3

ONE HEALTH AMR

3. One Health AMR

3.1 Introduction

One Health is defined as a unified approach to optimize the health of people, animals and the environment, under which multiple sectors must collaborate at varying levels [www.who.int].

DANMAP was established with the aim of understanding the drivers of AMR in humans and in the livestock industry and their interconnectedness. The monitoring programme has always been considered an integrated approach to research and surveillance, but with integration taking place at the coordination level rather than at the level of data collection and management. Hence, data are stored in separate databases by the animal and human sectors, however interpretation of results is done in cooperation whenever possible. Moreover, integration happens when discussing resistance findings in indicator and pathogenic bacteria and using it as a basis for recommendations and treatment guidelines. Finally, DANMAP supports the development and definition of strategies and action plans to reduce AMR in a collaborative manner, by monitoring sector-specific targets and by fostering the dialogue between different actors and stakeholders across sectors.

However, there has always been the wish to get a more in-depth understanding of the possible relationship between the animal, food and human sectors concerning antimicrobial usage (AMU) and development of antimicrobial resistance (AMR). To be able to foresee if changes in one sector will have a possible significant impact on the other sector, it requires knowledge of the probable routes of transmission and the size and speed of transfer. This again calls for further harmonised data collection, to define common denominators and units and to be able to perform cross-analyses on data from both the veterinary and human sectors.

At the EU level, an attempt to perform cross-analysis has been made since 2015 in the JIACRA reports [JIACRA IV, 2019-2021, ECDC, EFSA, EMA; 2024]. At the national level, even in a country such as Denmark with a long-established detailed monitoring system based on stable delivery of high-quality data, there are a few challenges in the implementation of integrated data analysis. Data are collected in the animal, food and human sectors often under different premises - following different legislation, with varying sampling strategies and magnitudes.

Here we cross-analyse antimicrobial resistance data from monitoring in livestock animals, meat and humans in Denmark. We map the frequency of multi-locus sequence types (MLST) and resistance genes and mutations of extended spectrum beta-lactamase-producing *E. coli* (here abbreviated to ESBL Ec) recovered from livestock animals and meat and from humans with bloodstream infections. Several recent studies [Aziz, et al 2024. *Microbiology Spectrum*. 12. e0341523; Nadimpalli et al 2023, *Frontiers in Ecology and the Environment*. 21. 10.1002/fee.2639; Liu et al 2023. *One Health*, 16: 100518; Roer, et al. 2019. *J Antimicrob Chemother* 74(3):557- 560; Valcek, et al. 2019. *J Antimicrob Chemother* 74(8):2171- 2175] report possible zoonotic transmission of ESBL Ec, both in high-income and low- and middle-income countries, underlining the importance of monitoring the occurrence of these bacteria in animals and humans, and assessing the possibility of transfer across sectors. A very recent modelling study [Brinch et al. 2025. *Zoonotic Diseases* 5(1): 7] performed in Denmark including the ESBL Ec isolates that have also been reported in DANMAP, has contributed to the body of work that assesses the likelihood of zoonotic transmission of ESBL Ec (see Textbox 3.1).

The annual number of bloodstream infections in humans in Denmark caused by ESBL Ec decreased during the COVID-19 pandemic, but has since resurged (see Chapter 8, section 8.2.1). Among animal and food sources, a significant reduction in ESBL Ec has been observed in Danish broilers (see Chapter 7, section 7.3.1), cattle and pigs (see DANMAP 2023, Chapter 7, section 7.3.1), as well as among most domestic and imported meat (DANMAP 2023, 2024, Chapter 7, section 7.3.1) with the exception of imported broiler meat in 2024. In this chapter, we investigate possible relationships between ESBL Ec from different sources in Denmark.

Despite its undoubtful integrated nature, the DANMAP programme continues to fall short on the monitoring of antimicrobials and antimicrobial resistance in the environment, as recently reported (see DANMAP 2021, Chapter 3, Textbox 3.1). The 2024 revision of the Urban Waste Water Treatment Directive (UWWTD) is expected to foster new national environmental monitoring activities in the near future, which will hopefully strengthen the focus on AMR of the already existing national surveillance program for aquatic environment and nature (NOVANA) (see Textbox 3.2).

