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STATENS SERUM INSTITUT

CELEBRATING 30 YEARS DANMAP 2025

# DANMAP 2025

## The Danish Integrated Antimicrobial Resistance Monitoring and Research Programme



Diagnostic Infectious Disease Preparedness, Statens Serum Institut
National Food Institute, Technical University of Denmark

## DANMAP 2025

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**Printing:** Pekema A/S

DANMAP 2025 - November 2026 - ISSN 1600-2032

**Text and tables may be cited and reprinted only with reference to this report:**
DANMAP 2025 - Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark. ISSN 1600-2032

The report is available from www.danmap.org

# DANMAP 2025

Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark

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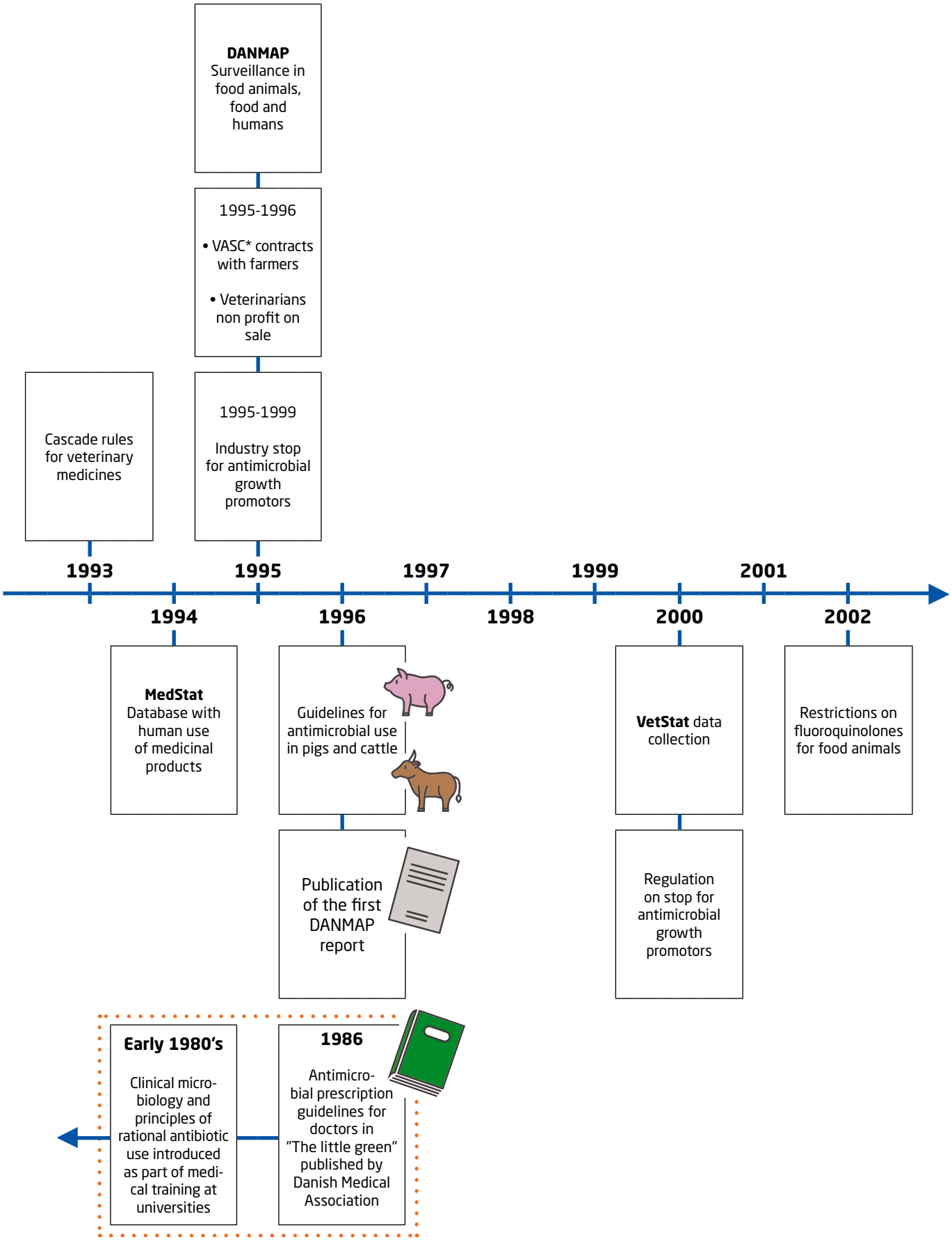
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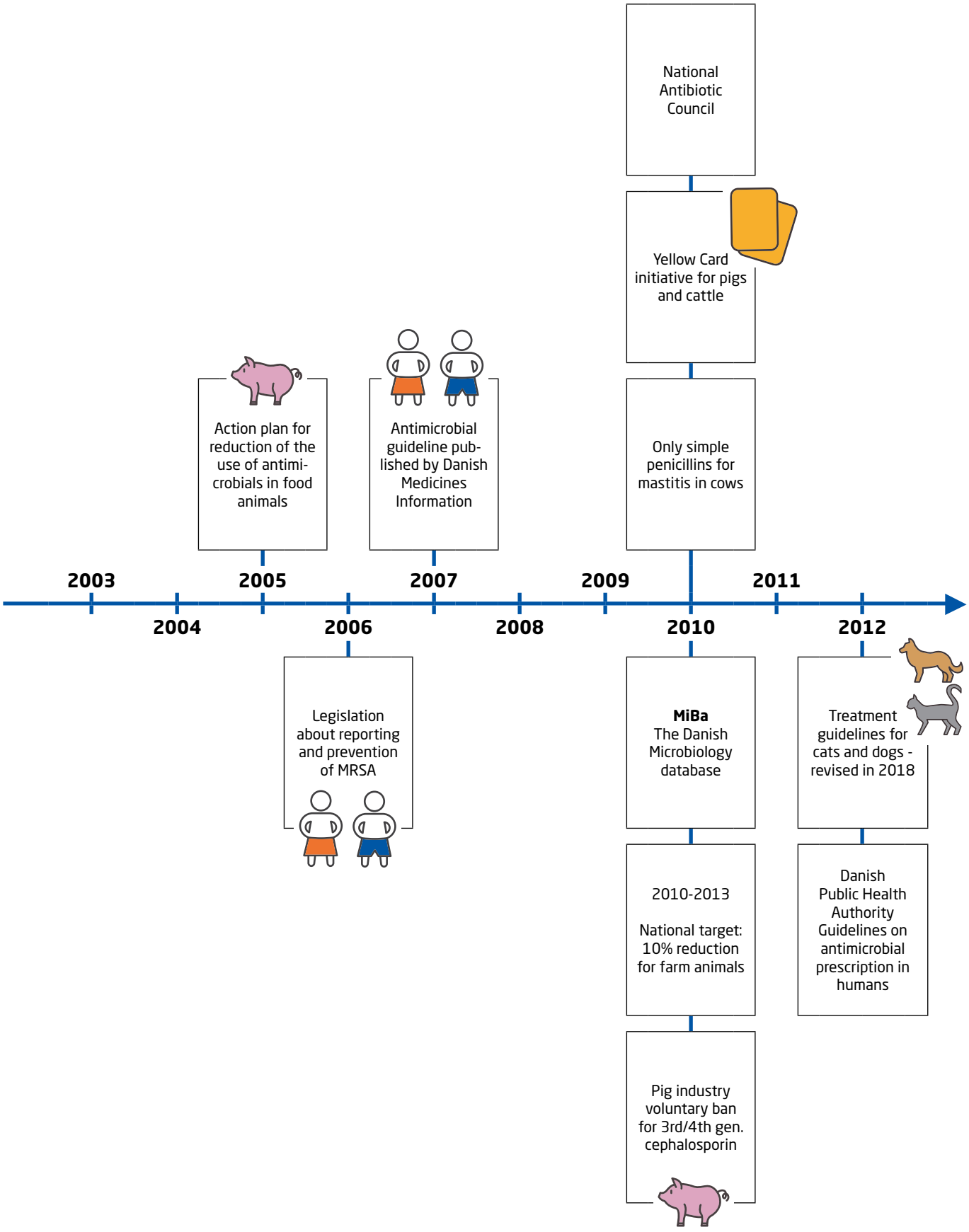
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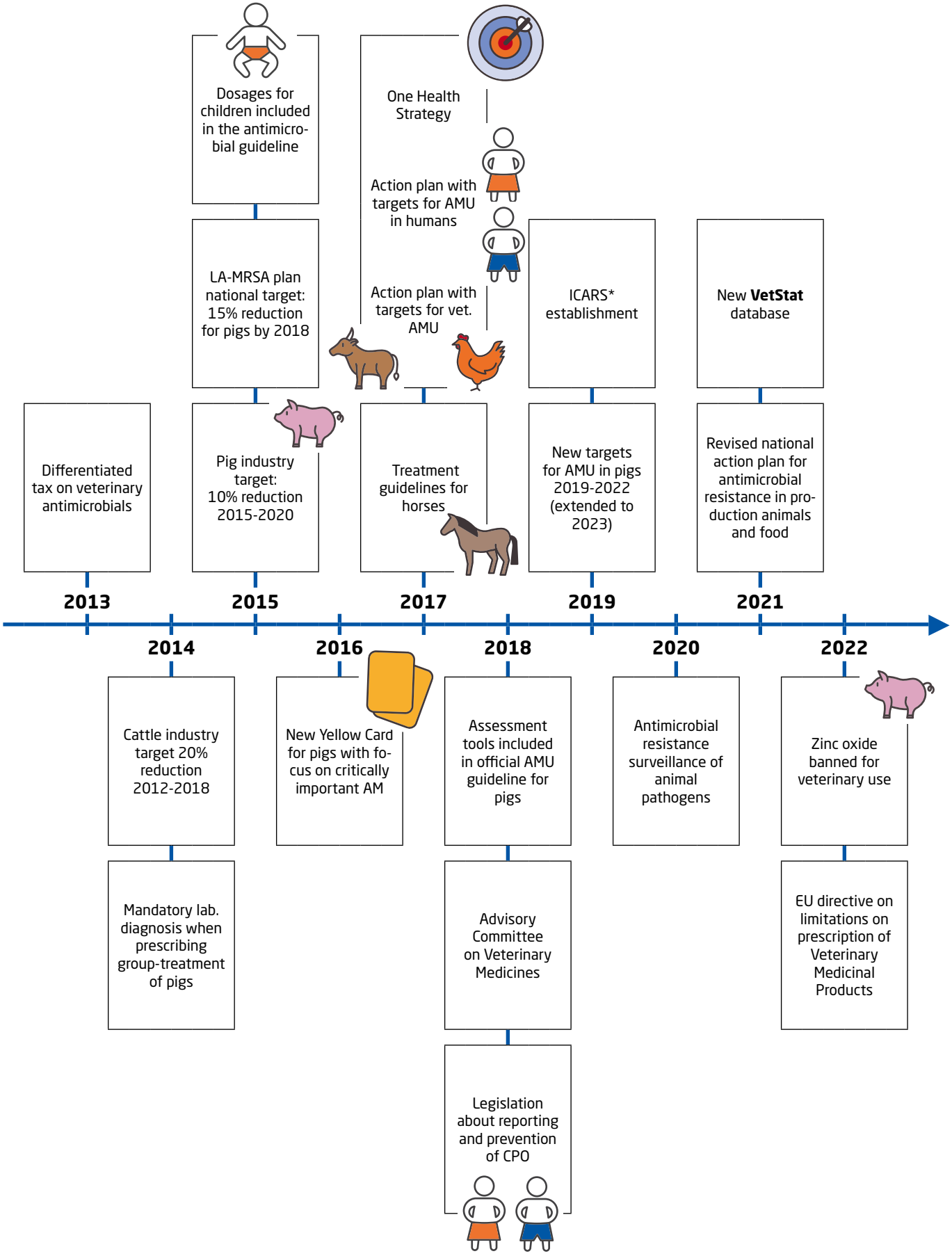
**Timeline with initiatives for the prevention and control of AMR and prudent antimicrobial use in animals and public health in Denmark**



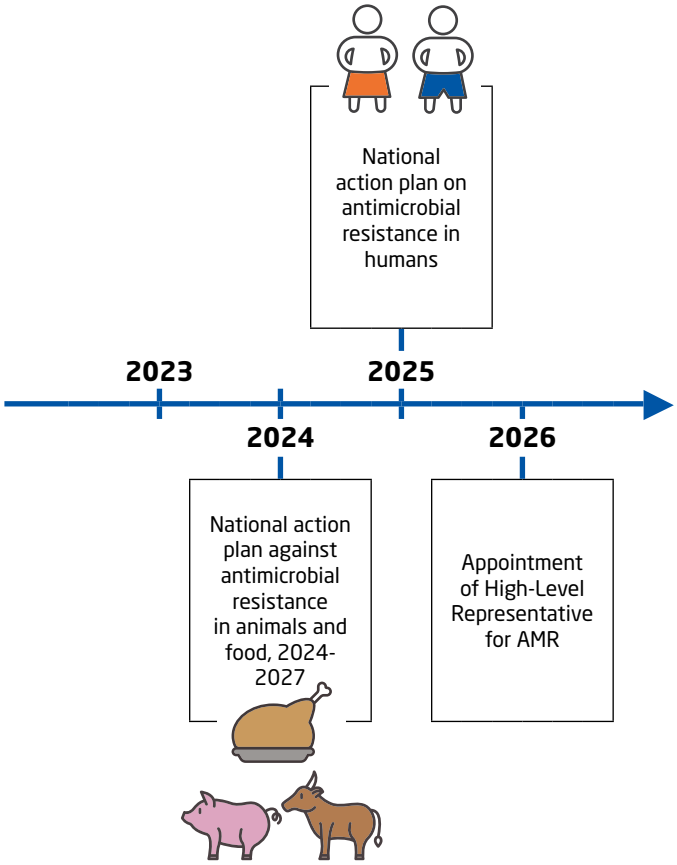

* Veterinary Advisory Service contracts


National Antibiotic Council
Yellow Card initiative for pigs and cattle
Only simple penicillins for mastitis in cows
Action plan for reduction of the use of antimicrobials in food animals
Antimicrobial guideline published by Danish Medicines Information
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012
Legislation about reporting and prevention of MRSA
MiBa The Danish Microbiology database
Treatment guidelines for cats and dogs - revised in 2018
2010-2013 National target: 10% reduction for farm animals
Danish Public Health Authority Guidelines on antimicrobial prescription in humans
Pig industry voluntary ban for 3rd/4th gen. cephalosporin

## continued ... Timeline of DANMAP




* The International Centre for Antimicrobial Resistance Solutions.


National action plan on antimicrobial resistance in humans
2023
2025
2024
2026
National action plan against antimicrobial resistance in animals and food, 2024-2027
Appointment of High-Level Representative for AMR

# 1. Editorial

## Three decades of surveillance, decades to come - what awaits us?

Commitment, Continuity, Collaboration - this year the DANMAP programme issues its thirtieth annual report, and these three words stand as important pillars and sum-up the core qualities from long-standing surveillance of antimicrobial consumption and resistance in humans, animals and food.

Thirty years is a considerable period for a surveillance programme. It is long enough to document changes in antimicrobial consumption and resistance, to assess the consequences of interventions and to establish a body of knowledge that extends beyond individual reports. As editors of the report, we would like to use the opportunity to consider not only what has been achieved but also what is required to maintain its value in the years to come.

DANMAP was established in 1995, when the possible, and probable relation between antibiotic usage in animals and occurrence of resistance in humans was gaining increased attention, not only in Denmark but across Europe. It became an area of concern for researchers and politicians alike. The idea behind was simple, yet the task complex: antimicrobial resistance cannot be adequately understood by examining data and findings in a single sector in isolation. The first results covering the food producing and human health sectors were published in 1997, making it evident that a systematic, continuous surveillance programme was necessary to gain more understanding and deliver data for policymaking in the area.

Covering both animals and humans, the programme delivered - and still delivers - a common evidence base for decisions that may otherwise be difficult to evaluate. DANMAP has documented the effects of many measures over time and in many ways, some of them will be addressed below.

From the very beginning of DANMAP, initiatives to reduce antimicrobial use in livestock, including the discontinuation of antimicrobial growth promoters and restrictions on both total and selected antimicrobial agents, led to marked changes, particularly in the pig industry. When VetStat was established in 2000 it further strengthened the possibilities for monitoring veterinary medicine use, while the concurrent development of microbiological diagnostics and national data systems supported increasingly detailed analyses and data comparisons. These again made it possible to look into potential sources and causes for emerging antimicrobial resistances using a a cross-sectoral approach. This led to measures aimed at reducing total usage or shifting toward a more rational application of antimicrobials, both of which have clearly contributed to maintaining low overall resistance levels in Denmark. Such achievements reflect the value of sustained cooperation and data-sharing across the sectors and across research institutions, authorities, farmers and clinical practitioners.

But surveillance is not simply a matter of collecting data and performing cross-analyses. Its value lies in maintaining consistent methods, interpreting findings in their appropriate context and making results available to those responsible for policy and practice. The annual report provides a record against which both progress and emerging problems can be assessed. That record is particularly valuable when the effects of an intervention become apparent only over several years.

However, the speed and order of developments are not always aligned, and progress in one area does not guarantee progress in another. While antimicrobial usage in pigs, after years of continuous reductions from 2011 to 2017, has levelled off in recent years despite strengthened efforts to reduce it further, antimicrobial consumption in humans has shown similar declines a decade ago and, after the fluctuations associated with the COVID-19-pandemic from 2020 to 2023, continues now its markedly declining trends.

Unfortunately, at the same time resistance to certain antibiotics continues to rise in the human sector: resistance to piperacillin-tazobactam among invasive *E. coli* increased over the longer term, causing worries in clinical departments as this is often the common choice of antibiotic treatment of patients upon admission to hospitals. Similarly, the number of carbapenemase-producing enterobacterales (CPE) continued its steep rise in 2025. Although CPE are currently either sporadically imported or outbreak-related and seem to be kept at bay, not showing in the resistance levels of the standard monitoring of bacteraemias yet, these are worrying trends that demand hospital resources and local actions. These developments underline the need to follow individual pathogens, resistance mechanisms and antimicrobial groups rather than relying on aggregate indicators alone.

The food chain represents another important dimension in surveillance, spanning and connecting the food production and the human health sectors. Along with the monitoring of antimicrobial use in the three main food-producing animal species in Denmark, the occurrence of resistance to a wide panel of antimicrobials, including compounds of both veterinary- and human medicine relevance, has been monitored in indicator and foodborne zoonotic bacteria recovered from animals and meat since the establishment of the programme. With the monitoring of resistance in indicator *E. coli* from healthy animals sampled at slaughter, DANMAP has continuously followed the trends of resistance in the Danish animal food-production sector over three decades. Such trends are interpreted in an integrated manner, alongside the trends in antimicrobial consumption, which has repeatedly provided valuable insights for policymakers and other stakeholders.

Similarly, the routine collaborative analysis and reporting of resistances in the foodborne pathogens *Salmonella* and *Campylobacter*, recovered from human patients, animals and meat has been an integral part of the programme since its inception, and it has contributed to monitor and inform the control of resistance in important human pathogens at the animal reservoir level. DANMAP has also repeatedly shown that resistance levels may differ between bacteria from domestically produced and imported meat. The low occurrence of resistance to third- and fourth-generation cephalosporins in *E. coli* from Danish meat is encouraging, while the higher resistance levels often reported in imported meat warrants attention. In a food market characterized by international trade, national production practices alone cannot determine the resistance patterns to which Danish consumers are exposed.

The next phase of DANMAP should build on its established strengths while being attentive to limitations of the programme. The implementation of whole-genome sequencing (WGS) in both outbreak detection and parts of the surveilled areas was a game changer, strengthening the programme´s ability to characterise resistant bacteria and investigate further on relationships between isolates from humans, animals and food. By identifying shared resistance genes and bacterial lineages, and providing evidence relevant to possible transmission between sectors, it has added a new layer of understanding. However, genetic similarity alone does not always establish the direction, frequency or epidemiological importance of transmission. For this, epidemiological information and well-designed sampling still remain essential.

There are also important gaps in the available data. National figures may follow overall trends, but they cannot always demonstrate whether an intervention actually changed prescribing at the level of the individual patient, healthcare unit, farm or production site. Nor does a passive surveillance system constructed around the collection of data from routine clinical isolates necessarily provide a representative picture of the levels of resistance in society or in certain population groups, such as residents of nursing homes.

Addressing these gaps requires choices about priorities, sampling and resources. More or, more detailed data does not necessarily make them better data. Introducing new surveillance activities should always be a response to clearly defined questions, addressing whether it improves the interpretation of existing results or supports decisions that could not be adequately informed by current methods. At the same time, it is important not to withdraw on existing methods or sampling schemes without considering how this can impact the ability to compare results over time.

The conditions under which DANMAP operates are changing. In Denmark, an ageing population demanding changes in healthcare provision and the recently introduced healthcare reform will change the landscape and probably impact sampling and diagnostic schedules. It may also impact the need for effective antibiotics over time.

Another concern is the availability of antimicrobial medicines for both humans and animals and of vaccines for animal production. Shortages may alter prescribing practices and increase the use of alternative agents. It can also stimulate the development of new antimicrobials or new alternatives to antimicrobials, a development that we look forward to, but which should be taken into account when readjusting surveillance programmes.

Food production is also evolving. Foreseen politically demanded changes in production volume, farm management and disease prevention practices may affect antimicrobial use. As production systems and supply chains change and develop, surveillance must remain sufficiently flexible to detect the following changes in bacteria and their resistome.

Also, the political landscape and context are important and can play a crucial role. While national action plans and goals need to be developed according to national needs, they also need to be aligned with and adjusted to international development, the direction set by the European Commission and the recommendations issued by the United Nations and important bodies such as the World Health Organisation, the Food and Agriculture Organisation and the World Organisation for Animal Health. In recent years, this also includes the United Nations Environmental Programme.

DANMAP can contribute by documenting whether intended changes occur and by identifying unintended consequences. Its role is to provide an independent evidence base, always keeping an arms-length distance to the political and professional decisions that follow from it.

In the future, environmental surveillance may become a more prominent part of this work. Resistant bacteria and antimicrobial residues in wastewater, agricultural environments and other environmental compartments can provide information not captured by current human, animal and food surveillance. However, the environmental dimension is methodologically demanding. New sampling approaches and indicators must be sufficiently standardised to allow meaningful interpretation, and their inclusion should be guided by a clear assessment of what they add to the existing programme.

A programme with DANMAP's responsibilities depends on more than scientific methods. It requires stable funding, access to high-quality data, skilled personnel, functioning laboratory networks and effective cooperation between institutions. These conditions should not be taken for granted. Public budgets and political priorities change, while the demands placed on surveillance continue to grow.

There is a risk that the value of long-running surveillance becomes less visible precisely because it has become an established part of the national infrastructure. The absence of a dramatic change in a given year may be reassuring, but it does not mean that the underlying surveillance is unnecessary. Reliable conclusions about trends, interventions and emerging resistance depend on data collected consistently over many years. Interruptions or poorly planned changes may compromise the ability to distinguish real developments from changes in measurement.

On a more practical level, it is important to consider how DANMAP can remain useful to its readers. The detailed annual reports have aimed at delivering satisfactory details and knowledge to researchers, laboratories, clinicians, veterinarians and authorities. The more accessible short report - or summary - has in recent years tried to accommodate the wish for easier and faster communication about main findings. It is a continuous challenge to hit the balance right, to make results easier to understand without simplifying away uncertainty or overstating what the data demonstrate.

Finally, in 2026, Denmark has appointed its high-level representative for AMR.DANMAP looks forward to contributing to this work in order to maintain the awareness on prudent use of antimicrobials and on AMR nationally but certainly also globally.

The 30th anniversary is an opportunity to recognise what DANMAP has achieved, but it should not become a reason for complacency. The programme's enduring strength lies in its continuity, its cross-sector perspective and its ability to turn data into a basis for action. Its future value will depend on maintaining these characteristics while adapting to new scientific possibilities and changing needs. After 30 years, the overall positive developments that DANMAP has reported in antimicrobial consumption and resistance in Denmark demonstrate why surveillance remains necessary. Having little to look for does not mean that we should stop looking. A surveillance programme should be able to document progress without overlooking unfavourable developments, and to distinguish between a temporary fluctuation, a sustained trend and a change that requires intervention, also when the trends are favourable.

At the end remains Commitment, Collaboration and Consistency, words that highlight the engagement and dedication that has been put into DANMAP work over the years. We hope that these words and values will carry DANMAP into its next 30 years. Enjoy reading!

***DANMAP team of editors,***
*Ana Sofia Ribeiro Duarte*
*Majda Attauabi*
*Mikkel Lindegaard*
*Vibe Andersen*
*Ute Wolff Sönksen*

# DANMAP 30 years in the service of One Health

It was a very different time 30 years ago; the Berlin wall had just come down and a new reunified Europe emerged, new molecular techniques were rapidly transforming classical microbiology, digital connectivity and data science were in their early stages, and both political and technical optimism about a new open, free and globally connected world began to take shape.

We hadn't yet worried about climate change, mass extinction of species or political nationalism and AI was not yet invented. However, antimicrobial resistance (AMR) was already a serious concern, and the prospect of humanity losing the race between our ability to discover new antimicrobials and the rapid emergence of new multidrug-resistant pathogens was becoming increasingly realistic.

In Denmark, the detection of vancomycin-resistant *Enterococcus faecium* in food animals, and the association to the routine feeding of avoparcin (a glycopeptide) to food animals as growth promoters, had caused both public and political alarm. The Minister of Food and Agriculture at the time, Henrik Dam Kristensen, boldly banned the use of avoparcin for food animals in Denmark.

Antimicrobial growth promoters were regulated by EU legislation, so a unilateral ban required solid scientific evidence that the banned substance represented an unacceptable threat to human or animal health. The time to provide this comprehensive evidence was a matter of weeks. It quickly became apparent how little data Denmark had on antimicrobial usage and antimicrobial resistance in humans and animals, and in particular in the interface between animals and humans.

We convinced the Minister that in order for Denmark to succeed in Brussels, we would need much better data on the association between antimicrobial use in humans and animals and antimicrobial resistance in human and animal infections, and also continuous data, to document the effect of the ban, as well as the risks to the health of humans and animals.

It was fortunate that Denmark just a little more than one year prior had established the Danish Zoonosis Center, with a mission to document the zoonosis situation in the country annually to the European Commission, and thus an elaborate system for collecting samples from animals, food and humans had been put in place recently, and also a governance and coordination structure involving all public, civic and private relevant stakeholders in the one health arena. The main institutions in the Danish Zoonosis Centre were Statens Serum Institut and Danish Veterinary Institute, and it was those two institutions that prepared the plan for the DANMAP program.

The plan reflected the purpose as well as the surveillance structures already in place in different contexts, not least the Danish integrated zoonosis monitoring program. Unique features of the programme included the diversity of microbial organisms; pathogens and indicators, the sampling system, the harmonized antimicrobial susceptibility testing methods, the antimicrobial consumption data collection and the epidemiological data analysis and visualization framework. The report preparation process, design, lay-out, printing and distribution was copied from the annual report on zoonosis, so we were able to move from plan to execution in a very short time, and the first DANMAP report was published less than a year after the program's initiation.

The DANMAP programme was instrumental in supporting the process of documenting the consequences of the use of, and the effects of terminating the use of antimicrobials for growth promotion. It provided a comprehensive situation report of the AMR situation in Denmark and has continued to do so for thirty years now. That is unique, and DANMAP has rightfully earned its nickname as the "mother of all AMR monitoring programs".

The European ban of the use of antimicrobials for animal growth promotion use remains the world's largest intervention to reduce the selective pressure for AMR globally, but also the voluntary as well as regulatory control of the use of critically important antimicrobials in animals and humans, as well as early detection and response to emerging pathogens such as MRSA, CRO's and others have been crucial. Sadly, antibiotics as growth promoters are still used outside Europe.

DANMAP remains the most comprehensive AMR and AMU monitoring programme globally, and it has been an international role model for many countries worldwide, including the EU integrated AMR monitoring program. DANMAP data has been used in thousands of scientific publications and reports and ensured a constant high level of awareness of the AMR situation in Denmark, informing guideline and regulatory developments as well.

Consistency in sampling plan and analysis methods has been a hallmark of DANMAP, however, in the future, a gradual replacement of conventional laboratory methods by genomic methods seems like a relatively safe prediction. This will however not happen rapidly and will require extensive evaluation and documentation to ensure that genomic data can be translated into phenotypic data of clinical relevance.

Despite the successes of DANMAP, the AMR problems of Denmark and the world around us have definitely not disappeared, on the contrary, thus it is our hope that the programme, which we initiated thirty years ago, will continue to produce solid data to inform experts and decision makers for many decades onwards, as well as inspire other countries to do the same. On this note, we are happy that Henrik can now not only apply and integrate the insights and knowledge gained from his years with AMR surveillance, but also utilize future DANMAP results in his work as the Danish High Level Representative on AMR.

DANMAP remains among the finest Danish solutions to this date.

*Niels Frimodt-Møller and Henrik C. Wegener*

# Acknowledgements

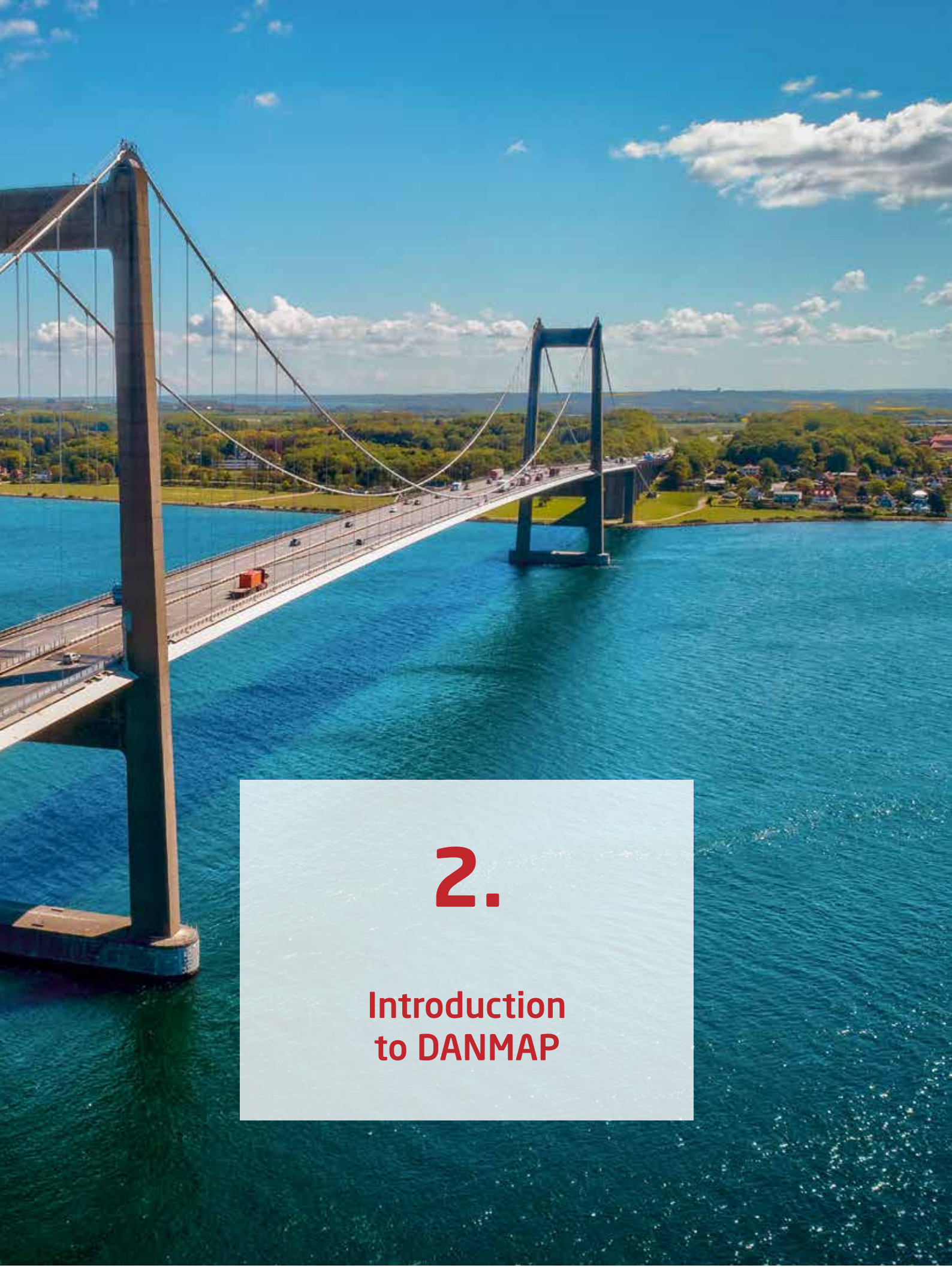
**DANMAP is based on a strong collaboration between several institutions and on the contributions from highly skilled staff from many specialties and professions. Without their knowledge and engagement, there would be no DANMAP surveillance.**

## The DTU National Food Institute would like to thank the following:

- The meat inspection staff and company personnel at the participating slaughterhouses for collecting samples from animals at slaughter
- The staff of local Veterinary and Food inspections units for collecting food and animal samples
- The staff of the Danish Veterinary and Food Administration's Laboratory, Ringsted for analysing animal and food samples
- The Danish Veterinary and Food Administration's Food and Feed Safety Division, for collecting and transmitting data on antimicrobial resistance in food and animal samples and for discussing data interpretation
- The Danish Veterinary and Food Administration's Animal Medicine and Veterinary Trade Division, for collecting and transmitting data on veterinary consumption of antimicrobial agents from VetStat and discussing the interpretation of the data
- Colleagues at the National Food Institute, DTU, for valuable discussions on many topics related to the report
- All data providers for textboxes and textbox authors

## Statens Serum Institut would like to thank the following:

- The Departments of Clinical Microbiology and the DANRES group - Danish Study Group for Antimicrobial Resistance Surveillance - for providing data on resistance in bacteria from human clinical samples and discussing many of the topics included in the report
- The staff of the Neisseria and Streptococcus Typing Unit at SSI for providing data on samples and resistance in beta-haemolytic streptococci, *H. influenzae* and *Neisseria gonorrhoeae*
- The staff of the Foodborne Pathogens Unit at SSI for providing data on resistance in *Campylobacter* and *Salmonella* from human clinical isolates
- The staff of the Staphylococcus Laboratory at SSI for providing data on invasive staphylococcal infections as well as all MRSA
- The staff of the Antimicrobial Resistance Reference Laboratory and Surveillance Unit at SSI for providing data on resistance in the referred *E. coli*, *K. pneumoniae*, *A. baumannii*, *P. aeruginosa* and vancomycin and linezolid-resistant enterococci
- The staff at the Unit of Mycology at SSI for providing resistance data for human *Candida* and *Aspergillus*
- Colleagues at the Infectious Disease Epidemiology & Prevention Unit at SSI
- Colleagues at the Data Integration and Analysis Secretariat at SSI
- The Danish Health Data Authority and the Register of Medicinal Products Statistics for providing data on antimicrobial consumption on healthcare activity
- All Danish hospital pharmacies for providing data on antimicrobials consumed at hospitals through special deliverances
- All data providers for textboxes and textbox authors



# 2.

# Introduction to DANMAP

# 2. Introduction to DANMAP

## 2.1 The DANMAP surveillance system

DANMAP, the Danish Integrated Antimicrobial Resistance Monitoring and Research Programme, is a surveillance system with five key objectives:

- To establish the state-of-nation in regards to the use of antimicrobial agents in food-producing animals and humans
- To carry out surveillance of the occurrence of antimicrobial resistance in bacteria isolated from food-producing animals, food of animal origin (meat) and humans
- To identify areas for further research, e.g. antimicrobial resistance transmission or possible associations between antimicrobial consumption and antimicrobial resistance
- To deliver data to veterinarians, medical doctors and other health professionals for the development of antibiotic treatment guidelines
- To act as a knowledge base for authorities, academia and politicians when performing risk assessment and management, thus supporting decision making in the prevention and control of resistant bacterial infections

Since 2021, DANMAP also provides an integrated analysis of resistance in bacteria from humans and food animals. The monitoring programme was initially developed in 1995 by researchers, based on frequent discussions and exchange of knowledge and results from research. Since then, DANMAP has evolved into a governmentally supported programme. However, much of the design of the programme, including participation of the human laboratories and referral of strains is based on a voluntary principle.

DANMAP surveillance relies on four equally important components: well-established and well-functioning diagnostic systems, well-designed and representative surveys, reliable registers as well as mutual trust and openness between all collaborators.

A positive effect of the regular meetings and exchange between stakeholders is that these prove helpful in other aspects, for example, by contributing to a common knowledge pool regarding laboratory methods. This ensures and contributes to continuous improvements and harmonisation of the laboratory work. Meetings across sectors and between different stakeholders also contribute to a better mutual understanding, facilitating development and work towards mutual goals.

Surveillance is a complex undertaking and DANMAP encompasses many different surveillance components and covers resistance in different populations and contexts.

These categories of bacteria are included in DANMAP:

- Human clinical isolates to reflect the antimicrobial resistance levels in the human population that seeks medical care
- Foodborne zoonotic bacteria along the whole farm-to-patient chain to monitor the levels of antimicrobial resistance in shared pathogens
- Indicator bacteria from healthy food-producing animals to monitor status of antimicrobial resistance in the animal reservoirs
- Clinical isolates from sick food-producing animals to monitor resistance

The National Food Institute at the Technical University of Denmark (DTU) and the National AMR reference laboratory at Statens Serum Institut (SSI) are responsible for data interpretation and output communication mainly via the annual DANMAP report and seminar. Interpretations are independent of policy, risk management and private industries.

The DANMAP programme is funded jointly by the Ministry of Health and the Ministry of Food, Agriculture and Fisheries. Support from the ministries has also helped build the databases and maintaining the registers, which the current surveillance system relies upon.

For further information on the development and history of DANMAP, please read Chapter 2, "DANMAP – A 20 year perspective" in DANMAP 2015 and Chapter 1, "DANMAP - the beginning" in DANMAP 2020.

**Organisation and data flow**

Since 1995, a main purpose of DANMAP has been to monitor the entire chain from farm to fork to patient. The organisation and collection of DANMAP data and the interdisciplinary collaboration between sectors and organisations is presented in Figure 2.1.

The introduction of whole genome sequencing (WGS) has been a big step forward for surveillance purposes and in outbreak situations and has become routine standard in many clinical laboratories and most reference laboratories. However, phenotypical testing is still considered relevant, more feasible, cheaper and sometimes faster, especially in a clinical setting. Phenotypical testing also continues to be used in combination with WGS to describe and determine which resistance genes are relevant to look for when using molecular analysis. Furthermore, it complies with EU regulations in food and animal testing.

**Figure 2.1 Organisation DANMAP regarding data and data flow**

DANMAP 2025

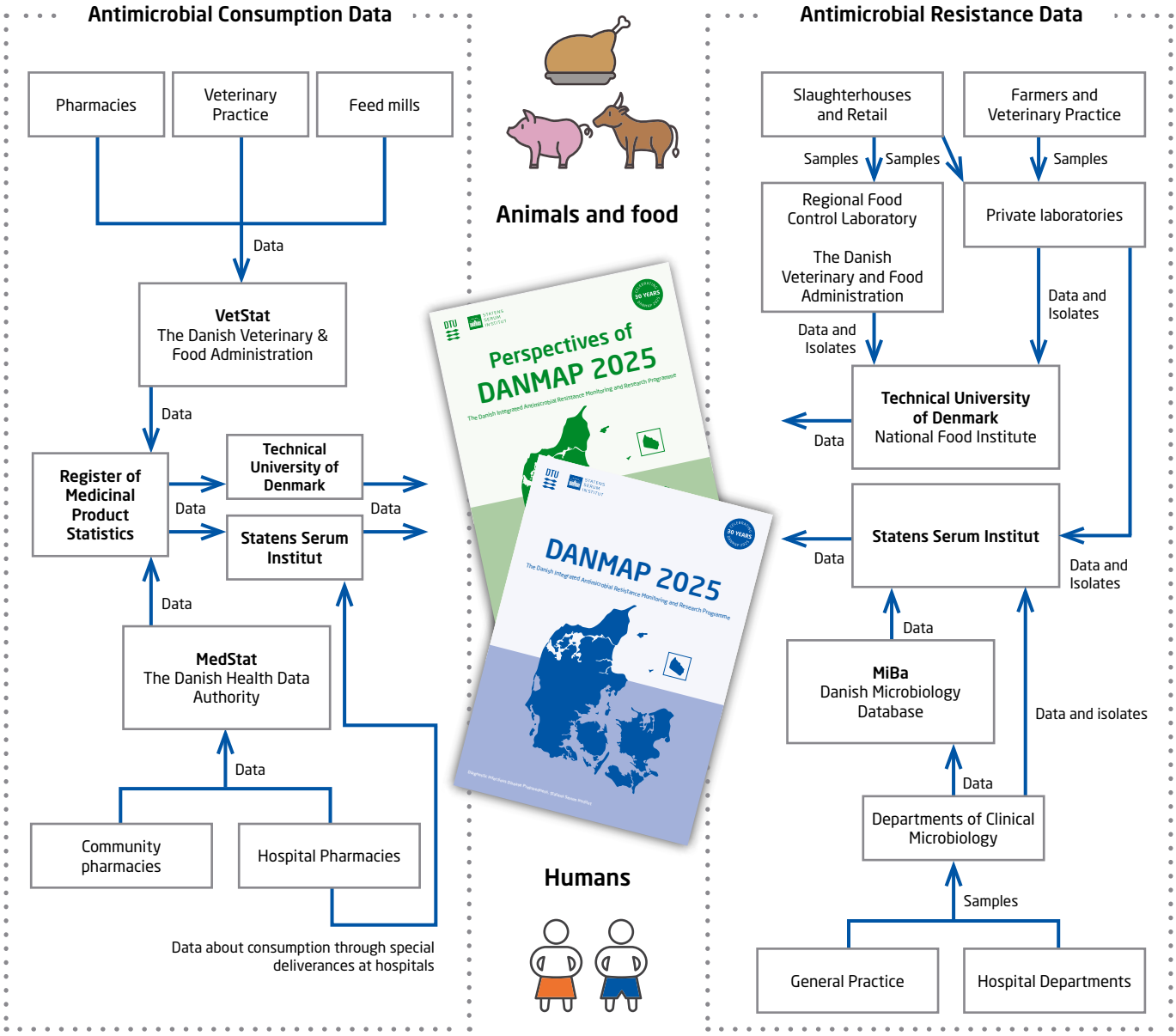


**Figure 2.2 The five Danish healthcare regions and their respective population distributions. In addition, the ten DCMs are marked by black dots. The grey dot indicates the national reference laboratories (NRL) situated at Statens Serum Institut** DANMAP 2025




| | |
|---|---|
| **North Denmark Region** | |
| No. of inhabitants | 592,768 |
| No. of inhabitants/km$^2$ | 75 |
| No. of inhabitants/GP | 1,780 |
| **Central Denmark Region** | |
| No. of inhabitants | 1,373,799 |
| No. of inhabitants/km$^2$ | 106 |
| No. of inhabitants/GP | 1,713 |
| **Capital Region of Denmark** | |
| No. of inhabitants | 1,930,793 |
| No. of inhabitants/km$^2$ | 753 |
| No. of inhabitants/GP | 1,775 |
| **Region Zealand** | |
| No. of inhabitants | 854,793 |
| No. of inhabitants/km$^2$ | 118 |
| No. of inhabitants/GP | 1,956 |
| **Region of Southern Denmark** | |
| No. of inhabitants | 1,240,472 |
| No. of inhabitants/km$^2$ | 101 |
| No. of inhabitants/GP | 1,615 |

GP = General Practioner
DCM = Department of Clinical Microbiology
NRL = National Reference Laboratories

Data source: Statistics Denmark [www.dst.dk] and the Danish Medical Association [www.laeger.dk]

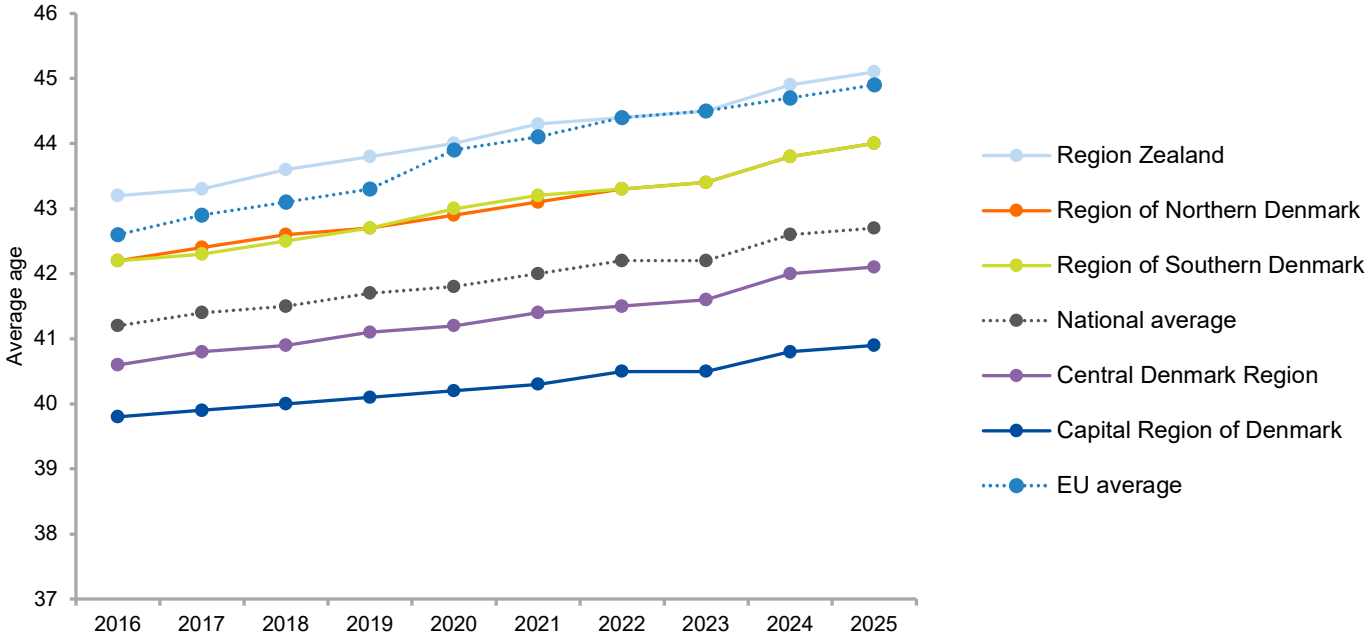
## 2.2 Information on demographics and health care system

During the past 30 years, the human population in Denmark has increased from approximately 5.2 million inhabitants in 1995 to 6.0 million in 2025 [www.dst.dk]. Simultaneously, the average age has increased gradually. In 2023, the national average age was 42.6 years. The population and the respective regional distribution, in 2024, is presented in Figure 2.2, while regional differences and changes in age are presented in Figure 2.3.

In Denmark, microbiological analyses are carried out by ten hospital departments of clinical microbiology (DCMs) situated at the main regional hospitals, Figure 2.2. The analyses performed cover all samples from public hospitals and most samples from general practitioners (GPs). In addition, some GPs perform culturing of urinary samples from their patients. In the Capital Region of Denmark one private laboratory also performs additional analyses for the GPs.

Data on regional and national health care activity at hospitals in 2016 and 2025 are presented in Table 2.1. Denmark has a very high bed occupancy rate at hospitals and can reach maximum capacity during winter time for example due to high influenza activity. In 2025, the number of admissions at Danish somatic hospitals was registered to be 717,733 and the number of bed-days was registered to be 2,682,883. From 2016-2025, the number of bed-days decreased by 35%, the number of admissions decreased by 17% whereas the Danish population grew by 5%.

**Figure 2.3 Changes in average age, Denmark and EU, 2016-2025** DANMAP 2025




Data source: Statistics Denmark and Eurostat.

**Table 2.1 Activity at Danish hospitals, 2016 and 2025** DANMAP 2025

| Region | Number of bed-days in somatic hospitals | | Number of admission to somatic hospitals | | Population | |
|---|---|---|---|---|---|---|
| | 2016 | 2025 | 2016 | 2025 | 2016 | 2025 |
| Capital Region of Denmark | 1,594,507 | 866,369 | 311,228 | 237,447 | 1,789,174 | 1,930,793 |
| Region Zealand | 594,881 | 407,059 | 118,794 | 107,276 | 827,499 | 854,902 |
| Region of Southern Denmark | 760,292 | 558,088 | 176,776 | 144,234 | 1,211,770 | 1,240,472 |
| Central Denmark Region | 768,818 | 561,350 | 181,522 | 154,951 | 1,293,309 | 1,373,799 |
| North Denmark Region | 378,815 | 290,017 | 79,462 | 73,825 | 585,499 | 592,768 |
| Denmark | 4,097,313 | 2,682,883 | 867,782 | 717,733 | 5,707,251 | 5,992,734 |

Data: Activity at somatic hospitals.
Data source: The National Patient Register.

## 2.3 Information on animal population and food production system

Denmark is an agricultural country, with more than half of its area managed by the agricultural sector. Approximately 25% of Danish agricultural enterprises are specialized in livestock production, focusing primarily on pigs, cattle, and chickens. In 2025, Danish exports of food, biobased products and agricultural technology totalled DKK 211.9 billion (Danish Agriculture & Food Council, 2026).

The production of food-producing animals as well as the production of meat and milk are presented in Table 2.2 and 2.3.

**Table 2.2 Production (1,000 heads) of food animals, Denmark, 2016-2025** DANMAP 2025

| | Pigs | | Cattle | | Poultry | |
|---|---|---|---|---|---|---|
| Year | Total | Exported [a] | Slaughter cattle | Dairy cows | Broilers | Turkeys [b] |
| 2016 | 31660 | 13280 | 540 | 572 | 120359 | 1095 |
| 2017 | 31662 | 14173 | 509 | 570 | 122854 | 841 |
| 2018 | 32571 | 14449 | 533 | 575 | 130626 | 602 |
| 2019 | 31694 | 14897 | 518 | 567 | 127642 | 356 |
| 2020 | 32018 | 14736 | 500 | 567 | 122748 | 455 |
| 2021 | 32649 | 14096 | 506 | 564 | 123189 | 306 |
| 2022 | 31681 | 13867 | 506 | 557 | 116035 | 443 |
| 2023 | 29353 | 14865 | 499 | 547 | 121968 | 395 |
| 2024 | 30784 | 16452 | 490 | 547 | 121224 | 382 |
| 2025 | 31966 | 16683 | 492 | 549 | 126736 | 742 |

Source: Statistics Denmark (www.dst.dk). Export data for poultry from Statistics Denmark.
a) Export of live pigs. These are included in total number of heads.
b) Since 2006, more than 99% of the turkeys have been exported for slaughter.

**Table 2.3 Production (mill kg) of meat, milk and fish, Denmark, 2016-2025** DANMAP 2025

| | | | | | | Farmed fish [c] | |
|---|---|---|---|---|---|---|---|
| Year | Pork | Beef | Broiler meat [a] | Turkey meat | Milk [b] | Land based | Marine net ponds |
| 2016 | 1943 | 142 | 177 | 16 | 5892 | 36 | 12 |
| 2017 | 1896 | 135 | 185 | 13 | 6088 | 37 | 14 |
| 2018 | 1967 | 142 | 219 | 9 | 6305 | 38 | 14 |
| 2019 | 1864 | 137 | 205 | 5 | 6323 | 41 | 14 |
| 2020 | 1952 | 133 | 201 | 7 | 6394 | 36 | 11 |
| 2021 | 2066 | 134 | 203 | 4 | 6390 | 37 | 12 |
| 2022 | 1957 | 131 | 193 | 7 | 6392 | 32 | 14 |
| 2023 | 1663 | 130 | 203 | 6 | 6377 | 30 | 14 |
| 2024 | 1734 | 126 | 200 | 6 | 6325 | 34 | 12 |
| 2025 | 1841 | 127 | 218 | 11 | 6337 | - | - |

Source: Statistics Denmark (www.dst.dk). Export data for poultry and average weight after slaughter from Statistics Denmark (personal communication).
a) In 2022, a final slaughtered weight of 1.74 kg per broiler produced and 12.93 kg per turkey produced was estimated.
b) conventional and organic.
c) Data are based on accounts statistics for aquaculture. The production of farmed fish includes fish transferred from one production facility to another.

## 2.4 Registered antimicrobial agents

Table 2.4 shows the antimicrobial agents registered to treat bacterial infections in humans and animals. Some of these are listed on the highest priority list of medically important antimicrobials for the treatment of bacterial infections in humans, according to definitions made by the World Health Organization [WHO 2026]. In order to be considered critically important or highest priority critically important an antimicrobial class or subclass with authorized use in humans and animals must meet two criteria; 1) be the only - or one of a limited number of compounds available to treat serious human infections and 2) be used to treat infections caused by bacteria that are either possibly transmitted from non-human sources, or carry resistance genes from non-human sources.

Furthermore, when both criteria are met, two prioritization factors are applied: 1) the antimicrobial class contains at least one antimicrobial that is both on the WHO Essential Medicines List (EML) and is classified as Watch or Reserve on the AWaRe classification list; 2) the antimicrobial class is used to treat human infections, often invasive and life-threatening, for which there is extensive evidence of transmission of resistance from non-human sources. When both prioritization factors are met, the antimicrobial is Highest Priority Critically Important (HPCIA), otherwise it is classified as Critically Important (CIA). Thus, in the newest list revision from 2024, four drug classes were considered highest priority critically important: 3rd and 4th generation cephalosporins, quinolones, polymyxins and phosphonic acid derivatives. Additionally, three antimicrobial classes were considered critically important: aminoglycosides, macrolides and ansamycins. In Denmark, the use of HPCIA classes in food-producing animals has generally been absent or reduced through either voluntary or legislative restrictions, while there is some use of the CIA classes aminoglycosides and macrolides. See Chapter 4 for more information.

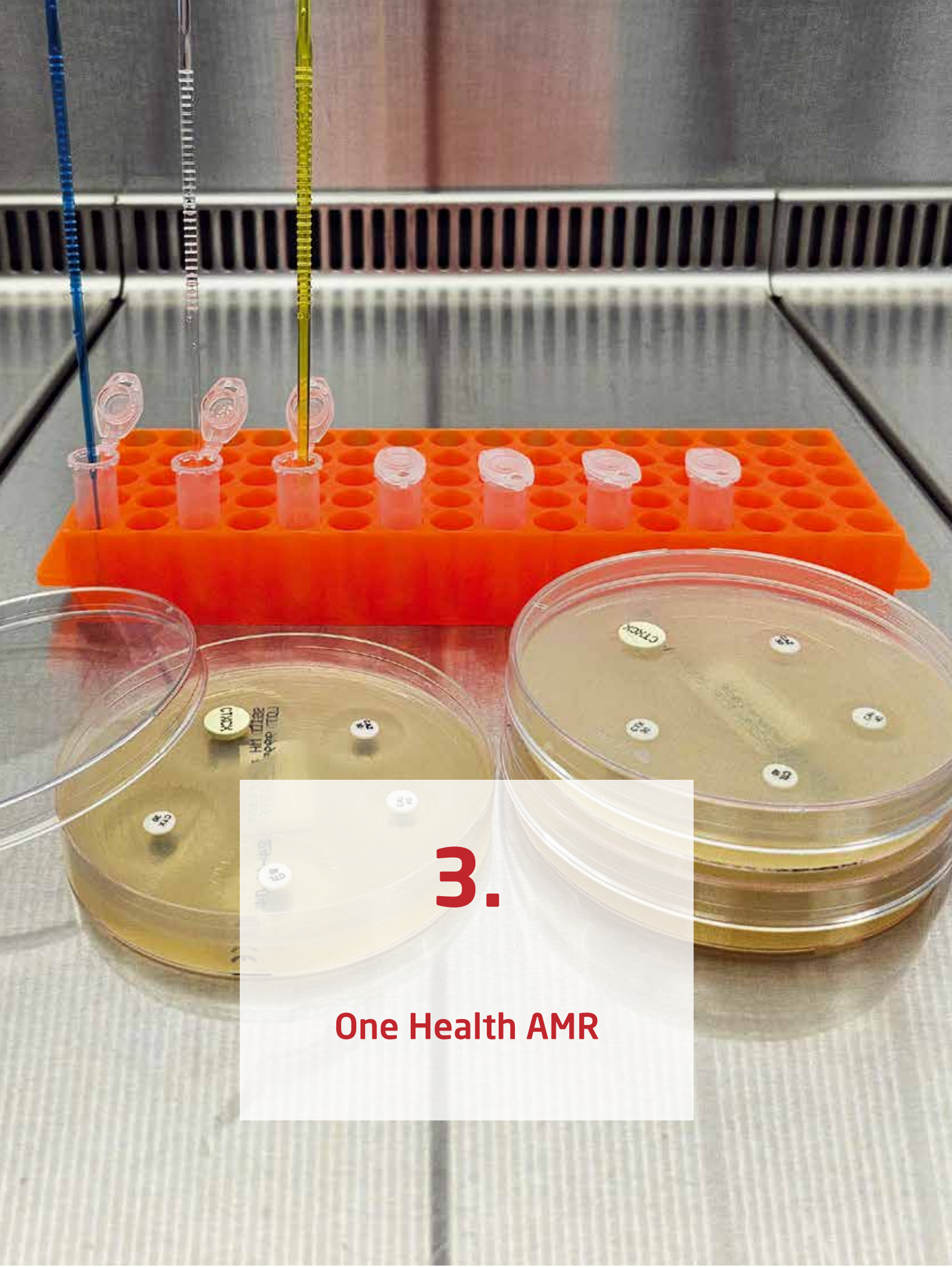
Furthermore, other antimicrobials may also be restricted due to national risk mitigation. For trends and preferred therapeutic choices in the antimicrobial treatment of humans, see Chapter 5.

Growth promoters are no longer used for animals in Denmark and are shown in parentheses in Table 2.4. Most of these influenced Gram-positive bacteria. Since 1995, the indicator enterococci from animals and meat have been used to monitor resistance towards former growth promoters.

**Table 2.4 Antimicrobial agents registered for systemic and veterinary intramammary therapeutic use in animals and humans, Denmark** DANMAP 2025

| ATC \| ATCvet codes [a] | Therapeutic group | Antimicrobial agents within the therapeutic groups | |
|---|---|---|---|
| | | Animals | Humans |
| J01AA \| QJ01AA, QJ51AA | Tetracyclines | Chlortetracycline, doxycycline, oxytetracycline, tetracycline | Doxycycline, eravacyclin, lymecycline, tetracycline, tigecycline |
| QJ01BA | Amphenicols | Florfenicol | |
| J01CA \| QJ01CA, QJ51RC | Penicillins with extended spectrum | Amoxicillin, ampicillin | Amoxicillin, amoxicillin, pivmecillinam |
| J01CE \| QJ01CE, QJ01RA, QJ01RV, QG51AG, QJ51CE, QJ51RC | Beta-lactamase-sensitive penicillins | Benethamine penicillin, benzathine benzylpenicillin, benzylpenicillin, penethamate hydroiodide, phenoxymethylpenicillin | Benzylpenicillin, phenoxymethylpenicillin |
| J01CF \| QJ51CF, QJ51RC | Beta-lactamase-resistant penicillins | Cloxacillin, nafcillin | Cloxacillin, dicloxacillin, flucloxacillin |
| J01CR \| QJ01CR | Combinations of penicillins and beta-lactamase inhibitors | Amoxicillin/clavulanic acid | Amoxicillin/clavulanic acid, piperacillin/tazobactam |
| J01DB \| QJ01DB, QJ51DB | First-generation cephalosporins | Cefadroxil, cefalexin, cefapirin | Cefazolin |
| J01DC | Second-generation cephalosporins | | Cefuroxime |
| J01DD \| QJ01DD, QJ51DD | Third-generation cephalosporins, including combinations with beta-lactamase inhibitors | Cefoperazone, cefovecin, ceftiofur | Cefotaxime, ceftazidime, ceftazidime/avibactam, ceftriaxone |
| J01DE \| QJ01DE, QJ51DE | Fourth-generation cephalosporins | Cefquinome | Cefepime |
| J01DF | Monobactams | | Aztreonam, aztreonam/avibactam |
| J01DH | Carbapenems | | Cilastatin, ertapenem, imipenem, meropenem |
| J01DI | Fifth-generation cephalosporins, including combinations with beta-lactamase inhibitors | | Ceftaroline fasamil, cefiderocol, ceftobiprol, ceftolozan/tazobactam |
| J01EA | Trimethoprim and derivatives | Trimethoprim | Trimethoprim |
| J01EB \| QJ01EQ, QG51AG | Short-acting sulfonamides | Sulfadiazine, sulfadimidine, sulfamerazine, sulfathiazole | Sulfamethizole, sulfapyridine |
| J01EE \| QJ01EW, QJ51RE | Combinations of sulfonamides and trimethoprim, including derivatives | Sulfadiazine/trimethoprim, sulfadimidine/trimethoprim, sulfadoxine/trimethoprim, sulfamethoxazole/trimethoprim, sulfatroxazole/trimethoprim | Sulfamethoxazole/trimethoprim |
| J01FA \| QJ01FA, QJ01RA | Macrolides | Gamithromycin, spiramycin, tildipirosin, tilmicosin, tulathromycin, tylosin, tylvalosin | Azithromycine, clarithromycine, erythromycine, roxithromycine |
| J01FF \| QJ01FF, QJ51FF, QJ51RF, QJ51RG | Lincosamides | Clindamycin, lincomycin, pirlimycin, spectinomycin | Clindamycin |
| QJ01FG [b] | Streptogramins | (Virginiamycin) | Framycetin |
| J01GA \| QJ01GA | Streptomycins | Dihydrostreptomycin | |
| J01GB \| QJ01GB, QJ01RA, QJ01RV, QJ51RF, QJ51RC, QJ51RG, QA07AA | Aminoglycosides | Apramycin, framycetin, gentamicin, neomycin, paromomycin, tobramycin | Amikacin, gentamicin, tobramycin |
| J01MA \| QJ01MA | Fluoroquinolones | Danofloxacin, difloxacin, enrofloxacin, ibafloxacin, marbofloxacin, moxifloxacin, orbifloxacin, pradofloxacin | Ciprofloxacin, levofloxacin, moxifloxacin |
| QJ01MB | Other quinolones | Oxolinic acid | |
| QJ01MQ [b] | Quinoxalines | (Carbadox, olaquindox) | |
| J01XA, A07AA \| Not in ATCvet [b,c] | Glycopeptides | (Avoparcin) | Dalbavancin, teicoplanin, vancomycin |
| J01XB \| QA07AA, QJ51RC [b] | Polypeptides, including polymyxins | Bacitracin, colistin | Colistin |
| J01XC | Steroid antibacterials | | Fusidic acid |
| J01XD, P01AB \| QJ01RA, QJ01XD [c] | Imidazole derivatives | Metronidazole | Metronidazole |
| J01XE | Nitrofuran derivatives | | Nitrofurantoin |
| J01XX | Other antibacterials | | Daptomycin, fosfomycin, linezolid, methenamine |
| QJ01XQ | Pleuromutilins | Tiamulin, valnemulin | |
| QP51AG06 | Antiprotozoals, sulfonamides | Sulfaclozine | |
| Not in ATCvet [b] | Oligosaccharides | (Avilamycin) | |
| Not in ATCvet [b] | Flavophospholipols | (Flavomycin) | |

a) ATCvet codes start with a Q.
b) Animal growth promoters used before 1999 are listed in parentheses.
c) Intestinal antiinfectives (A07AA) and imidazole derivatives for protozoal diseases (P01AB) were, for the first time, included in DANMAP 2014, since their widespread use in the treatment of *Clostridium difficile* infections makes them belong to the most used antibiotics in human infections in Denmark.



# 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 the human and animal sectors.

But antimicrobial resistance is a One Health challenge that extends beyond human and animal populations into the wider environment. Despite its undoubtful integrated nature, the DANMAP programme continues to fall short on the monitoring of antimicrobials and antimicrobial resistance in the environment (see DANMAP 2021, Chapter 3, Textbox 3.1). Environmental compartments such as surface waters, wastewater systems, soils, sediments, and wildlife can act as reservoirs, mixing points, and transmission pathways for antimicrobial-resistant bacteria, resistance genes, and antimicrobial residues. Consequently, there is growing international interest in establishing surveillance systems capable of detecting AMR emergence, tracking dissemination pathways, and assessing environmental drivers of resistance selection.

Despite the growing focus in this One Health pillar, environmental AMR monitoring is still at a relatively early stage of development, not only in Denmark, but worldwide. Key challenges include identifying suitable indicators, selecting representative sampling locations and matrices, harmonizing analytical methods, and determining how environmental data can inform risk assessments and policy decisions (see Textbox 3.1).

## 3.2 Integrated reporting

An aim of the DANMAP program has always been the in depth understanding of the possible relationship between the animal, food and human sectors concerning antimicrobial usage (AMU) and development of antimicrobial resistance (AMR). In addtion to the AMU and AMR data presented in the other DANMAP chapters, investigations of the interplay between sectors imply knowledge about antimicrobial resistance mechanisms, routes of transmission of pathogens and factors that may enhance the impact of resistance transmission.

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 and purposes, with varying sampling strategies and magnitudes. Some of these obstacles can be circumvented by investigating the genetic characteristics of resistant bacteria recovered from livestock animals, meat and humans.

Here, 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 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 DANMAP 2024, Textbox 3.1).

ESBL/AmpC-procuding *E. coli* is one of the organisms that DANMAP has monitored by use of WGS of isolates from animals and imported and domestic food products (see chapter 7, section 7.3.1), as well as from human infections (see chapter 8, section 8.3.1). In this chapter, we investigate possible relationships between ESBL Ec from different sources in Denmark.

### 3.2.1 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 2025; 120 isolates of animal origin and 188 isolates from humans, totaling a dataset of 2,579 ESBL isolates from humans and animals from 2018 through 2025. The 1,639 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: 110, broiler meat: 164, cattle: 75, beef: 53, pigs: 329, pork: 67, and turkey meat: 142) stem from the EU mandatory screening programme from healthy animals and meat products (see Chapter 10 for more information).

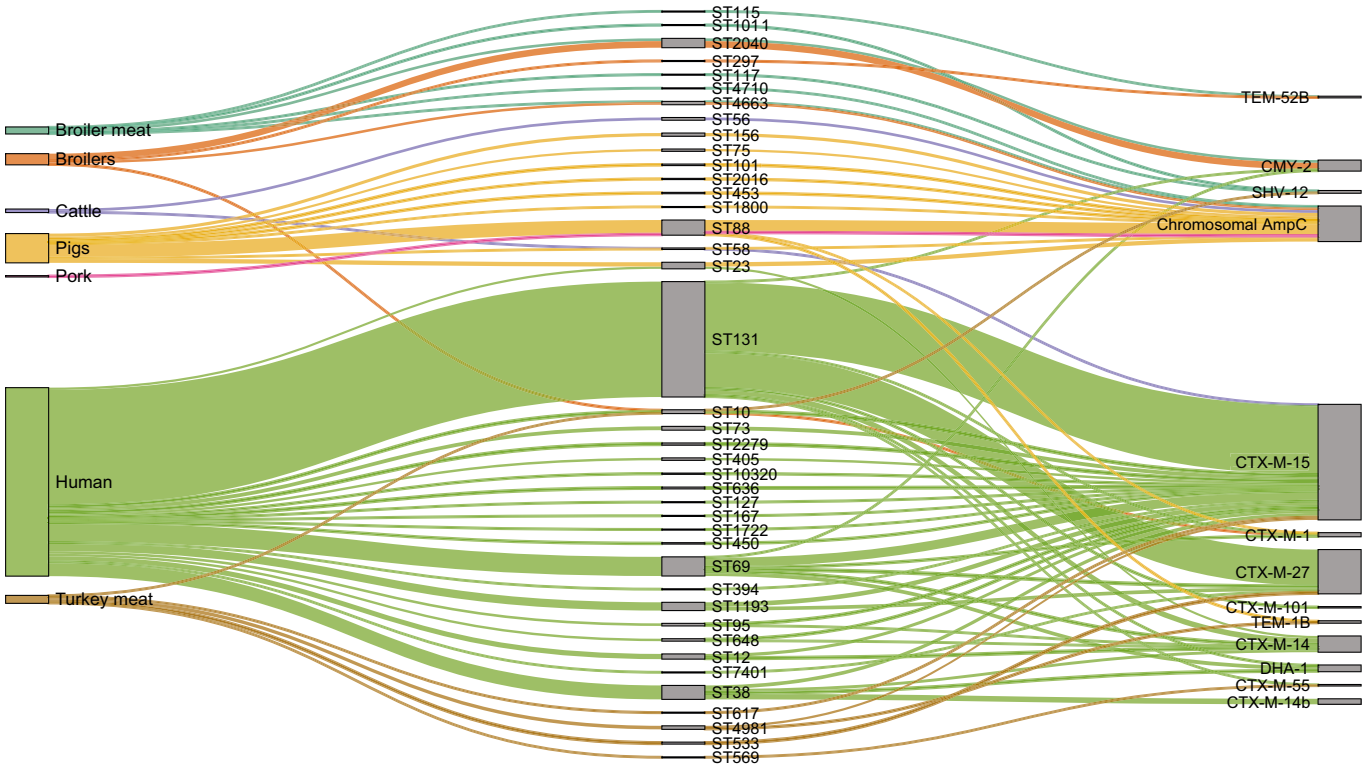
Each isolate has been sequenced as part of the surveillance activities, and the MLST and ESBL/AmpC genotype were extracted from the whole genome sequence. For an overview of sequence types and ESBL/AmpC genotypes detected in 2024 in *E. coli* from bloodstream infections, and from pigs, cattle, pork and beef, 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.

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, 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 1,624 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 2025




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 eight years, and when considering the occurrence of ESBL/AmpC genotypes in different sequence types. Many genes encoding for ESBL-producing phenotypes can be harboured by plasmids, and hence horizontally transmitted between different, reservoir-specific *E. coli* sequence types. The analysis here performed does not allow to investigate the occurrence of plasmid transmission across reservoirs. Further research into slow transmission over longer time spans, as well as more in-depth genomic analyses are of continued interest and on-going.

## 3.3 Towards a future of environmental AMR surveillance

There is recent increased international focus on developing practical monitoring approaches and on defining the scientific framework needed to support routine environmental AMR surveillance. Such initiatives occur both within research, as well as national AMR monitoring programmes, and focus on various environmental compartments.

### 3.3.1 AMR monitoring in wildlife

A study performed in Germany investigated whether wildlife can be used as indicator of AMR circulating in the environment [Plaza-Rodríguez et al. 2021. Front Vet Sci. 7:627821]. Samples were collected from wild boar, roe deer, and wild ducks and geese across Germany through the national zoonoses monitoring programme. While the overall prevalence of resistant bacteria was relatively low, ESBL/AmpC-producing *E. coli* were detected in a small percentage of animals across all sampled species, and resistance to various critically important antimicrobials was sporadically identified. The authors recommended continuous wildlife surveillance as an early-warning system for environmental AMR monitoring.

A more recent systematic review focused exclusively on wild birds and reinforced their potential as large-scale, cost-effective sentinel species for environmental AMR surveillance [Cocos et al 2025. Antibiotics 14(9):905]. This systematic review synthesized evidence from studies investigating antimicrobial-resistant *Enterobacteriaceae* in free-ranging wild birds across Europe and found that resistant bacteria are widely distributed among European wild bird populations, including numerous reports of ESBL-producing isolates across bird species and geographic regions. Furthermore, birds frequenting urban areas, landfills, wastewater-affected environments, and agricultural

landscapes generally exhibited higher prevalence of resistant *Enterobacteriaceae*, supporting evidence of the important effect of anthropogenic AMR pollution.

In addition to wild birds, small mammals can complement bird-based surveillance and provide information on local environmental AMR contamination. Hedgehogs living near urbanized or human-impacted environments have been identified as useful indicators of anthropogenic AMR pollution, also in Denmark [Rasmussen et al 2019. PLOS ONE 14(9): e0222031]. A recent study performed in Italy also investigated the occurrence of β-lactam and carbapenem resistance in hedgehogs [Di Francesco et al 2026. Vet Res Commun 50:267] and identified several β-lactam resistance genes in hedgehog-associated bacteria, as well as genes associated with resistance to critically important antimicrobials, including carbapenems.

These and other similar studies support the idea that AMR surveillance programs should not focus solely on the human sector and livestock production systems but should also include wildlife inhabiting agricultural and urban environments. Wildlife species may acquire resistant bacteria from human- or livestock-associated environmental contamination and subsequently contribute to their further dissemination. A recent review [González-Martín et al 2026. Animals 16(12):1859] examined the role of interactions between wildlife and livestock occupying shared habitats in the dissemination of ESBL/AmpC-producing *E. coli*. After reviewing the available evidence, the authors concluded that bacteria could move in both directions across the wildlife-livestock interface, and that a One Health approach should be adopted when designing AMR surveillance programs.

### 3.3.2 AMR monitoring in surface water

Parallel initiatives across the world are focusing on developing methods and protocols for AMR monitoring in surface waters.

In the United States, a study conducted within the National Antimicrobial Resistance Monitoring System (NARMS) evaluated advanced genomic methods for AMR surveillance in surface waters [Ottesen et al 2022. PLOS Water 1(12): e0000067]. Sampling was performed both in an urban creek located near a hospital and at a reservoir used for recreation and drinking water supply, and the samples were analysed both with direct shotgun metagenomics and with quasimetagenomics (shotgun sequencing after selective enrichment). This study showed that quasimetagenomics detected NARMS priority AMR targets to a wider extent than standard metagenomics. Furthermore, quasimetagenomics enabled detection of clinically important resistance genes, resistance-associated plasmids and differences in resistance-gene abundance between the two sampled sites.

Similar initiatives to monitor surface waters were also recently taken in Europe. The European Environment Agency (EEA) and partners have launched a pilot study to establish harmonised AMR monitoring in European surface waters [https://water.europa.eu/freshwater/europe-freshwater/amr/documentation]. The study findings have informed subsequent guidance documents that aim at supporting harmonized monitoring and data reporting across Europe. This represents one of the first coordinated efforts in Europe to move environmental AMR surveillance from research into routine regulatory monitoring.

### 3.3.3 AMR monitoring in wastewater

Wastewater is increasingly viewed as a strategic AMR surveillance matrix because it integrates resistance signals from large human populations and can serve as an indicator of the potential pollution from wastewater plants to the environment.

The revised Urban Wastewater Treatment Directive (EU) 2024/3019 introduced, for the first time, a requirement for monitoring AMR in urban wastewater as part of the EU's One Health response to AMR. The Directive recognizes wastewater as an important pathway through which resistant bacteria and antimicrobial resistance genes originating from human populations enter the environment, and it requires Member States to implement AMR monitoring in wastewater from large urban agglomerations (those serving 100,000 population equivalents or more), develop harmonised surveillance approaches, and generate data. It represents thus a major shift from research-based surveillance towards routine, harmonised monitoring of AMR in wastewater across Europe.

Research focused on AMR detection in wastewater has been ongoing for several years and has contributed with evidence that supports regulatory initiatives such as those of the revised Urban Wastewater Treatment Directive. The latest study published by the Global Sewage Consortium represents one of the largest investigations of AMR in wastewater to date [Martiny et al 2025. Nature Communications 16:10278]. Researchers analysed 1,240 sewage samples from 351 cities across 111 countries to understand the factors shaping the global distribution of antimicrobial resistance genes (ARGs) in urban wastewater. The study applied metagenomic sequencing of sewage samples to characterize the acquired and latent ARGs in the resistome. Findings suggest that wastewater monitoring programmes should focus not only on clinically important acquired resistance genes but also on the broader environmental resistome that may serve as a source of future resistance threats.

### 3.3.4 Future perspectives

Collectively, these and other similar studies and regulatory initiatives will support the development of future national and international One Health AMR surveillance systems, by providing valuable insights into the strengths, limitations and needs of environmental monitoring. Eventually, such efforts may enable the future implementation of multi-layered frameworks in monitoring programmes like DANMAP, where AMR monitoring in wildlife, surface-water, wastewater and other environmen-

tal compartments is considered. Some countries have already initiated that journey. For example, the study on USA surface waters supports the plans to implement surface water AMR monitoring in the NARMS program. Another example is the One Health Report on Antimicrobial Use and Resistance in Belgium (BELMAP), which has already introduced the reporting of antimicrobial residues in surface water, wastewater, sediments, and agricultural environments, as well as information on fungicide application and fungal resistance, and data on sales of biocidal products such as disinfectants, and antiseptics, which can act as co-selective agents for antimicrobial resistance.

The DANMAP partners, Statens Serum Institut and the National Food Institute, integrate various consortia of international studies that aim both at understanding AMR ecology in the environment and assessing how the future of AMR environmental monitoring can look like. Examples of such consortia are the European Partnership on Animal Health and Welfare [https://www.eupahw.eu] and the EU-WISH project [https://www.eu-wish.eu].

DANMAP is committed to introducing environmental monitoring as the missing One Health pillar in the programme. The 2024 revision of the Urban Waste Water Treatment Directive 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 DANMAP 2024, Textbox 3.2). Along that journey, thorough considerations regarding conceptual frameworks and data requirements must be taken.

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## Textbox 3.1

# Environmental AMR surveillance: From detection to decisions

**The purpose of environmental AMR surveillance**

Taking action against AMR without surveillance data to base mitigation decisions on has been likened to "flying blind" [1]. Along the same lines, one could argue that AMR surveillance without a clear objective is similar to getting into the cockpit without knowing the directions to the destination. It would take an awful lot of time and resources figuring out where to go with the plane in the air, which is why commercial air flights are – of course – planned meticulously. The same should be true for AMR surveillance: we need to know *why* we want to do surveillance and *what* we want to achieve before we start. This is particularly true for environmental surveillance, which easily becomes a task of figuring out what everything AMR-related looks like everywhere, all the time.

In clinical and veterinary AMR surveillance, surveillance data could influence the prescription and use of antimicrobials and can often be specific to particular pathogens and antimicrobial treatment regimes. The value then comes in the form of damage control, but also an opportunity to get ahead of the curve and detect emerging AMR threats before they become common in clinics or among production animals [2].

Such direct application links are harder to establish for environmental AMR surveillance. One could organize the environmental surveillance efforts into three different overarching 'use cases':

- Track AMR circulating in populations (e.g. a city or a farm) through wastewater.
- Evaluate environmental releases, dissemination and potential exposure to resistant microbes.
- Identify emerging resistance mechanisms before they become established clinical or veterinary problems.

None of these use cases does by itself provide a clear actionable outcome for the surveillance. Say that an increase in a gene providing resistance to a last-resort antibiotic is detected in Copenhagen wastewater; what action would that warrant? Covid-style lockdowns? Screening of incoming patients to hospitals? Protective measures towards the elderly? All these options are disproportional to the evidence, making it clear that we need prior definitions of:

1) What risks are we aiming to reduce through AMR surveillance?
2) What meaningful actions could we take based on surveillance to reduce these risks? Who would be responsible for taking these actions?
3) What would be the different 'trigger levels' measured in surveillance to initiate such actions?
4) How can we assess the efficiency of the measures taken?

**The risks and actions landscape**

The risks associated with AMR can be divided into two major groups: transmission risks and emergence risks, and both can be further subdivided. The transmission risks constitute the spread of resistant pathogens or mobile genetic elements carrying antibiotic resistance genes in various settings (hospital, agriculture, wastewater and so on). Actions to reduce those transmission risks involve hygiene, isolation of carriers, separation of animals, reducing releases of AMR into the environment and measures to avoid exposure of animals and humans to environmentally transmitted AMR [2]. Those measures are well understood, but generally not easy or popular to implement.

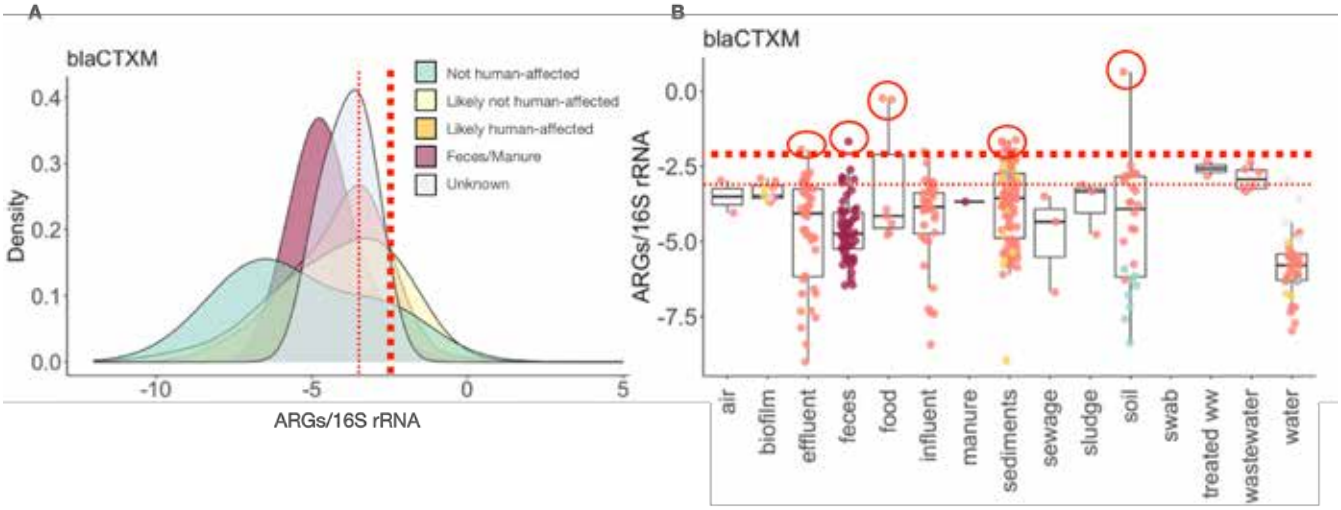
The emergence risks, on the other hand, are connected to new forms of resistance appearing in pathogens, through selection, mutations, or transfer of new resistance genes into pathogens. Here, any mitigation efforts would need to target the flow of AMR into human or animal populations, or trying to contain transmission early. For this type of risks, only two courses of action are available: preventive measures to avoid AMR flow into humans and animals, or early-warning monitoring coupled to isolation of patients or sick animals [3].

continued ... Textbox 3.1

**What is a meaningful change?**

The other major issue is to couple actions to measurements. What detections would warrant a certain set of responses? Here, it is crucial to define what are the normal, expected variations of a given AMR target in a specific setting. This requires repeated sampling to establish baselines and understand, for example, seasonal variation [4]. It may also be important to consider what the host organism and genetic context is for a particular resistance gene, and if it is associated with mobile genetic elements. Once such background data is obtained, it is possible to make priorities and set levels that would trigger specific actions (Figure 1).

**Figure 1 Example of a 'trigger level' method for AMR surveillance** DANMAP 2025




Example of the 'trigger level' method suggested in Abramova et al. (2023) [4], using 10 times the third quartile (3Q) abundance values for a given ARG to determine the upper limit for what should be viewed as a deviation from normal background levels in the environment. In the example, the overall levels of blaCTX-M is shown with the 3Q indicated in thin dots and the 10x trigger level indicated by the thick dotted line (A). in (B), the same approach is taken but on an environment basis, showing the samples that would have triggered potential actions in red circles at the top.

**Beyond established surveillance targets**

For the emergence risks, AMR surveillance is dependent on being able to identify new forms of high-priority resistance before it has appeared (or become widely spread) among pathogens. In order to do that, we need to know what forms of resistance we are looking for. That, in turn, means that there is a need for characterizing and prioritizing new forms of AMR that have a high potential to transfer to pathogens. Recent work has shown that there is a substantial reservoir of resistance genes that conventional analyses overlook [5]. Most of these genes exist in harmless environmental or commensal bacteria and never make it into pathogens; the important task is to identify the ones that are able to early. This would involve investigating candidates for evidence of resistance function, mobility and occurrence in species that are close relatives to pathogens. For such purposes, it is also important to keep track of non-clinical resistance genes across strains of bacteria, environments and studies. This is one of the purposes of the recently launched CLEVER database (https://microbiology.se/clever/), that keeps track of both clinically established and latent resistance genes, giving them names and organizing them by verification status and mobility. This type of information can help prioritizing resistance genes that are likely to become clinical problems, rather than blindly looking for all forms of AMR.

**Conclusions**

In the end, AMR surveillance shouldn't start with detection and work towards decisions. It should start with the decisions and work its way backwards to the appropriate settings, methods and frequencies for detection. All AMR surveillance efforts, but particularly those in the environment, should be evaluated by whether they identify important changes, inform appropriate responses and have measurable intervention effects. With the EU now strongly pushing for wastewater surveillance of AMR, the issue of purpose has become urgently pertinent [6]. The question we should all ask before we venture into surveillance should be: "What decision will this measurement enable?"

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**References**

[1] Bengtsson-Palme 2024: Surveillance of antimicrobial resistance – flying blind or flying behind? doi: 10.17044/scilifelab.27045433
[2] Bengtsson-Palme et al. 2023: Towards monitoring of antimicrobial resistance in the environment: For what reasons, how to implement it, and what are the data needs? doi: 10.1016/j.envint.2023.108089
[3] Hess & Bengtsson-Palme 2023: A Risk Management Framework for Emergence of Novel Antibiotic Resistance Determinants. doi: 10.2139/ssrn.4615467
[4] Abramova et al. 2023: A global baseline for qPCR-determined antimicrobial resistance gene prevalence across environments. doi: 10.1016/j.envint.2023.108084
[5] Inda-Díaz et al. 2023: Latent antibiotic resistance genes are abundant, diverse, and mobile in human, animal, and environmental microbiomes. doi: 10.1186/s40168-023-01479-0
[6] European Parliament: Directive (EU) 2024/3019 of the European Parliament and of the Council of 27 November 2024 concerning urban wastewater treatment (recast).



