *C. jejuni*, 19% *C. coli*) were collected, with 355 sequenced. Free-range flocks exhibited greater diversity, with nearly half of the flocks containing more than one *Campylobacter* type based on cgMLST. For conventional farms, transmission between flocks within the same house was more pronounced in 2021 (50%) compared to 2020 (20%). For free-range farms, there was significant transmission between houses within the same rotation (80%) and between flocks within the same house (60%). Additionally, some types persisted across both years and cross-farm types were detected among conventional and free-range farms indicating transmission between farms or shared infection sources.

Funding: Fjerkræsafgiftsfonden, 2021 (Campylobacter *smittedynamik i slagtekyllinger*).

6.8 A new sequence-based typing method for detection and investigation of *Campylobacter* transmission in poultry production, the porA-method

The aim of this study was to develop and evaluate a novel sequence-based typing method, the porA-method, for improved detection and investigation of *Campylobacter* contamination within poultry production. Furthermore, this method was established to enable detection and typing directly on complex samples thus omitting the culturing step normally necessary for typing of *Campylobacter* for surveillance purposes.

The porA-method was tested on samples collected from one poultry slaughterhouse, including cloacal swabs (140 samples), leg-skin samples (70 samples), and environmental swabs (70 samples) from 14 broiler flocks slaughtered on seven days. Additionally, artificial samples with pre-mixed

Campylobacter strains were included for performance evaluation. Validation was performed through comparison with conventional culturing and WGS).

The porA-method demonstrated similar sensitivity to conventional culturing, detecting *Campylobacter* in 47% of samples compared to 45% detected by culturing. Comparison with WGS showed reliable detection of the same types in 20 out of 25 selected samples. Notably, the porA-method revealed a broader diversity of porA-types, particularly in leg-skin and environmental samples, than conventional methods. It also identified cross-contamination during slaughter, as porA-types from one flock were sometimes detected in subsequent flocks.

This pilot study demonstrates that the porA-method is a promising tool for detecting and characterizing *Campylobacter* in poultry production, offering a sensitive and cost-effective alternative to conventional typing methods. Its application could provide valuable insights into *Campylobacter* diversity in broilers and significantly enhance efforts to trace contamination routes and improve food safety.

Challenges remain in detecting *C. coli* in mixed samples, and further optimization to reduce sequencing noise and enhance the bioinformatics pipeline is recommended.

Funding: Fjerkræsafgiftsfonden, 2024 (*Ny sekvensbaseret typningsmetode til detektion og smitteudredning af* Campylobacter *i fjerkræproduktionen*).

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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 Appendix Table A26 and Table A27, respectively, including reference 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 Statens Serum Institut (SSI) through different channels depending on the disease:

- Notifiable through the laboratory surveillance system: *Salmonella*, *Campylobacter*, *Yersinia*, Shiga toxin-producing *E. coli* (STEC), *Brucella* and *Listeria*.
- Individually notifiable zoonotic pathogens: *Chlamydia psittacci* (ornithosis), *Leptospira* (Weils disease), *Mycobacterium bovis*, Var. Creutzfeldt-Jakob Disease, HUS-inducing STEC 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 laboratory 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* and *Yersinia* cases are extracted from MiBa and STEC and *Listeria* are reported to SSI directly from the clinical microbiology laboratories. Furthermore,

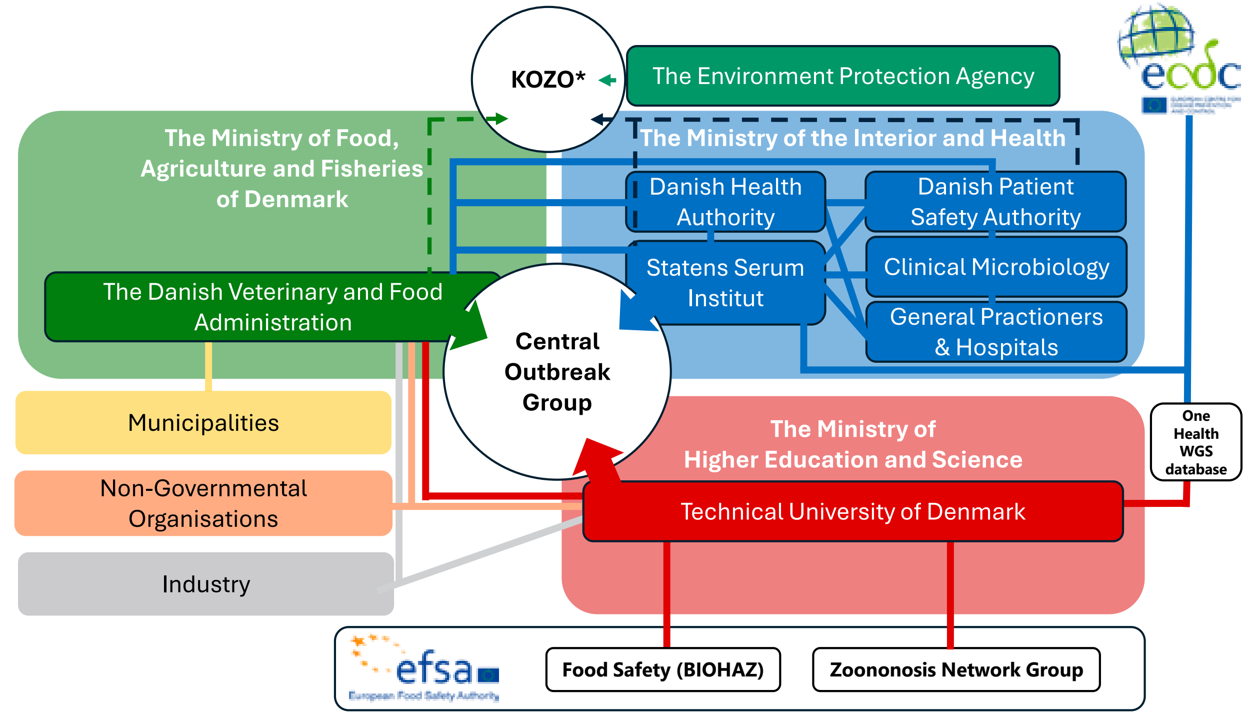


*Figure 7.1. Overview of the monitoring and outbreak investigation network for reporting infectious diseases in humans, animals, feed and food in Denmark. *) KOZO, "Myndighedsgruppen til KOordinering af ZOonoser" (The Group of Authorities for the Coordination of Zoonoses)*

all culturable *Salmonella* and STEC and a subset of *Yersinia* and *Campylobacter* isolates are sent to SSI for further characterisation and the results are recorded in the Register of Enteric Pathogens. Cases are reported as episodes, i.e., each patient-infectious agent combination is only recorded once in any six-month period. Overviews of results from the Register of Enteric Pathogens are presented as follows:

- All laboratory-confirmed human cases are presented in Appendix Table A1.
- STEC O-group distribution in humans is presented in Appendix Table A2.
- The *Salmonella* serovar distribution is presented in Appendix Table A4.

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 National Food Institute at the Technical University of Denmark (DTU Food) and the Danish Veterinary and Food Administration (DVFA) in collaboration. These institutions may also aid in the investigation of regional or local outbreaks. Representatives from these institutions meet regularly in the Central Outbreak Management Group to discuss surveillance results, compare the reported occurrence of zoonotic agents in animals, food and feedstuffs with that in humans, and coordinate the investigation of outbreaks. The formal responsibility of investigating food or waterborne outbreaks is currently divided between three ministries based on the outbreak source: The Ministry of 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 DVFA if the food they served or produced are suspected to have caused illness. Individuals who experience illness related to food intake in settings such as restaurants or workplace cafeterias may report these incidents directly to the Food Inspection Unit. General practitioners and hospitals are obliged to report all suspected food- and waterborne infections to the Danish Patient Safety Authority and to SSI.