3.2 Genotypic comparison of ESBL/AmpC-producing *E. coli* from humans, animals and food

Since 2022 (DANMAP 2021, Chapter 3), DANMAP has compared the distributions of multi-locus sequence types (MLSTs or STs) and ESBL/AmpC genes and mutations among ESBL Ec from humans, food-producing animals and meat to identify any major overlaps between sectors suggesting a zoonotic link.

In the present report, we added new data from 2024; 89 isolates of animal origin and 146 isolates from humans, totaling a dataset of 2068 ESBL isolates from humans and animals from 2018 through 2024. The 1,300 human isolates were clinical isolates from bloodstream infections sent voluntarily from the departments of clinical microbiology to the SSI reference laboratory for antimicrobial susceptibility testing. The animal and meat isolates (broilers: 109, broiler meat: 164, cattle: 56, beef: 41, pigs: 219, pork: 50, and turkey meat: 129) stem from the

EU mandatory screening programme from healthy animals and meat products (see Chapter 10 for more information).

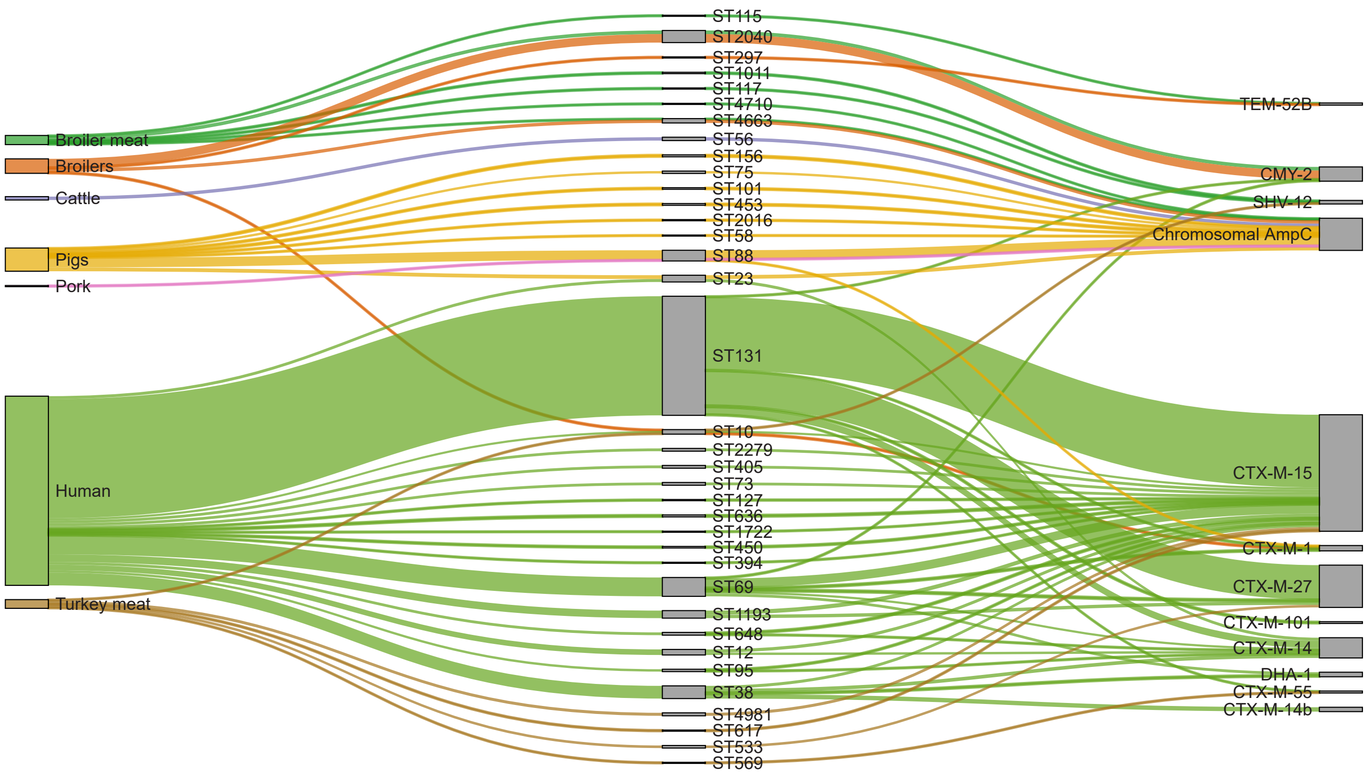
Each isolate has been sequenced as part of the surveillance activities, and the MLST and ESBL/AmpC genotype were extracted from the whole genome sequence. For an overview of sequence types and ESBL/AmpC genotypes detected in 2024 in *E. coli* from bloodstream infections, and from broilers, broiler meat and turkey meat, see Chapter 8 (Tables 8.14-16), and Chapter 7 (Table 7.3), respectively. For the purpose of the visual demonstration of the abundance of STs and resistance genes in the different reservoirs, we selected only flows of five or more isolates, thus limiting the analysis to a selection of data (Figure 3.1). The results described below refer to the selected isolates.