# 4.

# Antimicrobial consumption in animals

# 4. Antimicrobial consumption in animals

## Highlights

In 2025, total antimicrobial consumption in animals amounted to 88.44 tonnes of active compounds, representing a 1.14% increase compared with 2024. Pigs accounted for 84.68% of total consumption, followed by cattle (9.27%) and poultry (1.52%). Pig production remained the principal driver of antimicrobial consumption in Danish livestock production, despite cattle representing the largest share of estimated live biomass.

Antimicrobial consumption in **pig** production totaled 74.88 tonnes, corresponding to an increase of 2.03% from 2024. During the same period, the estimated live biomass increased by 0.38%, primarily due to increased production of 30 kg pigs intended for export. Taken together, these changes resulted in a 2.41% increase in the treatment proportion (DAPD). On any given day, an estimated 1.80% of sows and piglets, 11.57% of weaners, and 1.89% of finishers received antimicrobial treatment. Among sows and piglets, DAPD increased only for lincosamides (165.47%), while amphenicols (17.65%), pleuromutilins (17.32%), other penicillins (10.96%) and macrolides (5.55%) decreased. In weaners, amphenicols (19.02%), lincosamides (11.37%), and macrolides (9.88%) increased, while pleuromutilins (7.89%), aminoglycosides (4.48%), and beta-lactamase-sensitive penicillins (4.84%) decreased. In finishers, lincosamides (537.49%), macrolides (14.90%), and pleuromutilins (8.61%) increased, while amphenicols (58.66%), sulfonamides and trimethoprim (36.71%), and aminoglycosides (11.54%) decreased.

In **cattle**, antimicrobial consumption decreased to 8.20 tonnes, corresponding to a reduction of 0.72% compared with 2024, while the estimated live biomass declined by 1.05%. On any given day, an estimated 0.26% of adult cattle and 0.85% of young cattle received antimicrobial treatment. Among adult cattle, DAPD of lincosamides, aminoglycosides, macrolides and other penicillins increased by 56.77%, 8.08%, 3.74% and 4.35%, respectively, whereas amphenicols, beta-lactamase-sensitive penicillins, and tetracyklines decreased by 18.45%, 5.06% and 2.44%, respectively. The use of cephalosporins for systemic administration increased by 19.12 kg of active compound, corresponding to a 334.18% increase compared with 2024. Among young cattle, DAPD of macrolides, other penicillins and amphenicols increased by 21.29%, 7.60% and 4.73%, respectively, while lincosamides, tetracyclines, beta-lactamase-sensitive penicillins and aminoglycosides decreased by 28.48%, 22.94%, 5.44% and 3.95%, respectively. Beta-lactamase-sensitive penicillins continued to dominate intramammary treatments.

Antimicrobial consumption in **poultry** increased by 17.95% compared with 2024. Despite this increase, overall use remained very low and continued to be strongly influenced by disease outbreaks affecting a limited number of flocks.

In **horses** and **pets**, fluoroquinolone consumption was 12.75 kg in 2025 and was prescribed almost exclusively for these species. Cephalosporin consumption remained low at 42.03 kg, with pets accounting for 42.04% of total cephalosporin use.

## 4.1 Introduction

The DANMAP programme has monitored national antimicrobial consumption in both humans and animals since 1995. From the early 1990s, growing political and public concern over antimicrobial use in Danish animal production led to significant changes, including the discontinuation of antimicrobials for growth promotion and the implementation of several initiatives, such as voluntary bans on the use of 3rd and 4th generation cephalosporins in pig and cattle production. These initiatives were complemented by regulatory measures governing the therapeutic use of these antimicrobials.

Figure 4.1 presents the total antimicrobial consumption in animals and humans since 1990 and 1997, respectively. The expansion and intensification of Danish pig production during this period contributed to the overall trends in antimicrobial consumption.

The observed decline in antimicrobial consumption after 1994 was primarily attributed to the discontinuation of antimicrobials for growth promotion. Additional contributing factors likely included: 1) restrictions on veterinary practitioners' profits from the sales of medicines, 2) the implementation of Veterinary Advisory Service Contracts (VASCs), which introduced regular veterinary visits aimed at promoting preventive strategies and optimizing antimicrobial use, and 3) the enforcement of the "cascade rule" [Order (DK) 142/1993], which limited the prescription of less expensive extemporaneously produced medicines.

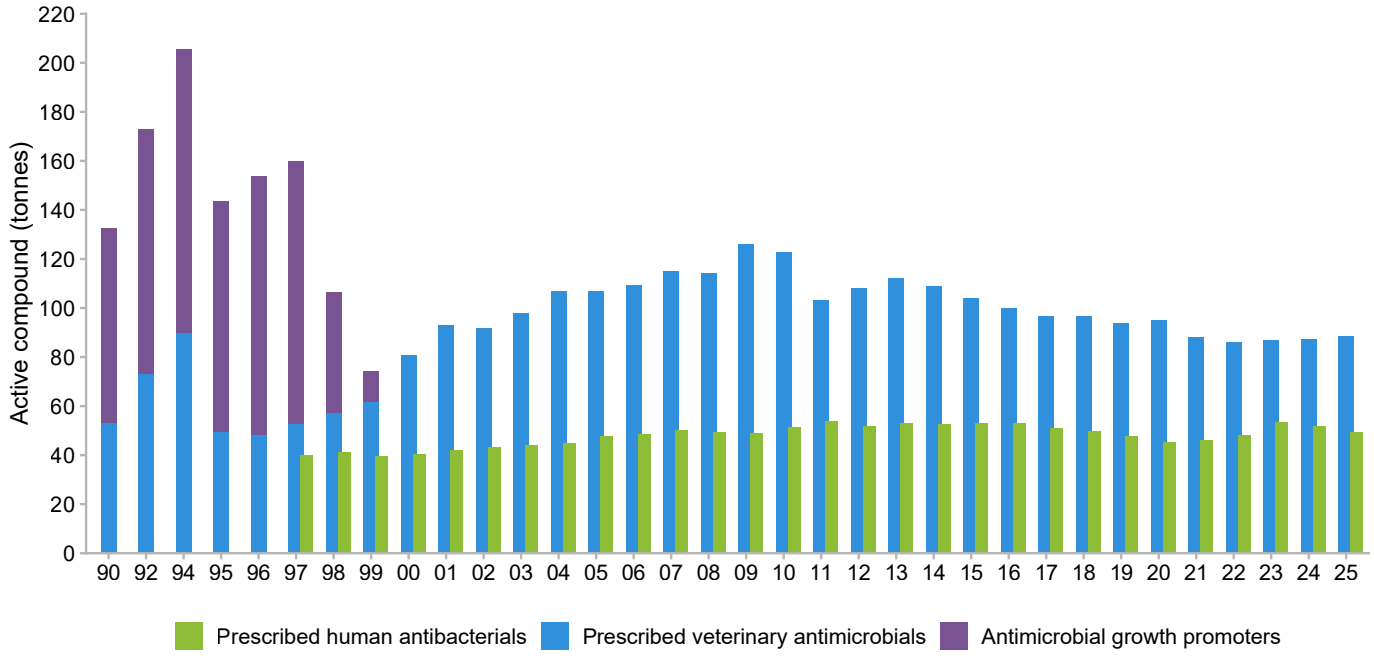
Other important interventions included legislative restrictions on the use of fluoroquinolones in production animals, introduced in 2002–2003, followed by a voluntary ban on the use of cephalosporins in pig production in 2010, which was extended to dairy cattle production in 2014.

The national action plan against antimicrobial resistance has evolved over time, setting progressively more targeted goals to curb antimicrobial use. Initially, the plan aimed for a 10% reduction in antimicrobial consumption in production animals by 2014, using 2009 levels as the baseline. In 2015, a new objective was introduced under the national strategy to combat livestock-associated MRSA, targeting a 15% reduction in antimicrobial use in pig production between 2015 and 2018.

To support the goals outlined in the national action plan, the Yellow Card initiative was introduced in 2010, establishing herd-level surveillance of antimicrobial consumption in pig production. Under this system, antimicrobial use is monitored at the herd level against legally defined thresholds, enabling authorities to take action against farmers with excessive use per pig [DANMAP 2010].

**Figure 4.1 Antimicrobial consumption for humans and all animal species, tonnes of active compound, Denmark, 1990-2025**

DANMAP 2025




Sources: Human therapeutics: The Danish Health Data Authority. Antimicrobials for animals: Data are based on reports from the pharmaceutical industry of total annual sales (until 2001), from the Federation of Danish pig producers and slaughterhouses (1994-1995), from the Danish Medicines Agency and Danish Plant Directorate (1996-2000), and since 2001 from VetStat.
Data for 2025 were extracted from VetStat on 31 July 2026.

The implementation of the Yellow Card system led to a noticeable reduction in antimicrobial consumption at the national level, particularly during its initial rollout from 2010 to 2011 and again following its revisions between 2016 and 2018. In 2016, the initiative was updated to include multiplication factors that adjusted the weighting of specific antimicrobials within the monitoring system. Tetracyclines were initially assigned a factor of 1.2, which was increased to 1.5 in 2017. Fluoroquinolones, cephalosporins, and colistin were assigned the highest multiplication factor of 10 [DANMAP 2017], reflecting their critical importance and the need to discourage their use.

Other legislative measures have also likely influenced antimicrobial prescribing practices. For instance, in 2014, regulations governing group medication in pig herds were tightened [Order (DK) 534 of 27/05/2014]. These changes required more rigorous diagnostic procedures, including thorough laboratory testing, as well as more frequent veterinary visits. The aim was to ensure that antimicrobials administered orally to groups of pigs via water or feed were prescribed only when clearly justified, thereby encouraging more targeted treatments such as individual injectable administration.

In 2017, the Ministry of Environment and Food and the Ministry of Health presented a new One Health strategy to combat antimicrobial resistance. This strategy established a comprehensive framework aimed at reducing the development and spread of AMR across both human and animal populations. In the same year, Denmark launched its first national action plan targeting antimicrobial resistance in animals, setting specific goals to further reduce antimicrobial use in animal production over the following years. This was followed by a second action plan in 2021. Most recently, in June 2024, a new national action plan against AMR in animals and food was adopted.

To help reduce the need to dispose of excess antimicrobials, a regulation introduced in 2019 [Order (DK) 1655/2018] permitted veterinarians and pharmacies to dispense individual immediate packages from a veterinary medical product package when necessary to avoid the disposal of surplus medicine. This initiative not only minimizes waste but may also improve surveillance by narrowing the gap between the quantities of antimicrobials prescribed and those actually consumed.

Official treatment guidelines for pigs and cattle have been available since 1996. Over time, the Danish Veterinary and Food Agency (DVFA) has continuously updated these guidelines in collaboration with stakeholders and academic experts [DANMAP 2010, www.foedevarestyrelsen.dk].

In 2012, the Danish Veterinary Association (DVA) published treatment guidelines to promote the prudent use of antimicrobials in dogs and cats. These guidelines were developed by clinical specialists and experts from the Faculty of Health and Medical Sciences at the University of Copenhagen and the National Food Institute at the Technical University of Denmark. A revised edition of the guidelines for dogs and cats was published in 2018. Similarly, in 2017, the DVA released treatment guidelines for the responsible use of antimicrobials in horses.

Alongside these sector-specific targets, guidelines issued by the DVFA emphasize disease prevention, improved udder health and the use of narrow-spectrum antimicrobials when treatment is required.

By 2020, the Danish dairy and beef producers' board had set a strategic goal to reduce antimicrobial use for mastitis and other cattle diseases by 20% compared to 2012 levels. Another objective was to lower the geometric mean bulk tank somatic cell count to 150,000 cells/ml. The strategy also promotes the use of simple penicillins (beta-lactamase-sensitive) for dry-cow therapy and mastitis treatment.

For the period 2021–2023, the board renewed its strategy for disease prevention in calves and cows, including updated udder health targets. The goals included a 10% annual reduction in antimicrobial use for cattle under 1 year of age and a 3% annual reduction for cattle over 1 year of age. Additionally, the strategy aimed to reduce the proportion of milk producers with somatic cell counts >200,000 cells/mL from 60% to 30%.

Since 28 January 2022, Regulation (EU) 2019/6 on veterinary medicinal products has been in force in Denmark. This regulation places particular emphasis on reducing the risk of antimicrobial resistance. It includes several key provisions regarding the prescription and use of veterinary medical products. These include limiting prescriptions to the exact quantity required for treatment, restricting the use of antimicrobials for metaphylactic or prophylactic purposes, and ensuring that all VMPs are used in accordance with their marketing authorizations (SPC). Furthermore, the regulation prohibits the routine use of antimicrobials to compensate for poor hygiene or management practices and designates certain critically important antimicrobials, listed in Regulation (EU) 2022/1255, as being reserved exclusively for the treatment of specific infections in humans [DANMAP 2022, Textbox 4.1].

In line with recommendations from the European Medicines Agency (EMA) and a subsequent decision by the European Commission in 2017, Denmark along with all EU Member States was required to phase out the use of veterinary medicinal products (VMPs) containing zinc oxide in food-producing animals by June 2022. As a result, the use of prescribed zinc oxide in pig production has been prohibited in Denmark since that date [DANMAP 2022, Textbox 4.2].

In September 2024, DVFA launched its third National Action Plan Against Antimicrobial Resistance in Animals and Food (2024–2027), continuing Denmark's One Health approach to combating antimicrobial resistance. The action plan focuses on four priority areas: strengthened surveillance, healthy livestock with prudent and low antimicrobial use, targeted

communication, and national and international collaboration. In accordance with the Food and Veterinary Agreement 2024–2027, the plan includes a national target of reducing antimicrobial consumption in pigs by 8% by 2027 compared with the 2018 baseline, while maintaining a high level of animal health through improved biosecurity, disease prevention, and prudent antimicrobial use.

To support this objective, the DVFA revised the Yellow Card scheme by lowering the antimicrobial consumption threshold values for weaners and finishers by 20%, effective from 31 December 2025. The revised thresholds are intended to encourage a further reduction in antimicrobial use in pig production, whereas the threshold values for sows, gilts, boars, and piglets remain unchanged.

**Data sources**

In Denmark, antimicrobials are available only by prescription, and data on antimicrobial consumption have been systematically collected since 1990.

Since 2001, data on all medicines prescribed for animal use have been systematically recorded in the national database VetStat. Since 2010, VetStat has been hosted and maintained by the DVFA. In June 2021, DVFA launched an updated version of the VetStat platform.

The 2025 data presented in this report were extracted from VetStat on 31 July 2026. Data extraction, analysis, and interpretation were carried out by the National Food Institute at the Technical University of Denmark on behalf of DANMAP.

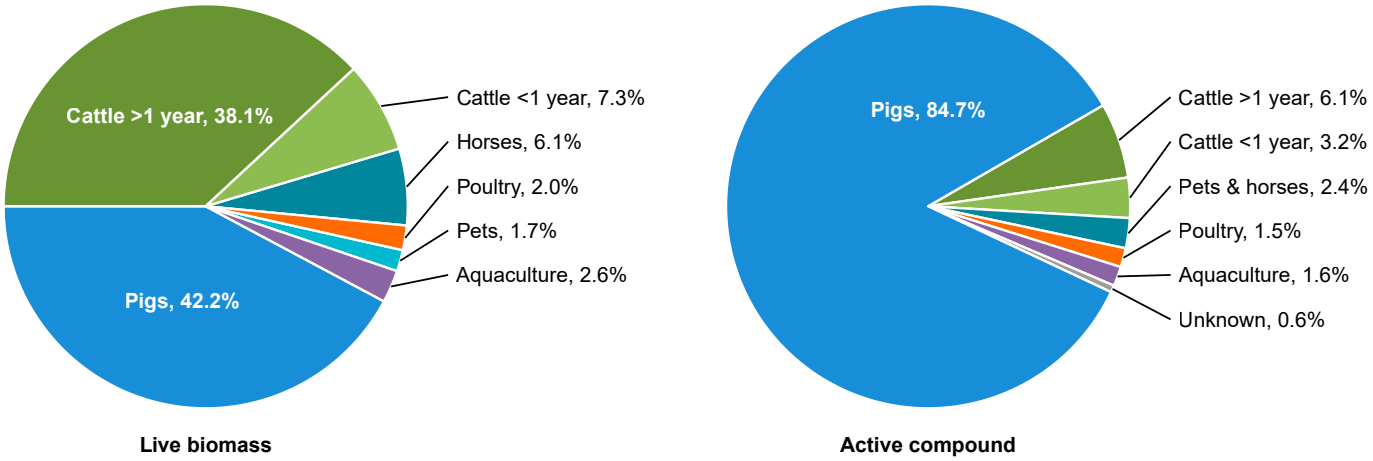
## 4.2 Total antimicrobial consumption in animals

In 2025, the total consumption of antimicrobials in animals amounted to 88.44 tonnes of active compound, representing a 1.14% (995.30 kg) increase compared to 2024 (Figure 4.1). Of this total, antimicrobial consumption in pigs accounted for 84.68%, followed by cattle at 9.27%, and poultry at 1.52% (Figure 4.2, Table 4.1).

Pig production is the primary driver of antimicrobial consumption in animals in Denmark. While cattle account for the largest share of live biomass, a substantial proportion of this biomass consists of dairy cows, which have significantly lower antimicrobial usage compared to growing animals such as those in slaughter pig production.

Between 2000 (the introduction of VetStat) and 2009, the total amount of antimicrobial active compounds used in animals increased by 61.7% (Figure 4.1). During this period, both the number of finishers produced and the proportion of live pigs exported at approximately 30 kg increased. From 2009 to 2021, antimicrobial consumption declined, while the proportion of exported pigs increased. Between 2022 and 2025, overall antimicrobial use increased modestly by 2.47%. Over the same period, the number of finishers produced fell by 14.02% compared to 2022, while the number of live pigs exported increased by 16.43%.

**Figure 4.2 Distribution of live biomass and antimicrobial consumption in main animal species, tonnes, Denmark, 2025** DANMAP 2025




The live biomass is estimated from census data (pigs, cattle, and companion animals) and production data (poultry and aquaculture).
The estimation procedures are described in Chapter 10, Section 10.2.
Data for 2025 were extracted from VetStat on 31 July 2026.

**Table 4.1 Antimicrobial consumption by animal species and age group, kg active compound, Denmark, 2024-2025** DANMAP 2025

| | Aminoglycosides | Amphenicols | Cephalosporins [a] | Fluoroquinolones | Lincosamides | Macrolides | Other antimicrobials [b] | Other quinolones | Penicillins, beta-lactamase-sensitive | Penicillins, others | Pleuromutilins | Sulfonamides and trimethoprim | Tetracyclines | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Pigs** | 18541.0 | 466.0 | - | - | 1761.1 | 12214.4 | - | - | 11663.2 | 8336.9 | 6147.1 | 5296.8 | 10456.6 | 73396.2 | 74883.1 |
| Sows, piglets, gilts and boars | 2151.5 | 208.1 | - | - | 257.6 | 305.9 | - | - | 6166.2 | 1913.0 | 582.9 | 3819.2 | 982.3 | 16664.2 | 16386.7 |
| Weaners, =<30 kg | 16280.1 | 249.2 | - | - | 1159.9 | 8262.1 | - | - | 1656.8 | 5714.5 | 2087.5 | 1449.7 | 6886.8 | 42997.4 | 43746.6 |
| Finishers and polts | 109.4 | 8.7 | - | - | 343.6 | 3646.4 | - | - | 3840.2 | 709.4 | 3476.7 | 27.9 | 2587.4 | 13734.6 | 14749.8 |
| **Cattle** | 766.6 | 1107.0 | 58.0 | - | 5.7 | 440.5 | - | - | 4079.4 | 682.0 | - | 386.3 | 670.7 | 8255.6 | 8196.1 |
| Cows, bulls, heifers and steers >24 months | 202.3 | 10.2 | 24.0 | - | 0.8 | 86.0 | - | - | 3330.8 | 362.4 | - | 284.5 | 456.0 | 4933.6 | 4757.0 |
| Intramammaries | 23.8 | - | 33.8 | - | 4.8 | - | - | - | 221.5 | 177.0 | - | 0.0 | - | 469.1 | 460.9 |
| Calves <12 months | 524.0 | 1090.7 | 0.0 | - | 0.1 | 350.6 | - | - | 440.7 | 132.6 | - | 100.3 | 198.1 | 2707.0 | 2837.1 |
| Young cattle btw 12 and 24 months | 16.5 | 6.1 | 0.1 | - | 0.0 | 3.9 | - | - | 86.3 | 9.9 | - | 1.5 | 16.7 | 145.9 | 141.1 |
| **Poultry** | 84.2 | - | - | - | 21.2 | 180.5 | - | - | 259.0 | 341.0 | 0.1 | 100.8 | 358.8 | 1140.9 | 1345.7 |
| Broilers | 39.5 | - | - | - | 16.9 | 66.0 | - | - | 40.0 | 201.2 | - | 96.6 | 119.6 | 552.7 | 579.8 |
| Layer hens | 31.5 | - | - | - | - | 103.4 | - | - | 82.9 | 13.6 | - | - | 34.1 | 247.2 | 265.5 |
| Turkeys | 8.6 | - | - | - | 4.3 | - | - | - | 135.9 | 104.8 | - | - | 161.0 | 285.8 | 414.5 |
| Other poultry | 4.7 | - | - | - | - | 11.1 | - | - | 0.3 | 21.4 | 0.1 | 4.2 | 44.1 | 55.2 | 85.9 |
| **Other production animals** | 2.2 | 123.2 | - | - | 0.0 | 0.1 | - | 277.0 | 0.6 | 6.2 | - | 981.7 | 2.7 | 1832.0 | 1393.6 |
| Aquaculture | 1.4 | 123.1 | - | - | - | - | - | 277.0 | - | - | - | 979.8 | 2.0 | 1812.1 | 1383.3 |
| Fur animals | 0.0 | - | - | - | - | - | - | - | 0.1 | 5.6 | - | 1.8 | 0.6 | 17.7 | 8.1 |
| Other | 0.7 | 0.1 | - | - | 0.0 | 0.1 | - | - | 0.5 | 0.7 | - | 0.0 | 0.1 | 2.2 | 2.2 |
| **Companion animals** | 6.4 | 0.6 | 42.0 | 12.7 | 72.6 | 0.4 | 29.0 | - | 14.9 | 453.0 | 0.4 | 1446.3 | 49.5 | 2268.6 | 2127.7 |
| Horses | 4.0 | 0.0 | 0.0 | 0.0 | 0.0 | - | 0.2 | - | 7.0 | 0.2 | - | 174.2 | 14.2 | 181.4 | 200.0 |
| Pets | 1.7 | 0.2 | 17.2 | 4.1 | 16.4 | 0.4 | 10.3 | - | 7.8 | 80.3 | 0.4 | 158.0 | 22.7 | 372.6 | 319.5 |
| Unspecified | 0.7 | 0.4 | 24.8 | 8.6 | 56.2 | - | 18.5 | - | - | 372.5 | - | 1114.1 | 12.6 | 1714.6 | 1608.2 |
| **Unknown** [c] | 56.1 | 4.8 | 0.8 | 0.0 | 1.9 | 11.8 | 0.0 | 1.0 | 277.3 | 48.8 | 11.3 | 12.2 | 67.4 | 551.0 | 493.4 |
| **Total** | 19456.4 | 1701.7 | 100.8 | 12.7 | 1862.6 | 12847.7 | 29.0 | 278.0 | 16294.3 | 9867.9 | 6158.9 | 8224.0 | 11605.6 | 87444.3 | 88439.6 |

Data for 2025 were extracted from VetStat on 31 July 2026.
Combination products are split into active compounds.
a) In 2025, 3rd generation cephalosporins were used in companion animals (0.75 kg) and cattle (0.03 kg).
b) Including other antiinfectives, dermatologicals, otological, ophthalmologicals, polymyxin, quinolones, and sulfonamides (plain).
c) Including data with no information on animal species/age group or mismatch between animal species and age group.
A dash (-) indicates no antimicrobial usage, and 0.0 indicates a consumption less than 0.05.

## 4.3 Antimicrobial consumption by animal species

### 4.3.1 Antimicrobial consumption in pigs

In 2025, a total of 74.88 tonnes of antimicrobials were used in pig production, representing an increase of 2.03% (1,486.9 kg) compared to 2024 (Table 4.1). During the same period, the estimated live biomass of pigs increased by 0.38%, primarily due to an increase in the number of exported pigs.

The total antimicrobial use was distributed across production stages, with approximately 16.39 tonnes used for sows and piglets, 43.75 tonnes for weaners, and 14.75 tonnes for finishers (Table 4.1).

The treatment proportion (DAPD) of the total population serves as an indicator of antimicrobial selection pressure within the population. DAPD is calculated as the number of standard doses per kg of animal divided by the estimated live biomass in the age group or the total population (in tonnes) (Chapter 10, Section 10.2). Figures 4.3, 4.4, and 4.5 illustrate DAPD values for the overall population of pigs, as well as for specific age groups of pigs and cattle.

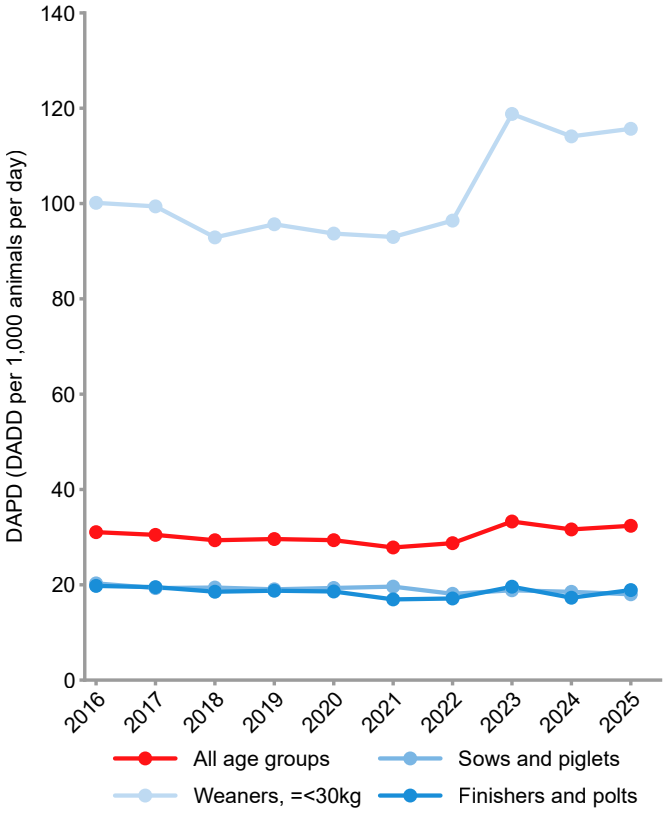
From 2004 to 2009, the DAPD showed a steady increase across all age groups. This was followed by a marked decline in 2010 and 2011, coinciding with the introduction of the Yellow Card initiative. Between 2013 and 2016, a slight but consistent downward trend in treatment proportion was observed (data not shown). This downward trend continued from 2016 to 2021 (Figure 4.3).

This trend reversed between 2021 and 2023, when DAPD increased by approximately 19.57%, primarily driven by increased antimicrobial use in weaners.

In 2025, the overall DAPD increased by 2.41% compared to 2024. However, trends varied across age groups. DAPD decreased by 2.80% in sows and piglets. In contrast, DAPD increased by 1.39% in weaners and by 9.32% in finishers (Figure 4.3).

In 2025, it is estimated that on any given day, approximately 1.80% of sows and piglets, 11.57% of weaners and 1.89% of finishers were treated with antimicrobials.

**Figure 4.3 Total antimicrobial consumption in the pig production, Denmark, 2011-2025** DANMAP 2025




The age group "Sows and piglets" includes treatment of boars, where boars constitute approximately 0.86% of the estimated live biomass for the age group.
DAPDs are calculated as the number of standard doses for one kg animal divided by the estimated live biomass in the age group or the total population (in tonnes).
Data for 2025 were extracted from VetStat on 31 July 2026.

For 2025 compared to 2024, antimicrobial consumption in the overall population increased for lincosamides (46.73%), macrolides (8.62%) and sulfonamides and trimethoprim (1.63%). In contrast, usage declined for amphenicols (3.96%) and aminoglycosides (3.95%). From 2024 to 2025, changes in the use of pleuromutilins, other penicillins, beta-lactamase-sensitive penicillins, and tetracyclines were all below 1% (Figure 4.4).

Among sows and piglets, the change from 2024 to 2025 in DAPD values showed an increase only in lincosamides, from 0.09 DAPD to 0.24 DAPD (165.47%). The use of beta-lactamase-sensitive penicillins remained at 6.86 DAPD. In contrast, usage declined for amphenicols (17.65%), pleuromutilins (17.32%), other penicillins (10.96%), macrolides (5.55%), tetracyclines (2.84%), and aminoglycosides (2.49%) (Figure 4.4).

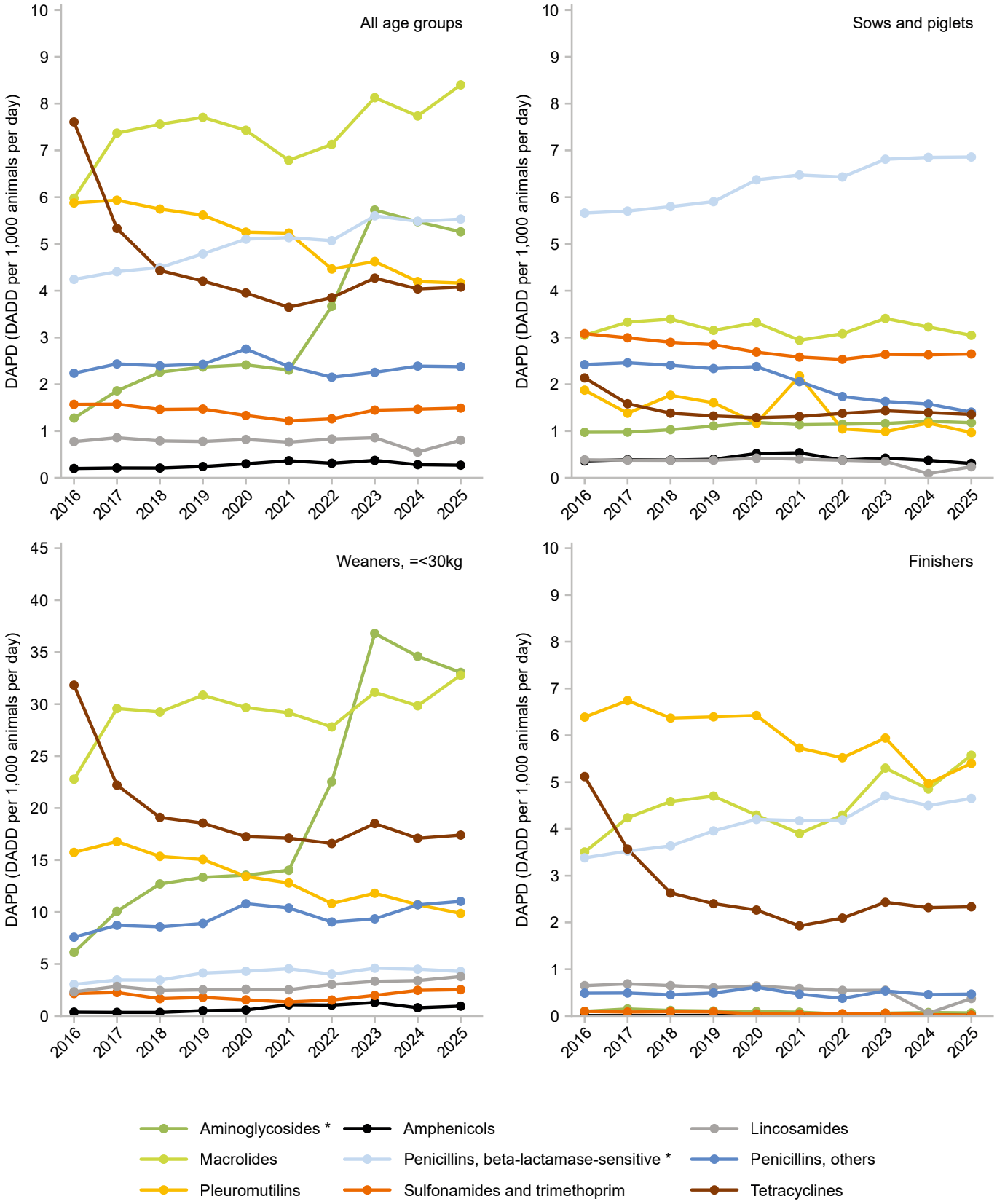
Following the ban on prescribed zinc oxide in pig production (effective June 2022), and the discontinuation of colistin, the use of aminoglycosides, neomycin and apramycin, in weaners increased significantly (Table 4.2). The DAPD values of aminoglycosides rose from 14.02 in 2021 to 34.60 in 2024. In 2025, usage declined to 33.05 DAPD, representing a 4.48% decrease compared to the previous year (Figure 4.4). Regarding additional changes in weaners from 2024 to 2025, the DAPD of amphenicols, lincosamides, macrolides, other penicillins, sulfonamides and trimethoprim, and tetracyclines increased by 19.02%, 11.37%, 9.88%, 3.15%, 2.73%, and 1.79%, respectively. There were reductions in DAPD of pleuromutilins (7.89%) and beta-lactamase-sensitive penicillins (4.84%) (Figure 4.4).

In finishers, the change from 2024 to 2025 showed that the DAPD increased from 0.06 DAPD to 0.37 DAPD (537.49%) for lincosamides. Moreover, the use of macrolides, pleuromutilins, beta-lactamase-sensitive penicillins and other penicillins increased by 14.90%, 8.61%, 3.37% and 2.02%, respectively. Meanwhile, amphenicols, sulfonamides and trimethoprim and aminoglycosides declined by 58.66%, 36.71%, and 11.54% (Figure 4.4).

In 2025, the three most commonly used active compounds in sows and piglets were procaine benzylpenicillin, tulathromycin, and sulfadiazin with trimethoprim. Among weaners, the most frequently used compounds were tylosin, doxycycline, and neomycin. For finishers, tiamulin, procaine benzylpenicillin, and tylosin were the predominant choices (Table 4.2).

**Figure 4.4 Antimicrobial consumption in the total pig production and in each age group at antimicrobial class level, Denmark, 2016-2025**

DANMAP 2025




* Please note that the reported level differs noticeably from DANMAP reports before 2024 due to DADD revisions.
The age group "Sows and piglets" includes treatment of boars, where boars constitute 0.86% of the estimated live biomass for the age group.
DAPDs are calculated as the number of standard doses for one kg animal divided by the estimated live biomass in the age group or the total population (in tonnes).
Data for 2025 were extracted from VetStat on 31 July 2026.
Combination products are split into active compounds.

**Table 4.2 Antimicrobial consumption in each age group of pig production at antimicrobial class and active compound level, DAPD, Denmark, 2016-2025** **DANMAP 2025**

| Antimicrobial class | Active compound | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Sows, piglets, gilts and boars** | | | | | | | | | | | |
| Aminoglycosides | Apramycin | 0.13 | 0.08 | 0.08 | 0.15 | 0.15 | 0.16 | 0.14 | 0.15 | 0.14 | 0.17 |
| | Dihydrostreptomycin | 0.60 | 0.51 | 0.51 | 0.53 | 0.59 | 0.59 | 0.64 | 0.67 | 0.67 | 0.69 |
| | Gentamicin | 0.02 | 0.03 | 0.04 | 0.03 | 0.03 | 0.01 | 0.01 | 0.03 | 0.00 | 0.00 |
| | Neomycin | - | 0.10 | 0.17 | 0.15 | 0.13 | 0.11 | 0.10 | 0.08 | 0.10 | 0.08 |
| | Paromomycin | 0.01 | 0.01 | 0.02 | 0.03 | 0.05 | 0.09 | 0.10 | 0.09 | 0.15 | 0.12 |
| | Spectinomycin | 0.21 | 0.24 | 0.23 | 0.22 | 0.23 | 0.18 | 0.16 | 0.14 | 0.14 | 0.13 |
| Amphenicols | Florfenicol | 0.36 | 0.39 | 0.38 | 0.40 | 0.52 | 0.54 | 0.38 | 0.42 | 0.37 | 0.31 |
| Cephalosporins | Cefquinome | - | 0.00 | 0.00 | - | - | - | - | - | - | - |
| | Ceftiofur | 0.00 | 0.00 | 0.00 | - | - | - | - | - | - | - |
| Lincosamides | Lincomycin | 0.38 | 0.38 | 0.37 | 0.38 | 0.42 | 0.40 | 0.38 | 0.35 | 0.09 | 0.24 |
| Macrolides | Gamithromycin | 0.51 | 1.19 | 1.32 | 1.35 | 1.40 | 1.01 | 0.86 | 0.73 | 0.49 | 0.37 |
| | Spiramycin | 0.00 | - | - | - | - | - | - | - | - | - |
| | Tildipirosin | 0.28 | 0.19 | 0.19 | 0.15 | 0.13 | 0.10 | 0.07 | 0.08 | 0.06 | 0.04 |
| | Tilmicosin | 0.14 | 0.14 | 0.16 | 0.09 | 0.08 | 0.06 | 0.04 | 0.03 | 0.02 | 0.02 |
| | Tulathromycin | 1.88 | 1.61 | 1.50 | 1.32 | 1.38 | 1.38 | 1.71 | 2.20 | 2.36 | 2.40 |
| | Tylosin | 0.23 | 0.20 | 0.17 | 0.19 | 0.31 | 0.39 | 0.39 | 0.37 | 0.30 | 0.21 |
| | Tylvalosin | 0.00 | 0.01 | 0.06 | 0.05 | 0.02 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Other antimicrobials | Colistin | 0.36 | 0.12 | 0.00 | 0.00 | 0.00 | - | - | - | - | - |
| Penicillins, beta-lactamase-sensitive | Benzylpenicillin | 0.04 | 0.00 | - | - | - | - | - | - | - | - |
| | Penethamate hydriodide | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Procaine benzylpenicillin | 5.62 | 5.70 | 5.79 | 5.90 | 6.37 | 6.47 | 6.43 | 6.81 | 6.85 | 6.86 |
| Penicillins, others | Amoxicillin | 2.33 | 2.40 | 2.32 | 2.25 | 2.27 | 1.97 | 1.64 | 1.58 | 1.53 | 1.36 |
| | Amoxicillin (beta-lactamase inhibitor) | 0.09 | 0.06 | 0.09 | 0.08 | 0.11 | 0.09 | 0.10 | 0.06 | 0.04 | 0.05 |
| Pleuromutilins | Tiamulin | 1.87 | 1.38 | 1.76 | 1.61 | 1.17 | 2.18 | 1.04 | 0.99 | 1.17 | 0.97 |
| | Valnemulin | - | 0.00 | - | - | - | - | - | - | - | - |
| Sulfonamides and trimethoprim | Sulfadiazine | 1.93 | 1.83 | 1.65 | 1.64 | 0.66 | - | - | 0.00 | 0.51 | 1.42 |
| | Sulfadoxine | 0.63 | 0.65 | 0.74 | 0.72 | 1.57 | 2.15 | 2.11 | 2.19 | 1.68 | 0.78 |
| | Sulfamethoxazole | 0.00 | 0.01 | 0.03 | 0.01 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 |
| | Trimethoprim | 0.51 | 0.50 | 0.48 | 0.47 | 0.45 | 0.43 | 0.42 | 0.44 | 0.44 | 0.44 |
| Tetracyclines | Chlortetracycline | 0.04 | 0.03 | 0.04 | 0.03 | 0.03 | 0.06 | 0.03 | 0.03 | 0.03 | 0.02 |
| | Doxycycline | 0.22 | 0.13 | 0.15 | 0.11 | 0.08 | 0.07 | 0.14 | 0.14 | 0.06 | 0.03 |
| | Oxytetracycline | 1.88 | 1.42 | 1.20 | 1.17 | 1.18 | 1.18 | 1.21 | 1.27 | 1.31 | 1.31 |
| **Weaners, =<30 kg** | | | | | | | | | | | |
| Aminoglycosides | Apramycin | 0.69 | 0.66 | 0.61 | 0.89 | 1.27 | 1.64 | 3.61 | 13.85 | 13.18 | 11.36 |
| | Dihydrostreptomycin | 1.07 | 1.07 | 1.04 | 1.25 | 1.41 | 1.43 | 1.27 | 1.51 | 1.45 | 1.52 |
| | Gentamicin | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | - |
| | Neomycin | - | 2.69 | 6.19 | 6.18 | 5.78 | 5.89 | 11.54 | 14.67 | 12.95 | 12.46 |
| | Paromomycin | 0.07 | 0.04 | 0.06 | 0.08 | 0.08 | 0.12 | 0.15 | 0.18 | 0.20 | 0.16 |
| | Spectinomycin | 4.29 | 5.61 | 4.80 | 4.94 | 5.01 | 4.94 | 5.95 | 6.58 | 6.81 | 7.55 |
| Amphenicols | Florfenicol | 0.37 | 0.35 | 0.35 | 0.51 | 0.58 | 1.08 | 1.04 | 1.29 | 0.79 | 0.95 |
| Cephalosporins | Cefquinome | 0.00 | 0.00 | - | - | - | - | - | - | - | - |
| | Ceftiofur | 0.00 | - | 0.00 | 0.00 | 0.00 | - | - | - | - | - |
| Lincosamides | Lincomycin | 2.33 | 2.84 | 2.45 | 2.52 | 2.57 | 2.53 | 3.03 | 3.33 | 3.40 | 3.79 |
| Macrolides | Gamithromycin | 0.41 | 0.98 | 0.91 | 1.30 | 1.69 | 1.21 | 0.89 | 0.68 | 0.64 | 0.55 |
| | Tildipirosin | 0.35 | 0.26 | 0.22 | 0.23 | 0.24 | 0.20 | 0.14 | 0.13 | 0.11 | 0.10 |
| | Tilmicosin | 4.97 | 5.29 | 5.06 | 5.88 | 6.40 | 6.49 | 5.28 | 5.55 | 4.95 | 5.30 |
| | Tulathromycin | 1.04 | 1.08 | 0.89 | 0.89 | 1.00 | 1.15 | 1.32 | 2.07 | 2.55 | 3.27 |
| | Tylosin | 14.75 | 18.90 | 17.81 | 18.05 | 16.38 | 16.54 | 15.88 | 17.19 | 16.40 | 18.18 |
| | Tylvalosin | 1.25 | 3.07 | 4.34 | 4.49 | 3.97 | 3.57 | 4.30 | 5.51 | 5.20 | 5.39 |

DAPDs are calculated as the number of standard doses for one kg animal divided by the estimated live biomass in the age group or the total population (in tonnes).
Data for 2025 were extracted from VetStat on 31 July 2026.
Combination products are split into active compounds.
A dash (-) indicates no antimicrobial usage, and 0.00 indicates a consumption less than 0.005.

**continued ... Table 4.2 Antimicrobial consumption in each age group of pig production at antimicrobial class and active compound level, DAPD, Denmark, 2016-2025** DANMAP 2025

| Antimicrobial class | Active compound | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **continued ... Weaners, =<30 kg** | | | | | | | | | | | |
| Other antimicrobials | Colistin | 8.21 | 3.14 | 0.01 | - | - | - | - | - | - | - |
| Penicillins, beta-lactamase-sensitive | Benzylpenicillin | 0.07 | 0.00 | - | - | - | - | - | - | - | - |
| | Penethamate hydriodide | 0.00 | - | 0.00 | - | - | - | - | - | - | - |
| | Procaine benzylpenicillin | 2.96 | 3.46 | 3.45 | 4.13 | 4.30 | 4.54 | 4.01 | 4.59 | 4.50 | 4.28 |
| Penicillins, others | Amoxicillin | 6.81 | 8.25 | 8.37 | 8.65 | 10.26 | 9.71 | 8.09 | 8.50 | 9.74 | 8.97 |
| | Amoxicillin (beta-lactamase inhibitor) | 0.77 | 0.47 | 0.21 | 0.24 | 0.54 | 0.67 | 0.94 | 0.84 | 0.96 | 2.06 |
| | Ampicillin | 0.00 | - | - | - | - | - | - | - | - | - |
| Pleuromutilins | Tiamulin | 15.65 | 16.12 | 14.99 | 14.86 | 13.27 | 12.78 | 10.82 | 11.81 | 10.71 | 9.86 |
| | Valnemulin | 0.09 | 0.65 | 0.37 | 0.20 | 0.15 | 0.01 | - | - | - | - |
| Sulfonamides and trimethoprim | Sulfadiazine | 0.88 | 0.99 | 0.57 | 0.63 | 0.24 | 0.01 | - | - | 0.64 | 1.15 |
| | Sulfadoxine | 0.23 | 0.24 | 0.28 | 0.36 | 0.61 | 0.87 | 1.09 | 1.48 | 1.27 | 0.79 |
| | Sulfamethoxazole | 0.69 | 0.65 | 0.54 | 0.51 | 0.45 | 0.25 | 0.19 | 0.17 | 0.15 | 0.18 |
| | Trimethoprim | 0.36 | 0.38 | 0.28 | 0.30 | 0.26 | 0.23 | 0.26 | 0.33 | 0.41 | 0.42 |
| Tetracyclines | Chlortetracycline | 5.28 | 4.07 | 3.47 | 3.29 | 2.66 | 2.07 | 1.16 | 0.98 | 0.80 | 0.94 |
| | Doxycycline | 22.26 | 14.02 | 12.07 | 11.55 | 11.43 | 11.99 | 12.39 | 14.04 | 12.82 | 13.15 |
| | Oxytetracycline | 4.29 | 4.13 | 3.55 | 3.71 | 3.17 | 3.05 | 3.05 | 3.48 | 3.47 | 3.31 |
| **Finishers and polts** | | | | | | | | | | | |
| Aminoglycosides | Apramycin | - | 0.00 | - | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Dihydrostreptomycin | 0.02 | 0.03 | 0.02 | 0.03 | 0.03 | 0.03 | 0.02 | 0.02 | 0.01 | 0.01 |
| | Gentamicin | - | - | - | - | 0.00 | - | - | - | 0.00 | - |
| | Neomycin | - | 0.00 | 0.01 | 0.02 | 0.03 | 0.03 | 0.01 | 0.02 | 0.03 | 0.02 |
| | Paromomycin | - | 0.00 | - | 0.00 | 0.00 | - | - | 0.00 | - | - |
| | Spectinomycin | 0.08 | 0.12 | 0.08 | 0.06 | 0.04 | 0.03 | 0.02 | 0.02 | 0.03 | 0.03 |
| Amphenicols | Florfenicol | 0.01 | 0.01 | 0.01 | 0.01 | 0.02 | 0.03 | 0.02 | 0.02 | 0.03 | 0.01 |
| Cephalosporins | Ceftiofur | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | - | - | - | - | - |
| Lincosamides | Lincomycin | 0.65 | 0.69 | 0.65 | 0.60 | 0.64 | 0.59 | 0.55 | 0.55 | 0.06 | 0.37 |
| Macrolides | Gamithromycin | 0.01 | 0.02 | 0.02 | 0.03 | 0.03 | 0.02 | 0.01 | 0.01 | 0.02 | 0.02 |
| | Tildipirosin | 0.01 | 0.02 | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Tilmicosin | 0.05 | 0.06 | 0.06 | 0.07 | 0.07 | 0.05 | 0.05 | 0.01 | 0.01 | 0.02 |
| | Tulathromycin | 0.02 | 0.03 | 0.02 | 0.02 | 0.04 | 0.02 | 0.02 | 0.03 | 0.06 | 0.09 |
| | Tylosin | 3.05 | 3.39 | 3.56 | 3.48 | 3.17 | 2.99 | 3.03 | 3.34 | 3.00 | 3.45 |
| | Tylvalosin | 0.37 | 0.73 | 0.92 | 1.10 | 0.98 | 0.82 | 1.18 | 1.91 | 1.76 | 2.00 |
| Other antimicrobials | Colistin | 0.03 | 0.01 | - | - | - | - | - | - | - | - |
| Penicillins, beta-lactamase-sensitive | Benzylpenicillin | 0.00 | - | - | - | - | - | - | - | - | - |
| | Penethamate hydriodide | - | - | 0.00 | - | - | - | - | - | - | - |
| | Procaine benzylpenicillin | 3.38 | 3.52 | 3.64 | 3.96 | 4.20 | 4.18 | 4.19 | 4.70 | 4.50 | 4.65 |
| Penicillins, others | Amoxicillin | 0.48 | 0.49 | 0.45 | 0.49 | 0.61 | 0.46 | 0.37 | 0.53 | 0.46 | 0.47 |
| | Amoxicillin (beta-lactamase inhibitor) | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.01 | 0.00 | 0.00 |
| Pleuromutilins | Tiamulin | 6.38 | 6.68 | 6.25 | 6.26 | 6.35 | 5.72 | 5.52 | 5.94 | 4.97 | 5.40 |
| | Valnemulin | 0.01 | 0.07 | 0.12 | 0.14 | 0.07 | 0.00 | - | - | - | - |
| Sulfonamides and trimethoprim | Sulfadiazine | 0.03 | 0.02 | 0.02 | 0.03 | 0.01 | - | 0.00 | - | 0.00 | 0.01 |
| | Sulfadoxine | 0.01 | 0.00 | 0.01 | 0.01 | 0.01 | 0.02 | 0.02 | 0.02 | 0.01 | 0.01 |
| | Sulfamethoxazole | 0.04 | 0.04 | 0.05 | 0.04 | 0.02 | 0.02 | 0.02 | 0.03 | 0.01 | 0.00 |
| | Trimethoprim | 0.02 | 0.01 | 0.02 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.00 | 0.00 |
| Tetracyclines | Chlortetracycline | 0.80 | 0.59 | 0.46 | 0.43 | 0.34 | 0.22 | 0.14 | 0.08 | 0.08 | 0.08 |
| | Doxycycline | 3.10 | 1.88 | 1.37 | 1.15 | 1.18 | 1.09 | 1.30 | 1.56 | 1.51 | 1.54 |
| | Oxytetracycline | 1.22 | 1.10 | 0.80 | 0.83 | 0.74 | 0.62 | 0.66 | 0.78 | 0.72 | 0.72 |

DAPDs are calculated as the number of standard doses for one kg animal divided by the estimated live biomass in the age group or the total population (in tonnes).
Data for 2025 were extracted from VetStat on 31 July 2026.
Combination products are split into active compounds.
A dash (-) indicates no antimicrobial usage, and 0.00 indicates a consumption less than 0.005.

### 4.3.2 Antimicrobial consumption in cattle

In 2025, approximately 8.20 tonnes of active antimicrobial compounds were recorded for use in cattle, representing a decrease of 0.72% compared to 2024 (Table 4.1). During the same period, the estimated live biomass of cattle decreased by 1.05%.

Of this amount, approximately 0.46 tonnes were used for intramammary therapeutic purposes or dry-cow treatment. Approximately 2.84 tonnes of antimicrobials were used for systemic treatment in young cattle (<1 year), with the remaining 4.90 tonnes used in adult cattle (>1 year) (Table 4.1).

Except for 2024, systemic antimicrobial consumption in adult cattle declined over the past decade: it was 3.41 DAPD in 2016 and 2.73 DAPD in 2024. In 2025, the DAPD was 2.64, thus a 3.29% decline compared to 2024 (Figure 4.5). During the same period, systemic antimicrobial consumption in young cattle increased until 2024 (8.13 DAPD). In 2025, the use for young cattle increased by 4.30% compared to 2024. The estimated live biomass of young cattle declined by approximately 1.00% in the same period.

In 2025, it is estimated that on any given day approximately 0.26% of adult cattle and 0.85% of young cattle were treated with systemic antimicrobials.

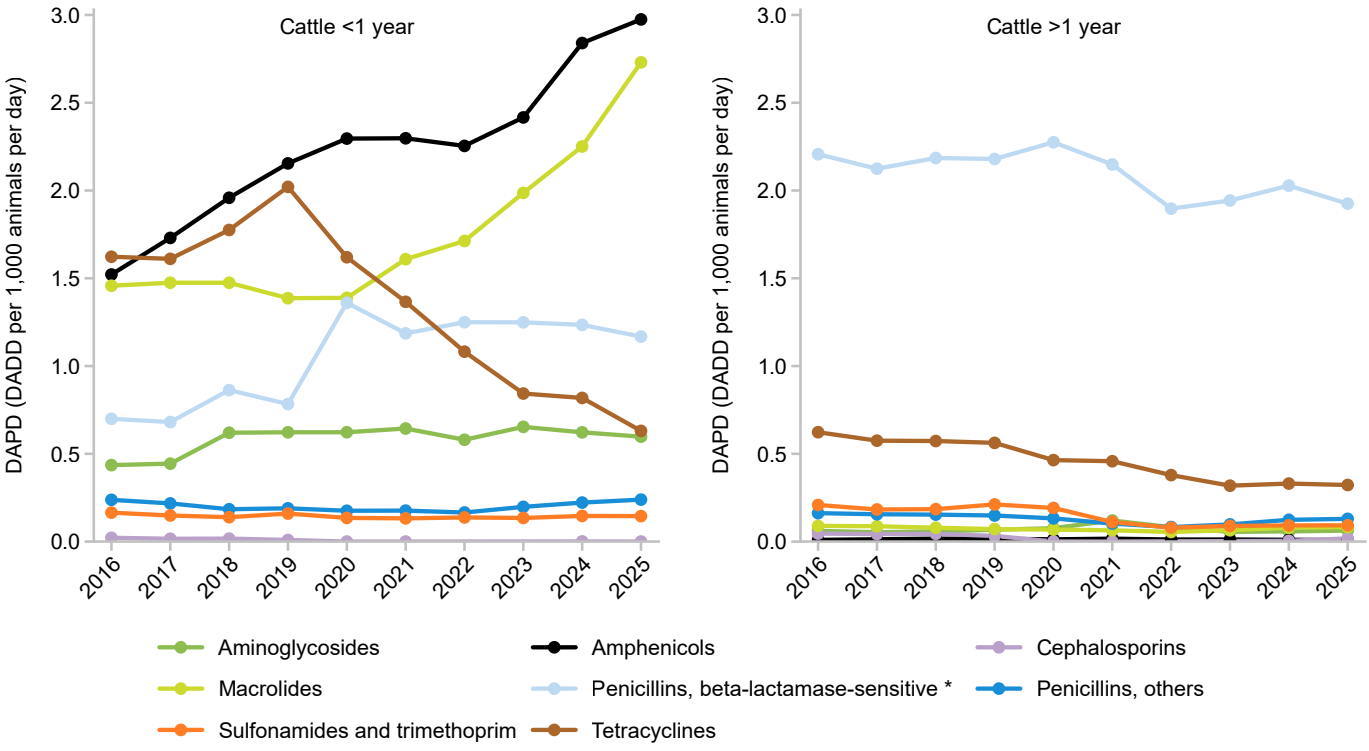
Among adult cattle, the change from 2024 to 2025 in DAPD values showed increased usage of cephalosporins (334.18%), lincosamides (56.77%), aminoglycosides (8.08%), macrolides (4.74%) and other penicillins (4.35%). In contrast, amphenicol use decreased by 18.45%, beta-lactamase-sensitive penicillins by 5.06% and tetracyclines by 2.44%. In 2025, treatments with beta-lactamase-sensitive penicillins accounted for 72.87% of the total DAPD (Figure 4.5).

In young cattle, the change from 2024 to 2025 in DAPD values showed increased usage of macrolides (21.29%), other penicillins (7.60%) and amphenicols (4.73%), while lincosamides decreased by 28.48%, tetracyclines by 22.94%, beta-lactamase-sensitive penicillins by 5.44% and aminoglycosides by 3.95% (Figure 4.5).

In 2025, the most frequently used active compounds for systemic treatments in adult cattle were procaine benzylpenicillin and oxytetracycline. Among young cattle, the most frequently used compounds were florfenicol, tulathromycin and procaine benzylpenicillin (Table 4.3).

**Figure 4.5 Systemic antimicrobial consumption in cattle production by age groups at antimicrobial class level, Denmark, 2016-2025**

DANMAP 2025




* Please note that the reported level differs noticeably from DANMAP reports before 2024 due to DADD revisions.
DAPDs are calculated as the number of standard doses for one kg animal divided by the estimated live biomass in the age group or the total population (in tonnes).
Intramammary applications are not included (since it is calculated as DADDs per dairy cow, not DAPD).
The DAPDs of amphenicols in cattle <1 year differ from reports before 2021, due to missing data in the old VetStat.
Data for 2025 were extracted from VetStat on 31 July 2026.
Combination products are split into active compounds.

**Table 4.3 Systemic antimicrobial consumption in each age group of cattle production at antimicrobial class and active compound level, DAPD, Denmark, 2016-2025** DANMAP 2025

| Antimicrobial class | Active compound | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **Cattle <1 year** | | | | | | | | | | | |
| Aminoglycosides | Apramycin | 0.02 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.04 | 0.01 | 0.01 |
| | Dihydrostreptomycin | 0.17 | 0.15 | 0.22 | 0.20 | 0.18 | 0.16 | 0.16 | 0.23 | 0.20 | 0.18 |
| | Neomycin | - | 0.01 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | - | 0.00 | 0.00 |
| | Paromomycin | 0.25 | 0.28 | 0.38 | 0.41 | 0.42 | 0.47 | 0.41 | 0.39 | 0.41 | 0.41 |
| | Spectinomycin | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Amphenicols | Florfenicol | 1.52 | 1.73 | 1.96 | 2.15 | 2.30 | 2.30 | 2.25 | 2.42 | 2.84 | 2.97 |
| Cephalosporins | Cefalexin | - | - | - | - | - | - | - | - | - | 0.00 |
| | Cefquinome | 0.01 | 0.01 | 0.01 | 0.01 | 0.00 | 0.00 | - | - | - | - |
| | Ceftiofur | 0.01 | 0.01 | 0.01 | 0.00 | 0.00 | - | - | - | 0.00 | - |
| Lincosamides | Lincomycin | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Macrolides | Gamithromycin | 0.11 | 0.13 | 0.12 | 0.10 | 0.12 | 0.12 | 0.06 | 0.05 | 0.04 | 0.04 |
| | Spiramycin | 0.00 | 0.00 | - | 0.00 | - | - | - | - | - | - |
| | Tildipirosin | 0.41 | 0.43 | 0.46 | 0.43 | 0.39 | 0.34 | 0.20 | 0.07 | 0.04 | 0.02 |
| | Tilmicosin | 0.14 | 0.13 | 0.14 | 0.10 | 0.14 | 0.17 | 0.14 | 0.08 | 0.11 | 0.06 |
| | Tulathromycin | 0.73 | 0.73 | 0.69 | 0.69 | 0.69 | 0.94 | 1.27 | 1.69 | 1.99 | 2.28 |
| | Tylosin | 0.07 | 0.05 | 0.06 | 0.06 | 0.05 | 0.04 | 0.05 | 0.10 | 0.06 | 0.32 |
| Other antimicrobials | Colistin | 0.07 | 0.03 | 0.02 | 0.01 | - | - | - | - | - | - |
| Penicillins, beta-lactamase-sensitive | Benzylpenicillin | 0.02 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Penethamate hydriodide | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.01 | 0.00 | 0.01 | 0.00 | 0.00 |
| | Procaine benzylpenicillin | 0.68 | 0.68 | 0.86 | 0.78 | 1.35 | 1.18 | 1.25 | 1.24 | 1.23 | 1.16 |
| Penicillins, others | Amoxicillin | 0.21 | 0.20 | 0.17 | 0.18 | 0.17 | 0.17 | 0.16 | 0.19 | 0.22 | 0.23 |
| | Amoxicillin (beta-lactamase inhibitor) | 0.03 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 |
| | Ampicillin | 0.00 | - | - | 0.00 | - | - | - | - | - | - |
| Sulfonamides and trimethoprim | Sulfadiazine | 0.12 | 0.11 | 0.10 | 0.12 | 0.06 | 0.01 | 0.00 | 0.00 | 0.03 | 0.04 |
| | Sulfadoxine | 0.02 | 0.01 | 0.02 | 0.02 | 0.05 | 0.10 | 0.11 | 0.11 | 0.09 | 0.09 |
| | Sulfamethoxazole | - | - | - | 0.00 | - | - | - | - | - | - |
| | Trimethoprim | 0.03 | 0.02 | 0.02 | 0.03 | 0.02 | 0.02 | 0.02 | 0.02 | 0.02 | 0.02 |
| Tetracyclines | Chlortetracycline | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Doxycycline | 0.25 | 0.27 | 0.31 | 0.47 | 0.37 | 0.27 | 0.18 | 0.10 | 0.12 | 0.09 |
| | Oxytetracycline | 1.37 | 1.34 | 1.47 | 1.55 | 1.25 | 1.09 | 0.90 | 0.74 | 0.70 | 0.54 |
| **Cattle >1 year** | | | | | | | | | | | |
| Aminoglycosides | Apramycin | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | - |
| | Dihydrostreptomycin | 0.06 | 0.05 | 0.06 | 0.06 | 0.07 | 0.12 | 0.08 | 0.05 | 0.06 | 0.06 |
| | Gentamicin | - | - | - | - | 0.00 | - | - | - | - | - |
| | Neomycin | - | - | - | 0.00 | 0.00 | 0.00 | 0.00 | - | - | - |
| | Paromomycin | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Spectinomycin | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Amphenicols | Florfenicol | 0.01 | 0.01 | 0.02 | 0.02 | 0.01 | 0.02 | 0.01 | 0.01 | 0.01 | 0.01 |
| Cephalosporins | Cefalexin | - | - | - | - | - | - | - | - | 0.00 | 0.02 |
| | Cefquinome | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | - | - | - | - |
| | Ceftiofur | 0.04 | 0.04 | 0.04 | 0.03 | 0.00 | 0.00 | - | - | 0.00 | 0.00 |
| Lincosamides | Lincomycin | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| Macrolides | Gamithromycin | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Spiramycin | 0.00 | 0.00 | 0.00 | - | - | - | - | - | - | - |
| | Tildipirosin | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Tilmicosin | - | 0.00 | - | 0.00 | 0.00 | 0.00 | - | - | - | - |
| | Tulathromycin | 0.00 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 |
| | Tylosin | 0.08 | 0.07 | 0.07 | 0.06 | 0.06 | 0.05 | 0.05 | 0.06 | 0.06 | 0.07 |
| Other antimicrobials | Colistin | 0.00 | 0.00 | 0.00 | 0.00 | - | - | - | - | - | - |

DAPDs are calculated as the number of standard doses for one kg animal divided by the estimated live biomass in the age group or the total population (in tonnes).
Intramammary applications are not included (since it is calculated as DADDs per dairy cow, not DAPD).
Data for 2025 were extracted from VetStat on 31 July 2026.
Combination products are split into active compounds.
A dash (-) indicates no antimicrobial usage, and 0.00 indicates a consumption less than 0.005.

**continued ... Table 4.3 Antimicrobial consumption in each age group of cattle production at antimicrobial class and active compound level, DAPD, using new DADD, Denmark, 2016-2025** DANMAP 2025

| Antimicrobial class | Active compound | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **continued ... Cattle >1 year** | | | | | | | | | | | |
| Penicillins, beta-lactamase-sensitive | Benzylpenicillin | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.01 | 0.01 | 0.01 | 0.02 |
| | Penethamate hydriodide | 0.10 | 0.15 | 0.17 | 0.18 | 0.18 | 0.17 | 0.18 | 0.20 | 0.21 | 0.20 |
| | Procaine benzylpenicillin | 2.10 | 1.97 | 2.01 | 2.00 | 2.09 | 1.97 | 1.70 | 1.73 | 1.81 | 1.71 |
| Penicillins, others | Amoxicillin | 0.16 | 0.16 | 0.15 | 0.15 | 0.13 | 0.10 | 0.08 | 0.10 | 0.12 | 0.13 |
| | Amoxicillin (beta-lactamase inhibitor) | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Ampicillin | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | - | - | - | - |
| Pleuromutilins | Tiamulin | - | - | - | - | - | - | - | - | 0.00 | - |
| Sulfonamides and trimethoprim | Sulfadiazine | 0.16 | 0.14 | 0.14 | 0.16 | 0.06 | 0.00 | 0.00 | 0.00 | 0.02 | 0.04 |
| | Sulfadoxine | 0.02 | 0.02 | 0.02 | 0.02 | 0.10 | 0.09 | 0.07 | 0.07 | 0.06 | 0.04 |
| | Trimethoprim | 0.03 | 0.03 | 0.03 | 0.04 | 0.03 | 0.02 | 0.01 | 0.01 | 0.02 | 0.02 |
| Tetracyclines | Chlortetracycline | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| | Doxycycline | 0.00 | 0.00 | 0.01 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | - | - |
| | Oxytetracycline | 0.62 | 0.57 | 0.56 | 0.55 | 0.46 | 0.45 | 0.38 | 0.32 | 0.33 | 0.32 |

DAPDs are calculated as the number of standard doses for one kg animal divided by the estimated live biomass in the age group or the total population (in tonnes).
Intramammary applications are not included (since it is calculated as DADDs per dairy cow, not DAPD).
Data for 2025 were extracted from VetStat on 31 July 2026.
Combination products are split into active compounds.
A dash (-) indicates no antimicrobial usage, and 0.00 indicates a consumption less than 0.005.

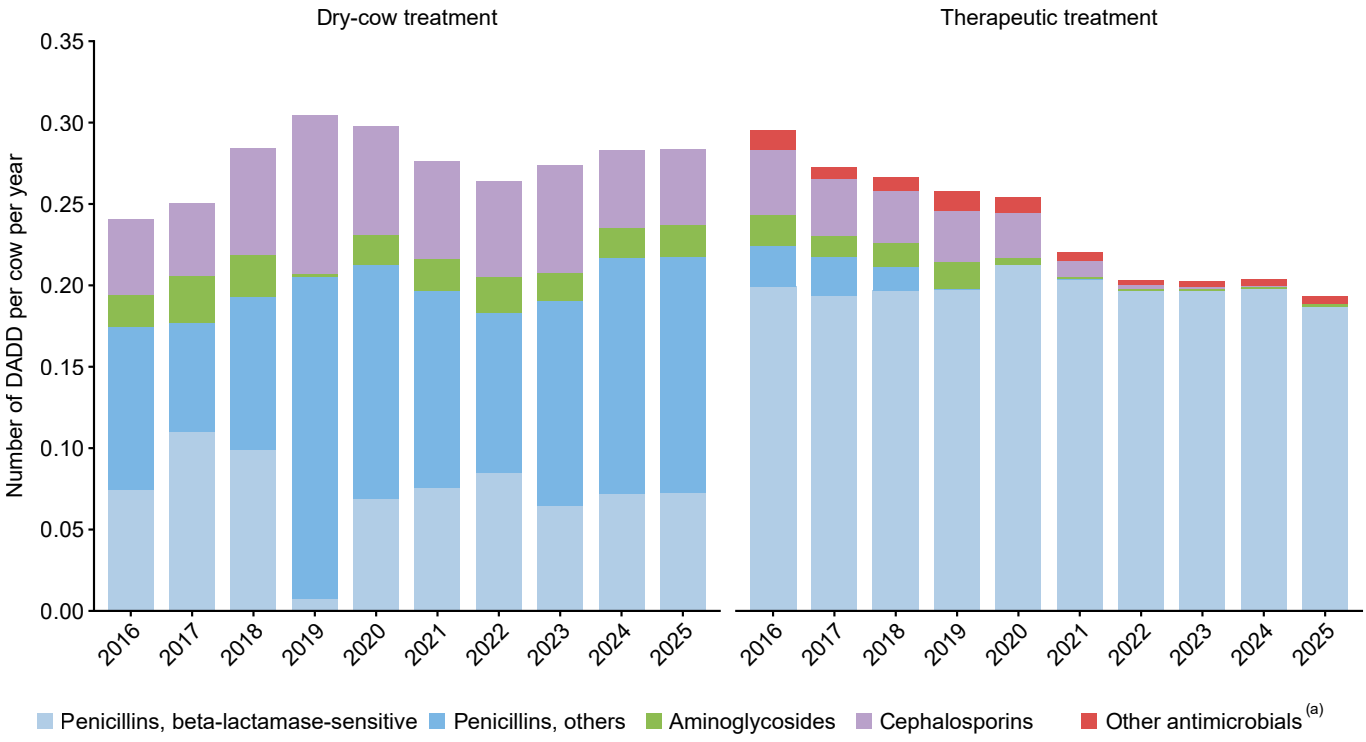
The consumption of intramammary treatments, measured as DADD per cow per year, is presented in Figure 4.6. From 2016 to 2024, usage declined by 9.08%, and in 2025 usage declined by 2.13% compared to 2024.

In 2019, a notable shift occurred in dry-cow treatments: the use of beta-lactamase-sensitive penicillins for this purpose almost ceased, while the use of other penicillins, particularly cloxacillin, increased substantially. This shift resulted from a product shortage in which the primary beta-lactamase-sensitive penicillins for dry-cow treatment were unavailable for extended periods during 2019. Consequently, other penicillins, especially products containing cloxacillin, had to be used as alternatives [Personal communication; Michael Farre, Danish Agriculture and Food Council] (Figure 4.6).

In 2025, other penicillins remained the most frequently used antimicrobials for dry-cow treatment, accounting for 51.31% of this use, followed by beta-lactamase-sensitive penicillins at 25.61% (Figure 4.6).

For therapeutic intramammary treatments, beta-lactamase-sensitive penicillins remained the dominant antimicrobial class from 2016 to 2024, and in 2025, they accounted for 96.89% of all therapeutic intramammary treatments.

**Figure 4.6 Consumption of antimicrobials for intramammary application in cattle, Denmark, 2016-2025** DANMAP 2025




For intramammary therapeutic treatments, 1 DADD is defined as the dose to treat two teats for 24 hours. For dry-cow treatment, 1 DADD is defined as the dose to treat four teats.
Data for 2025 were extracted from VetStat on 31 July 2026.
Combination products are split into active compounds.
a) Includes lincomycin for dry-cow treatments. For therapeutic treatments, mainly sulfonamides and trimethoprim, but also lincomycin and bacitracin.

### 4.3.3 Antimicrobial consumption in poultry

Poultry production in Denmark comprises broiler chickens, laying hens, and turkeys, supplemented by smaller-scale farming involving ducks, geese, and game birds. Among these sectors, conventional broiler production is characterized by stringent biosecurity protocols, which contribute to comparatively low antimicrobial usage relative to other livestock sectors. However, due to the low overall baseline usage, disease outbreaks on a limited number of farms can have a substantial influence on national antimicrobial consumption statistics (Table 4.4).

Marked fluctuations in antimicrobial usage, both increases and decreases, are frequently attributable to disease outbreaks affecting multiple flocks within a single production unit [personal communication; Susanne Kabel, Danish Agriculture and Food Council].

Historically, the Danish VetStat surveillance system lacked the resolution to disaggregate antimicrobial usage data by specific poultry production types. This limitation was addressed through the revised VetStat system, which has enabled more granular reporting since June 2021. As longitudinal data accumulates, this enhancement will facilitate more precise monitoring of antimicrobial usage trends across distinct poultry production categories.

In 2025, total antimicrobial consumption in the poultry sector increased by 17.95% in terms of kilograms of active compound compared to 2024. By antimicrobial class, the use of pleuromutilins decreased by 99.13%, macrolides by 22.50%, and lincosamides by 1.98%, while the usage of beta-lactamase-sensitive penicillins increased by 66.39%, aminoglycosides by 64.64%, sulfonamides and trimethoprim by 38.84%, tetracyclines by 23.80%, and other penicillins by 12.63% (Table 4.4).

**Table 4.4 Consumption of antimicrobials in poultry, kg active compound, Denmark, 2016-2025** DANMAP 2025

| | Aminoglycosides | Amphenicols | Fluoroquinolones | Lincosamides | Macrolides | Other antimicrobials [a] | Other quinolones | Penicillins, beta-lactamase-sensitive | Penicillins, others | Pleuromutilins | Sulfonamides and trimethoprim | Tetracyclines | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2016 | 60.19 | 4.83 | - | 23.77 | 175.58 | 8.00 | - | 264.55 | 257.65 | 0.38 | 111.00 | 764.56 | 1670.51 |
| 2017 | 64.87 | 5.06 | - | 31.75 | 244.87 | - | 1.00 | 355.55 | 334.77 | 0.45 | 84.60 | 487.45 | 1610.37 |
| 2018 | 50.56 | - | - | 25.28 | 194.95 | - | - | 357.82 | 242.58 | 0.82 | 36.60 | 521.12 | 1429.73 |
| 2019 | 54.80 | 0.23 | 0.01 | 27.36 | 274.83 | - | - | 368.37 | 234.30 | 0.64 | 64.25 | 694.27 | 1719.07 |
| 2020 | 58.19 | - | - | 29.01 | 156.91 | - | - | 334.10 | 237.34 | 0.22 | 54.60 | 1590.93 | 2461.31 |
| 2021 | 58.87 | - | - | 27.69 | 168.64 | - | - | 115.38 | 204.10 | 0.38 | 34.80 | 656.61 | 1266.46 |
| 2022 | 50.42 | - | - | 14.98 | 433.96 | - | - | 232.70 | 139.88 | 19.38 | 12.60 | 442.43 | 1346.35 |
| 2023 | 50.23 | - | - | 15.28 | 176.34 | - | - | 315.90 | 203.06 | 16.88 | 31.20 | 496.92 | 1305.80 |
| 2024 | 51.15 | - | - | 21.65 | 232.94 | - | - | 155.68 | 302.75 | 14.38 | 72.60 | 289.78 | 1140.92 |
| 2025 | 84.21 | - | - | 21.22 | 180.54 | - | - | 259.02 | 341.00 | 0.12 | 100.80 | 358.76 | 1345.67 |

Data for 2025 were extracted from VetStat on 31 July 2026.
Combination drugs are divided into active compounds.
a) Other antibacterials also include other polymyxins.
A dash (-) indicates no antimicrobial usage, and 0.00 indicates a consumption less than 0.005.

### 4.3.4 Antimicrobial consumption in aquaculture, fur animals, and companion animals

**Aquaculture**

Antimicrobial consumption in aquaculture is mainly driven by summer air temperature and the number of hours of sunlight, because bacterial diseases are more likely to occur when water temperatures are high [Villumsen and Bojesen, 2022. Microbiol Spectr. 10(5):e0175222]. Although the aquaculture production continues to focus on developing improved vaccination strategies to reduce the risk of bacterial diseases requiring antimicrobial treatment, antimicrobial use varies significantly from year to year. In 2025, antimicrobial consumption decreased by 27.82% compared to the average consumption over the previous five years. The decrease was primarily due to decreased usage of combination products of sulfonamides and trimethoprim (Table 4.5).

In 2025, three antimicrobial classes were used to treat bacterial infections in aquaculture: 70.83% of sulfonamides and trimethoprim, 20.02% of other quinolones (oxolinic acid), and 8.90% of amphenicols (florfenicol) (Table 4.5).

**Companion animals - horses and pets**

The information available on antimicrobial consumption in companion animals is less precise than that available for production animals, since veterinarians are not required to report antimicrobial use for these animal species in VetStat. Table 4.6 shows the antimicrobial consumption registered for companion animals in three categories: Horses, Pets, and Unspecified.

The total amount of antimicrobials estimated for consumption in companion animals in 2025 was 2127.70 kg (Table 4.1 and 4.6). As in previous years, a substantial amount of sulfonamides and trimethoprim registered as used for pets or unspecified is an oral paste, a product normally used for horses. Thus, a substantial amount of sulfonamide/trimethoprim included in Table 4.6 is likely to have been used for horses (1114.05 kg in 2025).

A large proportion of antimicrobials for dogs and cats are prescribed for the treatment of chronic or recurrent diseases, mainly dermatitis. Due to the close contact between owners and their pets, repeated use of critically important antimicrobials may pose a risk to the owners, and the use of these antimicrobials is therefore monitored carefully.

Since the treatment guidelines by DVA were published in 2012 (revised in 2018), the use of cephalosporins has been reduced from 272.70 kg in 2012 to 42.03 kg of active compound in 2025. Pets accounted for 42.04% of all the cephalosporins consumed in animals (Table 4.1 and 4.6).

In 2025, the consumption of fluoroquinolones in companion animals, mainly dogs and cats, was 12.75 kg active compound (Table 4.1 and 4.6).

**Table 4.5 Consumption of antimicrobials in aquaculture, kg active compound, Denmark, 2016-2025** DANMAP 2025

| | Aminoglycosides | Amphenicols | Other antibacterials [a] | Other quinolones | Penicillins, beta-lactamase-sensitive | Penicillins, others | Sulfonamides and trimethoprim | Tetracyclines | Total |
|---|---|---|---|---|---|---|---|---|---|
| 2016 | - | 315.34 | - | 893.07 | - | 13.55 | 1085.88 | 0.40 | 2308.24 |
| 2017 | - | 350.26 | - | 636.81 | 0.04 | 35.02 | 679.34 | 0.10 | 1701.57 |
| 2018 | - | 323.47 | - | 899.34 | - | 51.58 | 2292.56 | 0.50 | 3567.45 |
| 2019 | - | 292.56 | - | 446.88 | - | 43.90 | 1720.93 | 22.00 | 2526.28 |
| 2020 | - | 341.19 | - | 565.26 | - | 27.05 | 1030.20 | 1.00 | 1964.70 |
| 2021 | - | 295.42 | 0.12 | 366.33 | 1.71 | 19.50 | 1088.90 | 1.42 | 1773.39 |
| 2022 | - | 143.85 | - | 366.53 | - | - | 1940.76 | 0.60 | 2451.74 |
| 2023 | - | 124.93 | - | 523.98 | - | - | 931.70 | - | 1580.61 |
| 2024 | 8.40 | 134.83 | - | 316.78 | - | - | 1352.08 | - | 1812.09 |
| 2025 | 1.40 | 123.10 | - | 277.00 | - | - | 979.85 | 2.00 | 1383.35 |

Data for 2025 were extracted from VetStat on 31 July 2026.
Combination products are split into active compounds.
a) Other antibacterials also include lincosamides.
A dash (-) indicates no antimicrobial usage, and 0.00 indicates a consumption less than 0.005.

**Table 4.6 Estimated consumption of antimicrobials for horses, pets and unspecified animals, kg active compound, Denmark, 2016-2025**

DANMAP 2025

| | Aminoglycosides | Amphenicols | Cephalosporins | Fluoroquinolones | Lincosamides | Macrolides | Other antimicrobials [a] | Other quinolones | Penicillins, beta-lactamase-sensitive | Penicillins, others | Pleuromutilins | Sulfonamides and trimethoprim | Tetracyclines | Total |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Horses** | | | | | | | | | | | | | | |
| 2016 | 0.78 | - | 0.13 | 0.01 | - | - | 0.01 | - | 5.21 | 0.02 | - | 108.02 | 5.30 | 119.48 |
| 2017 | 0.86 | 0.09 | 0.11 | 0.00 | - | - | 0.01 | - | 5.38 | 0.06 | - | 106.44 | 2.98 | 115.93 |
| 2018 | 0.70 | 0.04 | 0.15 | - | - | 0.08 | 0.02 | - | 5.96 | 0.01 | - | 100.56 | 3.78 | 111.31 |
| 2019 | 0.95 | - | 0.08 | 0.00 | - | 0.02 | 0.01 | - | 4.92 | 0.09 | - | 94.19 | 3.82 | 104.08 |
| 2020 | 1.71 | - | 0.00 | 0.00 | - | - | 0.01 | - | 5.32 | 0.03 | - | 111.46 | 3.52 | 122.05 |
| 2021 | 0.20 | - | 0.01 | 0.00 | 0.00 | 0.02 | 0.05 | - | 5.19 | 0.13 | - | 106.03 | 1.99 | 113.61 |
| 2022 | 0.35 | 0.00 | 0.04 | 0.00 | 0.02 | 1.00 | 0.15 | - | 5.07 | 0.39 | - | 137.09 | 7.32 | 151.43 |
| 2023 | 0.30 | 0.00 | 0.01 | 0.02 | 0.01 | - | 0.24 | - | 5.91 | 0.57 | - | 167.02 | 7.67 | 181.75 |
| 2024 | 0.61 | - | 0.02 | 0.00 | 0.00 | 0.01 | 0.15 | - | 6.72 | 0.17 | - | 166.84 | 6.88 | 181.39 |
| 2025 | 4.01 | 0.00 | 0.02 | 0.00 | 0.00 | - | 0.21 | - | 7.04 | 0.22 | - | 174.22 | 14.24 | 199.97 |
| **Pets** | | | | | | | | | | | | | | |
| 2016 | 3.39 | 0.43 | 55.31 | 5.38 | 21.78 | 2.31 | 1.46 | 0.06 | 9.81 | 131.16 | 0.25 | 269.09 | 21.49 | 521.91 |
| 2017 | 3.80 | 0.70 | 41.70 | 5.22 | 18.38 | 1.66 | 2.18 | - | 9.16 | 125.79 | 0.12 | 272.44 | 19.34 | 500.49 |
| 2018 | 3.93 | 0.28 | 35.86 | 4.94 | 17.51 | 1.66 | 5.98 | 1.00 | 10.00 | 113.72 | 0.50 | 253.22 | 21.12 | 469.71 |
| 2019 | 3.73 | 0.26 | 32.33 | 4.45 | 17.19 | 7.35 | 6.08 | - | 10.35 | 108.43 | 0.62 | 236.83 | 14.79 | 442.42 |
| 2020 | 4.34 | 0.56 | 30.68 | 5.06 | 19.07 | 3.84 | 7.52 | - | 12.88 | 103.42 | 0.50 | 262.32 | 17.75 | 467.92 |
| 2021 | 3.20 | 0.67 | 27.98 | 4.74 | 19.25 | 2.16 | 9.34 | - | 11.46 | 100.15 | 0.12 | 270.77 | 23.66 | 473.50 |
| 2022 | 1.69 | 0.01 | 22.30 | 3.87 | 16.48 | 0.23 | 10.51 | - | 9.39 | 79.53 | 0.12 | 165.50 | 22.26 | 331.89 |
| 2023 | 2.21 | 0.64 | 21.56 | 4.31 | 17.72 | 2.19 | 10.15 | - | 10.02 | 86.54 | 0.16 | 194.37 | 18.81 | 368.68 |
| 2024 | 1.38 | 0.12 | 16.69 | 4.15 | 16.88 | 0.36 | 10.29 | - | 8.45 | 89.17 | 0.12 | 206.62 | 18.34 | 372.57 |
| 2025 | 1.73 | 0.22 | 17.24 | 4.11 | 16.39 | 0.36 | 10.30 | - | 7.82 | 80.28 | 0.38 | 158.00 | 22.67 | 319.49 |
| **Unspecified** | | | | | | | | | | | | | | |
| 2016 | 37.45 | 0.38 | 81.64 | 9.71 | 48.91 | 0.27 | 2.72 | - | 2.21 | 455.07 | - | 1015.35 | 17.02 | 1670.73 |
| 2017 | 33.22 | 0.21 | 69.14 | 9.27 | 50.12 | 0.00 | 5.24 | - | 1.94 | 456.72 | - | 1071.67 | 14.71 | 1712.25 |
| 2018 | 36.52 | 1.32 | 61.41 | 9.76 | 45.80 | - | 11.75 | - | 1.84 | 441.45 | - | 1136.63 | 12.96 | 1759.42 |
| 2019 | 35.36 | 0.23 | 60.64 | 9.87 | 48.83 | 0.13 | 14.05 | - | 1.90 | 434.53 | 0.12 | 1140.68 | 16.04 | 1762.40 |
| 2020 | 28.29 | 0.42 | 56.90 | 10.70 | 52.24 | 0.06 | 15.84 | - | 2.90 | 440.04 | - | 1221.66 | 15.65 | 1844.69 |
| 2021 | 21.40 | 0.39 | 49.36 | 10.11 | 57.52 | - | 20.86 | - | 0.79 | 451.35 | - | 1284.34 | 14.46 | 1910.59 |
| 2022 | 1.28 | 0.40 | 38.82 | 8.76 | 54.30 | - | 24.94 | - | - | 389.36 | - | 1100.12 | 11.94 | 1629.92 |
| 2023 | 1.04 | 0.41 | 36.93 | 8.73 | 55.63 | - | 22.99 | - | - | 385.05 | - | 1233.67 | 12.82 | 1757.26 |
| 2024 | 0.91 | 0.39 | 29.29 | 8.83 | 58.61 | - | 19.28 | - | - | 381.47 | - | 1202.96 | 12.85 | 1714.60 |
| 2025 | 0.66 | 0.37 | 24.77 | 8.64 | 56.24 | - | 18.46 | - | - | 372.49 | - | 1114.05 | 12.56 | 1608.24 |

Data for 2025 were extracted from VetStat on 31 July 2026.
Combination products are split into active compounds.
The estimates include all veterinary approved antimicrobials for use in horses, pets, as well as products without a specified animal species (unknown).
a) Other antibacterials also include other otologicals, pleuromutilins, polymyxins, and sulfonamides (plain).
A dash (-) indicates no antimicrobial usage, and 0.00 indicates a consumption less than 0.005.

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## Textbox 4.1

# VetStat: 25 Years of Monitoring Veterinary Antimicrobial Use

The overall purpose of the Danish database VetStat is to support the monitoring and prudent use of veterinary medicinal products through the collection of data on prescription medicine use, thereby contributing to the fight against antimicrobial resistance and promoting a One Health approach. VetStat has been in operation for 25 years. Over time, it has evolved from a research database into a cornerstone of Danish surveillance of veterinary antimicrobial use and an essential data source for DANMAP and international reporting.

**Establishment of VetStat**

A national register to collect data on veterinary use of prescription medicine was conceived in the late 1990s following the phase-out of antimicrobial growth promoters in the Danish animal production, partly to monitor trends in antimicrobial use. VetStat was subsequently developed in 1999 by the Danish Technical University (DTU) and launched in 2000. Initially, the database and its data were maintained by DTU and the main use of data was for research purposes, including the relationship between antimicrobial use and antimicrobial resistance, and as the foundation for DANMAP's chapters on antimicrobial use.