A list of verified outbreaks (not including household outbreaks) reported to the Food- and waterborne Outbreak Database are presented in Appendix Table A3 and some of the outbreaks from 2024 are outlined 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 25 years. The first plan targeted *Salmonella* in the broiler production and was developed as a response to an increase in the number of human cases related to eating broiler meat. Since then, plans have been developed for *Salmonella* in pigs and pork, *Salmonella* in layers (eggs), *Campylobacter* in broilers and *S.* Dublin in cattle and beef.

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

At EU level, harmonised surveillance programmes and common targets have been set for the broiler and laying egg production. An overview on the status on the targets can be seen in Table A25.

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

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

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

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

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

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

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

7.4 Official testing of zoonotic pathogens in foodstuffs

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

- To verify that food business operators comply with microbiological criteria laid down in the legislation.
- To verify the microbiological safety of food for which no microbiological criteria are laid down at EU Community level.
- To monitor the effect of established risk management procedures to evaluate if these provide the desired results or need to be reconsidered.
- To generate data for the preparation of risk profiles and risk assessments to support microbial risk management
- To discover emerging problems with microbiological contaminants.

Appendix Table A24 provides information on the centrally coordinated studies conducted in 2024.

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

In 2024, Statens Serum Institut (SSI) extracted 1266 registered *Salmonella* cases including the available travel information from the Danish Microbiology Database (MiBa) that receives copies of reports from all Danish departments of clinical microbiology. Travel information was available from 70.3% of the *Salmonella* cases in 2024. The proportion of travel-related cases were similar to 2023 with 44.7% in 2024 and 46.0% in 2023 (Table 7.1 - Top ten *Salmonella* serotypes). A significant decrease in the total number of *S.* Enteritidis cases was seen from 384 in 2023 to 274 in 2024 (Table A1). This reflects that only a few outbreaks were reported with *S.* Enteritidis in 2024 compared to several large outbreaks *S.* Enteritidis in 2023 (Table A3 + Annual Report on Zoonoses in Denmark 2023).

In 2024, an increase in domestically acquired *S.* Typhimurium and S. 1,4,[5],12:i:- cases was seen from 68.9% and 73.7% in 2023 to 83.9% and 83.6% (Table 7.1 - Top ten *Salmonella* serotypes) caused by different outbreaks (Chapter 1 + Table A3). This increase also affected the total number of *S.* Typhimurium and S. 1,4,[5],12:i:- cases, from 174 in 2023 to 310 in 2024 (Table A1).

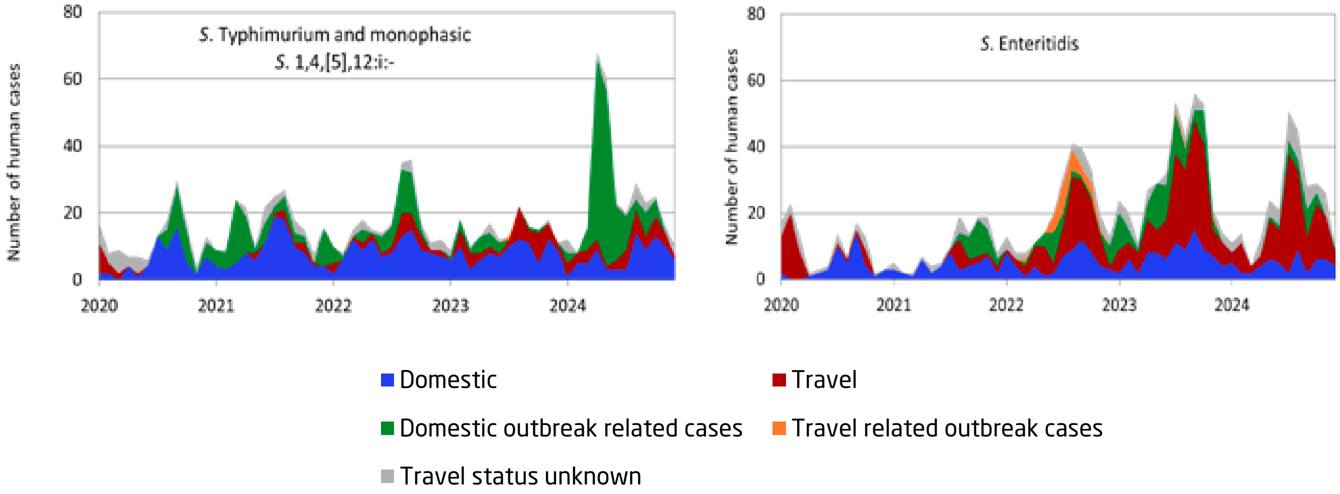
Table 7.2. Top 10 Salmonella *serotypes in humans and information about travel abroad, 2023-2024*

2024	Number of patients (%)	% of patients[a] infected Abroad[b]	Domestically	2023	Number of patients (%)	% of patients[a] infected Abroad[b]	Domestically
Enteritidis	274 (21.6)	66.1	33.9	Enteritidis	384 (31.8)	52.2	47.8
Typhimurium	177 (14.0)	16.1	83.9	Typhimurium	93 (7.7)	31.1	68.9
1,4,[5],12:i:-	133 (10.5)	16.4	83.6	1,4,[5],12:i:-	81 (6.7)	26.3	73.7
Stanley	33 (2.6)	64.3	35.7	Infantis	43 (3.6)	80.6	19.4
Paratyphi B var. Java	29 (2.3)	81.5	18.5	Muenchen	38 (3.1)	5.9	94.1
Newport	28 (2.2)	56.5	43.5	Stanley	33 (2.7)	70.0	30.0
Chester	26 (2.1)	57.1	42.9	Bareilly	20 (1.7)	70.0	30.0
Umbilo	24 (1.4)	0.0	100.0	Saintpaul	20 (1.7)	61.1	38.9
Agona	18 (1.4)	64.3	35.7	Newport	20 (1.7)	17.6	82.4
Infantis	17 (1.3)	78.6	21.4	Chester	17 (1.4)	13.3	86.7
Other serotypes	295 (23.3)	51.7	48.3	Other serotypes	458 (37.9)	57.1	42.9
Total	1,266	44.7	55.3	Total	1,207	46.0	54.0

a) Patients with unknown travel information (16.7% of all patients in 2024 and 10.2% in 2023) were excluded from the percentage calculations.
b) Infected abroad is defined as travel abroad in a seven-day period prior to disease onset.