As in the previous years, limited overlap was found in both STs and ESBL/AmpC genes and mutations in isolates from humans vs. animals and food (Figure 3.1).

Regarding the distribution of MLSTs, one or few sequence types predominated among the isolates of each source. Isolates from humans were mostly from ST131, followed by ST69 and ST38 (see also Chapter 8, Table 8.16). The most abundant STs of animal and meat isolates were ST2040 for broilers and broiler meat, ST4981 for turkey meat, ST88 for pigs and pork, and ST56 for cattle. In accordance with former findings (see DANMAP 2015, Textbox 7.3), ST23 was found in both humans and pigs, although the ESBL/AmpC genotype differed between the human and pig strains. The pig isolates from ST23 harboured AmpC C-42T mutations, whereas the human isolates harboured the ESBL gene *CTX-M-14*. Additionally, ST10 was found in broilers, turkey meat and humans, but also harbouring different resistance mechanisms – *CTX-M-1*, *SHV-12* and *CTX-M-15*, respectively.

As observed in previous years, the AmpC plasmid-mediated gene *CMY-2*, and the ESBL genes *CTX-M-1*, *CTX-M-15*, *CTX-M-27* were found in both humans and food-producing animals or meat. Additionally, in 2024, also the ESBL genes *CTX-M-55* and *SHV-12* were detected across sectors. Interestingly, turkey meat isolates were those with the largest overlap with human isolates regarding the detected ESBL genotypes, including carriage of *CTX-M-15* and *CTX-M-27* (the two most common ESBL genes among human isolates; see also Chapter 8, Table 8.15), as well as *CTX-M-55*, although by different MLSTs.
The *CMY-2* AmpC gene was almost exclusively found among isolates from broilers and broiler meat from ST2040, but also in human isolates of ST69 and ST131. The *CTX-M-1* gene was mostly found among human isolates, but also in pig isolates of ST88 and ST10 isolates from broilers. All isolates from cattle harboured a C-42T mutation, which was not detected among the selected human isolates.

Figure 3.1 A Sankey diagram comprised of 1,272 ESBL Ec MLST-gene/mutation combinations from humans, animals and food showing the relationship between the isolates' source, sequence type and ESBL/AmpC gene or mutation DANMAP 2024



In general, sequence types seem to strongly associate with species, whereas there is more variance in combinations of STs and ESBL/AmpC genes and mutations. In the 2018 DANMAP report Textbox 7.2, Roer, et al., used whole genome sequencing on a similar, but smaller, dataset to investigate for possible zoonotic links. A possible link was found in ST69/*CTX-M-1*, but the SNP-distance was not indicative of an outbreak or a direct transmission, but rather of a clonal relationship.

In conclusion, it remains challenging to find clear evidence of zoonotic transmission of ESBL Ec between animals and humans in Denmark, within the investigated time frame of seven years, and when considering the occurrence of ESBL/AmpC genotypes in different sequence types. Further research into slow transmission over longer time spans, as well as more in-depth genomic analyses are of continued interest and on-going.