**From Research Tool to Regulatory Instrument**

After a rise in the veterinary use of antibiotics up throughout the 2000s it was decided, that the data in VetStat should be used more actively in policy making and initiatives. As a result, the responsibility for maintaining VetStat and its data was transferred from DTU to the Danish Veterinary and Food Administration (DVFA) in 2011. One of the most prominent examples of the regulatory use of VetStat data was the Yellow Card Initiative, targeting the highest users of antibiotics in the Danish pig production. VetStat also became an important tool for monitoring progress in national efforts to reduce antimicrobial use in animal production. Even though the responsibility was transferred from academia to the public sector, the data in VetStat continued and continues to play a key role in DANMAP and academic research into national antimicrobial use and resistance.

**Modernization and Improved Data Quality**

In 2017 it was decided that VetStat required modernization, both in terms of the user interface, improving data quality, balancing data access, and complying with increasing IT security demands. Additionally, it was decided to merge VetStat with the DVFA's register of authorized veterinarians, VetReg, to support data validation and user access management. The modernization of VetStat took place from 2018 to 2021 and the new platform was launched on 1 June 2021. Among other things, the modernized platform introduced improved data granularity regarding where medicine is being used, data quality validation, and improved data on intended animal species - especially for poultry and aquaculture. Even after its launch, New VetStat has continuously been improved and refined to enhance data quality, provide greater insights on medicine use, and support evolving regulatory needs.

**Future Developments and Reporting Requirements**

Apart from data in VetStat being used nationally in DANMAP, it also provides the foundation for Denmark's international reporting to the World Organization of Animal Health (WOAH) and to the European Union's European Sales and Use of Antimicrobials for Veterinary Medicine (ESUAvet) initiative. Especially the latter will expand VetStat's coverage of antimicrobial use in horses and companion animals, further strengthening national and international surveillance. ESUAvet will start collecting data on antimicrobial use in horses from 2027 and in companion animals from 2030, meaning that data must be collected in 2026 and 2029, respectively.

VetStat already collects sales data from pharmacies anytime prescription medicine is being sold for use in horses and companion animals; however, the total use data is incomplete, as veterinarians are currently not obligated to report their use of antimicrobials for these animal species. To meet these reporting requirements, equine veterinarians will be required to report their use of antimicrobials from 2027, followed by mandatory reporting for companion animal veterinarians from 2029. Additionally, sales for use in companion animals are currently reported collectively, but as ESUAvet requires antimicrobial use to be specified for dogs and cats, the reporting requirements for companion animals will have to follow suit.

As reporting requirements continue to expand, VetStat will remain a central tool for surveillance, research, and policy development related to veterinary antimicrobial use in Denmark.

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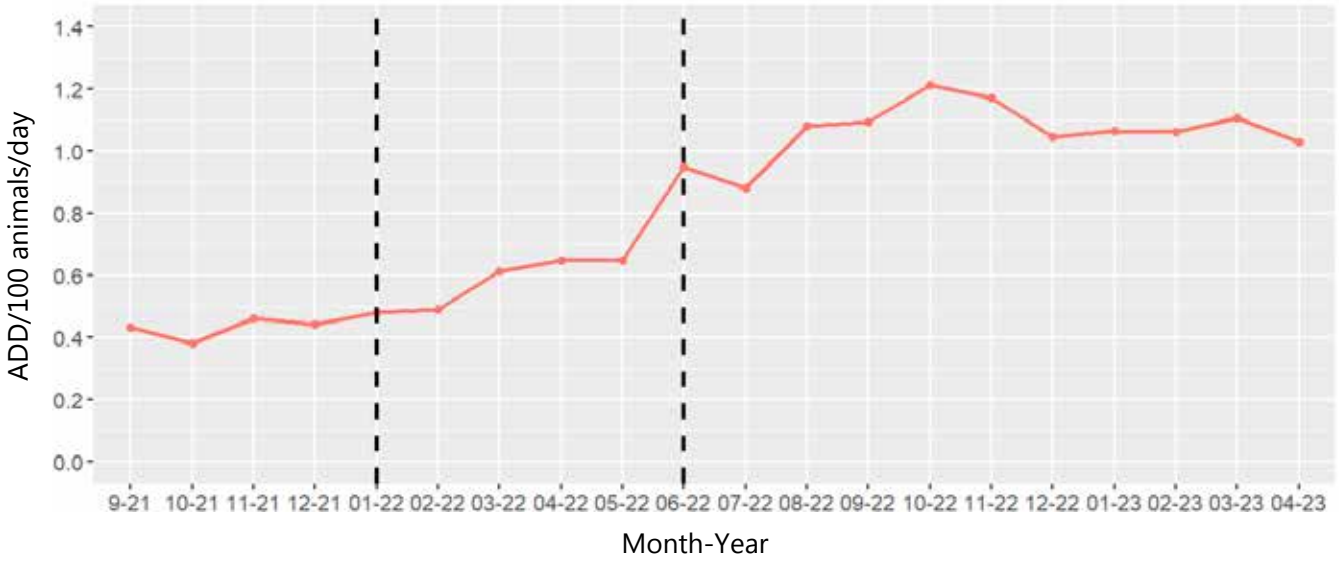
## Textbox 4.2

# Effect of the new Veterinary Medicinal Products Regulation on the antimicrobial use in Danish Weaners

The new Veterinary Medicinal Product Regulation came into force in January 2022. In June same year, medicinal zinc oxide was phased out and an increase in the national yearly antimicrobial use (AMU) was seen between 2021 and 2022. The increase in AMU was mainly driven by an increase in use of products prescribed for gastrointestinal indications in weaners. Medicinal zinc oxide was widely used in the Danish pig production to prevent post weaning diarrhoea. Thus, it seems reasonable to attribute the increase in AMU to the phasing out of medicinal zinc oxide. However, with the new regulation, the veterinarians were obliged to prescribe antimicrobials in accordance with the Summary of Product Characteristics (SPC). In Denmark, many antimicrobial products were prescribed with a shorter treatment duration than stated in the SPC. This was to keep the AMU as low as possible and below the yellow card limits. With the new regulation, this was not allowed, and the expectation was that the individual farmer would either increase AMU due to a longer treatment duration or change to products with a shorter treatment duration.

VetStat data were analysed to investigate the effect of the new Veterinary Medicinal Products Regulation on AMU for Danish Weaners on a monthly national. Data consisted of all antimicrobial products prescribed for oral administration and gastrointestinal indications in weaners from January 2020 – December 2023. The AMU was measured in ADD per 100 animals per day and the percentage changes in antimicrobial use between 2021 and 2022 were calculated for each product. The project focused on the products with an increase in use above 50% or a decrease in use below 50%. Veterinarians in Danish pig practice were consulted about the previous treatment regimens for the specific products, and this was compared with the requirements in the SPC.

**Figure 1 Monthly prescriptions of *Neomay* for gastrointestinal indications in weaners** DANMAP 2025




Monthly prescriptions of the antimicrobial product Neomay (active ingredient is Neomycin) in the period from September 2021 to April 2023. National prescriptions are summarised per month and measured in ADD per 100 animals per day. The first dotted line marks the New Veterinary Medicinal Product regulation coming into force (January 2022). The second dotted line marks the phasing out of medicinal zinc oxide (June 2022).

The use of *Doxycyclin "ScanVet" Vet.* increased with 500% from 2021-2022. The products *Apravet, Neomay* and *Lismay* increased with 171%, 121% and 88%, respectively. The use of *Octacillin Vet.* decreased with 79%. The use of *Doxx-Sol* decreased with 91% for gastrointestinal indications, but increased equally for respiratory indications, which is the officially approved indication for *Doxx-Sol*. These changes were observed already before the phasing out of medicinal zinc oxide, which could indicate an effect of the new regulation. The veterinarians who were consulted confirmed that the changes seen could be attributed to the difference between the previous treatment regimens and the SPC for these products. For example, for *Neomay*, the SPC requires a treatment duration of 3-4 days, which according to the veterinarians was previously used in a double dose but only as a one-day treatment. The change in monthly prescriptions for *Neomay* is illustrated in Figure 1.

A further increase was seen after the phasing out of medicinal zinc oxide, which again can be attributed to more farmers implementing longer treatment duration, but also to an increased need for treatment when weaning pigs without the use of medicinal zinc oxide.

This project was part of the veterinary contingency work carried out by the VetStat cluster at University of Copenhagen under the veterinary public service agreement. The results are presented in this report (In Danish): https://dkvet.dk/rapporter/Analyse af veterin rl gemiddelforordningens art. 106 stk 1s p virkning p udviklingen af antibiotikaforbrug til grise.pdf.

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## Textbox 4.3

# Challenges in quantifying and presenting cattle antimicrobial use: Insights from studies of Danish rosé veal calf farms

Monitoring antimicrobial use (AMU) is essential for antimicrobial stewardship. However, quantifying and presenting AMU can be challenging. Measures such as the weight of active compound and standardised doses are commonly used and related to the population at risk, as in DANMAP. Antimicrobial use is frequently stratified by species, age groups, or indication. Understanding how quantified AMU reflects the underlying on-farm use can provide valuable context for interpreting the reported results.

As part of the PhD project *Improving quantification and understanding of patterns in antimicrobial use in Danish cattle*, VetStat data on antimicrobial sales for cattle were combined with treatment records and observations collected in a field study of Danish rosé veal farms. Experiences from this project are summarised in three key points:

**Transparency in quantification methods is crucial**
Methods used to quantify AMU vary and, in some cases, differ even when using the same data. For example, data from VetStat form the basis of both DANMAP and VetStat reports, yet the definition and calculations of animal daily doses differ between the two. In VetStat, a daily dose per kilogram live weight of an animal is defined for each unique product, whereas DANMAP defines daily doses for active compounds. Furthermore, the standardised animal is based on an assigned fixed weight in VetStat and on average live weight in DANMAP.

Additional factors that may influence animal daily dose calculations include dosage intervals, age-specific dosing recommendations, and durations of effect that are shorter or longer than one day. The approach to standardising a dose is not always clearly communicated. Consequently, an animal daily dose is the result of a series of methodological decisions, and differences in approach may significantly affect the summarised statistics presented. Transparency regarding methodological choices is therefore essential.

**The composition of groups should be considered when making comparisons**
AMU can be presented in many ways. Stratification by species, age groups, or indications preserves information that might otherwise be lost in aggregated summaries. Applying meaningful subgroups and maintaining clear, concise, and relevant reporting is a continuous balancing exercise.

Stratification choices can influence comparisons and benchmarking across farms, sectors, and national borders. Age groups provide a relevant example. In VetStat, the group 'calves' includes all animals younger than one year of age and is assigned a standard weight of 200 kg. Calves undergo a substantial weight gain during the first year, which is likely to affect the AMU estimates, as doses for most systemic antibiotics are calculated based on body weight. Using a standard weight is not inherently problematic, as it is merely a standardisation method applied equally across farms. Challenges arise when comparing farms, sectors, production types, and populations with marked differences in age distribution and, consequently, body weight at treatment.

Different treatment patterns can also pose a challenge for comparisons. Different production types or stages of production are often associated with different disorders. In VetStat, treatments for omphalitis (navel infection) and interdigital phlegmon (a hoof infection) are registered in the same indication group but they typically appear at different stages of a calf's life. When comparing AMU, the composition of the population within each stratified group should always be carefully considered.

**Standardisation helps identify patterns, but reality is often more complex**

Quantifying and standardising allow summaries of complex data across farms, regions, and borders in a more approachable way. This provides valuable insights into overall trends and patterns.

Results from studies in this project showed that the individual farm was an important explanatory factor for both the level of AMU and the way antimicrobials were used. Differences between farms were both visually and statistically significant. Each farm had its own strengths and challenges regarding antimicrobial use. These findings highlight the importance of farmers and local conditions in the ongoing effort to understand and evaluate AMU. The project was part of the veterinary contingency work carried out by the VetStat cluster at University of Copenhagen under the veterinary public service agreement. The project was co-funded by the Danish Cattle Levy Fund.

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# 5.

# Antimicrobial consumption in humans

# 5. Antimicrobial consumption in humans

## Highlights

Antimicrobial consumption in Denmark has been monitored in DANMAP since 1996. During the initial years of surveillance, the consumption was estimated to be 13-14 DDD per 1000 inhabitants per day (DID). From 2001 consumption increased markedly and continuously, reaching its peak of 18,90 DID in 2011, an increase of more than 30%. Since 2011 consumption has decreased again. In 2025, antimicrobial consumption was 15.35 DID, 12.4% lower than consumption in 2016 (17.53 DID) and 6% lower than in 2024 (16.27 DID). Use of the AWaRe classification of antimicrobials on consumption in Denmark shows that 82% in 2025 consisted of access antimicrobials (WHO´s goal is minimum 60% access antimicrobials).

**In primary health care**, total antimicrobial consumption was 13.48 DID in 2025, 6% lower than in 2024 (14.35 DID) and 14% lower than in 2016 (15.67 DID). The four groups of penicillins constituted 65% of the total antimicrobial consumption and beta-lactama sesensitive penicillins were the most used antimicrobials (accounting for 24% of total consumption in primary health care).

**Antimicrobials prescribed for children** decreased in 2025: among the 0–4-year-olds, consumption was on average 203 treated patients per 1,000 inhabitants, a 12% decrease compared to 230 in 2024. For the 5–9-year-olds, 118 patients per 1,000 inhabitants were treated in 2025 compared to 172 in 2024 (32% decrease). The years 2022 and 2023 had seen severe and prolonged outbreaks of both Group A streptococci and *Mycoplasma pneumoniae* infections in children, as well as high rates of viral infections, in particular early and more severe RSV and influenza seasons. The decrease in consumption in 2024 and 2025 highlights a return to lower rates of respiratory infections.

**Older inhabitants** living in care homes during 2025 continued to receive notably more antimicrobials than older inhabitants living in their own homes. Urinary tract infections were the main indication driving the high treatment frequency at care homes (991 versus 433 prescriptions for urinary tract infections per 1,000 older inhabitants, respectively, in 2025).

**Antimicrobial consumption in hospital care** was 1.87 DID in 2025. When accounting for hospital activity, the consumption in 2025 was 144.7 DDD per 100 bed-days (DBD) and 540.7 DDD per 100 admissions (DAD), similar to the consumption in 2024. However, consumption of combinations of penicillins, including beta-lactamase inhibitors, decreased since 2024 (4-5% in 2025) after several years of increasing consumption. Over the decade, the overall hospital consumption at acute care hospitals has increased by 56% and 23%, when measured in DBD and DAD, respectively.

## 5.1 Introduction

In Denmark, antimicrobials are available by prescription from medical doctors, veterinarians and dentists. Sale is restricted to licensed pharmacies that have exclusive rights to sell medicine on prescription. No over-the-counter sale takes place. All consumption of medicinal products for humans is recorded through the Register of Medicinal Product Statistics at the Danish Health Data Authority (see Figure 2.1). This includes sales data from all public and private healthcare providers. Antimicrobial sales data have been submitted from the primary care sector since 1994 and from the hospital sector since 1997.

Registration of medicine consumption in the primary care sector covers sales from pharmacies to individuals and private clinics. Sales data contain an identifier of the prescriber and the patient in addition to information about the prescribed antimicrobial. This includes the ATC code, formulation, package size and number of packages sold. Since 2004, the Register of Medicinal Product Statistics also receives information about the indication on prescriptions. This allows a very detailed and near-complete surveillance of all systemic antimicrobials used in Denmark in primary health care.

For the hospital sector, antimicrobial consumption data from all public somatic hospitals with an acute care function (referred to as somatic hospitals) are included in the report. Data from psychiatric hospitals, private hospitals and hospices are excluded, since they only account for a minor share of antimicrobial consumption and no reliable denominator for measuring antimicrobial consumption in these facilities is available.

In this chapter, the term 'antimicrobials' covers all systemic antibacterial agents for human use listed in the Anatomical Therapeutic Chemical (ATC) Classification under the code J01. Metronidazole (ATC code P01AB01) and for hospitals vancomycin (ATC code A07AA09) have been included since 2014. Consumption of tuberculostatica, antifungal drugs and antivirals are not included.

The Danish Healthcare system has undergone changes in recent years, which has led to functions being reassigned from hospitals to ambulatory care and further on to smaller health units, rehabilitation centers and general practice. Based on the recommendations from The Danish Resilience Commission, September 2023, future changes will include the establishment of regional and local health councils and the merger of the Capital Region and Region Zealand as from January 2027. In addition, psychiatry will administratively be placed together with the somatic functions, which means that data and registers from these functions are expected to also be merged in the future. Such changes in organization may impact consumption trends per healthcare sector but may also demand rethinking of commonly used denominators such as DDD per bed-day or per admission.

For over 30 years, larger Danish hospitals have driven diagnostically anchored antimicrobial stewardship (AMS) through their Departments of Clinical Microbiology. In recent years, this framework has expanded via infectious disease specialists enrolling in AMS training programs and establishing dedicated AMS teams across clinical wards.

In 2017, the Danish Regions developed criteria on better use of critically important antibiotics via the Danish Learning and Quality Teams. This led to the establishment of antibiotic committees locally and across the Regions.

Concurrently, primary care initiatives have been supported by the Danish Research Center for General Medicine and the Association of General Practitioners.

The new Danish National Action Plan against antimicrobial resistance in humans from June 2025 aims to further strengthen the work. The action plan is monitored in the separate publication "Perspectives of DANMAP 2025".

## 5.2 Total antimicrobial consumption in the Danish healthcare system

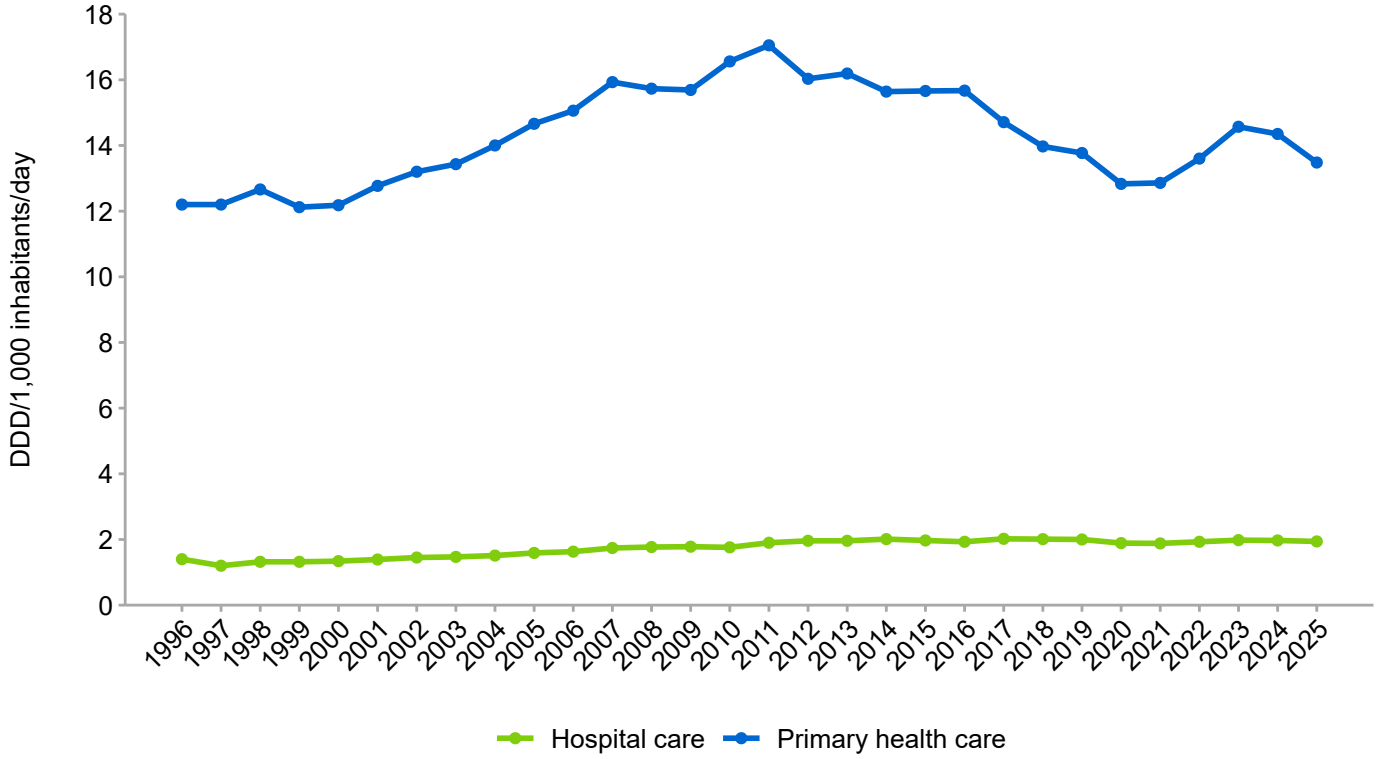
During the first five years of surveillance from 1996 to 2000, the consumption of systemic antimicrobials in Denmark showed no significant changes and consumption was estimated to be 13 to 14 Defined Daily Doses per 1,000 inhabitants per day (DID), (Figure 5.1). Data are not fully comparable to later years' reporting due to changes in data collection and systems.

From 2001 to 2011, consumption increased steadily and peaked at a total of 18.95 DID (34%). From 2011 to 2025, consumption decreased overall (-19% compared to 2011), albeit with more fluctuations, the most notable being a marked drop during the COVID-19 pandemic, followed by an equally marked resurgence during 2022 and 2023. The observed decreases were driven by reduced prescribing in primary care, which accounts for 88% of antibiotic consumption in Denmark (Figure 5.2).

For comparison, antimicrobial consumption at hospitals fluctuated more, moving between the highest level of 1.95 DID in 2017 and the lowest level of 1.81 DID in 2021. The notably lower consumption in 2020 and 2021 is considered an exception due to the COVID-19 pandemic.

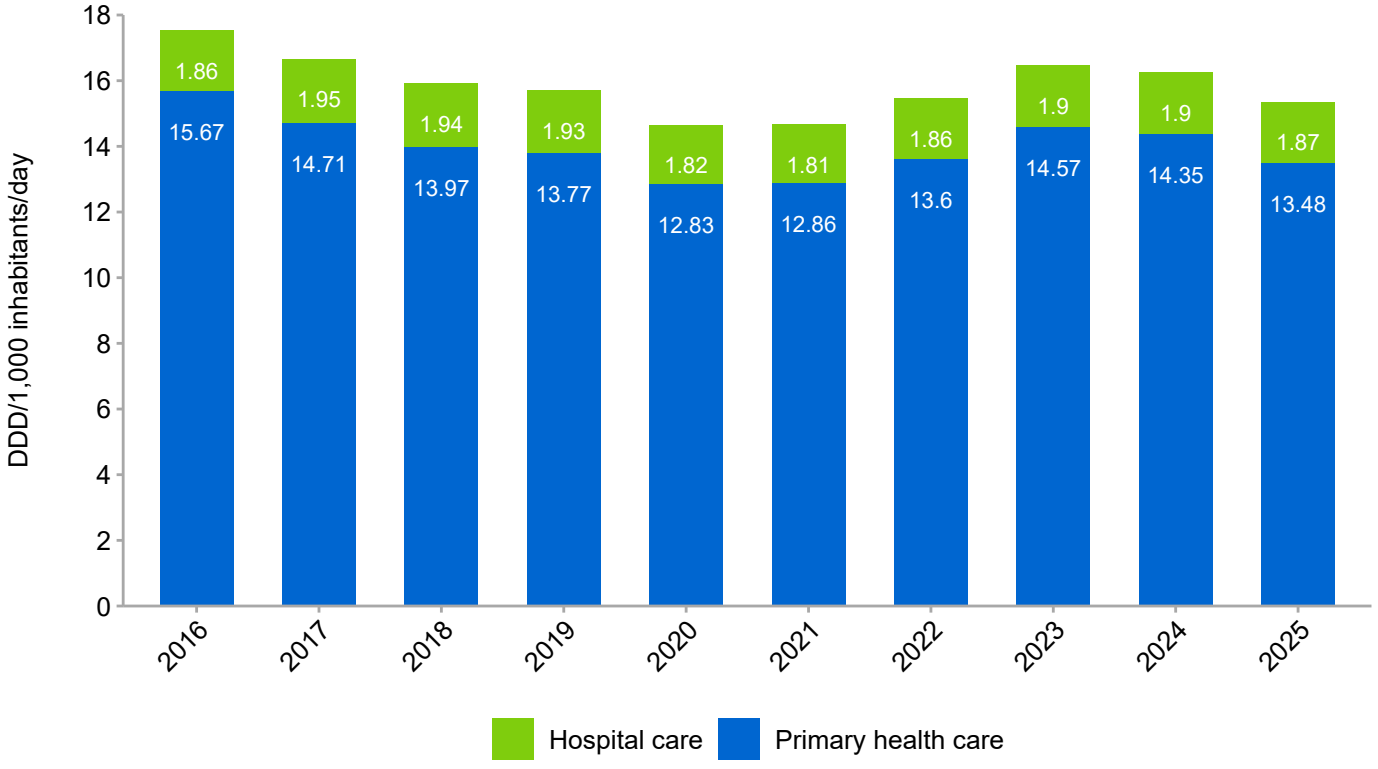
The total consumption of antimicrobials in primary health care and at somatic hospitals in the five Danish health regions is presented in Figure 5.3. The trends in consumption are similar for all five regions. Region Zealand showed the highest total consumption of 16.12 DID in 2025, whereas the Central Region of Denmark had the lowest total consumption of 13.67 DID. Figure 5.4 presents the drug classes used in primary health care and at hospitals; both sectors show a high share of penicillins in their usage patterns. Broad-spectrum antibiotics, such as cephalosporins, aminoglycosides and carbapenems, are predominantly used in hospitals. Assessed by WHO's Access, Watch and Reserve (AWaRe) classification system, "access antimicrobials" have constituted at least 80% since 2014 and constituted 82% in 2025.

**Figure 5.1 Antimicrobial agents in Danish healthcare system, DDD per 1,000 inhabitants per day, Denmark, 1996-2025** DANMAP 2025



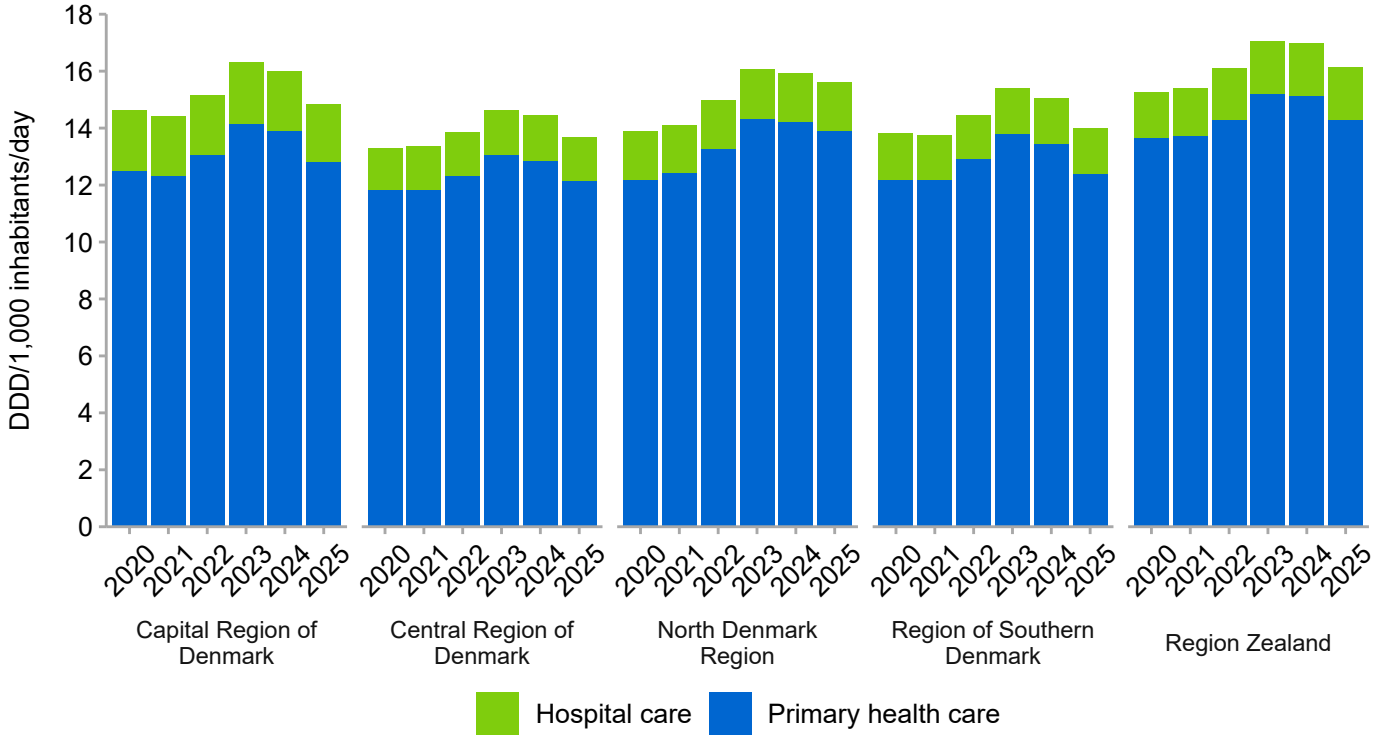

Data: Sales of antimicrobials in Denmark.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

**Figure 5.2 Total consumption of systemic antimicrobial agents in humans per health care sector, DDD per 1,000 inhabitants per day, Denmark, 2016-2025** DANMAP 2025



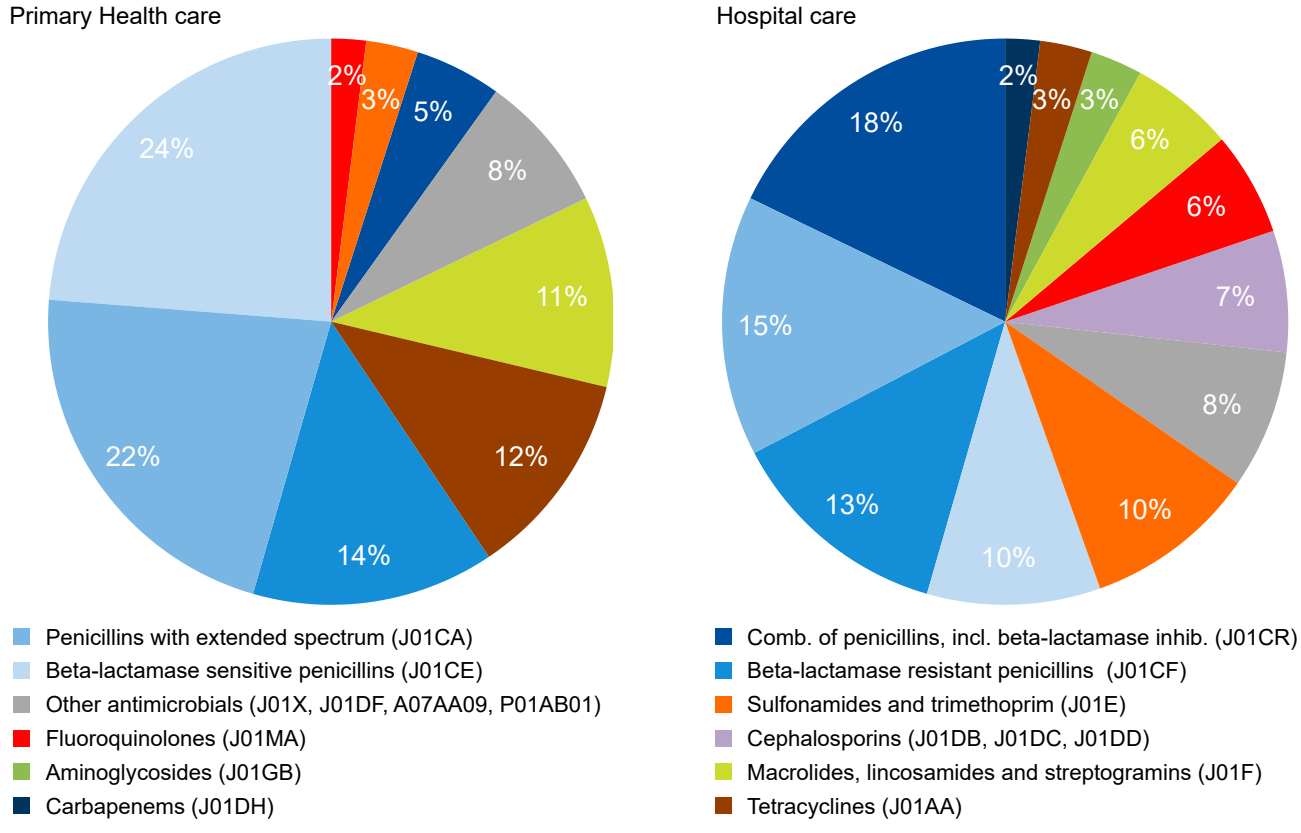

Data: Sales of antimicrobials in Denmark.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

**Figure 5.3 Consumption of systemic antimicrobial agents in primary health care and somatic hospitals, DDD per 1,000 inhabitants per day, Danish regions, 2020-2025**
DANMAP 2025




Data: Registered sales of antimicrobials to individuals and to somatic hospital departments.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

**Figure 5.4 Percentage distribution of antimicrobial agent groups in primary health care and hospital care, DDD, Denmark, 2025**
DANMAP 2025




Data: Registered sales of antimicrobials to individuals and to somatic hospital departments.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

## 5.3 Antimicrobial consumption in primary health care

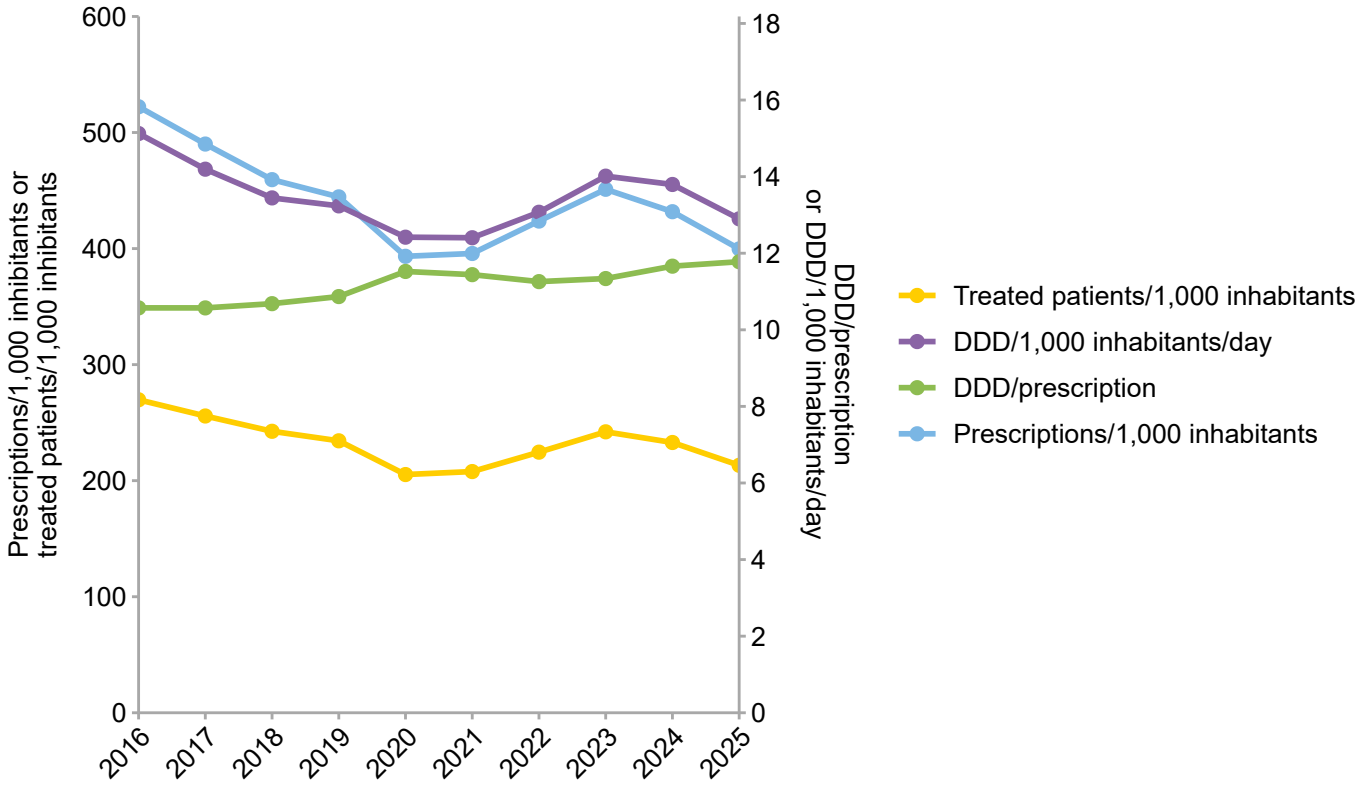
In the following sections, the consumption of antimicrobials in primary health care is described by the units DDD per 1,000 inhabitants per day, number of prescriptions per 1,000 inhabitants and number of treated patients per 1,000 inhabitants. Data are based on sales to individuals and do not include the approximately 4% of antimicrobials, mainly penicillins, sold to clinics and doctors on call (out-of-hours service).

### 5.3.1 Overall antimicrobial consumption in primary health care

Comparison of trends over time by different indicators showed decreases in the number of treated patients and issued prescriptions from 2014-2020, no change from 2020-2021 and increased consumption from 2021-2023 (Figure 5.5). In 2025, an average of 213 patients per 1,000 inhabitants were treated and 400 prescriptions per 1,000 inhabitants were issued (7-8% lower than in 2024). The number of DDD per 1,000 inhabitants was 12.90 (6.5% lower than in 2024).

A decade earlier, in 2016, the number of treated patients per 1,000 inhabitants was 270, the number of prescriptions per 1,000 inhabitants was 522, and the number of DDD per 1,000 inhabitants was 15.13 (Table 5.1, Table 5.2 and Table 5.3). The change in the number of treated patients and issued prescriptions over the decade corresponds to a 21% and a 24% decrease, respectively. However, doses per prescription have increased, primarily due to a switch to antibiotics that contribute with more DDDs per treatment, e.g., the switch to pivmecillinam as the drug of choice for the treatment of urinary tract infections and the switch to tetracycline as the drug of choice for the treatment of chlamydia.

**Figure 5.5 Consumption of systemic antimicrobial agents in primary health care, Denmark, 2016-2025** DANMAP 2025




Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

**Table 5.1 Consumption of antimicrobial agents for systemic use in primary health care, DDD per 1,000 inhabitants per day, Denmark, 2006 and 2016-2025**

DANMAP 2025

| ATC group | Therapeutic group | 2006 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| J01CA | Penicillins with extended spectrum | 2.55 | 3.33 | 3.36 | 3.35 | 3.28 | 3.19 | 3.17 | 3.26 | 3.28 | 3.05 | 2.96 |
| J01CE | Beta-lactamase sensitive penicillins | 5.41 | 4.16 | 3.88 | 3.61 | 3.44 | 2.84 | 2.89 | 3.23 | 3.96 | 3.49 | 3.20 |
| J01CF | Beta-lactamase resistant penicillins | 1.05 | 1.48 | 1.56 | 1.6 | 1.63 | 1.58 | 1.61 | 1.72 | 1.78 | 1.85 | 1.83 |
| J01CR | Combinations of penicillins, including beta-lactamase inhibitors | 0.08 | 0.95 | 0.79 | 0.66 | 0.63 | 0.52 | 0.55 | 0.63 | 0.71 | 0.74 | 0.65 |
| J01D | Cephalosporins and other betalactam antibiotics | 0.03 | 0.03 | 0.03 | 0.03 | 0.03 | 0.03 | 0.03 | 0.02 | 0.02 | 0.02 | 0.02 |
| J01EA | Trimethoprim and derivates | 0.47 | 0.56 | 0.56 | 0.53 | 0.45 | 0.43 | 0.42 | 0.39 | 0.41 | 0.35 | 0.34 |
| J01EB | Short-acting sulfonamides | 0.35 | 0.16 | 0.15 | 0.14 | 0.13 | 0.11 | 0.09 | 0.09 | 0.08 | 0.07 | 0.03 |
| J01EE | Combination of sulfonamides and trimethoprim, including derivates | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.01 | 0.01 | 0.01 | 0.01 |
| J01FA | Macrolides | 2.33 | 1.82 | 1.62 | 1.46 | 1.41 | 1.15 | 1.11 | 1.17 | 1.3 | 1.57 | 1.34 |
| J01FF | Lincosamides | 0.02 | 0.06 | 0.06 | 0.06 | 0.06 | 0.07 | 0.07 | 0.07 | 0.08 | 0.09 | 0.09 |
| J01GB | Aminoglycosides | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 |
| J01MA | Fluroquinolones | 0.37 | 0.48 | 0.44 | 0.41 | 0.37 | 0.33 | 0.32 | 0.34 | 0.33 | 0.30 | 0.30 |
| J01XC | Steroid antibacterials (combination fusidic acid) | 0.01 | 0.01 | 0.01 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| J01XE | Nitrofuran derivates (nitrofurantoin) | 0.47 | 0.43 | 0.26 | 0.15 | 0.27 | 0.27 | 0.28 | 0.27 | 0.12 | 0.19 | 0.22 |
| J01XX | Other antibacterials (metheamine >99%) | 0.27 | 0.27 | 0.28 | 0.29 | 0.32 | 0.34 | 0.39 | 0.43 | 0.47 | 0.55 | 0.64 |
| J01AA | Tetracyclines | 1.38 | 1.62 | 1.42 | 1.4 | 1.48 | 1.69 | 1.64 | 1.7 | 1.74 | 1.83 | 1.59 |
| J01XD and P01AB01 | Imidazole derivatives and metronidazole | 0.22 | 0.28 | 0.25 | 0.24 | 0.24 | 0.23 | 0.24 | 0.24 | 0.25 | 0.21 | 0.24 |
| J01 and P01AB01 | All antimicrobial agents for systemic use | 15.02 | 15.65 | 14.68 | 13.94 | 13.75 | 12.79 | 12.82 | 13.58 | 14.55 | 14.33 | 13.47 |

Data: Registered sales in primary health care.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

**Table 5.2 Number of treated patients per 1,000 inhabitants for leading antimicrobial agents in primary health care, Denmark, 2006 and 2016-2025**

DANMAP 2025

| ATC group | Therapeutic group | 2006 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| J01AA | Tetracyclines | 12.25 | 11.04 | 10.35 | 9.69 | 10.10 | 14.43 | 12.99 | 13.64 | 14.06 | 13.42 | 11.91 |
| J01CA | Penicillins with extended spectrum | 75.78 | 74.05 | 74.04 | 73.56 | 71.97 | 67.14 | 68.60 | 71.45 | 72.42 | 66.04 | 64.58 |
| J01CE | Beta-lactamase sensitive penicillins | 171.29 | 125.69 | 119.32 | 110.90 | 104.70 | 84.93 | 87.69 | 100.09 | 116.67 | 105.69 | 95.38 |
| J01CF | Beta-lactamase resisistant penicillins | 29.38 | 29.70 | 29.96 | 31.10 | 31.06 | 30.52 | 30.89 | 32.92 | 33.77 | 33.42 | 33.34 |
| J01CR | Combinations of penicillins, incl. beta-lactamase inhibitors | 2.27 | 22.17 | 19.89 | 17.73 | 17.33 | 14.43 | 15.50 | 17.90 | 20.28 | 21.16 | 19.70 |
| J01E | Sulphonamides and trimethoprim | 36.56 | 21.17 | 19.87 | 18.42 | 16.63 | 15.04 | 13.66 | 12.67 | 12.47 | 10.50 | 8.09 |
| J01FA | Macrolides | 67.03 | 53.21 | 46.01 | 40.11 | 38.45 | 25.13 | 24.97 | 27.16 | 30.06 | 38.55 | 27.72 |
| J01MA | Fluoroquinolones | 13.09 | 14.37 | 13.36 | 12.26 | 10.74 | 9.01 | 8.52 | 9.10 | 8.87 | 8.01 | 7.53 |
| J01X | Other antibacterials (methenamine >99%) | 7.70 | 7.47 | 5.01 | 3.62 | 5.66 | 5.80 | 5.95 | 5.91 | 2.65 | 5.17 | 6.05 |
| P01AB01 | Metronidazole | 13.77 | 16.03 | 14.84 | 14.05 | 13.57 | 13.36 | 13.77 | 13.94 | 14.11 | 11.88 | 13.75 |
| J01 and P01AB01 | All antimicrobial agents for systemic use | 313.4 | 269.7 | 255.7 | 242.6 | 234.3 | 205.3 | 207.9 | 224.6 | 242.1 | 232.9 | 213.3 |

Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

**Table 5.3 Number of prescriptions per 1,000 inhabitants for leading antimicrobial agents in primary health care, Denmark, 2006 and 2016-2025**

DANMAP 2025

| ATC group | Therapeutic group | 2006 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| J01AA | Tetracyclines | 20.63 | 17.18 | 15.89 | 14.63 | 15.11 | 20.19 | 18.25 | 18.71 | 19.11 | 17.84 | 15.13 |
| J01CA | Penicillins with extended spectrum | 111.39 | 113.16 | 114.37 | 114.31 | 112.19 | 105.93 | 107.97 | 112.19 | 114.05 | 103.92 | 101.86 |
| J01CE | Beta-lactamase sensitive penicillins | 226.74 | 157.13 | 148.52 | 136.81 | 128.77 | 104.07 | 107.28 | 122.87 | 145.45 | 129.57 | 116.51 |
| J01CF | Beta-lactamase resisistant penicillins | 41.36 | 41.87 | 41.87 | 43.35 | 43.16 | 42.87 | 43.17 | 45.66 | 47.05 | 46.42 | 46.44 |
| J01CR | Combinations of penicillins, incl. beta-lactamase inhibitors | 3.38 | 31.13 | 27.09 | 23.71 | 23.07 | 19.14 | 20.36 | 23.45 | 26.32 | 27.36 | 25.73 |
| J01E | Sulphonamides and trimethoprim | 56.68 | 36.41 | 34.29 | 31.74 | 28.14 | 25.59 | 23.07 | 21.26 | 21.30 | 18.31 | 14.10 |
| J01FA | Macrolides | 91.77 | 68.85 | 60.00 | 52.64 | 50.71 | 33.66 | 33.80 | 36.94 | 40.32 | 49.77 | 38.33 |
| J01MA | Fluoroquinolones | 17.11 | 18.74 | 17.37 | 15.97 | 13.99 | 12.07 | 11.41 | 11.96 | 11.57 | 10.48 | 10.00 |
| J01X | Other antibacterials (methenamine >99%) | 16.93 | 15.82 | 10.18 | 6.76 | 10.29 | 10.62 | 10.70 | 10.72 | 5.47 | 9.88 | 11.54 |
| P01AB01 | Metronidazole | 16.13 | 18.63 | 17.26 | 16.31 | 15.78 | 15.62 | 16.00 | 16.17 | 16.25 | 13.55 | 15.83 |
| J01 and P01AB01 | All antimicrobial agents for systemic use | 603.6 | 522.2 | 490.1 | 459.4 | 444.5 | 393.3 | 395.8 | 423.7 | 451.1 | 431.8 | 399.7 |

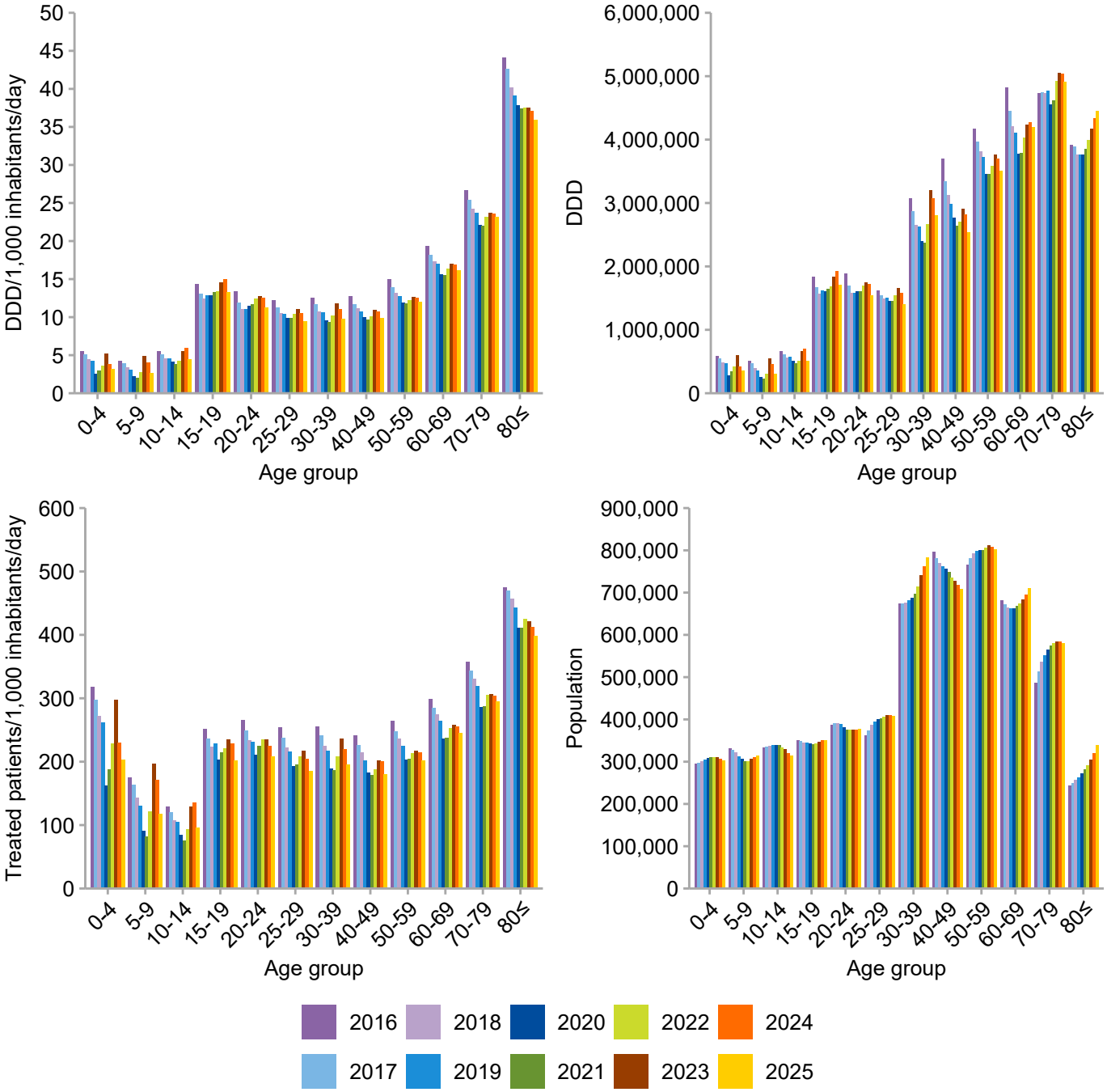
Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

### 5.3.2 Antimicrobial consumption by patient case mix

Antimicrobial consumption is highly affected by patient case mix. The need for antimicrobials differs throughout life and for the two genders. Antimicrobial consumption is also affected by sociodemographic factors such as civil status, educational level, employment status and country of birth (DANMAP 2022, Textbox 5.2). Figure 5.6a-c presents consumption of antimicrobials by age group based on different denominators: Figure 5.6a presents consumption in DDD per 1,000 inhabitants per day; Figure 5.6b in crude DDD, i.e., not corrected for population size; Figure 5.6c presents the number of patients treated per 1,000 inhabitants; Figure 5.6d presents population size by age group. Children and adolescents are presented in five-year age groups, while adults are clustered in 10-year age groups.

Estimates of antimicrobial consumption for children based on DDD should be interpreted with caution since the DDD is defined as "maintenance dose per day for its main indication in adults". The maintenance dose per day for children may differ from the one for adults due to different pharmacodynamics and -kinetics. Furthermore, infants and young children in the same age group might be treated with different doses based on body weight. Therefore, other units of measurement might be more suitable to monitor consumption in children, e.g., number of treated patients per 1,000 inhabitants and number of prescriptions per 1,000 inhabitants.

**Figure 5.6 Consumption of systemic antimicrobial agents in primary health care by age group, measured in a) DDD per 1,000 inhabitants per day, b) DDD, c) treated patients per 1,000 inhabitants and d) population size, Denmark, 2016-2025** DANMAP 2025

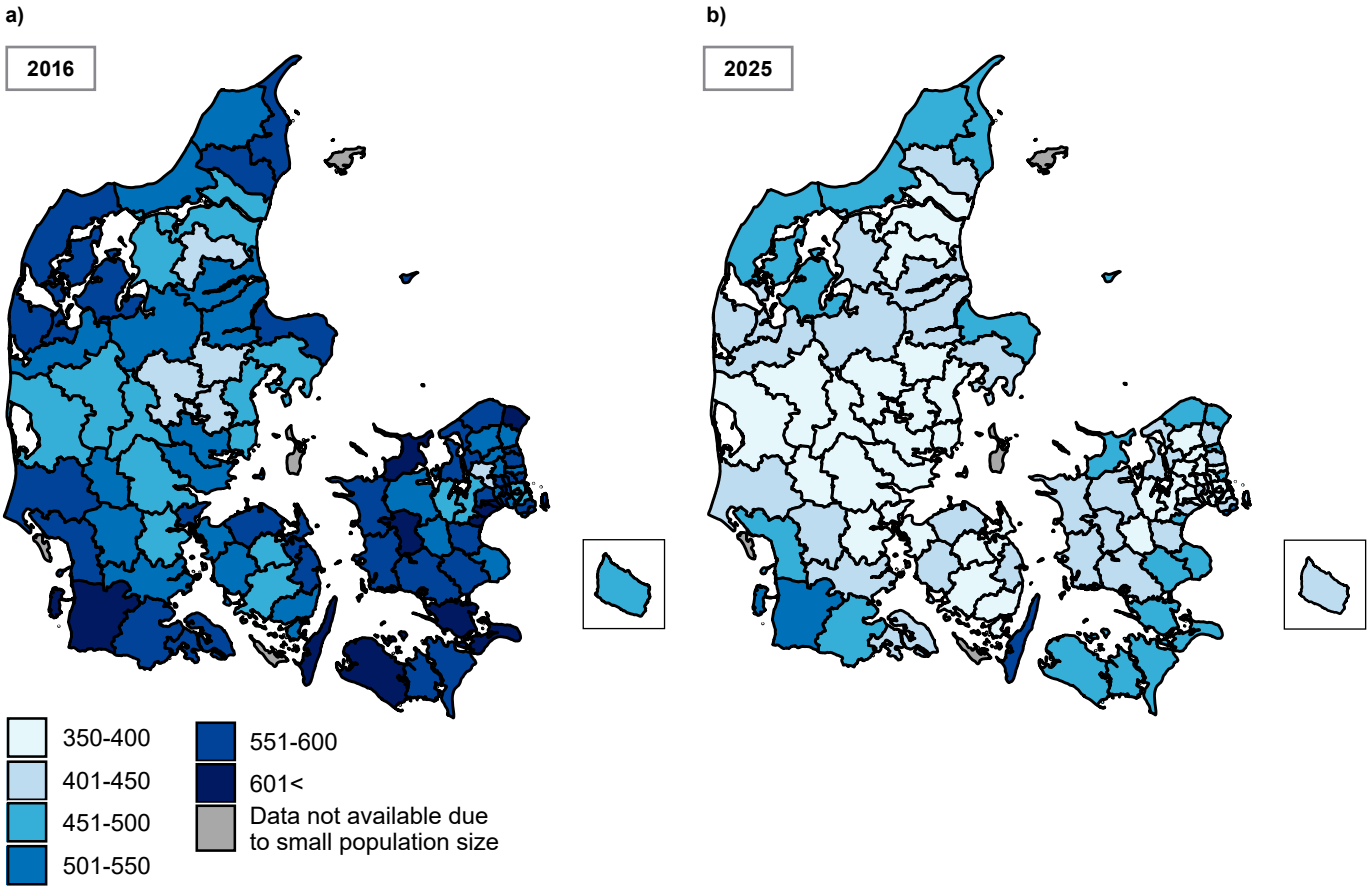



Children and adolescents are presented in five-year age groups, while adults are clustered in 10-year age groups.
Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics, the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system and Statistics Denmark.

Interregional differences in the levels of prescribing have been described in DANMAP since 2017 (Table 5.4). In general, the Danish population is relatively homogeneous and health care is of standardized quality, which, combined with several initiatives to educate GPs in appropriate prescribing, diminishes potential differences in prescribing trends. However, observed variations in prescribing may owe to differences in population density (distance to the nearest general practitioner), differences in age and comorbidity of the population (younger populations in bigger cities and in the Capital Region) as well as behavioral differences between urban and rural populations.

**Figure 5.7 Number of prescriptions in primary health care per 1,000 inhabitants in Danish municipalities in a) 2016 and b) 2025**

DANMAP 2025




Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

Figure 5.7 shows the number of prescriptions per 1,000 inhabitants at municipality level in 2016 and 2025, respectively. In 2025, the consumption ranged from 335 to 568 prescriptions per 1,000 inhabitants. In 2016, the range was 434-727 prescriptions per 1,000 inhabitants. 2016 was the baseline year for the first Danish action plan on reducing antimicrobial use in human health care (see Textbox 5.1 in DANMAP2021), whereas 2025 is the baseline year for the current national action plan, see Perspectives of DANMAP 2025. Of note is that prescribers in all regions reduced their prescribing activities in the shown period. Demographic differences might impact the range of prescribing. The distribution of older inhabitants over 60 across the municipalities closely follows that of prescriptions per 1,000 inhabitants with higher prescription rates in municipalities with larger populations of older inhabitants above 60 years (data not shown).

**Table 5.4 Consumption of antimicrobial agents for systemic use in primary health care at regional level, Denmark, 2021-2025**

DANMAP 2025

| Region | Indicator | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|
| Capital Region of Denmark | DDD/1.000 inhabitants/day | 12.32 | 13.03 | 14.14 | 13.90 | 12.79 |
| | Prescriptions/1.000 inhabitants | 378 | 409 | 443 | 423 | 384 |
| Central Region of Denmark | DDD/1.000 inhabitants/day | 11.83 | 12.32 | 13.07 | 12.86 | 12.14 |
| | Prescriptions/1.000 inhabitants | 380 | 402 | 425 | 408 | 382 |
| North Denmark Region | DDD/1.000 inhabitants/day | 12.42 | 13.26 | 14.33 | 14.23 | 13.91 |
| | Prescriptions/1.000 inhabitants | 400 | 431 | 458 | 438 | 428 |
| Region of Southern Denmark | DDD/1.000 inhabitants/day | 12.17 | 12.91 | 13.78 | 13.43 | 12.37 |
| | Prescriptions/1.000 inhabitants | 405 | 434 | 460 | 440 | 402 |
| Region Zealand | DDD/1.000 inhabitants/day | 13.71 | 14.31 | 15.21 | 15.14 | 14.29 |
| | Prescriptions/1.000 inhabitants | 440 | 466 | 489 | 470 | 435 |

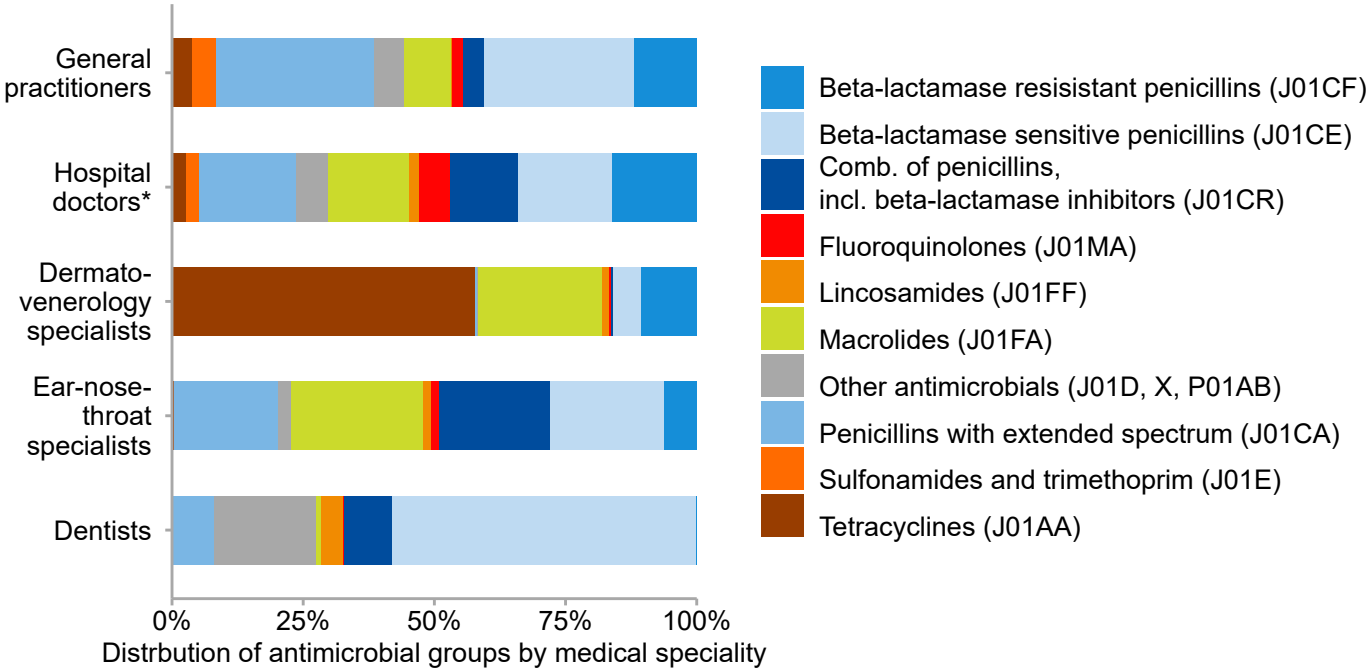
Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

### 5.3.3 Antimicrobial consumption by prescriber

Prescribing trends in primary health care clearly differ by prescribers' specialties. Table 5.5 shows an overview of the number of prescriptions issued by different specialists, including hospital doctors issuing prescriptions for patients at hospitals, which are then redeemed at a community pharmacy. Figure 5.8 shows the main antimicrobial groups prescribed by medical specialty in primary health care in 2025. In general practice, beta-lactamase sensitive penicillins and penicillins with extended spectrum were the most prescribed (29% and 30%, respectively) indicating adherence to the guidelines recommending beta-lactamase sensitive penicillins as the drug of choice in many common infections. In 2025, 58% of antimicrobial prescriptions from dermato-venerology specialists were tetracyclines, which are indicated for treatment of severe acne and sexually transmitted chlamydia/mycoplasma infections. The majority of prescriptions by dentists were narrow-spectrum beta-lactamase sensitive penicillins (58%) reflecting adherence to the recommended first-line treatment for common dental infections in primary health care.

General practitioners have access to their own prescribing data through ordiprax+, an online dashboard with personal log-in visualising prescription data and enabling comparisons with other practices at the regional level (DANMAP 2020 Textbox 5.2). Additionally, general practitioners are organized in quality clusters where improvement of antimicrobial prescribing is discussed among other topics.

**Figure 5.8 Antimicrobial groups prescribed by main medical specialties in primary health care, Denmark, 2025** DANMAP 2025




*Hospital doctors issuing prescriptions for patients in ambulatory care or upon discharge from hospital.
Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

**Table 5.5 Number of prescriptions per 1,000 inhabitants by main medical specialties, Denmark, 2021-2025** DANMAP 2025

| Prescriber | | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|
| General practitioners | Prescriptions per 1,000 inhabitants | 279 | 300.9 | 323.1 | 305.5 | 0 |
| | DDD per prescription | 11 | 10.8 | 10.9 | 11.2 | 11.3 |
| Hospital doctors* | Prescriptions per 1,000 inhabitants | 63.5 | 62 | 65.6 | 64.3 | 31.4 |
| | DDD per prescription | 13.2 | 13.6 | 13.7 | 14.4 | 15 |
| Ear-nose-throat specialists | Prescriptions per 1,000 inhabitants | 6.9 | 8.1 | 8.5 | 8.1 | 7.5 |
| | DDD per prescription | 8.3 | 8.1 | 8 | 8.1 | 8.2 |
| Dermato-venerology specialists | Prescriptions per 1,000 inhabitants | 5 | 4.6 | 4.4 | 4.4 | 3.9 |
| | DDD per prescription | 35.4 | 35 | 34.6 | 37.1 | 35.4 |
| Dentists | Prescriptions per 1,000 inhabitants | 28.9 | 34.4 | 33.1 | 32.8 | 35.2 |
| | DDD per prescription | 7.7 | 7.7 | 8.2 | 8.2 | 8 |

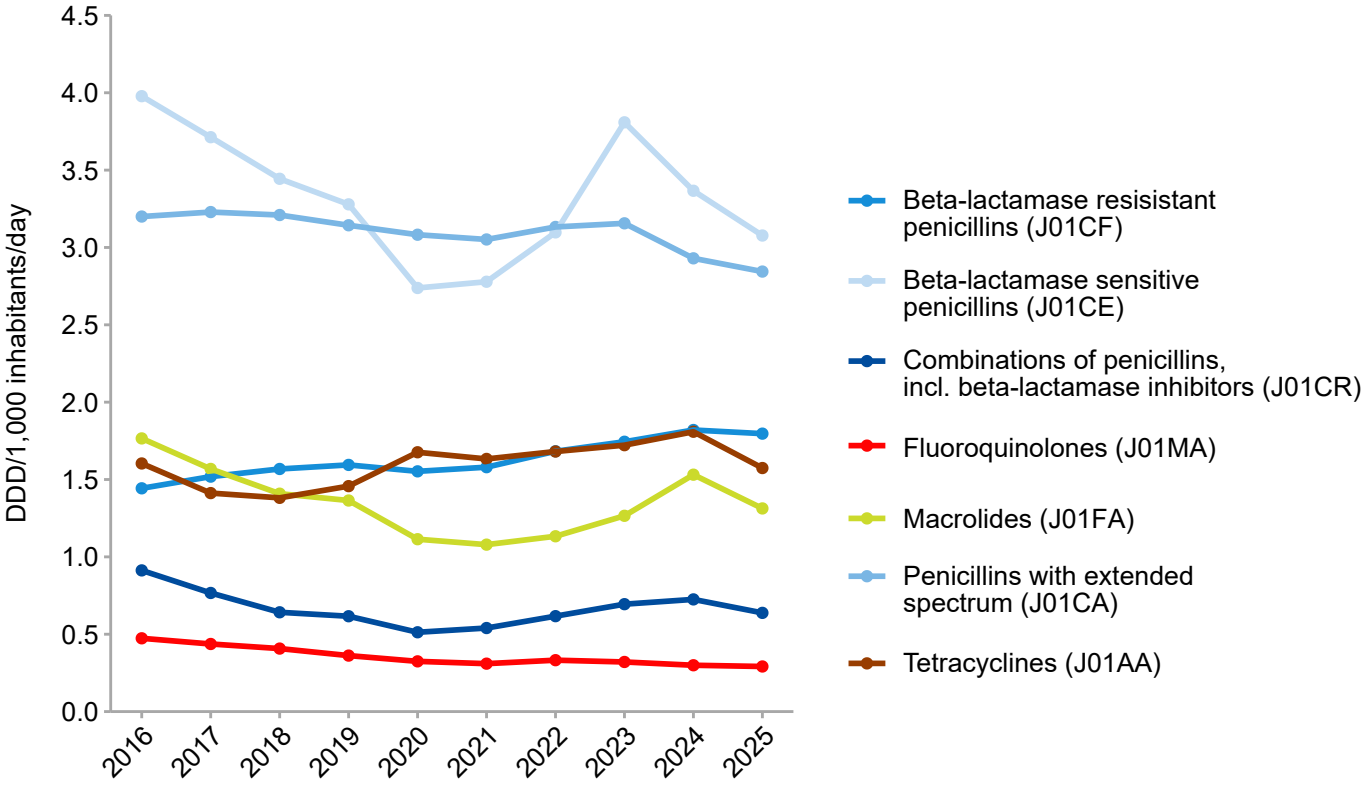
*Hospital doctors issuing prescriptions for patients in ambulatory care or upon discharge from hospital.
Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

### 5.3.4 Consumption of antimicrobial groups

In compliance with treatment guidelines, beta-lactamase sensitive penicillins have been the most used antimicrobials in primary health care in Denmark for decades (Figure 5.9). In 2025, beta-lactamase sensitive penicillins accounted for 24% of total consumption in primary health care. The steep increase of these penicillins, observed post COVID-19 and attributed to a renormalized circulation of airway infections, discontinued in 2024, (-11.6% from 2023 to 2024). Altogether, the four penicillin groups (penicillins with extended spectrum; beta-lactamase sensitive penicillins; beta-lactamase resistant penicillins; combinations of penicillins, including beta-lactamase inhibitors) accounted for 8.36 DID corresponding to 65% of antimicrobials consumed in primary health care in 2025. Other beta-lactams such as cephalosporins, monobactams and carbapenems were either used at an extremely low level or restricted to hospital use only. Consumption of macrolides increased by 21% from 2023 to 2024 attributed to the Group A streptococcal pandemic that circulated among children and their parents. In 2025, consumption of macrolides was 14% lower than in 2024.

**Figure 5.9 Consumption of leading antimicrobial groups for systemic use in primary health care, DDD per 1,000 inhabitants per day, Denmark, 2016-2025**

DANMAP 2025

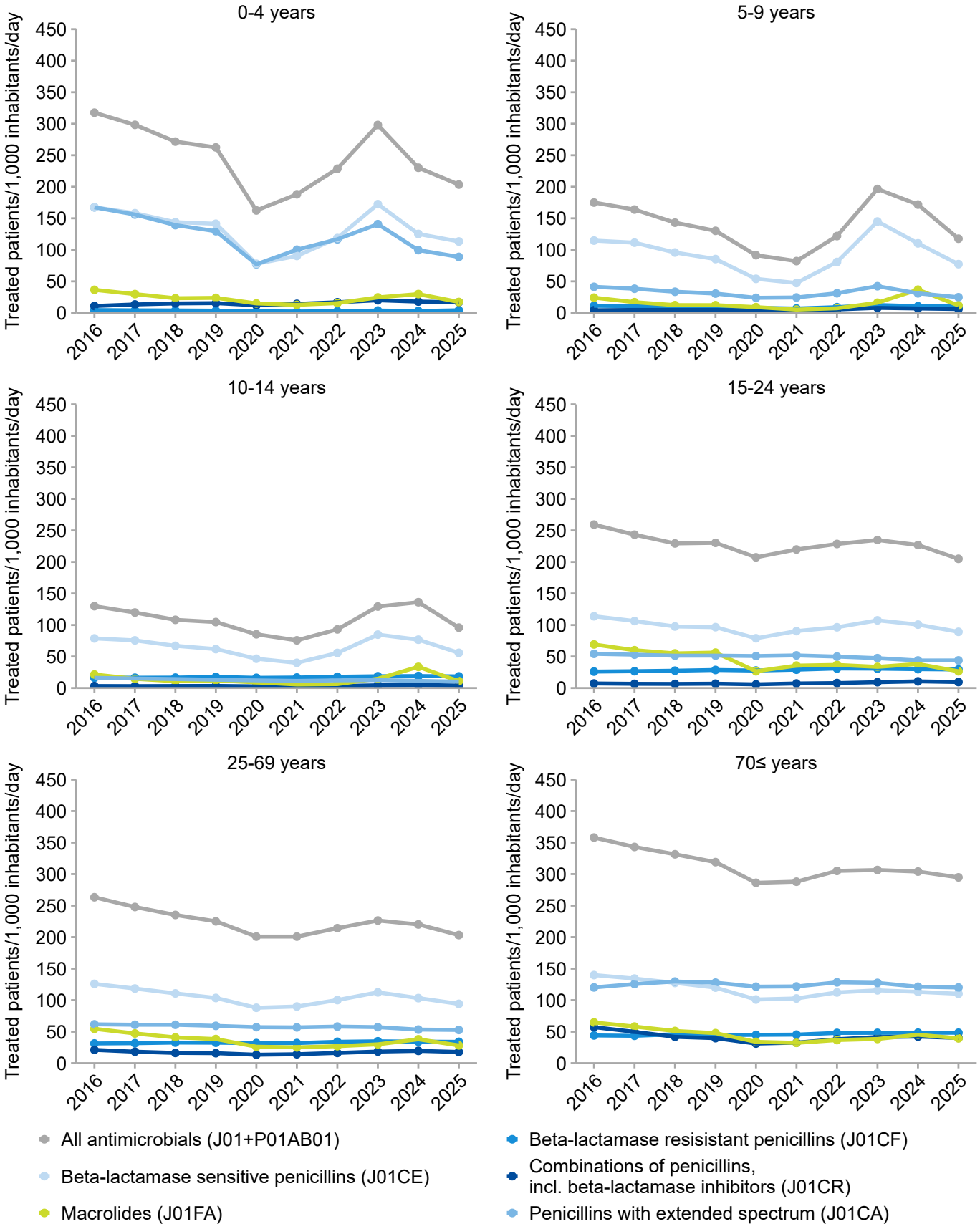



Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

Macrolides play an important role in the treatment of bacterial respiratory tract infections in children and adolescents (Figure 5.10). Macrolides were also used as first-line treatment for chlamydia infections until the change in guidance (described in DANMAP2020), which may be the reason for the relatively high, but in recent years decreasing, consumption of macrolides in the 15-24-year-olds. However, penicillins continued to be the most used antimicrobial agents for children and adolescents, constituting between 67% and 89% of all antimicrobials prescribed depending on age group in 2025 (Figure 5.10).

**Figure 5.10 Consumption of main antimicrobial agents by age group, treated patients/1,000 inhabitants, Denmark, 2016-2025**

DANMAP 2025




Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

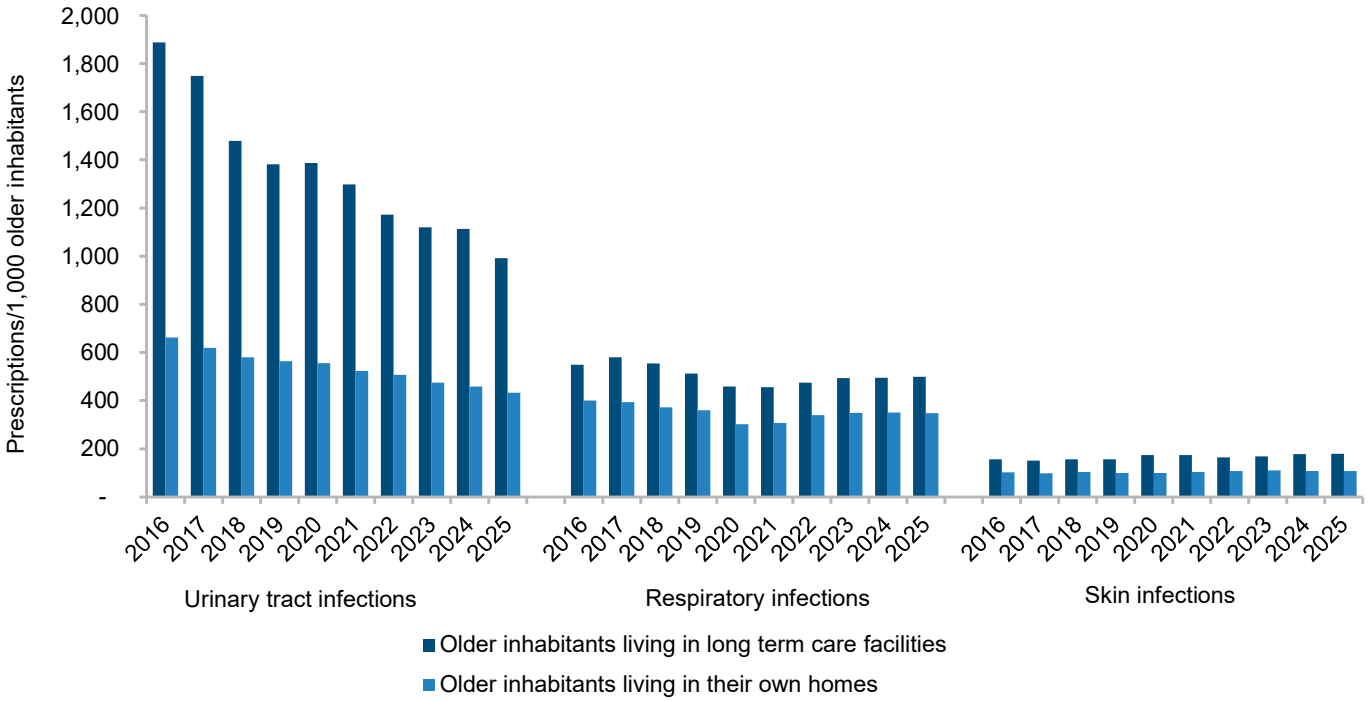
## 5.4 Antimicrobials among older inhabitants

One of the more recent additions to the DANMAP program is surveillance of antimicrobial consumption in older inhabitants aged 65 years and above. Close monitoring of infections in this population is necessary, as it is one of the most fragile populations in society. Surveillance of antimicrobial consumption contributes to high-quality treatment of infections and thereby prevents the emergence of antimicrobial resistant pathogens.

Based on data in the Danish Care Home Register and the Danish Civil Registry, it is possible to divide older inhabitants into two populations; older living in their own homes and older living at long-term care facilities. Figure 5.11 shows decreasing antimicrobial consumption for older inhabitants aged 65 years and above in 2016-2025, with a steeper decrease in consumption for older living at care homes. The figure compares trends in prescription codes for different infectious entities.

**Figure 5.11 Consumption of antimicrobials in primary health care for older inhabitants (≥65 years) living in long-term care facilities or in their own homes, Denmark, 2016-2025**

DANMAP 2025

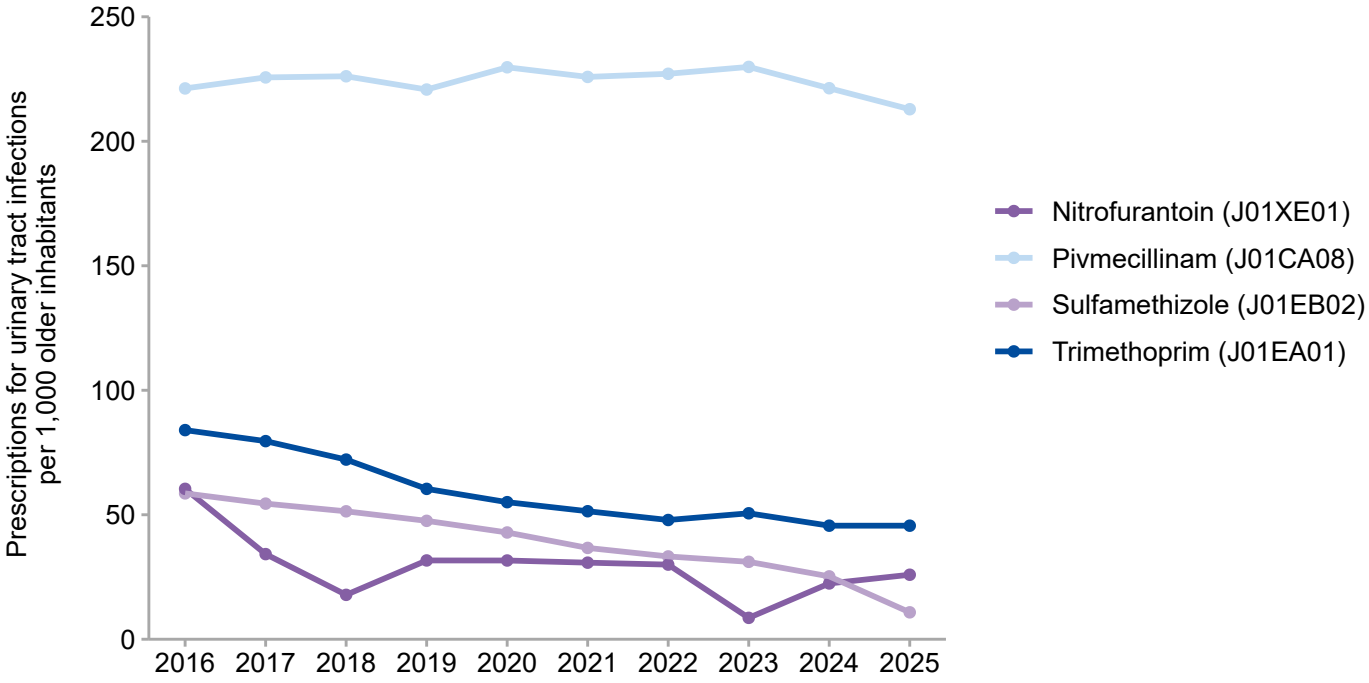



Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics, and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system, Care Home Register and Danish Civil Registry.

The main indication for antimicrobial treatment among older patients is urinary tract infections. Higher prevalence of urinary tract infections among older people at long-term care facilities has been observed for many years (Figure 5.11). In 2025, 991 prescriptions were issued per 1,000 inhabitants at long-term care facilities, whereas 433 prescriptions were issued per 1,000 inhabitants living in their own homes. The difference was less pronounced for respiratory (449 and 347 prescriptions per 1,000 inhabitants, respectively), and skin infections (179 and 108 prescriptions per 1,000 inhabitants, respectively). Figures 5.12, 5.13 and 5.14 show the consumption of antimicrobial agents for specific infections based on the indication on prescriptions for older inhabitants (≥70 years).

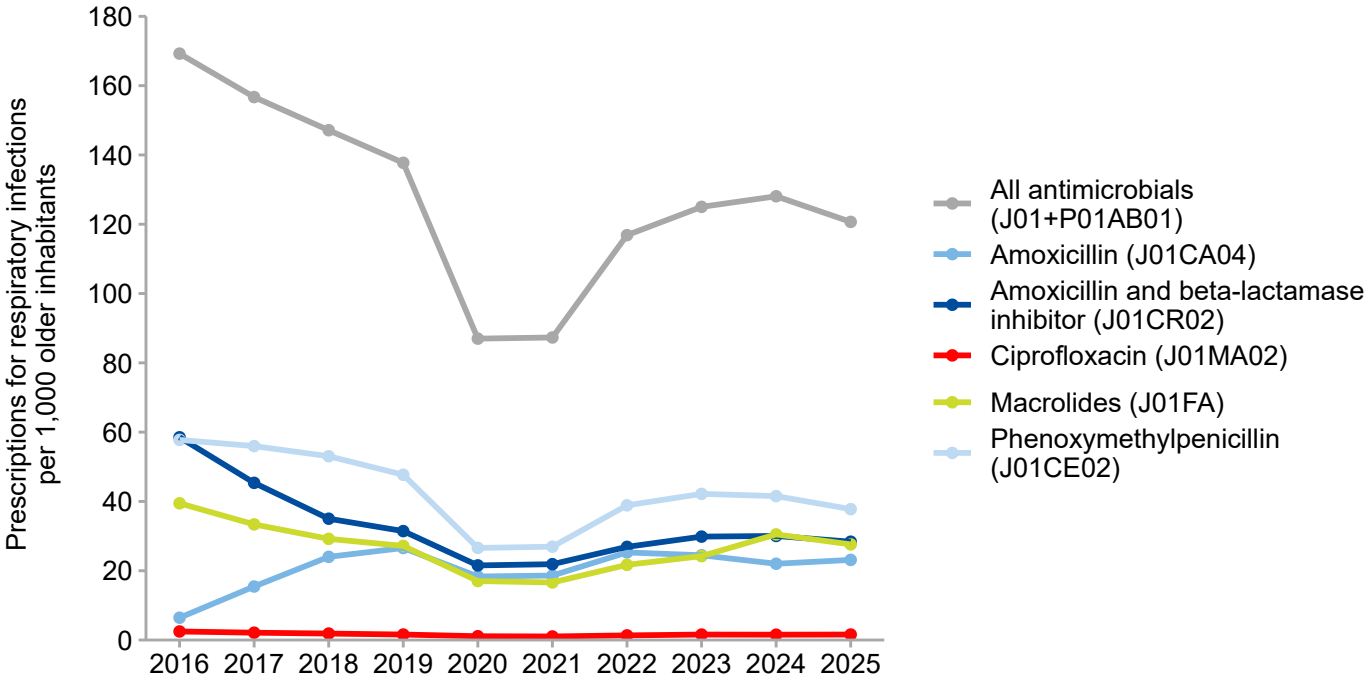
The Danish national action plan about antimicrobial resistance in human health emphasizes the importance of improving knowledge and awareness about infection prevention and control at long-term care facilities, but also among the older in general.