Source: Statens Serum Institut

Figure 7.3. Monthly distribution of S. *Enteriditis and* S. *Typhimurium incl. monophasic S. 1,4,[5],12i- cases, 2020-2024*



Human disease and outbreak data

Table A1. Zoonoses in humans, number of laboratory-confirmed cases, 2019-2024

	Incidence per 100,000 inhabitants	Reported no. of cases					
Zoonotic pathogen	2024	2024	2023	2022	2021	2020	2019
Bacteria							
Brucella abortus/melitensis[a,b]		1	1	1	1	1	7
Campylobacter	92.9	5,546	5,186	5,142	3,740	3,742	5,389
Chlamydia psittaci	0.6	35	17	16	25	27	32
Leptospira spp.	0.4	25	13	6	10	14	14
Listeria monocytogenes	1.0	61	54	86	62	43	62
Mycobacterium bovis	0.0	0	2	0	0	0	0
Salmonella total	21.2	1,266	1,207	899	692	614	1,120
S. Enteritidis	4.6	274	384	251	114	117	310
S. Typhimurium[c]	5.2	310	174	208	205	149	272
Other serotypes	7.9	470	649[d]	344	301	302	449
Shigella/EIEC[e]	12.2	728	709	-	-	-	-
Shigella[f]	2.3	140	139	-	-	-	-
EIEC	1.4	82	63	-	-	-	-
STEC total[g]	21.2	1,269	1,431	1,330	927	448	630
O157	0.5	32	38	47	32	39	60
Other O-groups or non-typeable	5.2	310	375	394	376	198	359
Yersinia enterocolitica total[h]	21.7	1,296	1199	747	454	413	374
Yersinia enterocolitica (Biotype 2,3,4 and 5)	1.7	99	118	174	137	106	139
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 (S. 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) A subset of *Yersinia enterocolitica* (18.2%) was isolated and sent from the local clinical departments to SSI for surveillance. Characterisation disclosed 62,8% (266 isolates) being apathogenic biotype 1a, and these are excluded from the total number for 2024.

Source: Statens Serum Institut

Table A2. STEC[a] O-group distribution in humans, 2024

O-group[b]	Number of episodes	Proportion of total (%)
O146	37	2.9
O26	33	2.6
O157	32	2.5
O103	31	2.4
O27	15	1.2
O145	15	1.2
O63	14	1.1
O128	13	1.0
O91	11	0.9
Other O groups	141	11.1
Isolate not avaliable	927	73.0
Total	1,269	

Continued in the next column

a) Shiga toxin-producing *Escherichia coli* (STEC).
b) All O-groups that resulted in ten or more episodes are listed.

Source: Statens Serum Institut

Table A3. Food- and waterborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD) (n = 55), 2024

Pathogen[a]	No. of patients[b]	Patients laboratory confirmed[b]	Setting	Source	FUD no.
Bacillus cereus	27	0	Kindergarten	Bread with carrots	2398
Campylobacter coli ST8195	6	6	National	Chicken meat	2374
Campylobacter jejuni ST19	6	6	National	Chicken meat	2335
Campylobacter jejuni ST19	5	5	National	Unknown	2354
Campylobacter jejuni ST19	5	5	National	Chicken meat	2356
Campylobacter jejuni ST19	12	12	National	Chicken meat	2379
Campylobacter jejuni ST21	5	5	National	Unknown	2402
Campylobacter jejuni ST52	7	7	National	Chicken meat	2368
Campylobacter jejuni ST61	7	7	National	Unknown	2352
Campylobacter jejuni ST464	6	6	National	Chicken meat (imp)	2400
Campylobacter jejuni ST6461	8	8	National	Chicken meat	2355
Campylobacter, STEC O103:H2 ST17 (stx2a, eae)	10	2	Farm	Raw cow's milk	2377
Clostridium perfringens	20	0	Workplace catering	Meat sauce	2326
Clostridium perfringens	95	0	Catering	Mixed food	2358
Clostridium perfringens	91	1	Canteen	Pork roast	2366
Hepatitis A, 3A	5	5	National	Unknown	2331
Listeria monocytogenes ST1	4	4	National	Unknown	2319
Listeria monocytogenes ST5	2	2	National	Unknown	2318

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Table A3. Food- and waterborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD) (n = 55), 2024 (Continued from previous page)

Pathogen[a]	No. of patients[b]	Patients laboratory confirmed[b]	Setting	Source	FUD no.
Listeria monocytogenes ST7	7	7	National	Fish patties	2369
Listeria monocytogenes ST8	4	4	International	Salmon	2339
Listeria monocytogenes ST1607	5	5	International	Fish products	2262
Listeria monocytogenes ST416	2	2	National	Unknown	2375
Norovirus	25	3	Restaurant	Buffet meals	2298
Norovirus	10	0	Restaurant	Sushi	2329
Norovirus	47	2	Restaurant	Unknown	2330
Norovirus	30	2	Restaurant	Unknown	2350
Norovirus	37	3	Workplace catering	Unknown	2353
Norovirus	7	0	Restaurant	Open sandwich	2360
Norovirus	15	2	Canteen	Unknown	2362
Norovirus	15	0	Restaurant	Mixed food	2363
Norovirus	20	3	Restaurant	Unknown	2370
Norovirus	9	0	Restaurant	Sushi	2372
Norovirus	15	3	Restaurant	Unknown	2373
Norovirus	10	3	Restaurant	Unknown	2384
Norovirus	15	3	Restaurant	Frozen blackberries	2385
Norovirus	14	0	Regional	Oysters (imp)	2390
Norovirus	60	3	Restaurant	Unknown	2391
Norovirus	75	0	Catering	Mixed food	2399
Norovirus and Rotavirus	17	2	Restaurant	Mixed food	2297
Salmonella Enteritidis ST11	10	10	National	Unknown	2340
Salmonella Enteritidis ST11	6	6	National	Unknown	2371
Salmonella Enteritidis ST11	5	5	National	Unknown	2393
Salmonella Mikawasima	5	5	International	Unknown	2388
Salmonella 4,[5],12,i- ST34	66	66	National	Minced beef	2328
Salmonella 4,[5],12,i- ST36	6	6	National	Unknown	2338
Salmonella Typhimurium ST19	5	5	National	Unknown	2315
Salmonella Typhimurium ST19	70	70	International	Minced beef (imp)	2325
Salmonella Typhimurium ST19	11	11	National	Unknown	2376
Salmonella Umbilo ST2014	22	22	International	Rocket salad and spinach (imp)	2345
STEC O132:H34 ST582 (stx2f, eae)	4	4	Regional	Unknown	2392
STEC O26:H11 ST21 (stx1a, stx2a)	4	4	National	Unknown	2367
Unknown	31	0	Regional	Oysters (imp)	2316
Unknown	48	0	National	Porridge for infants	2337

Continued on the next page

Table A3. Food- and waterborne disease outbreaks reported in the Food- and waterborne Outbreak Database (FUD) (n = 55), 2024 (Continued from previous page)

Pathogen[a]	No. of patients[b]	Patients laboratory confirmed[b]	Setting	Source	FUD no.
Unknown	43	0	Restaurant	Buffet meals	2351
Unknown	30	0	Catering	Beef tenderloin stew	2381
Total	1,126	342			

a) ST = Sequence Type
STEC = Shigatoxin-producing *Escherichia coli*
b) Data only include outbreak cases from 2024
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, carcasses, Danish and imported meat, 2024. N=number of culture positive units*[a]

	Human cases N=1,266	Pork[b] batches N=80	Beef[c] batches N=4	Broiler[d] flocks N=14	Layer[d] flocks N=3
Agona	1.4	-	-	-	-
Chester	2.1	-	-	-	-
Dublin	0.9	-	50.0	-	-
Enteritidis	21.6	-	-	-	-
Infantis	1.3	6.3	-	7.14	33.3
Mikawasima	0.9	-	-	-	-
Newport	2.2	-	-	-	33.3
Oranienburg	1.0	-	-	-	-
Paratyphi B var. Java	2.3	-	-	-	-
Poona	0.9	-	-	-	-
Saintpaul	1.2	-	-	-	-
Stanley	2.6	-	-	-	-
Typhimurium	14.0	16.3	25.0	7.14	-
4,5,12:i:- & 4,(5),12:i:-	10.5	27.5	-	-	-
Umbilo	1.9	-	-	-	-
Other	18.2	43.8[e]	25.0[f]	85.7[g]	33.3[h]
Unknown	16.7	6.3	-	-	-

a) One isolate per serotype per unit is included, thus the number of isolates may exceed the number of units.
b) Sampling of pork carcasses at slaughterhouses according to the surveillance programme (Table A33).
c) Sampling of beef carcasses at slaughterhouses according to the surveillance programme (Table A32).
d) Sampling of production flocks prior to slaughter according to surveillance programmes (Tables A30).
e) Brandenburg (1), Derby (22), Give (1), Senftenberg (1), 4.12:i:- (10)
f) S. Havana (1)
g) S. Anatum (1), S. Coeln (1), S. Derby (5), S. Montevideo (1), S. Parathyphi.B (2)
h) S. 4.12:I:- (1)