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Textbox 3.1

Understanding the spread of extended-spectrum cephalosporin-resistant *E. coli*: Insights from a dual modelling study

Background
Extended-spectrum cephalosporin-resistant *Escherichia coli* (ESC-EC) is an increasing public health concern, as it is now frequently detected not only in clinical settings but also in healthy individuals and various animal species. This study used two complementary modelling approaches to explore the spread of ESC-EC in Denmark: a compartmental model to simulate the risk of transmission in various sub-populations, and a Bayesian source attribution model to estimate the relative contribution of different sources to human infections based on genetic resistance profiles [1].

Method
The compartmental model
A compartmental model was developed to simulate ESC-EC transmission, capturing four stages of infection: susceptible, colonised, infected, and infected receiving antibiotic treatment. The Danish population was divided into three subpopulations: the general public, farmers, and pet owners, reflecting different patterns of exposure. Transmission pathways included person-to-person spread, foodborne exposure (from both domestic and imported meat), direct contact with animals such as livestock and pets, and colonisation following international travel.

Animal- and food-related exposures were quantified using an exposure indicator, which incorporated the proportion of resistant bacteria in each source, contact frequency, and the likelihood of transmission at the point of exposure, e.g., accounting for risk-reducing factors such as cooking or hygiene practices. The model estimated the total number of ESC-EC infections and evaluated the impact of individual sources by simulating scenarios in which each was removed. The additional burden of infections due to earlier antibiotic use was also assessed.

The Bayesian source attribution model
To complement the dynamic model, a Bayesian source attribution model was applied to estimate the contribution of different reservoirs to human ESC-EC infections, based on the distribution of resistance genes. The model compared the frequency of resistance gene combinations in human clinical isolates with those from isolates from various potential sources, including pets, domestic and imported food, and healthy human carriers. Data from DANMAP Chapter 3 formed the core of the dataset, supplemented with data from Swedish surveillance [2] and published literature.

Results
The compartmental model estimated a total of 61,067 ESC-EC infections annually in Denmark, with 3.2% linked to increased infection risk due to earlier antibiotic use. Human-to-human transmission was identified as the most significant pathway, and removing this route alone led to a 79% reduction in total infections. Excluding livestock sources resulted in a 59% decrease in infections, with cattle being the most influential species, responsible for 27% of the total burden. Foodborne transmission was responsible for 17% of infections; within this category, imported meat contributed more substantially than domestically produced meat. Pets, particularly dogs, accounted for 9% of infections. In contrast, colonisation via returning international travellers had only a modest impact, with their exclusion reducing total infections by just 3%.

In total, 2,696 *E. coli* isolates were included in the source attribution analysis: 1,295 from clinical cases, 265 from healthy colonised individuals, and 1,136 from non-human sources. A total of 101 distinct resistance gene combinations were identified, 21 of which were shared between infected humans and at least one of the different sources.