**Figure 5.12 Antimicrobial prescriptions indicated for treatment of urinary tract infections in primary health care, prescriptions per 1,000 older inhabitants (≥70 years), Denmark, 2016-2025** DANMAP 2025



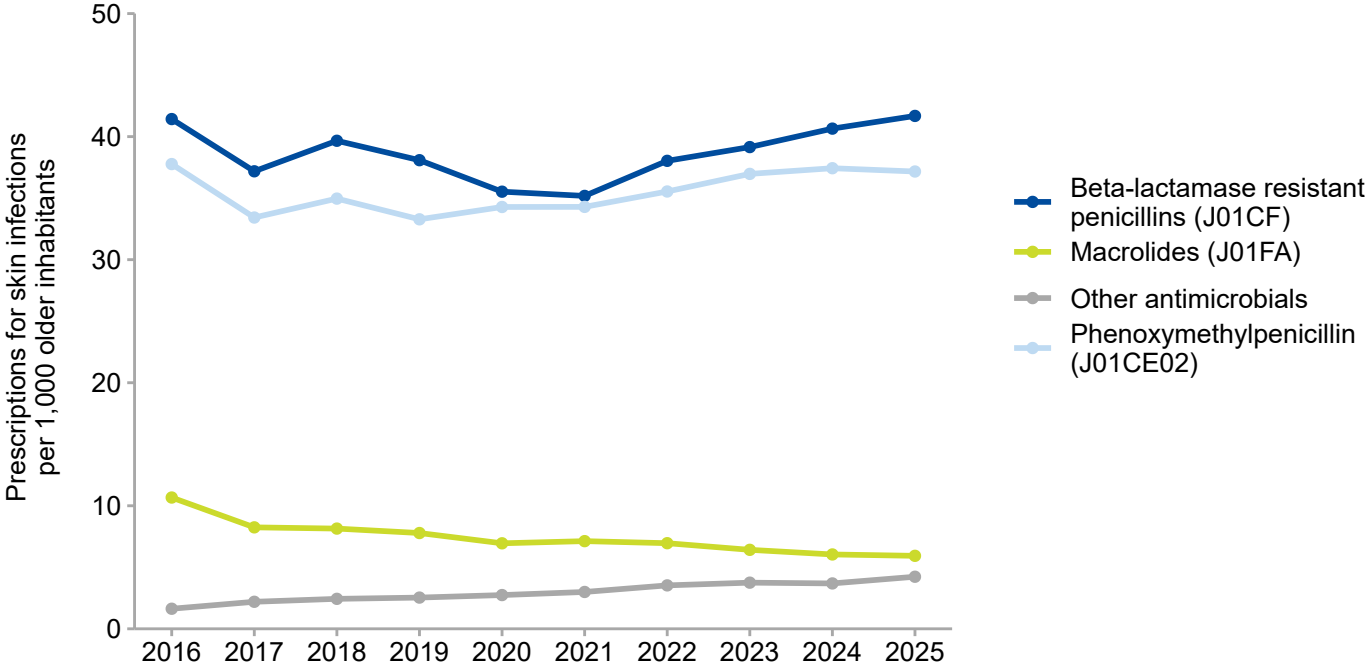

Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

**Figure 5.13 Antimicrobial prescriptions indicated for treatment of respiratory tract infections in primary health care, prescriptions per 1,000 older inhabitants (≥70 years), Denmark, 2016-2025** DANMAP 2025




Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

**Figure 5.14 Antimicrobial prescriptions indicated for treatment of skin infections in primary health care, prescriptions per 1,000 older inhabitants (≥70 years), Denmark, 2016-2025**
DANMAP 2025



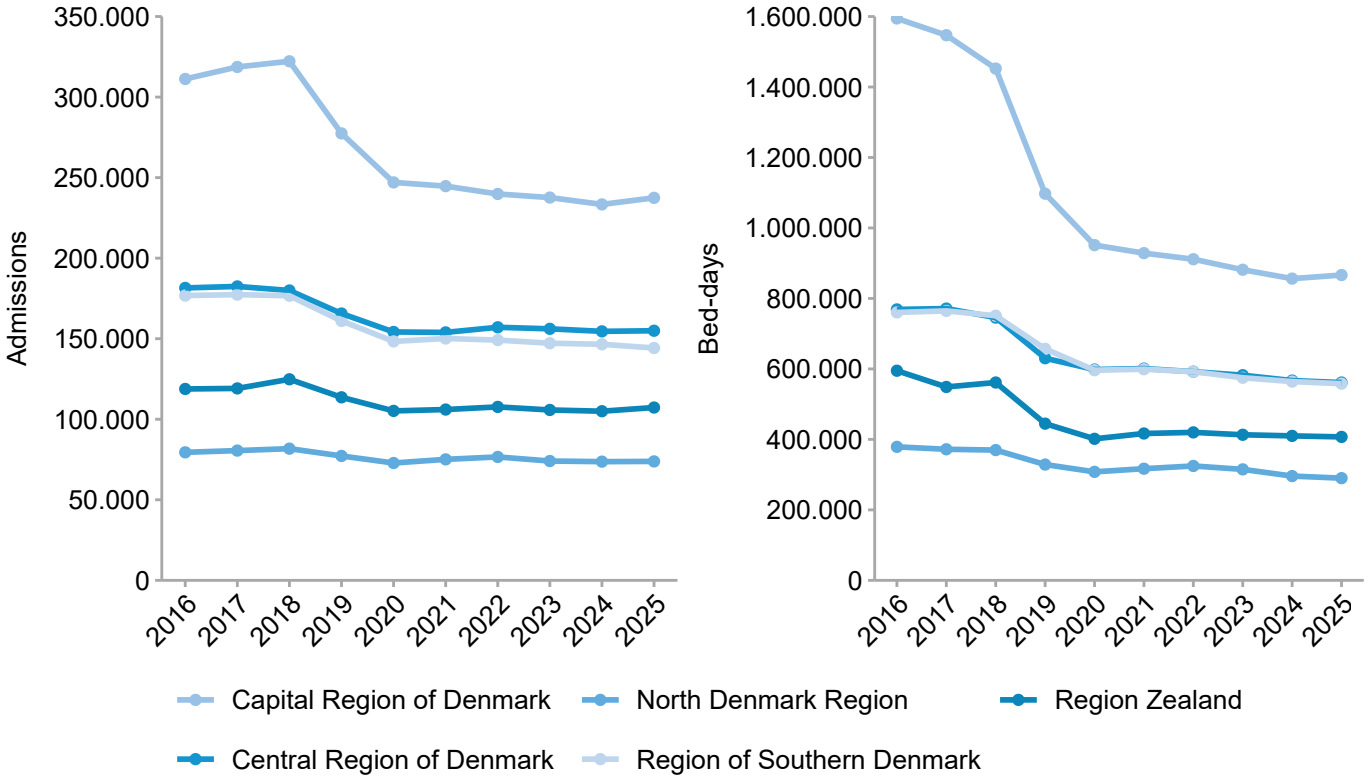

Data: Registered sales of antimicrobials to individuals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

## 5.5 Antimicrobial consumption in hospital care

Surveillance of antimicrobial consumption in hospital care is based on sales of systemic antimicrobials (ATC codes J01, P01AB01 and A07AA09) from Danish hospital pharmacies to hospitals, excluding private hospitals and psychiatric departments (approximately 2-3% of the total hospital consumption). Antimicrobial consumption data are presented as DDD per 100 occupied bed-days (DBD) and per 100 admissions (DAD) to account for hospital activity. The consumption is also presented as DDD per 1,000 inhabitants per day to enable comparison with consumption in primary health care and to correct for changes in consumption data based on changes in hospital activity, the background population being a more stable denominator.

Hospital activity has changed over the years with a decreasing number of bed-days and admissions, although at differing rates (Figure 5.15). Earlier discharge of patients, increasing ambulatory care functions in the community as well as in care homes and changed workflow due to new electronic systems all affect the activity and need to be considered when interpreting antimicrobial consumption trends in hospitals. Information on consumption at the patient level is currently not available to DANMAP for the hospital sector. This information is expected to become available to DANMAP through the "Hospital Medicine Register" in the coming years.

**Figure 5.15 Activity at somatic hospitals, bed-days and admissions, Denmark, 2016-2025** DANMAP 2025



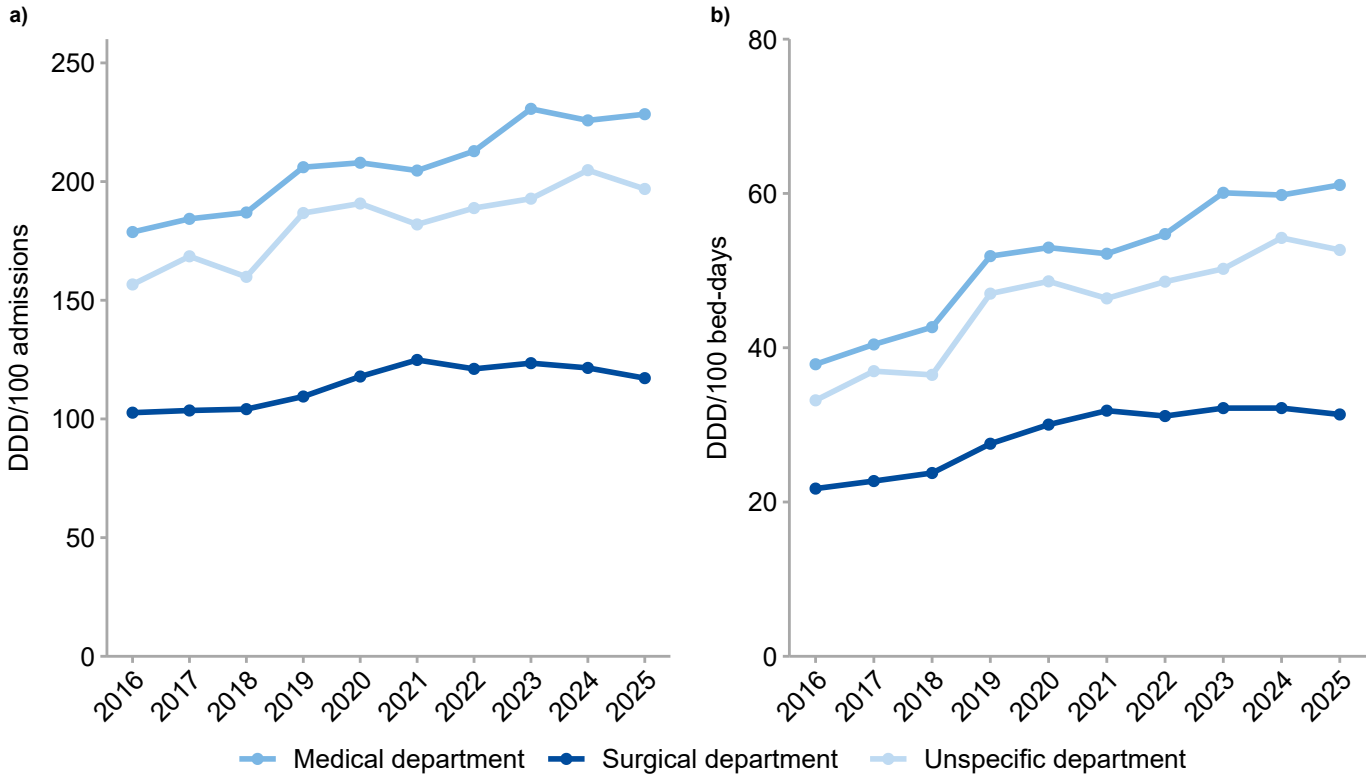

Data source: National Patient Register.
Data from the National Patient Register are subject to change due to continuous development of the new National Patient Register. This means that data will be continuously updated.

### 5.5.1 Antimicrobial consumption at public somatic hospitals accounting for hospital activity

Antimicrobial consumption at hospitals can be monitored based on the type of department. Figure 5.16 shows the highest share of consumption at medical departments (42%) in 2025, whereas surgical departments accounted for 22%. However, a significant part of the consumption could not be assigned to a specific hospital department (36%) which necessitates careful interpretation of data at this hospital organizational level.

**Figure 5.16 Antimicrobial consumption at hospitals by type of department, a) DDD per 100 admissions and b) DDD per 100 bed-days, Denmark, 2016-2025**

DANMAP 2025




Data: Antimicrobial consumption at somatic hospitals.
Data source: Register of Medicinal Product Statistics, the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system and The National Patient Register.

In 2025, the consumption of antimicrobial agents at somatic hospitals was 144.7 DBD. This is similar to 2024 (145.2 DBD) and 55% higher than a decade ago (92.8 DBD in 2016) (Table 5.6). The four penicillin groups (penicillins with extended spectrum, beta-lactamase sensitive penicillins, beta-lactamase resistant penicillins and combinations of penicillins, including beta-lactamase inhibitors) accounted for 80.6 DBD, corresponding to 56% of the total consumption of antimicrobials at somatic hospitals in Denmark in 2025. The main group of antimicrobials in 2025; combinations of penicillins, including beta-lactamase inhibitors increased by 75% since 2016 (Figure 5.18). However, the conusmption started decreasing since 2024, in 2025 by 3.5% compared to 2024.

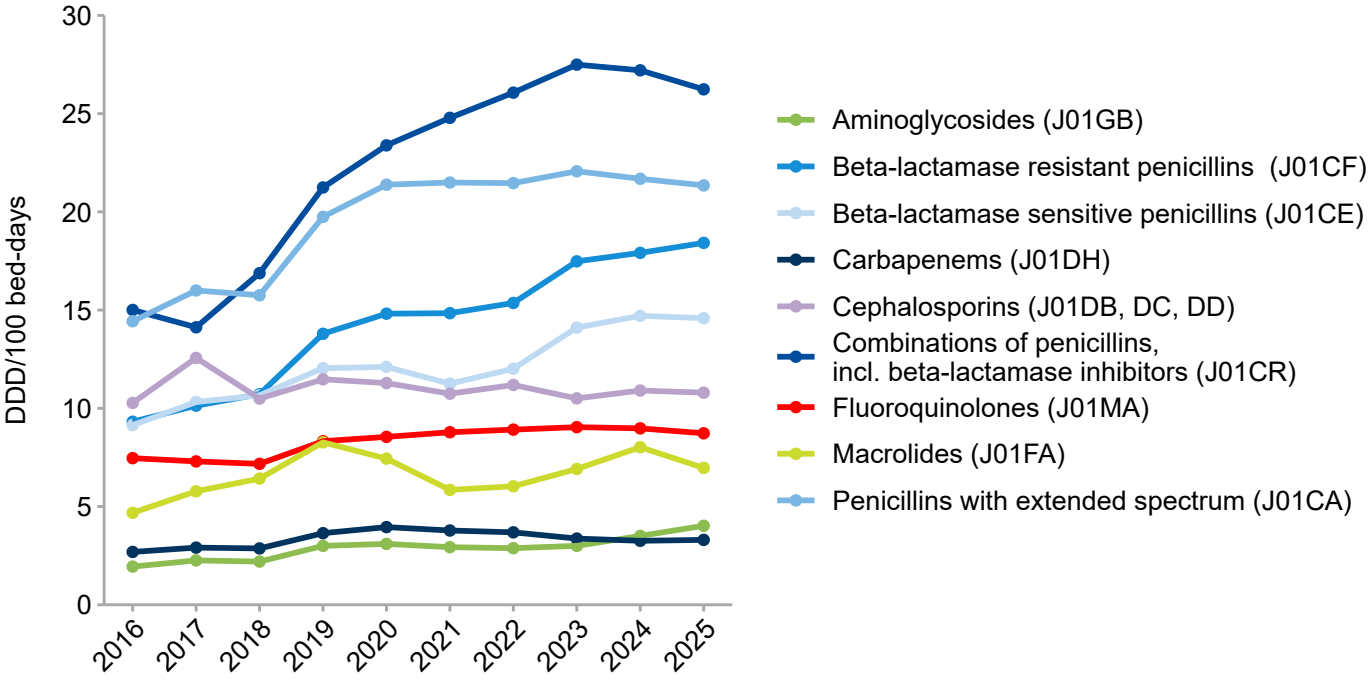
Much has changed within the choice and usage of antimicrobials at Danish hospitals, an example being the increase in combination penicillins as an attempt to reduce the usage of cephalosporins, while recent initiatives now include the combination penicillins among the broad-spectrum antimicrobials that should be closely monitored and, whenever possible, replaced by narrow-spectrum penicillins (Figure 5.17). These initiatives were included in the latter and the new Danish national action plan against antimicrobial resistance (DANMAP2021, Textbox 5.1 and DANMAP2024, Textbox 1.1).

Linezolid consumption was 0.64 DBD in 2025 which is 12% lower than in 2024 (0.73 DBD). The consumption of linezolid has shown fluctuating trends but increased by 78% over the past decade (0.36 DBD in 2016). Consumption of daptomycin has been stable in recent years at 0.13 DBD since 2022 (Table 5.6).

Although the overall consumption of both antimicrobials is low, sudden changes are of concern due to the high risk of resistance in enterococci and staphylococci. Moreover, the consumption is concentrated at highly specialized tertiary care hospitals in Denmark, which can result in local selection pressure for resistant bacteria.

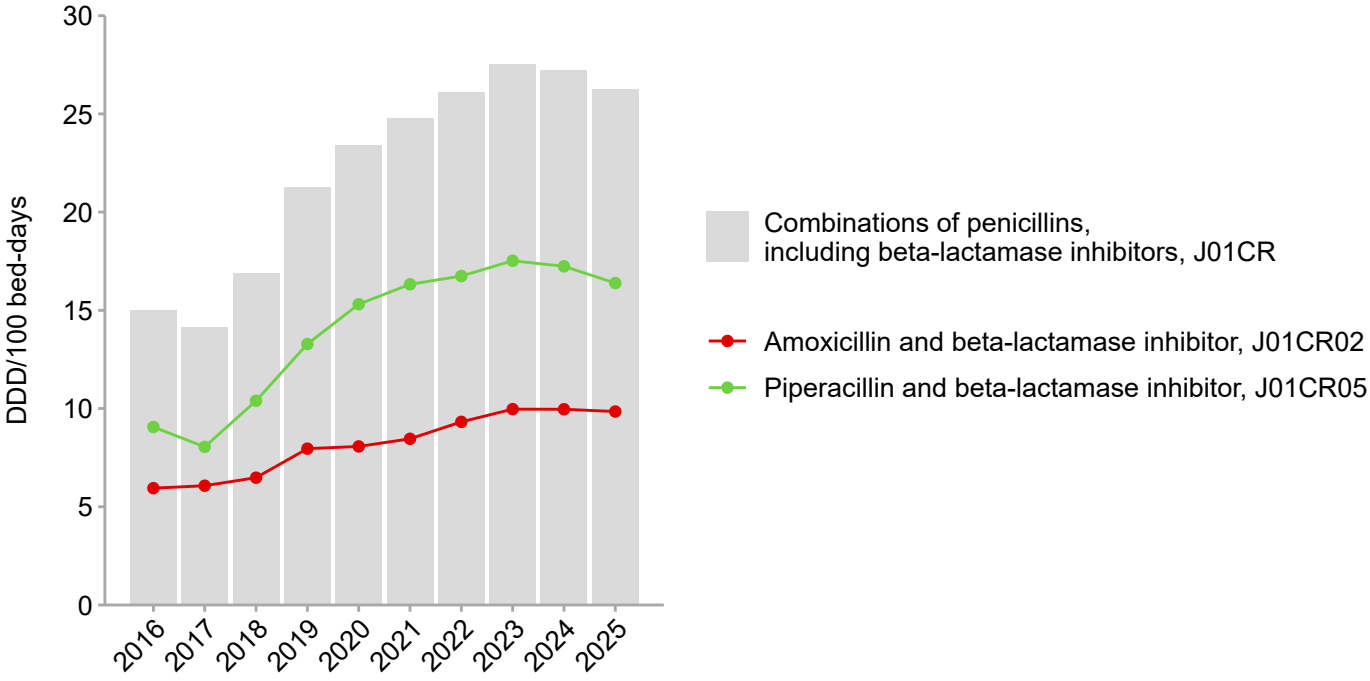
The consumption data at hospitals are presented in Table 5.6 by number of bed-days and in Table 5.7 by number of admissions.

**Figure 5.17 Consumption of leading groups of antimicrobial agents at somatic hospitals, DDD per 100 bed-days, Denmark, 2016-2025** DANMAP 2025




Data: Antimicrobial consumption at somatic hospitals.
Data source: Register of Medicinal Product Statistics, the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system and The National Patient Register.

**Figure 5.18 Consumption of combination penicillins at somatic hospitals, DDD per 100 bed-days, Denmark, 2016-2025** DANMAP 2025




Data: Antimicrobial consumption at somatic hospitals.
Data source: Register of Medicinal Product Statistics, the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system and National Patient Register.

**Table 5.6 Consumption of antimicrobial agents for systemic use in somatic hospitals, DDD per 100 bed-days, Denmark, 2016-2025**

DANMAP 2025

| ATC group | Therapeutic group | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| J01AA | Tetracyclines | 2.09 | 2.07 | 2.43 | 3.87 | 3.29 | 3.40 | 3.69 | 4.20 | 4.49 | 4.06 |
| J01CA | Penicillins with extended spectrum | 14.43 | 16.00 | 15.76 | 19.74 | 21.38 | 21.49 | 21.46 | 22.07 | 21.68 | 21.35 |
| J01CE | Beta-lactamase sensitive penicillins | 9.15 | 10.32 | 10.66 | 12.04 | 12.11 | 11.25 | 12.01 | 14.11 | 14.71 | 14.59 |
| J01CF | Beta-lactamase resistant penicillins | 9.32 | 10.14 | 10.72 | 13.79 | 14.82 | 14.84 | 15.36 | 17.48 | 17.91 | 18.42 |
| J01CR | Comb. of penicillins. incl. beta-lactamase inhibitors | 15.01 | 14.12 | 16.88 | 21.24 | 23.38 | 24.78 | 26.07 | 27.49 | 27.20 | 26.24 |
| J01DB | First-generation cephalosporins | 0.04 | 0.04 | 0.04 | 0.03 | 0.04 | 0.04 | 0.03 | 0.03 | 0.01 | 0.00 |
| J01DC | Second-generation cephalosporins | 9.21 | 11.18 | 9.23 | 9.98 | 9.79 | 9.26 | 9.56 | 8.94 | 9.32 | 9.27 |
| J01DD | Third-generation cephalosporins | 1.03 | 1.35 | 1.23 | 1.46 | 1.45 | 1.45 | 1.59 | 1.54 | 1.58 | 1.52 |
| J01DF | Monobactams | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.02 | 0.01 | 0.03 | 0.04 |
| J01DH | Carbapenems | 2.69 | 2.91 | 2.87 | 3.64 | 3.95 | 3.78 | 3.69 | 3.37 | 3.26 | 3.30 |
| J01EA | Trimethoprim and derivatives | 0.37 | 0.42 | 0.45 | 0.49 | 0.55 | 0.51 | 0.48 | 0.45 | 0.40 | 0.39 |
| J01EB | Short-acting sulfonamides | 0.10 | 0.10 | 0.10 | 0.11 | 0.08 | 0.08 | 0.06 | 0.05 | 0.05 | 0.03 |
| J01EE | Comb. of sulfonamides and trimethoprim. incl. derivatives | 5.34 | 5.67 | 6.14 | 8.19 | 8.86 | 9.71 | 10.04 | 11.20 | 12.10 | 13.71 |
| J01FA | Macrolides | 4.68 | 5.78 | 6.42 | 8.27 | 7.44 | 5.85 | 6.03 | 6.91 | 8.02 | 6.97 |
| J01FF | Lincosamides | 0.62 | 0.65 | 0.78 | 0.91 | 0.88 | 0.83 | 0.85 | 0.91 | 0.94 | 1.01 |
| J01GB | Aminoglycosides | 1.94 | 2.26 | 2.20 | 3.00 | 3.10 | 2.93 | 2.88 | 3.00 | 3.51 | 4.02 |
| J01MA | Fluoroquinolones | 7.46 | 7.30 | 7.17 | 8.33 | 8.55 | 8.78 | 8.92 | 9.04 | 8.98 | 8.73 |
| J01XA | Glycopeptides | 1.08 | 1.33 | 1.30 | 1.64 | 1.82 | 1.83 | 1.78 | 1.66 | 1.90 | 1.97 |
| J01XB | Polymyxins | 0.19 | 0.19 | 0.23 | 0.27 | 0.29 | 0.29 | 0.30 | 0.36 | 0.47 | 0.36 |
| J01XC | Steroid antibacterials (fusidic acid) | 0.11 | 0.07 | 0.06 | 0.07 | 0.06 | 0.07 | 0.05 | 0.06 | 0.05 | 0.02 |
| J01XD | Imidazole derivatives | 4.50 | 4.71 | 4.44 | 5.05 | 5.19 | 4.79 | 4.64 | 4.57 | 4.46 | 4.33 |
| J01XE | Nitrofuran derivatives (nitrofurantoin) | 0.24 | 0.26 | 0.28 | 0.35 | 0.43 | 0.38 | 0.38 | 0.46 | 0.38 | 0.32 |
| J01XX05 | Methenamine | 0.08 | 0.07 | 0.11 | 0.10 | 0.10 | 0.14 | 0.13 | 0.15 | 0.13 | 0.14 |
| J01XX08 | Linezolid | 0.36 | 0.38 | 0.54 | 0.65 | 0.60 | 0.61 | 0.68 | 0.68 | 0.73 | 0.64 |
| J01XX09 | Daptomycin | 0.05 | 0.08 | 0.15 | 0.08 | 0.12 | 0.15 | 0.13 | 0.13 | 0.13 | 0.13 |
| A07AA09 | Vancomycin | 0.48 | 0.53 | 0.51 | 0.67 | 0.81 | 0.70 | 0.82 | 0.87 | 0.91 | 0.94 |
| P01AB01 | Metronidazole | 2.17 | 2.06 | 1.99 | 2.35 | 2.42 | 2.32 | 2.26 | 2.28 | 1.81 | 2.15 |
| J01, P01AB01, A07AA09 | All antimicrobial agents for systemic use, incl. metronidazole and vancomycin | 92.8 | 100.0 | 102.7 | 126.3 | 131.5 | 130.3 | 133.9 | 142.0 | 145.2 | 144.7 |

Data: Antimicrobial consumption at somatic hospitals.
Data source: The Register of Medicinal Product Statistics, the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system and National Patient Register.

**Table 5.7 Consumption of antimicrobial agents for systemic use in somatic hospitals, DDD per 100 admissions, Denmark, 2016-2025**

DANMAP 2025

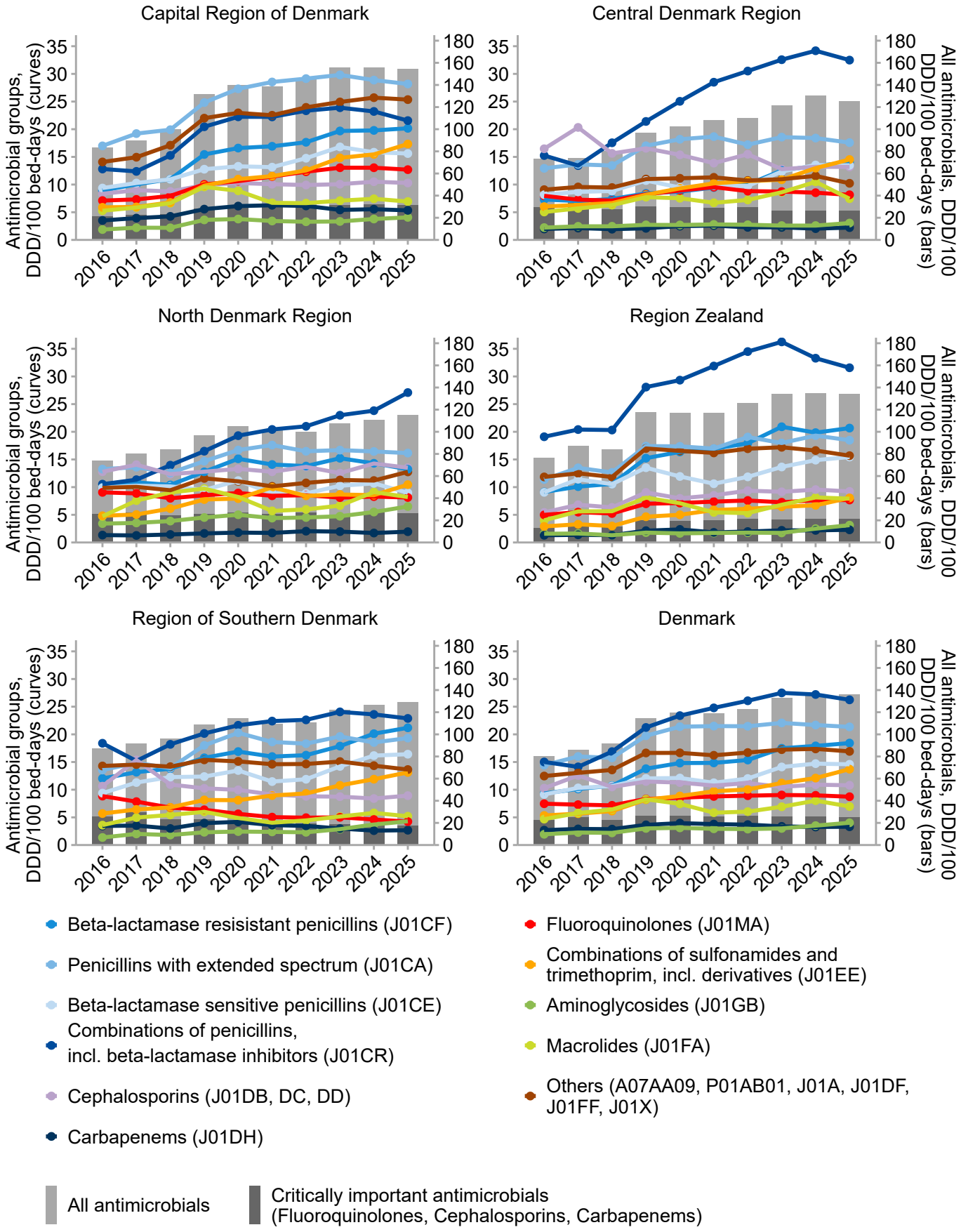
| ATC group | Therapeutic group | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| J01AA | Tetracyclines | 9.88 | 9.44 | 10.66 | 15.36 | 12.93 | 13.35 | 14.33 | 16.14 | 16.97 | 15.16 |
| J01CA | Penicillins with extended spectrum | 68.14 | 72.94 | 69.04 | 78.43 | 83.93 | 84.28 | 83.45 | 84.70 | 81.88 | 79.80 |
| J01CE | Beta-lactamase sensitive penicillins | 43.19 | 47.05 | 46.72 | 47.83 | 47.53 | 44.12 | 46.72 | 54.16 | 55.54 | 54.53 |
| J01CF | Beta-lactamase resistant penicillins | 43.99 | 46.21 | 46.97 | 54.79 | 58.15 | 58.20 | 59.74 | 67.10 | 67.64 | 68.85 |
| J01CR | Comb. of penicillins. incl. beta-lactamase inhibitors | 70.86 | 64.39 | 73.96 | 84.37 | 91.78 | 97.19 | 101.36 | 105.53 | 102.73 | 98.07 |
| J01DB | First-generation cephalosporins | 0.20 | 0.19 | 0.17 | 0.13 | 0.15 | 0.14 | 0.13 | 0.11 | 0.05 | 0.02 |
| J01DC | Second-generation cephalosporins | 43.47 | 50.95 | 40.43 | 39.64 | 38.43 | 36.32 | 37.18 | 34.32 | 35.18 | 34.66 |
| J01DD | Third-generation cephalosporins | 4.85 | 6.14 | 5.39 | 5.82 | 5.70 | 5.67 | 6.19 | 5.90 | 5.95 | 5.67 |
| J01DF | Monobactams | 0.05 | 0.03 | 0.03 | 0.05 | 0.04 | 0.02 | 0.06 | 0.03 | 0.12 | 0.13 |
| J01DH | Carbapenems | 12.70 | 13.26 | 12.57 | 14.47 | 15.52 | 14.83 | 14.34 | 12.93 | 12.30 | 12.35 |
| J01EA | Trimethoprim and derivatives | 1.76 | 1.91 | 1.96 | 1.95 | 2.14 | 2.01 | 1.86 | 1.74 | 1.53 | 1.47 |
| J01EB | Short-acting sulfonamides | 0.47 | 0.47 | 0.45 | 0.43 | 0.30 | 0.30 | 0.24 | 0.18 | 0.19 | 0.12 |
| J01EE | Comb. of sulfonamides and trimethoprim. incl. derivatives | 25.23 | 25.83 | 26.90 | 32.54 | 34.76 | 38.08 | 39.06 | 42.98 | 45.68 | 51.25 |
| J01FA | Macrolides | 22.11 | 26.33 | 28.14 | 32.84 | 29.19 | 22.93 | 23.45 | 26.54 | 30.29 | 26.04 |
| J01FF | Lincosamides | 2.94 | 2.98 | 3.42 | 3.62 | 3.44 | 3.25 | 3.31 | 3.49 | 3.56 | 3.79 |
| J01GB | Aminoglycosides | 9.17 | 10.29 | 9.63 | 11.91 | 12.16 | 11.49 | 11.20 | 11.52 | 13.24 | 15.03 |
| J01MA | Fluoroquinolones | 35.23 | 33.27 | 31.43 | 33.07 | 33.54 | 34.44 | 34.67 | 34.70 | 33.91 | 32.63 |
| J01XA | Glycopeptides | 5.11 | 6.05 | 5.69 | 6.52 | 7.15 | 7.16 | 6.90 | 6.38 | 7.16 | 7.37 |
| J01XB | Polymyxins | 0.91 | 0.89 | 1.02 | 1.07 | 1.14 | 1.12 | 1.15 | 1.37 | 1.77 | 1.35 |
| J01XC | Steroid antibacterials (fusidic acid) | 0.54 | 0.31 | 0.28 | 0.28 | 0.25 | 0.27 | 0.21 | 0.22 | 0.18 | 0.09 |
| J01XD | Imidazole derivatives | 21.24 | 21.45 | 19.44 | 20.06 | 20.36 | 18.77 | 18.05 | 17.55 | 16.83 | 16.19 |
| J01XE | Nitrofuran derivatives (nitrofurantoin) | 1.12 | 1.17 | 1.21 | 1.37 | 1.67 | 1.47 | 1.49 | 1.76 | 1.43 | 1.20 |
| J01XX05 | Methenamine | 0.37 | 0.33 | 0.47 | 0.38 | 0.41 | 0.54 | 0.51 | 0.59 | 0.50 | 0.52 |
| J01XX08 | Linezolid | 1.71 | 1.71 | 2.35 | 2.59 | 2.34 | 2.39 | 2.63 | 2.61 | 2.74 | 2.38 |
| J01XX09 | Daptomycin | 0.23 | 0.38 | 0.64 | 0.32 | 0.46 | 0.59 | 0.52 | 0.50 | 0.47 | 0.50 |
| A07AA09 | Vancomycin | 2.29 | 2.40 | 2.22 | 2.66 | 3.18 | 2.76 | 3.19 | 3.34 | 3.45 | 3.51 |
| P01AB01 | Metronidazole | 10.24 | 9.37 | 8.73 | 9.35 | 9.50 | 9.12 | 8.77 | 8.74 | 6.85 | 8.02 |
| J01, P01AB01, A07AA09 | All antimicrobial agents for systemic use, incl. metronidazole and vancomycin | 438.0 | 455.7 | 449.9 | 501.9 | 516.2 | 510.8 | 520.7 | 545.1 | 548.1 | 540.7 |

Data: Antimicrobial consumption at somatic hospitals.
Data source: The Register of Medicinal Product Statistics, the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system and National Patient Register.

Figures 5.19 and 5.20 show antimicrobial consumption at hospitals by health care region. The overall trends are similar to national level trends; however, the figures show different levels of antimicrobial consumption as well as different compositions of the consumption in the regions. Regions with highly specialised hospitals treating complicated infections, show higher and broader consumption of antimicrobials.

**Figure 5.19 Consumption of antimicrobial agents for systemic use at hospitals in the five health regions, DDD per 100 bed-days, Denmark, 2016-2025**

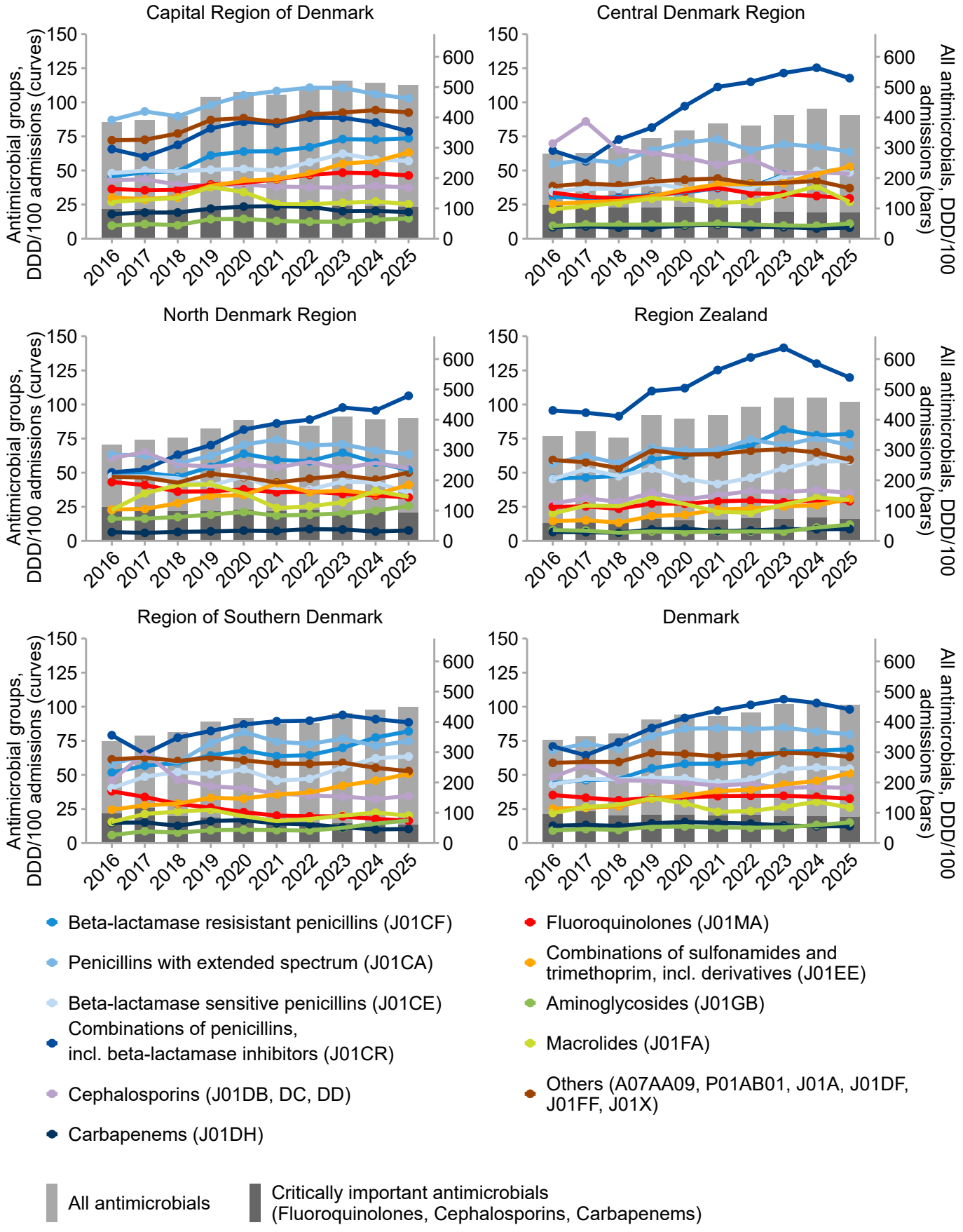
DANMAP 2025




Data: Antimicrobial consumption at somatic hospitals.
Data source: Register of Medicinal Product Statistics, and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system and National Patient Register.

**Figure 5.20 Consumption of antimicrobial agents for systemic use at hospitals in the five health regions, DDD per 100 admissions, Denmark, 2016-2025**

DANMAP 2025



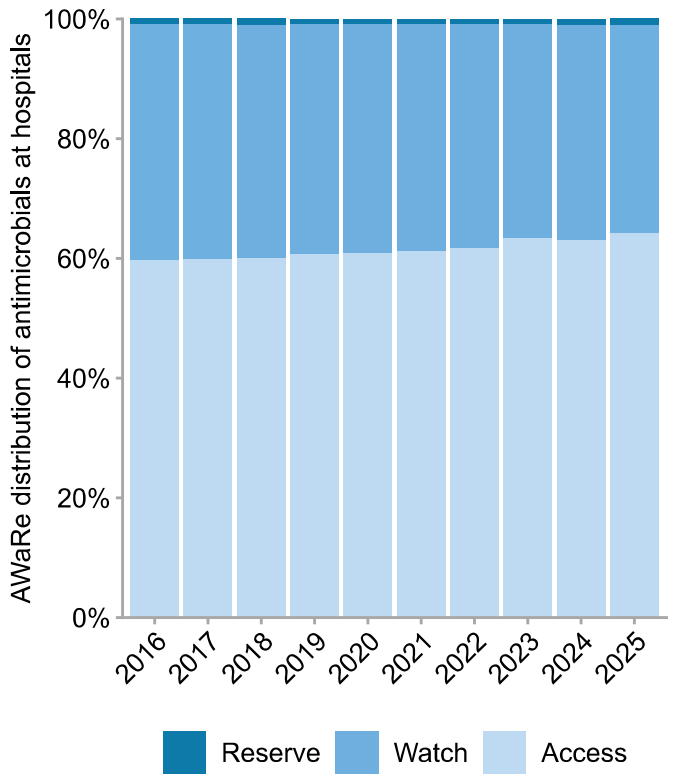

Data: Antimicrobial consumption at somatic hospitals.
Data source: Register of Medicinal Product Statistics, and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system and National Patient Register.

### 5.5.2 AWaRe classification of antimicrobials at Danish somatic hospitals

The World Health Organization (WHO) has developed the AWaRe classification system as a tool to assist antibiotic stewardship and to reduce antimicrobial resistance. Antibiotics are classified into three groups to emphasise the importance of their appropriate use:

- Access: Antibiotics used to treat common susceptible pathogens with lower resistance potential than antibiotics in the other groups. 60% of total antimicrobial consumption should consist of access agents.
- Watch: Antibiotics that have higher resistance potential, including most of the highest priority agents. These antibiotics should be prioritised as key targets of stewardship programs and monitoring.
- Reserve: Antibiotics reserved for treatment of confirmed or suspected infections due to multi-drug resistant organisms. These antibiotics should be considered as "last resort" options.

**Figure 5.21 Percentage distribution of antimicrobials at somatic hospitals according to WHO AWaRe classification, DDD, Denmark, 2016-2025** DANMAP 2025




Data: Antimicrobial consumption at somatic hospitals.
Data source: Register of Medicinal Product Statistics and the 2026 edition of the Anatomical Therapeutic Chemical (ATC) classification system.

Antimicrobial consumption at Danish somatic hospitals has consisted of more than 60% "access antimicrobials" since 2016, and in 2025 the share was 64%. "Reserve antimicrobials" constituted 1% in all years (Figure 5.21).

Several hospitals work with a stricter classification of antimicrobials and have set up local criteria for the use of certain antimicrobials associated with observed increasing levels of resistance. For instance, amoxicillin and beta-lactamase inhibitor are moved from the access group to watch, and meropenem from the watch group to reserve.

### 5.5.3 Shortage of antimicrobials

Issues with supply chains of antimicrobials can lead to product shortages. Some shortages do not reach the patient due to the substitution rules in Denmark. Shortages can also be solved by using non-marketed antimicrobials on special delivery, which requires permission from the Danish Medicines Agency.

In 2025, levofloxacin and metronidazole were the most purchased antimicrobials via special deliveries (Table 5.8). In 2023, nitrofurantoin was hit by a shortage and even with increased supply via special deliveries, it was not possible to cover the whole need, which is why other antimicrobials were chosen for treatment.

In 2022, penicillin/beta-lactamase inhibitor combinations decreased sharply in July and August due to product shortages. However, prescribers had access to penicillin/beta-lactamase inhibitor combinations via special deliveries. Approximately 70,000 DDD of penicillin/betalactamase inhibitor combinations were purchased through special delivery in 2022, whereas in 2019-2021 the number was approximately 4,000 DDD (not shown). Special deliveries could not meet the demand for penicillin/beta-lactamase inhibitor combinations in 2017, which led to a significant decrease in consumption that year (Figure 5.17). Simultaneously, an increase in consumption of cephalosporins was observed.

Danish authorities have launched several initiatives at national, Nordic and European levels to improve and secure access to antimicrobials (Textbox 5.1 in DANMAP 2024).

**Table 5.8 Consumption of selected antimicrobials on special delivery to hospitals, DDD, 2016-2025** DANMAP 2025

| Antimicrobial | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|
| J01MA12 Levofloxacin | 463 | 435 | 392 | 412 | 320 | 180 | 193 | 214 | 199 | 8,728 |
| P01AB01 Metronidazole | | | | | | | | | 525 | 4,025 |
| J01FA09 Clarithromycin | | | | 6,895 | 6,840 | 4,790 | 3,850 | 2,620 | 2,780 | 3,365 |
| J01GB01 Tobramycin | 6,704 | 8,188 | 7,596 | 7,136 | 3,094 | 7,985 | 2,610 | 3,760 | 2,502 | 1,235 |
| J01EE01 Sulfamethoxazole and trimethoprim | 1,195 | 690 | 766 | 726 | 1,028 | 908 | 935 | 890 | 985 | 960 |
| J01CF05 Flucloxacillin | | | | 125 | 500 | 225 | 325 | 275 | 700 | 870 |
| J01MA02 Ciprofloxacin | 160 | 160 | 200 | 425 | 390 | 466 | 1,067 | 533 | 856 | 728 |
| J01CR02 Amoxicillin and beta-lactamase inhibitor | 3,276 | 2,579 | 3,882 | 4,348 | 4,277 | 3,934 | 4,177 | 1,726 | | |
| J01CR05 Piperacillin and beta-lactamase inhibitor | | 16,465 | 4,457 | | | | 63,808 | | | |
| J01XE01 Nitrofurantoin | | | | | | | | 7,950 | 425 | |

Data: Consumption of antimicrobials on special delivery.
Data source: Danish Hospital Pharmacies.

We would like to acknowledge Maja Laursen from the National Health Data Authority in Denmark for data on antimicrobial consumption. We would also like to acknowledge all hospital pharmacies in Denmark for data on special delivery of antimicrobials to the hospitals. Finally, we would like to acknowledge the panel of experts from clinical microbiology laboratories and from research centers for general practice for their valuable input to this chapter.

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## Textbox 5.1

# The Danish Hospital Medication Register: new opportunities for examining antibiotic therapy in Danish hospitals

The Danish Hospital Medication Register provides patient-level data on medication administered in all public hospitals and affiliated hospital outpatient clinics in Denmark (1, 2). This register expands opportunities for pharmacoepidemiological research by enabling analyses of hospital medication use, including antibiotic treatment choices such as de-escalation strategies, and the transition from intravenous to oral therapy across different patient populations. Opposite the aggregated annual data reported in the DANMAP reports, the Danish Hospital Medication Register provides patient-level information on actual medication administrations. The Danish Hospital Medication can be linked with other Danish health registries, including the Danish National Prescription Registry, the Danish Microbiology Database, and the Danish National Patient Register, which provides a unique opportunity to examine complete antibiotic treatment courses spanning both hospital and community settings.

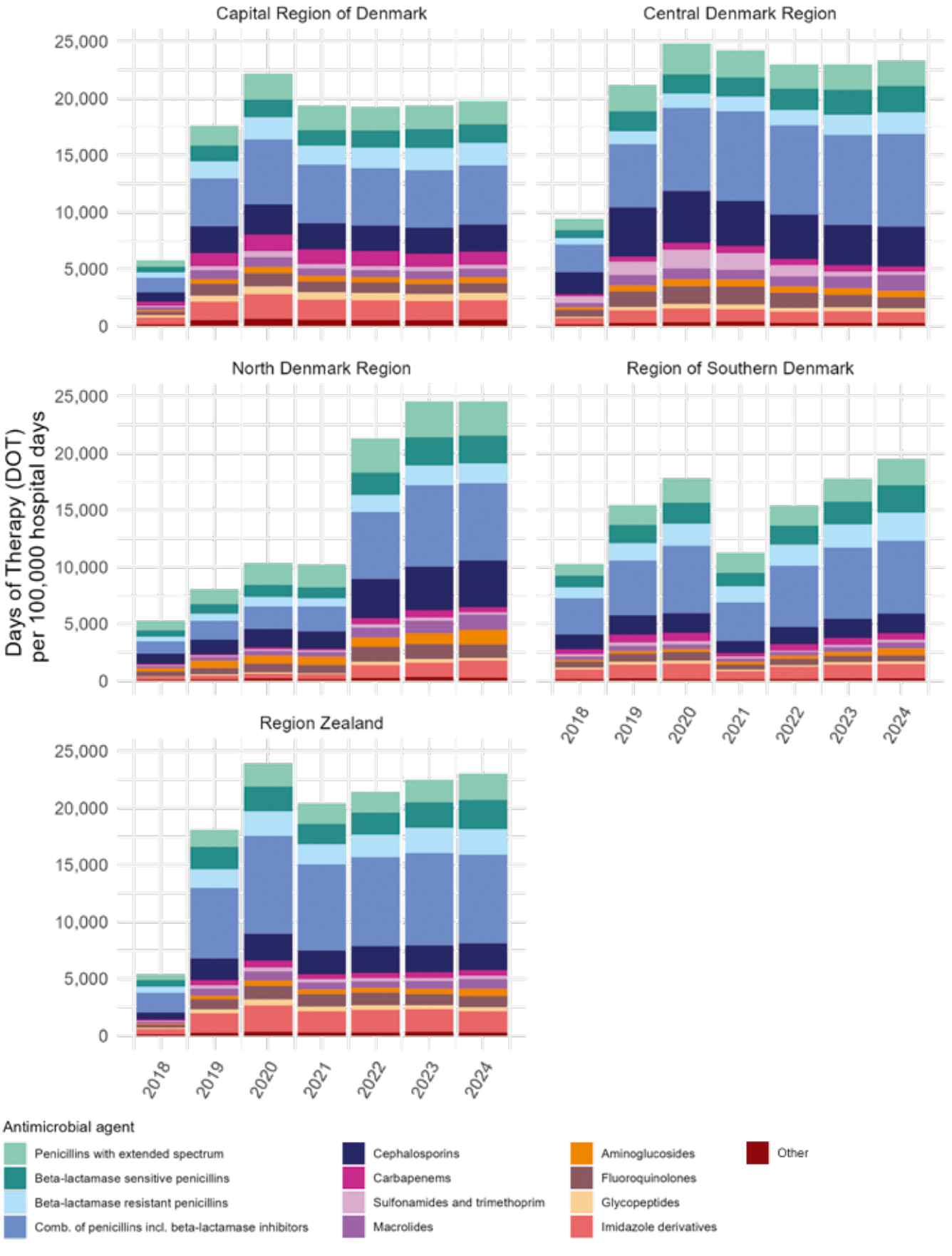
However, important differences in data recording should be considered. The Danish Hospital Medication Register records each medication administration, whereas the Danish National Prescription Registry records redeemed prescriptions, resulting in uncertainty regarding treatment duration and medication adherence. The patient-level data from the Danish Hospital Medication Register also enable calculation of measures relevant to antimicrobial stewardship such as the number of treated patients or Days of Therapy (DOT) (3). However, some variables, such as dose units, are incompletely recorded and/or coded using a wide range of different units, requiring substantial data management before analysis. No published studies have evaluated the validity of the Danish Hospital Medication Register.

This textbox aims to characterize the use of antimicrobial agents administered during hospitalization across hospital regions and age groups. The analyses include all antibiotics (ATC code group J01) recorded in the Danish Hospital Medication Register between 15 May 2018 and 11 November 2024. DOT were defined as the administration of at least one dose of a specific antimicrobial agent to an individual on a given calendar day (3). Each antimicrobial agent was counted separately (3). Therefore, a patient receiving several antimicrobial agents on the same day contributed one DOT per antimicrobial agent. Hospital days were defined as the total number of calendar days on which an individual had inpatient or outpatient hospital contact during the study period. A calendar day counts as one hospital day regardless of the number of hours spent at the hospital by the patient.

The number of DOT per 100,000 hospital days appeared lower in 2018 across all regions, likely reflecting incomplete reporting during the initial implementation of the register. In the North Denmark Region, DOT per 100,000 hospital days remained substantially lower until 2022, suggesting incomplete reporting during this period. Across all regions and years, combinations of penicillins including beta-lactamase inhibitors, accounted for the largest proportion of DOT. The distribution of antimicrobial agents was similar across hospital regions. The overall DOT per 100,000 hospital days was lower in the Region of Southern Denmark than in the other regions throughout the study period. In the Capital Region of Denmark, the Central Denmark Region, and Region Zealand, DOT per 100,000 hospital days was highest in 2020 (Figure 1).

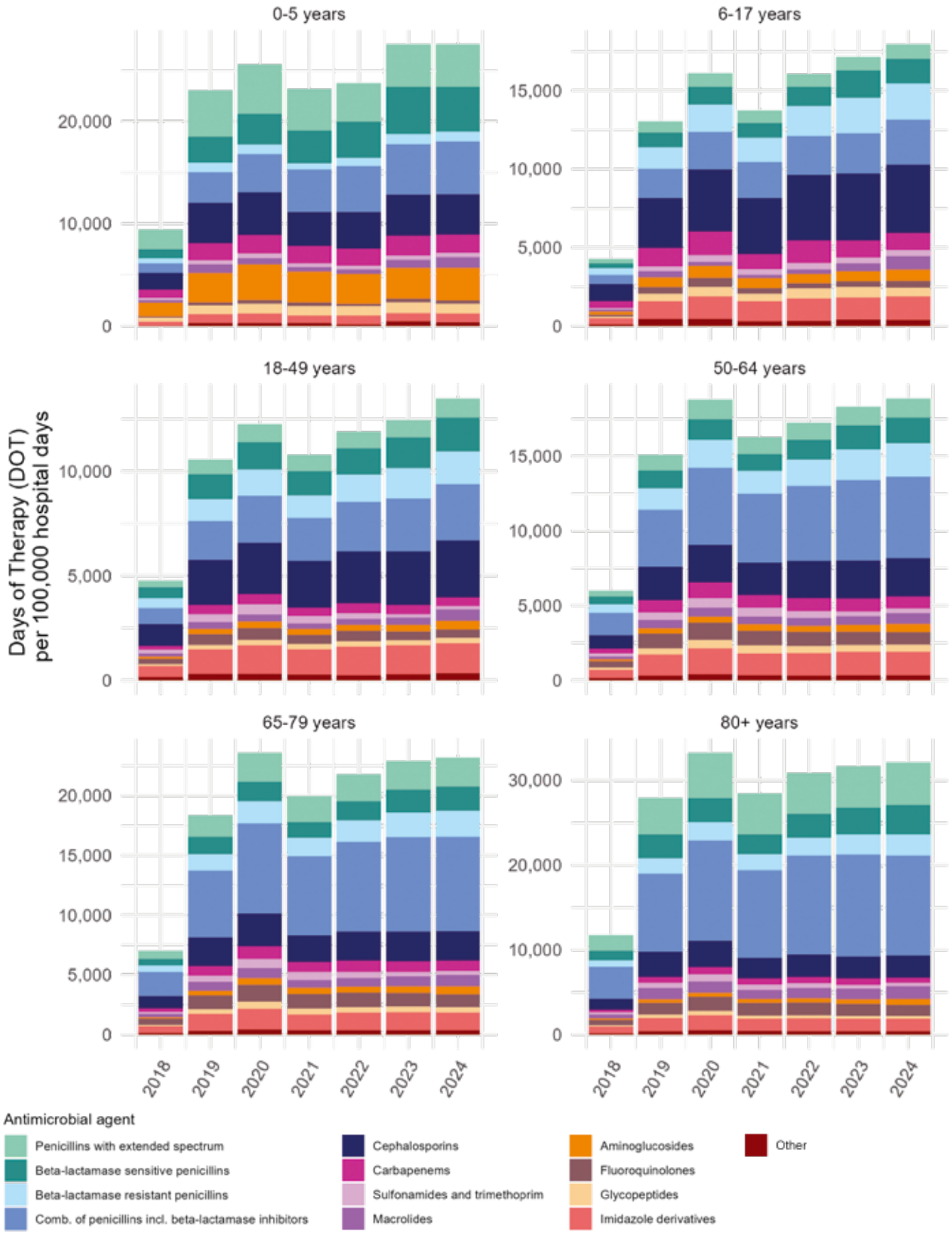
The overall DOT per 100,000 hospital days, summed across all antimicrobial agents, was highest among individuals aged 80 years and older, followed by children aged 0-5 years and individuals aged 65-79 years. Among individuals aged 0-5 years, 50-64 years, 65-79 years, and 80 years and older, combinations of penicillins including beta-lactamase inhibitors, accounted for the largest proportion of DOT. In contrast, cephalosporins accounted for the largest proportion of DOT among individuals aged 6-17 years and 18-49 years. Aminoglycosides contributed a higher proportion of DOT among children aged 0-5 years compared with the other age groups (Figure 2).

**Figure 1. Days of Therapy (DOT) per 100,000 hospital days stratified by antimicrobial agent and hospital region** DANMAP 2025



continued ... Textbox 5.1

**Figure 2. Days of Therapy (DOT) per 100,000 hospital days stratified by antimicrobial agent and age group** DANMAP 2025



In summary, the use of antimicrobial agents during hospitalization was similar across Danish regions, with combinations of penicillins including beta-lactamase inhibitors being the most commonly used antimicrobial agents. The overall DOT per 100,000 hospital days was highest among patients aged 80 years and older, while patterns of antimicrobial administration differed across age groups. Lower recorded use of antimicrobial agents in 2018 and in North Denmark until 2022 likely reflect incomplete reporting.

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**References**

[1] Rosenkrantz O, Wheler J, Westphal Thrane MC, Pedersen L, Sørensen HT. The Danish National Hospital Medication Register: A Resource for Pharmacoepidemiology. Clin Epidemiol. 2024;16:783-92.
[2] Andersen MA, Jensen TL, Petersen TS. Data Resource Profile: The Danish National Hospital Medicine Register. Pharmacoepidemiol Drug Saf. 2024;33(11):e70054.
[3] Yarrington ME, Moehring RW. Basic, Advanced, and Novel Metrics to Guide Antibiotic Use Assessments. Current Treatment Options in Infectious Diseases. 2019;11(2):145-60.

## Textbox 5.2

# IMAGINE – improving antibiotic use in European nursing homes

**Combining infection prevention and antimicrobial stewardship**

Nursing home residents are particularly vulnerable to infections and are often treated with antibiotics. Suspected urinary tract infection (UTI) is the most common reason for antibiotic treatment[1], yet more than half of the treatments may be unnecessary[2]. This highlights the need for interventions that not only support appropriate diagnosis and antibiotic use but also strengthen infection prevention in nursing homes.

The aim of the European IMAGINE project – *Improving antibiotic use in long-term care facilities through infection prevention and control and antimicrobial stewardship* – was therefore to develop, in close collaboration with nursing home staff, a multifaceted intervention suitable for nursing homes across Europe. The intervention was designed to strengthen infection prevention and control (IPC) and antimicrobial stewardship (AMS), ultimately reducing unnecessary antibiotic use by targeting staff in nursing homes across eight European countries: Greece, Hungary, Lithuania, Poland, Slovakia, Slovenia, Spain, and Denmark.

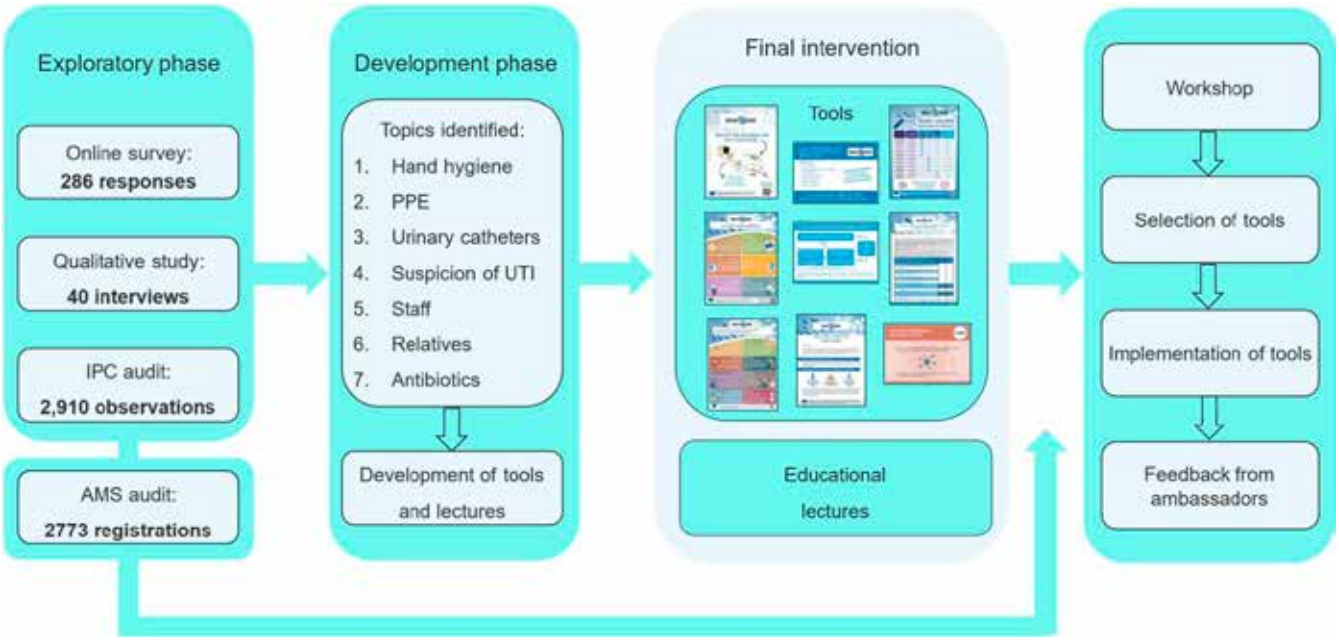
**Not just an intervention *for* nursing home staff – but *with* them**

A central feature of IMAGINE was the use of Participatory Action Research (PAR). Nursing home staff were recruited as IMAGINE ambassadors and participated as partners throughout the project. They collected audit data, contributed with their knowledge on everyday nursing home practice, participated in workshops and helped implement the intervention locally[3].

The intervention was designed around an exploratory phase. It included an online survey[4], a qualitative study[5], IPC audit, and AMS audit[6] (Figure 1). Data obtained were combined with input from nursing home staff to identify seven priority areas: hand hygiene, personal protective equipment, urinary catheters, suspicion of UTI, staff competences, relatives and antibiotics (Figure 1).

Based on these findings, ten practical tools were developed, ranging from posters and leaflets to an infection prevention quiz, educational material for newly employed staff and a pocket card with an decision algorithm for suspected UTI – (see Figure 1). The intervention also included educational sessions and workshops in each participating country.

**Figure 1 Overview of the development and implementation of the IMAGINE intervention** DANMAP 2025



**Did it make a difference?**

A total of 109 nursing homes across the participating countries signed on IMAGINE. 103 completed the project and participated in both the IPC and AMS audits conducted in spring 2024 and repeated one year later in spring 2025.

Overall, adherence improved significantly for 17 of the 29 assessed IPC practices. Improvements were particularly evident for the availability of IPC resources and practices related to the handling of indwelling urinary catheters, although considerable variation was observed between countries[7].

Antibiotic use for suspected UTI also changed. Among residents without an indwelling urinary catheter, the proportion of antibiotic treatments classified as potentially unnecessary decreased from 52.9% before the intervention to 46.1% after the intervention. The overall result, however, conceals considerable variation between countries.

Interestingly, the incidence of antibiotic-treated UTI, across the 103 nursing homes decreased from a mean of 12.2% to 8.9%, corresponding to a relative reduction of approximately 27%. Denmark showed a reduction from 17.0% to 9.7%, corresponding to a 43% reduction[7] (Table 1). In Denmark, this reduction was accompanied by a marked change in diagnostic practice, where the use of urinary dipsticks for suspected UTI decreased by 77%. Changes in antibiotic-treated UTI were smaller in most of the other participating countries, and Slovakia showed an increase.

**Table 1 Incidence of antibiotic-treated UTIs during a three-month period among residents at 103 nurs-ing homes in eight European countries before and after the IMAGINE intervention, 2024-2025** DANMAP 2025

| Country | Number of residents at participating nursing homes | First registration (2024) | Second registration (2025) | Paired t-test |
|---|---|---|---|---|
| | | Mean UTI incidence (%) | Mean UTI incidence (%) | P-value |
| Denmark | 1,066 | 17.0 | 9.7 | 0.026 |
| Greece | 440 | 17.8 | 16.0 | 0.405 |
| Hungary | 1,536 | 11.0 | 8.3 | 0.165 |
| Lithuania | 779 | 4.8 | 3.8 | 0.546 |
| Poland | 1,441 | 3.7 | 3.4 | 0.878 |
| Slovakia | 918 | 4.4 | 6.8 | 0.153 |
| Slovenia | 2,414 | 14.3 | 12.6 | 0.176 |
| Spain | 1,124 | 26.6 | 13.3 | 0.006 |
| Total | 9,718 | 12.2 | 8.9 | 0.000 |

**What can we learn from IMAGINE?**

The IMAGINE project was based on a before-and-after study without a control group, and the observed changes therefore cannot with certainty be attributed to the intervention. Nor can we determine which of the individual components – audit and feedback, education, practical tools, peer discussion or staff involvement – contributed most to the observed changes.

Nevertheless, the findings suggest an important direction for antimicrobial stewardship in nursing homes. Preventing infections and improving antibiotic use may be most effective when approached together.

**One size can fit all**

Despite differences in healthcare systems, organization and culture, IMAGINE identified common challenges across the 103 nursing homes, allowing the same core tools to be used in all eight countries – suggesting that sometimes "one size" may actually fit quite many.

**continued ... Textbox 5.2**

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**References**

[1] European Centre for Disease Prevention and Control. *Point Prevalence Survey of Healthcare-Associated Infections and Antimicrobial Use in European Long-Term Care Facilities: 2023 2024*. (Publications Office, LU, 2025). doi:10.2900/5735023.

[2] Llor, C. *et al.* Assessment of potentially unnecessary antibiotic use for suspected urinary tract infections in nursing homes using a simplified algorithm. *Expert Rev Anti Infect Ther* 1–7 (2025) doi:10.1080/14787210.2025.2456860.

[3] Theut, M. *et al.* Development of a participatory action research-based intervention to enhance infection prevention and antimicrobial stewardship among European nursing home staff. *JAC Antimicrob Resist* **8**, dlag158 (2026).

[4] Chalkidou, A. *et al.* Symptoms associated with Urinary Tract Infection in Nursing Home Residents: A Study Among Nursing Home Staff Across Eight European Countries. *Infection Prevention in Practice* 100563 (2026) doi:10.1016/j.infpip.2026.100563.

[5] Theut, M. *et al.* Factors influencing urinary tract infection prevention and antibiotic stewardship in European nursing homes: an interview study with staff. *Eur Geriatr Med* **16**, 2293–2303 (2025).

[6] Theut, M. *et al.* Signs and symptoms attributed to urinary tract infections in nursing home residents across eight European countries | European Geriatric Medicine | Springer Nature Link. https://link.springer.com/article/10.1007/s41999-026-01427-9.

[7] Jensen JN *et al.* Impact of a multifaceted intervention integrating infection prevention and control and antibiotic stewardship in the management of urinary tract infections in nursing homes in eight European countries, 2023-2025. (Forthcoming). Accepted for publication in Eurosurveillance, August 2026.

## Textbox 5.3

# *Free from UTI* in the Region of Southern Denmark

**An initiative to prevent urinary tract infections among nursing home residents**
The aim of this initiative is to reduce the incidence of urinary tract infections (UTIs) among nursing home residents and to reduce antibiotic consumption within the nursing home sector.

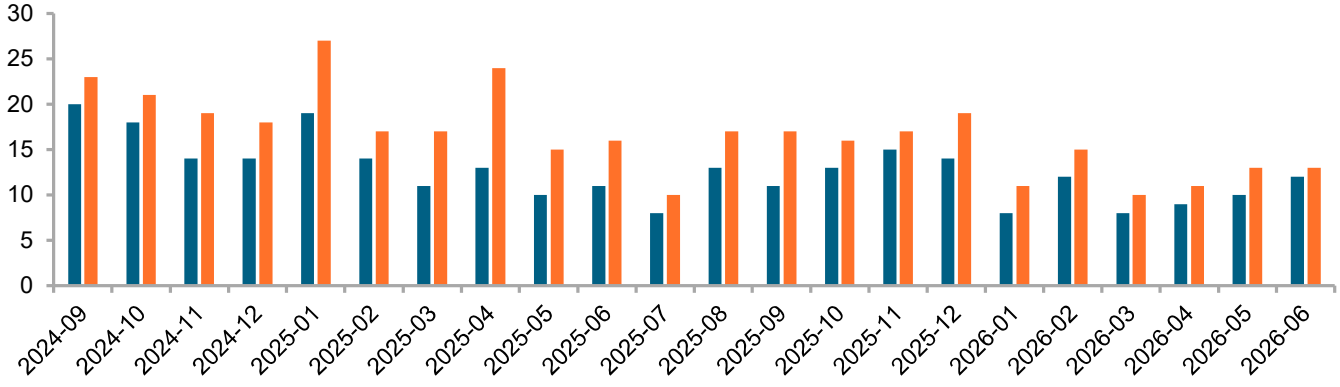
Antibiotic consumption is high among Danish nursing home residents compared with other European countries [1]. The majority is prescribed against UTI, though more than half of these treatments may be unnecessary as diagnostic criteria for UTI are not met [2]. There is a great potential for reducing the number of antibiotic prescriptions for nursing home residents and thereby reducing unnecessary adverse effects.

**The pilot project**
*Free from UTI* began as a pilot project in 2024 at two selected nursing homes in Nyborg and Odense [3]. Drawing inspiration from other initiatives in Denmark and abroad, the Department of Clinical Microbiology at Odense University Hospital developed a two-hour interactive training seminar in close collaboration with Nyborg and Odense municipalities. This seminar, including short instructional sessions, exercises, and case discussions, was attended by all staff at the two nursing homes. The seminar covered the basics of UTI and antibiotics as well as prevention of UTI and basic hygienic measures. Decision-support tools were developed to assist nursing home staff in assessing residents with suspected UTI. The use of urine dipsticks was discontinued as part of the project.

Both nursing homes succeeded in significantly reducing the incidence of UTIs and antibiotic consumption. One nursing home achieved a 66% reduction in the total number of UTI treatments (from 65 in 2023 to 22 in 2024). The other nursing home achieved a 46% reduction (from 67 in 2024 to 36 in 2025).

**Continuation of the project**
In 2025, *Free from UTI* was implemented at the remaining public nursing homes in Nyborg and Odense by a "train-the-trainers" method. Key staff members such as specialist nurses, managers, and nursing home doctors were trained to implement *Free from UTI* in their own settings. This effort has been well received in general and antibiotic consumption continues to decline (Figures 1 and 2). Successful implementation of *Free from UTI* principles depends on interdisciplinary collaboration and requires strong leadership commitment. Furthermore, it is essential to have permanent staff members acting as project ambassadors to maintain the effect. The aim is to expand the initiative to nursing homes throughout the Region of Southern Denmark.

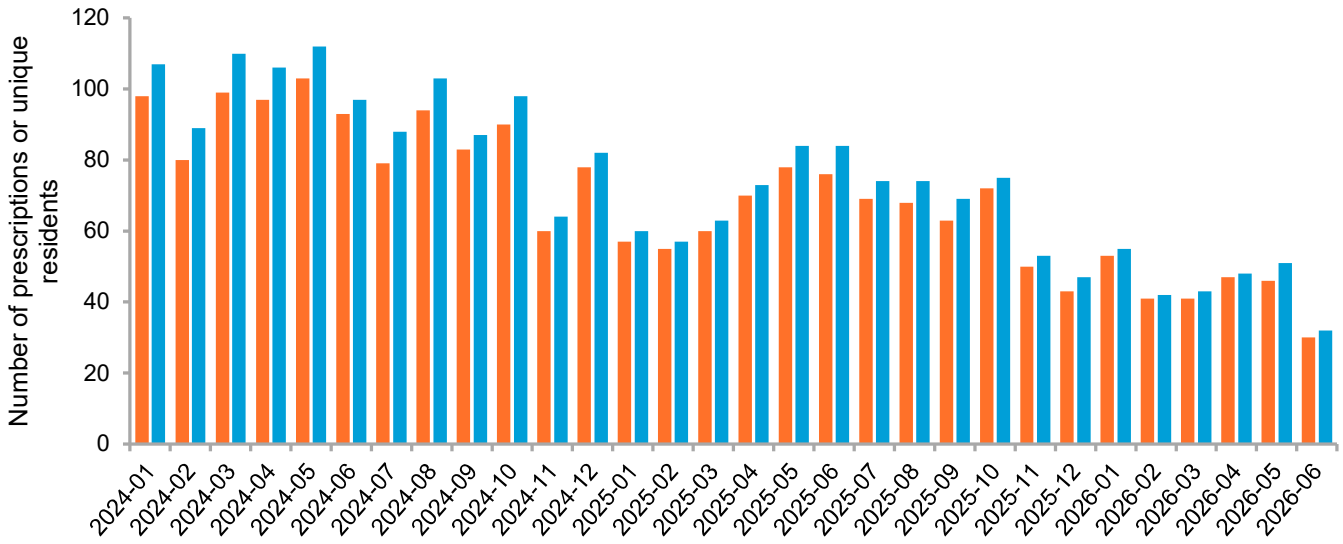
**Figure 1 Use of antibiotics against UTI among nursing home residents in Nyborg from September 2024 to June 2026** DANMAP 2025




Number of prescriptions against UTI (orange) and number of unique residents treated against UTI (blue) per month in public nursing homes in Nyborg (approximately 186 residents in total).
The figure is based on cumulated medicine data from the municipality. Data is not adjusted for date of residency; some treatments may have been initiated before moving into the nursing home. Prescriptions of UTI specific antibiotics cover pivmecillinam, trimethoprim, sulfamethizol, or nitrofurantoin.

continued ... Textbox 5.3

**Figure 2 Use of antibiotics against UTI among nursing home residents in Odense from January 2024 to June 2026** DANMAP 2025




Number of prescriptions against UTI (orange) and number of unique residents treated against UTI (blue) per month in public nursing homes in Odense (approximately 929 residents in total).
The figure is based on cumulated medicine data from the municipality. Data is not adjusted for date of residency; some treatments may have been initiated before moving into the nursing home. Prescriptions of UTI specific antibiotics cover pivmecillinam, trimethoprim, sulfamethizol, or nitrofurantoin.

*Klinisk Mikrobiologisk Afdeling, Odense Universitetshospital & Nyborg og Odense Kommuner*
*For further information: Anne Marie Rosendahl Madsen, Anne.Rosendahl@rsyd.dk*

**References**

[1] European Centre for Disease Prevention and Control. Point Prevalence Survey of Healthcare-Associated Infections and Antimicrobial Use in European Long-Term Care Facilities: 2023 2024. (Publications Office, LU, 2025). doi:10.2900/5735023.
[2] Llor, C. et al. Assessment of potentially unnecessary antibiotic use for suspected urinary tract infections in nursing homes using a simplified algorithm. Expert Rev Anti Infect Ther. 2025 Feb-Apr;23(2-4):235-241. doi: 10.1080/14787210.2025.2456860.
[3] Klinisk Mikrobiologisk Afdeling, Odense Universitetshospital et al. Fri for UVI, Forebyg Urinvejsinfektion på Plejehjem. https://ouh.dk/media/e4un0ffw/rapport_fri-for-uvi_20250319-tvs-opdateret-og-webtilgaengelig.pdf (2025).



# 6.

# Resistance in zoonotic bacteria

# 6. Resistance in zoonotic bacteria

**Highlights:** The **levels of resistance in *Campylobacter jejuni* and *C. coli* in Denmark in 2025 were consistent with the overall pattern observed in previous years,** with high levels of resistance to ciprofloxacin and tetracycline, and low levels of resistance to chloramphenicol, erythromycin, and gentamicin among isolates from humans and broilers. Ciprofloxacin resistance was observed in 57% and 72% of *C. jejuni* isolates from domestic and travel associated human cases, respectively, and in 45% of isolates from broilers.

**Ciprofloxacin resistance in domestic human and broiler isolates was higher than in previous years.** The increase was prompted by two major human domestic outbreaks caused by two distinct ciprofloxacin resistant clones, which were also detected in broilers. This illustrates how the emergence of individual clones can influence resistance levels in both human and broiler isolates.

**Macrolide resistance remained rare in *C. jejuni* and *C. coli*.** Erythromycin resistance was detected in 1% of human *C. jejuni* isolates and was not observed among broiler isolates. The continued low prevalence of macrolide resistance supports the use of macrolides as first line treatment for severe human campylobacteriosis.

**In *Salmonella* spp., azithromycin resistance was observed in 1% of human isolates,** with no resistance detected among domestically acquired cases. Resistance to third-generation cephalosporins was observed in 2% of isolates, while no resistance to meropenem was detected. Ciprofloxacin resistance was observed in 16% of isolates, with resistance levels of 9% in domestic cases (up from 5% in 2024) and 23% among travel-related cases. Gentamicin resistance was seen in 3% of *Salmonella* spp. isolates and in 9% of human monophasic *S.* Typhimurium cases, the highest level recorded in the last 5 years.

**Resistance to critically important antimicrobials,** namely quinolones, third-generation cephalosporins, colistin or carbapenems, **remained uncommon in *Salmonella* spp. from Danish pigs and pork** and no resistance to colistin, meropenem or quinolones was observed. One *S.* Derby isolate from a pig displayed an unusual ceftazidime-resistant phenotype, although no genetic ESBL or AmpC resistance determinants were identified. Increased levels of gentamicin resistance were also observed among *S.* Derby and *S.* Typhimurium isolates from domestic pigs and pork. The **increasing occurrence of gentamicin resistance in *Salmonella* warrants continued attention.**

Whole genome sequencing showed that changes in the frequency of resistance determinants among human *S.* Typhimurium and monophasic *S.* Typhimurium correlated with changes in the circulating resistant and susceptible *Salmonella* clones. **Genetic determinants conferring resistance to clinically important antimicrobials remained uncommon** and were detected only sporadically in 2025.

*Salmonella* sequence data isolates collected from **Danish pork samples** indicates the presence of a broad set of common resistance genes as well as a **sporadic occurrence of variants conferring resistance to gentamicin and azithromycin.**

## 6. 1 Introduction

### 6.1.1 Introduction to resistance in zoonotic bacteria

Zoonoses are infectious diseases transmitted between animals and humans through direct contact or indirectly via contaminated food, water or environment. In DANMAP, information on antimicrobial resistance (AMR) in zoonotic bacteria is collected from the national programme for monitoring and control on zoonoses. For more information see the Annual Report on Zoonoses in Denmark 2025 [www.food.dtu.dk].

In humans, AMR is monitored in all clinical *Salmonella* spp. isolates, except for *S.* Enteritidis, for which only a subset of isolates is tested. For *Campylobacter jejuni* and *C. coli*, a geographically stratified selection of clinical isolates is tested. The testing is performed in accordance with the ECDC recommendations (see Chapter 10, section 10.9). Travel histories of the patients are collected when possible.

In Denmark, antimicrobials are generally not recommended for patients with acute bacterial gastroenteritis, as most infections are self-limiting. Treatment with antibiotics may be considered in case of severe illness, specific risk factors, or signs of systemic infection. Azithromycin (macrolide) is the recommended oral empirical treatment for acute bacterial gastroenteritis and is active against both *Campylobacter* and non-typhoidal *Salmonella* spp. For non-typhoidal *Salmonella* gastroenteritis, ciprofloxacin may be used as an alternative to azithromycin if susceptibility is confirmed. For *Campylobacter* bacteraemia, intravenous clarithromycin (macrolide) is recommended, with the possible addition of a single dose of gentamicin. For suspected bacteraemia or sepsis caused by non-typhoidal *Salmonella*, empirical treatment with ceftriaxone (third-generation cephalosporin) is recommended, with a switch to ciprofloxacin if susceptibility is confirmed. Information regarding concrete antimicrobial usage in diarrheal patients on patient level is currently not available.

Isolates from food-producing animals for antimicrobial susceptibility testing were obtained from healthy animals at slaughter. *Salmonella* spp. was obtained from swab samples of pork and cattle carcasses, and caecal samples from pigs and cattle. *Campylobacter* isolates were obtained from caecal samples of pigs, cattle, and broilers. Antimicrobial susceptibility testing of *Campylobacter* and *Salmonella* from animals and meat was done in accordance with the Commission Implementing Decision 2020/1729/EU of 17 November 2020 (see Chapter 10 for further details).

In Danish food-producing animals, macrolides are often used to treat infections, particularly in pigs. Fluoroquinolones and third- and fourth-generation cephalosporins are not used in production animals. The use of antimicrobials in the Danish poultry sector is low and limited to a few antimicrobial classes, primarily tetracyclines (see Chapter 4, Table 4.1).

## 6.2 *Campylobacter* spp.

In 2025 a total of 234 human isolates of *C. jejuni* (195 domestic, 36 travel-associated, and three with unknown travel history) and 44 isolates of *C. coli* (33 domestic, 10 travel-associated, and one with unknown travel history) were tested for antimicrobial susceptibility.

In animals, all *C. jejuni* isolates recovered from broilers (51), cattle (171), and pigs (8), as well as all *C. coli* from broilers (3), cattle (5), and pigs (165) were tested for antimicrobial susceptibility. Due to low numbers of isolates recovered, resistance data for *C. jejuni* in pigs and *C. coli* in broilers and cattle are not reported.

### 6.2.1 Resistance in *Campylobacter jejuni*

The resistance levels recorded in *C. jejuni* isolates from humans, Danish broilers and cattle at slaughter in 2025 are shown in Table 6.1. The ten-year trends in resistance to selected antimicrobials are shown in Figure 6.1.

In 2025, 39% of isolates from human cases (42% domestically acquired and 28% from travel related cases), 53% of *C. jejuni* from broilers, and 68% from cattle were fully susceptible to all tested antimicrobials. The percentage of fully susceptible *C. jejuni* isolates from human cases, broilers, and cattle has overall remained stable over the past decade (Figure 6.1).

Except for ciprofloxacin, antimicrobial resistance levels among *C. jejuni* isolates from human cases have remained relatively stable over the past ten years. In general, resistance levels have been higher among isolates from travel-associated cases than among those from domestically acquired cases. Human isolates also have generally higher levels of resistance than isolates from broilers and cattle.

Resistance to ciprofloxacin and tetracycline is common in *C. jejuni* from both humans and food-producing animals, except in cattle.

In 2025, 60% of *C. jejuni* isolates from human cases were resistant to ciprofloxacin, with resistance levels of 57% and 72% among isolates from domestic and travel-associated cases, respectively. The overall level of resistance to tetracycline was 25%, while resistance levels of 21% and 42% were observed among isolates from domestic and travel-associated cases, respectively.

The percentage of ciprofloxacin resistance among isolates from domestic human cases was higher in 2025 than in previous years. This increase was associated with two large outbreaks traced to Danish broiler meat, caused by two distinct ciprofloxacin resistant *C. jejuni* clones [Benedetti et al., Euro Surveill. 2025;30(47)]. This coincided with increased levels of ciprofloxacin resistance observed in broiler isolates in 2025. A similar situation was observed in 2019 among human isolates, when another specific clone also contributed substantially to an elevated level of ciprofloxacin resistance. This indicates that the levels of ciprofloxacin and tetracycline resistance in *C. jejuni* is affected by the composition of the *C. jejuni* population circulating in the food chain at a given time.

In 2025, an increase in tetracycline and ciprofloxacin resistance was observed in *C. jejuni* isolates from cattle, 6% and 32%, respectively (1% and 26% in 2024). In broilers a level of 25% tetracycline and 45% ciprofloxacin resistant *C. jejuni* isolates was observed, an increase from 2024 (17% and 29%) (Table 6.1).

As in previous years, combined resistance to ciprofloxacin and tetracycline in *C. jejuni* isolates was common; 25% from human cases (47% in travel-related and 20% in domestically acquired cases) and 24% from broilers (Table 6.1 and Figure 6.1). Over the last 10 years, the prevalence of isolates with this resistance profile has fluctuated slightly in domestic human cases and in broilers but remained stable for travel-related cases and cattle (Figure 6.1).

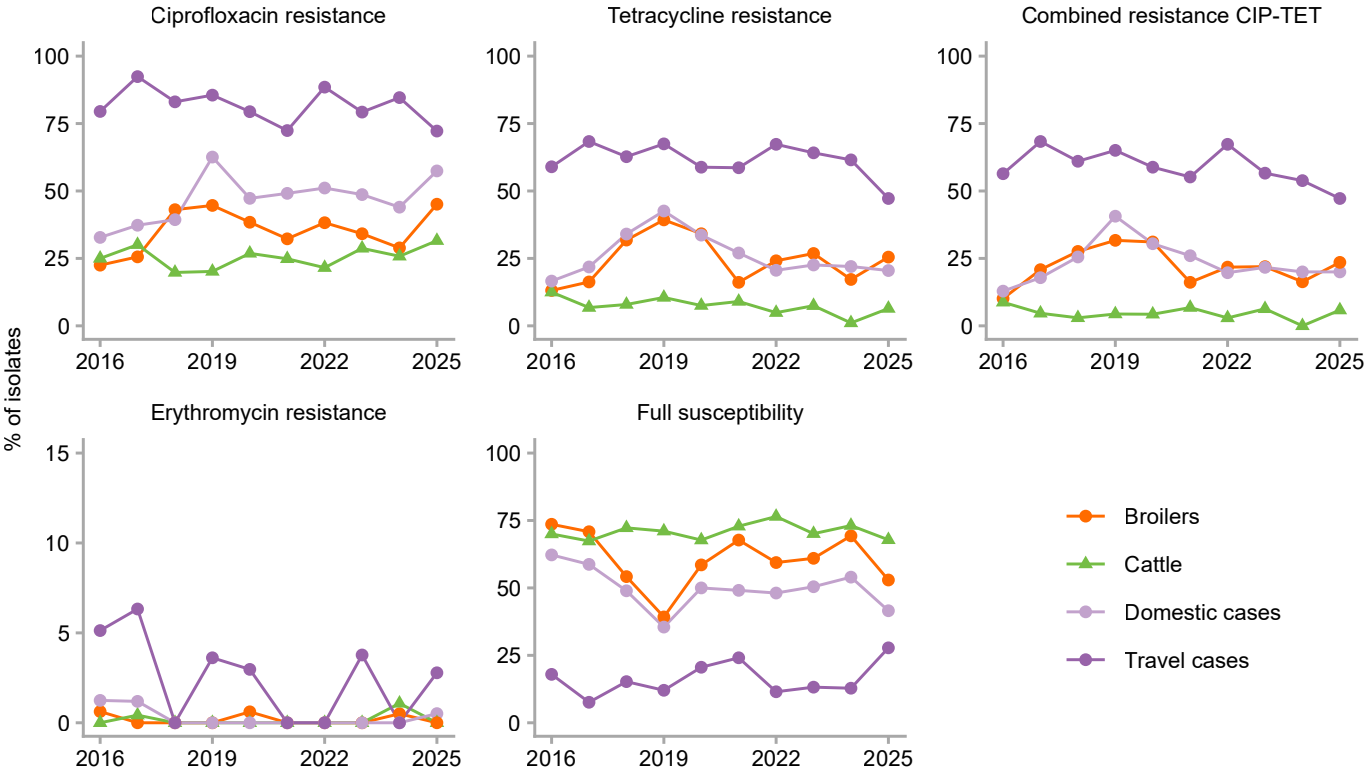
In 2025, macrolide (erythromycin) resistance was observed in two human isolates, one domestic and one travel-related, respectively, while no macrolide resistance was observed in broiler and cattle *C. jejuni* isolates. Resistance to macrolides is of concern since macrolides are frequently used for the treatment of patients. The two erythromcyin resistant isolates were simultaneously resistant towards ciprofloxacin and tetracycline. The genetic basis for the resistance was one isolate with mutations in the ribosomal 23S DNA and one isolates harboured the *erm*B gene.