Source: Danish Veterinary and Food Administration and Statens Serum Institut

Table A5. Occurrence of Salmonella *in the table egg production*[a]*, 2014-2024*

	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
2014	22	0	8	0	150	0	347	2
2015	15	0	8	0	123	0	344	0
2016	15	0	10	0	132	0	426	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[d]	364	2[e]

a) See Tables A28 and A30 for description of the surveillance programmes.
b) *Salmonella* was not detected in grandparent flocks (2) during rearing period.
c) *Salmonella* was not detected in grandparent flocks during adult (0) period.
d) *S.* 4,12:I:- (1)
e) *S.* Newport (1), *S.* Infantis (1)

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

Table A6. Occurrence of Salmonella *in the table egg layer flocks sorted by type of production, 2014-2024*

	Deep litter		Free range		Organic		Cage	
	N	Positive	N	Positive	N	Positive	N	Positive
2014	97	0	30	0	125	1	95	1
2015	108	0	29	0	172	0	86	0
2016	125	1	31	0	196	1	74	1
2017	126	0	42	1	217	2	61	0
2018	139	4	46	1	227	4	42	3
2019	135	1	34	2	220	5	22	0
2020	151	3	40	1	216	4	25	0
2021	151	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[a]	21	0

a) *S.* Newport (1), *S.* Infantis (1)

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

Table A7. Occurrence of Salmonella *in the broiler production*[a]*, 2014-2024*

	Rearing period[b] (parent flocks)		Adult period[c] (parent flocks)		Broiler flocks		Slaughterhouse[d] (flocks/batches)	
	N	Positive	N	Positive	N	Positive	N	Positive
2014	121	2	131	3	3,470	26	277	4
2015	91	0	289	1	3,631	23	148	0
2016	184	0	182	3	3,606	21	203	1
2017	170	2	250	1	4,290	25	259	0
2018	184	1	149	1	4,245	35	249	1
2019	210	0	137	1	4,012	12	254	0
2020	357	0	217	2	3,604	13	231	0
2021	154	0	290	1	3,758	6	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[e]	233	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.* Anatum (1), *S.* Coeln (1), *S.* Derby (5), *S.* Infantis (1), *S.* Montevideo (1), *S.* Paratyphi (2), *S.* Typhimurium (1).

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

Table A8. Occurrence of Salmonella *in turkey flocks, 2014-2024*

	Turkey flocks[a]	
	N	Positive
2014	10	0
2015	80	1
2016	76	0
2017	24	1
2018	13	0
2019	85[b]	0
2020	198	0
2021	115	0
2022	132	3
2023	151	1[c]
2024	109	1[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.* Infantis

d) *S.* Newport

Source: Danish Veterinary and Food Administration

Table A9. Occurrence of Campylobacter *in broiler flocks, 2014-2024*[a]

	Cloacal swabs at slaughter		Neck skin samples at slaughter[b]	
	N (Flocks)	% pos	N (Batches)	% pos[c]
2014	3,474	27.7	-	-
2015	3,274	19.6	-	-
2016	3,184	20.8	-	-
2017	3,316	16.6	-	-
2018	3,411	24.6	1,120	9.7
2019	3,327	22.7	1,063	7.4
2020	3,189	20.2	985	7.0
2021	3,332	19.1[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

a) See Table A29 for a description of the surveillance programmes. In 2014 the sampling method changed from boot swabs collected in the stable 7-10 days before slaughter to cloacal swabs at slaughter according to Danish Order no. 1512 of 13/12/2013.
b) In 2018, additional sampling of neck skin began at the slaughterhouses according to Regulation (EC) 2073/2005, see Table A29 for further description.
c) Percent positive samples >1000 cfu/g.
d) Corrected from 2022 report.

Source: Danish Agriculture and Food Council

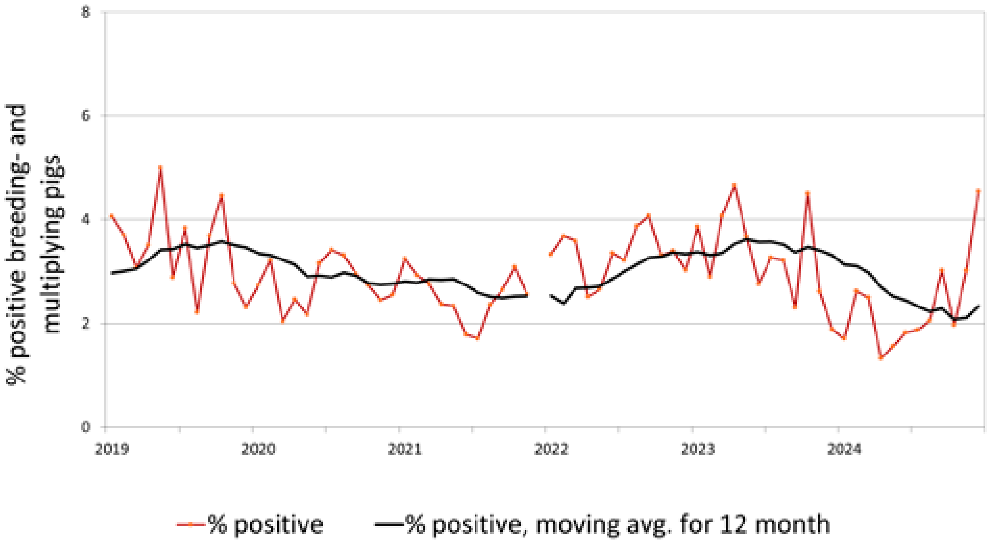
Table A10. Occurrence of Campylobacter *in non-heat treated chilled broiler meat samples at slaughter and retail*[a]*, 2018-2024*

		At slaughter[b]		At retail			
		Denmark		Denmark		Import	
		N (samples)	% pos	N (samples)	% pos[c]	N (samples)	% pos[c]
2018	Conventional	1,250	31.3	-	-	-	-
	Organic/free-range	199	91.5	-	-	-	-
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[d]	33	63.6[f]
	Organic/free-range	97	50.5	143	23.1[e]	33	75.8[g]

a) Centrally coordinated studies (see Table A24 and section 7.3 for description). Limit of quantification: 10 cfu/g.
b) Leg-skin samples.
c) The prevalence is calculated as a mean of quarterly prevalences, except organic/free-range results.
d) *C. jejuni* (75.3%), *C. coli* (24.7%)
e) *C. jejuni* (83.8%), *C. coli* (16.2%)
f) *C. jejuni* (57.1%), *C. coli* (42.9%)
g) *C. jejuni* (52.6%), *C. coli* (47.4%)