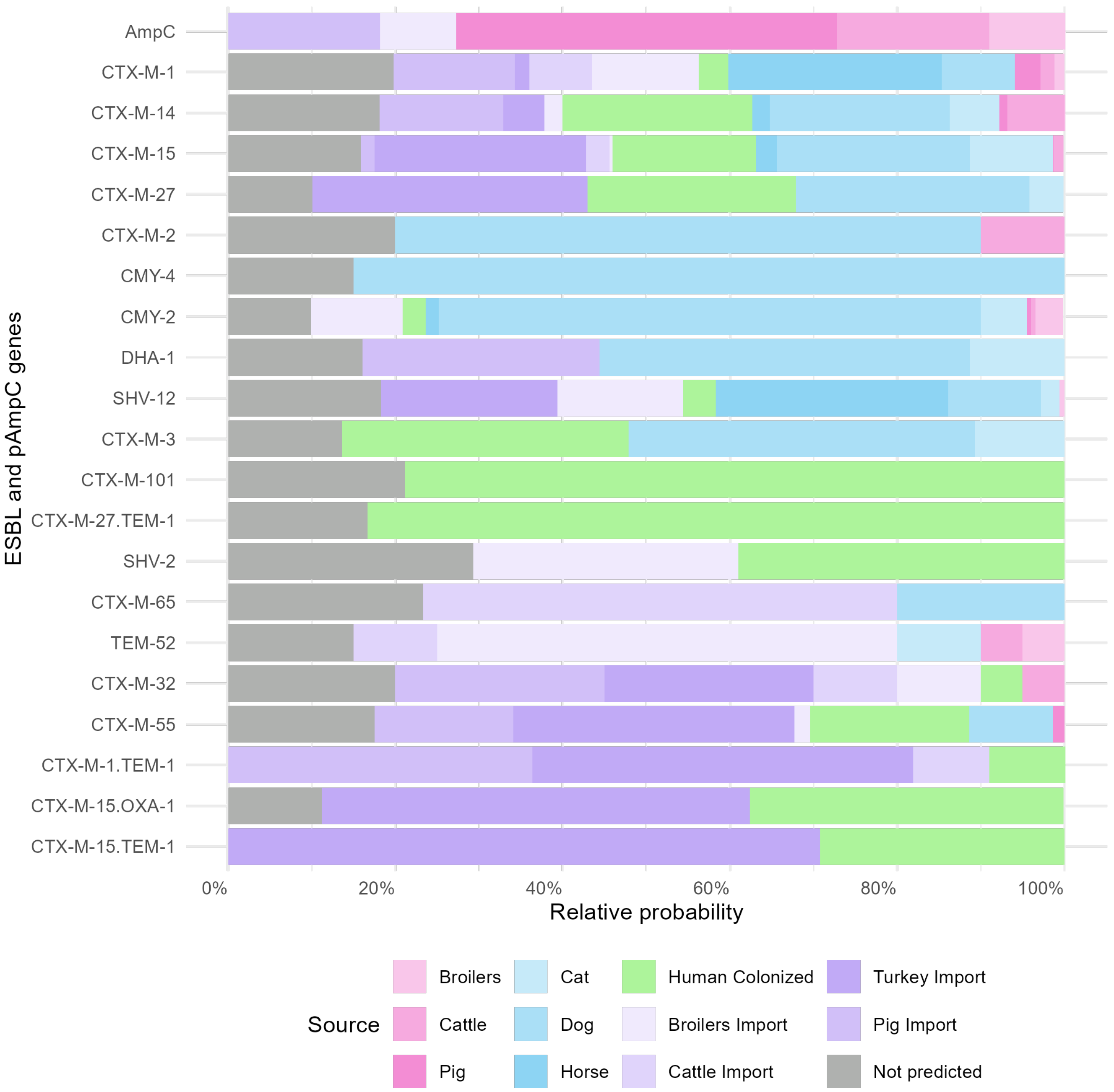
The Bayesian model estimated that dogs were the most significant contributor, accounting for 20.3% of human cases. This was followed by imported turkey meat (18.7%) and colonised humans (16.0%). Gene-specific attribution (Figure 1) revealed that pets (blue shades) and imported meat (purple shades) generally had higher attribution probabilities. For example, CMY-4 was exclusively attributed to dogs, while AmpC promoter mutations were the only resistance determinants present in infected humans and strongly linked to domestic animal sources, particularly pigs. In contrast, CTX-M-101 and CTX-M-27+TEM-1 were found only in colonised and infected humans, and not in any non-human reservoirs, suggesting possible human-adapted lineages.

continued ... Textbox 3.1

Conclusion

The findings of this study underscore the dominant role of human-to-human transmission in the spread of ESC-EC, while also highlighting the significant contributions from livestock, food, and pets. Although the impact of international travel was relatively limited in this model, it may still serve as a route for the introduction of novel resistant strains. Overall, the complexity of transmission dynamics revealed by this study supports the application of a One Health framework—integrating human, animal, and environmental health—to guide future surveillance, intervention, and policy efforts targeting antimicrobial resistance.

Figure 1 ESC gene-specific attribution in individuals infected with *E. coli*, shown as relative probabilities (%) DANMAP 2024



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[2] Swedres-Svarm 2022. Sales of antibiotics and occurrence of resistance in Sweden. Solna/Uppsala ISSN2001-7901.

Textbox 3.2

Antibiotics in wastewater and surface water

A) Current and forthcoming regulation on antibiotics in wastewater.

The Urbane Wastewater Treatment Directive
Antibiotics, as active pharmaceutical ingredients or partly degraded compounds, can be excreted to urban wastewater as a result of human consumption.