**Table 6.1 Resistance (%) in *Campylobacter jejuni* isolates from broilers, cattle and human cases, Denmark, 2025** DANMAP 2025

| | Broilers | Cattle | | Human | |
|---|---|---|---|---|---|
| | Danish | Danish | All | Domestically acquired | Travel abroad reported |
| Antimicrobial agent | % | % | % | % | % |
| Chloramphenicol | 0 | 0 | 0 | 0 | 0 |
| Ciprofloxacin | 45 | 32 | 60 | 57 | 72 |
| Ertapenem | 2 | 0 | 2 | 1 | 6 |
| Erythromycin | 0 | 0 | 1 | <1 | 3 |
| Gentamicin | 0 | 0 | 0 | 0 | 0 |
| Tetracycline | 25 | 6 | 25 | 21 | 47 |
| CIP-TET | 24 | 6 | 25 | 20 | 47 |
| Fully susceptible | 53 | 68 | 39 | 42 | 28 |
| Number of isolates | 51 | 171 | 234 | 195 | 36 |

An isolate is categorised as domestically acquired if the patient did not travel outside Denmark one week prior to the onset of disease. The threshold for resistance to ertapenem in Campylobacter has not been validated by the European Committee on Antimicrobial Susceptibility Testing (EUCAST), ECOFF as provided by EFSA [EFSA Supporting publication 2023:EN-7826]. CIP-TET: all isolates with both ciprofloxacin and tetracycline resistance. Fully susceptible: isolates sensitive to all antimicrobial agents included in the test panel (See Chapter 10, Table 10.3).

**Figure 6.1 Resistance to ciprofloxacin, tetracycline, erythromycin, combined ciprofloxacin and tetracycline resistance and full susceptibility (%) among *Campylobacter jejuni* from broilers, cattle and human cases, Denmark, 2016-2025** DANMAP 2025




An isolate is categorised as domestically acquired if the patient did not travel outside Denmark one week prior to the onset of disease. CIP-TET: all isolates with both ciprofloxacin and tetracycline resistance. Fully susceptible: isolates sensitive to all antimicrobial agents included in the test panel (see Chapter 10, Table 10.2).

Resistance to chloramphenicol and gentamicin was rare and in 2025, no resistance to chloramphenicol and gentamicin was seen among human, broiler and cattle *C. jejuni* isolates.

Ertapenem resistance has been monitored in *Campylobacter* since 2021. There has not been established any generally recognized epidemiological cut-off (ECOFF) or clinical breakpoints for ertapenem resistance. Therefore, the clinical relevance of human isolates resistant to ertapenem is unclear. The EU Reference Laboratory for AMR (EURL-AMR) and the European Food Safety Authority (EFSA) have established a provisional ECOFF of 0.5 mg/L (Chapter 10, Table 10.2), and this has been adopted in DANMAP.

In 2025, two *C. jejuni* isolates from domestic human cases, two from travel-related cases, and one from broilers, were above the ECOFF for ertapenem.

### 6.2.2 Resistance in *Campylobacter coli*

The 2025 resistance data for *C. coli* isolates from humans and Danish fattening pigs at slaughter are presented in Table 6.2.

The data from the 44 human *C. coli* isolates indicate high levels of resistance in *C. coli*. In travel related cases resistance to ciprofloxacin and tetracycline was observed in 80% and 80% of the isolates, respectively. The similar level in domestic cases was 58% for ciprofloxacin and 55% for tetracycline. These levels are comparable to those observed in 2023 and 2024, the first years of reporting human data. Seven percent (three isolates) of the human *C. coli* isolates in 2025 were resistant to erythromycin. The resistance in these isolates was mediated by point mutations in the 23S ribosomal DNA. The three isolates were also resistant towards ciprofloxacin and tetracycline.

In 2025, an increase in fully susceptible *C. coli* isolates from pigs (64%) was observed compared to 2023 (53%) (Table 6.2). Resistance towards ciprofloxacin and tetracycline was observed in 13% and 30%, respectively, of *C. coli* isolates from pigs. This is a decrease from 2023, where 25% ciprofloxacin and 35% tetracycline resistant *C. coli* from pigs were reported. Resistance to erythromycin was observed in 3% (five isolates) of *C. coli* isolates from pigs, a decrease from 2023 (6%).

In 2025 chloramphenicol resistance was not observed in *C. coli* isolates from humans and pigs. Gentamicin resistance was observed in one of the human travel-related *C. coli* isolate, but was not observed in isolates from pigs.

As for *C. jejuni*, ertapenem resistance has been monitored in *C. coli* since 2021 using a provisional ECOFF of 0.5 mg/L (Chapter 10, Table 10.2). While in 2023, no isolates above the ECOFF for ertapenem were reported in *C. coli* from pigs, in 2025 one *C. coli* isolate above the ertapenem ECOFF from pigs was observed.

**Table 6.2 Resistance (%) in *Campylobacter coli* from fattening pigs and human cases, Denmark, 2025** DANMAP 2025

| | Pigs | Human | | |
|---|---|---|---|---|
| | Danish | All | Domestically acquired | Travel abroad reported |
| Antimicrobial agent | % | % | % | % |
| Chloramphenicol | 0 | 0 | 0 | 0 |
| Ciprofloxacin | 13 | 64 | 58 | 80 |
| Ertapenem | 1 | 32 | 33 | 20 |
| Erythromycin | 3 | 7 | 6 | 10 |
| Gentamicin | 0 | 2 | 0 | 10 |
| Tetracycline | 30 | 61 | 55 | 80 |
| Fully susceptible (%) | 64 | 30 | 33 | 20 |
| Number of isolates | 165 | 44 | 33 | 10 |

An isolate is categorised as domestically acquired if the patient did not travel outside Denmark one week prior to the onset of disease. The threshold for resistance to ertapenem in Campylobacter has not been validated by the European Committee on Antimicrobial Susceptibility Testing (EUCAST), ECOFF as provided by EFSA [EFSA Supporting publication 2023:EN-7826].

## 6.3 *Salmonella* spp.

In 2025 a total of 669 human isolates of *Salmonella* spp., including 337 domestic, and 250 travel-related cases were tested for antimicrobial susceptibility. The isolates represented 93 different serotypes. The predominant serotypes were *S.* Typhimurium (137 isolates), monophasic *S.* Typhimurium with the antigenic formula 4,[5],12:i:- (79 isolates), and *S.* Enteritidis (39 isolates). Except for *S.* Enteritidis, the tested isolates represented all clinical Danish isolates and included outbreak isolates. These included 49 outbreak isolates of fully susceptible *S.* Typhimurium, 12 outbreak isolates of monophasic *S.* Typhimurium, and 29 outbreak isolates of fully susceptible *S.* Strathcona, as well as isolates from a few other smaller outbreaks.

Also in 2025, a total of 205 *Salmonella* spp. isolates from pigs (116 isolates) and pork meat (89 isolates) were tested for antimicrobial susceptibility. The most prevalent serotypes reported in domestic pigs and pork were *S.* Derby (103 isolates), monophasic *S.* Typhimurium (52 isolates), and *S.* Typhimurium (23 isolates).

The current report only presents available data from domestic pig and Danish pork isolates. The lack of AMR data from isolates from a wider variety of sources limits the possibilities for comparison of resistance levels between animals at slaughter, food, and humans. Another limitation for comparison of resistance levels over the years in isolates from food-producing animals and food, is that only a small number of isolates are recovered yearly, and domestic pigs are only sampled every second year. It is known that there are other sources of human salmonella infections than domestic pork.

Clonal dissemination plays an important role in the occurrence of antimicrobial resistance, in particular among *S.* Typhimurium and monophasic *S.* Typhimurium.

Historically, DANMAP has focused on phenotypic resistance in *S.* Typhimurium and the related monophasic variant 4,[5],12:i:-, as these serotypes are prevalent in both human isolates and isolates from food-producing animals and derived products.

The resistance levels recorded among *Salmonella* spp. isolates from humans are presented in Table 6.4. Resistance data from domestic pigs and pork isolates are presented in Table 6.3 for *S.* Typhimurium and monophasic *S.* Typhimurium, and in Figure 6.5 for *S.* Derby.

### 6.3.1 Resistance in human *Salmonella* spp. isolates

The resistance levels in human isolates are presented in Table 6.4.

**Table 6.4 Resistance (%) in *Salmonella* from humans, Denmark, 2025** DANMAP 2025

| | Other *Salmonella* serovars | | |
|---|---|---|---|
| | Human | | |
| | Domestically acquired | Travel abroad reported | Total |
| Antimicrobial agent | % | % | % |
| Amikacin | <1 | <1 | <1 |
| Ampicillin | 21 | 18 | 19 |
| Azithromycin | 0 | 3 | 1 |
| Cefotaxime | 1 | 5 | 2 |
| Ceftazidime | 1 | 5 | 2 |
| Chloramphenicol | 6 | 8 | 7 |
| Ciprofloxacin | 9 | 27 | 16 |
| Colistin | 6 | 5 | 6 |
| Gentamicin | 2 | 5 | 3 |
| Meropenem | 0 | 0 | 0 |
| Nalidixic acid | 7 | 16 | 10 |
| Sulfamethoxazole | 19 | 17 | 18 |
| Tetracycline | 22 | 21 | 22 |
| Tigecycline | 1 | 2 | 1 |
| Trimethoprim | 6 | 10 | 7 |
| ASuT | 7 | 2 | 5 |
| MDR | 18 | 19 | 18 |
| Fully susceptible (%) | 66 | 60 | 63 |
| Number of isolates | 337 | 250 | 669 |

An isolate is categorised as domestically acquired if the patient did not travel outside Denmark one week prior to the onset of disease. Total number of human cases includes travel cases and infections of unknown origin. An isolate susceptible to all antimicrobial agents included in the test panel is considered fully susceptible (Chapter 10, Table 10.3).

Azithromycin resistance was observed in 1% of the isolates, with no resistance detected among domestically acquired cases. Resistance to third-generation cephalosporins was observed in 2% of the isolates, while no resistance to meropenem was detected. Ciprofloxacin resistance was observed in 16% of the isolates, with resistance levels of 9% and 23% among domestically acquired and travel-related cases, respectively. Among domestically acquired cases, ciprofloxacin resistance increased from 5% in 2024 to 9% in 2025. Gentamicin resistance was seen in 3% of all *Salmonella* spp. isolates in 2025.

Polymyxin (colistin) resistance is mainly seen in *S.* Dublin and *S.* Enteritidis isolates. Both serotypes, in particular *S.* Dublin, are regarded as intrinsically resistant towards polymyxins.

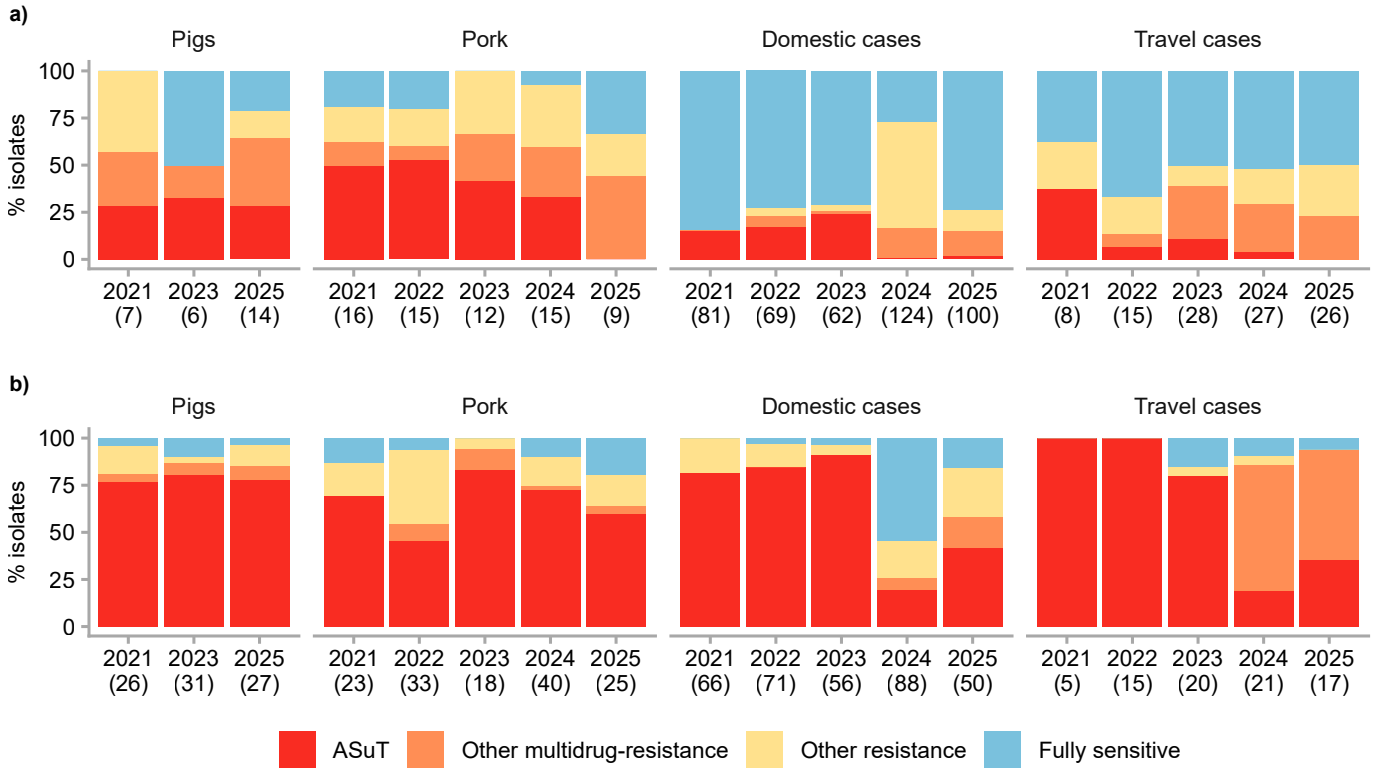
### 6.3.2 Resistance in *S.* Typhimurium and monophasic *S.* Typhimurium

The resistance levels observed for *S.* Typhimurium and monophasic *S.* Typhimurium isolates from human cases, domestic pigs, and pork in 2025, are presented in Table 6.3. The relative distribution (%) of AMR profiles from 2021 to 2025 for *S.* Typhimurium and monophasic *S.* Typhimurium in human domestic and travel-related cases, pigs, and pork are shown in Figure 6.2. The ten-year trends for resistance towards azithromycin, ciprofloxacin, and gentamicin, for *S.* Typhimurium and monophasic *S.* Typhimurium isolates combined from human domestic and travel-related cases, pigs, and pork are shown in Figure 6.3.

The resistance levels recorded in *S.* Typhimurium and monophasic *S.* Typhimurium isolates from human cases and pigs in 2025 are shown in Table 6.3. The levels of resistance in *S.* Typhimurium in humans are overall in accordance with the levels observed in the previous years. There is a numerical decrease in the resistance levels, but this is mainly a reflection of the 49 fully susceptible outbreak isolates. The resistance levels for monophasic *S.* Typhimurium are also overall in accordance with the normal picture, after a 2024, that deviated due to a human outbreak caused by an unusual clone that were susceptible to ampicillin, tetracycline, sulfamethoxazole. Importantly it should be noted that the level of gentamicin resistance in 2025 was 9% in monophasic *S.* Typhimurium, the highest level recorded the last five years.

Figure 6.2 presents the relative distribution (%) of AMR profiles for *S.* Typhimurium and monophasic *S.* Typhimurium combined from pigs, domestic pork and human domestic- and travel-related cases from 2021 to 2025.

**Figure 6.2 Relative distributions (%) of AMR profiles among *Salmonella* Typhimurium (a) and monophasic *S.* Typhimurium (b) from pigs, pork and human cases, Denmark, 2021-2025**
DANMAP 2025




Number of isolates included each year is presented in parentheses. Includes isolates verified as monophasic variants of S. Typhimurium with antigenic formula S. 4,[5],12:i:-. An isolate is considered fully susceptible if sensitive to all antimicrobial agents included in the test panel, and multidrug-resistant if resistant to three or more of all antimicrobial classes included in the test panel (See Chapter 10, Table 10.3). ASuT are multidrug-resistant isolates resistant to ampicillin, sulfamethoxazole and tetracycline. Caution in data interpretation should be taken in years with small numbers (n<15) of isolates from domestic pork, pigs and travel-associated cases. No data available for pigs in 2022 and 2024.

**Table 6.3 Resistance (%) in *Salmonella* Typhimurium and monophasic *S.* Typhimurium isolates from pigs, domestic pork and humans, Denmark, 2025** DANMAP 2025

| | *S.* Typhimurium | | Monophasic *S.* Typhimurium | | *S.* Typhimurium | | | Monophasic *S.* Typhimurium | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Pigs | Pork | Pigs | Pork | Human | | | Human | | |
| | Danish | Danish | Danish | Danish | Domestically acquired | Travel abroad reported | Total | Domestically acquired | Travel abroad reported | Total |
| Antimicrobial agent | % | % | % | % | % | % | % | % | % | % |
| Amikacin | 7 | 0 | 0 | 0 | 0 | 4 | 1 | 2 | 0 | 1 |
| Ampicillin | 50 | 33 | 89 | 68 | 13 | 4 | 10 | 76 | 82 | 77 |
| Azithromycin | 14 | 11 | 0 | 0 | 0 | 4 | 1 | 0 | 0 | 1 |
| Cefotaxime | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| Ceftazidime | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| Chloramphenicol | 29 | 33 | 19 | 24 | 9 | 15 | 10 | 8 | 6 | 8 |
| Ciprofloxacin | 0 | 0 | 0 | 0 | 3 | 31 | 8 | 4 | 18 | 8 |
| Colistin | 0 | 0 | 0 | 0 | 1 | 0 | 2 | 2 | 0 | 1 |
| Gentamicin | 29 | 11 | 7 | 8 | 2 | 4 | 2 | 8 | 6 | 9 |
| Meropenem | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Nalidixic acid | 0 | 0 | 0 | 0 | 1 | 8 | 2 | 2 | 12 | 5 |
| Sulfamethoxazole | 71 | 44 | 93 | 76 | 20 | 35 | 23 | 64 | 77 | 68 |
| Tetracycline | 57 | 11 | 85 | 60 | 22 | 39 | 26 | 70 | 65 | 70 |
| Tigecycline | 7 | 11 | 4 | 0 | 1 | 4 | 2 | 0 | 0 | 1 |
| Trimethoprim | 21 | 56 | 26 | 40 | 3 | 12 | 4 | 14 | 6 | 11 |
| ASuT | 29 | 0 | 78 | 60 | 2 | 0 | 2 | 42 | 35 | 42 |
| MDR | 36 | 44 | 7 | 4 | 13 | 23 | 14 | 58 | 59 | 61 |
| Fully susceptible (%) | 21 | 33 | 4 | 20 | 74 | 50 | 69 | 16 | 6 | 15 |
| Number of isolates | 14 | 9 | 27 | 25 | 100 | 26 | 137 | 50 | 17 | 79 |

Results are shown separately for *S.* Typhimurium and monophasic *S.* Typhimurium with antigenic formula *S.* 4,[5],12:i:-. Isolates from Danish pork were recovered from carcass swabs collected at slaughter. An isolate is categorised as domestically acquired if the patient did not travel outside Denmark one week prior to the onset of disease. Total number of human cases includes travel cases and infections of unknown origin. An isolate is considered fully susceptible if sensitive to all antimicrobial agents included in the test panel. An isolate is considered MDR, multi drug resistance, if resistant to three or more classes of antimicrobials (Chapter 10, Table 10.3).

The ten-year trends in resistance to azithromycin, ciprofloxacin, and gentamicin among *S.* Typhimurium and monophasic *S.* Typhimurium combined from human cases, domestic pigs, and pork are shown in Figure 6.3. Azithromycin resistance remained relatively stable throughout the period. Ciprofloxacin resistance was consistently higher among human isolates than among isolates from pigs and domestic pork. Among human cases, ciprofloxacin resistance was also higher in travel-related cases than in domestically acquired cases.

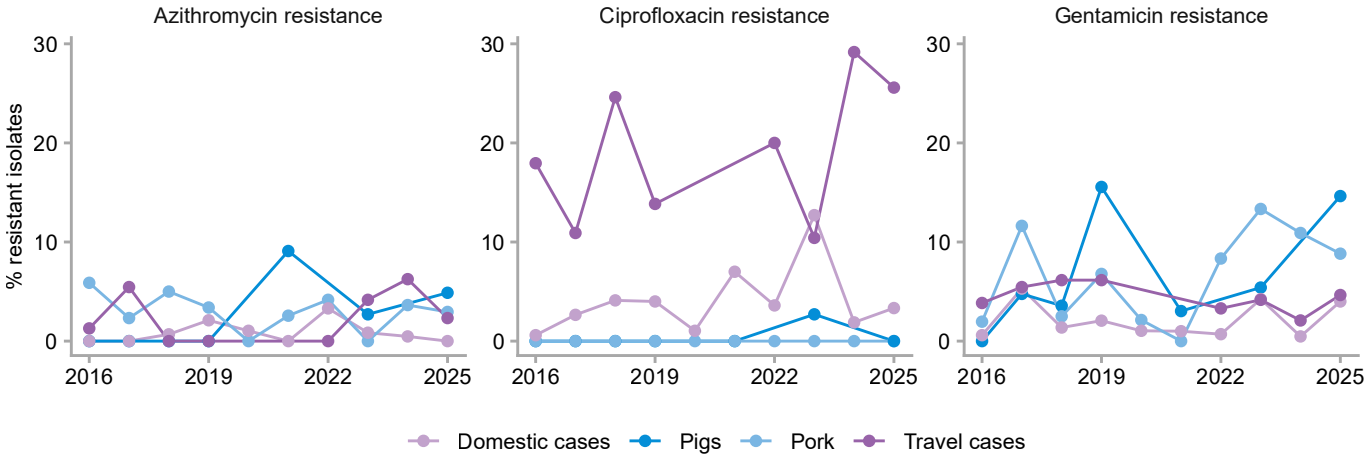
As in previous years, the occurrence of resistance in *S.* Typhimurium and monophasic *S.* Typhimurium continued to be overall higher in isolates from domestic pigs and pork than in isolates from humans.

The level of full susceptibility in *S.* Typhimurium (21%) and monophasic *S.* Typhimurium (4%) from pigs showed a decrease compared to 2023, while the level of full susceptibility in *S.* Typhimurium (33%) and monophasic *S.* Typhimurium (20%) from pork showed an increase compared to 2024 (Figure 6.2A and B).

No resistance towards critically important antimicrobials in *S.* Typhimurium and monophasic *S.* Typhimurium from domestic pigs and pork, were observed in 2025. In this context, critically important antimicrobials are quinolones, third- & fourth-generation cephalosporins, colistin or carbapenems, as defined in the national order on critical resistant *Salmonella* in poultry, cattle, and pigs (Bekendtgørelse 523 20/05/2025). As in previous years, resistance to third-generation cephalosporins (cefotaxime and ceftazidime), was not observed in 2025 (Table 6.3), and no resistance towards colistin, meropenem, or ciprofloxacin was reported. As shown in Figure 6.3, ciprofloxacin resistance has not been observed in domestic pork for more than 10 years and only few ciprofloxacin resistant isolates have been observed in domestic pigs in 2023.

The occurrence of resistance to tetracycline in monophasic *S.* Typhimurium from domestic pigs and pork remained high (85% and 60%, respectively). For pigs this is similar to levels found in 2023, while for pork the level of tetracycline resistance has decreased compared to 2023 (89%) and 2024 (80%). In 2025, the level of resistance to tetracycline in *S.* Typhimurium isolates from pigs (57%) were higher compared to 2023 (33%), while in pork (11%) it was lower than in 2024 (47%). However, caution in data interpretation should be taken, since only few isolates were recovered from domestic pork and pigs.

**Figure 6.3 Ciprofloxacin, azithromycin and gentamicin resistance (%) among *S.* Typhimurium and its monophasic variants from pigs, domestic pork and human cases, Denmark, 2016-2025** DANMAP 2025




Includes isolates of *S.* Typhimurium and monophasic *S.* Typhimurium with antigenic formula S. 4,[5],12:i:-. An isolate is categorised as domestically acquired if the patient did not travel outside Denmark one week prior to the onset of disease. Due to the low number of isolates (N<15), travel-associated cases are not shown separately for 2020 and 2021. No data available for pigs in 2020, 2022 and 2024.

As in previous years, in 2025, multidrug-resistance (MDR) towards ampicillin, sulfamethoxazole and tetracycline (ASuT) in monophasic *S.* Typhimurium is common in isolates from domestic pigs (78%) and pork (60%) (Figure 6.2). Other MDR-profiles were observed in 7% of pig and 4% of pork monophasic *S.* Typhimurium isolates.

Similar to previous years, most *S.* Typhimurium isolates recovered from domestic pigs and pork were resistant to several antimicrobials, with the ASuT-profile reaching 29% and 0%, respectively, and other MDR-profile levels reaching 36% and 44%, respectively.

As shown in Figure 6.2, there is a marked difference in S. Typhimurium and monophasic *S.* Typhimurium levels of MDR, especially for the ASuT-profile.

Minor fluctuations were observed for amikacin, ampicillin, azithromycin, chloramphenicol, sulfamethoxazole, tetracycline, tigecycline, and trimethoprim in domestic pigs and pork, however, this should be interpreted with caution due to the low number of isolates (Table 6.3). In 2025, an increase in resistance towards gentamicin was observed in *S.* Typhimurium isolates from domestic pigs compared to 2023, while the level of gentamicin resistance in *S.* Typhimurium from domestic pork (11%) remains similar to levels in 2022-2024 (Figure 6.3).

### 6.3.3 Genotypic resistance in *S.* Typhimurium and monophasic *S.* Typhimurium

Whole Genome Sequencing (WGS) can be used to complement antimicrobial susceptibility tests by identifying the genetic resistance mechanisms behind phenotypically expressed antimicrobial resistance. These mechanisms can be either induced by the specific genes or combination of genes, and/or point mutations. WGS makes it possible to investigate the dissemination of different genotypes within and across reservoirs.

*S.* Typhimurium and monophasic *S.* Typhimurium from domestic pork and human clinical isolates collected from 2021 to 2025 were investigated for genetic AMR determinants. A detailed description of the selection of isolates and methods used is included in Chapter 10.

In total, 633 *S.* Typhimurium isolates (443 domestic, 106 travel-associated) and 482 monophasic *S.* Typhimurium (335 domestic, 79 travel-associated) obtained from human cases in the period from 2021 to 2025, were included in the analysis of genetic AMR determinants. Overall, 62.9% of *S.* Typhimurium isolates and 16.8% of monophasic *S.* Typhimurium isolates did not carry any AMR determinants. Among the remaining isolates, 59 and 77 unique genetic AMR determinants were identified in *S.* Typhimurium and monophasic *S.* Typhimurium isolates from humans, respectively.

All the sequenced *S.* Typhimurium (58) and monophasic *S.* Typhimurium (121) isolates from Danish pork collected from 2021 to 2025 in accordance with the EU rules for AMR monitoring were included.

The occurrence of selected AMR determinants (%) among *S.* Typhimurium and monophasic *S.* Typhimurium from domestic pork and human cases from 2021 to 2025 is presented in Figure 6.4. The determinants shown were selected to highlight i) predominant and/or outbreak-associated resistance clones identified among human isolates, ii) resistance to clinically important antimicrobials, and iii) other commonly occurring or relevant AMR determinants. To illustrate the influence of specific clones on the occurrence of AMR determinants, selected determinants are grouped according to their association with outbreak-related clones or the predominant lineages. These determinants are not exclusive to the respective clones and may also occur in other isolates and AMR gene combinations.

**Resistance determinants in human *S.* Typhimurium isolates**
In both domestic and travel-associated human *Salmonella* Typhimurium isolates, *tet(A), sul2, aph(3")-Ib* and *aph(6)-Id* were among the most frequently detected AMR determinants (Outbreak 1 – associated, Figure 6.4a). In domestic isolates, the marked increase in these determinants observed in 2024 was followed by a marked decline in 2025. The high occurrence in 2024 was driven by an outbreak-associated *S.* Typhimurium clone carrying the resistance profile *aph(3")-Ib/aph(6)-Id/sul2/tet(A)*.

An increased occurrence of *aadA2*, *floR*, *sul1*, *blaCARB-2* and *tet(G)* observed in domestic isolates between 2022 and 2024 declined in 2025 (Multiple clone - associated, Figure 6.4a). The increased occurrence of these genes during 2022–2024 was largely associated with circulation of multiple *S.* Typhimurium clones carrying the multidrug resistance profile *aadA2/blaCARB-2/floR/qacEdelta1/sul1/tet(G)* with a subset of isolates harboring additional quinolone resistance determinants.

In contrast to these commonly occurring resistance profiles, determinants conferring resistance to clinically important antimicrobials remained uncommon and were detected only sporadically throughout the study period. The findings described below highlight the observations made in 2025.

A noteworthy finding in 2025 was the detection of a travel-associated isolate carrying a previously unobserved combination of clinically important resistance determinants comprising *aac(3)-VIa*, *aadA1*, *armA*, *mph(E)*, *msr(E)*, *qnrB7*, *sul1* and *tet(B)*. The isolate exhibited high-level resistance to amikacin (MIC 128 mg/L), gentamicin (MIC >16 mg/L) and azithromycin (MIC 64 mg/L), together with reduced susceptibility to ciprofloxacin (MIC 0.25 mg/L). No other known quinolone or azithromycin resistance determinants were identified in this isolate.

Other clinically relevant resistance determinants detected in 2025 included the plasmid-mediated quinolone resistance genes *qnrS1*, *qnrB2* and *qnrB19*, *gyrA* mutations D87N and D87Y and the gentamicin resistance determinant *aac(3)-IVa*.

The *blaCMY-2* gene, conferring resistance to third-generation cephalosporins, was detected in a single domestic isolate in 2025. Interestingly, this isolate and *blaCMY-2* positive isolate detected in 2021 carried an identical multidrug resistance profile comprising *aph(3")-Ib, aph(6)-Id, blaCMY-2*, *floR*, *sul2* and *tet(A)*.

As in previous years, determinants conferring resistance to colistin or carbapenems were not detected in 2025.

**Resistance determinants in pork *S.* Typhimurium isolates**
*S.* Typhimurium isolates collected from Danish pork samples in the years 2021 to 2025 have consistently shown a prevalence of resistance genes conferring resistance to beta-lactams (*blaTEM-1*), streptomycin (*aph(3")-Ib, aph(6)-Id, aadA2*), sulfamethoxazole (*sul2, sul1*), tetracycline (*tet(B), tet(A)*), and trimethoprim (*dfrA12*). Common and noteworthy gene prevalences are shown in Figure 6.4.

Of note is the continued presence of the gentamicin/apramycin resistance gene *aac(3)-IVa* in two isolates sampled in 2025, similar to the three isolates found in 2024. Furthermore, there were two isolates where macrolide resistance variants were detected: one isolate carried the R717L mutation of *acrB*, associated with azithromycin resistance, the other isolate carried *mph(E)* and *msr(E)* genes, which confer resistance to erythromycin and azithromycin. These findings are all the more noteworthy considering that only eight *S.* Typhimurium isolates from Danish pork were investigated in 2025.

In line with previous years, as well as with phenotypical results in 2025, no genes conferring resistance to carbapenems, cephalosporins, fluoroquinolones or polymyxins were detected in *S.* Typhimurium isolates from pork in 2025 (Table 6.3).

**Figure 6.4 Prevalence (%) of genetic determinants of antimicrobial resistance among *S.* Typhimurium (a) and its monophasic variant (b) from domestic pork and human cases, Denmark, 2021-2025**

DANMAP 2025




Number of isolates included each year is presented in parentheses. Outbreak-, Multiple clone-, and ST34-associated determinants may also occur in other isolates and AMR gene combinations, see text for details. OB 3 = Outbreak 3. Some rows show aggregate values for several genetic variants, these are: 1: *gyrA_D87G, gyrA_D87N, gyrA_D87Y, gyrA_S83A, gyrA_S83F, gyrA_S83Y;* 2: *qnrB19, qnrB2, qnrB7, qnrS1, qnrS13, qnrVC;* 3: *acrB_R717L, acrB_R717Q, mef(B), mph(A), mph(E), msr(E);* 4: *aac(3)-IId, aac(3)-IIe, aac(3)-IIg, aac(3)-IVa, aac(3)-VIa, aac(6')-Ic, armA;* 5: *mcr-1.1, mcr-3.1, mcr-3.40;* 6: *blaCTX-M-1, blaCTX-M-14, blaCTX-M-55, blaSHV-12.*

**Resistance determinants in human monophasic *S.* Typhimurium isolates**

In both domestic and travel-associated human monophasic *Salmonella* Typhimurium isolates, *blaTEM-1, tet(B), sul2, aph(3")-Ib* and *aph(6)-Id* were the most frequently detected AMR determinants. Together, these genes constituted the most common AMR genotype identified among the isolates in this study and are characteristic of the epidemic multidrug-resistant monophasic *S.* Typhimurium ST34 lineage circulating among human cases in Europe. In domestic isolates, the marked decline in these determinants in 2024, associated with a large outbreak caused by a fully susceptible monophasic *S.* Typhimurium clone, was followed by a return to levels comparable to those observed before 2024 (ST34 – associated, Figure 6.4b).

The increased occurrence of *aadA2* and *dfrA12* was observed in domestic isolates in 2025 (Outbreak 3 – associated, Figure 6.4b). This was largely explained by an outbreak of monophasic *S.* Typhimurium carrying these two genes. One of the eight outbreak isolates additionally carried *tet(A).*

Determinants conferring resistance to clinically important antimicrobials remained uncommon throughout the study period. The findings described below highlight the observations made in 2025.

In 2025, the plasmid-mediated quinolone resistance genes *qnrS1*, *qnrB19*, and the *gyrA* mutation S83A were detected. As in previous years, *qnrS1* and *qnrB19* occurred more frequently in travel-associated than domestic human isolates. The *gyrA* mutation S83A was present in a travel-associated isolate and was detected for the first time in a whole study period. Two aminoglycoside resistance determinants associated with gentamicin resistance, *aac(3)-IId* and *aac(3)-IVa*, were also detected in 2025.

In three of the monophasic *S.* Typhimurium that phenotypically were resistant to gentamicin it was not possible to identify the genetic basis for the resistance. The three isolates all exhibited a MIC value of 4, which is close to the ECOFF. One of the three strains were additionally resistant towards amikacin and the and the two other strains had MIC value that deviated one dilution range to the ECOFF.

Resistance determinants conferring resistance to third-generation cephalosporins, azithromycin and colistin were detected sporadically during 2021-2024, but none were identified in 2025. Carbapenem resistance determinants were absent throughout the whole study period.

**Resistance determinants in pork monophasic *S.* Typhimurium isolates**

The most common AMR profile in monophasic *S.* Typhimurium isolates obtained from Danish pork samples continues to match known resistances of the widespread ST34 lineage: while resistance gene prevalences found in 2025 differ slightly from previous years (Figure 6.4b), *blaTEM-1*, *sul2*, and *tet(B)* remain as the largest drivers of resistance to beta-lactams, sulfamethoxazole, and tetracycline.

Just as in the previous year, in 2025 there were again three isolates which each carried one of three noteworthy aminoglycoside resistance genes: *aac(3)-IId* (gentamicin), *aac(3)-IVa* (apramycin/gentamicin/tobramycin), and *aph(3')-Id* (amikacin/kanamycin). These genes were also detected in monophasic *S.* Typhimurium isolated from pork samples in 2022 and 2023.

Two isolates with genotypic macrolide resistance were found in 2025. Both isolates carried the two genes *rdmCL* and *mph(B)* which are associated with resistance to tylosin and erythromycin. This is in line with previous sporadic detections of macrolide resistance, for instance resistance to azithromycin via the gene *mph(A)* in 2024 as well as via the *acrB* mutations R717Q and R717L in 2021 and 2022.

Finally, there were no genotypes associated with resistance to critically important antimicrobials in monophasic *S.* Typhimurium isolated from pork samples in 2025. This has been true in previous years as well, going back as far as 2020.

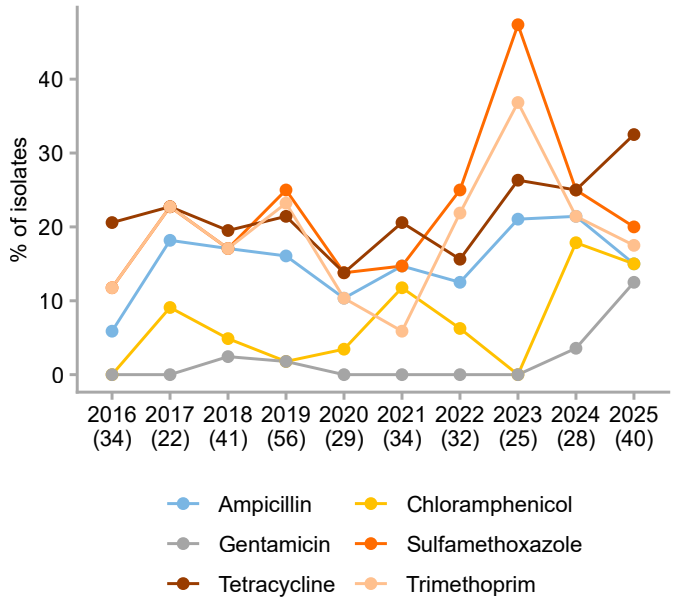
### 6.3.4 Resistance in other *Salmonella* serotypes from domestic pigs and pork

*S.* Derby was the most prevalent serotype in domestic pork and pigs, with 40 isolates recovered from pork and 63 from pigs. The occurrence of resistance in *S.* Derby is generally lower than in *S.* Typhimurium and monophasic *S.* Typhimurium. In 2025, 62.5% of *S.* Derby isolates from domestic pork and 73% of *S.* Derby isolates from domestic pigs were fully susceptible to all tested antimicrobials. This is comparable to what was seen in 2024 (64%) for domestic pork and in 2023 (70%) for domestic pigs.

Resistance levels to ampicillin, tetracycline, sulfamethoxazole, and trimethoprim in *S.* Derby from domestic pork and pigs remained similar to 2024, a decrease since the spike observed in 2023 (Figure 6.5).

In 2025, resistance to gentamicin was observed in 12.5% of domestic pork (five isolates) and 1.6% domestic pig (one isolate) *S.* Derby isolates, respectively. This is an increase from previous years, where 4% gentamicin resistant *S.* Derby isolates were observed in 2024, while no gentamicin resistance was observed in 2020-2023 (Figure 6.5).

**Figure 6.5 Resistance (%) among *Salmonella* Derby from domestic pork, Denmark, 2016-2025** DANMAP 2025




In 2025, resistance to critically important antimicrobials remained rare in *S.* Derby isolates from domestic pork and pigs. No resistance to colistin, meropenem, or fluoroquinolones in *S.* Derby or other non-Typhimurium/-monophasic serotype isolates from domestic pork and pigs was observed, comparable to data from 2024.

One *S.* Derby isolate from domestic pigs showed phenotypic resistance to the third-generation cephalosporin ceftazidime. Furthermore, resistance to ampicillin, chloramphenicol, tetracycline, and ceftazidime combined with clavulanic acid was observed in the isolate. The observed ceftazidime resistant phenotype is unusual and not explained by the resistance genes detected in the isolate. The isolate lacks recognised extended-spectrum beta-lactamases (ESBLs) and plasmid-mediated AmpC beta-lactamases, and remains susceptible to cefotaxime, cefepime and cefoxitin. The result could reflect an atypical effect of the *bla*ROB-1 gene; however, further investigation is required.

Resistance to azithromycin was observed in 5% of domestic pork and 1.6% of domestic pig *S.* Derby isolates, respectively. No resistance to tigecycline resistance was observed in 2025, which is a decrease compared to domestic pork in 2024 (7%), but comparable to 2023 (0%) for domestic pigs.

Resistance to amikacin was not observed in domestic pork *S.* Derby isolates in 2025, similar to 2024. However, in 2025, amikacin resistance was observed in one *S.* Derby isolate (1.6%) from domestic pig.

## 6.4 Conclusions and future perspectives

The levels of antimicrobial resistance in *C. jejuni*, and *C. coli* in Denmark in 2025 remained overall in accordance with the normal pattern from the previous years, with high levels of resistance to ciprofloxacin and tetracycline and low levels of resistance towards chloramphenicol, erythromycin, and gentamicin in isolates from humans and broilers. From a human health perspective, it is particularly important to follow the level of erythromycin resistance as azithromycin is the preferred antimicrobial in the cases where treatment is necessary.

The data from 2025 also shows that the dissemination of successful clones substantially can influence observed resistance levels. This was demonstrated by the increased occurrence of ciprofloxacin-resistant *C. jejuni* associated with two large outbreaks linked to Danish broiler meat. This was also the case for some of the fluctuations in resistance among human *S.* Typhimurium, that were impacted by outbreak-associated clones.

In human isolates, gentamicin resistance reached the highest level observed *Salmonella* spp. and in monophasic *S.* Typhi murium during the last five years, while increased levels were also observed among *S.* Derby and *S.* Typhimurium isolates from domestic pigs and pork. The increasing occurrence of gentamicin resistance in *Salmonella* warrants continued attention.

Resistance to critically important antimicrobials remained uncommon in *Salmonella* from domestic pigs and pork. No resistance to fluoroquinolones, colistin or carbapenems were detected, and resistance to third-generation cephalosporins remained exceptionally rare. A notable finding was the detection of one *S.* Derby isolate from pigs, displaying an unusual ceftazidime-resistant phenotype, which could not be explained by recognised ESBL or AmpC resistance determinants and therefore warrants further investigation.

Among human *Salmonella* isolates, resistance determinants conferring resistance to clinically important antimicrobials, including third-generation cephalosporins, quinolones and azithromycin, were detected only sporadically and primarily associated with travel-related cases.

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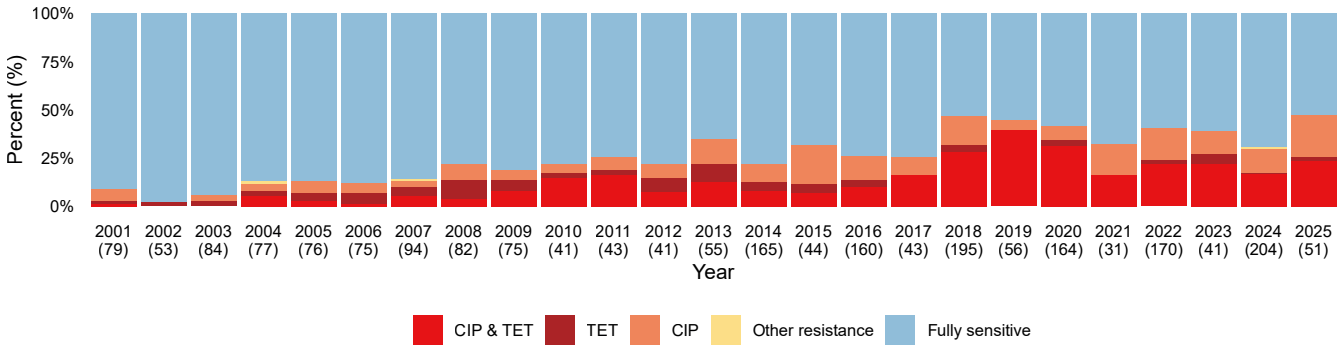
## Textbox 6.1

# 30 years of *Campylobacter jejuni* surveillance in Denmark

Denmark has had a nationwide surveillance of antimicrobial resistance in *Campylobacter* recovered from healthy food-producing animals since 1995. A retrospective comparison of resistance patterns in *Campylobacter jejuni* over the past 25 years of the DANMAP programme[1] was performed. *C. jejuni* is a common cause of bacterial gastrointestinal infection in humans in Denmark, and broilers are an important zoonotic reservoir. It is hence of public health interest to continuously monitor the development of antimicrobial resistance in *C. jejuni* from broilers.

A total of 2,199 *C. jejuni* isolates from broilers were collected and reported in DANMAP between 2001 and 2025.

**Figure 1 Relative distributions (%) of AMR profiles among *C. jejuni* from broilers by year, Denmark, 2001-2025** DANMAP 2025



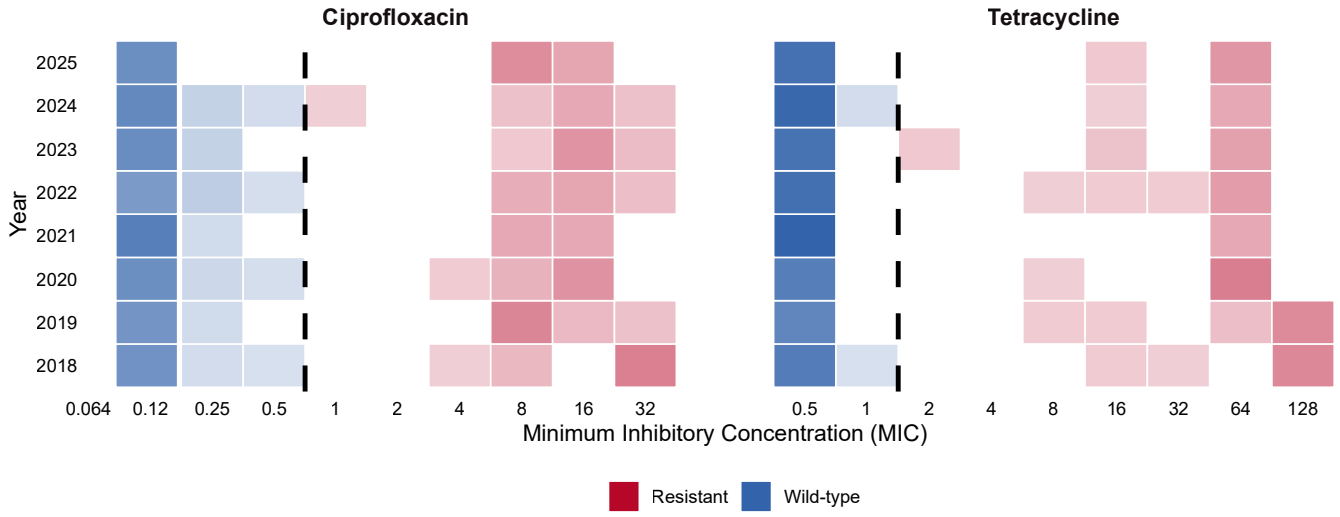

The bars show the percentage of isolates classified as having resistance to ciprofloxacin (CIP), tetracycline (TET), both CIP and TET, other resistance or being fully sensitive (sensitivity to all antimicrobial substances tested). The number of isolates included for each year is given in parentheses below each bar.

The relative occurrence of the different resistance profiles fluctuated over the 25-year period, with overall resistance (CIP, TET, CIP & TET and Other resistance) becoming more prominent from the late 2000s onwards and remaining common in the most recent years. In the early years, most isolates were fully sensitive. A first increase in the occurrence of resistance was observed in 2004, followed by a stable level until 2007, and a gradual increase from 2008 onwards for several years (see textbox 6.1. in DANMAP 2023). No statistically significant differences in the proportion of fully sensitive isolates were observed between years in 2018-2025, during which 31-47% of isolates had some form of resistance. Across the surveillance period, resistance was mainly associated with ciprofloxacin and tetracycline, either alone or in combination. Resistance to TET alone was more consistently observed, although at relatively low frequencies after 2016, while resistance to CIP alone became more frequent from 2013 onwards. Resistance to both CIP and TET became particularly prominent from 2018 onwards, while resistance classified as other resistance was rarely observed throughout the whole period.

MIC distributions for ciprofloxacin and tetracycline were examined for selected years to assess changes in the distribution of MIC values over time (Figure 2). Statistical comparisons were performed separately for wild-type and resistant isolates for each antimicrobial using the Kruskal-Wallis test followed by Dunn's post hoc test with Bonferroni correction, to assess whether the MIC distributions changed across the years considered.

[1] Although *C. jejuni* surveillance in DANMAP was established in 1995, MIC results are included from 2001 onwards as data from 1995-2000 was digitally unavailable at the time of writing.

**Figure 2 Distribution of MIC values from *C. jejuni* from broilers by antimicrobial substance and year** DANMAP 2025




Blue indicates wild-type isolates while red indicates resistant isolates. The intensity of the colour shading represents the percentage of isolates with the respective MIC value within each year, with darker shading indicating higher percentages. The dashed line represents the ECOFF value applied for interpretation.

For ciprofloxacin, significant differences in the MIC distribution of sensitive isolates were observed between 2018 and 2022 (with a slight shift towards the ECOFF) and between 2022 and 2025 (shift towards lower MIC values), whereas no significant differences were observed between the other years. The MIC distribution for resistant isolates differed significantly between 2018 and the subsequent years (except for 2023), with the distribution remaining stable from 2019 through 2025.

For tetracycline, no significant differences in the MIC distribution were observed among sensitive isolates in the selected years, although among resistant isolates there was a shift towards lower MIC values from 2020 onwards compared with 2018 and 2019.

Overall, combined resistance to ciprofloxacin and tetracycline, as well as resistance to ciprofloxacin alone in *C. jejuni* from broilers was more common in the later years of the programme. Some changes were also observed in the MIC distribution among both sensitive and resistant isolates, for ciprofloxacin and tetracycline, respectively, between the years 2018-2019 and the more recent years. An expanded analysis of the MIC distribution among ciprofloxacin-resistant isolates with and without combined CIP & TET resistance may provide further insights into the development of ciprofloxacin resistance in *C. jejuni* isolates from Danish broilers.

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## Textbox 6.2

# 30 years of *Salmonella* surveillance in Denmark

Denmark has had a nationwide surveillance of antimicrobial resistance in *Salmonella* spp. recovered from healthy food-producing animals since 1995. A retrospective comparison of resistance patterns in *Salmonella* isolates over time was performed. *Salmonella* has been monitored in different sources including pigs, pork, cattle and broilers, although most consistently in pigs and pork, considered important sources of *Salmonella* infections in humans. This textbox focuses on *Salmonella* Derby, monophasic *Salmonella* Typhimurium and *Salmonella* Typhimurium, the most commonly detected serotypes in pigs and pork in Denmark, collected between 2000 and 2025[1].

A total of 9,841 *Salmonella* Derby, monophasic *Salmonella* Typhimurium and *Salmonella* Typhimurium isolates from pig and pork samples have been collected and reported in DANMAP between 2000 and 2025. The number of isolates varies by year, sample origin and serotype. For pigs, sampling has most recently only been done in alternating years, following the rules of the EU harmonized antimicrobial resistance monitoring [Commission Implementing Decision (EU) 2020/1729].

The relative distribution of antimicrobial resistance profiles varies by serotype, sample origin and year (Figure 1). The occurrence of resistance in *S.* Derby is generally lower than in *S.* Typhimurium and monophasic *S.* Typhimurium for both pigs and pork across the 26 years.

Among *S.* Derby from pigs, the proportion of fully sensitive isolates accounted for 45–50% in 2000-2005, followed by an increase in 2015 reaching a maximum of 73%. Since then, the level has fluctuated annually, reaching values of 70% or above in 2021, 2023 and 2025. In contrast, the proportion of fully sensitive *S.* Derby from pork has shown a gradual decrease since 2021, reaching a minimum of 42.1% in 2023.

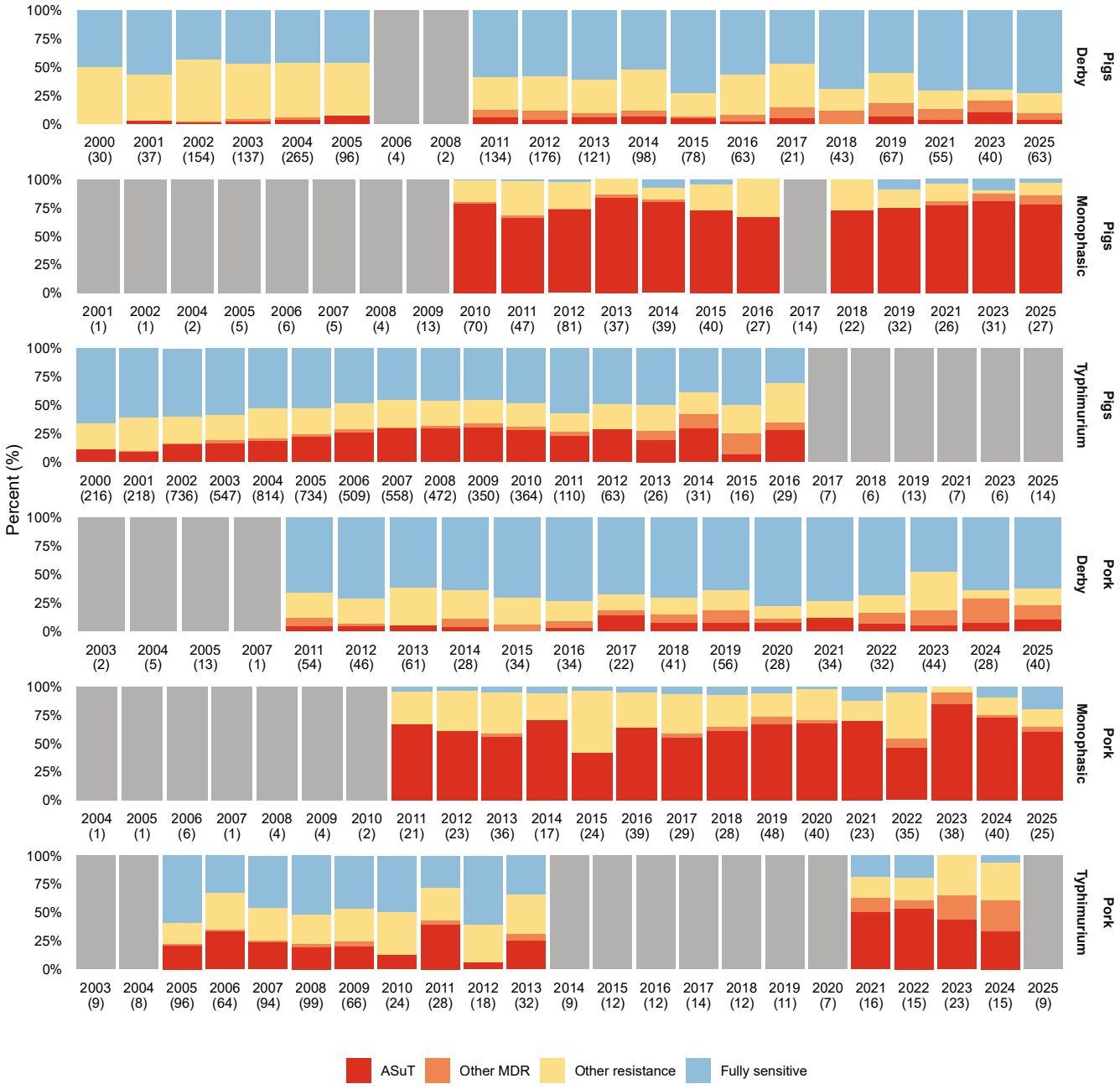
Among monophasic *S.* Typhimurium from pigs, ASuT remained the predominant resistance profile across all years, with proportions accounting for 66–84% of isolates, and the highest value observed in 2013. Among isolates from pork, ASuT accounted for 55–71% of isolates during 2011–2021, except in 2015, when the proportion was 41.7%. This was followed by a decrease in 2022 and an increase again in 2023 and 2024. Both in pigs and pork, the frequency of other MDR profiles in monophasic *S.* Typhimurium became more pronounced and consistent in the period 2022-2025, although this has not been a statistically significant change.

Among *S.* Typhimurium from pigs, the proportion of ASuT isolates increased from 10.6% in 2000 to 29.0% in 2008 and remained at a similar level through 2016 except for in 2015 (note that only 15 isolates were reported in this year). After 2016, very few *S.* Typhimurium isolates (<15) have been recovered from pigs under the scope of DANMAP sampling. Among *S.* Typhimurium from pork, the proportion of ASuT isolates varied between 19% and 33% during 2005–2009, followed by a more pronounced variation in 2010-2013. In the most recent years, ASuT accounted for 33-53%. In comparison to the earlier years, in the latest years the occurrence of complete sensitivity was markedly lower, and the occurrence of other MDR profiles markedly higher.

Overall, resistance profiles differed between serotypes, with lower resistance occurrence observed among *S.* Derby, followed by *S.* Typhimurium and higher occurrence observed among monophasic *S.* Typhimurium, where ASuT remained the predominant resistance profile across the monitoring period.

[1] Although Salmonella surveillance in DANMAP was established in 1995, MIC results are included from 2000 onwards as data from 1995-1999 was digitally unavailable at the time of writing.

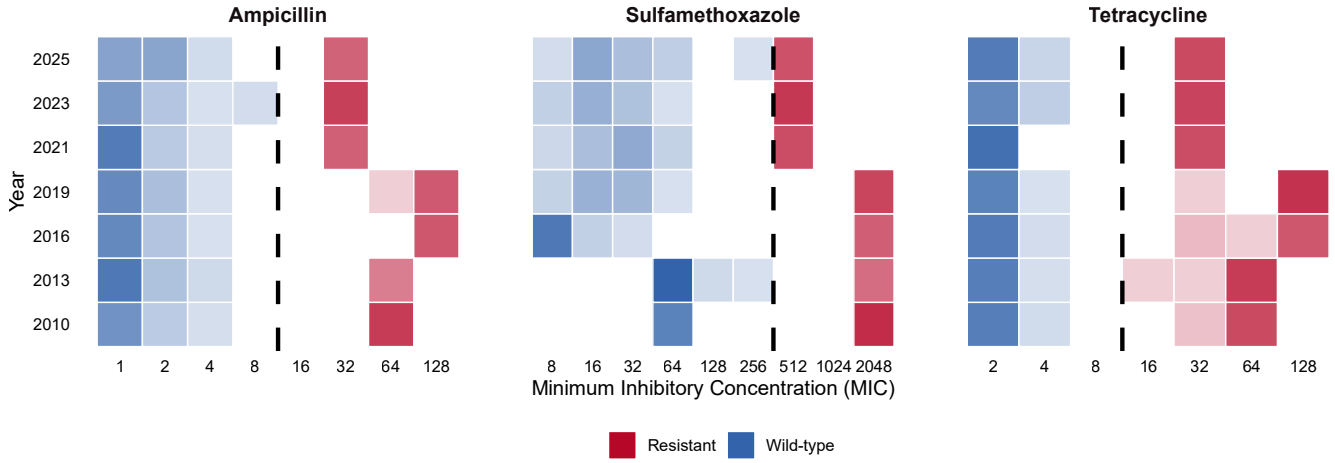
**Figure 1 Relative distributions (%) of AMR profiles among *Salmonella* Derby, monophasic *Salmonella* Typhimurium and *Salmonella* Typhimurium from pigs and pork by serotype and year, Denmark, 2000-2025** DANMAP 2025




The bars show the percentage of isolates classified as ASuT (resistant to at least ampicillin, sulfamethoxazole and tetracycline), other MDR (other multidrug resistance profiles than ASuT), other resistance (resistance to one or two antimicrobial classes), or fully sensitive (sensitivity to all antimicrobial substances tested). Isolates included are shown separately for S. Derby, S. Typhimurium and monophasic S. Typhimurium with antigenic formula S 4,[5],12:i:-, and separately for pigs and pork. The number of isolates included for each year is given in parentheses below each bar. Bars with fewer than 15 isolates per year and serotype are coloured grey.

continued ... Textbox 6.2

**Figure 2 Distribution of MIC values from *Salmonella Derby*, monophasic *Salmonella* Typhimurium and *Salmonella* Typhimurium isolates from pigs by antimicrobial substance and year** DANMAP 2025




Blue indicates wild-type isolates while red indicates resistant isolates. The intensity of the colour shading represents the percentage of isolates with the respective MIC value within each year, with darker shading indicating higher percentages. The dashed line represents the ECOFF value applied for interpretation.

MIC distributions for ampicillin, sulfamethoxazole and tetracycline were examined for selected years to assess changes in the distribution of MIC values over time (Figure 2). Statistical comparisons were performed separately for wild-type and resistant isolates for each antimicrobial using the Kruskal-Wallis test followed by Dunn's post hoc test with Bonferroni correction, to assess whether the MIC distributions changed across the years considered.

Among ampicillin-sensitive isolates, the MIC distribution below the ECOFF remained relatively stable from 2010 to 2023, followed by a significant shift towards the ECOFF in 2025. However, the 2025 distribution did not differ significantly from those observed in the individual years of 2019 and 2023. For sulfamethoxazole, the MIC distribution of sensitive isolates differed significantly between the period 2010-2013 and the year 2016, and between 2016 and the period 2019-2025, with observed MIC values being lower in 2016 than in 2010-2013 and higher in 2019-2025 compared to 2016. For tetracycline-sensitive isolates, the MIC distribution below the ECOFF remained stable from 2010 through 2021. A significant shift was observed in 2023 towards higher MIC values, while the 2025 distribution was not significantly different from either the preceding years or 2023.

Among isolates resistant to each of the three ASuT substances, there has been a clear shift towards lower MIC values in the years 2021, 2023 and 2025, which could in time also lead to a decrease in the occurrence of ASuT resistance among *Salmonella* isolates recovered from pigs. An apparent ongoing reduction in ASuT occurrence has already been observed among *S.* Typhimurium and monophasic *S.* Typhimurium from pork in the period 2023-2025 (Figure 1). However, due to the relatively low number of isolates recovered particularly from pork every year, caution should be taken in the interpretation of resistance trends in this source.

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# 7.

# Resistance in indicator bacteria

# 7. Resistance in indicator bacteria

## Highlights

In 2025, the occurrence of **fully susceptible indicator *E. coli*** increased further in broilers to 66%, remained stable in pigs at 41%, and decreased from 93% to 88% in cattle compared with 2024.

The occurrence of **multidrug-resistant (MDR) indicator *E. coli*** remained stable in broilers (13%) and pigs (34%), while in cattle it increased to 11%, returning to levels observed before the marked decline reported in 2024. Combined resistance to ampicillin, sulfamethoxazole and tetracycline (ASuT) continued to be a common MDR profile in pigs.

Compared with 2024, **resistance levels in *E. coli*** from broilers and pigs changed only marginally (1 to 3 percentage points) for most antimicrobials. In cattle, resistance to ampicillin, trimethoprim, chloramphenicol, sulfamethoxazole and tetracycline increased, returning to levels similar to those observed in 2021-2022.

Resistance to ciprofloxacin in indicator *E. coli* from broilers continued its downward trend and reached 9% in 2025. Resistance to fluoroquinolones remained very low in cattle (<1%) and pigs (2%). No resistance to colistin, meropenem, or third-generation cephalosporins was detected among indicator *E. coli* isolates.

The specific monitoring of **ESBL/AmpC-producing *E. coli*** detected an increase in occurrence in Danish pigs from 18% in 2023 to 22% in 2025, while prevalence in cattle, beef and pork remained largely unchanged, fluctuating by only 1 to 2 percentage points. ESBL/AmpC-producing *E. coli* continued to occur more frequently in imported pork (10%) than in Danish pork (1%).

No **carbapenemase-producing (CP) *E. coli*** were detected in any retail meat samples. Among ESBL/AmpC-producing isolates, resistance to colistin, meropenem and tigecycline remained absent. From 2023 to 2025, ciprofloxacin resistance and resistance to cefepime increased among ESBL/AmpC-producing *E. coli* from pigs, by 6 and 9 percentage points respectively, while ertapenem resistance was no longer detected.

Among **enterococci** from pigs, the proportion of fully susceptible isolates was 18% for *E. faecalis* and 10% for *E. faecium*. Compared with previous monitoring years, resistance increased for several antimicrobials, most notably erythromycin, chloramphenicol and daptomycin in *E. faecalis*, and ampicillin, ciprofloxacin and quinupristin/dalfopristin in *E. faecium*. Notably, resistance to linezolid or tigecycline were detected among few enterococci. No vancomycin resistance was detected.

## 7.1 Introduction

*Escherichia coli* and *Enterococcus* are included in the DANMAP programme to monitor the occurrence of antimicrobial resistance (AMR) in different reservoirs throughout the food chain for the following reasons: i) they are present as commensals in the gut microbiota of healthy animals and humans, ii) they can acquire antimicrobial resistance both via mutations in chromosomal genes and horizontal transfer of antimicrobial resistance genes, and iii) they have the potential to cause infections in both animals and humans, and to transfer antimicrobial resistance to pathogenic bacteria of the same or other species.

*E. coli* exhibiting resistance to third generation cephalosporins via the production of extended-spectrum beta-lactamases (ESBLs) and AmpC beta-lactamases (AmpCs) are among the fastest spreading antimicrobial resistance threats in both humans and food-producing animals worldwide.

Carbapenemase-producing *Enterobacteriaceae* (CPE) pose a great threat to human health, as carbapenems are last-line antimicrobial drugs for the treatment of infections caused by multidrug-resistant Gram-negative bacteria.

Isolation and antimicrobial susceptibility testing of indicator *E. coli*, indicator enterococci and ESBL-, AmpC- and carbapenemase (CP)-producing *E. coli* are performed in accordance with the rules for the EU harmonised monitoring of antimicrobial resistance [Decision 2020/1729/EU].

In 2025, isolates were obtained from randomly selected caecal samples collected from healthy broilers, cattle (calves under one year of age), and fattening pigs at slaughter. Additionally, for the specific monitoring of ESBL-, AmpC- and CP-producing *E. coli*, fresh meat from pigs and cattle was collected at retail.

Details on sampling, analysis, susceptibility testing and interpretation of results are presented in Chapter 10.

## 7.2 Indicator *Escherichia coli*

Indicator *E. coli* isolates were obtained from 95% of caecal samples from broiler flocks (130/137), 97% of samples from pigs (173/179), and 96% of samples from cattle (177/184).

### 7.2.1 Indicator *Escherichia coli* from broilers, cattle and pigs

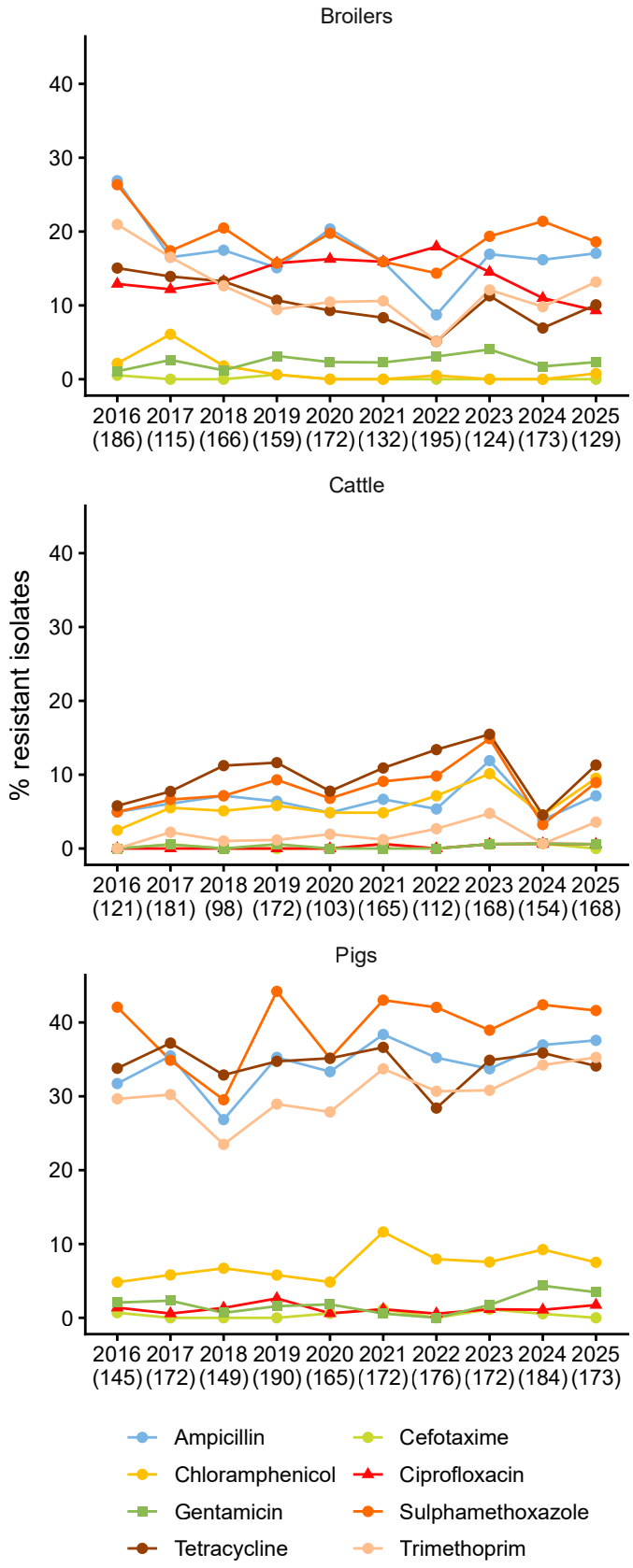
As in 2024, the percentage of broiler isolates susceptible to all antimicrobials in the test panel continued to increase in 2025 (66%, 2 percent points higher than in the previous year). After an observed increase to 93% of full-susceptibility in isolates from cattle in the previous year, in 2025 the level decreased to 88%. Among isolates from pigs, the occurrence of full-susceptibility remained similar to what was observed in 2024 (41%), with a one percent point oscillation (Table 7.1, Figure 7.2).

**Table 7.1 Resistance (%) in *Escherichia coli* isolates from broilers, cattle and pigs, Denmark, 2025** DANMAP 2025

| | Broilers | Cattle | Pigs |
|---|---|---|---|
| | Danish | Danish | Danish |
| | % | % | % |
| Amikacin | <1 | 0 | 2 |
| Ampicillin | 17 | 7 | 38 |
| Azithromycin | 0 | 0 | 6 |
| Cefotaxime | 0 | 0 | 0 |
| Ceftazidime | 0 | 0 | 0 |
| Chloramphenicol | <1 | 10 | 8 |
| Ciprofloxacin | 9 | <1 | 2 |
| Colistin | 0 | 0 | 0 |
| Gentamicin | 2 | <1 | 3 |
| Meropenem | 0 | 0 | 0 |
| Nalidixic acid | 9 | 0 | 2 |
| Sulphamethoxazole | 19 | 9 | 42 |
| Tetracycline | 10 | 11 | 34 |
| Tigecycline | 0 | 0 | <1 |
| Trimethoprim | 13 | 4 | 35 |
| Fully susceptible (%) | 66 | 88 | 41 |
| Number of isolates | 129 | 168 | 173 |

An isolate is considered fully susceptible if sensitive to all antimicrobial agents included in the test panel (Chapter 10, Table 10.2).

**Figure 7.1 Resistance (%) among *Escherichia coli* isolates from broilers, cattle and pigs, Denmark, 2016-2025** DANMAP 2025




The number of isolates included each year is shown in the parentheses.

For *E. coli* isolates from broilers and pigs, the fluctuations in the occurrence of resistance to most antimicrobials in the test panel were minor between 2024 and 2025 (1-3% points). Resistance to some antimicrobials among isolates from cattle increased more markedly in 2025, after the decrease observed in 2024. Specifically, there was 3% points increase for ampicillin and trimethoprim resistance, 5% points for chloramphenicol resistance and 6% points for sulphametoxazole and tetracycline resistance; these resistance levels are similar to those observed in the period of 2021-2022 (Figure 7.1).

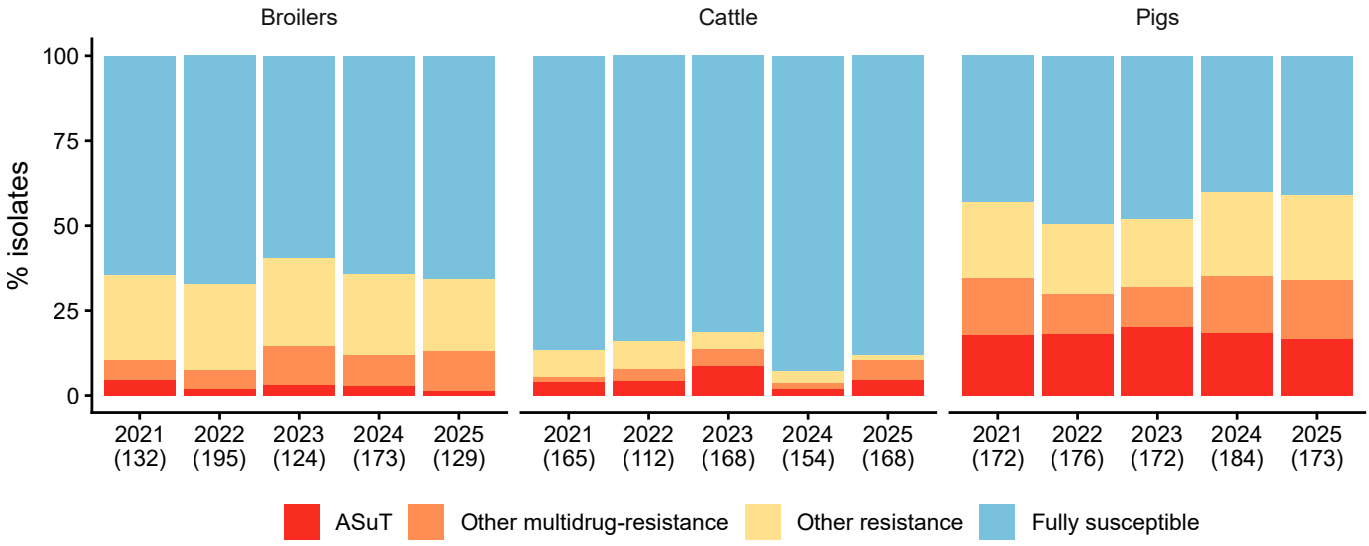
Remarkably, the occurrence of resistance to ciprofloxacin in *E. coli* from broilers continued decreasing in 2025, after the decrease already observed in the two previous years, with fluoroquinolone resistance reaching the level of 9%. These findings reinforce the hypothesis of an ongoing decreasing trend.

Notably, in pig isolates (although by a limited magnitude), the increase in resistance to macrolides already observed in 2024 continued in 2025 (azithromycin: from 4% to 6%), while the occurrence of resistance to aminoglycosides remained somewhat stable (amikacin: 2%; gentamicin: 3%).

As in previous years, no isolates resistant to colistin or meropenem were detected in 2025. Similarly, resistance to third generation cephalosporins was not detected in indicator *E. coli* using non-selective methods. Resistance to fluoroquinolones continues to be very low (up to 2%) in isolates from cattle and pigs, and higher (9%) among broiler isolates. Among pig isolates, one was resistant to tigecycline, three were resistant to amikacin and eleven were resistant to azithromycin. A single isolate from broilers was resistant to amikacin (Table 7.1).

In 2025, the occurrence of multidrug-resistance (MDR) in *E. coli* from broilers, including combined resistance to ampicillin, sulfamethoxazole and tetracycline (ASuT) and other MDR profiles, was 13%, like that observed in 2024. In pigs, occurrence of MDR and other resistance profiles also appeared relatively stable in comparison with the previous year (34%), and ASuT resistance was as frequent as the joint occurrence of other MDR profiles. Notably, in cattle, following the marked decrease observed in 2024, the occurrence of MDR *E. coli* returned to 11% (5% ASuT and 6% other MDR profiles) in 2025 (Figure 7.2).

**Figure 7.2 Relative distributions (%) of fully susceptible, resistant and multidrug-resistant *Escherichia coli* isolates from broilers, cattle and pigs, Denmark, 2021-2025** DANMAP 2025




The number of isolates included each year is shown in parentheses. An isolate is considered fully susceptible if sensitive to all antimicrobial agents included in the test panel, and multidrug-resistant if resistant to 3 or more of the 12 antimicrobial classes included in the test panel (Chapter 10, Table 10.3). ASuT are the multidrug-resistant isolates resistant to ampicillin, sulphamethoxazole and tetracycline.

## 7.3 ESBL/AmpC- and carbapenemase-producing *E. coli*

In 2025, caecal samples collected from pigs and cattle at slaughter, and from packages of fresh, chilled pork and beef collected from Danish wholesale and retail outlets were subject to the specific monitoring of ESBL/AmpC- and CP-producing *E. coli* and the corresponding results are reported in this chapter. Furthermore, samples from consignments of imported pork and beef were sampled at Danish border control posts (BCP) in agreement with the EU harmonized AMR monitoring [Decision 2020/1729/EU]. None of the samples collected at BCPs tested positive for ESBL/AmpC- or CP-producing *E. coli*, and due to the low sample size the results of the BCP monitoring are not included in the chapter.

Among the samples randomly collected at retail, 26% (83 out of 323) of pork samples and 51% (149 out of 293) of beef samples were imported products. The distribution of the country of origin of the sampled imported pork meat did not change considerably compared to 2023, with the same two EU countries representing 84% of all samples in 2025 (previously 92%). The distribution of the country of origin of the sampled imported beef changed somewhat compared to the previous reporting year. In 2023, the collected samples originated predominantly (57%) from one of three EU countries. In 2025, only two of those countries remained as a predominant origin of beef samples (43%), with other two countries, one EU (15%) and one non-EU (19%), also being highly represented. Still, the predominant country representing most samples of imported pork and beef did not change between 2023 and 2025.

As in previous years, the selective procedures for detection of CP-producing *E. coli* (including oxacillinase-producing OXA-48-like enzymes), recovered no isolates from retail meat.

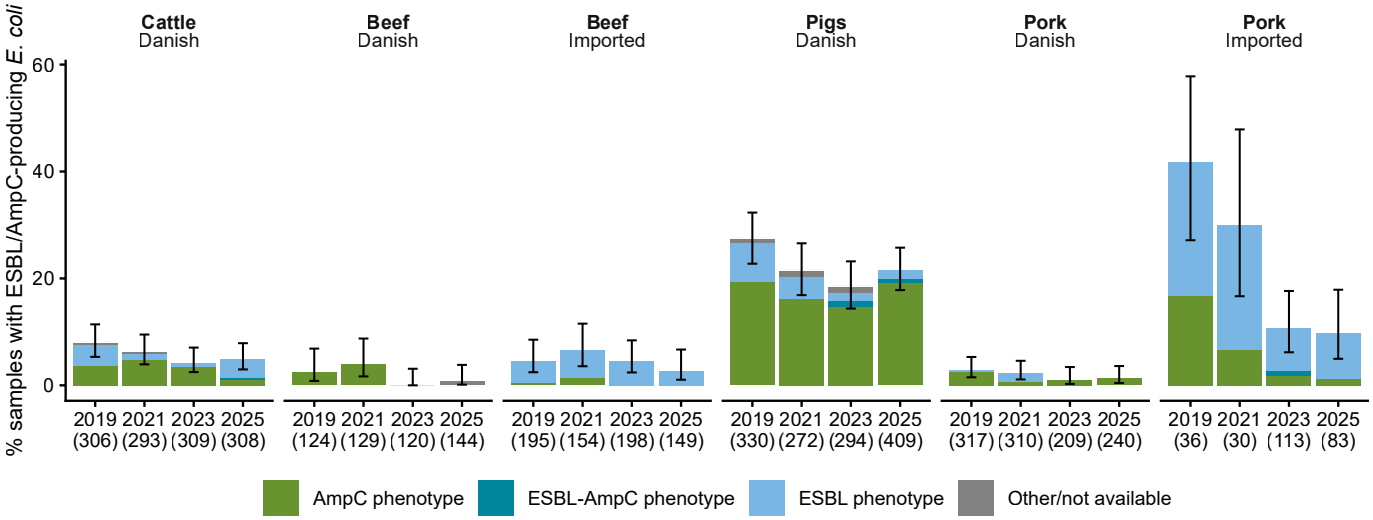
### 7.3.1 Prevalence of ESBL/AmpC-producing *E. coli* in animals and meat

Following selective enrichment, ESBL/AmpC-producing isolates, i.e. *E. coli* resistant to third generation cephalosporins (cefotaxime and/or ceftazidime), here abbreviated as ESBL/AmpC *E. coli*, were obtained from 88/409 samples from pigs (22%; CI 95%: 18-26%), 3/240 samples from Danish pork (1%; CI 95%: 0.4-4%), 8/83 samples from imported pork (10%; CI 95%: 5-18%), 15/308 samples from cattle (5%; CI 95%: 3-8%), 1/144 samples from Danish beef (1%; CI 95%: 0.1-4%), and 4/149 samples from imported beef (3%; CI 95%: 1-7%) (Figure 7.3, Table 7.2).

In 2025, in comparison to 2023, the prevalence of ESBL/AmpC *E. coli* has increased in Danish pigs by 4% points (from 18% to 22%) and fluctuated in Danish and imported pork by 1-2% points. As previously, ESBL/ AmpC *E. coli* continued to show higher occurrence in imported pork compared to Danish pork.

Similarly, in 2025 compared to 2023, the prevalence of ESBL/AmpC *E. coli* in Danish calves and domestic and imported beef oscillated only by 1-2% points, and as seen previously the discrepancy in occurrence between domestic and imported meat is not as marked as that observed in pork (Figure 7.3, Table 7.2).

**Figure 7.3 Occurrence (%) of samples with phenotypic ESBL- or AmpC-producing *E. coli* from animals and meat recovered by selective enrichment, Denmark 2019-2025** DANMAP 2025




Number of samples tested per year is presented in the parentheses. Confidence intervals for total proportion of samples positive for phenotypic ESBL and/or AmpC producing *E. coli* - calculated as 95% binomial proportion Wilson intervals. Classification of ESBL and AmpC phenotypes according to the scheme provided by EFSA (Chapter 10, Section 10.7.2).

### 7.3.2 Phenotypic resistance in ESBL/AmpC-producing *E. coli*

The distribution of phenotypes seems relatively stable across the samples tested for specific monitoring of ESBL/AmpC-producing *E. coli*, apart from a shift to a higher proportion of ESBL phenotypes and a lower proportion of AmpC phenotypes among isolates from cattle in 2025 (Figure 7.3). Due to the overall low number of isolates recovered from cattle and retail meat, it is important to carefully interpret any increasing or decreasing trends in the occurrence of resistance in these samples.

As in previous years, all the recovered ESBL/AmpC *E. coli* isolates were resistant to both third generation cephalosporins (cefotaxime and ceftazidime) and ampicillin. In 2025, 87% of the cattle isolates, all isolates from imported beef, 33% of the pig isolates and 88% of isolates from imported pork were also resistant to fourth generation cephalosporins (cefepime). Among isolates from pigs, cefepime resistance occurrence has increased from 24% (of a total of 54 isolates) in 2023 to 33% (of a total of 88 isolates) in 2025 (Table 7.2).

From 2023 to 2025, the observed resistance to fluoroquinolones (ciprofloxacin) has also increased in ESBL/AmpC *E. coli* from Danish pigs (from 6% in 2023 to 12% in 2025).

Unlike the previous monitoring year, in 2025 ertapenem resistance was not observed in any ESBL/AmpC *E. coli* isolates (previously 11% in isolates from imported pork). Resistance against meropenem was also not observed, and a single isolate from pigs showed resistance to imipenem, a decrease compared to the 6% occurrence observed in 2023.

As previously, there was no occurrence of colistin or tigecycline resistance among the recovered ESBL/AmpC *E. coli*, and temocillin resistance was detected in 3% of the isolates from pigs.

Opposed to 2023, in 2025, azithromycin resistance was not observed in cattle or beef isolates, and it was detected in pig and pork isolates (16% in pigs, a single isolate from Danish pork and two isolates from imported pork). Notably, among cattle isolates, the occurrence of gentamicin resistance increased from 8% in 2023 (from a total of 13 isolates) to 27% in 2025 (from a total of 15 isolates), while it decreased among pig isolates, from 11% in 2023 to 7% in 2025.