Source: National Food Institute and Danish Veterinary and Food Administration

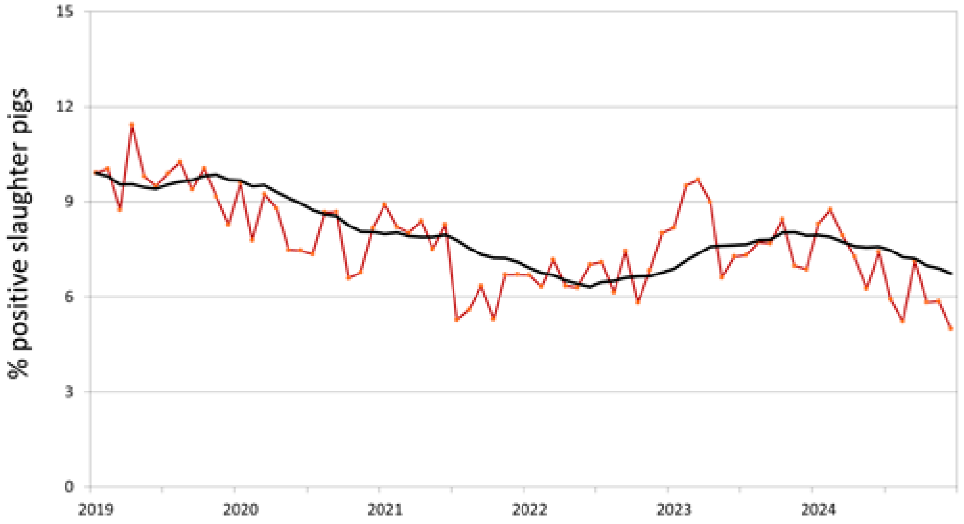
Figure A1. Serological surveillance of Salmonella *in breeding and multiplying pigs*[a] *based on monthly testing of blood samples, 2019-2024*[b]



a) For more information about the surveillance program, see Table A33.
b) Monthly data for the month of December 2021 not available. Therefore, the monthly moving average from January 2022 to November 2022 is based on 11 months' data.

Source: Danish Agriculture and Food Council

Figure A2. Serological surveillance of Salmonella *in slaughter pigs*[a]*, 2019-2024. Percentage of seropositive meat juice samples (first sample per herd per month)*



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

Source: Danish Agriculture and Food Council

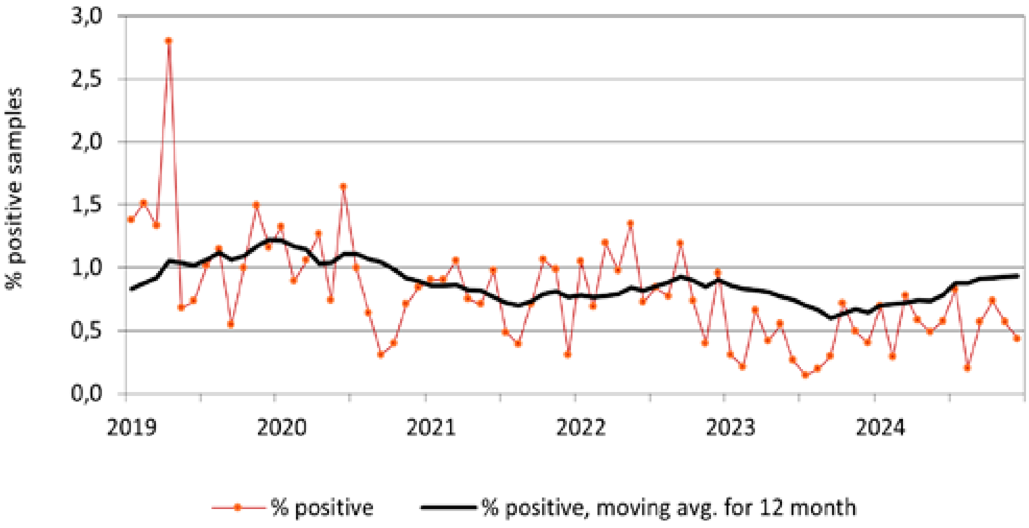
Table A11. Occurrence of zoonotic pathogens in pigs and pork in Denmark, 2024

	Herds		Animals/Samples		
Zoonotic pathogen	N	Pos	N	Pos	% pos
At slaughterhouse (slaughter pigs)					
Salmonella spp.[a,b]	4,185	89[g]	-	-	-
Salmonella spp.[a,c] (slaughtering >30,000 pigs/year)	-	-	15,570	-	0.85[h]
Salmonella spp.[a,c] (slaughtering 1,000 or more and less than 30,000 pigs/year)	-	-	53	-	0
Salmonella spp.[a,d]	-	-	-	-	-
Trichinella spp.[e]	-	-	14,364,453	0	-
Mycobacterium spp.[f]	-	-	14,364,453	0	-
Echinococcus granulosis/multilocularis[f]			14,364,453	0	-

a) See Table A33 for description of the *Salmonella* surveillance programme.
b) Data are from December 2020. Slaughter pig herds monitored using serological testing of meat juice samples collected at slaughter.
c) Swab samples from 4 designated areas after 12 hours chilling (4x100 cm^2).
d) Caecum samples are randomly collected from slaughter pigs at slaughter.
e) Samples collected from slaughter pigs at slaughter were examined using the method described in Regulation (EU) 2015/1375. In 2014, an amendment to EU regulation (EC) No 2075/2005 came into force stating that slaughter pigs, sows and boars kept under "controlled housing conditions" in Denmark are exempted testing for *Trichinella*. Free range pigs must be tested for *Trichinella*.
f) Slaughter pigs were examined by meat inspectors at slaughter.
g) Includes herds belonging to *Salmonella* level 2 and 3 only (See Table A33).
h) When estimating the prevalence of *Salmonella*, both the loss of sensitivity and probability of more than one sample being positive in a pool are taken into consideration. A conversion factor has been determined on the basis of comparative studies, as described in Annual Report 2001. Furthermore, the prevalence has been adjusted for double sampling carried out in slaughterhouses with a prevalence of 2% or above (12-month average).

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

Figure A3. Salmonella *in pork, monitored at slaughterhouses*[a]*, 2019-2024*



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

Source: Danish Veterinary and Food Administration

Table A12. Occurrence of zoonotic pathogens in cattle and beef in Denmark, 2024

	Animals/Samples		
Zoonotic pathogen	N	Pos	% Pos
At farm			
Brucella spp.[a]	726	0	0
Mycobacterium Tuberculosis Complex (MTBC)[b,c]	525	0	0
Coxiella burnetii[d]	88	1	1.1
At slaughterhouse			-
Salmonella spp.[e,f](slaughtering ≥7,500 cattle/year)	3,620	3	0.1[g]
Salmonella spp.[e,f](slaughtering ≥250 and <7,500 cattle/year)	92	1	1.1
Mycobacterium bovis[b]	432,700	0	-
Echinococcus granulosis/multilocularis	432,700	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.

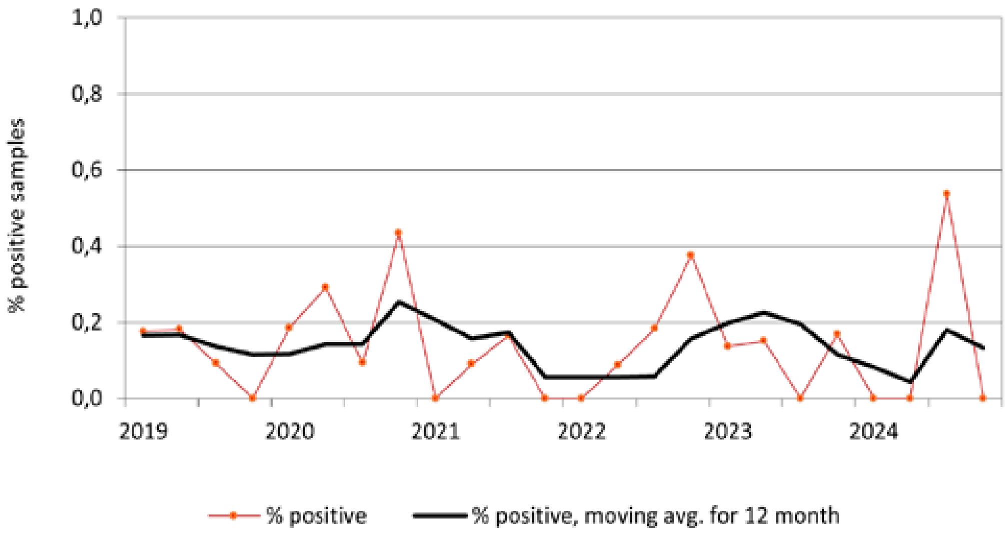
e) Swap samples from 4 designated areas after 12 hours chilling (4x100 cm^2)

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 being positive in a pool are taken into consideration. A conversion factor has been determined on the basis of comparative studies, as described in Annual Report 2001.