In November 2024, a revised Urban Waste Water Treatment Directive (UWWTD) was approved[1]. The directive sets the legal framework for the collection, treatment and discharge of urban wastewater.

The revised UWWTD has determined a requirement for establishment of a quaternary treatment step on wastewater treatment plants to remove micropollutants – including pharmaceuticals and thus antibiotics – from urban wastewater. All urban wastewater treatment plants of 150.000 p.e.[2] and above shall provide quaternary treatment, and for wastewater treatment plants of 10.000 -149.999 p.e. quaternary treatment must be established for wastewater treatment plants discharging effluent to areas identified as sensitive to pollution with micropollutants. The requirement of quaternary treatment shall gradually be implemented at all relevant wastewater treatment plants from 2033 to 2045.

Requirements for the quaternary treatment step is a minimum 80 percent removal of minimum six out of 13 indicator compounds all of which are pharmaceuticals. The list of indicator compounds include one antibiotic.

The additional costs related to installation of new treatment technologies at urban wastewater treatment plants has to be paid through an extended producer responsibility system. An assessment of micropollutants in urban wastewater determined that pharmaceuticals and cosmetic residues contribute to 92% of the total toxic load of untreated wastewater, of this pharmaceuticals account for 66% and cosmetic products for 26%[3]. Thus, producers of compounds from these two product categories will be included in the extended producer responsibility system in accordance with the polluter pays principle.

The UWWTD further requires monitoring of a broad number of compounds in influent and effluent from wastewater treatment plants; - minimum two samples per year for wastewater treatment plants of 150.000 p.e. and above and at least one sample every two years for wastewater treatment plants of between 10.000 p.e. and 150.000 p.e. The monitoring scheme will thus give continuous data on the content of a broad number of micropollutants expected to include antibiotics.

Current Danish regulation on wastewater
In Denmark, discharge of wastewater from wastewater treatment plants to surface water requires a discharge permit issued by the municipalities. The municipalities is also the legal authority to issue permit for discharge of wastewater from hospitals to surface water. The Danish Environmental Protection Agency issues discharge permit for wastewater directly to surface water from pharmaceutical industry. The permit must secure that discharge of micropollutants – including pharmaceuticals – to surface water does not compromise compliance with EU and nationally established environmental quality standards and criteria or other ecotoxicological threshold values (proposed no effect concentration values).

If wastewater from pharmaceutical industry or hospitals is connected to sewers leading to waste water treatment plants, this requires a connection permit issued by the municipalities, which must secure that micropollutants in the effluent does not prevent the wastewater treatment plants from complying with their discharge permits.

B) National surveillance of antibiotics in surface water and wastewater.

The national surveillance program for aquatic environment and nature (NOVANA[4]) monitors the status of the aquatic and terrestrial environments in Denmark and ensures that Denmark meets national legislation, EU directives, and international conventions. Furthermore, NOVANA provides data supporting the national action plans to support fulfillment of the water frame directive. The monitoring is carried out by the Agency for Green Transition and Aquatic Environment in Denmark.

As part of NOVANA, the presence of micropollutants in the aquatic environment is monitored. Thus, a wide range of different substances are measured in samples from streams, lakes, and marine areas. The list of substances monitored includes pharmaceuticals, such as antibiotics, metals, pesticides, plasticizers, and PFAS. The substances are monitored in water, sediment or biota (fish or mussels) depending mainly on their physical-chemical properties. Selected substances are also monitored at point sources such as wastewater treatment plants and storm water overflows, in order to identify which substances are emitted as a direct result of human consumption with wastewater.

Results

In 2017 a total of four antibiotics - trimethoprim, sulfamethiazole, sulfamethoxazole, and sulfadiazine, was included in the NOVANA surveillance program of surface water. The antibiotics are monitored in freshwater from streams as this is where the highest concentrations is expected to be found. Reviewing the collected data from 2017-24, sulfamethiazole has been found most frequently in 20% of the samples in concentrations ranging from 0.005 to 1.1 µg/L. The remaining antibiotics have been found in approximately 5% of the samples (table 1). None of the detected concentrations exceed the national environmental quality standards (EQS) for trimethoprim (100 µg/L) and sulfadiazine (4.6 µg/L).