**Table 7.2 Resistance (%) and resistance phenotypes in specific monitoring of ESBL/AmpC-producing *Escherichia coli* from animals and meat recovered by selective enrichment, Denmark, 2025** DANMAP 2025

| | Cattle | Beef | | Pigs | Pork | |
|---|---|---|---|---|---|---|
| Antimicrobial agent | Danish % | Danish % | Import % | Danish % | Danish % | Import % |
| Amikacin | 7 | 0 | 0 | 1 | 0 | 0 |
| Ampicillin | 100 | 100 | 100 | 100 | 100 | 100 |
| Azithromycin | 0 | 0 | 0 | 16 | 33 | 25 |
| Cefepime | 87 | 0 | 100 | 33 | 0 | 88 |
| Cefotaxime | 100 | 100 | 100 | 100 | 100 | 100 |
| Cefotaxime/clavulanic acid | 20 | 100 | 0 | 90 | 100 | 12 |
| Cefoxitin | 27 | 0 | 0 | 92 | 100 | 12 |
| Ceftazidime | 100 | 100 | 100 | 99 | 100 | 100 |
| Ceftazidime/clavulanic acid | 20 | 100 | 0 | 90 | 100 | 12 |
| Chloramphenicol | 40 | 0 | 25 | 10 | 0 | 50 |
| Ciprofloxacin | 67 | 0 | 50 | 12 | 0 | 50 |
| Colistin | 0 | 0 | 0 | 0 | 0 | 0 |
| Ertapenem | 0 | 0 | 0 | 0 | 0 | 0 |
| Gentamicin | 27 | 0 | 0 | 7 | 0 | 12 |
| Imipenem | 0 | 0 | 0 | 1 | 0 | 0 |
| Meropenem | 0 | 0 | 0 | 0 | 0 | 0 |
| Nalidixic acid | 13 | 0 | 25 | 7 | 0 | 25 |
| Sulphamethoxazole | 53 | 0 | 50 | 58 | 67 | 38 |
| Temocillin | 0 | 0 | 0 | 3 | 0 | 0 |
| Tetracycline | 27 | 0 | 75 | 65 | 100 | 62 |
| Tigecycline | 0 | 0 | 0 | 0 | 0 | 0 |
| Trimethoprim | 20 | 0 | 0 | 67 | 67 | 75 |
| Number of AmpC phenotypes | 3 | 0 | 0 | 78 | 3 | 1 |
| Number of ESBL phenotypes | 11 | 0 | 4 | 7 | 0 | 7 |
| Number of ESBL+AmpC phenotypes | 1 | 0 | 0 | 3 | 0 | 0 |
| Other phenotypes | 0 | 1 | 0 | 0 | 0 | 0 |
| Number of isolates (%) | 15 (5%) | 1 (1%) | 4 (3%) | 88 (22%) | 3 (1%) | 8 (10%) |
| Number of samples | 308 | 144 | 149 | 409 | 240 | 83 |

Classification of ESBL-, AmpC- and AmpC+ESBL phenotypes is based on the MIC results (Chapter 10, Section 10.7.2). AmpC, ESBL and AmpC+ESBL phenotypes indicate the number of isolates expressing each specific phenotype.

### 7.3.3 Genotypic resistance in ESBL/AmpC-producing *E. coli*

The genetic basis for ESBL and AmpC enzymes was detected in most ESBL/AmpC-producing isolates, with the detected enzymes mainly corresponding to the phenotypes derived from susceptibility testing. A single isolate from Danish beef did not show an AmpC-producing phenotype, while whole genome sequencing revealed an upregulated AmpC promotor C-42T mutation. Another isolate from cattle showed an ESBL and AmpC-producing phenotype, even though the genomic analysis only revealed an ESBL genotype. Finally, two isolates from pigs showed an AmpC phenotype but an ESBL genotype (Tables 7.2 and 7.3).

Among the AmpC-producing isolates recovered in 2025, resistance was, as observed in previous years, mainly conferred by upregulated AmpC promotor C-42T mutations (three isolates from cattle, one from Danish beef, 76 from pigs, three from Danish pork and one from imported pork). However, among isolates from pigs, the plasmid-mediated AmpC beta-lactamase encoding genes blaCMY-2 (one isolate) and blaDHA-1 (six isolates) were also observed (Table 7.3).

Among all ESBL-producing isolates, nine different ESBL genes were detected. Overall, the most observed ESBL encoding genes across all categories of animals and meat sampled in 2025 were blaCTX-M-15 (9 isolates), blaCTX-M-14 (7 isolates), blaCTX-M-1 and blaCTX-M-55 (6 isolates). While the CTX-M-1 and CTX-M-14 enzymes were most common among pig isolates, CTX-M-15 and CTX-M-55 were most abundant among isolates from cattle. The ESBL genes blaCTX-M-8, blaTEM-106 and blaTEM-126 were only detected in single isolates from pigs. Among the two pig isolates that harbored both ESBL and AmpC genotypes, upregulated AmpC promotor C-42T mutation was detected, together with the ESBL genes blaTEM-106 and blaTEM-126 (one isolate) and blaTEM-207 (one isolate).

In total, 32 MLSTs were observed among all ESBL/AmpC-producing *E. coli* isolates. The most common MLST was ST88, followed by ST156. These frequencies were mostly due to the overrepresentation of pig isolates. Among cattle isolates, ST58 was most commonly observed, while only two ST88 were detected and ST156 was absent.

**Table 7.3 Number of ESBL and AmpC enzymes detected in beta-lactamase-producing *E. coli* isolates from animals and meat recovered by selective enrichment, Denmark, 2025** DANMAP 2025

| | Cattle | Beef | | Pigs | Pork | |
|---|---|---|---|---|---|---|
| Enzymes | Danish | Danish | Import | Danish | Danish | Import |
| CTX-M-1 | 1 | | 1 | 3 | | 1 |
| CTX-M-14 | | | 1 | 4 | | 2 |
| CTX-M-15 | 6 | | 2 | | | 1 |
| CTX-M-27 | 1 | | | | | 1 |
| CTX-M-55 | 4 | | | 1 | | 1 |
| CTX-M-8 | | | | 1 | | |
| TEM-106 | | | | 1 | | |
| TEM-126 | | | | 1 | | |
| TEM-207 | | | | 2 | | 2 |
| CMY-2 | | | | 1 | | |
| DHA-1 | | | | 6 | | |
| Chromossomal AmpC (C-42T) | 3 | 1 | | 71 | 3 | 1 |
| Number of AmpC genotypes | 3 | 1 | | 76 | 3 | 1 |
| Number of ESBL genotypes (two or more enzymes) | 12 | | 4 | 9 (2) | | 6 (2) |
| Number of AmpC+ESBL genotypes | | | | 2 | | |
| Number (%) positive samples | 15 (5%) | 1 (1%) | 4 (3%) | 88 (22%) [a] | 3 (1%) | 8 (10%) [b] |
| Number of tested samples | 308 | 144 | 149 | 409 | 240 | 83 |

Number (%) positive samples are isolates recovered by selective enrichment methods for monitoring of beta-lactamase-producing *E. coli* ESBL/AmpC enzymes were determined by whole genome sequencing of the recovered isolates (Chapter 10, Section 10.6). [a] WGS was only available for 87 of the 88 isolates; [b] WGS was only available for 7 of the 8 isolates.

## 7.4 Indicator *Enterococci*

Enterococci were obtained from 204 (42%) out of 490 faecal samples taken from pigs at slaughter, and antimicrobial susceptibility testing was subsequently performed on 122 *E. faecalis* isolates and on 80 *E. faecium* isolates.

### 7.4.1 *E. faecalis* and *E. faecium* from pigs

Overall, 18% of the *E. faecalis* isolates and 10% of the *E. faecium* isolates were susceptible to all antimicrobials in the test panel (Table 7.4).

As in 2023, the previous year of *E. faecalis* monitoring in pigs, no *E. faecalis* isolates showed resistance to ampicillin, ciprofloxacin, or vancomycin. However, in 2025, resistance to chloramphenicol, daptomycin, and erythromycin have increased by 14%, 10% and 10% points, respectively. Furthermore, resistance to linezolid (2%) and to tigecycline (3%) were detected among *E. faecalis* isolates. Resistance to erythromycin and tetracycline, followed by chloramphenicol, continued to be the most common (Table 7.4). The increase in resistance to erythromycin and chloramphenicol observed among *E. faecalis* isolates in 2025, follows a previous increase already observed in 2023 compared to 2021 (Figure 7.4).

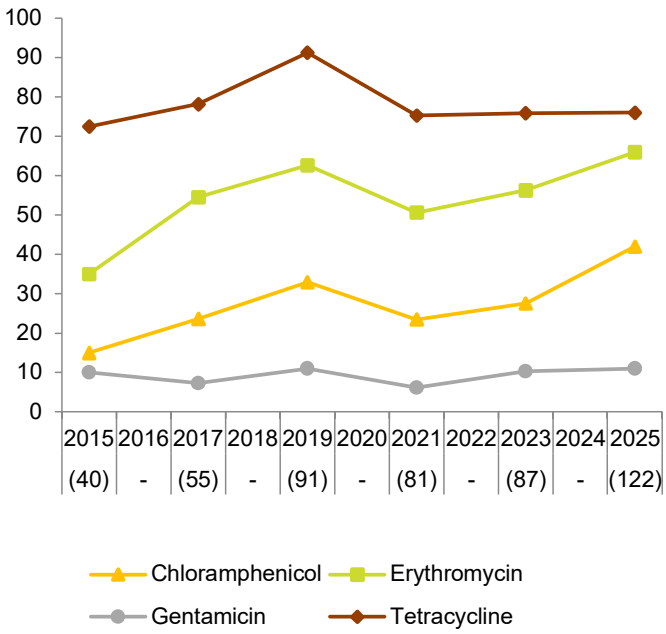
Compared to 2019, the last year of *E. faecium* monitoring in pigs, in 2025 there was an overall increase in the resistance levels to most tested antibiotics. Most notably, there was a marked increase in resistance to ampicillin (from 12% to 28%), ciprofloxacin (from 5% to 12%) and quinupristin/dalfopristin (when interpreted with ECOFF, from 71% to 85%). It should be noted that the interpretation of the cutoff values for quinupristin/dalfopristin has changed. 2019 data has been re-analysed with the new cutoff and the value here reported differs therefore from previously reported values. Furthermore, linezolid resistance was detected in 1% of the isolates in 2025 (Table 7.4).

**Table 7.4 Resistance (%) in Enterococci isolates from pigs, Denmark, 2025** DANMAP 2025

| | *Enterococcus faecalis* | *Enterococcus faecium* |
|---|---|---|
| Antimicrobial agent | % | % |
| Ampicillin | 0 | 28 |
| Chloramphenicol | 42 | 2 |
| Ciprofloxacin | 0 | 12 |
| Daptomycin | 12 | 0 |
| Erythromycin | 66 | 24 |
| Gentamicin | 11 | 0 |
| Linezolid | 2 | 1 |
| Quinupristin/dalfopristin | 100 | 85 |
| Teicoplanin | 0 | 0 |
| Tetracycline | 76 | 58 |
| Tigecycline | 3 | 0 |
| Vancomycin | 0 | 0 |
| Fully susceptible (%) | 18 | 10 |
| Number of isolates | 122 | 80 |

*E. faecalis* are assumed inherently resistant to streptogramins (Quinupristin/Dalfopristin).
An isolate is considered fully susceptible if sensitive to all antimicrobial agents included in the test panel (Chapter 10, Table 10.3).

**Figure 7.4 Resistance (%) among *E. faecalis* isolates from pigs, Denmark, 2015-2025** DANMAP 2025




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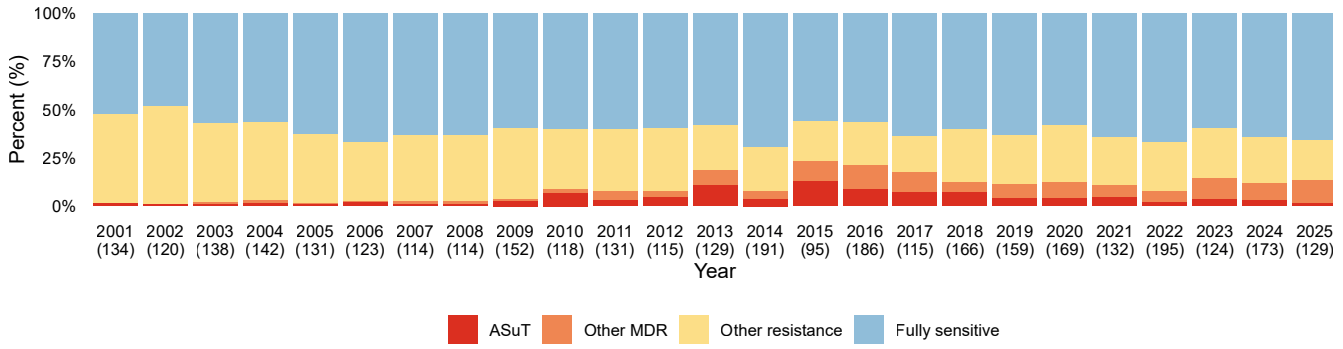
## Textbox 7.1

# 30 years of *Escherichia coli* surveillance in Danish broilers

Denmark has had a nationwide surveillance of antimicrobial resistance in indicator *Escherichia coli* recovered from healthy food-producing animals since 1995. A retrospective comparison of resistance patterns in *E. coli* over the past 25 years of the DANMAP programme[1] was performed.

A total of 3,495 *E. coli* isolates from broilers were collected and reported in DANMAP between 2001 and 2025. The sampling strategy has changed over time, with a more standardized approach being implemented after 2014, following the introduction of the harmonized antimicrobial resistance monitoring in the European Union [Commission Implementing Decision (EU) 2020/1729].

**Figure 1 Relative distributions (%) of AMR profiles among *E. coli* from broilers by year, Denmark, 2001-2025** DANMAP 2025



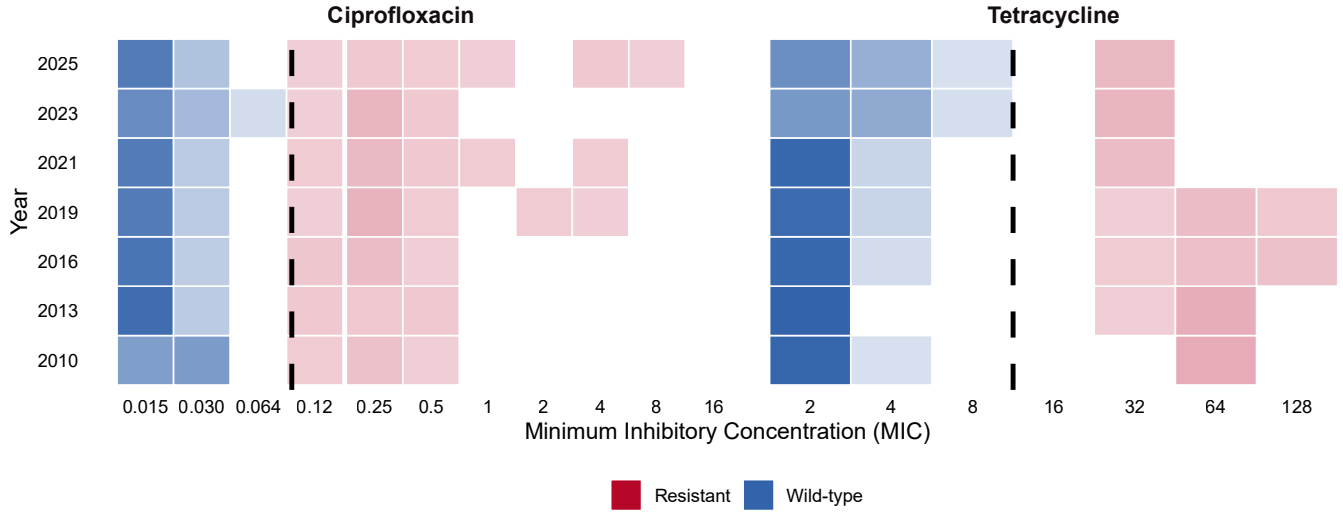

The bars show the percentage of isolates classified as ASuT (resistant to at least ampicillin, sulfamethoxazole and tetracycline), other MDR (other multidrug resistance profiles than ASuT), other resistance (resistance to one or two antimicrobial classes), or fully sensitive (sensitivity to all antimicrobial substances tested). The number of isolates included for each year is given in parentheses below each bar.

The relative distribution of antimicrobial resistance profiles varied between years (Figure 1). Fully sensitive *E. coli* isolates were dominant across all years, ranging from 52% to 70%, except in 2002, when 48% of the isolates were fully sensitive and 51% had other resistance. The proportion of ASuT and other MDR was generally low and increased from 2009, reaching a maximum of 23% in 2015 before decreasing and plateauing from 2019 onwards.

MIC distributions for ciprofloxacin and tetracycline were examined for selected years to assess changes in the distribution of MIC values over time (Figure 2). Statistical comparisons were performed separately for wild-type and resistant isolates for each antimicrobial using the Kruskal-Wallis test followed by Dunn's post hoc test with Bonferroni correction, to assess whether the MIC distributions changed across the years considered.

[1] Although *E. coli* surveillance in DANMAP was established in 1995, MIC results are included from 2001 onwards as data from 1995-2000 was digitally unavailable at the time of writing.

**Figure 2 Distribution of MIC values from *E. coli* from broilers by antimicrobial substance and year** DANMAP 2025




Blue indicates wild-type isolates while red indicates resistant isolates. The intensity of the colour shading represents the percentage of isolates with the respective MIC value within each year, with darker shading indicating higher percentages. The dashed line represents the ECOFF value applied for interpretation.

Among wild-type isolates, the MIC distribution for ciprofloxacin shifted towards lower MIC values after 2010 and remained similar in 2013, 2016, 2019 and 2021. In 2023, the distribution shifted towards higher MIC values, closer to the ECOFF, and was significantly different from 2013 and 2016. In 2025, a significant shift towards lower MIC values was observed compared with 2023. For tetracycline, the distribution in 2023 and 2025 differed significantly from the previous years, shifting towards higher MIC values and closer to the ECOFF. Among resistant isolates, no significant differences were observed in the distribution of MIC values across years for ciprofloxacin except in 2025. In recent years, higher MIC values have been observed, although not at a level significantly different from previous years. For tetracycline, the MIC distribution among resistant isolates was significantly different in 2025, 2023 and 2021 compared to previous years.

Overall, changes in resistance profiles and MIC distributions were observed over time for *E. coli* in broilers, with a tendency towards higher MIC values in recent years while the overall distribution of resistance profiles remained similar.

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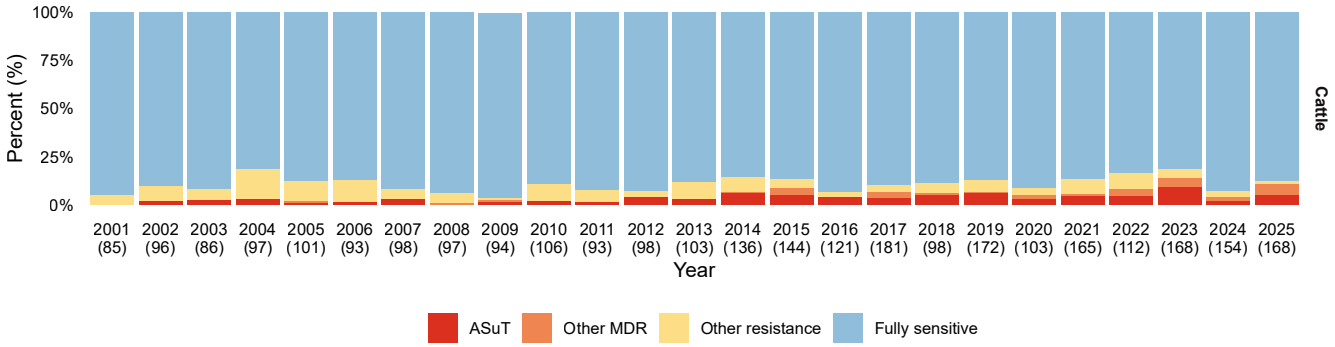
## Textbox 7.2

# 30 years of *Escherichia coli* surveillance in Danish cattle

Denmark has had a nationwide surveillance of antimicrobial resistance in indicator *Escherichia coli* recovered from healthy food-producing animals since 1995. A retrospective comparison of resistance patterns in *E. coli* over the past 25 years of the DANMAP programme[1] was performed.

A total of 2,969 *E. coli* isolates from cattle were collected and reported in DANMAP between 2001 and 2025. The sampling strategy has changed over time, with a more standardized approach being implemented after 2014, following the introduction of the harmonized antimicrobial resistance monitoring in the European Union [Commission Implementing Decision (EU) 2020/1729].

**Figure 1 Relative distributions (%) of AMR profiles among *E. coli* from cattle by year, Denmark, 2001-2025** DANMAP 2025



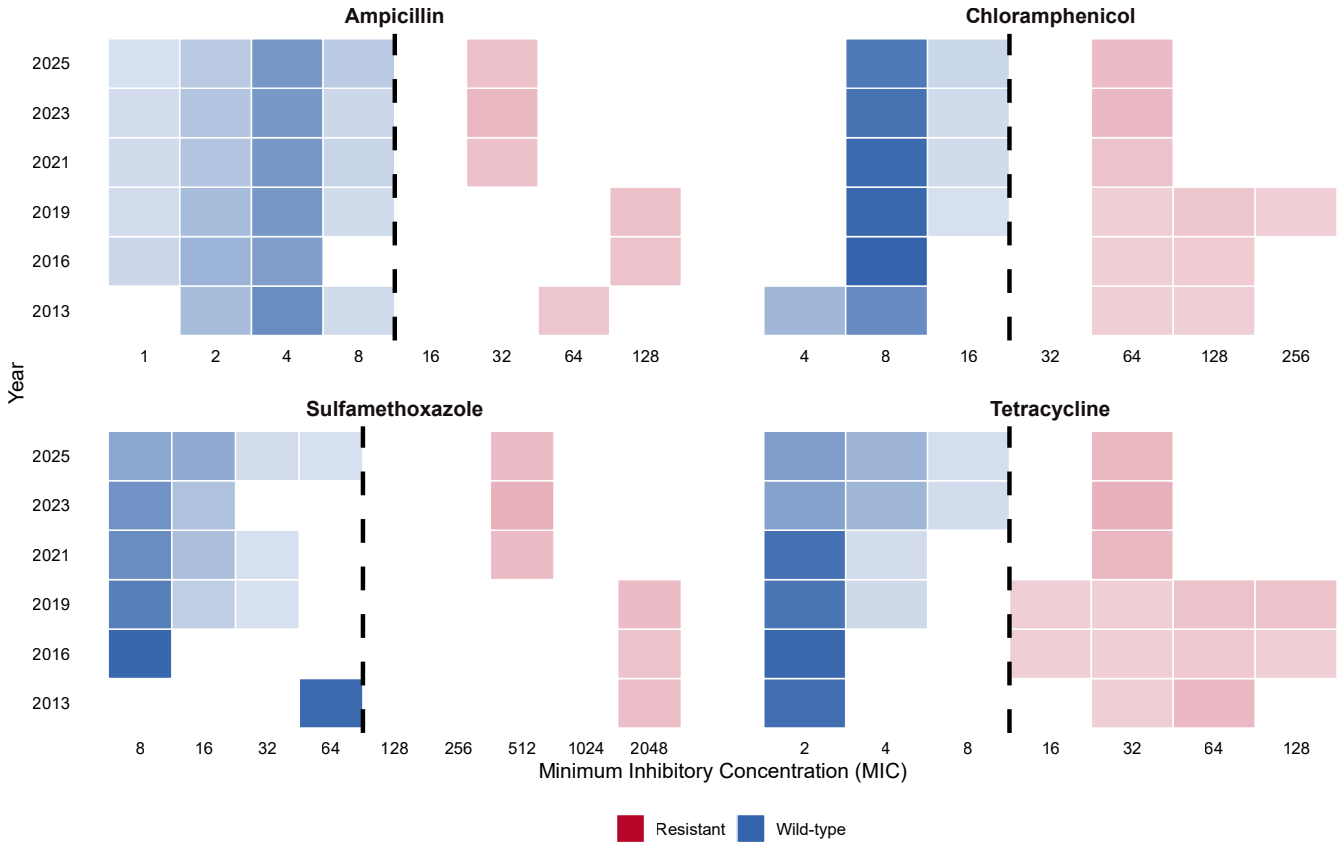

The bars show the percentage of isolates classified as ASuT (resistant to at least ampicillin, sulfamethoxazole and tetracycline), other MDR (other multidrug resistance profiles than ASuT), other resistance (resistance to one or two antimicrobial classes), or fully sensitive (sensitivity to all antimicrobial substances tested). The number of isolates included for each year is given in parentheses below each bar.

The relative distribution of antimicrobial resistance profiles varied between years (Figure 1). Fully sensitive *E. coli* isolates were dominant across all years, ranging from 81% to 97%. ASuT was the predominant resistance profile throughout the study period, although other MDR accounted for a larger proportion of isolates in 2025. Although the proportion of ASuT isolates was generally low from 2001 to 2013, it subsequently fluctuated without a significant trend, reaching a maximum of 9% in 2023.

MIC distributions for ampicillin, chloramphenicol, sulfamethoxazole and tetracycline were examined for selected years to assess changes in the distribution of MIC values over time (Figure 2). Statistical comparisons were performed separately for wild-type and resistant isolates for each antimicrobial using the Kruskal-Wallis test followed by Dunn's post hoc test with Bonferroni correction, to assess whether the MIC distributions changed across the years considered.

[1] Although *E. coli* surveillance in DANMAP was established in 1995, MIC results are included from 2001 onwards as data from 1995-2000 was digitally unavailable at the time of writing.

**Figure 2 Distribution of MIC values from *E. coli* from cattle by antimicrobial substance and year** DANMAP 2025




Blue indicates wild-type isolates while red indicates resistant isolates. The intensity of the colour shading represents the percentage of isolates with the respective MIC value within each year, with darker shading indicating higher percentages. The dashed line represents the ECOFF value applied for interpretation.

Among wild-type isolates, the MIC distribution for tetracycline remained similar in the earlier years, followed by a significant shift towards the ECOFF in 2023 and 2025. For chloramphenicol, a significant shift towards higher MIC values was observed after 2013. For sulfamethoxazole, the MIC distribution showed more pronounced differences between years. The distribution in 2013 differed significantly from those observed in all subsequent years, while the distributions in 2019, 2021 and 2023 were similar. In 2025, a significant shift towards higher MIC values and closer to the ECOFF was observed compared with all previous years. For ampicillin, the MIC distribution remained relatively stable across years, although significant differences were observed between 2016 and 2021, 2023 and 2025. The distribution in 2025 also differed significantly from 2019.

Among resistant isolates, a shift in the MIC distributions was observed from 2019 onwards. For sulfamethoxazole and ampicillin, this was characterised by a significant shift towards lower MIC values in the later years. For tetracycline and chloramphenicol, the MIC distributions observed in 2019 differed significantly from those observed in 2021, 2023 and 2025.

Overall, the MIC distributions appear to be moving towards the ECOFF, with wild-type isolates shifting towards higher MIC values, and resistant isolates shifting towards lower MIC values.

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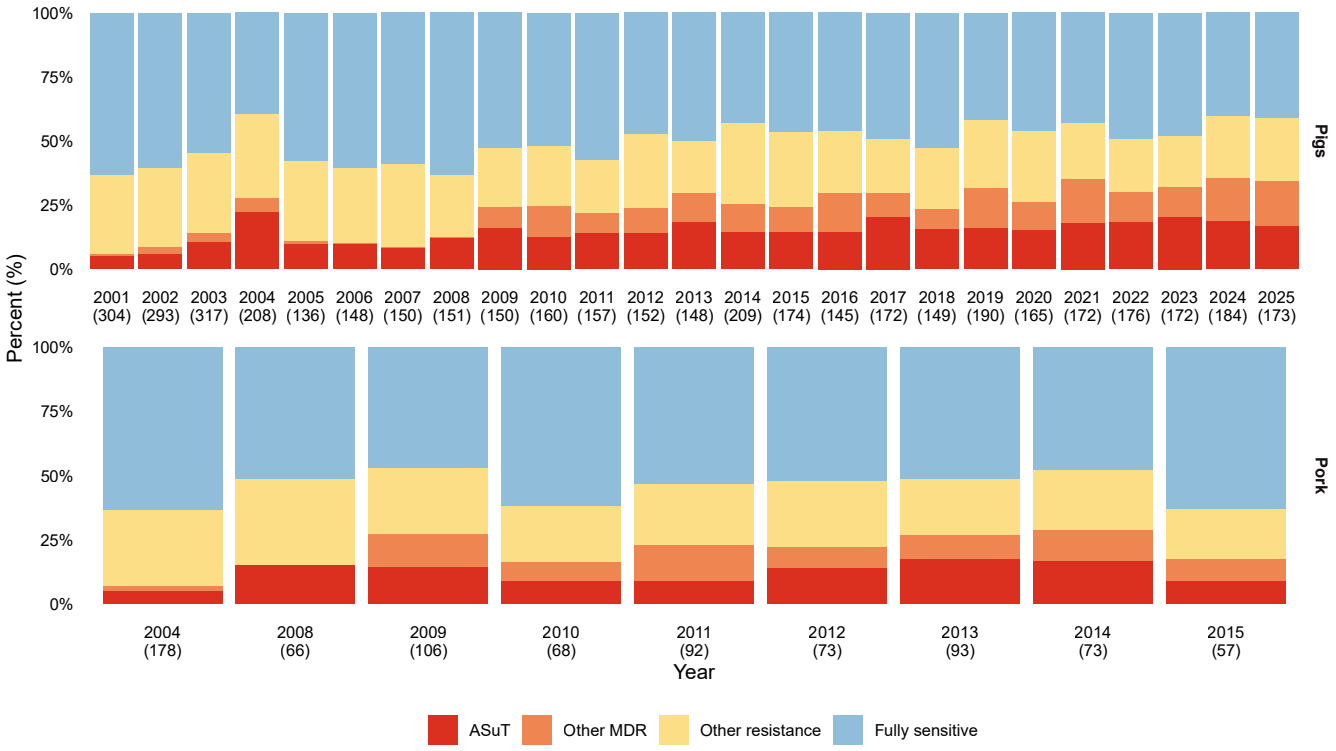
## Textbox 7.3

# 30 years of *Escherichia coli* surveillance in Danish pigs and pork

Denmark has had a nationwide surveillance of antimicrobial resistance in indicator *Escherichia coli* recovered from healthy food-producing animals since 1995. A retrospective comparison of resistance patterns in *E. coli* over the past 25 years of the DANMAP programme[1] was performed.

A total of 4,546 *E. coli* isolates from pigs and 806 *E. coli* isolates from pork have been collected and reported in DANMAP from 2001 to 2025. Isolates from pigs were collected consistently throughout the 25-year period, whereas isolates from pork were only collected in 2004 and from 2008 to 2015. The sampling strategy has changed over time, with a more standardized approach being implemented after 2014, following the introduction of the harmonized antimicrobial resistance monitoring in the European Union [Commission Implementing Decision (EU) 2020/1729].

**Figure 1 Relative distributions (%) of AMR profiles among *E. coli* from pigs and pork by year, Denmark, 2001-2025** DANMAP 2025

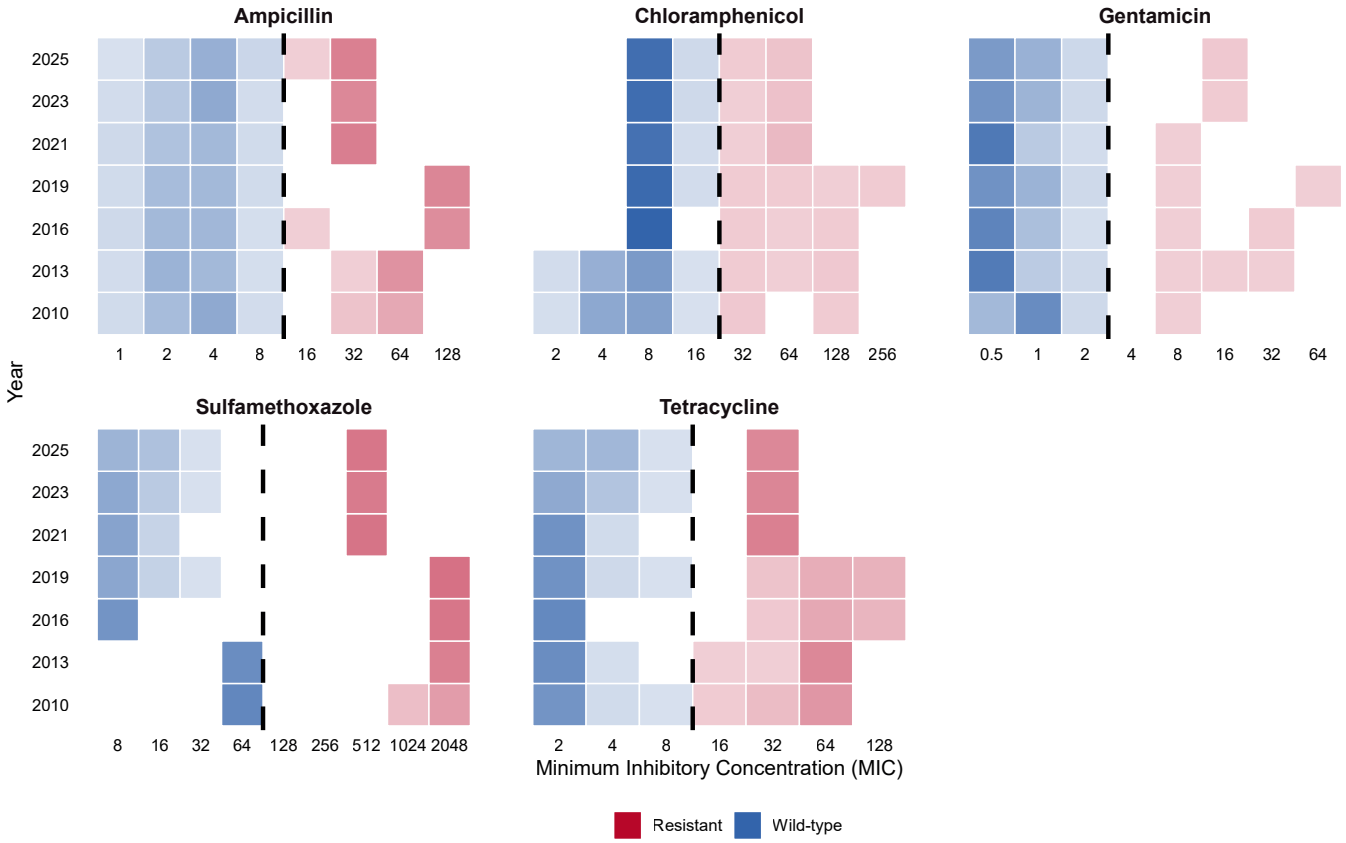



The bars show the percentage of isolates classified as ASuT (resistant to at least ampicillin, sulfamethoxazole and tetracycline), other MDR (other multidrug resistance profiles than ASuT), other resistance (resistance to one or two antimicrobial classes), or fully sensitive (sensitivity to all antimicrobial substances tested). The number of isolates included for each year is given in parentheses below each bar.

The relative distribution of antimicrobial resistance profiles varies between sample origin and year (Figure 1). Fully sensitive *E. coli* isolates were dominant in both pigs and pork across all years, ranging from 40% to 64% among pigs and from 47% to 64% among pork. Among resistant isolates from pigs, ASuT was the predominant resistance profile for most of the surveillance period. In pig isolates, the proportion of ASuT increased from 5% in 2001 to approximately 12% in 2009 and remained at a statistically similar level thereafter. However, in 2016 and 2025, other MDR accounted for a larger proportion of isolates than ASuT. A similar pattern was observed in pork, with the prevalence of ASuT increasing from 2004 to 2008 and then stabilizing (note that no data were available for the years 2005-2007, so this observation must be interpreted with caution).

[1] Although *E. coli* surveillance in DANMAP was established in 1995, MIC results are included from 2001 onwards as data from 1995-2000 was digitally unavailable at the time of writing.

**Figure 2 Distribution of MIC values from *E. coli* from pigs and pork by antimicrobial substance and year** DANMAP 2025




Blue indicates wild-type isolates while red indicates resistant isolates. The intensity of the colour shading represents the percentage of isolates with the respective MIC value within each year, with darker shading indicating higher percentages. The dashed line represents the ECOFF value applied for interpretation.

Among isolates from pigs, MIC distributions for ampicillin, sulfamethoxazole, tetracycline, gentamicin and chloramphenicol were examined for given years to assess changes in the distribution of MIC values over time (Figure 2). Statistical comparisons were performed separately for wild-type and resistant isolates for each antimicrobial using the Kruskal-Wallis test followed by Dunn's post hoc test with Bonferroni correction, to assess whether the MIC distributions changed across the years considered.

Among wild-type isolates, for ampicillin, the MIC distribution remained stable from 2010 to 2023, with no pairwise differences. Differences in the MIC distribution were observed in 2025 compared with 2013, 2016, 2019 and 2021 (with a slight shift towards the ECOFF). For sulfamethoxazole, the MIC distribution differed significantly between the early years (2010 and 2013) and the later part of the surveillance period. Furthermore, the MIC distribution in 2025 differed significantly from the distribution in 2016. For tetracycline, the MIC distribution remained stable from 2010 to 2021, followed by a shift towards the ECOFF in 2023 and 2025. For chloramphenicol, the MIC distribution shifted significantly towards the ECOFF from 2016 onwards compared with 2010 and 2013, after which the distribution remained stable through 2025. For gentamicin the distribution fluctuated over time, shifting away from the ECOFF in 2013 compared with 2010, followed by a shift back towards the ECOFF in 2019. The distribution then shifted away from the ECOFF again in 2021 before moving towards the ECOFF in 2023, where it remained stable through 2025.

Among resistant isolates, for ampicillin, the MIC distribution above the ECOFF had three phases, with similar distributions in 2010-2013, 2016-2019, and 2021-2025. For tetracycline, a similar pattern was observed, although the 2013 MIC distribution did not differ significantly from the distributions observed in 2010, 2016, or 2019. For sulfamethoxazole, the MIC distribution above the ECOFF shifted significantly towards the ECOFF in 2021 compared with 2010-2019 and remained stable through 2025.

**continued ... Textbox 7.3**

No significant differences were observed for the MIC distributions above the ECOFF for gentamicin and chloramphenicol, although the distribution appeared to shift away from the ECOFF for gentamicin and towards the ECOFF for chloramphenicol in the most recent years.

Overall, the relative occurrence of ASuT profiles in indicator *E. coli* from pigs has remained similar with minor non-significant fluctuations from 2010 to 2025, while the MIC distributions showed changes. For all five antimicrobials, the MIC distribution among wild-type isolates appeared to fluctuate over time, with distributions in the most recent years tending to be closer to the ECOFF. This shift may be indicative of future changes in the proportion of isolates classified as resistant, and hence an early signal of a possible increase in ASuT resistance in the near future. However, in 2023 and 2025 the occurrence of other MDR profiles also seems to have increased (Figure 1).

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# 8.

# Resistance in human pathogens

# 8. Resistance in human pathogens

## Highlights

**Number of invasive cases:** All monitored species apart from ***Enterococcus faecium*** increased in number, some significantly from 2016 to 2025: *E. coli* from 4,841 to 6,056 cases (25% increase), *S. aureus* from 1,963 to 2,543 cases (30%) and *K. pneumoniae* complex from 1,156 to 1,718 cases (49%).

***Escherichia coli*:** Invasive cases showed continuously slow rises in resistance to ciprofloxacin, cefuroxime, 3rd generation cephalosporins and gentamicin, but combined resistance to the three antimicrobial classes decreased. Also increasing resistance to piperacillin-tazobactam has been observed, 2025 at 6.5%. Resistance to carbapenems remained below 1%.

***Klebsiella pneumoniae*:** In 2025, reporting changed from *K. pneumoniae* to include the entire *K. pneumoniae* complex; data were corrected retrospectively, but from 2023 to 2025 this led to an increase of approximately 15% in the total number of reported cases. From 2015 to 2021, particularly for cephalosporins decreasing trends in resistance were observed. From 2022 to 2025, resistance levels reverted and showed increases for most of the monitored antibiotics. Of particular interest is the almost continuous increase in resistance levels to piperacillin-tazobactam, which increased from 5.9% in 2015 to 10.0% in 2025 in total, albeit with a small drop from 2024 to 2025. The resistance level to carbapenems remained low (<1%) as did combined resistance to ciprofloxacin, cephalosporins and gentamicin (0.9% in 2025).

***Staphylococcus aureus*:** A substantial increase in the number of bacteraemia with methicillin-resistant *S. aureus* was observed with 66 cases whereof seven were LA-MRSA. Mortality remained the same for MSSA and MRSA. There were 3,301 cases of MRSA from screening (42% of cases) or infections (58%). Thirty-six MRSA outbreaks were registered at hospitals, nursing homes and other institutions for a total of 127 cases with 60 being infections.

***Streptococcus pneumoniae*:** An increase in the number of invasive cases from 2024 (600 cases) to 2025 (685 cases) was observed, which was the highest number since 2018 (798 cases). Fifty isolates were reported as having either susceptibility to penicillin at increased exposure or as resistant – equating to 7.2% of all culture-positive *S. pneumoniae* isolates compared to 6.3% in 2024.

***Neisseria gonorrhoeae*:** In 2025, the reference laboratory at SSI examined 1,797 isolates from 1,893 culture positive unique cases of gonorrhoea. Ceftriaxone resistance was found isolates from two patients, both of whom had been infected in Asia. The overall ciprofloxacin resistance rate was 54%, while the azithromycin resistance rate was 9%.

***Shigella* spp.:** The levels of resistance observed in the *Shigella* spp. isolates in Denmark were generally in concordance with the levels that are reported internationally. It is notable that there was a number of isolates that simultaneously were resistant towards azithromycin, 3rd generation cephalosporins, and ciprofloxacin, in particular for *S. sonnei*.

## 8.1 Introduction

The Danish national surveillance programme for monitoring of antimicrobial resistance in human clinical bacteria collects data on routine diagnostics from all of Denmark. It is an active digital catchment system collecting results from all clinical and screening samples from patients at hospitals and in general praxis. Data coverage is high and near complete, including all results from phenotypical susceptibility testing (AST) at Danish hospitals and a high share of AST performed on samples from general practitioners. Included are data from invasive infections and urines, and in selected cases data from other specimen or sample sites. In addition, the programme includes phenotypic resistance and typing results from the reference laboratories at SSI. Isolates are submitted to SSI either as part of the programme on mandatory notifiable diseases or based on voluntary submission of bacterial species carrying resistance mechanisms of concern. Table 8.1 gives an overview of inclusion criteria for data from the digital surveillance system and the reference laboratories.

### 8.1.1 Surveillance based on data from the Danish Microbiology Database (MiBa)

An important part of the national surveillance programme consists of systematically extracted data from a register (EpiMiBa) linking to the Danish Microbiology Database (MiBa). MiBa was established in 2010 with the aim of building a cross-national database that included and made available all microbiology analyses performed by the individual Department of Clinical Microbiology (DCM). MiBa simultaneously delivers real time patient data to the DCMs for clinical use and data to SSI for national surveillance. Until the establishment of MiBa, surveillance was based on voluntary manual reporting from the individual DCM, in the beginning (1995) hosting data from just two DCMs, but quickly expanding to cover more than fifty percent of the DCMs. Since 2015, all DCMs have contributed to the program resulting in a 100% coverage of hospitalised patients and – since the DCMs perform microbiology analyses for GPs and private specialists as well – also a very high coverage of results from the primary sector. A description of MiBa and the usage and validation of data from the associated database EpiMiBa can be found on the following homepage [https://mibaen.ssi.dk/] and in DANMAP 2018, Textbox 8.1.

The MiBa-based surveillance includes all invasive isolates of *Escherichia coli*, *Klebsiella pneumoniae* complex, *Enterococcus faecalis*, *Enterococcus faecium*, *Pseudomonas aeruginosa* and *Acinetobacter* species and all urine isolates of *E. coli* and *K. pneumoniae* complex. For inclusion, the following case definition applies: The first sample of each given bacterial species per individual patient per year, by date of sample collection; an approach identical to the surveillance performed by the European Antimicrobial Resistance Surveillance Network (EARS-Net). All duplicates, patient-related or sample-related within the year of observation, are excluded. Materials and methods are further described in paragraph 10.10 in Chapter 10.

### 8.1.2 Surveillance based on data from the reference laboratories

Submission of isolates to the reference laboratories at SSI began in 1957 with the voluntary referral of *S. aureus* from bloodstream infections. Still today, many isolates are sent as part of voluntary programmes; however, the majority of isolates are referred as part of surveillance programmes for notifiable diseases. The mandatory programme collects information on methicillin-resistant *S. aureus* (MRSA) and carbapenemase-producing organisms (CPO) from clinical and screening samples, *S. pneumoniae* and *Haemophilus influenzae* serotype b (Hib) from invasive infections and *Neisseria gonorrhoeae* from all clinical samples. The latter three are collected irrespectively of findings of antimicrobial resistance, but resistance mechanisms are investigated both locally and at SSI (Table 8.1). The voluntary programme includes referral of vancomycin-resistant enterococci, ESBL-positive *E. coli*, beta-haemolytic streptococci and *S. aureus*, all from blood or other sterile sites. In addition, the reference laboratory for antimicrobial resistance at SSI receives highly resistant strains or strains carrying atypical antimicrobial resistance mechanisms of specific concern irrespective of bacterial species. Referral frequency varies between the reporting DCM and may be day-to-day or on a monthly or periodical basis. Since 2015/2016, characterisation of antimicrobial resistance mechanisms in bacteria has been performed primarily by whole genome sequencing (WGS).

### 8.1.3 Number of invasive cases

Figure 8.1 presents the number of invasive cases according to DANMAP and EARS-Net definitions (one case pr patient pr year with *E. coli, K. pneumoniae, S. aureus, P. aeruginosa, E. faecalis, E. faecium* and/or *S. pneumoniae*, e.g. each patient-species case is counted once per year) from 2016 to 2025. During the decade, the number of invasive cases increased by 18% from 10,442 to 12,738 cases: *E. coli* 4,841 to 6,056 cases (20% increase), *S. aureus* 1,963 to 2,543 cases (23%) and *K. pneumoniae* complex 1,156 to 1,718 cases (33%). Invasive cases caused by Acinetobacter species are not shown in the figure due to the small number of isolates (between 55 and 97 cases/year for 2016 to 2025).

Figure 8.2a shows the incidence of the monitored invasive cases per 100,000 inhabitants in Denmark per year from 2016 to 2025. During this period, the Danish population increased by 5.0% (from 5,707,251 inhabitants in 2016 to 5,992,734 inhabitants in 2025). For comparison, Figure 8.2b shows the total number of blood cultures taken per 100,000 inhabitants per year (38% increase) and the number of patients with minimum one blood culture taken per 100,000 inhabitants per year, (from 2,652 patients per 100,000 inhabitants in 2016 to 3,127 patients per 100,000 inhabitants in 2025, 18% increase) for the same period. The combined incidence of positive blood cultures with one of the monitored species increased from 483 per 100,000 inhabitants in 2016 to 635 per 100,000 inhabitants in 2025, (24%).

The following sections present trends in resistance for the individual bacterial species and/or resistance types under surveillance.

**Table 8.1 Bacterial species and types included in the national antimicrobial resistance surveillance in humans, Denmark**

DANMAP 2025

| **MiBa* data - AST** routine diagnostics performed by departments of clinical microbiology at Danish hospitals** | |
|---|---|
| **Species** | **Inclusion criteria** |
| *Escherichia coli*<br>*Klebsiella pneumoniae* | First isolate per patient per year from blood or cerebrospinal fluid, from urine in hospitalised patients and from urine from primary health care |
| *Pseudomonas aeruginosa*<br>*Acinetobacter* species<br>*Enterococcus faecalis*<br>*Enterococcus faecium* | First isolate per patient per year from blood or cerebrospinal fluid |
| **Data from the reference laboratories at SSI - voluntary submitted isolates, selected resistance mechanisms** | |
| **Species or type** | **Inclusion criteria** |
| *Staphylococcus aureus*<br>Beta-haemolytic streptococci | One isolate per patient per episode from blood or cerebrospinal fluid |
| *Neisseria gonorrhoeae* | One isolate per patient per episode from any sample site |
| 3rd generation cephalosporin-resistant *Escherichia coli* | First isolate per patient within 12 months from blood |
| Vancomycin-resistant enterococci | First isolate per patient within 12 months from any sample site (excluding screening samples) |
| Enterococci with specific phenotype of concern (e.g. linezolid, daptomycin and tigecycline R) | First isolate per patient within 12 months from any sample site (clinical and screening samples) |
| All bacterial species with other exceptional phenotypes (e.g. acquired colistin resistance) | One isolate per patient per episode from any sample site |
| **Data from the reference laboratories at SSI - mandatory submitted isolates, selected resistance mechanisms** | |
| **Species or type** | **Inclusion criteria** |
| Carbapenemase-producing organisms | First isolate per patient within 12 months from any sample site (clinical and screening samples) |
| Methicillin-resistant *Staphylococcus aureus* | First isolate from all new cases of MRSA postive patients from any sample site (clinical and screening samples) |
| *Streptococcus pneumoniae* | One isolate per patient per episode from blood or cerebrospinal fluid |
| *Haemophilus influenzae* serotype b, Hib | All invasive isolates |

Regarding submissions of isolates to the reference laboratories normally more isolates are received, but for the statistics one patient only counts once.
* MiBa = the microbiological database, ** AST = antimicrobial susceptibility testing.

**Figure 8.1 Number of invasive cases for bacterial species under surveillance, Denmark, 2016-2025** DANMAP 2025

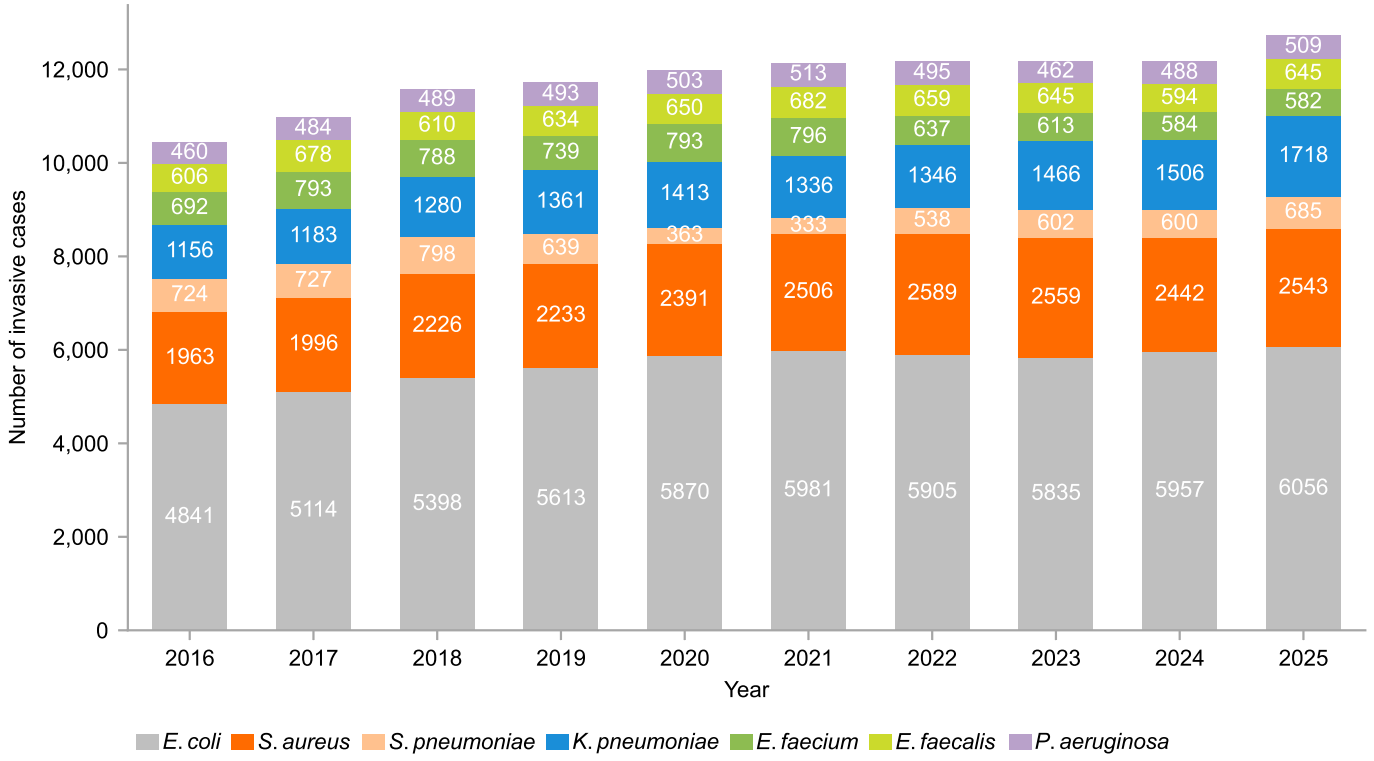
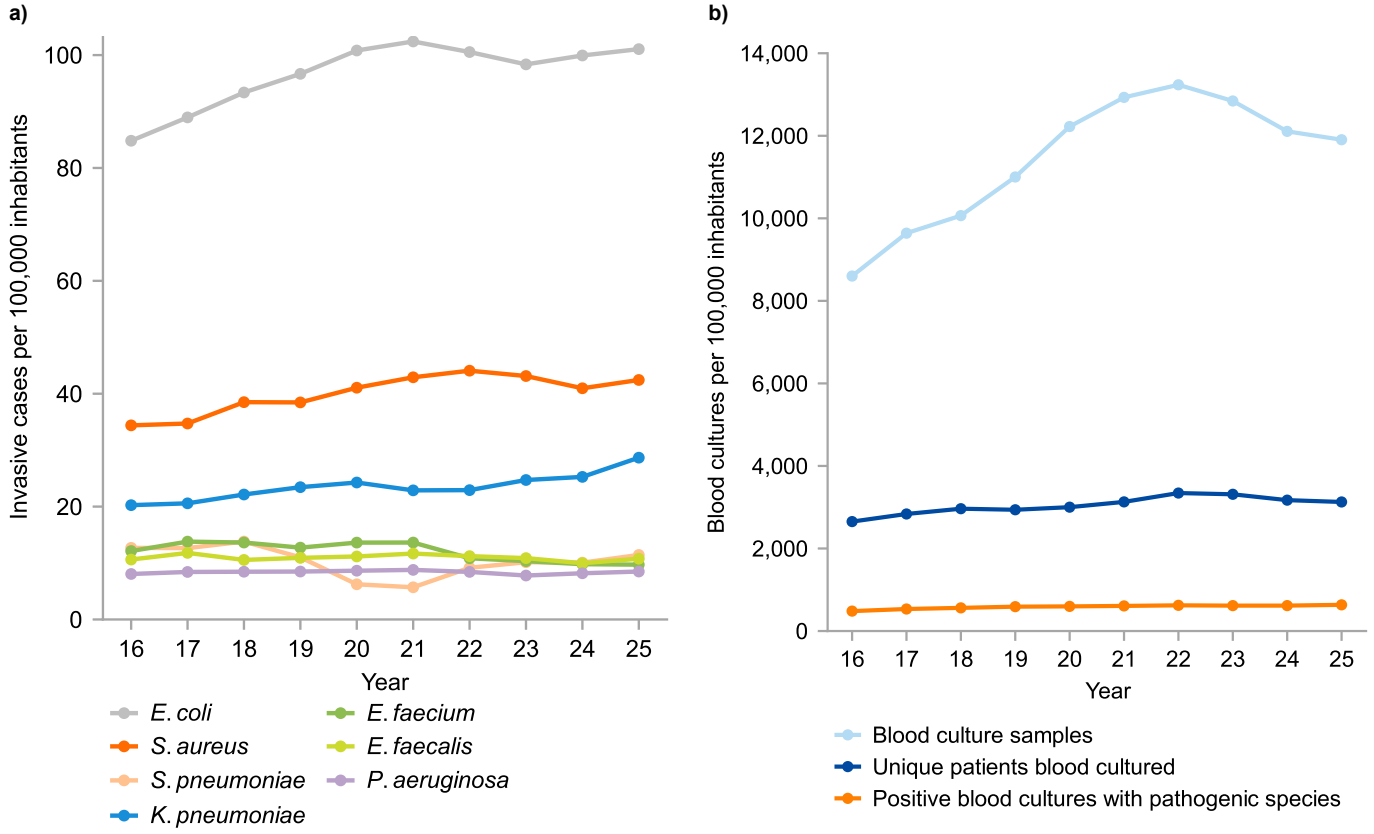



**Figure 8.2 Incidence of a) Invasive cases and b) blood cultures taken per 100,000 inhabitants, Denmark, 2016-2025** DANMAP 2025



## 8.2 Results from MiBa data surveillance

### 8.2.1 *Escherichia coli*

Escherichia coli is by far the most frequent cause of community and hospital acquired bacteraemia and urinary tract infections (UTI) in Denmark. The pathogen is part of the normal intestinal flora in both animals and humans, where it comes into close proximity to many other bacterial species. Transferable resistance mechanisms are frequently seen in these gut bacteria as well as resistance conferred by mutations. Since *E. coli* is the most frequent cause of UTI and bacteraemia, it is also responsible for a large proportion of the antimicrobials used to treat these conditions. The percentages of resistance in invasive *E. coli* isolates for each key antimicrobial are presented in Table 8.2, as are urine samples from hospitals and primary health care (see details in later paragraphs).

**Invasive cases from hospital patients**

In 2025, a total of 6,056 individual patients with invasive *E. coli* isolates were identified in EpiMiBa. Antimicrobial susceptibility test results for key antimicrobials were also extracted (see Chapter 10 'Material and methods'). Figure 8.3 and Table 8.3 show the total annual number of invasive isolates and proportion of resistant isolates by region between 2016 and 2025. Resistance levels have appeared relatively stable for the last decade. However, slow increases in resistance to ciprofloxacin, cefuroxime and 3rd generation cephalosporins have been noticeable for the past five years. Also resistance to piperacillin-tazobactam has been on an upwards trend for the last decade. Resistance to carbapenems remained below 1%. The percentages of multidrug resistant invasive isolates are presented in Table 8.4. Combined resistance to ciprofloxacin, cephalosporins and gentamicin decreased from 1.8% in 2016 to 1.1% in 2025 and combined resistance to ampicillin and gentamicin decreased from 5.8% to 4.3%.

**Urinary cases from hospitals**

In 2025, *E. coli* was isolated from urine samples of 38,050 individual hospital patients. As for invasive *E. coli* increasing resistance to ciprofloxacin, cefuroxime and 3rd generation cephalosporins has been observed for the past five years. In Table 8.2 summarized antimicrobial susceptibility results for *E. coli* isolates (invasive and urine specimen) are shown. In Figure 8.4 and Table 8.5, resistance for *E. coli* urine isolates from hospitalised patients are shown for 2016-2025.

**Urinary cases from primary health care**

In 2025, *E. coli* were isolated from urine samples from 106,767 individual patients in primary health care. In 2024, a change in workflow at one of the DCMs in the Capital Region caused data from that DCM to be excluded for *E. coli* from the analysis for that specific year. Susceptibility results for all tested antimicrobials are shown in Table 8.2. In Figure 8.5 and Table 8.6, resistance for *E. coli* urine isolates from primary health care are shown for the past decade.

**Conclusion**

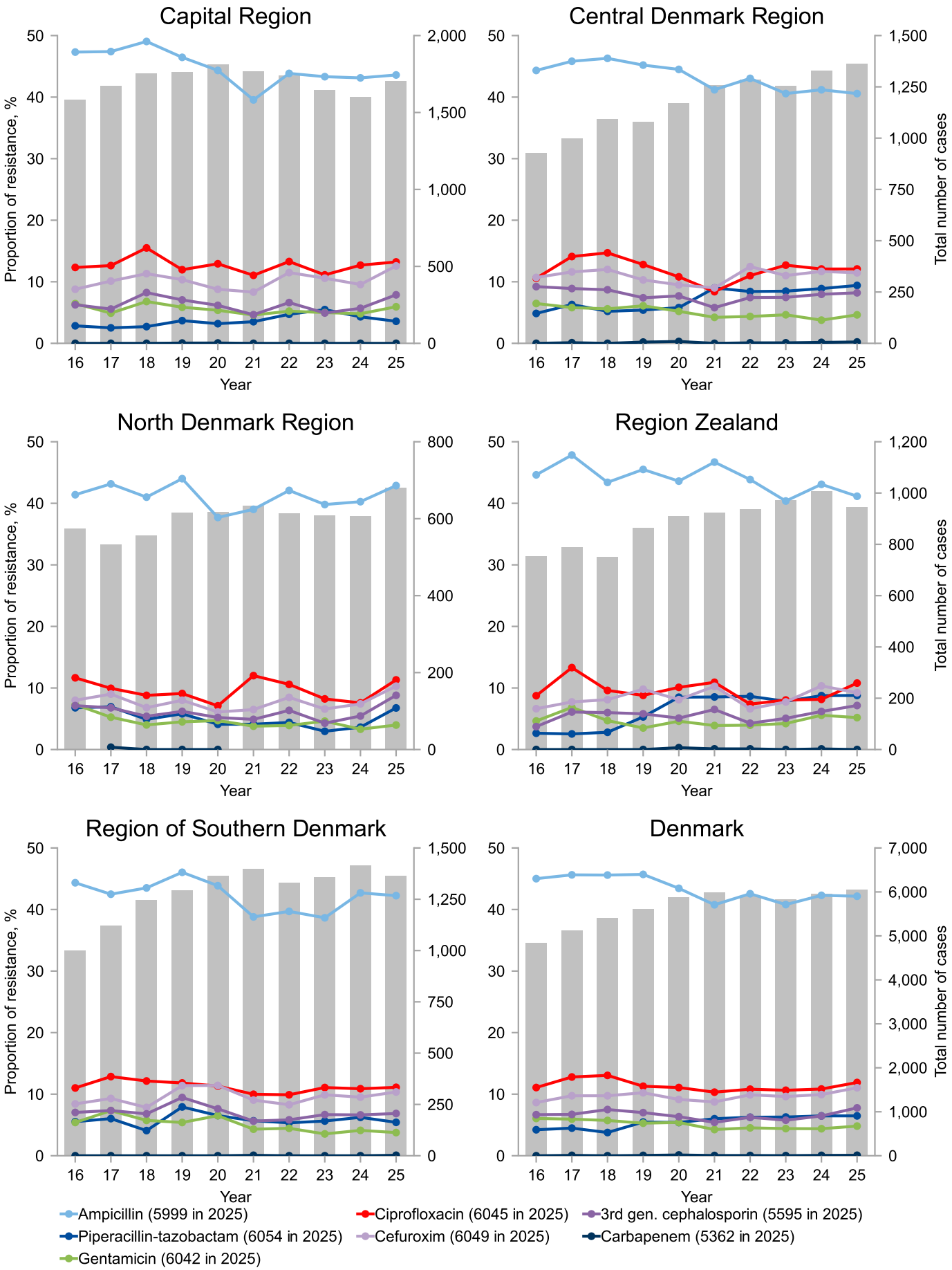
The number of invasive cases of *E. coli* appears to have reached a plateau. Resistance levels are generally stable for all specimen types, however, the slow rise in ciprofloxacin, cefuroxime, 3rd generation cephalosporins and piperacillin-tazobactam resistance in *E. coli* from invasive infections and hospital urines are cause for concern.

**Table 8.2 *Escherichia coli*. Resistance (%) in isolates from humans, Denmark, 2025** DANMAP 2025

| Substance | Invasive isolates, hospitals % | Urine isolates, hospitals % | Urine isolates, primary health care % |
|---|---|---|---|
| Ampicillin | 42 | 38 | 34 |
| Mecillinam | 5.6 | 6.9 | 4.1 |
| Piperacillin-tazobactam | 6.5 | 5.9 | 3.4 (2) |
| Amoxicillin/clavulanic acid | 27 (4) | 10.6 | 7.0 |
| Sulfonamide | | 29 (5) | 22.3 |
| Trimethoprim | | 22 | 19.7 |
| Nitrofuratoin | | 0.8 | 0.5 |
| Gentamicin | 4.8 | 4.8 | 3.3 (2) |
| Ciprofloxacin | 11.9 | 11.2 | 8.8 |
| Cefuroxime | 11 | 9.9 | 6.3 (3) |
| 3rd generation cephalosporins | 7.8 | 8.2 | 5.6 |
| Carbapenem | 0.1 | 0.0 | 0.0 (3) |
| Max. number of isolates tested for resistance to the presented antibiotics | 6,054 | 37,898 | 106,528 |

Included are results from all DCMs where >75% of the isolates in each antibiotic/sample group were susceptibility tested.
Numbers in parantheses indicate the number of DCMs included if less than six.

**Figure 8.3 Antimicrobial resistance in invasive *Escherichia coli* isolates from humans by region, Denmark, 2016-2025** DANMAP 2025




Number in parentheses indicates number tested.

**Table 8.3 Invasive *Escherichia coli* isolates from humans, resistance (%) and annual number of individual cases, Denmark, 2016-2025** DANMAP 2025

| | Resistance (%) in invasive *E. coli* isolates | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Substance | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
| Ampicillin | 45.0 | 45.6 | 45.5 | 45.7 | 43.4 | 40.7 | 42.6 | 40.8 | 42.3 | 42.2 |
| Piperacillin-tazobactam | 4.2 | 4.5 | 3.8 | 5.5 | 5.4 | 6.0 | 6.3 | 6.3 | 6.5 | 6.5 |
| Gentamicin | 6.1 | 6.0 | 5.7 | 5.3 | 5.4 | 4.3 | 4.5 | 4.4 | 4.4 | 4.8 |
| Ciprofloxacin | 11.1 | 12.8 | 13.0 | 11.3 | 11.1 | 10.3 | 10.8 | 10.6 | 10.8 | 11.9 |
| Cefuroxime | 8.6 | 9.7 | 9.8 | 10.2 | 9.2 | 8.7 | 9.9 | 9.6 | 9.9 | 11.0 |
| 3rd gen.cephalosporins | 6.7 | 6.7 | 7.3 | 6.9 | 6.2 | 5.4 | 6.2 | 5.8 | 6.5 | 7.8 |
| Carbapenem | 0.0 | 0.1 | 0.0 | 0.1 | 0.1 | 0.0 | 0.0 | 0.0 | 0.1 | 0.1 |
| Total number of isolates | 4,841 | 5,114 | 5,398 | 5,613 | 5,870 | 5,981 | 5,905 | 5,835 | 5,957 | 6,056 |

**Table 8.4 Invasive *Escherichia coli* isolates from humans. Combined resistance to 1) ampicillin and gentamicin and 2) 3rd generation cephalosporins, ciprofloxacin, and gentamicin (multiresistance), Denmark, 2016-2025** DANMAP 2025

| | | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Combination | | % (N) | % (N) | % (N) | % (N) | % (N) | % (N) | % (N) | % (N) | % (N) | % (N) |
| AMP/GEN | Resistance | 5.8 (278) | 5.8 (289) | 5.5 (284) | 5.2 (275) | 5.1 (287) | 4.0 (229) | 4.1 (233) | 4.1 (231) | 4.0 (235) | 4.3 (259) |
| | Percentage (no.) of isolates tested | 99 (4,816) | 98 (5,015) | 96 (5,170) | 95 (5,308) | 95 (5,583) | 96 (5,745) | 96 (5,679) | 96 (5,602) | 99 (5,903) | 99 (5,993) |
| 3GC/CIP/GEN | Resistance | 1.8 (87) | 1.8 (88) | 2.0 (100) | 1.8 (93) | 1.5 (82) | 1.1 (60) | 1.3 (70) | 1.2 (63) | 1.0 (54) | 1.1 (63) |
| | Percentage (no.) of isolates tested | 98 (4,763) | 95 (4,883) | 93 (4,997) | 94 (5,259) | 93 (5,470) | 93 (5,564) | 93 (5,474) | 93 (5,417) | 93 (5,515) | 92 (5,585) |
| | Total number of invasive isolates | 4,841 | 5,114 | 5,398 | 5,613 | 5,870 | 5,981 | 5,905 | 5,835 | 5,957 | 6,056 |

**Table 8.5 *Escherichia coli* from hospital urines, levels of resistance (%), Denmark, 2016-2025** DANMAP 2025

| | Resistance in E. coli urine isolates from hospitals | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Substance | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
| Ampicillin | 41 | 41.9 | 42.1 | 43.7 | 40.6 | 39.2 | 40.0 | 39.4 | 39.6 | 39.6 |
| Mecillinam | 7.4 | 7.5 | 7.4 | 8.1 | 7.3 | 6.9 | 6.8 | 6.5 | 6.7 | 6.9 |
| Piperacillin-tazobactam | 3.3 | 3.7 | 3.5 | 4.4 | 4.3 | 4.5 | 5.4 | 5.4 | 5.6 | 5.9 |
| Sulfonamide | 34.9 | 31.1 | 31* | 31.4* | 29.4* | 28.5* | 28.2* | 30.9* | 30.0* | 29.3* |
| Gentamicin | 5.3 | 4.9 | 4.7 | 4.6 | 4.6 | 4.2 | 4.3 | 4.5 | 4.9 | 4.8 |
| Ciprofloxacin | 10.9 | 10.4 | 11 | 10.6 | 9.6 | 8.7 | 9.3 | 9.9 | 10.2 | 11.2 |
| Cefuroxime | 6.8 | 7.1 | 7.2 | 7.8 | 7.2 | 6.7 | 7.5 | 7.7 | 8.1 | 9.9 |
| 3rd gen. cephalosporins | 5.9 | 6.2 | 6.4 | 6.9 | 6.3 | 5.8 | 6.2 | 6.5 | 6.9 | 8.2 |
| Carbapenem | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 |
| Total number of isolates | 46,865 | 46,884 | 47,914 | 47,235 | 48,962 | 49,986 | 48,559 | 44,389 | 40,624 | 38,050 |

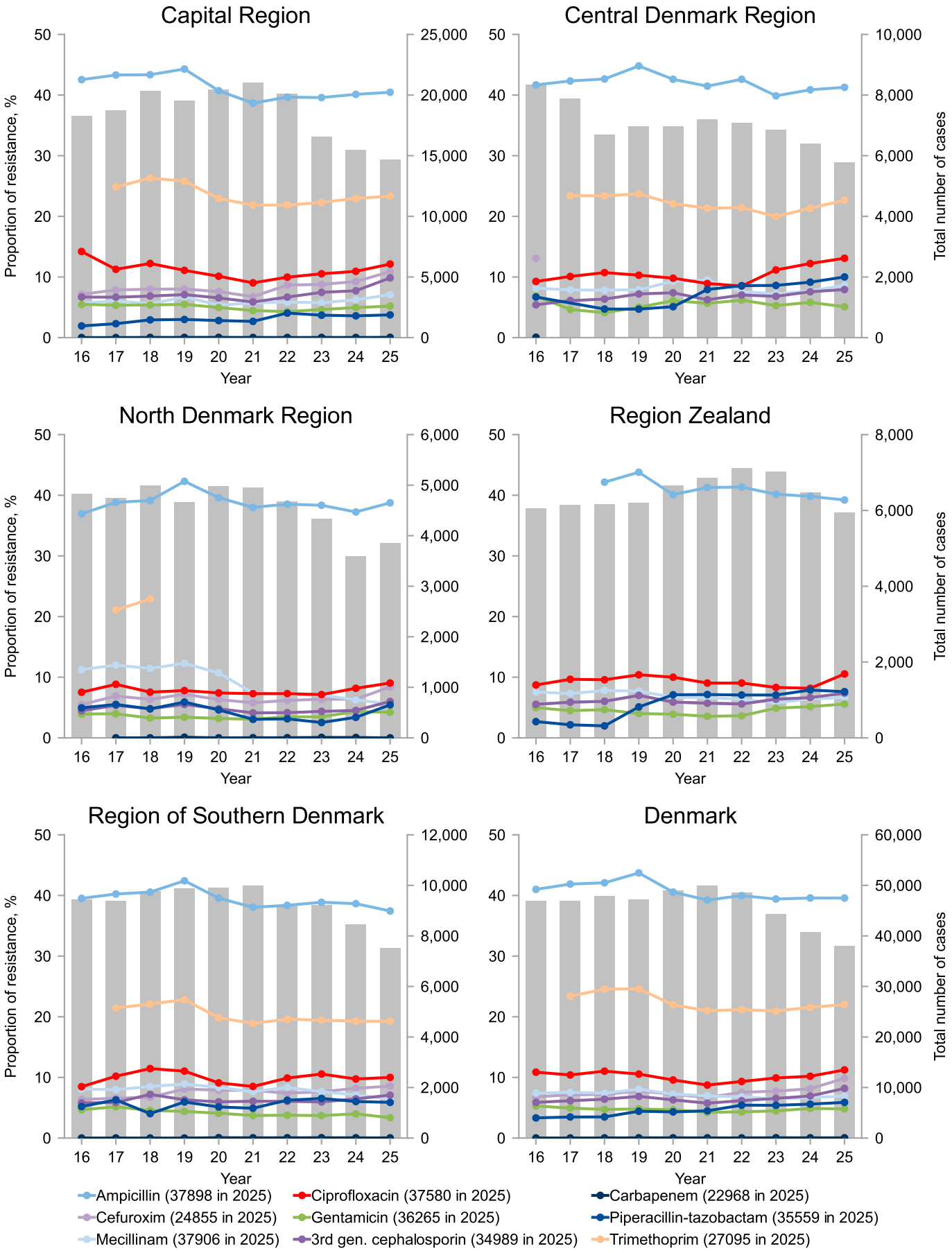
* Indicates less than 6 DCMs reported routine susceptibility testing.

**Table 8.6 *Escherichia coli* from urines from primary health care, levels of resistance (%), Denmark, 2016-2025** DANMAP 2025

| | Resistance in *E. coli* urine isolates from primary health care | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Substance | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
| Ampicillin | 38.3 | 37.9 | 37.4 | 38.1 | 36.5 | 34.3 | 34.6 | 34.2 | 34.3 | 33.8 |
| Mecillinam | 5.6 | 5.5 | 5.1 | 5.3 | 4.9 | 4.6 | 4.3 | 4.0 | 3.9 | 4.1 |
| Sulfonamide | 29.5 | 29.1 | 28.3 | 27.9 | 26.7 | 25.2 | 25.0 | 25.5 | 23.7 | 22.3 |
| Ciprofloxacin | 10.1 | 8.4 | 8.1 | 8 | 7.5 | 6.9 | 6.9 | 7.5 | 7.7 | 8.8 |
| 3rd gen. cephalosporins | 4.3 | 4.5 | 4.9 | 5.2 | 5 | 4.4 | 4.8 | 5.3 | 5.6 | 5.6 |
| Total number of isolates | 67,798 | 73,497 | 80,851 | 86,508 | 88,462 | 99,077 | 104,376 | 106,236 | 93,436 | 106,767 |

**Figure 8.4 Antimicrobial resistance in *Escherichia coli* isolates from urines in humans (individual cases at hospitals) by region, Denmark, 2016-2025**

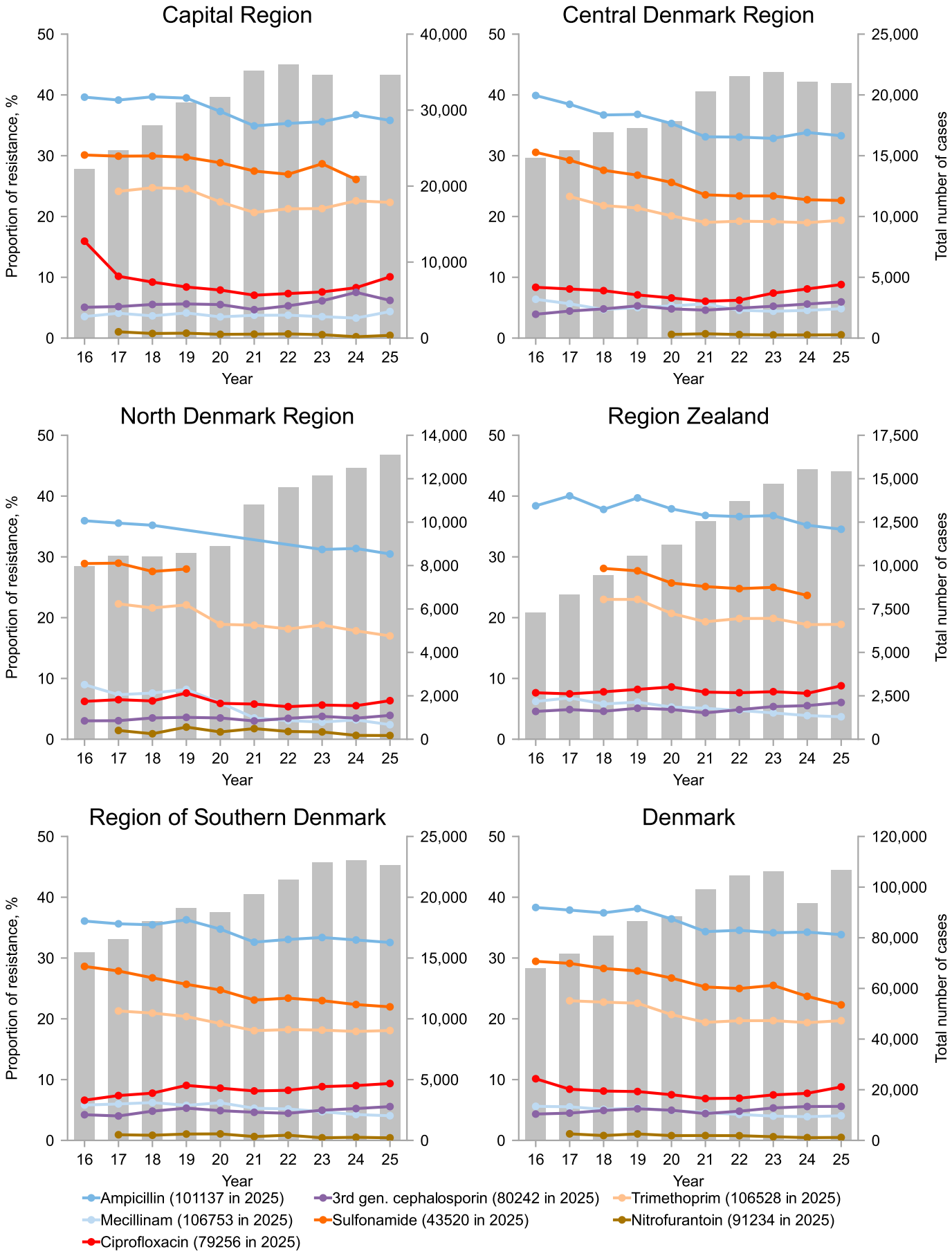
DANMAP 2025




Number in parentheses indicates number tested.

**Figure 8.5 Antimicrobial resistance in *Escherichia coli* isolates from urines in humans (individual cases from primary health care) by region, Denmark, 2016-2025**

DANMAP 2025




Number in parentheses indicates number tested.

### 8.2.2 *Klebsiella pneumonia* complex

*Klebsiella pneumoniae* is part of the human intestinal tract. The bacteria cause urinary tract infections, intra-abdominal infections, bacteraemia and ventilator-associated pneumonia (VAP). *K. pneumoniae* may cause nosocomial outbreaks. *K. pneumoniae* frequently displays plasmid-mediated resistance mechanisms, which are transferrable to other bacterial species. The percentage of resistance in *K. pneumoniae* isolates for key antimicrobials in isolates from invasive infections, urines from hospitals and urines from general praxis, respectively, is presented in Table 8.7. Due to changes in reporting, this section that earlier reported on *Klebsiella pneumoniae* now includes the entire *Klebsiella pneumoniae* complex. Data has been corrected retrospectively where necessary, which has caused changes from 2023 and onwards.

#### Invasive cases from hospitals

In 2025, a total of 1,718 individual patients were registered in MiBa with invasive *K. pneumoniae* complex isolates. From 2015 to 2021, particularly for cephalosporins decreasing trends in resistance were observed. From 2022 to 2025, resistance levels reverted and showed increases for most of the monitored antibiotics. Of particular interest is the almost continuous increase in resistance levels to piperacillin-tazobactam, which increased from 5.9% in 2015 to 10.0% in 2025 in total, albeit with a small drop from 2024 to 2025. The resistance level to carbapenems remained low (<1%) as did combined resistance to ciprofloxacin, cephalosporins and gentamicin (0.9% in 2025).

Figure 8.6 shows total annual numbers and numbers and percentages of resistance in invasive isolates by region and in total, for 2016 to 2025. The proportions of isolates resistant to key antimicrobials for the decade are presented in Table 8.8. The percentages of multidrug resistant invasive isolates are presented in Table 8.9.

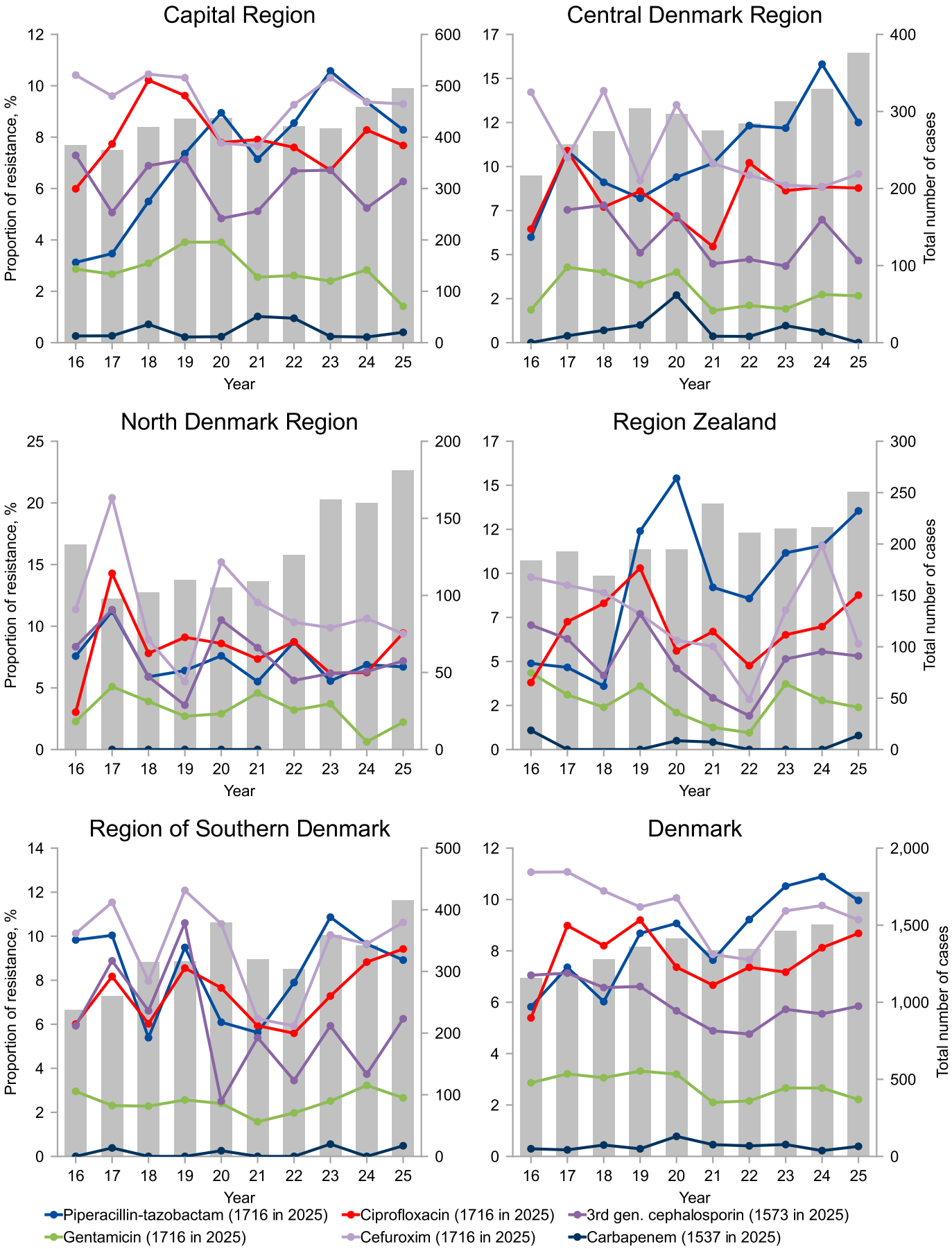
**Table 8.7 *Klebsiella pneumoniae* complex. Resistance (%) in isolates from humans, Denmark, 2025** DANMAP 2025

| Substance | Invasive isolates, hospitals % | Urine isolates, hospitals % | Urine isolates, primary health care % |
|---|---|---|---|
| Mecillinam | 7.1 | 9.6 | 7.7 |
| Piperacillin/tazobactam | 10.0 | 10.6 | 6.9 (2) |
| Amoxicillin/clavulanic acid | 15.1 (4) | 6.8 | 4.8 (4) |
| Sulfonamide | | 24.9 (4) | 10.4 (5) |
| Trimethoprim | | 15.7 | 11.4 |
| Nitrofuratoin | | 11.5 (4) | 24.3 |
| Gentamicin | 2.2 | 2.4 | 0.9 (1) |
| Ciprofloxacin | 8.7 | 8.4 | 5.5 (5) |
| Cefuroxime | 9.2 | 11.2 | 6.0 (2) |
| 3rd generation cephalosporins | 5.8 | 6.0 | 3.9 |
| Carbapenem | 0.4 | 0.3 | 0.0 (2) |
| Max. number of isolates tested for resistance to the presented antibiotics | 1,716 | 7,798 | 13,521 |

Included are results from all DCMs where >75% of the isolates in each antibiotic/sample group were susceptibility tested.
Numbers in parantheses indicate the number of DCMs included if less than six.

**Figure 8.6 Antimicrobial resistance in invasive *Klebsiella pneumoniae* complex isolates from humans (individual cases) by region, Denmark, 2016-2025**

DANMAP 2025




Number in parentheses indicates number tested.