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

Figure A4. Salmonella *in beef, monitored at slaughterhouses*[a]*, 2019-2024*



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

Source: Danish Veterinary and Food Administration

Table A13. Cattle herds in the Salmonella *Dublin surveillance programme*[a]*, December 2024*

			Non-milk producing herds		Milk producing herds	
Salmonella Dublin level			N	%	N	%
Level 1		On the basis of milk samples	-	-	1,813	87.3
		On the basis of blood samples	10,856	97.1		
	Total	Probably *S.* Dublin free	10,856	97.1	1,813	87.3
Level 2		Titer high in blood- or milk samples	168	1.5	213	10.3
		Contact with herds in level 2	113	1	25	1.2
		Other causes	38	0.3	26	1.3
	Total	Non *S.* Dublin free	319	2.9	264	12.7
Total number of herds			11,175		2,077	

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]*, 2024*

Category of processing plant	Own-check samples		Product samples	
	N	Positive	N	Positive
1+2: By-products of this material cannot be used for feeding purposes	255	3	295	1
2: By-product of this material may be used for feed for fur animals[b]	0	0	0	0
3: By-products from healthy animals slaughtered in a slaughterhouse. Products of these may be used for pet food[c] and for feed for fur animals	468	0	683	0
Total	723	3	978	1

a) Regulation (EC) No 1774 of 03/10/2002 as amended.
b) No production.
c) For cats and dogs. Only by-products from pigs are used in this pet food.

Source: Daka Denmark A/S

Table A15. Control of Salmonella *in feed processing and feed material (batch-based data), 2022-2024*

	2024		2023		2022	
	N	Positive	N	Positive	N	Positive
Feed materials, farm animals[a]	61	0	69	0	60	1
Feed processing plants (process control)[b]:						
Ordinary inspections[c]	281	7[d]	282	11	284	8

a) Predominantly products of soybean, fish meal, and rapeseed cake.
b) Presence of *Salmonella* in compound feed is indirectly monitored by environmental samples collected during feed processing. Companies are sampled one to four times per year.
c) Primarily findings of *Salmonella* in the unclean zone.
d) *S.* Ikeja (1), *S.* Havana (5) *S.* Yoruba (1)

Source: Danish Veterinary and Food Administration

Table A16. Feed business operators own sampling of Salmonella *in compound feeds, feed processing and feed material (batch-based data), 2022-2024*

	2024		2023		2022	
	N	Positive	N	Positive	N	Positive
Compound feed, farm animals	3,305	6[d]	2,504	1	2,600	1
Feed materials, farm animals[a]	1,908	30[e]	1,837	36	1,969	27
Feed processing plants (process control):						
Ordinary inspections - clean zone[b]	7,564	13[f]	6,197	26	8,656	20
Ordinary inspections - unclean zone[b]	705	65[g]	563	32	1,232	25
Transport vehicles, clean zone/hygiene samples[c]	867	0	1,176	1	1,263	5
Transport vehicles, unclean zone/hygiene samples[c]	107	16[h]	108	15	165	6

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 (3), *S.* Lille (1), *S.* Rissen (1), *S.* Senftenberg (1).
e) *S.* Aarhus (1), *S.* Cubana (1), *S.* Livingstone (1), *S.* Mbandaka (4), *S.* Molade (3), *S.* Orion var. 15,34 (1), *S.* Rissen (2), *S.* Senftenberg (5), *S.* Soerenga (1), *S.* Typhimurium (1).
f) *S.* Falkensee(10), *S.* Mbandaka (3).
g) *S. Enterica* subspecies diarizonae (IIIb) (1), *S.* Idikan (1), *S.* Lexington (1), *S.* Minnesota (1), *S.* Putten (25), *S.* Raus (1), *S.* Rissen (18), *S.* Schleissheim (17).
h) *S.* Putten (5), *S.* Rissen (11).

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

Table A17. Listeria monocytogenes *in Danish and non-Danish produced ready-to-eat (RTE) foods[a], 2024*

			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[d]	Wholesale	37	0	43	4
	Products made from bovine, RTE[d]	Wholesale	2	0	3	0
	Products made from pork, RTE[d]	Wholesale	4	0	3	0
	Products made from chicken, RTE[d]	Wholesale	1	0	1	0
	Other meats, RTE[d]	Wholesale	8	0	1	0
	Other, RTE[d]	Wholesale	71	1	36	0
Non-Danish[e]	Crustaceans, RTE[e]	Border inspection	21	0	0	0
	Products made from pork, RTE[e]	Border inspection	3	0	0	0
	Products made from chicken, RTE[e]	Border inspection	1	0	0	0
	Surimi, RTE[e]	Border inspection	1	0	0	0
	Total		149	1	87	4

a) Samples are collected by the local food control offices according to EU Regulation (EC) No 2073/2005.
b) *Listeria monocytogenes* present in 10 or 25 g sample of the product.
c) Levels >10 cfu/g.
d) Ready-to-eat.
e) Samples from Canada, Chile, China, Greenland, United States, Vietnam.

Source: Danish Veterinary and Food Administration

Table A18. Histamine in batches of Danish and non-Danish fish products[a,b], 2024

		Danish		Non-Danish[c]	
Food category	Sampling place	N	Positive	N	Positive
Fish, unspecified, canned	Border Inspection	-	-	180	7
Fish, unspecified, raw	Border Inspection	-	-	54	0
Total				227	7

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 Canada, Colombia, Ecuador, Ghana, Mauritius, Seychelles, El Salvador, Philippines, Thailand, United Kingdom and Vietnam

Source: Danish Veterinary and Food Administration

Table A19. Salmonella *in Danish and non-Danish produced food items[a], 2024*

		Danish		Non-Danish[b]	
Food category	Sampling place	N	Positive	N	Positive
Products made from beef, intended to be cooked	At processing	190	0	-	-
Products made from pork, intended to be cooked	At processing	209	6[d]	-	-
Meat from bovine animals and pig, intended to be cooked	At processing	5	0	-	-
Products made from poultry, intended to be cooked	At border inspection	-	-	25	0
	At processing	75	0	-	-
Meat from other animal species, RTE[c]	At processing	15	0	-	-
Meat from other animal species, intended to be cooked	At processing	15	0	-	-
Products made from beef, RTE[c]	At processing	15	0	-	-
Products made from pork, RTE[c]	At processing	25	0	-	-
Crustaceans, RTE[c]	At border inspection	-	-	29	1[f]
	At processing	-	-	75	0
Molluscan shellfish, RTE[c]	At border inspection	-	-	15	0
	At processing	-	-	10	0
Vegetables, RTE[c]	At processing	168	2[e]	-	-
Seeds, sprouted, RTE[c]	At processing	10	0	-	-
Infant formula, dried	At processing	90	0	-	-
Infant formula, liquid	At processing	30	0	-	-
Other products of animal origin	At border inspection	-	-	15	0
Other food	At processing	5	0	-	-
Total		852	8	170	1