Table 1 Overview of data from the national surveillance of antibiotics in surface water (streams) DANMAP 2024

	Parameter	CAS	Incl. in NOVANA	Number of samples	Detection frequency (%)	Range of concentrations (µg/L)
1478	Trimethoprim	738-70-5	2017-25	1297	3	0.001-0.45
912	Sulfamethiazole	144-82-1	2017-25	678	19	0.005-1.1
915	Sulfamethoxazole	723-46-6	2017-25	685	4	0.01-0.2
909	Sulfadiazine	68-35-9	2017-25	1080	3	0.0077-0.98

At point sources a total of six antibiotic (azithromycine, clarithromycine, erythromycine, sulfamethiazole, sulfamethoxazole, and trimethoprim) are monitored in samples from wastewater treatment plants and storm water overflows through NOVANA. Based on the results from the surveillance program, national mean concentrations[5] of discharges are estimated for each type of point source[6, 7]. For sulfamethiazole a national mean concentration of 0.58 µg/L is found in effluent from advanced wastewater treatment plants while a national mean concentration of 4.8 µg/L is found in effluent from mechanical treatment plants. It is, at this point, not possible to establish reliable national mean concentrations for the remaining antibiotics. Approximately 95% of the total amount of wastewater in Denmark is treated in advanced treatment plants and the remaining 5% in mechanical treatment plants.

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1 DIRECTIVE (EU) 2024/3019 OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL of 27 November 2024 concerning urban wastewater treatment
2 One population equivalent' or '(1 p.e.)' means the organic biodegradable load per day, having a five-day biochemical oxygen demand (BOD5) of 60 g of oxygen per day.
3 Feasibility of an EPR system for micropollutants. Final Report (070201/2020/837586/SFRA/ENV.C.2)
4 https://www2.mst.dk/Udgiv/publikationer/2023/09/978-87-7038-556-5.pdf
5 National mean concentrations signify the best estimate of the national Danish annual mean value of the concentration of a substance
6 https://www2.mst.dk/Udgiv/publikationer/2021/03/978-87-7038-287-8.pdf
7 https://www2.mst.dk/Udgiv/publikationer/2022/01/978-87-7038-386-8.pdf

Textbox 3.3

Infection prevention and control and prevention of antimicrobial resistance are interconnected

In Denmark there are numerous activities concerning infection prevention and control (IPC) and antimicrobial resistance (AMR) - both on the national and on the international level. Across Europe as well as globally it is increasingly stressed that controlling AMR in human health must be based on aligning efforts within surveillance, antimicrobial stewardship (AMS) and IPC.

IPC is for the first time in a Danish action plan on AMR specifically mentioned as one out of four central focus areas in the newly issued national action plan (NAP) on AMR as of 11 June 2025[1]. In June 2023, the European Union recommended to step up EU actions to combat antimicrobial resistance with a One Health approach[2]. To support the countries in stepping up the AMR actions the European Commission has invested 50 million Euros in EU-JAMRAI 2 four-year-project (2024-2027)[3] under the EU4health programme[4].

EU-JAMRAI 2 (European Joint Action on Antimicrobial Resistance and Healthcare-Associated Infections) seeks to implement concrete actions to monitor, prevent and effectively tackle AMR across human, animal and environmental health domains through a "One-Health" approach and to make Europe a best practice region. The project focuses on multiple areas, such as AMS, surveillance, awareness raising, capacity building, IPC, behavioral science and updating NAPs on AMR with a focus on both AMR and IPC[5].

The project was launched at a kick-off meeting in Paris in February 2024 and an annual meeting took place in Bilbao in March 2025[6]. The project is progressing well and the first results will be available and presented from autumn 2025 and onwards.

Among the 10 work packages (WP) in EU-JAMRAI 2, Denmark participates in WP5 (National Action Plans), WP6 (Antimicrobial Stewardship), WP7 (Infection Prevention and Control), WP8 (One Health Surveillance) and WP9 (Access to antibiotics).