**Table 8.8 Invasive *Klebsiella pneumoniaecomplex* in isolates from humans, resistance (%), Denmark, 2016-2025** DANMAP 2025

| | Resistance (%) in invasive *K. pneumoniae* complex isolates | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Substance | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
| Piperacillin/tazobactam | 5.8 | 7.4 | 6.1 | 8.7 | 9.1 | 7.5 | 9.2 | 10.5 | 10.9 | 10.0 |
| Gentamicin | 2.9 | 3.2 | 3.1 | 3.3 | 3.2 | 2.1 | 2.2 | 2.7 | 2.7 | 2.2 |
| Ciprofloxacin | 5.4 | 9.0 | 8.1 | 9.2 | 7.4 | 6.7 | 7.4 | 7.2 | 8.1 | 8.7 |
| Cefuroxime | 11.1 | 11.1 | 10.3 | 9.7 | 10.1 | 7.9 | 7.7 | 9.6 | 9.8 | 9.2 |
| 3rd gen. cephalosporins | 7.3 | 7.1 | 6.1 | 6.6 | 5.3 | 4.9 | 4.8 | 5.7 | 5.5 | 5.8 |
| Carbapenem | 0.3 | 0.3 | 0.5 | 0.3 | 0.8 | 0.5 | 0.4 | 0.5 | 0.2 | 0.4 |
| Total number of isolates | 1,156 | 1,183 | 1,280 | 1,361 | 1,413 | 1,336 | 1,346 | 1,466 | 1,506 | 1,718 |

**Table 8.9 Invasive *Klebsiella pneumoniae* complex in isolates from humans. Combined resistance to 3rd generation cephalosporins, ciprofloxacin, and gentamicin (multidrug-resistance), Denmark, 2016-2025** DANMAP 2025

| | 2016<br>% (N) | 2017<br>% (N) | 2018<br>% (N) | 2019<br>% (N) | 2020<br>% (N) | 2021<br>% (N) | 2022<br>% (N) | 2023<br>% (N) | 2024<br>% (N) | 2025<br>%(N) |
|---|---|---|---|---|---|---|---|---|---|---|
| Resistance | 1.6 (18) | 2.4 (27) | 1.7 (20) | 2.4 (30) | 1.5 (19) | 1.0 (13) | 1.0 (13) | 1.8 (24) | 1.4 (19) | 0.9 (14) |
| Percentage (no.) of isolates tested for combined resistance (multiresistance) | 98<br>(1,131) | 95<br>(1,122) | 93<br>(1,188) | 94<br>(1,275) | 93<br>(1,308) | 93<br>(1,248) | 94<br>(1,259) | 92<br>(1,344) | 92<br>(1,386) | 91<br>(1,571) |
| Total number of invasive isolates | 1,156 | 1,183 | 1,280 | 1,361 | 1,413 | 1,336 | 1,346 | 1,466 | 1,506 | 1,718 |

**Table 8.10 *Klebsiella pneumoniae* complex from hospital urines, levels of resistance (%), Denmark, 2016-2025** DANMAP 2025

| | Resistance (%) in *K. pneumoniae* urine isolates from hospitals | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Substance | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
| Mecillinam | 8.9 | 15.7 | 16.9 | 13.2 | 11.7 | 10.6 | 9.4 | 10.0 | 9.9 | 9.6 |
| Piperacillin/tazobactam | 5.6 | 6.7 | 8.7 | 8.5 | 8.0 | 8.7 | 9.9 | 10.5 | 10.8 | 10.6 |
| Gentamicin | 3.2 | 3.6 | 3.2 | 3.0 | 2.9 | 2.4 | 2.3 | 2.3 | 3.3 | 2.4 |
| Ciprofloxacin | 6.1 | 7.6 | 8.9 | 7.4 | 7.2 | 7.2 | 7.2 | 7.4 | 8.4 | 8.4 |
| Cefuroxime | 9.1 | 9.4 | 9.5 | 8.6 | 8.5 | 8.4 | 8.1 | 9.3 | 9.3 | 11.2 |
| 3rd gen. cephalosporins | 6.8 | 7.1 | 6.8 | 6.0 | 5.5 | 5.4 | 4.7 | 5.7 | 6.2 | 6.0 |
| Total number of isolates | 7,467 | 8,106 | 8,047 | 7,926 | 7,814 | 7,701 | 7,911 | 7,910 | 7,554 | 7,798 |

**Table 8.11 *Klebsiella pneumoniae* complex from urines from primary health care, levels of resistance (%), Denmark, 2016-2025** DANMAP 2025

| | Resistance (%) in *K. pneumoniae* urine isolates from primary health care | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Substance | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
| Mecillinam | 8.8 | 9.4 | 9 | 16.6 | 15.9 | 11.5 | 9.4 | 8.6 | 7.9 | 7.2 | 7.9 | 7.7 |
| Sulfonamide | 17.1 | 18.7 | 19.3 | 25.5 | 24.6 | 18.9 | 15.5 | 13.8 | 11.9 | 13.1 | 14.1 | 10.4 |
| Ciprofloxacin | 6.5 | 5.2 | 5.6 | 5.4 | 6.4 | 5.5 | 5.2 | 4.9 | 5.1 | 5.2 | 5.3 | 5.5 |
| 3rd gen. cephalosporins | 4.7 | 4.8 | 5.4 | 4.9 | 5.3 | 4.5 | 4.4 | 3.7 | 3.4 | 4.5 | 4.4 | 3.9 |
| Total number of isolates | 4,246 | 6,372 | 7,615 | 8,948 | 9,227 | 9,696 | 9,387 | 10,196 | 11,039 | 12,160 | 12,626 | 13,521 |

**Figure 8.7 *Klebsiella pneumoniae* complex isolates from urines in humans (hospitals): proportion of resistant isolates and annual number of individual cases, Denmark, 2016-2025**

DANMAP 2025

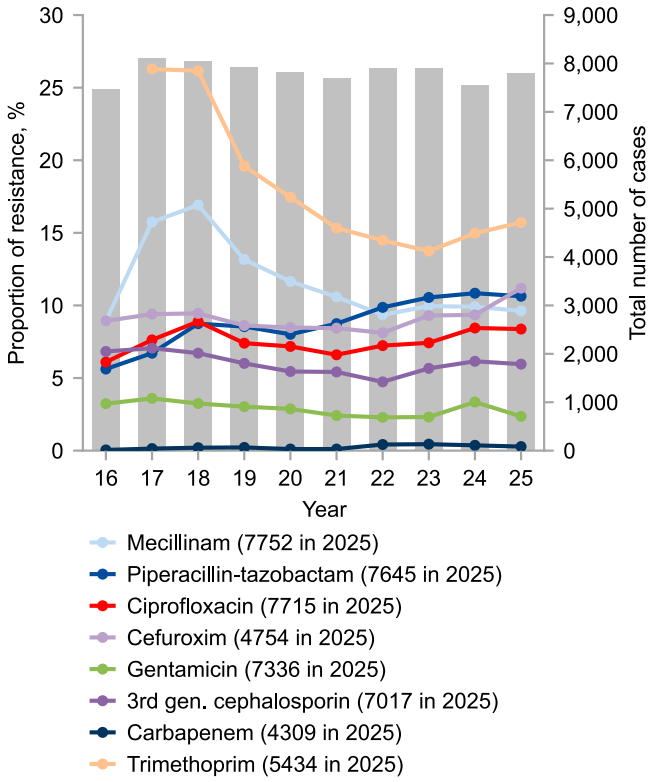
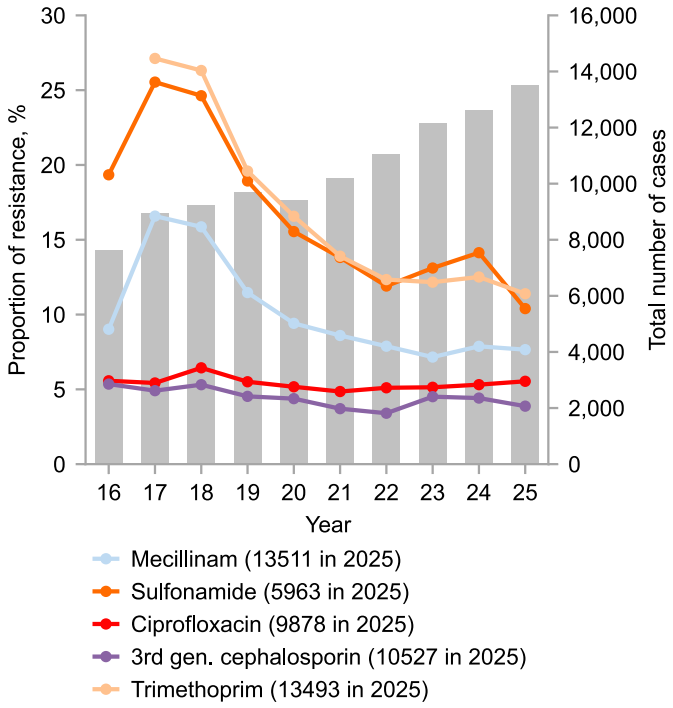



**Figure 8.8 *Klebsiella pneumoniae* complex isolates from urines in humans (primary health care): proportion of resistant isolates and annual number of individual cases, Denmark, 2016-2025**

DANMAP 2025




**Urinary cases from hospitals**

In 2025, *K. pneumoniae* complex from urine samples were isolated from 7,798 individual hospital patients in Denmark. Summarized antibiotic-specific susceptibility results for *K. pneumoniae* complex isolates (invasive and urine specimen) for 2025 are shown in Table 8.7. In Figure 8.7 and Table 8.10, resistance for *K. pneumoniae* complex urine isolates from hospitals is shown for 2016-2025.

**Urinary cases from primary health care**

In 2025, *K. pneumoniae* complex was isolated from urine samples of 13,521 individual patients in primary health care.

As for the results from invasive isolates and isolates from hospital urine samples susceptibility results for all tested antimicrobials are shown in Table 8.7. In Figure 8.8 and Table 8.11, resistance for *K. pneumoniae* complex urine isolates from primary health care is shown for the past decade.

**Conclusion**

The number of invasive cases of *K. pneumoniae* complex have increased by 33% since 2016. As for *E. coli*, a concerning trend is seen with regards to ciprofloxacin, cefuroxime, 3rd generation cephalosporins and piperacillin-tazobactam resistance, which has been trending upwards for the past five to ten years.

### 8.2.3 *Pseudomonas aeruginosa*

*Pseudomonas aeruginosa* is an opportunistic pathogen that can colonise the lung, urinary tract, burn wounds, superficial wounds and cause invasive infections. The pathogen is capable of biofilm formation and has the ability to colonise medical devices (e.g. indwelling catheters and implants) which in many cases causes complicated infections requiring prolonged and combination treatment with two broad spectrum antimicrobials. *P. aeruginosa* infections are more prevalent in certain at-risk groups such as immunocompromised, diabetes and cystic fibrosis patients. *P. aeruginosa* exhibits intrinsic resistance to various antimicrobial agents through chromosomal gene mutations and has the ability to acquire β-lactamases (extended-spectrum β-lactamases (ESBLs) and carbapenemases (especially class B carbapenemases or metallo-β-lactamases [MBLs]) by horizontal transmission.

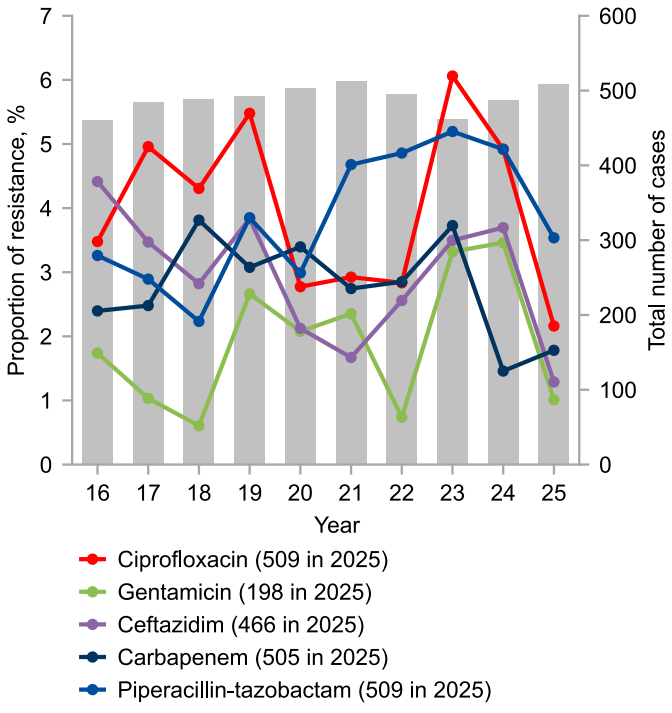
#### Invasive cases from hospital patients

In 2025, a total of 509 individual patients with invasive *P. aeruginosa* isolates were registered in Denmark. Figure 8.9 shows the total annual number of invasive isolates and proportion of resistant isolates between 2016 and 2025.

#### Conclusion

The occurrence of invasive *P. aeruginosa* in Denmark is stable regarding the number of cases reported and resistance levels are low.

**Figure 8.9 Invasive *Pseudomonas aeruginosa* isolates from humans: resistant isolates (%) and annual number of individual cases, Denmark, 2016-2025** DANMAP 2025




### 8.2.4 *Acinetobacter* species

The genus *Acinetobacter* includes several species and is found widespread in nature (soil and water) as well as in animals and humans. In humans, *Acinetobacter* species (spp.) can colonise the skin and wounds but may also cause hospital-acquired infections such as central line-associated bloodstream infections, nosocomial pneumonia, UTIs and wound infections, most often in severely ill patients. Many of the different subspecies are phenotypically alike, and thus identification at species level can be difficult. Species belonging to the *A. baumannii* group are considered as the most clinically important. *Acinetobacter* spp. is intrinsically resistant to a broad range of antimicrobials mediated by a low membrane permeability and constitutive expression of various efflux systems.

#### Invasive cases from hospitals

In 2025, a total of 96 individual patients with invasive *Acinetobacter* species were reported. Data are presented in Table 8.12 and in Figure 8.10.

#### Conclusion

The number of invasive *Acinetobacter* spp. appears to have stabilized at a new level compared to the marked increase from 2020 to 2021; however, the proportion of invasive isolates resistant to key antimicrobials remained low in Denmark.

**Figure 8.10 Invasive *Acinetobacter* spp. isolates from humans: resistant isolates (%) and annual number of individual cases, Denmark, 2016-2025** DANMAP 2025

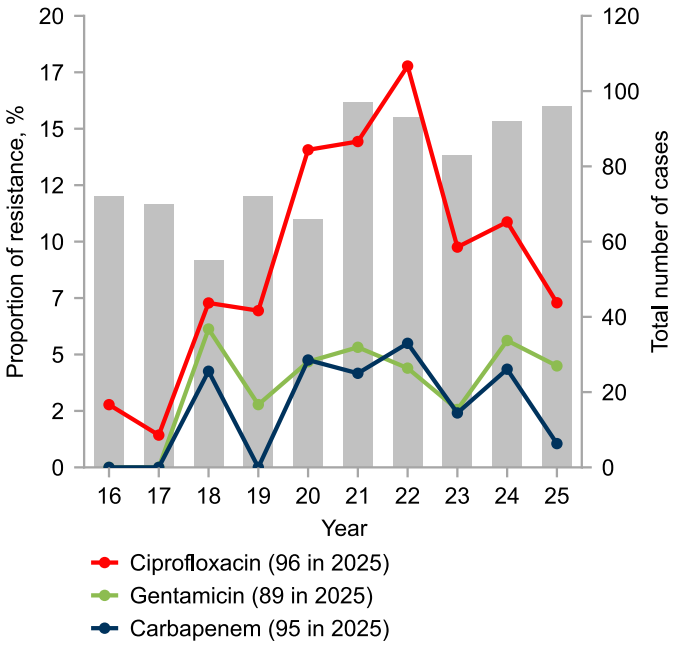


**Table 8.12 *Acinetobacter* spp. tested and resistant invasive isolates, Denmark, 2016-2025** DANMAP 2025

| | 2016 | | 2017 | | 2018 | | 2019 | | 2020 | | 2021 | | 2022 | | 2023 | | 2024 | | 2025 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | res. | n | res. | n | res. | n | res. | n | res. | n | res. | n | res. | n | res. | n | res. | n | res. | n |
| Ciprofloxacin | 2 | 72 | 1 | 70 | 4 | 55 | 5 | 72 | 9 | 64 | 14 | 97 | 16 | 92 | 8 | 89 | 10 | 92 | 7 | 96 |
| Gentamicin | 0 | 70 | 0 | 70 | 3 | 49 | 2 | 72 | 3 | 64 | 5 | 94 | 4 | 92 | 2 | 85 | 5 | 89 | 4 | 89 |
| Carbapenem | 0 | 69 | 0 | 67 | 2 | 47 | 0 | 72 | 3 | 63 | 4 | 96 | 5 | 93 | 2 | 90 | 4 | 92 | 1 | 95 |
| Total number of invasive isolates | 72 | | 70 | | 55 | | 72 | | 66 | | 97 | | 93 | | 90 | | 92 | | 96 | |

res. = number of resistant isolates. n = number of tested isolates.

### 8.2.5 Enterococci

Enterococci are part of the normal intestinal microbiota in humans and animals. More than 54 species belonging to the genus *Enterococcus* have been described. The majority of human infections are caused by *E. faecalis* and *E. faecium* and in rare cases by *E. casseliflavus, E. gallinarum* and *E. raffinosus*. Most common clinical infections include urinary tract infections, intra-abdominal infections, bacteraemia and infective endocarditis. Enterococci are intrinsically resistant to many groups of antimicrobials which gives them a selective advantage in e.g. ospitalized patients under antibiotic treatment, leading to colonization or infection. The source of hospital infection is often associated with invasive medical devices and abdominal catastrophes.

#### Invasive cases from hospitals

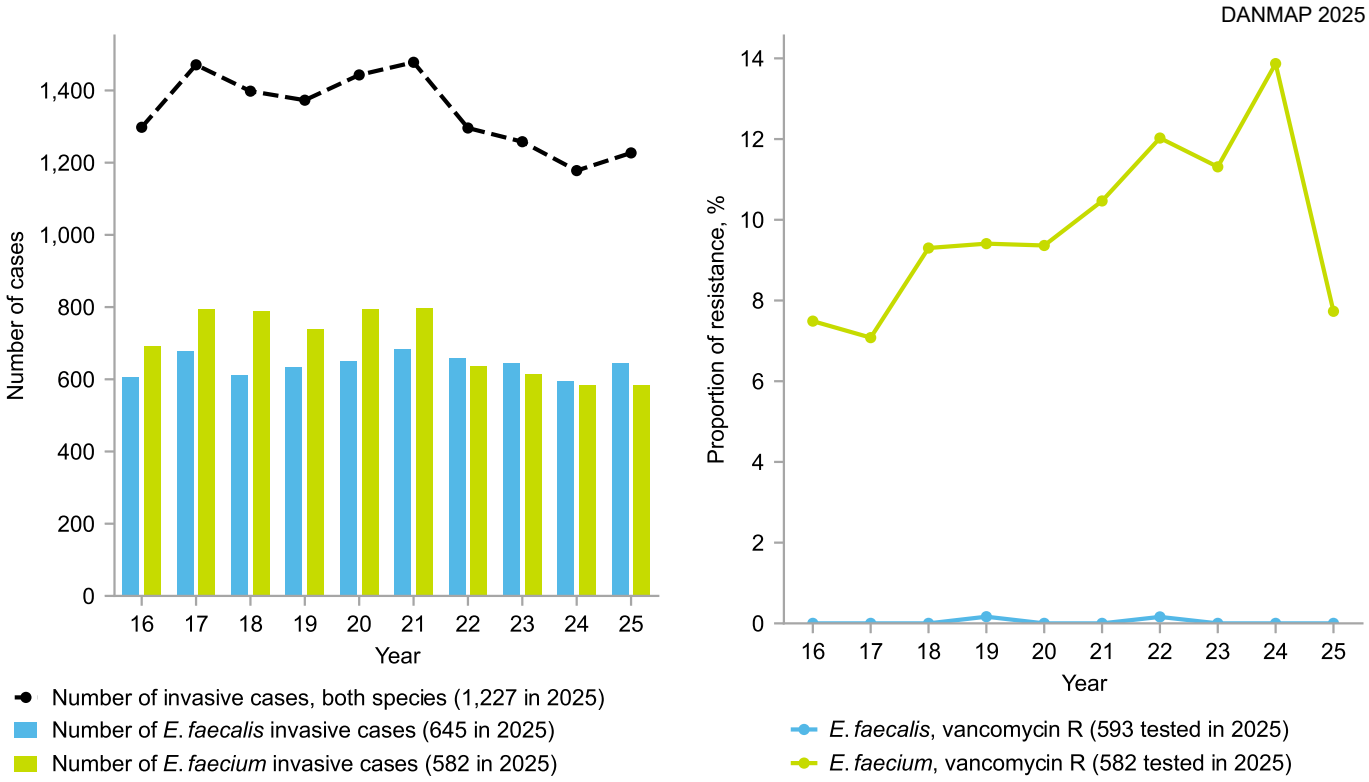
In 2025, a total of 645 and 582 individual patients were registered in Denmark with invasive *E. faecalis* and *E. faecium* isolates, respectively. Table 8.13 shows resistance percentages towards the most important antibiotics for both species for 2025 and Figure 8.11 shows the annual numbers of invasive isolates and resistance to vancomycin.

**Table 8.13 Enterococci. Resistance (%) in invasive isolates from humans, Denmark, 2025** DANMAP 2025

| | *E. faecalis* | *E. faecium* | Number of included isolates (number of DCM) | |
|---|---|---|---|---|
| | % | % | *E. faecalis* | *E. faecium* |
| Ampicillin | 0.0 | 88 | 644 (10) | 561 (9) |
| Vancomycin | 0.0 | 7,7 | 593 (9) | 582 (10) |
| Linezolid | 0,8 | 0,6 | 506 (7) | 462 (7) |
| Teicoplanin | 0.0 | 0,6 | 217 (2) | 172 (2) |
| Tigecycline | 2,8 | 0.0 | 106 (1) | 97 (1) |

All levels of resistance are presented for each antibiotic as a mean of the resistance rates reported by the DCMs. Included are all DCMs that report routine testing (>75% of the isolates). The number in parentheses tells the number of included DCMs.

**Figure 8.11 Invasive *Enterococci faecalis/faecium* isolates from humans:**
**a) annual number of isolates from individual cases and b) proportion of vancomycin resistant isolates, Denmark, 2016-2025**




**Conclusion**

The number of invasive cases for both *E. faecium* and *E. faecalis* has been decreasing since 2021, for *E. faecalis* following peaks during 2017 to 2021. Resistance to vancomycin has only rarely been observed in *E. faecalis* and no invasive cases with vancomycin resistance were detected in 2025. For *E. faecium,* it had been increasing for the last decade, but saw a marked drop from 2024 to 2025.

*Mikkel Lindegaard and Ute Wolff Sönksen*
*For further information: Mikkel Lindegaard, ldd@ssi.dk*

## 8.3 Results from the reference laboratories

### 8.3.1 Characterization of ESBL- and pAmpC-producing *Escherichia coli* from bloodstream infections

**Background**

Resistance to third-generation cephalosporins in *Escherichia coli* is commonly caused by the production of extended-spectrum beta-lactamases (ESBLs), carbapenemases or plasmid-mediated AmpC (pAmpC). It may also arise from mutations in the promoter/attenuator region of chromosomal AmpC (cAmpC), leading to overexpression or hyperproduction.

Since 2014, the Danish Departments of Clinical Microbiology (DCMs) have voluntarily submitted third-generation cephalosporin-resistant *E. coli* (3GC-R *Ec*) from bloodstream infections for further characterization at the National Reference Laboratory for Antimicrobial Resistance at Statens Serum Institut (SSI). Isolates were submitted according to the EUCAST criteria for reduced susceptibility towards cefpodoxime, ceftriaxone, cefotaxime or ceftazidime.

At SSI, the 3GC-R *Ec*'s collected in Denmark through 2025, were phenotypically tested for ESBL-production. ESBL- and/ or pAmpC-positive isolates from January, March, May, July, September, and November were selected for whole-genome sequencing and characterized according to Multilocus Sequence Types (MLSTs) and the encoding ESBL-, pAmpC- and carbapenemase genes.

**Results**

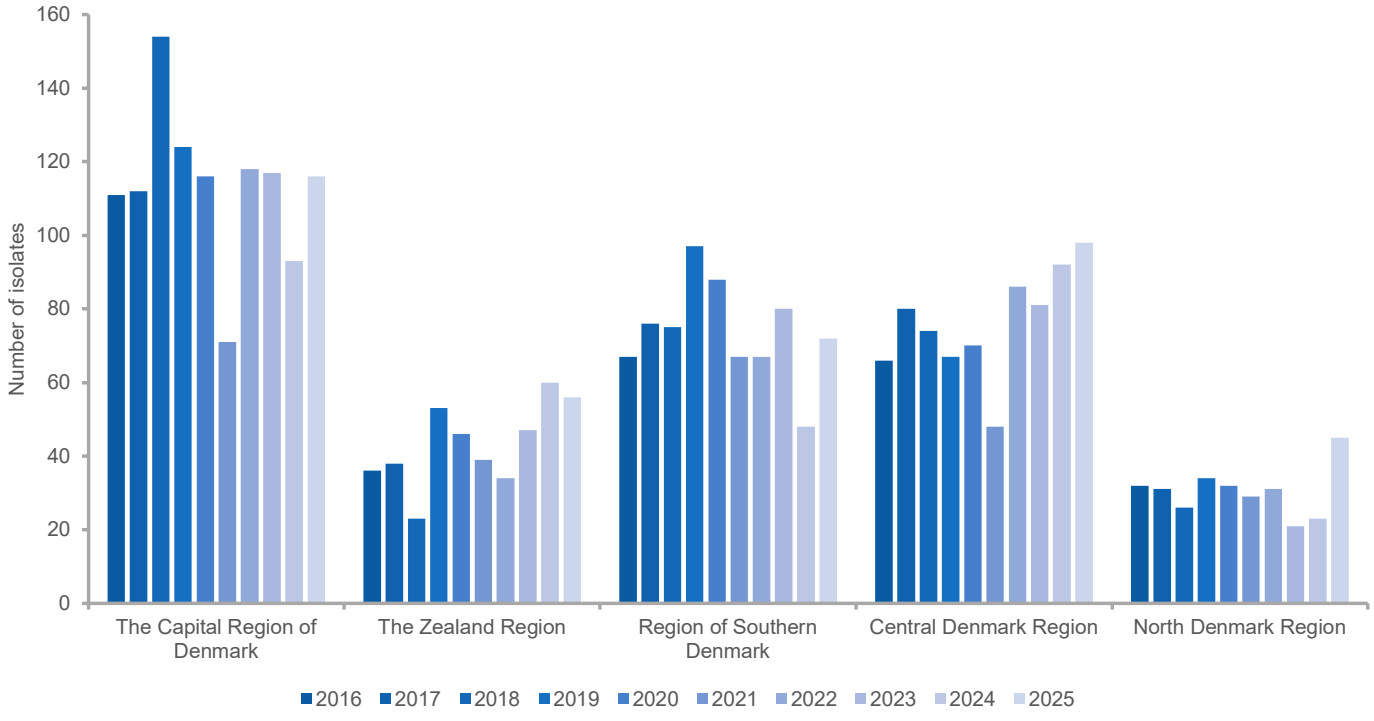
In 2025, a total of 387 *E. coli* blood isolates from unique patients, were identified by phenotypic testing as ESBL-, AmpC- and/or carbapenemase positive. This corresponds to a 22.5% relative increase compared to 2024, where 316 isolates were reported. Demographic data was available for all 387 *E. coli* isolates. The median age at diagnosis was 69 years, with an age range from below 1 year to 99 years. The proportion of 3GC-R *Ec* from male patients remained unchanged at 48% (187/387), compared to 2024.

The regional distribution of the 387 isolates with ESBL-, AmpC- or carbapenemase phenotype was compared to data from previous years (Figure 8.12 and Table 8.14). From 2024 to 2025, a tendency towards an increased proportion of observations from the North Denmark Region was observed, however this change did not reach statistical significance. Overall, no significant difference in the regional distribution was observed between 2024 and 2025.

Whole genome sequencing data were obtained from 192 *E. coli* isolates, as only isolates from every second month were subjected to sequencing.

Among the 192 sequenced isolates, 16 different genes associated with ESBL-, pAmpC- and carbapenemase enzymes were detected (Table 8.15). CTX-M-15 remained the frequently detected enzyme in 2025, and increased significantly in occurrence, from 40% in 2024 to 59% in 2025. Four carbapenemase producing isolates were identified among the sequenced bloodstream infection isolates from the included months (two OXA-244 producers, and two OXA-48 producers).

**Figure 8.12 ESBL/pAmpC producing *E. coli* from bloodstream infections by region, Denmark, 2016-2025** DANMAP 2025



The 192 whole-genome sequenced *E. coli* isolates belonged to 36 different sequences types (ST). ST131 remained the most common ST, accounting for 42% of the isolates, followed by ST69 and ST1193, each accounting for 9%. A notable observation in 2025 was the first detection of ST10320 in the Danish surveillance, comprising six isolates (3%). Apart from this finding, no further significant changes in the distribution of MLSTs were observed compared to 2024 (Table 8.16).

Among the 84 *E. coli* isolates belonging to ST131, CTX-M-15 (62%) was the most common enzyme, followed by CTX-M-27 (35%). In contrast, all six ST10320 isolates encoded the gene for CTX-M-15 as the only ESBL-related enzyme (100%).

**Table 8.14. Distribution of ESBL, pAmpC and Carbapenemase producing *E. coli* from bloodstream infections, Denmark, 2016-2025**

DANMAP 2025

| | DANMAP 2016 | DANMAP 2017 | DANMAP 2018 | DANMAP 2019 | DANMAP 2020 | DANMAP 2021 | DANMAP 2022 | DANMAP 2023 | DANMAP 2024 | DANMAP 2025 |
|---|---|---|---|---|---|---|---|---|---|---|
| Region | Numbers | Numbers | Numbers | Numbers | Numbers | Numbers | Numbers | Numbers | Numbers | Numbers |
| The Capital Region of Denmark | 111 | 112 | 154 | 124 | 116 | 71 | 118 | 117 | 93 | 116 |
| The Zealand Region | 36 | 38 | 23 | 53 | 46 | 39 | 34 | 47 | 60 | 56 |
| Region of Southern Denmark | 67 | 76 | 75 | 97 | 88 | 67 | 67 | 80 | 48 | 72 |
| Central Denmark Region | 66 | 80 | 74 | 67 | 70 | 48 | 86 | 81 | 92 | 98 |
| North Denmark Region | 32 | 31 | 26 | 34 | 32 | 29 | 31 | 21 | 23 | 45 |
| Total Numbers | 312 | 337 | 352 | 375 | 352 | 254 | 336 | 346 | 316 | 387 |

**Table 8.15 Most common ESBL enzymes and carbapenemases detected in *E. coli* from bloodstream infections, Denmark, 2021-2025**

DANMAP 2025

| | DANMAP 2021 | | DANMAP 2022 | | DANMAP 2023 | | DANMAP 2024 | | DANMAP 2025 | |
|---|---|---|---|---|---|---|---|---|---|---|
| Enzyme | Number* | % | Number* | % | Number* | % | Number* | % | Number* | % |
| CTX-M-1 | 6 | 4% | 1 | <1% | 3 | 2% | 0 | 0% | 5 | 3% |
| CTX-M-14 | 12 | 9% | 17 | 9% | 17 | 9% | 3 | 2% | 1 | <1% |
| CTX-M-14b | 0 | 0% | 3 | 2% | 2 | 1% | 10 | 7% | 4 | 2% |
| CTX-M-15 | 63 | 46% | 94 | 52% | 103 | 58% | 60 | 40% | 114 | 59% |
| CTX-M-27 | 29 | 21% | 34 | 19% | 32 | 18% | 40 | 27% | 41 | 21% |
| CTX-M-3 | 3 | 2% | 1 | <1% | 0 | 0% | 3 | 2% | 3 | 2% |
| CTX-M-55 | 5 | 4% | 3 | 2% | 1 | <1% | 4 | 3% | 3 | 2% |
| CMY-2 | 2 | 1% | 2 | 1% | 3 | 2% | 1 | <1% | 2 | 1% |
| CMY-4 | 1 | <1% | 1 | <1% | 1 | <1% | 4 | 3% | 2 | 1% |
| DHA-1 | 3 | 2% | 11 | 6% | 9 | 5% | 14 | 9% | 17 | 9% |
| SHV-12 | 3 | 2% | 3 | 2% | 3 | 2% | 3 | 2% | 2 | 1% |
| Other pAmpC variants | 0 | 0% | 0 | 0% | 0 | 0% | 1 | <1% | 0 | 0% |
| Other ESBL enzymes | 6 | 4% | 7 | 4% | 3 | 2% | 3 | 2% | 3 | 2% |
| Carbapenemase enzymes | 4 | 3% | 5 | 3% | 1 | <1% | 8 | 5% | 4 | 2% |

In some isolates more than one enzyme was detected.
* Numbers based on sequenced data from odd months.

**Table 8.16 Distribution of MLSTs in *E. coli* from bloodstream infections, Denmark, 2021-2025**

DANMAP 2025

| | DANMAP 2021 | | DANMAP 2022 | | DANMAP 2023 | | DANMAP 2024 | | DANMAP 2025 | |
|---|---|---|---|---|---|---|---|---|---|---|
| MLST | Number* | % | Number* | % | Number* | % | Number* | % | Number* | % |
| ST131 | 64 | 49% | 89 | 50% | 68 | 38% | 66 | 47% | 84 | 42% |
| ST69 | 7 | 5% | 9 | 5% | 27 | 15% | 19 | 13% | 17 | 9% |
| ST12 | 5 | 4% | 4 | 2% | 8 | 4% | 2 | 1% | 5 | 3% |
| ST38 | 1 | 1% | 11 | 6% | 7 | 4% | 13 | 9% | 13 | 7% |
| ST1193 | 9 | 7% | 5 | 3% | 7 | 4% | 6 | 4% | 18 | 9% |
| ST95 | 3 | 2% | 2 | 1% | 5 | 3% | 6 | 4% | 3 | 2% |
| ST73 | 1 | 1% | 5 | 3% | 5 | 3% | 4 | 3% | 10 | 5% |
| ST10320 | 0 | 0% | 0 | 0% | 0 | 0% | 0 | 0% | 6 | 3% |
| Other STs[1] | 40 | 31% | 53 | 30% | 47 | 26% | 25 | 18% | 36 | 18% |

[1] Found in less than 2% in 2025.
* Numbers based on sequenced data from odd months.

**Conclusion**
In 2025, the number of *E. coli* blood isolates with an ESBL-, AmpC- and/or carbapenemase phenotype increased compared to 2024, with 387 isolates reported from unique patients. The demographic distribution remained largely unchanged, including a stable proportion of isolates from male patients. No significant changes were observed in the regional distribution compared to 2024, although a non-significant tendency towards an increased proportion of observations from the North Denmark Region was noted.

Among the whole genome sequenced isolates, CTX-M-15 remained the most prevalent ESBL enzyme and increased significantly in relative occurrence compared to 2024. ST131 continued to be the dominant sequence type, followed by ST69 and ST1193. A notable finding in 2025 was the first observation of ST10320 in the Danish surveillance, comprising six isolates, all carrying CTX-M-15. Apart from this, no further significant changes in the MLST distribution were observed compared to the previous year.

Four carbapenemase-producing *E. coli* isolates were detected among the sequenced bloodstream infection isolates in 2025, consisting of two OXA-244 producers and two OXA-48 producers.

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### 8.3.2 Carbapenemase-producing organisms (CPO)

**Background**
Carbapenems comprise one of the only classes of antimicrobial agents that can be used for treatment of infections caused by multidrug-resistant Gram-negative bacteria like *Klebsiella pneumoniae, Escherichia coli, Pseudomonas aeruginosa* and *Acinetobacter baumannii*. Treatment options for infections with carbapenem-resistant bacteria are often none or suboptimal. Resistance can be expressed by the presence of various carbapenemases of which the five most frequently occurring are *K. pneumoniae* carbapenemase (KPC), Oxacillinase (OXA), Verona integrin encoded metallo-β-lactamase (VIM), New Delhi metallo-β-lactamase (NDM) and Imipenemase (IMP).

Carbapenemase-producing organisms (CPO) comprise two main groups: 1) Intestinal bacteria: Carbapenemase-producing *Enterobacterales* (CPE), e.g., *E. coli* and *K. pneumoniae*, and 2) environmental bacteria: *Pseudomonas* spp. and *Acinetobacter* spp. The term CPE is used to designate intestinal bacteria. Thus, CPE are a subset of CPO.

CPO have been notifiable in Denmark since the guideline from 5th September 2018 [https://www.retsinformation.dk/eli/lta/2018/1091]. Before this date, Danish departments of clinical microbiology (DCMs) have submitted carbapenem-resistant isolates for verification and genotyping at the National Reference Laboratory for Antimicrobial Resistance at Statens Serum Institut on a voluntary basis. This section describes findings for carbapenemase-producing Enterobacterales (CPE), *Pseudomonas* spp. and *Acinetobacter* spp.

During 2025, 760 CPOs were identified from 591 patients compared with 677 CPO isolates from 527 patients in 2024 (Figure 8.13, Table 8.17). More than one isolate from the same patient was included if the isolates belonged to different bacterial species and/or if the isolates harbored different carbapenemases. In 2025, 116 patients had more than one CPO isolate, ranging from two-seven isolates.

Collection of travel information is part of the CPO surveillance in Denmark. Thus, information of travelling abroad in the period of 6 months prior to testing positive for CPO is requested and reported to SSI, together with the clinical sample information.

**Carbapenemase-producing *Enterobacterales***
In 2025, 714 CPE isolates were reported from 565 patients compared with 616 CPE from 497 patients in 2024 (Figure 8.13, Table 8.17). In 2025, 36 of the 714 CPE isolates produced both NDM and OXA-48 group enzymes, 464 produced OXA-48-like enzymes alone and 173 were only NDM-producing. Furthermore, 34 KPC-, five VIM- as well as two KPC/NDM group, CPE isolate(s) were identified. The distribution of the five most common species is shown in Figure 8.14b. From 2020 to 2025, the species distribution has been stable. In 2025, 256 *E. coli*, 133 *K. pneumoniae* complex, 164 *C. freundii* complex, 34 *Enterobacter cloacae* complex, 65 *K. oxytoca* complex were detected.

**Figure 8.13 Number of CPO/CPE isolates and cases in Denmark from 2016-2025** DANMAP 2025

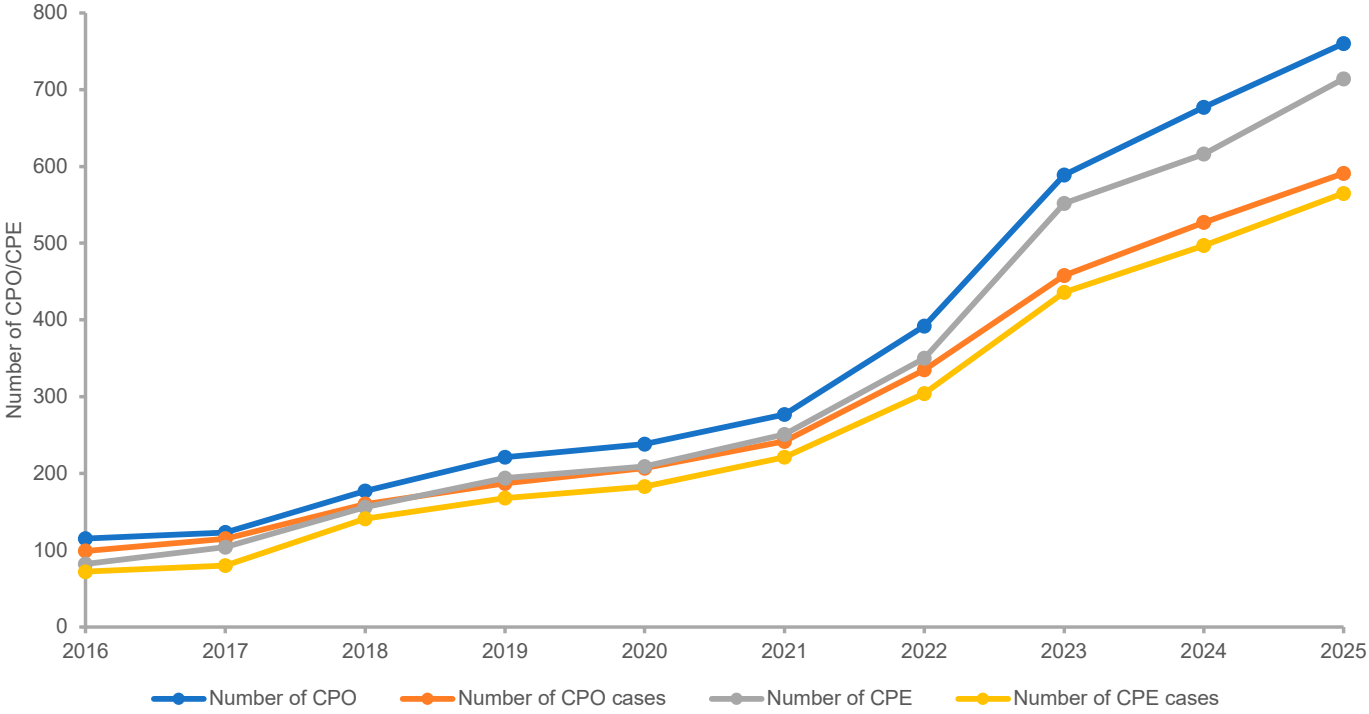
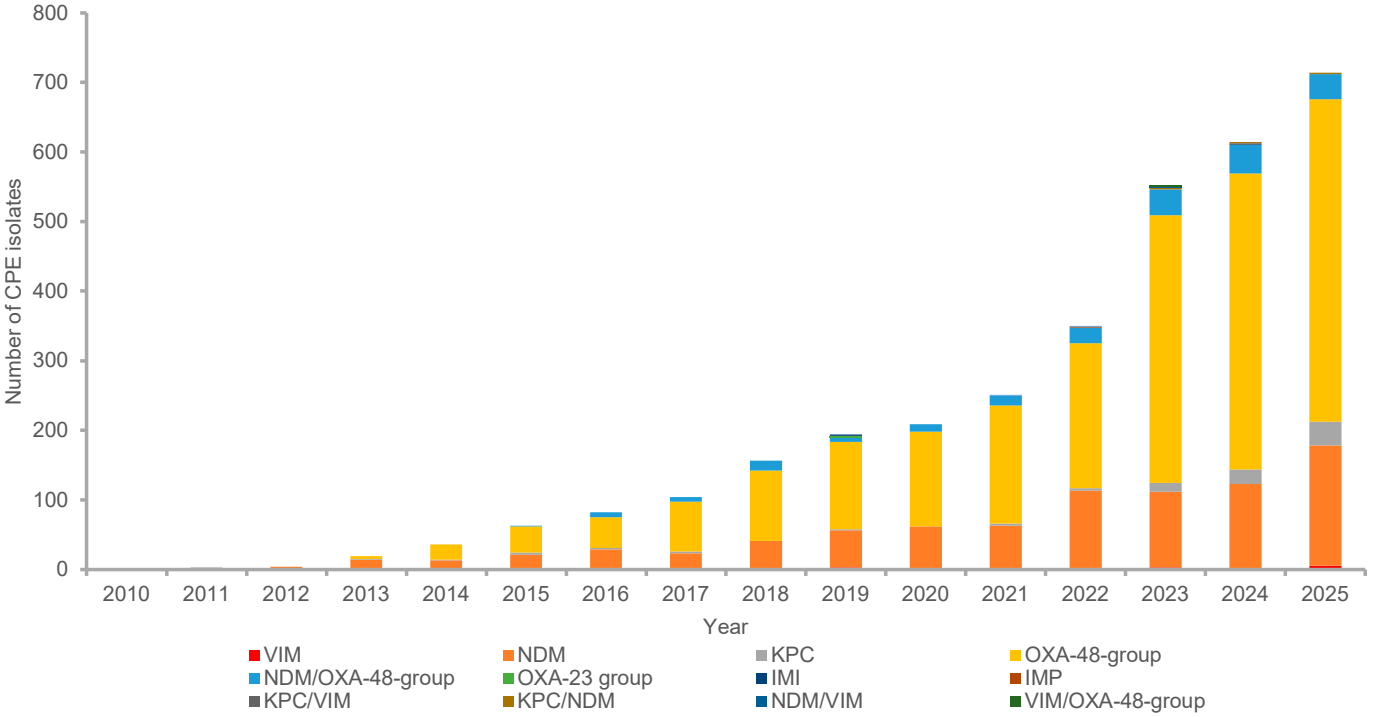



**Table 8.17 Number of CPO/CPE isolates and cases in Denmark from 2016-2025** DANMAP 2025

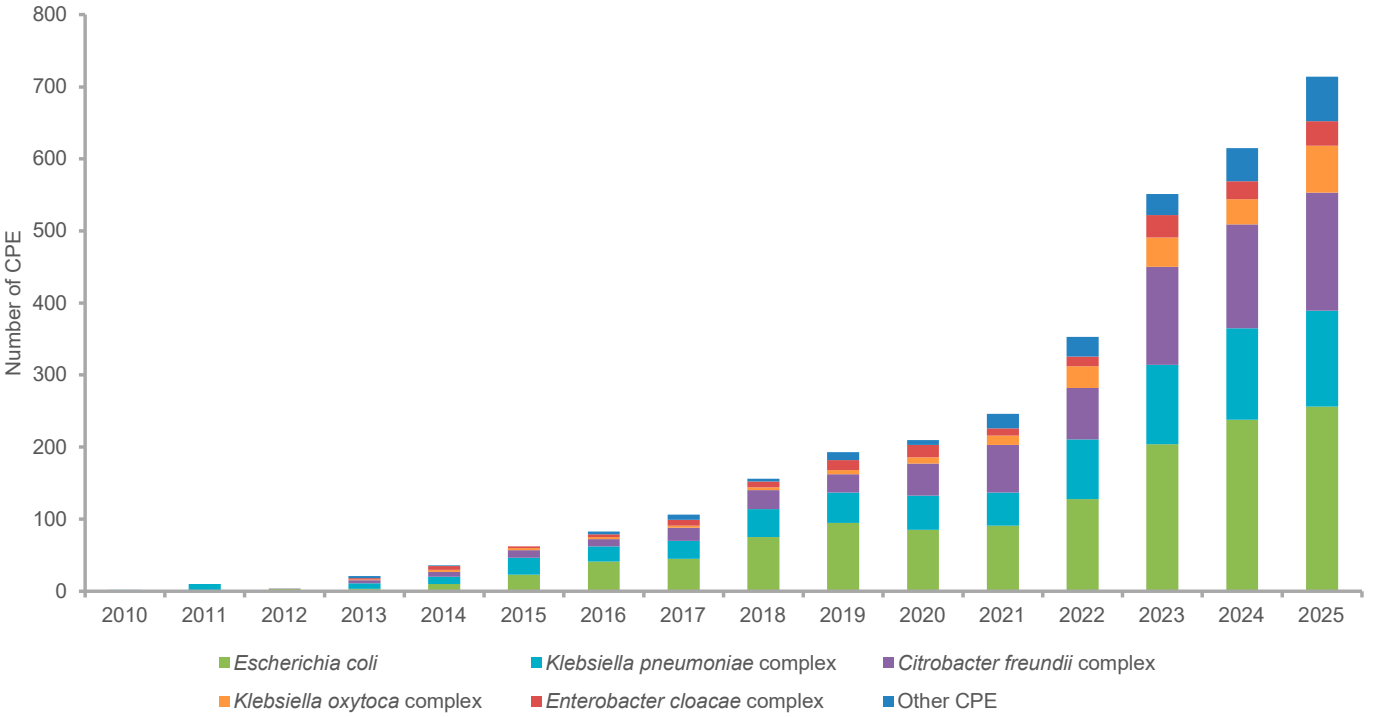
| | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|
| Number of CPO isolates | 115 | 123 | 177 | 221 | 238 | 277 | 392 | 589 | 677 | 760 |
| Number of CPO cases | 99 | 115 | 160 | 187 | 207 | 242 | 335 | 458 | 527 | 591 |
| Number of CPE isolates | 82 | 104 | 156 | 194 | 209 | 251 | 350 | 552 | 616 | 714 |
| Number of CPE cases | 72 | 80 | 141 | 168 | 183 | 221 | 304 | 436 | 497 | 565 |

**Figure 8.14a Genes identified in CPE** DANMAP 2025



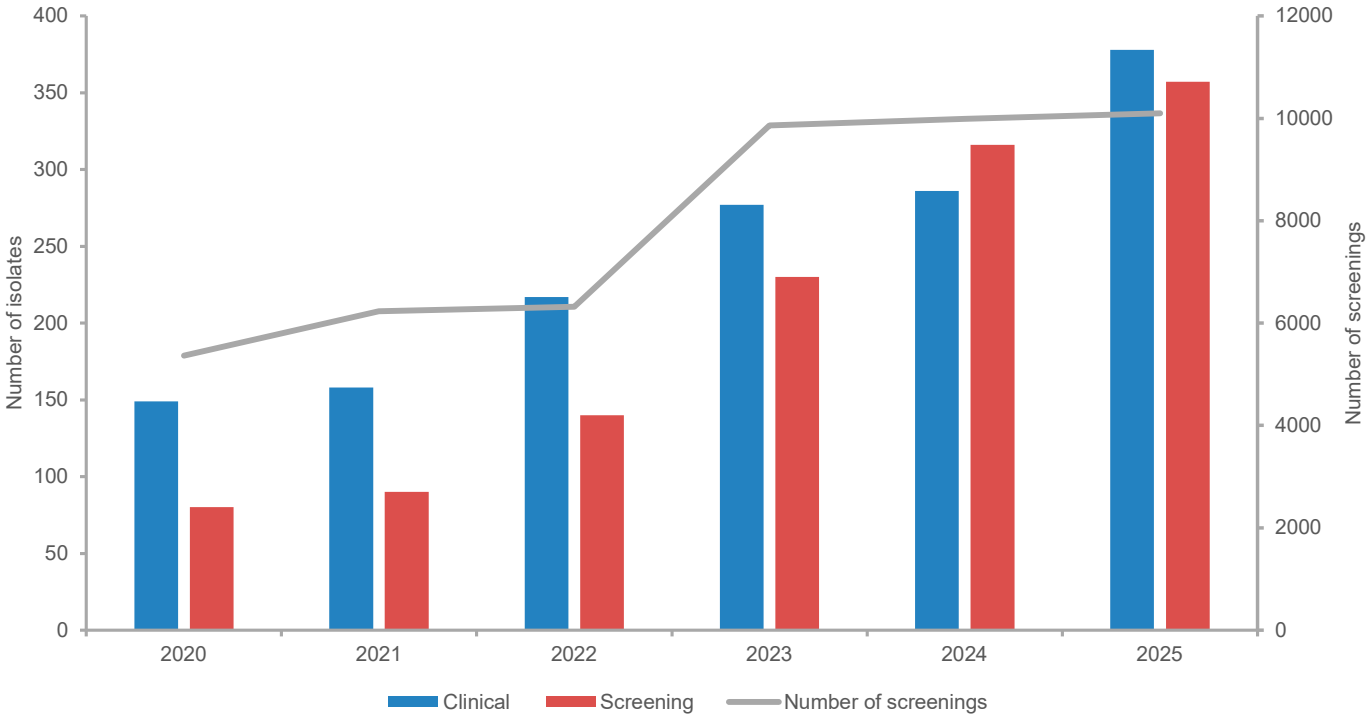

Isolates from the same patient were included if they belonged to different species or carried different carbapenemases.

**Figure 8.14b Species identified as CPE** DANMAP 2025




Isolates from the same patient were included if they belonged to different species or carried different carbapenemases.

**Figure 8.15 Number of patients with CPE-positive samples in the Danish Microbiology Database, 2020-2025. Numbers of patients with CPE-positive clinical (blue columns) and screening (red columns) samples, 2020-2025. Patients are included in both categories if they had both a positive screening and clinical sample in the same year. The grey line (secondary y-axis) represents the total number of screenings** DANMAP 2025



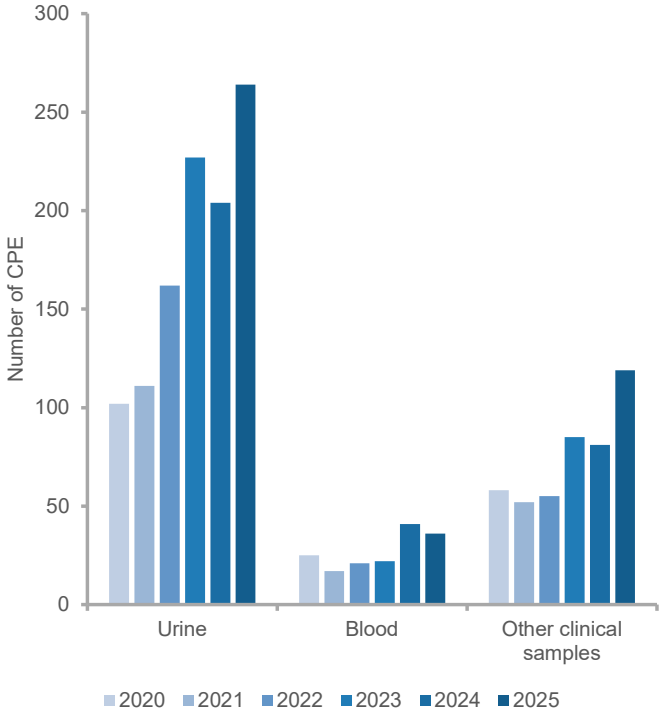

In this DANMAP report CPE-surveillance was supplemented with data from MiBa, which includes all microbiology reports from all ten Danish Departments of Clinical Microbiology. Data was extracted from MiBa for 2020-2025.

An increase in both CPE-positive screening and clinical samples was seen during the 6-years' period (Figure 8.15). During 2023-2025 the number of patients with CPE-positive screening samples increased, even though the screening activity, shown as total number of screenings taken, was stable.

Figure 8.16 shows CPE from clinical samples between 2020 and 2025 obtained from data from MiBa.

In all years, urine was the specimen, where CPE was most frequently found. In 2025, 264 patients were diagnosed with CPE in the urine. During 2020-2025, 17 to 41 patients per year were diagnosed with CPE-bacteremia, with the highest number in 2024, but no clear trend. In 2025, 36 patients were diagnosed with CPE-bacteremia.

**Figure 8.16 Numbers of patients with CPE-positive clinical samples, 2020-2025, stratified by specimen type. Patients can be included in >1 category and in >1 year** DANMAP 2025



**Carbapenemase-producing *Acinetobacter* spp.**
In 2025, 35 carbapenemase-producing *Acinetobacter* spp. isolates were reported from 35 patients, compared with 40 isolates from 39 patients in 2024. Twenty-two patients had been travelling abroad or had relation to Ukraine prior to identification of the carbapenemase-producing *Acinetobacter* spp. Denmark was reported for four of the patients and no information was reported for nine of the patients.

In 2025, 26 carbapenemase-producing *A. baumannii* with the following enzymes were identified: OXA-23 (13), OXA-72 (8), OXA-72/NDM (1), OXA-23/OXA-72 (1) and NDM group/OXA-23 (3). Furthermore, three NDM-1/OXA-97 producing *Acinetobacter johnsonii* and, six OXA-164 *Acinetobacter bereziniae* were identified. (Figure 8.17).

**Carbapenemase-producing *Pseudomonas* spp.**
In 2025, 11 carbapenemase-producing *Pseudomonas aeruginosa* isolates from 11 patients were reported compared to 20 isolates from 20 patients in 2024. Of these 11 patients, eight patients had been travelling abroad or had relation to Ukraine. No information was given for three patients prior to identification of the carbapenemase-producing *P. aeruginosa*. In 2025, 11 carbapenemase-producing *P. aeruginosa* with the following enzymes were identified: NDM (5), VIM (3) and IMP (3) (Figure 8.18).

**CPO-Place of origin 2019-2025**
The Departments of Clinical Microbiology or a clinical physician should report travel in the period of six months before a colonization with CPO is detected, and the CPO-patient will be classified as a travel-associated CPO-patient. In order to qualify the information regarding the origin of a colonization with CPO in a Danish patient, the reported CPO-data from 2019 to 2025 has been evaluated and categorized into four categories: 1) Denmark, 2) Danish outbreak, 3) travel outside the Nordic countries, and 4) unknown (Figure 8.19).

The Departments of Clinical Microbiology or a clinical physician can also report a CPO-patient to be colonized in Denmark implicating that the patient has not been travelling prior to colonization. A CPO-patient can be affected by a Danish nosocomial outbreak and will be classified as an outbreak-patient. For some patients, no information is reported and the classification for place of origin will be unknown. The presumed index patient (the first patient identified) in an outbreak will be registered according to possible travel information.

In 2025, the reported travel data show that 101 out of 591 CPO-positive cases reported travelling outside the Nordic countries. These cases were not part of a nosocomial outbreak. The number of cases in which no travel information was provided is high (28%). In total, there was no travel information for 165 cases, suggesting that the actual travel rate is higher. Denmark was reported as the origin of the CPO-infection or colonization in 41 of the cases.

The most frequent reported travel destinations in 2025 were Asia (29 cases), Southeastern Europe (18), Europe (15) and Middle East (9). The most single reported travel destinations were Turkey (14), Egypt (14), Thailand (9) and Pakistan (5).

**Figure 8.17 Carbapenemase-producing *Acinetobacter* spp. and enzymes identified, Denmark, 2008-2025** DANMAP 2025

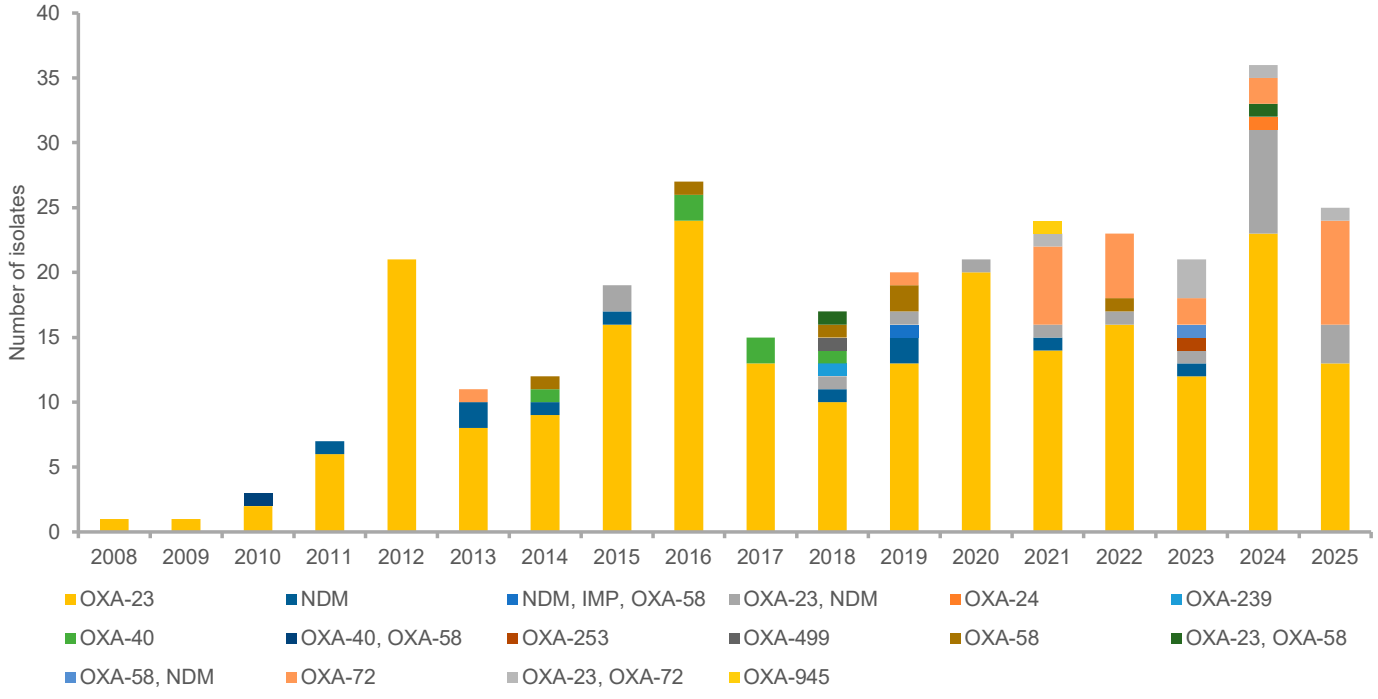


**Figure 8.18 Carbapenemase-producing *Pseudomonas* spp. and enzymes identified, Denmark, 2010-2025** DANMAP 2025

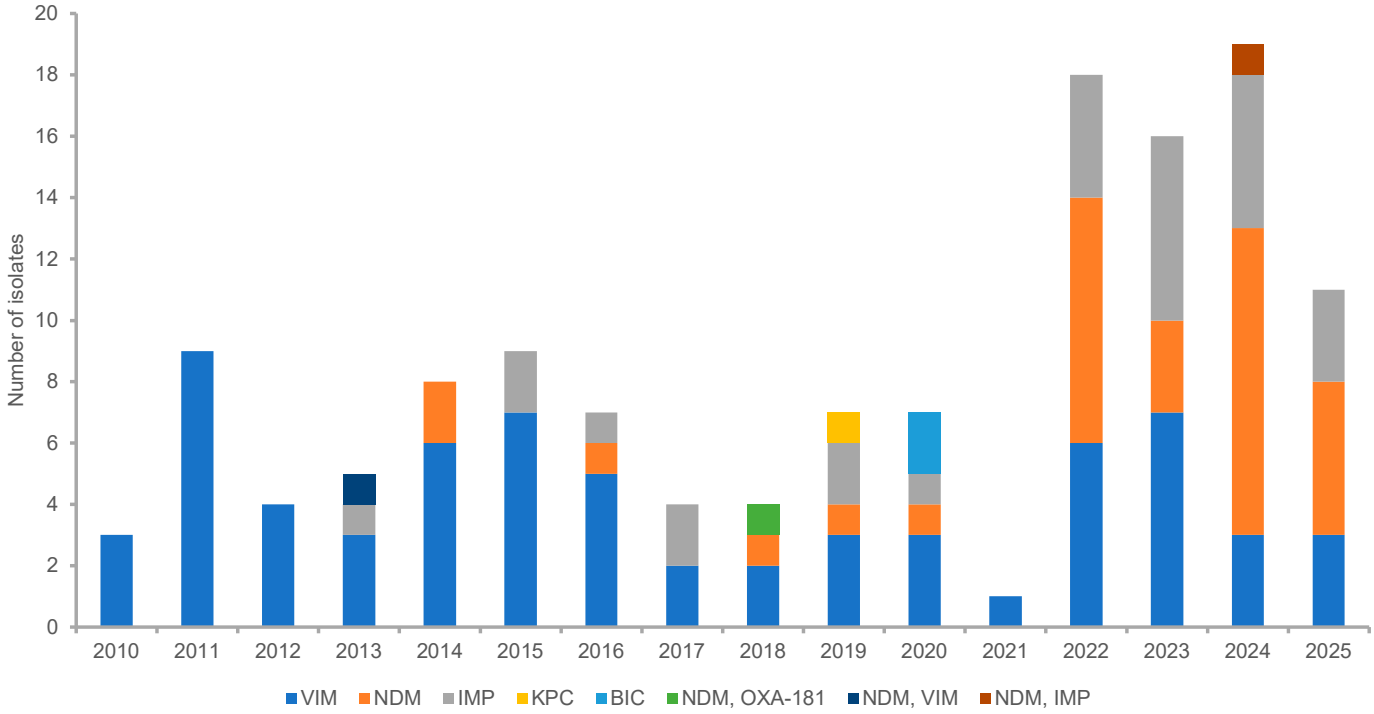
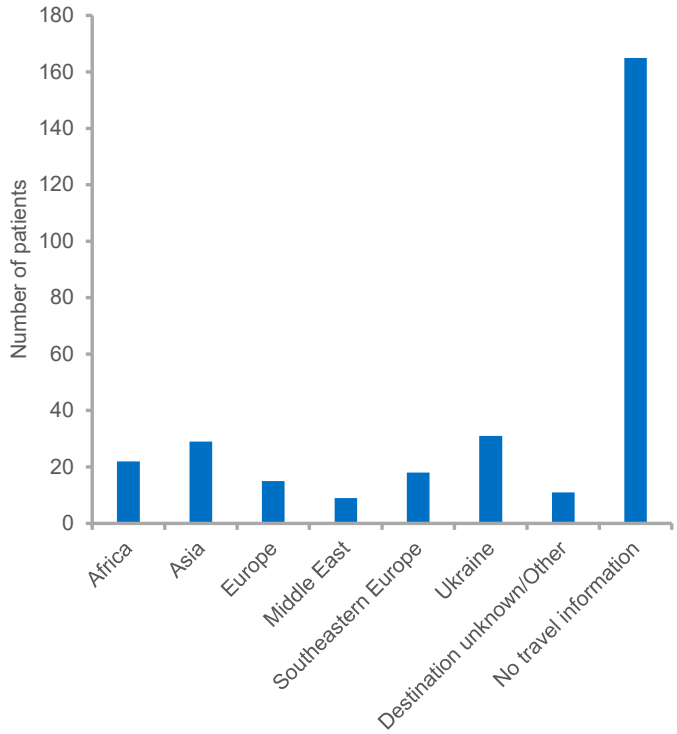



**Figure 8.19 Place of origin of CPO, 2019-2025** DANMAP 2025




Due to the still ongoing war in Ukraine, a number of patients from Ukraine are still receiving care in the Danish health care system. According to the Danish Health Authority, Denmark has received a total of 27 patients from Ukraine as part of medical evacuations in 2025. Some patients who were evacuated in previous years are still receiving medical treatment in Denmark. These patients are investigated for CPO according to the guideline. In 2025, a total of 60 CPO isolates were collected from 29 patients from Ukraine. More than one isolate was included from individual patients, if the isolates belonged to different bacterial species and/or had different carbapenemases. Among the 60 CPO, 45 were CPE isolates (of these were 36 *K. pneumoniae*), six were *Pseudomonas* ssp. and nine were *Acinetobacter* ssp. The findings show that the patients originating from Ukraine were colonized and/or infected by many CPO per patient [Stolberg, *et al.*, J Glob Antimicrob Resist. 2023 Sep:34:15-17].

**Outbreaks with CPO during 2025**

In Denmark, outbreaks caused by CPO in healthcare settings are registered at SSI in the national database (KURS). The database also includes CPO-outbreaks identified in community settings, e.g., nursing homes and travel related outbreaks. At SSI, CPO isolates are routinely characterized by whole genome sequencing (WGS). Cluster analysis is conducted on all isolates using cgMLST to detect possible clustering between the CPO isolates. A genomic cluster is defined as at least two isolates (from different patients) belonging to the same cgMLST cluster (or having less than 15 alleles difference between the isolates). Due to the risk of long-term colonization of the patients, cluster analysis is carried out regardless of the time of isolation. When epidemiological investigations can establish a link (e.g., the patients had been at the same hospital ward at the same time) between at least two patients in a genomic cluster, the patients are classified as belonging to a "verified outbreak". When no epidemiological link can be established, the patients related to the genomic cluster are classified as part of a possible outbreak (Materials and methods, section 9.12).

In 2025, a total of 34 CPO-outbreaks were registered compared to 33 CPO-outbreaks in 2024 (Table 8.18). In 17 of the outbreaks, an epidemiological link could be established between the main part of the patients, thereby indicating that the outbreaks were connected to healthcare settings. In health care settings the verified outbreaks were found to be caused by patients sharing the same ward or staying at the same hospital at the same time. In all, 18 of the 33 outbreaks have been ongoing for more than two years and three outbreaks for more than ten years, meaning that new patients have been identified as belonging to the same cgMLST cluster as found in the previous years.

In total, 176 new patients were associated with CPO-outbreaks in Denmark in 2025. Of these, six patients were part of more than one outbreak. This is a small increase compared to 2024 where 166 new patients were affected. Of the 34 outbreaks registered in 2025, six new small clusters were identified involving 2 – 5 patients each.

In Denmark, hospital outbreaks caused by the *Citrobacter freundii* complex are the most frequently reported CPO outbreaks and account for the majority of outbreak-associated cases. These outbreaks are often prolonged and challenging to control.

Some of the detected (clonal) outbreaks are most likely attributable to transfer of plasmids between different clones or species, suggesting that they are connected, but this is difficult to assess based on the current short-read sequencing methods used for the surveillance. Therefore, long-read sequencing is currently being implemented to enable tracking plasmid transfer across different CPO-outbreaks.

**Outbreaks with CPO of special interest**

Between April 2025 and September 2025, a total of 15 cases were detected from the Southern Denmark Region as belonging to the same outbreak. The cases were found to be infected/colonised with ST1344 NDM-5 producing *E. hormaechei*, confirmed via whole-genome sequencing of isolates as belonging to the specific core-genome multilocus sequence typing (cgMLST) cluster within ≤4 allelic differences. All cases in Denmark had been hospitalized. Notification by the Netherlands in the European surveillance portal for infectious diseases EpiPulse revealed the presence of cases also in the Netherlands. Investigations showed that the cases belonged to same specific cluster as the Danish cases. Subsequent cases were notified from Germany, Ireland, Austria, Norway and Luxembourg. In total, 57 cases have been identified. The simultaneous emergence of genetically highly related NDM-5-producing *E. hormaechei* ST1344 across several countries suggests a common source. The investigation of this outbreak is coordinated by ECDC, the European Centre for Disease Prevention and Control (Roer *et al.* Euro Surveill. 2026 Jun;31(25):2600460).

The ST18 NDM-1-producing *Citrobacter freundii* outbreak (ID41), which started in 2012 in the North Denmark Region, continued in 2025 [Hammerum *et al.* 2016, J. Antimicrob. Agents, 71:3117-3124]. Since 2012, the outbreak has spread to all five Danish regions. The main reason for the spread between regions is the movement of infected patients between regions. By the end of 2025, a total of 125 cases were involved in this outbreak. In 2025, a total of twelve new cases were identified. None of the cases had a history of travel.

Since 2015, another large outbreak (ID21) has been ongoing, primarily in two regions of the Zealand Region and in the Capital Region. The outbreak is associated with the spread of ST410 NDM-5/OXA-181 *E. coli*. [Roer *et al.* 2018, mSphere;3(4).]. Eleven new cases were detected as part of this outbreak. By the end of 2025, a total of 122 cases had been identified as part of this outbreak. With the exception of the initial cases reported in 2015, who had been traveling to Egypt [Overballe-Petersen *et al.* 2018, Genome Announc.6(5): e01542-17] none of the cases had a history of travel.

Since 2021, sixteen isolates have been found to belong to ST131 OXA-244 *E. coli* in the Danish surveillance of CPO (data not shown). The cases are distributed across the country and no epidemiological link to the Danish health care system has been identified. In March 2024, the national contact point for EURGen-Nets at Statens Serum Institut (SSI) contacted the European Centre for Disease Prevention and Control (ECDC) regarding the increasing detection of OXA-244-producing *E. coli* ST131 in Denmark. ECDC initiated a European investigation involving 17 countries. The investigation showed a considerable heterogeneity in the geographical distribution and speed of spread of specific carbapenemase genes. This heterogeneity was particularly evident in the recent rapid emergence of ST131 isolates carrying chromosomally localised $bla_{\text{OXA-244}}$ associated with large multi-country clusters [Kohlenberg, *et al.*, Euro Surveill. 2024 Nov;29(47)].

The hospital environment is a known reservoir for nosocomial infections, with bathroom plumbing increasingly implicated in the spread of carbapenemase-producing Enterobacterales (CPE). In the North Denmark Region an outbreak of CPE has been linked to *Klebsiella oxytoca* ST2. A study was conducted to investigate the environmental reservoirs and potential transmission routes of NDM-1-producing *K. oxytoca* isolates associated with patients and the environment. Whole genome sequencing (WGS) and plasmid analysis was used to assess genetic relationships between environmental and patient isolates. NDM-1-producing *K. oxytoca* ST2 was consistently detected in three toilets, each harboring distinct genomic sub-clades. Four patients were later found colonized with isolates genetically related to those from the toilets connected to the specific hospital ward of the patients. No evidence of direct patient-to-patient transmission was found, underscoring the role of toilets as reservoirs in the outbreak [Eriksen, *et al.*, Infect Prev Pract. 2025 Oct 9;7(4)].

**Table 8.18 Outbreaks of carbapenemase-producing Enterobacterales (CPE) during 2025, n=34, Denmark** DANMAP 2025

| Outbreak ID | Year | Patients total | Patients 2025 | Carbapene-mase | Type of outbreak | Species (clonal spread) | Regions | Status |
|---|---|---|---|---|---|---|---|---|
| 41 | 2012-2025 | 125 | 12 | NDM-1 | Clonal/plasmid | ST18 *C. freundii* | 1 / 2 / 3 / 4 / 5 | Verified |
| 48 | 2013-2025 | 46 | 2 | OXA-436/OXA-48 | Clonal/plasmid | ST90 *E. cloacae*/ST22 *C. freundii* | 1 / 4 / 5 | Verified |
| 1204 | 2013-2025 | 14 | 4 | NDM-1 | Plasmid | *E. coli / K. michiganensis /C. freundii* | 1 | Possible |
| 21 | 2015-2025 | 122 | 11 | NDM-5/OXA-181 | Clonal | ST410 *E. coli* | 1 / 2 / 5 | Verified |
| 22 | 2015-2025 | 16 | 2 | OXA-181 | Clonal | ST440 *E. coli* | 1 / 2 | Verified |
| 1066 | 2017-2025 | 81 | 18 | OXA-48 | Clonal | ST91 *C. freundii* | 1 / 5 | Verified |
| 1070 | 2017-2025 | 27 | 12 | OXA-48 | Clonal | *C. farmeri* | 5 | Verified |
| 1145 | 2017-2025 | 23 | 12 | OXA-48 | Clonal/plasmid | ST65 *C. freundii* | 3 | Verified |
| 1052 | 2018-2025 | 9 | 1 | NDM-1 | Clonal | ST18 *C. freundii* | 2 / 4 | Possible |
| 43 | 2019-2025 | 49 | 16 | OXA-48 | Clonal/plasmid | ST323 *C. freundii* | 1 / 5 | Verified |
| 1061 | 2020-2025 | 25 | 7 | OXA-181 | Clonal | ST22 *C. freundii* | 2 | Possible |
| 1221 | 2020-2025 | 6 | 4 | NDM-1 | Clonal/plasmid | ST22 *C. freundii* | 3 | Possible |
| 1122 | 2021-2025 | 8 | 6 | NDM-1 | Clonal | ST116 *C. freundii* | 2 | Possible |
| 1107 | 2022-2025 | 14 | 4 | OXA-181 | Clonal | ST636 *C. freundii* | 1 / 5 | Possible |
| 1113 | 2022-2025 | 16 | 6 | OXA-48 | Clonal | ST22 *C. freundii* | 5 | Verified |
| 1115 | 2022-2025 | 13 | 4 | NDM-1 | Clonal | ST2 *K. oxytoca* | 3 | Verified |
| 1148 | 2022-2025 | 6 | 2 | OXA-48 | Clonal | ST214 *C. freundii* | 5 | Possible |
| 1154 | 2022-2025 | 6 | 1 | KPC-3 | Clonal/plasmid | ST22 *C. freundii* | 4 | Possible |
| 1112 | 2023-2025 | 11 | 3 | OXA-244 | Clonal | ST10 *E. coli* | 1 / 4 | Verified |
| 1139 | 2023-2025 | 8 | 1 | OXA-181 | Clonal | ST65 *C. freundii* | 5 | Possible |
| 1190 | 2023-2025 | 7 | 6 | OXA-48 | Clonal | ST27 *K. michiganensis* | 2 | Verified |
| 1179 | 2024-2025 | 3 | 1 | OXA-232 | Clonal | ST18 *C. freundii* | 2 | Verified |
| 1180 | 2024-2025 | 4 | 2 | OXA-48 | Clonal | ST114 *C. freundii* | 5 | Possible |
| 1183 | 2024-2025 | 3 | 1 | OXA-181 | Clonal | ST98 *C. freundii* | 5 | Possible |
| 1189 | 2024-2025 | 2 | 1 | OXA-181 | Clonal | ST35 *K. oxytoca* | 1 | Verified |
| 1201 | 2024-2025 | 2 | 1 | OXA-48 | Clonal | ST636 *C. freundii* | 1 | Verified |
| 1218 | 2024-2025 | 3 | 2 | OXA-181 | Clonal | ST22 *C. freundii* | 2 | Possible |
| 1198 | 2025 | 3 | 3 | OXA-48 | Clonal | ST118 *E. hormaechei* | 1 | Verified |
| 1199 | 2025 | 5 | 5 | NDM-7 | Clonal/plasmid | ST91 *C. freundii* | 2 | Possible |
| 1200 | 2025 | 15 | 15 | NDM-5 | Clonal/plasmid | ST1344 *E. hormaechei* | 4 | Verified |
| 1217 | 2025 | 2 | 2 | OXA-181 | Clonal | *M. morganii* | 5 | Possible |
| 1223 | 2025 | 2 | 2 | OXA-48 | Clonal | ST65 *C. freundii* | 3 | Possible |
| Outbreaks of carbapenemase-producing organisms (CPO | | | | | | | | |
| 1203 | 2025 | 2 | 2 | NDM-1/OXA-97 | Clonal | *A. johnsonii* | 2 | Possible |
| 1215 | 2025 | 5 | 5 | OXA-164 | Clonal | *A. bereziniae* | 2 | Possible |

1 Regions will be listed as: 1) Capital Region, 2) Central Denmark Region, 3) North Denmark Region, 4) Southern Denmark Region and 5) Zealand Region.

**Conclusion**

The occurrence of CPOs in Denmark continued to increase throughout 2025. This increase may partly be explained by the arrival of patients from Ukraine, among whom CPO carriage has been frequently observed. Another contributing factor is the growing number of outbreaks caused by carbapenemase-producing Enterobacterales (CPE) in Danish hospitals. However, the overall number of CPE cases has also increased independently of recognised outbreaks. Isolates recovered from urine samples appear to account for a substantial proportion of these sporadic cases.

The number of newly detected nosocomial outbreaks increased from 2024 to 2025. Some of the reported outbreaks may be attributable to the transfer of carbapenemase-carrying plasmids between different bacterial species. The role of plasmid-mediated transmission in CPO outbreaks will be investigated further in the coming years. The *Citrobacter freundii* complex was the species most frequently associated with reported CPO outbreaks.

Travel outside the Nordic countries remains an important contributor to the number of CPO cases detected in Denmark. The most frequently reported travel destinations in 2025 were Asia and south-eastern Europe. However, travel information was unavailable for a substantial proportion of cases, limiting the ability to accurately assess the contribution of travel-associated acquisition to the epidemiology of CPOs in Denmark.

The increasing spread of carbapenemase-producing Enterobacterales (CPE) among patients in Denmark is of concern. Enterobacterales may colonise the gastrointestinal tract for prolonged periods, without causing symptoms, thereby facilitating transmission and complicating outbreak control. Furthermore, infections caused by CPE may limit available treatment options and are associated with increased healthcare burden.

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### 8.3.3 Vancomycin-resistant/vancomycin-variable enterococci

**Background**

Enterococci are intrinsically resistant to a number of first-line antimicrobial agents, including cephalosporins, which increases the risk of enterococci being selected for in-hospital environments and emerging in patients that receive cephalosporins for other conditions. Most hospital-acquired *Enterococcus faecium* are resistant to ampicillin, further limiting the treatment options. Vancomycin is an important drug for the treatment of severe *E. faecium* infections, however an increase in the occurrence of vancomycin resistant enterococci (VRE) has been observed within the last decade, both internationally as well as in Denmark. Newer antibiotics such as linezolid and daptomycin can be used for treatment of VRE, but both antimicrobial agents may lead to adverse events. The development of resistance is reported. In recent years, isolates of phenotypically vancomycin-susceptible *E. faecium* have been described to harbor a *vanA*-gene complex, in various countries. These isolates are referred to as vancomycin-variable enterococci (VVE).

**Surveillance of VRE/VVE**

Since 2005, Danish departments of clinical microbiology (DCMs) have voluntarily submitted clinical VRE (one VRE/VVE isolate per patient, isolated within 12 months) for species identification, genotyping and surveillance purposes to the Antimicrobial Resistance Reference Laboratory at Statens Serum Institut (SSI).

Since 2015, the received clinical VRE/VVE isolates have been analysed using whole-genome sequencing (WGS). In 2025, the VRE/VVE surveillance was changed, so only VRE/VVE isolates from bloodstream infection were WGS. The WGS data are used for *in silico* genotyping of isolate characteristics such as species identification, multilocus sequence typing (MLST), core genome sequence typing (cgMLST) and detection of van-genes and core genome MLST (cgMLST) used for clonal detection (see Section 9.13.3).

To determine any underreporting in the submissions of VRE isolates, the number of VRE isolates submitted to SSI since were compared to data from VRE from bloodstream infections in MiBa (the Danish Microbiology Database). These isolates were not genotyped, yet they are included in Figure 8.20.

Of the 38 clinical VRE isolates from bloodstream infection sequenced in 2025; 3 were *vanA E. faecium* and 35 *vanB E. faecium*. No vancomycin resistant *E. faecalis* were detected from bloodstream infections in 2025 (Figure 8.20). Until 2019, *vanA E. faecium* were most common, but hereafter *vanB E. faecium* dominated. In 2024, 93% of the *E. faecium* isolates had the *vanB* gene.

WGS-based cgMLST analysis was performed on the 38 *E. faecium* isolates using the MBioSEQ Ridom Typer (Ridom). The 38 *E. faecium* isolates belonged to unique 24 CT clusters. When investigating the composition of sequence types (ST) and clonal types (CT) for *E. faecium*, we observed a clustering tendency between isolates, where ST's and CT's were diverging while the allelic differences were minimal within each cluster. MST clusters were set up using the MST algorithm of MBioSEQ Ridom Typer, setting the maximal allelic distances to 20. Each complex type cluster were named according to the ST and CT of the earliest observed isolate within each cluster. One clonal group (covering several different CTs but presumably originating from the same clone) were predominant: The ST80-CT2406 *vanB E. faecium* group containing 26 isolates (68%) (Table 8.19). This clone has been the most common among the clinical VR*E. faecium* isolates in the previous year (DANMAP 2024).

**Figure 8.20 Overview and distribution of vancomycin resistance genes in vancomycin-resistant isolates from bloodstream infections, Denmark, 2016-2025**

DANMAP 2025




**Table 8.19 Description of the types of *vanA* or *vanB* Enterococcus faecium according to MLST and cgMLST, Denmark, 2025**

DANMAP 2025

| Van gene | ST | Local SLC Clones | Cluster type(s) | Numbers |
|---|---|---|---|---|
| *vanA* | ST80 | | 1965 (new) | 1 |
| | ST117 | 2505 | 2505 | 1 |
| | ST203 | 859 | 859 | 1 |
| *vanB* | ST17 | | 7023 | 2 |
| | ST80 (ST2412) | 2406 | 5211, 6254,6507, 6598, 8187, 8443, 8455, 8840, 9115, 9165, 9450, 9776, 9809, 10268 | 25 (1) |
| | ST80 | | 9180 (new) | 1 |
| | ST80 | | 9820 (new) | 1 |
| | ST80 | | 10066 (new) | 1 |
| | ST117 | 2505 | 2505, 2872, 7570 | 3 |

## Conclusion

The number of VRE cases from bloodstream infections have decreased from 2024 to 2025. This is a desired development.

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### 8.3.4 *Staphylococcus aureus*

*Staphylococcus aureus* (*S. aureus*) is part of the normal flora of the skin and mucosa. Approximately 50% of humans will be colonized with *S. aureus* in their nose or throat at any given time, some of these carrying the strain only intermittently, others for longer periods of time. *S. aureus* causes infections ranging from superficial skin infections e.g. impetigo and boils to deeper and invasive life-threatening infections such as bacteraemia, septic arthritis, osteomyelitis, endocarditis. The infections can be healthcare-associated such as postoperative wound infections and infections related to intravenous catheters and prosthetic devices or the bacteria can spread endogenously.

In Denmark, a voluntary surveillance program of all *S. aureus* bacteraemia cases was established in 1957. By comparison with the numbers of bacteraemia cases registered in the Danish Microbiology Database (MiBa) since 2010, the number of reported cases and bacterial isolates submitted to SSI has been almost complete (94-97%). Laboratory and clinical notification of all cases of methicillin-resistant *S. aureus* (MRSA) has existed since November 2006.

### Surveillance of *S. aureus* bacteraemia

The number of *S. aureus* bacteraemia cases were 2,375 in 2025 corresponding to 40 cases per 100,000 inhabitants. This is less compared to 2024 (N=2,461), and the long-term trend of an increasing number of cases seem to have been halted the last 2-3 years (Figure 8.21). Within 30 days from the bacteraemia onset, 522 (22%) patients died (all-cause mortality). Sixty-six (2.8%) of the bacteraemia cases were caused by methicillin-resistant *S. aureus* (MRSA). This is the highest prevalence since 2014 (2.9%). The prevalence is normally below 2% and remains below most other European countries participating in the European Antimicrobial Resistance Surveillance Network (EARS-Net) [EARS-Net 2023]. Livestock-associated MRSA (LA-MRSA) CC398 caused seven of the 66 MRSA bacteraemia cases. The 30-day all-cause mortality for the MRSA bacteraemia cases was 21%.

The antimicrobial susceptibility remained at the same level as the previous years for most agents (Table 8.20). The highest frequency of resistance to antimicrobials other than penicillin was observed for fusidic acid (13%), erythromycin (11%) and clindamycin (11%).