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.
d) 4,[5],12:i:- (2)
e) *S.* Give (1)
f) *S.* Brunei (1)

Source: Danish Veterinary and Food Administration

Table A20. Occurrence of zoonotic pathogens in pets and zoo animals in Denmark[a], 2024

	Pet animals						Zoo animals			
	Dogs		Cats		Others[c]		Mammals & reptiles		Birds	
Zoonotic pathogen	N	Pos	N	Pos	N	Pos	N	Pos	N	Pos
Chlamydia psittaci[b,c]	-	-	-	-	13	1	-	-	-	-
Echinococcus spp.	-	-	-	-	-	-	-	-	-	-
Lyssavirus (classical)	1	0	3	0	-	-	-	-	-	-
European Bat Lyssavirus	-	-	-	-	-	-	-	-	-	-
West Nile virus[c]	-	-	-	-	4	0	-	-	-	-
Highly pathogenic avian influenza	2	0	3	0	-	-	-	-	-	-

a) All samples are analysed based on suspicion of disease and does not reflect the country prevalence.
b) The number N and Pos represents cases. One case may contain more birds sampled at the same location /address.
c) In the case of *Chlamydia psittaci,* others refer to captive birds. In the case of West Nile virus, others refer to horses.

Source: Danish Veterinary Consortium and Danish Veterinary and Food Administration

Table A21. Occurrence of zoonotic pathogens in wild and farmed wildlife in Denmark[a], 2024

	Farmed wildlife						Wildlife			
	Wild boar		Mink & chinchillas		Birds		Mammals		Birds	
Zoonotic pathogen	N	Pos	N	Pos	N	Pos	N	Pos	N	Pos
Echinococcus multilocularis	-	-	-	-	-	-	313	7	-	-
Lyssavirus (classical)[b]	-	-	-	-	-	-	1	0	-	-
European Bat Lyssavirus[c]	-	-	-	-	-	-	80	0	-	-
West Nile virus[d,e]	-	-	-	-	-	-	28	0	461	0
Highly pathogenic avian influenza[f]	-	-	1	0	84[g]	0	77	1	638	85

a) All samples are analysed based on suspicion of disease or risk based and does not reflect the country prevalence
b) The mammal is a red fox. Samples are analysed using PCR.
c) The mammals are bats. These samples originate from both dead bats (brain material, n=31) and living bats (saliva, n=49).
d) The mammals are bats.
e) These samples originate from dead wild birds (brain material, n = 200) and living migratory wild birds (serum, n=261). No samples were positive for West Nile Virus, while approx. 3% of analysed serum samles (n=261) from living birds tested positive for antibodies.
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/.
g) The number equals number of subunits of Mallard ducks.

Source: Danish Veterinary Consortium and Danish Veterinary and Food Administration

Table A22. The Bovine Spongiform Encephalopathy (BSE) surveillance programme[a] for cattle, 2024

Type of surveillance	N[b]	Positive
Active surveillance		
Slaughtered animals	0	
Risk categories:		
Emergency slaughters	2,167	0
Slaughterhouse antemortem inspection revealed suspicion or signs of disease	0	
Fallen stock (>48 months)	18,706	0
Animals from herds under restriction	0	
Passive surveillance		
Animals suspected of having clinical BSE	0	
Total	20,873	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 and Food Administration, data extraction from the EFSA database, April 2025

Table A23. The Transmissible Spongiform Encephalopathy (TSE) surveillance programme[a] for sheep and goats, 2024

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)	86	0	325	0
Slaughtered for human consumption	0	0	0	0
Passive surveillance				
Animals suspected of having clinical TSE	0	0	0	0
Total	86	0	325	0

a) According to the EU Regulation (EC) 999/2001 as amended, Commission Decision 2009/719/EC as amended and Danish Order no. 1491 of 12/12/2019 as amended.
b) Samples (brain stem material) are tested using an IDEXX technique. Confirmatory testing is carried out using histopathology or immunohistochemistry. Further confirmation on autolysed material is performed at the European Union TSE reference laboratory.

Source: Danish Veterinary and Food Administration, data extraction from the EFSA database, April 2025

Table A24. Examples of centrally coordinated studies planned for 2024

Title of project	No. of planned samples	Pathogen surveyed	Further information
BU microbiology - slaughterhouses	120	Various	Not published
Campylobacter spp. in fresh, chilled Danish broiler meat at slaughteries (conventional)	1,250	*Campylobacter* spp.	To be published
Campylobacter spp. in fresh, chilled Danish broiler meat at slaughteries (organic)	100	*Campylobacter* spp.	To be published
Campylobacter spp. in fresh, chilled Danish broiler meat	100	*Campylobacter* spp.	Appendix Table A10
Campylobacter spp. in imported broiler meat	120	*Campylobacter* spp.	Appendix Table A10
Campylobacter spp. in imported and intratraded poultry meat	200	*Campylobacter* spp.	To be published[a]
Campylobacter spp. on cattle carcasses	175	*Campylobacter* spp.	To be published[a]
DANMAP - Antibiotic resistance in poultry, pork and cattle	220	AMR	To be published
DANMAP and EU surveillance Surveillance of antibiotic resistance in broiler, pork and cattle meat at retail (appendicitis samples)	630	AMR	To be published
EU surveillance of antibiotic resistance in retail	630	AMR	To be published
EU surveillance of antibiotic resistance in imported meat	12	AMR	To be published
Export - USA - environmental samples	100	*Listeria monocytogens*	Not published
Export - USA swab	468	*Salmonella*	Not published
IMPORT - Intensified control of Brazilian beef and poultry meat	50	*Salmonella, Listeria monocytogenes*	To be published
IMPORT - Microbiologic control of fish, fish products and bivale molluscan shellfish from 3rd.countries	110	*Listeria monoctogenes, Salmonella*	To be published
IMPORT - Microbiological control of food of animal origin, excluding fish	50	*Listeria monoctogenes, Salmonella*	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 products from Greenland	10	*Listeria monocytogenes, Salmonella spp., Escherichia coli, Staphylococci*	To be published
Microbiological classification of mussel production areas in Denmark	60	*Salmonella spp., Escherichia coli*	To be published
Part 6: Fish and fish products - wholesale	400	*Listeria monocytogenes*	To be published
Part 8: *Listeia monocytogenes* in other RTE products - wholesale	400	*Listeria monocytogenes*	To be published
Salmonella in feed materials from feed companies	60	*Salmonella* spp.	To be published
Salmonella in intratraded shell eggs retail	25	*Salmonella* spp.	To be published
Salmonella in intratraded shell eggs wholesale	25	*Salmonella* spp.	To be published

Continued on the next page

Table A24. Examples of centrally coordinated studies planned for 2024 (Continued from previous page)

Title of project	No. of planned samples	Pathogen surveyed	Further information
Salmonella process samples from feed companies	280	*Salmonella* spp.	To be published
Salmonella spp. and *Escherichia coli* in raw frozen scallops from Greenland	25	*Salmonella* spp., *Escherichia coli*	To be published
Salmonella in fresh poultry meat	700	*Salmonella* spp.	To be published
STEC in fermented sausages	25	STEC	To be published
Norovirus in soft berries	25	Norovirus	To be published