WP7 is about improving IPC actions within the human, veterinary and environmental sectors and has a general focus on behavior change strategies to support further uptake of IPC recommendations. Several subtasks are described within the human activities: Development of frameworks for implementation of IPC competencies and prioritizing EU standards in IPC programs, support the participating member states and associated countries in the implementation of IPC core components, give access to an IPC toolbox and, finally, organizing peer-to-peer activities and exchanges with IPC experts. Topics which constitute a challenge for IPC of today as e.g. lack of educated workforce, specialized care moving out of the hospitals and replaced by care at home, and IPC in the green transition will be included in the work.

As part of the EU-JAMRAI 2 project the Danish National Center for Infection Control (CEI) in close collaboration with our national IPC partners aim at improving the access to IPC knowledge and tools, strengthening IPC networking and the sharing of knowledge. A general focus is on how to improve and maintain IPC competencies. CEI follows a number of IPC implementation activities from around the country. Both municipalities, regions and projects across sectors are represented. The implementation and behavior change knowledge from these projects will later be shared. In 2025, as a part of the peer-to-peer programme, CEI has organized a national behavior change workshop and mediated a number of IPC webinars in collaboration with EUCIC (European Committee on Infection Control)[7]. CEI has launched a new site for IPC inspiration for the sharing of materials and tools among healthcare professionals working with IPC in Denmark. Read more about the Danish EU-JAMRAI 2 IPC activities at CEI SSI subsite[8].

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The Danish IPC guidelines are in place
All healthcare professionals are expected to be familiar with and act in compliance with the national guidelines for IPC (published by the National Centre for Infection Control at SSI); in Danish "NIR Generelle forholdsregler for sundhedssektoren"[9]. The supplemental national guideline includes specific guidance on VRE, ESBL and other multidrug-resistant microorganisms (MDRO) and should be followed when being in contact with a patient, for which either clinical infection or carriage of MDRO is suspected or known; "NIR Supplerende forholdsregler ved infektioner og bærertilstand i sundhedssektoren"[10].

The Guidance on Preventing the Spread of MRSA by the Danish Health Authority was issued in 2006, the year MRSA became notifiable. The applicable 3rd edition of the guideline is from 2016; Guidance on Preventing the Spread of MRSA - The Danish Health Authority (sst.dk)[11]. The guideline represents the national recommendations and strategic framework for preventing the spread of MRSA at hospitals and in other healthcare settings and nursing homes. A 16-year MRSA surveillance report[12] has shown that the national MRSA strategy has been successful in controlling the spread of MRSA at hospitals as the primary goal of the MRSA guideline and to stabilize the spread of livestock-associated MRSA.

The first national guideline on preventing the spread of CPO by the Danish Health Authority was issued in 2018 (only in Danish); "Vejledning om forebyggelse af spredning af CPO"[13]. The guideline provides a national strategic framework for detection and management of CPO in hospitals. The main purpose of the guideline is to maintain a low prevalence of disease caused by CPO associated with certain high-risk situations. Despite this national guideline CPO is increasing in Denmark (see chapter 8.3.2, carbapenemase-producing organisms, CPO) indicating that more needs to be done in order to combat the outbreaks at hospitals and at long-term care facilities. There are a lot of challenges in controlling these outbreaks as they are long-lasting.

The purpose of both guidelines is to minimize the spread of these often highly resistant bacteria to the ill and weak patients at hospitals and in long-term care facilities, simultaneously keeping the occurrence of these bacteria on a continued low level. The guidelines contain recommendations for active screening of patients on admission to hospital, based on assessment of certain risk situations, e.g. admission to a hospital abroad during the last six months. Both guidelines are free of charge and easy to download from the Danish Health Authority website www.sst.dk.

In hospitals, nursing homes and home care, it is necessary to supplement the general precautions with transmission based (isolation) precautions in the case of an outbreak: "Infektionshygiejniske retningslinjer for MRSA"[14] and "Infektionshygiejniske retningslinjer for CPO"[15].

All IPC guidelines emphasize the importance of all healthcare staff, irrespective of profession, to contribute to the management and prevention of infections and to prescribe antibiotics with care.

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5 https://ec.europa.eu/info/funding-tenders/opportunities/portal/screen/opportunities/projects-details/43332642/101127787/EU4H
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