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

Source: Danish Veterinary and Food Administration

Table A25. Status on targets for Campylobacter *and* Salmonella, 2024

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 prevalence in flocks in 2024 was 25,0% for conventional flocks and 50,8% 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 2024 2) Three out of the four slaughterhouses met their targets on proportion of positive samples >1000 cfu/g in the winter period 2023-2024 and two out of four met their targets in the summer period 2024
Salmonella in poultry[b]		
Laying hen flocks of *Gallus gallus*	Initially eradication, later a reduction strategy in the table egg production	2 positive flocks (1.9%) (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	0.85% (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]	12.7% of milk-producing herds and 2.9% 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 (N=109) (Table A8)
Regulation (EC) No. 200/2010		
Breeding flocks of *Gallus gallus*	Max. 1% adult flocks positive for *S.* Typhimurium[d], *S.* Enteritidis, *S.* Hadar, *S.* Infantis and *S.* Virchow	0% (0 flocks) (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	0% (0 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	0.03% (1 flock) 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 and Food Administration

Monitoring and surveillance programmes

Table A26. Overview of referral of isolates, individual and laboratory notifiable human diseases presented in this report, 2024

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]	10.0
Chlamydophila psittaci (Ornithosis)	Laboratory and clinical notification	Mandatory	NA
Listeria monocytogenes	Laboratory and clinical notification	Mandatory[d]	100
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]	83.3
Shigella spp. and EIEC[g]	Laboratory and clinical notification	Voluntary[d]	27.7
STEC[h]	Laboratory and clinical notification	Mandatory from patients with HUS, all other voluntary[d]	27.2
Yersinia enterocolitica	Laboratory	Voluntary[d]	18.2
Parasites			
Cryptosporidium spp.	Laboratory	Mandatory when outbreak 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, 2024

Pathogen	Notifiable	EU legislation	Danish legislation
Bacteria			
Brucella spp.	1920[a]		
Cattle	OBF in 1979[b]	Regulation (EU) 2021/620	Order no 1152 of 25/07/2022
Sheep and goats	ObmF in 1995[c]	Regulation (EU) 2021/620	Order no 1152 of 25/07/2022
Pigs	No cases since 1999	Regulation (EU) 2016/429	Order no 1392 of 12/12/2019
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[d]	Decision 2003/467/EC	Order no. 1290 of 10/11/2023
Coxiella burnetii	2005	-	Order no. 1246 of 20/11/2024
Salmonella spp.	1993[e]	-	-
Cattle	-	-	Order no. 1493 of 06/12/2022
Swine	-	-	Order no. 1226 af 25/11/2024
Eggs for consumption	-	-	Order no. 499 of 23/3/2021
Hatching eggs	-	-	Order no. 1247 of 23/10/2023
Poultry for slaugther	-	-	Order no. 1229 of 26/11/2024
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[f]	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) Officially Tuberculosis Free (OTF) implementing regulation (EU) 2021/620, and Commission Decision 2003/467/EC. No cases in since 1988 or in deer since 1994.

e) Only clinical cases notifiable.

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

Source: Danish Veterinary and Food Administration

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, 2024*

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 m^2 in total) or swab samples (>1 m^2 in total). Analysed as one pool	5 transport crates from one delivery: crate liners (>1 m^2 in total) or swab samples (>1 m^2 in total). Analysed as one pool
1st & 2nd week[b, c]	Per unit	-	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g
4th week[a,b,c]	Per unit	5 pairs of boot swabs (analysed as two pooled samples), or 1 faeces sample consisting of 2x150 g	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g
8th week[b,c]	Per unit	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g
2 weeks prior to moving[a,c,d]	Per unit	5 pairs of boot swabs (analysed as two pooled samples), or 1 faeces sample consisting of 2x150 g	2 pairs of boot swabs (analysed as one pooled sample) or 1 faeces sample of 60 g
Adult flocks		*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 faeces sample consisting of 2x150 g	5 pairs of boot swabs (analysed as two pooled samples), or 1 faeces 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 and Food Administration.

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 and Food Administration

Table A29. Salmonella *and* Campylobacter *surveillance programme for the broiler flocks, 2024*

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

Source: Danish Veterinary and Food Administration

Table A30. Salmonella *surveillance programme for the pullet-rearing, table egg layer and barnyard/hobby flocks in the table egg production, 2024*

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. 499 of 23/03/2021.
b) Samples collected by the food business operator.
c) Samples collected by the Danish Veterinary and Food Administration.
d) According to Regulation (EC) 2160/2003 sample collection must be carried out every 15 weeks as a minimum.
e) Voluntary for hobby flocks.
f) For flocks with 30 birds or less: No testing if only delivered to a well-known circle of users, who are informed about the fact that no *Salmonella* control was performed.
g) If samples are negative, sampling is repeated 14 days later.

Source: Danish Veterinary and Food Administration

Table A31. Salmonella *surveillance programme for the turkey flocks, 2024*

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

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

Source: Danish Veterinary and Food Administration

Table A32. Salmonella *surveillance programme[a] for the cattle production, 2024*

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. 1493 of 06/12/2022. It is compulsory to have an action plan to eradicate *Salmonella* Dublin in Level 2 herds. Prior to 1.st 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 and Food Administration and SEGES

Table A33. Salmonella *surveillance programme*[a] *for the pig production, 2024*

Time	Samples taken	Purpose/Comment
Breeding and multiplier herds		
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		
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		
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 (4x100 cm^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 (4x100 cm^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 (4x100 cm^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.

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, within the last month, finds a sample positive for *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 analyses with 5 samples in each.

Source: Danish Veterinary and Food Administration

Table A34. Typing methods used in the surveillance of foodborne pathogens in Denmark, 2024

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]	None
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 the Laboratory of the Danish Veterinary and Food Administration

Population and slaughter data

Table A35. Human population, 2024

Age groups (years)	Males	Females	Total
0-4	156,723	148,426	305,149
5-14	323,065	306,204	629,269
15-24	369,564	354,137	723,701
25-44	771,801	747,660	1,519,461
45-64	774,950	778,057	1,553,007
65+	573,519	668,314	1,241,833
Total	2,969,622	3,002,798	5,972,420

Source: Statistics Denmark, 15 May 2025

Table A36. Number of livestock establishments, livestock and animals slaughtered, 2024

	No. of establishments	Livestock (capacity)	Number slaughtered
Slaughter pigs	6,597	12,468,016	14,364,453
Cattle	13,833	1,427,796	432,700
Broilers	275	19,416,495	105,289,700
Layers (excl. barnyard)	448	6,771,464	-
Turkeys	28	337,118	1,500
Sheep & lambs	5,712	132,529	35,700
Goats	3,117	18,072	-
Horses	19,457	112,163	219

Source: Statistics Denmark and Danish Veterinary and Food Administration - the Central Husbandry Register, May 2025

Table A37. Number of establishments, flocks and livestock capacity in the broiler production, 2024

	No. of establishments	No. of flocks	Livestock (capacity)
Rearing period (grandparent)	2	2	50,000
Adult period (grandparent)	4	9	84,500
Rearing period (parent)	20	85	680,300
Adult period (parent)	48	135	1,098,200
Hatcheries	5	0	0
Broilers	275	699	19,416,495

Source: Danish Veterinary and Food Administration, May 2025

Table A38. Number of establishments, flocks and livestock capacity in the table egg production, 2024

	No. of establishments	No. of flocks	Livestock (capacity)
Rearing period (grandparent)	0	0	0
Adult period (grandparent)	0	0	0
Rearing period (parent)	2	2	28,500
Adult period (parent)	8	8	73,400
Hatcheries	5	0	0
Pullet-rearing	34	54	1,315,620
Layers (excl. barnyard)	201	226	4,757,560

Source: Danish Veterinary and Food Administration, May 2025

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