**Figure 8.21 Number of new *Staphylococcus aureus* bacteraemia cases, Denmark, 2016-2025** DANMAP 2025

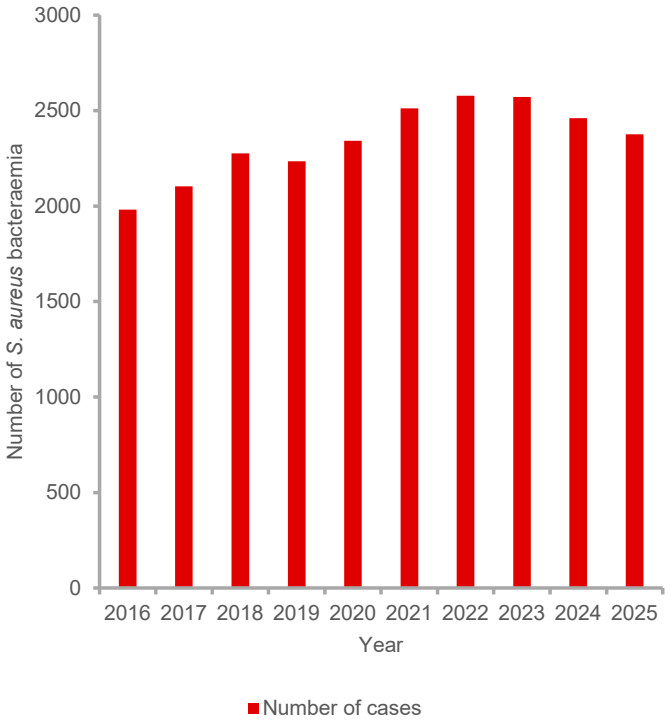



**Table 8.20 Resistance (%) in isolates from *Staphylococcus aureus* bacteraemia cases, Denmark, 2016-2025** DANMAP 2025

| Antimicrobial agent | 2016 % | 2017 % | 2018 % | 2019 % | 2020* % | 2021 % | 2022 % | 2023 % | 2024 % | 2025 % |
|---|---|---|---|---|---|---|---|---|---|---|
| Methicillin | 2.1 | 2.2 | 1.6 | 2.1 | 1.6 | 1.6 | 1.9 | 1.5 | 1.9 | 2.8 |
| Penicillin | 71 | 72 | 72 | 72 | 72 | 69 | 68 | 68 | 69 | 68 |
| Erythromycin | 7 | 6 | 5 | 9 | 7 | 7 | 9 | 9 | 9 | 11 |
| Clindamycin | 6 | 5 | 4 | 8 | 7 | 7 | 8 | 8 | 9 | 11 |
| Tetracycline | 3 | 3 | 3 | 2 | 3 | 2 | 3 | 2 | 3 | 3 |
| Fusidic acid | 12 | 14 | 17 | 14 | 14 | 13 | 13 | 12 | 13 | 13 |
| Rifampicin | <1 | <1 | <1 | <1 | <1 | <1 | <1 | <1 | 1 | 1 |
| Moxifloxacin# | 4 | 4 | 4 | 5 | 6 | 4 | 4 | 4 | 3 | 4 |
| Gentamicin | <1 | 1.1 | 1.0 | <1 | <1 | <1 | 1.1 | 1.2 | 1 | 1 |
| Linezolid | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Mupirocin | 0 | <1 | 0 | <1 | <1 | <1 | <1 | <1 | <1 | <1 |
| Trimethoprim-sulfamethoxazole | <1 | <1 | 0 | <1 | <1 | <1 | <1 | <1 | <1 | <1 |

* From 2020 and onwards, resistance data was extracted from the Danish Microbiology database, MiBa. # Prior to 2021 testing for fluoroquinolone resistance was reported for norfloxacin.

**Table 8.21 The ten most prevalent spa types in SAB cases, Denmark, 2025** DANMAP 2025

| *spa* type | CC group | No. of cases |
|---|---|---|
| t127 | CC1 | 135 |
| t084 | CC15 | 98 |
| t091 | CC7 | 89 |
| t1451 | CC398 | 89 |
| t002 | CC5 | 79 |
| t008 | CC8 | 59 |
| t701 | CC8 | 57 |
| t230 | CC45 | 57 |
| t012 | CC30 | 55 |
| t021 | CC30 | 51 |

Typing revealed a high diversity with 697 different *spa* types distributed in 27 different clonal complexes (CCs). The ten most prevalent *spa* types, representing 33% of the total number, are presented in Table 8.21. The distribution of the most prevalent *spa* types has been very stable over the last decade with only minor changes in the relative order. The PVL toxin was present in 44 (1.9%) cases of which 14 were MRSA. The 44 isolates with the PVL gene were distributed among 28 different *spa* types.

**Surveillance of methicillin-resistant *S. aureus***

In 2025, 3,301 MRSA new cases were detected (55 per 100,000 inhabitants), a small decrease compared to 2024 (3,372; Figure 8.22a). A case was defined as the first time an individual tested positive for a specific MRSA strain regardless of clinical context (infection or colonisation). A case was defined as infection or colonisation based on the information in the notification form. Infections constituted 58% of the cases. The proportion of infections in the years 2016 to 2025 has varied between 38% to 58% (Figure 8.22b).

**Figure 8.22a Number of new MRSA cases, Denmark, 1994-2025** DANMAP 2025

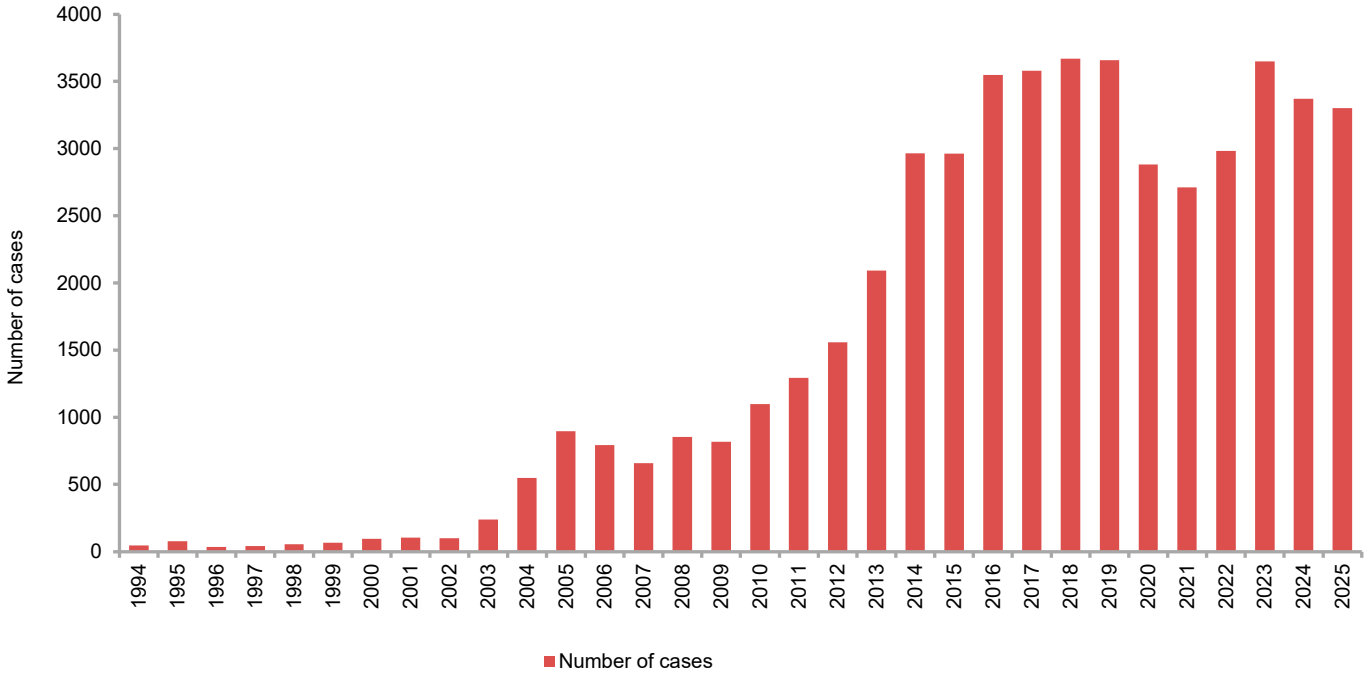
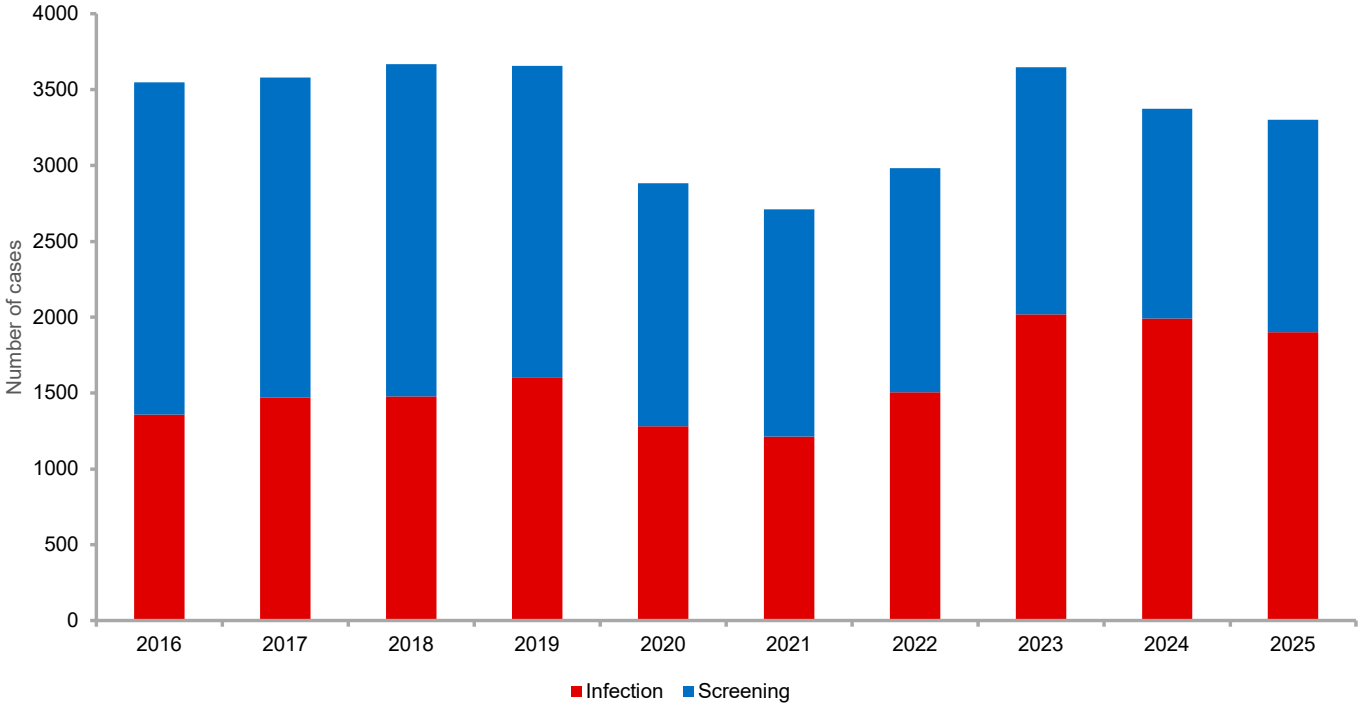



**Figure 8.22b Number of new MRSA cases divided in infection and screening samples, Denmark, 2016-2025** DANMAP 2025



LA-CC398 cases constituted 18% (n = 591) of new MRSA cases, the lowest proportion in the last decade. A higher proportion of LA-MRSA CC398 isolates (79%) were identified in healthy carriers compared to other MRSA types (36%), likely reflecting the active screening of patients with livestock contact upon admission to healthcare facilities.

MRSA isolates carrying *mecC* were detected in 37 cases (1%). Thirty of the cases (81%) had infections at the time of diagnosis. None of the patients reported contact to hedgehogs, which recently has been shown to be a major environmental reservoir for *mecC* MRSA. One patient had reported contact to pigs, two to horses, and three patients had contact to other animals. The remaining 31 patients did not report any contact to livestock or other animals.

*spa* typing revealed 438 different strain types. Among the infections, 358 *spa* types were identified. The 10 dominating non-LA-CC398 *spa* types isolated in 2025 are listed in Table 8.22. They constituted 44% of the total number of non-LA-CC398 MRSA isolates. Table 8.22 does not list *spa* types in CC398, which for many years has been the dominating CC. *spa* types t304 and t223 have been among the five most prevalent *spa* types since 2016, when their increase was linked to the refugee crisis following the civil war in Syria. For the third year in a row *spa* type t127 was the second most numerous. This type has been involved in several outbreaks in neonatal units in recent years but is also a common type among community associated cases.

The PVL encoding gene was detected in 26% of the infections and in 15% of the asymptomatic carriers and most often in relation to isolates with *spa* types t005 (n = 69), t008 (n = 59), t021 (n = 52), t355 (n = 39) and t034 (n = 39).

Thirty-six MRSA outbreaks were registered at hospitals, nursing homes and other institutions (Table 8.23). These outbreaks comprised a total of 127 cases of which 60 had an infection. Seven of the outbreaks occurred in neonatal departments, comprising a total of 42 cases. Additionally, 10 outbreaks were registered in other hospital department, comprising 24 patients and 15 outbreaks were observed in nursing homes or associated with home care (counting a total of 42 patients).

The total number of cases and the number of cases presenting with infection according to epidemiological classification are shown in Table 8.24. Most of the cases (84%) were as usual acquired in Denmark.

The trend of MRSA infections for 2016-2025 based on their epidemiological classification is shown in Figure 8.23. The number of infections in imported cases decreased in 2025 when compared to 2024. The number of infections among hospital-acquired MRSA was 53, an increase compared to 30 cases in 2024, but still constitutes the smallest fraction of the total number of infections.

**Table 8.22 The ten most prevalent *spa* types demonstrated in non-LA-CC398-MRSA, Denmark, 2025** DANMAP 2025

| *spa* type | CC group | No. of cases | No. causing infections (%) |
|---|---|---|---|
| t304 | CC6 | 277 | 151 (55) |
| t127 | CC1 | 148 | 77 (52) |
| t223 | CC22 | 125 | 73 (58) |
| t668 | CC5 | 124 | 82 (66) |
| t002 | CC5 | 113 | 73 (65) |
| t008 | CC8 | 111 | 72 (65) |
| t4549 | CC8 | 106 | 90 (85) |
| t005 | CC22 | 78 | 55 (71) |
| t021 | CC30 | 58 | 36 (62) |
| t3841 | CC5 | 56 | 31 (55) |

**Table 8.23 Outbreaks of methicillin-resistant *Staphylococcus aureus* (MRSA), Denmark, 2025** DANMAP 2025

| Start of outbreak (year) | Patients in total | Patients in 2024 | *spa* type | CC | Place of outbreak | Region |
|---|---|---|---|---|---|---|
| 2016 | 1 | 35 | t2846 | CC97 | Nursing home | Capital Region of Denmark |
| 2016 | 1 | 13 | t250 | CC7 | Hospital (neonatal) | North Denmark Region |
| 2017 | 3 | 25 | t3802 | CC6 | Hospital | Central Denmark Region |
| 2018 | 10 | 18 | t223 | CC22 | Nursing home | Capital Region of Denmark |
| 2019 | 15 | 147 | t127 | CC1 | Hospital (neonatal) | Capital Region of Denmark |
| 2019 | 4 | 20 | t148 | CC72 | Educational facility | Region of Southern Denmark |
| 2019 | 2 | 5 | t002 | CC5 | Nursing home | Capital Region of Denmark |
| 2020 | 5 | 8 | t015 | CC45 | Nursing home | Capital Region of Denmark |
| 2021 | 1 | 5 | t267 | CC97 | Nursing home | Central Denmark Region |
| 2022 | 3 | 18 | t553 | CC45 | Nursing home | Region Zealand |
| 2022 | 3 | 6 | t511 | CC45 | Nursing home | Capital Region of Denmark |
| 2022 | 3 | 5 | t111 | CC5 | Hospital | North Denmark Region |
| 2023 | 1 | 22 | t1776 | CC30 | Hospital (neonatal) | Central Denmark Region |
| 2023 | 3 | 63 | t272 | CC121 | Child care institution | Region of Southern Denmark |
| 2023 | 1 | 8* | t127 | CC1 | Hospital (neonatal) | Capital Region of Denmark |
| 2024 | 3 | 11 | t1476 | CC8 | Hospital (neonatal) | Central Denmark Region |
| 2024 | 2 | 6 | t359 | CC97 | Educational facility | Region of Southern Denmark |
| 2024 | 2 | 5 | t6980 | unknown | Nursing home | Central Denmark Region |
| 2025 | 18 | 18 | t693 | CC1 | Hospital (neonatal) | North Denmark Region |
| 2025 | 4 | 5* | t005 | CC22 | Nursing home | Region Zealand |
| 2025 | 6 | 6 | t304 | CC6 | Hospital | Capital Region of Denmark |
| 2025 | 4 | 5* | t311 | CC5 | Nursing home | Region of Southern Denmark |
| Multiple (14 smaller outbreaks) | 23 | 32* | Multiple | Multiple | Various | Denmark |

**Table 8.24 Epidemiological classification of new MRSA cases, Denmark, 2025** DANMAP 2025

| Epidemiologic classification | Exposure | No. of cases (% of total) | No. (%) of cases with infections (% of cases in same epi. class) |
|---|---|---|---|
| Imported (IMP) | | **525 (16)** | 342 (65) |
| Hospital-acquired (HA) | | **70 (2)** | 28 (40) |
| "Health-care associated, community onset (HACO)" | | **326 (10)** | |
| | with known exposure | 18 | 10 (56) |
| | without known | 308 | 269 (87) |
| Health care worker | | **40 (1)** | 25 (63) |
| Community-acquired (CA) | | **1,749 (53)** | |
| | with known exposure | 703 | 94 (13) |
| | without known | 1046 | 946 (90) |
| LA-MRSA CC398 | | **591 (18)** | |
| | with known exposure | 472 | 97 (21) |
| | without known | 119 | 91 (76) |
| **Total** | | **3,301** | **1,902** |

Numbers shown in bold are sub-totals.

**Figure 8.23 Number of MRSA infections according to epidemiological classification, Denmark, 2016-2025** DANMAP 2025

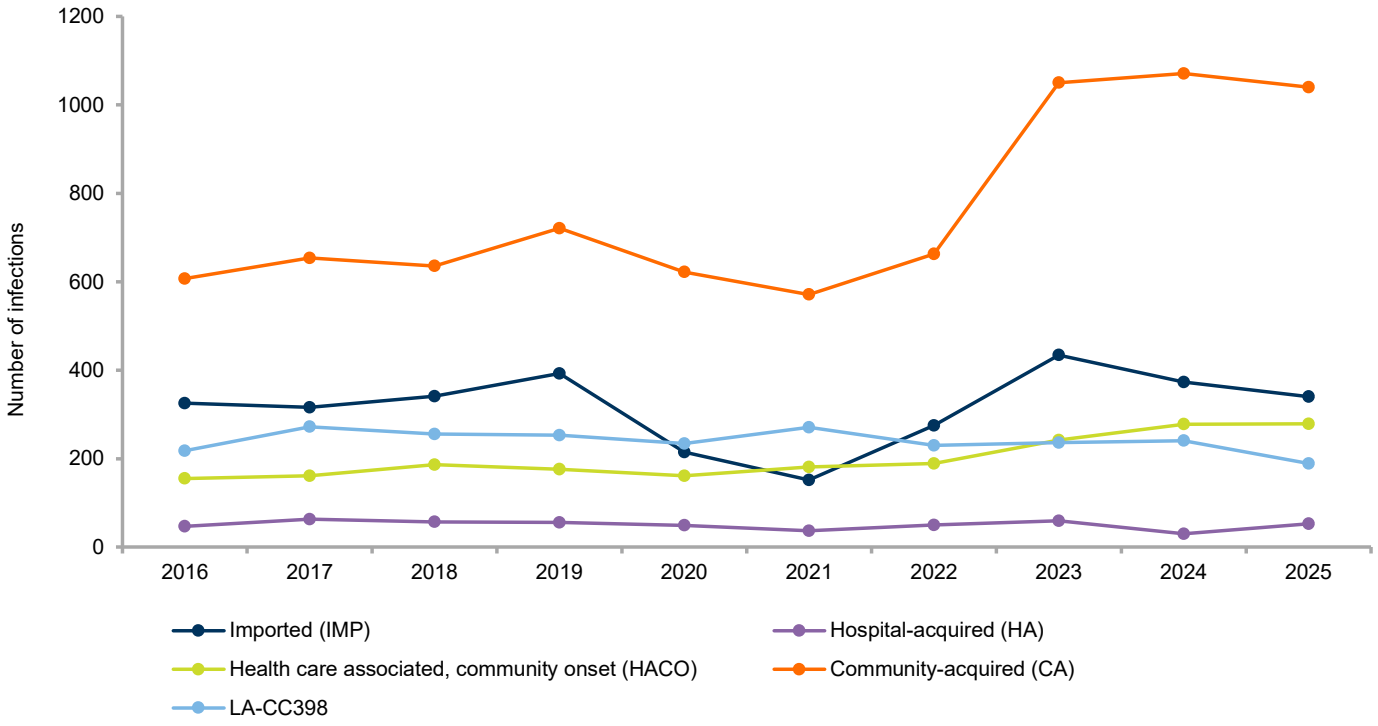



**Table 8.25 Resistance (%) in non-livestock-associated CC398 MRSA isolates, Denmark, 2016-2025** DANMAP 2025

| | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|
| Erythromycin | 34 | 34 | 33 | 33 | 30 | 29 | 34 | 32 | 33 | 35 |
| Clindamycin | 25 | 27 | 28 | 23 | 22 | 19 | 21 | 21 | 22 | 23 |
| Tetracycline | 26 | 24 | 26 | 22 | 22 | 21 | 23 | 21 | 24 | 23 |
| Fusidic acid | 18 | 16 | 18 | 23 | 22 | 21 | 22 | 26 | 27 | 29 |
| Rifampicin | 1 | 1 | 1 | <1 | <1 | <1 | <1 | 1 | <1 | <1 |
| Moxifloxacin# | 19 | 20 | 21 | 21 | 17 | 19 | 23 | 24 | 26 | 26 |
| Linezolid | <1 | 0 | <1 | 0 | <1 | <1 | <1 | <1 | <1 | <1 |
| Mupirocin | <1 | <1 | <1 | <1 | <1 | <1 | <1 | <1 | <1 | <1 |
| Trimethoprim-sulfamethoxazole | 2 | 3 | 3 | 4 | 2 | <1 | 1 | 1 | 2 | <1 |
| Number of tested isolates | 1,184 | 1,193 | 1,233 | 1,025 | 1,920* | 1,520* | 2,043* | 2,696* | 2,605* | 2,696* |

* Not all isolates were tested for all listed antimicrobials.
# Prior to 2021 testing for fluoroquinolone resistance was reported for norfloxacin.

### Resistance among MRSA isolates

Resistance data for non-LA-CC398 isolates are presented in Table 8.25. Resistance prevalences were similar to previous years, with the highest resistance to erythromycin (35%), fusidic acid (29%), moxifloxacin (26%), tetracycline (23%) and clindamycin (23%), and low resistance (<1%) to trimethroprim-sulfamethoxazole, linezolid, mupirocin and rifampicin.

### Conclusion

The number of *S. aureus* bacteraemia cases was 2,375 in 2025, a slight decrease compared to 2024. Of these, 66 cases (2.8%) were caused by methicillin-resistant *S. aureus* (MRSA) with seven being livestock-associated-MRSA (LA-MRSA).

There were 3,301 cases of MRSA from both screening (42% of cases) and infections (58%), which was a small decrease compared to 2024. Thirty-six MRSA outbreaks were registered at hospitals, nursing homes and other institutions for a total of 127 cases with 60 being infections.

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### 8.3.5 *Streptococcus pneumoniae*

**Background**

*Streptococcus pneumoniae*, also known as the pneumococcus, is a Gram-positive bacterium which can colonise the respiratory tract of humans and is a frequent cause of bacterial pneumonia worldwide. The pneumococcus causes a range of diseases which can be categorised as either invasive or non-invasive, with invasive infections, resulting in bloodstream infections and meningitis as well as infections at other normally sterile sites resulting in the development of an empyema, septic arthritis, endocarditis et cetera, being the most severe manifestation. Non-invasive infections such as acute otitis media, sinusitis, and infective exacerbations of bronchitis are much more commonly encountered than invasive infections. First-line treatment for infections caused by *S. pneumoniae* is penicillin, but the development of resistance to this agent through mutations in penicillin-binding proteins, is of global concern, and driven by the overuse of antibiotics.

A key virulence determinant of *S. pneumoniae* is its polysaccharide capsule, with variations in the polysaccharide component of the capsule allowing characterisation of *S. pneumoniae* into different serotypes, with over 100 serotypes currently documented. Persons aged over 65 years of age, children under 2 years of age as well as individuals with certain chronic illnesses are at higher risk of invasive pneumococcal disease (IPD), and prevention of both IPD and non-invasive disease through vaccination of vulnerable populations has been a key public health intervention. Pneumococcal vaccinations (Table 8.26) include capsular polysaccharides of the most common serotypes causing IPD either alone, the pneumococcal polysaccharide vaccine (PPV23), or conjugated to carrier proteins, the pneumococcal conjugate vaccine (PCV7, PCV13, PCV15, PCV20 and PCV21). The PCV has been included in the Danish childhood vaccination programme since 2007, initially with the PCV7, and subsequently with the PCV13 from 2010. In the Autumn of 2025, the PCV13 was replaced by the PCV15 to include two additional serotypes. For individuals at increased risk of IPD, the PPV23 is indicated for those over 2 years of age, the PCV20 can be given to individuals over the age of 6 weeks, and the PCV-21 is indicated for adults over the age of 18 years.

**Laboratory Surveillance**

IPD is a notifiable disease in Denmark and submission of isolates cultured from normally sterile sites to Statens Serum Institut (SSI) is mandatory. At the *Neisseria* and *Streptococcus* Reference (NSR) Laboratory at SSI, all isolates are phenotypically characterised into serotypes using agglutination-based methods and investigation of the Neufeld reaction which is observed when bacterial isolates belonging to one serotype are exposed to the corresponding antiserum. Information regarding the antimicrobial susceptibility testing of pneumococcal isolates in 2025 was extracted from the Danish Microbiology Database (MiBa) with results interpreted according to version 15 of the breakpoints published by the European Committee on Antimicrobial Susceptibility Testing (EUCAST) and valid from January 1st 2025. In short, an oxacillin 1µg disc or a benzylpenicillin MIC determination is used to screen for possible beta-lactam resistance mechanisms. Beta-lactam resistance mechanisms can be excluded in isolates with an oxacillin zone size ≥20 mm or a benzylpenicillin MIC ≤0.06 mg/L, and these isolates are considered susceptible to benzylpenicillin (S) as well as all other beta-lactam antibiotics. An oxacillin zone size ≤20 mm or benzylpenicillin MIC ≥0.06 mg/L indicates the presence of a beta-lactam resistance mechanism, and isolates are considered resistant (R) to benzylpenicillin in cases of meningitis or infective endocarditis. For treatment of disease other than meningitis or endocarditis, isolates with a benzylpenicillin (1 unit) zone size ≥14 mm, or a benzylpenicillin MIC between 0.06–1 mg/L, are considered susceptible to benzylpenicillin with increased exposure (I), i.e., a higher dose should be administered, and isolates with an observed zone size ≤14 mm, or MIC >1 mg/L are considered resistant (R) to benzylpenicillin. Previous iterations of DANMAP have categorised pneumococci as susceptible or penicillin non-susceptible *S. pneumoniae* (PNSP) based on the presence or absence of mutations conferring resistance to beta-lactams, this report will differentiate between isolates categorised as susceptible, susceptible with increased exposure and resistant.

**Table 8.26 Curect vaccines available and their coverage against serotypes of *S. pneumoniae*** DANMAP 2025

| Available vaccines | Serotypes included |
|---|---|
| PCV 13 | 1, 3, 4, 5, 6A, 6B, 7F, 9V, 14, 18C, 19A, 19F, 23F |
| PCV 15 | 1, 3, 4, 5, 6A, 6B, 7F, 9V, 14, 18C, 19A, 19F, 23F, 22F, 33F |
| PCV 20 | 1, 3, 4, 5, 6A, 6B, 7F, 9V, 14, 18C, 19A, 19F, 23F, 22F, 33F, 8, 10A, 11A, 12F, 15B |
| PCV 21 | 3, 6A, 7F, 19A, 22F, 33F, 8, 10A, 11A, 12F, 9N, 17F, 20A, 15A, 15C, 16F, 23A, 23B, 24F, 31, 35B |
| PPV 23 | 1, 3, 4, 5, 6B, 7F, 9V, 14, 18C, 19A, 19F, 23F, 22F, 33F, 8, 10A, 11A, 12F, 15B, 2, 9N, 17F, 20 |

## Results

In 2025, a total of 686 cases of IPD in which an isolate was cultured from blood or cerebrospinal fluid were recorded in Denmark (Table 8.27). A further 13 cases of meningitis were identified in which *S. pneumoniae* DNA was demonstrated by PCR from cerebrospinal fluid (CSF), but no isolate was cultured from either CSF or blood. Two CSF samples were sent to SSI for a serotype determination by PCR and one case was determined to be serotype 3, and the other case determined to be 23B. An additional 14 cases of IPD causing infection at other normally sterile sites were identified – 8 cases where *S. pneumoniae* was isolated from pleural fluid, 5 cases of septic arthritis, and one case of peritonitis. The results of antimicrobial susceptibility testing were available in 12 out of 14 cases, and in two cases *S. pneumoniae* DNA was demonstrated but culture was negative. Seven out of these 14 isolates were referred to SSI for serotyping.

The total number of IPD cases in 2025 was 715, compared to 634 cases in 2024 and 635 cases in 2023. This is equivalent to an incidence rate of 11.9 cases per 100,000 population, and represents an increase in comparison to the incidence rates of 10.6 cases per 100,000 in 2023 and 2024 (Figure 8.24). The following information presented in this chapter is based on the serotype determination and AST from culture-positive bloodstream infections (BSIs), meningitis and infections at other normally sterile sites due to *S. pneumoniae*.

**Table 8.27 The number of cases of IPD and the sample type/detection method** DANMAP 2025

| Sample type | Number | AST data available | Serotype available |
|---|---|---|---|
| Bloodstream isolates alone | 627 | 627 | 613 |
| CSF isolates | 42 | 42 | 40 |
| CSF - *S. pneumoniae* DNA detected with concurrent bloodstream infection | 17* | 17* | 17* |
| CSF – *S. pneumoniae* DNA detected | 15 | 0 | 2 |
| *S. pneumoniae* isolates from a normally sterile site | 12 | 12 | 7 |
| *S. pneumoniae* DNA detected from a normally sterile site (excluding CSF) | 2 | 0 | 0 |
| Total number of IPD cases | 715 | 698 | 679 |

*Serotype and AST data inferred bloodstream isolate.

**Figure 8.24 The incidence of invasive pneumococcal disease (IPD) and the percentage of penicillin non-susceptible IPD isolates, Denmark, 2000-2025** DANMAP 2025

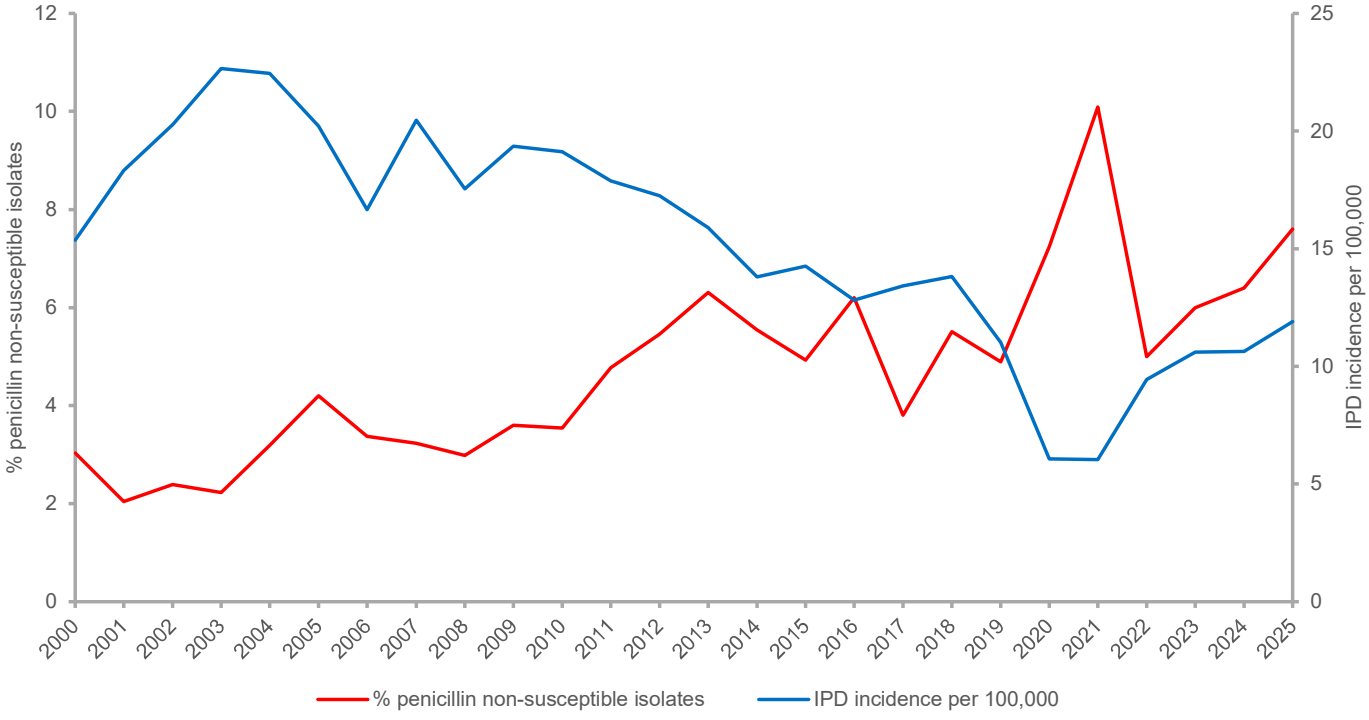


**Table 8.28 All IPD cases for which information on penicillin susceptibility was available, in order of serotype distribution, Denmark, 2025**

DANMAP 2025

| Serotype | Included in pneumococcus vaccines | | | | | Total number | Penicillin susceptible, numbers | | | % Pen-S or S, DD |
|---|---|---|---|---|---|---|---|---|---|---|
| | PCV13 | PCV15 | PCV20 | PCV21 | PPV23 | | S | I | R | |
| 3 | + | + | + | + | + | 118 | 114 | 4 | 0 | 100% |
| 8 | | | + | + | + | 94 | 92 | 2 | 0 | 100% |
| 9N | | | | + | + | 71 | 65 | 2 | 4 | 94% |
| 22F | | + | + | + | + | 55 | 54 | 1 | 0 | 100% |
| 15A | | | | + | | 32 | 30 | 2 | 0 | 100% |
| 33F | | + | + | + | + | 30 | 30 | 0 | 0 | 100% |
| 19A | + | + | + | + | + | 24 | 21 | 3 | 0 | 100% |
| 7C* | | | | | | 21 | 21 | 0 | 0 | 100% |
| 24F | | | | + | | 21 | 20 | 0 | 1 | 95% |
| 23A | | + | + | + | + | 21 | 18 | 3 | 0 | 100% |
| 10A | | | + | + | + | 15 | 14 | 1 | 0 | 100% |
| 19F | + | + | + | | + | 16 | 16 | 0 | 0 | 100% |
| 23B | | | | + | | 16 | 5 | 4 | 7 | 56% |
| 11A | | | + | + | + | 14 | 12 | 2 | 0 | 100% |
| 38* | | | | | | 11 | 11 | 0 | 0 | 100% |
| 15B | | | + | | + | 11 | 11 | 0 | 0 | 100% |
| 16F | | | | + | | 12 | 11 | 1 | 0 | 100% |
| 31 | | | | + | | 11 | 11 | 0 | 0 | 100% |
| 4 | + | + | + | | + | 11 | 11 | 0 | 0 | 100% |
| 35F* | | | | | | 10 | 9 | 1 | 0 | 100% |
| 6C* | | | | | | 10 | 8 | 2 | 0 | 100% |
| 12F | | | + | + | + | 9 | 8 | 1 | 0 | 100% |
| 35B | | | | + | | 8 | 8 | 0 | 0 | 100% |
| 15C | | | | + | | 6 | 6 | 0 | 0 | 100% |
| 10B* | | | | | | 5 | 4 | 1 | 0 | 100% |
| 17F | | | | + | | 5 | 3 | 2 | 0 | 100% |
| 20 | | | | + | | 3 | 3 | 0 | 0 | 100% |
| 34* | | | | | | 3 | 2 | 1 | 0 | 100% |
| 14 | + | + | + | + | | 2 | 1 | 1 | 0 | 100% |
| 33A* | | | | | | 2 | 2 | 0 | 0 | 100% |
| 1 | + | + | + | + | | 1 | 1 | 0 | 0 | 100% |
| 11B* | | | | | | 1 | 1 | 0 | 0 | 100% |
| 12A* | | | | | | 1 | 1 | 0 | 0 | 100% |
| 18A* | | | | | | 1 | 1 | 0 | 0 | 100% |
| 21* | | | | | | 1 | 1 | 0 | 0 | 100% |
| 37* | | | | | | 1 | 1 | 0 | 0 | 100% |
| 28F* | | | | | | 1 | 1 | 0 | 0 | 100% |
| 9L* | | | | | | 1 | 0 | 1 | 0 | 100% |
| 9V | + | + | + | + | | 1 | 0 | 0 | 1 | 0% |
| 5 | | | | | | 1 | 1 | 0 | 0 | 100% |
| Unknown | | | | | | 21 | 19 | 2 | 0 | 100% |
| Total | | | | | | 698 | 648 | 37 | 13 | 1.9% |

S = benzylpenicillin susceptible; I = benzylpenicillin susceptible, increased exposure; R = benzylpenicillin resistant; % Pen-S or S, DD = percentage of isolates susceptible to penicillin at standard dosing or increased exposure.
Serotypes marked with an asterisk indicate serotypes which are not present in currently available vaccines.

Of the 698 culture-positive cases of IPD, 677 were serotyped at the NSR. The remaining 21 isolates were either non-culturable once received at the NSR, or in some instances, no isolate was sent. Forty-two isolates causing meningitis were identified, and 11 of these cases arose without a concurrent BSI. In 17 cases, pneumococcal DNA was detected in cerebrospinal fluid in patientsassociated with a concurrent bloodstream infection. Sixteen of these isolates were fully susceptible to benzylpenicillin applying meningitis breakpoints, and the last isolate was resistant to benzylpenicillin in both blood and CSF. In 2025, 40 different serotypes were identified as causing IPD versus 43 serotypes in 2024. The leading serotype associated with IPD remains serotype 3, accounting for 118 cases (17.2%), followed by serotype 8 (n=94). Of the 644 BSIs, 11 were determined to be R to benzylpenicillin, with 5 out of the 11 resistant BSI isolates belonging to serotype 23B. Thirty-six bloodstream isolates were susceptible with increased exposure to benzylpenicillin. One of these serogroup 23B penicillin-resistant BSI isolates was associated with culture-negative meningitis. Of the 42 isolates cultured from CSF, 2 were resistant to benzylpenicillin, and both belonged to serotype 23B. Sixty-nine cases of IPD (10%) were caused by serotypes which are currently not included in available vaccines, of which 9 cases were associated with meningitis, 14.7% of all cases of meningitis due to *S. pneumoniae*. All non-vaccine serotypes associated with IPD in 2025 were susceptible to benzylpenicillin or susceptible to benzylpenicillin with increased exposure where serotype was available.

There were 10 episodes of IPD amongst children under 24 months of age, all BSIs, and all isolates were susceptible to benzylpenicillin. Three cases were caused by serotypes found in the PCV13, but the children were too young to have received vaccination at the time they developed IPD. A further 2 episodes were caused by serotype 22F which is found in the PCV15 vaccine, but not in the PCV-13 which had been in use in the vaccination programme at the time these children developed IPD.

In adults over 65 years of age, a total of 426 episodes of IPD were registered (Table 8.29), including 22 cases of meningitis. This is equivalent to an incidence rate of IPD of 33.8 cases per 100,000 in this age group. The three cases of meningitis caused by *S. pneumoniae* serotype 23B resistant to benzylpenicillin were amongst people in this age group. Four including the cases associated with meningitis, BSIs in this age group were caused by pneumococcal isolates resistant to benzylpenicillin, with 3 out 4 isolates belonging to serotype 23B.

**Conclusions**

The incidence of IPD in 2025 has increased to 11.9 cases per 100,000 population, following the lower incidence observed from 2020-2022 as a result of the Covid-19 restrictions in place during that period. Thirteeen isolates in total were categorised as resistant to benzylpenicillin, 1.9% of all culture-positive pneumococci. Benzylpenicillin-resistant isolates were most frequently observed amongst seroytpe 23B, with 44% of isolates (n=7) classified as such, and a further 4 out of 16 serotype 23B isolates were categorised as I. Resistance to benzylpenicillin was observed in 6% of isolates belonging to serotype 9N (n=4). There was one episode of IPD caused by serotype 9V, and this isolate was resistant to benzylpenicillin. Resistance to benzylpenicillin was observed in 2 isolates (3.4%) causing meningitis. Thirty-seven isolates were categorised as susceptible to benzylpenicillin with increased exposure, equivalent to 5.3% of all isolates. In total, 50 isolates were found either to have susceptibility to penicillin at increased exposure, or to be resistant to penicillin, and so categorised as PNSP. This equates to 7.2% of all culture-positive *S. pneumoniae* isolates, in comparison to 6.3% of isolates in 2024 and 6% of isolates in 2023.

**Table 8.29 IPD amongst people aged 65 years or older and vaccine coverage** DANMAP 2025

| IPD amongst persons aged 65 years and over | Number (%) |
|---|---|
| Total cases | 426 (100) |
| IPD cases caused by serotypes included in PPV-23 | 281 (66) |
| IPD cases caused by serotypes included in PCV-20 | 243 (57) |
| IPD cases caused by serotypes included in PCV 21 | 344* (81) |

* 85 cases of IPD caused by serotypes found in the PCV21 alone, including 6 isolates resistant to benzylpenicillin.

**Table 8.30 Serotypes accociated with benzylpenicillin resistance and sample site of isolation** DANMAP 2025

| Serotypes associated with benzypenicillin resistance | Number and sample site |
|---|---|
| 23B | 7-4 BSI alone<br>3 meningitis* |
| 9N | 4-BSI |
| 24F | 1-BSI |
| 9V | 1-BSI |

* 2 culture positive, 1 DNA detected with concurrent BSI.

Two changes in the Danish pneumococccal vaccination programme occurred in 2025, the PCV15 replaced the PCV13 in the childhood vaccination programme including serotypes 22F and 33F for children for the first time, and the PCV21 was authorised for use. The PCV21 includes serotypes which previously were not covered by other available vaccines, and covers 81% of the serotypes which caused IPD in those aged 65 years and older. Three out of four serotypes which were associated with resistance to benzylpenicillin are included in the PCV-21. The effects of these vaccines on the incidence of IPD as well as rates of PNSP in Denmark, remains to be seen, but will be closely monitored and included in future editions of DANMAP.

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### 8.3.6 *Neisseria gonorrhoeae*

*Neisseria gonorrhoeae* is the causative agent of the sexually transmitted infection gonorrhoea, which is usually located in the urethra in males and cervix in females. *N. gonorrhoeae* (gonococci) may also sometimes be demonstrated in specimens from the pharynx or rectum in either gender. In females, the finding of gonococci in ano-rectal specimens is usually due to contamination with vaginal secretion, while in men who have sex with men (MSM) it is due to unprotected anal sex leading to infection. In both genders, the condition is generally asymptomatic. Pharyngeal gonorrhoea is virtually always asymptomatic.

Complications of gonorrhoea include, e.g., salpingitis, epididymitis, orchitis, and prostatitis. Furthermore, conjunctivitis may occur in new-borns after transmission from an infected mother during labour and rarely in adults following direct or indirect inoculation. Rarely, gonococci cause bacteraemia with various manifestations from skin and connective tissue, and they may also cause purulent arthritis and sometimes reactive arthritis.

**Gonococcal surveillance**

Since 1962, the departments of clinical microbiology (DCMs) in Denmark have voluntarily submitted isolates of gonococci to the Neisseria and Streptococcus Reference (NSR) laboratory at Statens Serum Institut for national surveillance of antimicrobial resistance. While culture of primary specimens had been undertaken by all DCMs for many decades, the Mid Jutland Region and the Capital Region discontinued doing so in 2021 and 2022, respectively. Since then, the primary specimens from these regions are sent to NSR for culture and susceptibility testing.

Repetitive detections of gonococci in a patient are considered to represent unique cases of gonorrhoea if separated by more than 21 days. The same distinction is applied when enumerating unique episodes of testing.

Isolates with intermediary susceptibility are non-existing according to EUCAST breakpoints for ceftriaxone and azithromycin. Such isolates are exceedingly rare regarding ciprofloxacin, and for this antibiotic, resistant and intermediary susceptible isolates, i.e. susceptible at higher dosage, were categorized as resistant in this report.

As part of NSR's participation in ECDC's surveillance (Euro-GASP) of sexually transmitted infections since 2009, approximately 100-200 gonococcus isolates are collected consecutively each year in September-October and investigated for susceptibility to an expanded panel of antimicrobial agents. This panel includes cefixime and in selected years also tetracycline, spectinomycin, and sometimes gentamicin.

**Results and discussion**

The annual number of received examined isolates increased considerably from 2011 through 2017 (Figure 8.25). This was most likely due to the widespread use of combined nucleic acid amplifications tests (NAATs) for *Chlamydia trachomatis* and *N. gonorrhoeae* which have identified unexpected cases of gonorrhoea (sometimes followed by culture), and also to an increasing incidence of gonorrhoea, especially among young heterosexual persons, among whom an increasing proportion until 2016 were women. The proportion of female cases has decreased slightly since 2017, but it is still substantially higher than in the beginning of the observation period (2003-2016). A decrease in the annual number of isolates from unique cases was seen in 2018 followed by an increase in 2019-2021 and in particular from 2021 to 2023 (Pedersen *et al.*, 2024).

In 2025, there were 343,263 episodes of testing for gonococci (365,263 in 2024), for the most part consisting of dual testing for gonococci and *C. trachomatis*. Among these episodes of testing, 5,135 were positive for gonococci (5,108 in 2024), including 1,893 unique episodes of positive cultures (1,852 in 2024). The NSR laboratory performed susceptibility testing on isolates from 1,797 unique cases of gonorrhoea (1,301 males and 496 females). Only one isolate from each unique case is counted in this report. There were 735 cases which had been cultured at the DCMs, and 1,062 cases which had been cultured at the NSR.

If more than one isolate is received from a unique episode of gonorrhoea, the following hierarchy of the isolates are used, in accordance with the ECDC guidelines for Euro-GASP:

Males:
1. Pharyngeal
2. Rectal
3. Urethral
4. Other

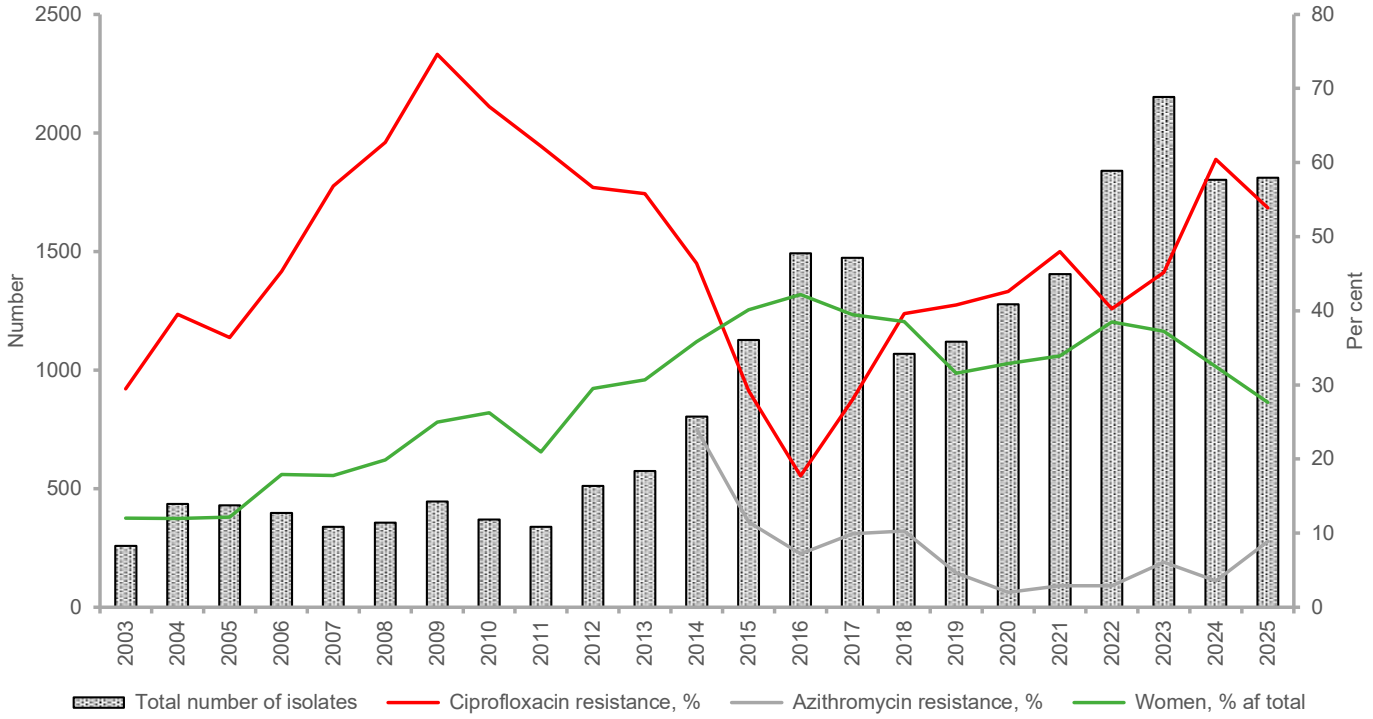
Females:
1. Pharyngeal
2. Cervical
3. Other anogenital (high vaginal swab/rectal/urethral)
4. Other

Among the 1,797 isolates from males and females included in this report for 2025, 1,376 were from urogenital sites, 148 from anorectal areas, 82 from pharynx, three from blood, three from conjunctiva, one from joint fluid, and 184 from uninformed or other anatomical sites. The high number of uninformed sites is mainly caused by sparse details given in electronic information accompanying the isolates.

The ciprofloxacin resistance rate was 54% in 2025 (61% in 2024, 63% in 2023 and 40% in 2022), (Figure 8.25). As in 2024, only 0.4% of the isolates were classified as ciprofloxacin susceptible, increased exposure (MIC 0.047-0.064 mg/L).

Azithromycin resistance (MIC above the present ECOFF >1 mg/L) was found in 9% of the tested isolates (3.5% in 2024 and 6% in 2023).

**Figure 8.25 Number of examined gonococcus isolates from unique cases of gonorrhoea in males and females, and the percentage of isolates with ciprofloxacin resistance and azithromycin resistance, Denmark, 2003-2025** DANMAP 2025




Ceftriaxone resistant gonococci (MIC >0.125 mg/L) as well as ceftriaxone treatment failure in patients with gonorrhoea have occurred in several countries during recent years. As shown in Figure 8.26, the ceftriaxone MIC distribution changed from 2003 through 2009 with the highly susceptible isolates becoming gradually less frequent. However, since then, this change has completely reversed. In 2017, there was a single case among the submitted isolates with ceftriaxone MIC of 0.25 mg/L (i.e., resistant) and azithromycin MIC of 0.25 mg/L. Secondary cases were not reported and no strains with ceftriaxone resistance have been encountered among the submitted isolates during 2017-2024.

In 2025, however, gonococci with ceftriaxone MIC at 0.19 and 0.25 mg/L were detected in urethral specimens from two males, who had acquired the infection in Asia. They were treated with ceftriaxone 500 mg i.m. An additional similar urethral isolate (ceftriaxone MIC 0.19 mg/L; aalso acquired in Asia) was detected in January 2026. The patient was cured by ceftriaxone 1000 mg i.m. Whole genome sequencing revealed that the three strains were not genotypically related.

Ceftriaxone resistant gonococci are particularly common in Cambodia and Viet Nam.

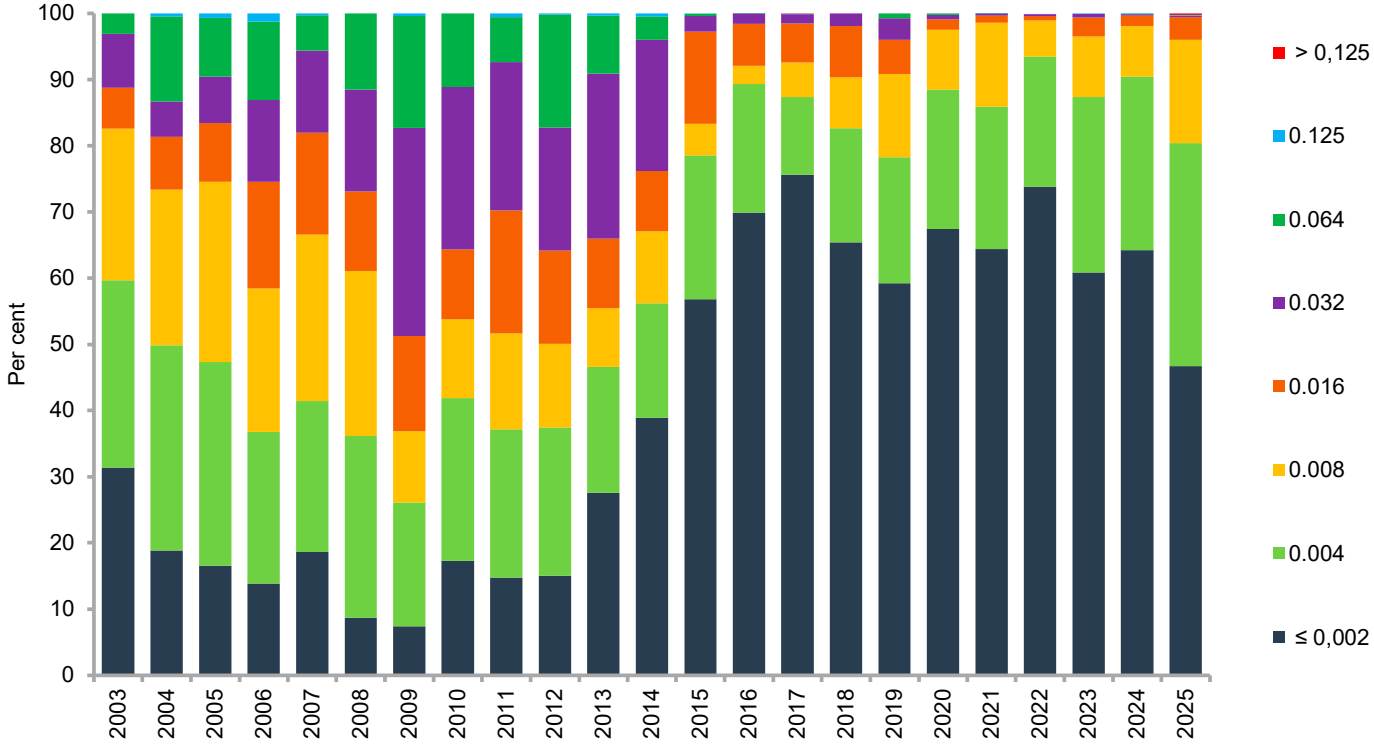
The Danish National Board of Health issued guidelines in 2015 for the diagnosis and treatment of sexually transmitted infections. A combination of high dose ceftriaxone (500 mg i.m.) and azithromycin (2 g p.o.) was recommended for the empiric treatment of gonorrhoea. This therapeutic regimen has gradually been abandoned during 2019 and onwards by most clinicians.

In 2025, the SSI recommended to increase the standard dose of ceftriaxone to 1000 mg i.m. (https://en.ssi.dk/news/epi-news/2025/no-41---2025).

Ciprofloxacin (500 mg p.o. as a single dose) may still be used for treatment if the strain is fully susceptible and if appropriate investigation has excluded pharyngeal gonorrhoea.

**Figure 8.26 Distribution of ceftriaxone MIC (mg/L) values in gonococci, Denmark, 2003–2025**

DANMAP 2025




### Participation in Euro-GASP

In a subset of 200 isolates tested as part of the Danish participation in Euro-GASP, resistance against cefixime (MIC >0.125 mg/L) was 0% like in 2023 (it was 1% in 2024, Figure 8.27. Cefixime is an oral cephalosporin that has never been used in Denmark.

Resistance against tetracycline (MIC >0.5 mg/L) was 50% (23% in 2024 and 33% in 2023), Figure 8.28. Susceptibility testing against spectinomycin and gentamicin are only performed in selected years and was not carried out in 2023 and 2024. The results for 2025 are shown in Table 8.31.

### Resistance findings by gender and anatomical origin of the isolates

In males, the ciprofloxacin resistance rate was slightly higher in anorectal and pharyngeal isolates than in urogenital isolates. In females, there was no substantial difference when comparing isolates from different sites of infections (Table 8.32).

In males as well as in females, the azithromycin resistance rate was substantialy higher in pharyngeal isolates than in anorectal and urogenital isolates (Table 8.33).

**Table 8.31 Susceptibility results for spectinomycin and gentamicin, 200 isolates in Euro-GASP 2025 (number of isolates)**

DANMAP 2025

| | MIC values (mg/L) | | | | | Breakpoint (mg/L) |
|---|---|---|---|---|---|---|
| | 1 | 2 | 4 | 8 | 16 | |
| Spectinomycin | 0 | 0 | 2 | 158 | 40 | S ≤1024 |
| Gentamicin | 3 | 79 | 118 | 0 | 0 | Not determined |

**Figure 8.27 Distribution of gonococcal isolates according to MIC values for cefixime; number of isolates (total number: 132 in 2023, 201 in 2024 and 200 in 2025). Breakpoint for susceptibility to cefixime, 0.125 mg/L** DANMAP 2025

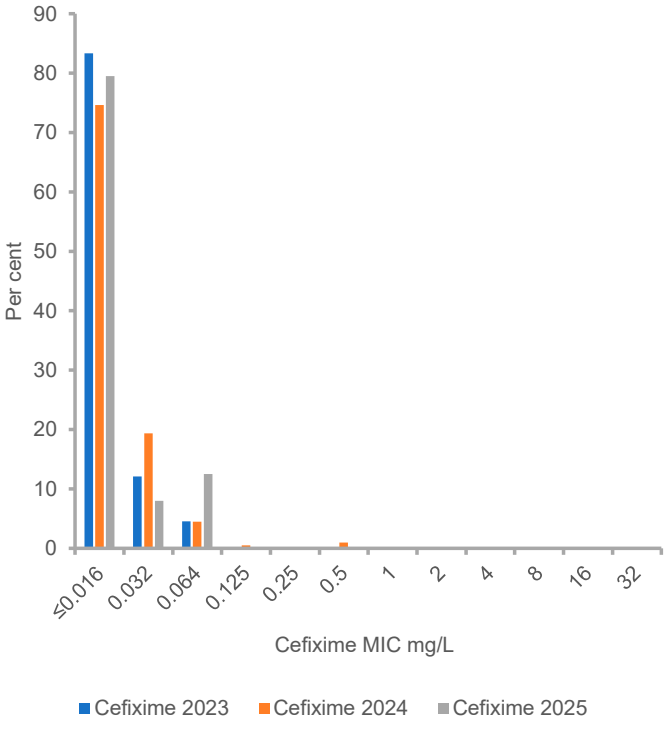



**Figure 8.28 Distribution of gonococcal isolates according to MIC values for tetracycline; number of isolates (total number: 132 in 2023, 201 in 2024 and 200 in 2025). Breakpoint for susceptibility to tetracycline, 0.5 mg/L** DANMAP 2025

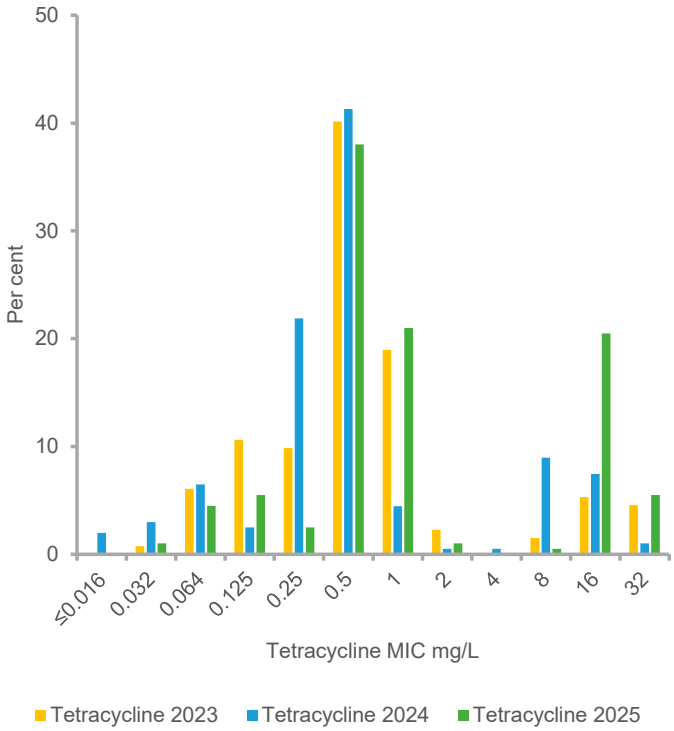



**Table 8.32 Ciprofloxacin resistance rates by gender and anatomical origin of the isolates, 2025** DANMAP 2025

| | Males | | Females | | Total | |
|---|---|---|---|---|---|---|
| | No. resistant / total no. | % resistant | No. resistant / total no. | % resistant | No. resistant / total no. | % resistant |
| Urogenital | 533 / 972 | 55 | 200 / 404 | 50 | 733 / 1,376 | 53 |
| Anorectal | 79 / 135 | 59 | 8 / 13 | 62 | 87 / 148 | 59 |
| Pharynx | 35 / 60 | 58 | 11 / 22 | 50 | 46 / 82 | 56 |
| Blood | 1 / 3 | 33 | 0 / 0 | - | 1 / 3 | 33 |
| Eye | 2 / 3 | 67 | 0 / 0 | - | 2 / 3 | 67 |
| Other or unknown | 73 / 128 | 57 | 28 / 57 | 49 | 101 / 185 | 55 |
| Total | 723 / 1,301 | 56 | 247 / 496 | 50 | 970 / 1,797 | 54 |

**Table 8.33 Azithromycin resistance rates by gender and anatomical origin of the isolates, 2025** DANMAP 2025

| | Males | | Females | | Total | |
|---|---|---|---|---|---|---|
| | No. resistant / total no. | % resistant | No. resistant / total no. | % resistant | No. resistant / total no. | % resistant |
| Urogenital | 76 / 972 | 7.8 | 40 / 404 | 9.9 | 116 / 1,376 | 8.4 |
| Anorectal | 7 / 135 | 5.2 | 1 / 13 | 7.7 | 8 / 148 | 5.4 |
| Pharynx | 9 / 60 | 15 | 5 / 22 | 22.7 | 14 / 82 | 17.1 |
| Blood | 0 / 3 | 0 | 0 / 0 | - | 0 / 3 | 0 |
| Eye | 0 / 3 | 0 | 0 / 0 | - | 0 / 3 | 0 |
| Other or unknown | 17 / 128 | 13.3 | 7 / 57 | 12.3 | 24 / 185 | 13 |
| Total | 109 / 1,301 | 8.4 | 53 / 496 | 10.7 | 162 / 1,797 | 9 |

**Conclusions**

The overall ceftriaxone MIC distribution was unchanged, except for the finding of two isolates with MIC values at 0.19 and 0.25 mg/L, both of which were diagnosed in males infected in South-East Asia. Whole genome sequencing revealed that that the two strains were not identical. The ciprofloxacin resistance rate was a little lower (54%) than in 2024 (61%) and in 2023 (63%) but still substantially higher than in 2022 (40%).

Although resistance problems among gonococci are still not present in Denmark, the frequent emergence globally of gonococcal resistance to antibiotics underlines the importance of maintaining the centralised national surveillance of antimicrobial resistance in gonococci. It is of the utmost importance to detect import of such strains as well as intra-country spread.

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### 8.3.7 *Haemophilus influenzae*

**Background**

*Haemophilus influenzae* commonly colonises the upper respiratory tract, with carriage varying by age. It is a frequent cause of respiratory tract infections, while invasive disease is infrequent. Invasive infections mainly affect young children and older adults, particularly those with underlying conditions such as chronic obstructive pulmonary disease or cancer. Most cases present as bacteraemia or sepsis, whereas meningitis is less frequent.

*H. influenzae* is divided into six encapsulated serotypes (a-f; Hia, Hib, Hic, Hid, Hie and Hif) as well as non-encapsulated strains, referred to as non-typeable *H. influenzae* (NTHi). Since the introduction of the type b conjugate vaccine in 1993, invasive disease caused by Hib has declined substantially. As a result, NTHi and non-b serotypes now account for a larger proportion of cases.

Antimicrobial resistance in *H. influenzae* is an increasing concern, especially for beta-lactam antibiotics. Resistance arises through a combination of beta-lactamase production and alterations in penicillin-binding proteins, primarily PBP3, encoded by the *ftsI* gene. Based on the presence or absence of these resistance mechanisms, isolates are commonly categorized as BLNAS, BLNAR, BLPAR, or BLPACR.

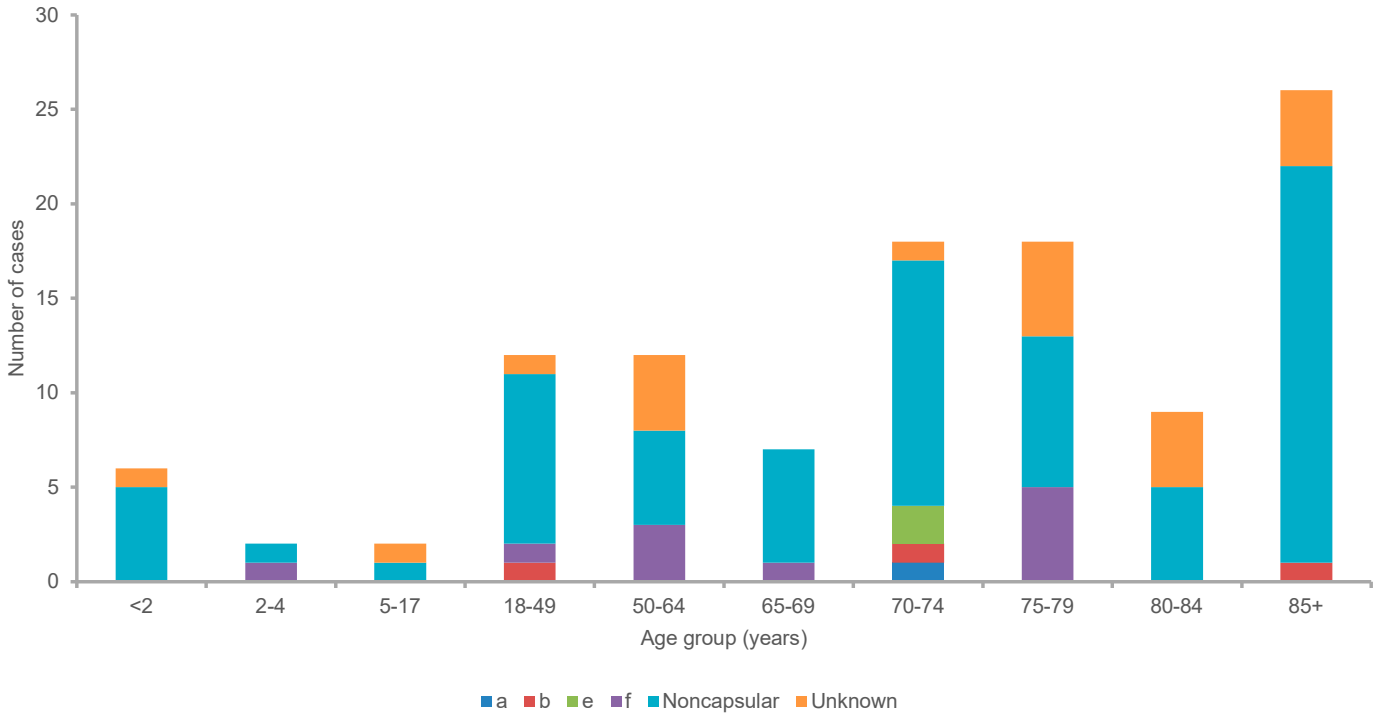
**Surveillance of *Haemophilus influenzae***

In Denmark, invasive *H. influenzae* infections are monitored through submission of clinical isolates to Statens Serum Institut (SSI). Cases without available clinical isolates are identified via MiBa. At SSI, isolates are analysed using whole-genome sequencing to determine serotype, sequence type, and genetic determinants of beta-lactam resistance. Phenotypic susceptibility data for beta-lactam antibiotics are retrieved from MiBa when available.

**Results**

In 2025, a total of 112 invasive H. influenzae cases were registered based on isolates from blood and cerebrospinal fluid. *H. influenzae* was isolated by culture from cerebrospinal fluid in five cases, four of which also had concurrent bacteraemia. The remaining 107 cases were based on isolates from blood. Patient age and serotype distribution of cases are shown in Figure 8.29.

**Figure 8.29 Distribution of invasive *H. influenzae* cases by age group and serotype (a, b, e, and f), Denmark, 2025** DANMAP 2025



Capsule type was available for 91 of 112 cases. NTHi was the most common, accounting for 74 cases (81%). Among the encapsulated isolates, Hif was the most frequent (11 cases; 12%), followed by Hib (3 cases; 3%), Hie (2 cases; 2%), and Hia (1 case; 1%). Among the five meningitis cases, three were NTHi, one was Hif, and one was Hie.

Overall, susceptibility to penicillin/ampicillin was high (79%) (Table 8.34). Resistance to ciprofloxacin and ceftriaxone was each observed in a single isolate. WGS data were available for 98 cases, of which 12 harboured the TEM-1 beta-lactamase gene, all of these were phenotypically resistant to ampicillin.

**Table 8.34 Phenotypic resistance against penicillin/ampicillin in *Haemophilus influenzae*, Denmark, 2025** DANMAP 2025

| Sensitivity | Number (%) |
|---|---|
| Resistant | 24 (21) |
| Susceptible | 88 (79) |
| Total | 112 |

A comparison between phenotypic beta-lactam susceptibility and underlying resistance mechanisms (BLNAS, BLPAR, BLNAR, and BLPACR) is presented in Table 8.35.

**Table 8.35 Phenotypic resistance against penicillin/ampicillin vs. beta-lactam resistance mechanism in *Haemophilus influenzae*, Denmark, 2025** DANMAP 2025

| Beta-lactam resistance mechanism | Pen/ampi resistant | Pen/ampi susceptible | Total (%) |
|---|---|---|---|
| BLNAS | 1 | 73 | 74 (76) |
| BLNAR | 10 | 3 | 13 (13) |
| BLPAR | 10 | 0 | 10 (10) |
| BLPACR | 1* | 0 | 1 (1) |
| Total | 21 | 76 | 98 |

BLNAS = beta-lactamase-negative, ampicillin-susceptible; BLPAR = beta-lactamase-positive, ampicillin-resistant; BLNAR = beta-lactamase-negative, ampicillin-resistant; BLPACR = beta-lactamase-positive, amoxicillin-clavulanic acid-resistant.
* Isolate R to amoxicillin-clavulanic acid.

Most isolates were categorized as BLNAS (74/98; 76%) and they were almost exclusively phenotypically susceptible to penicillin/ampicillin. In contrast, BLNAR (13%), BLPAR (10%), and BLPACR (1%) were associated with phenotypic resistance. Overall concordance between phenotypic susceptibility and genotypic resistance mechanisms was 96%.

**Conclusions**

In 2025, a total of 112 invasive *H. influenzae* cases were registered based on isolates from blood and cerebrospinal fluid. The majority of cases were caused by NTHi (81%), while Hif was the most frequent encapsulated serotype (12%) and Hib remained rare. Overall, susceptibility to penicillin/ampicillin was high. Resistance was primarily associated with BLNAR (13%) and BLPAR (10%), with one isolate exhibiting a BLPACR resistance mechanism.

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### 8.3.8 *Neisseria meningitidis*

**Introduction**

*Neisseria meningitidis* (meningococci) are capable of causing invasive meningococcal disease (IMD), usually meningitis or septicaemia or both, which may be life threatening and may cause permanent neurological sequelae. Asymptomatic throat carriage is very frequent and only rarely leads to invasive disease. IMD is usually treated with intravenous penicillin or ceftriaxone. Single-dose ciprofloxacin may be used for prophylaxis to close contacts to patients with IMD.

Meningococci are classified into serological groups (A, B, C, W, X, Y, Z, and 29E) according to antigenic properties of the polysaccharide capsule. In Denmark, serogroups B and C are the most frequent ones in most years, although serogroup W was quite frequent in 2016 through 2019 and serogroup Y has been increasingly prevalent during 2023-2025. Vaccination against meningococci has never been part of the Danish childhood immunization programme but is used for prophylaxis to close contacts to patients with IMD. Specific vaccines exist for group B and combined vaccines for groups A, C, W, and Y.

This report presents data on antimicrobial resistance in non-duplicate invasive isolates (i.e., usually from blood or cerebrospinal fluid) submitted from the departments of clinical microbiology (DCMs) during 2012-2025 to the Neisseria and Streptococcus Reference laboratory (NSR). Isolates are received from all DCMs in Denmark. As of November 1, 2023, it became mandatory to submit isolates of meningococci, but the coverage rate until then was estimated to be 100% when compared to the mandatory clinical notification system. The two surveillance systems continuously supplement each other.

**Results**

During the years 2012 through 2019, 18 to 52 isolates were received annually. In 2020, where restrictions to counteract the spread of COVID-19 were implemented, the number was 14, decreasing to 8 and 11, respectively, in 2021 and 2022. Figure 8.30 shows the number of isolates of groups B, C, W, and Y received during 2012-2025. In 2025 the reference laboratory received 25 isolates, of which 10 were serogroup B, 3 were serogroup W, and 12 were serogoup Y. Because of low numbers the following have been omitted: One isolate of group 29E (2017), three isolates of group X (2016, 2019 and 2023), and two isolates which were non-groupable (2019 and 2023). The susceptibility pattern of these four isolates did not show any specific deviations from the remaining findings and are therefore not further included in the present report.

**Figure 8.30 Number and serogroup of meningococcal isolates received during 2012-2025** DANMAP 2025

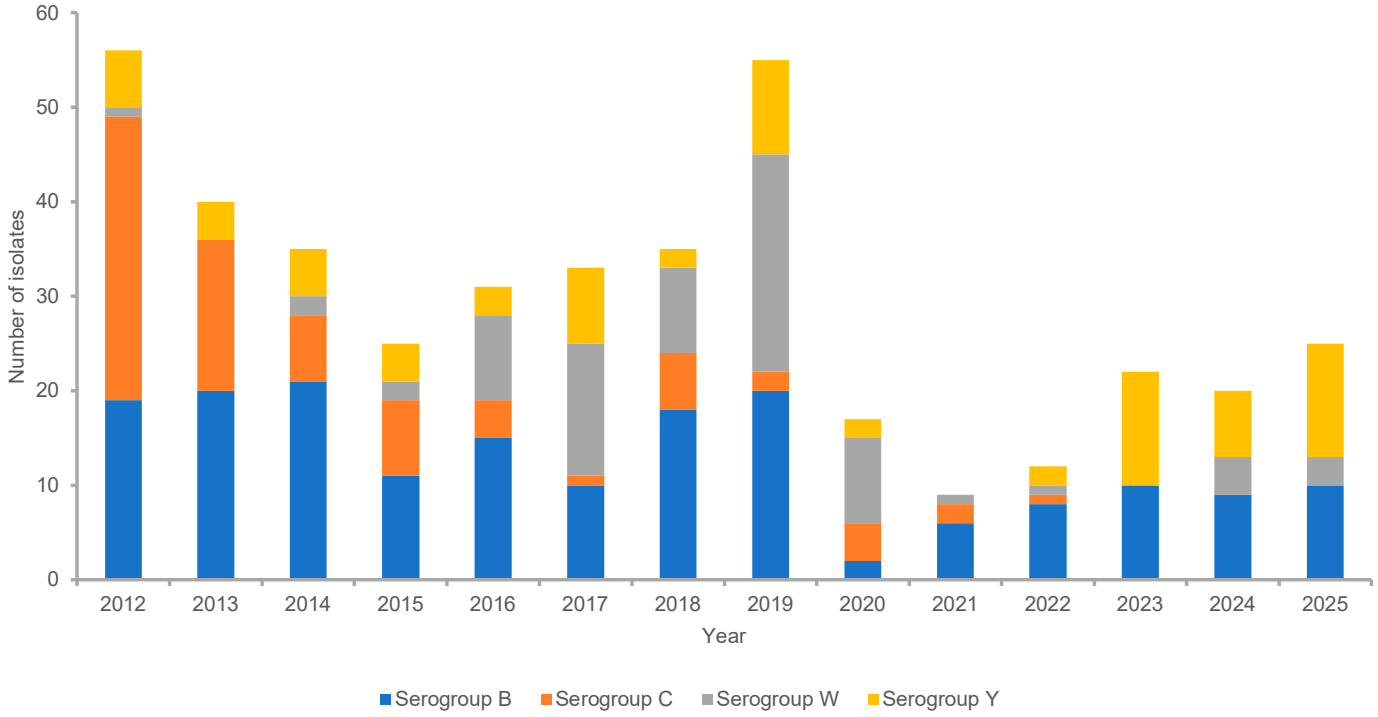



**Figure 8.31 Distribution of ceftriaxone MIC values (mg/L) by serogroup, 2012-2025** DANMAP 2025

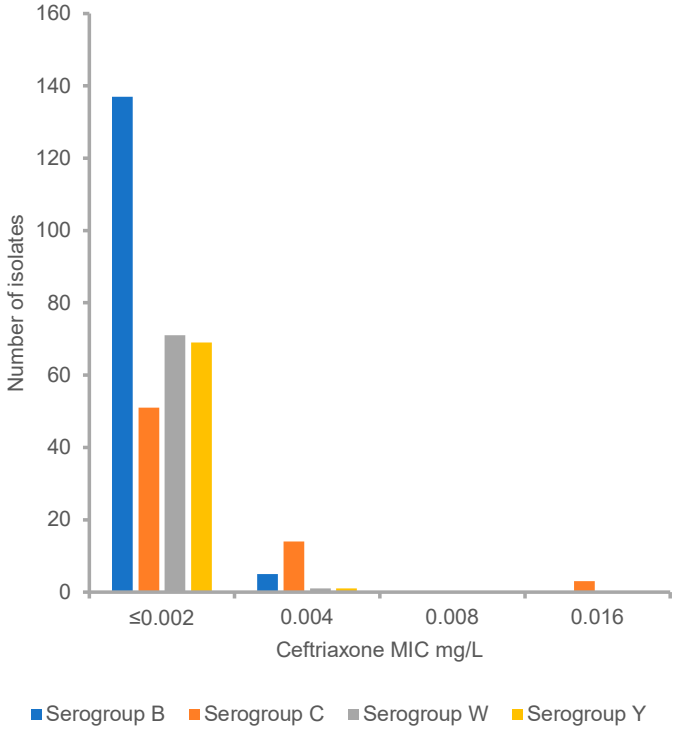



**Figure 8.32 Distribution of ciprofloxacin MIC values (mg/L) by serogroup, 201-2025** DANMAP 2025

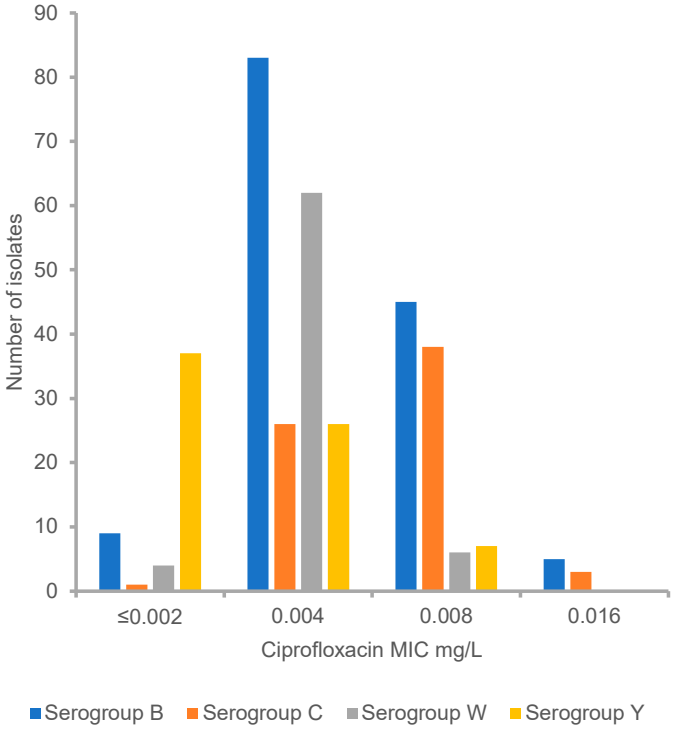


**Figure 8.33 Distribution of penicillin MIC values (mg/L) by serogroup, 2012-2025** DANMAP 2025

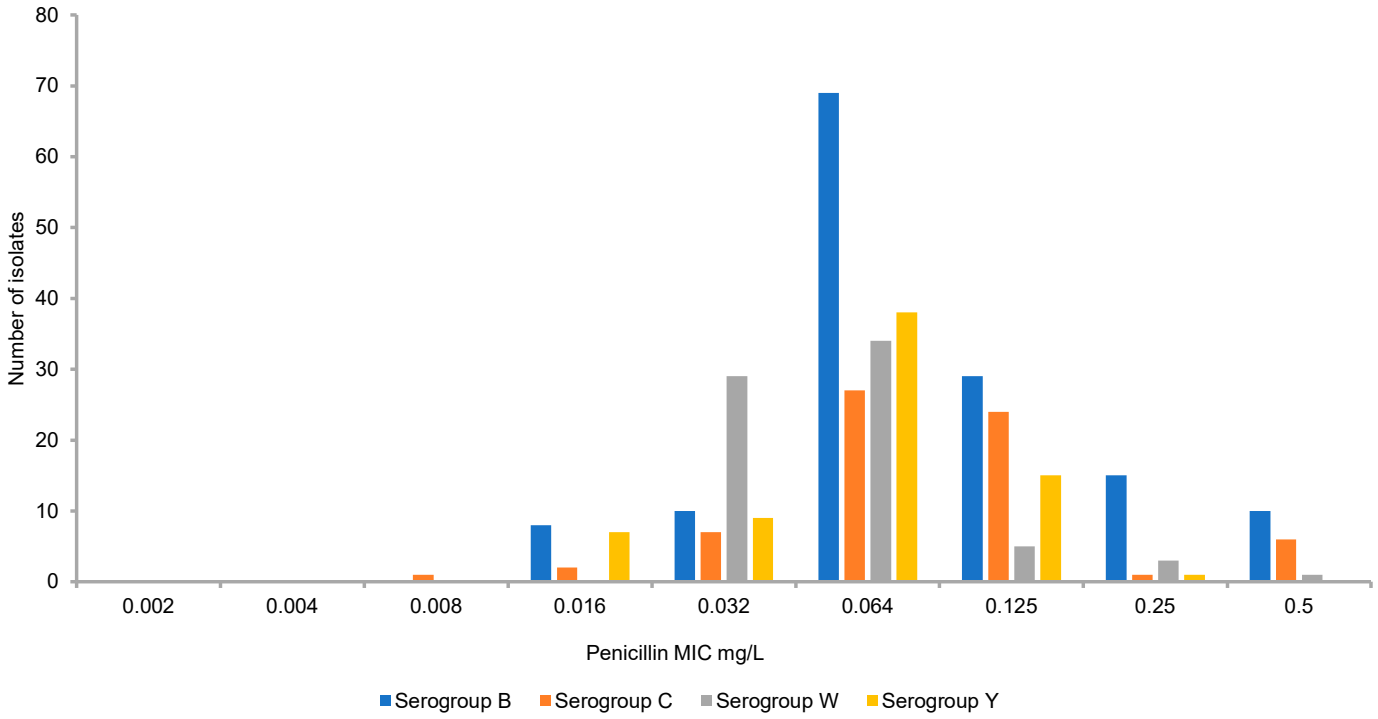



**Table 8.36 Number of penicillin-resistant meningococcal isolates (MIC >0.25 mg/L), serogroups B, C, and W, 2013-2025** DANMAP 2025

| | 2013 | 2014 | 2016 | 2017 | 2018 | 2020 | 2022 | 2023 | 2024 | 2025 |
|---|---|---|---|---|---|---|---|---|---|---|
| Serogroup B | 1 | 2 | 1 | 2 | - | - | 1 | 1 | 1 | 2 |
| Serogroup C | - | 1 | - | - | 2 | 3 | - | - | - | - |
| Serogroup W | - | - | - | - | - | - | - | - | - | 1 |

All isolates were susceptible to ceftriaxone (MIC ≤0.125 mg/L), Figure 8.31.

All isolates were susceptible to ciprofloxacin (MIC ≤0.016 mg/L), Figure 8.32. Isolates of serogroup W (none in 2023 and 4 in 2024) and serogroup Y (11 in 2023 and 7 in 2024) tended to have slightly lower levels of ciprofloxacin MIC values than isolates of serogroup C.

In total, 95% of the isolates during the study period were susceptible to penicillin (MIC ≤0.25 mg/L), Figure 8.33.

Eleven isolates of serogroup B, six isolates of serogroup C, and one isolate of group W were penicillin-resistant (MIC >0,25 mg/L), Table 8.36.

**Comments and conclusions**

The substantial decrease of received meningococcal isolates during and following 2020 is most likely due to the social restrictions implemented in April 2020 because of the COVID-19 pandemic. Likewise, the modest increase during 2023 and also in 2024-2025 probably represents the impact of the lifting of the restrictions which have enabled more respiratory transmission than during the preceding 2-3 years.

The antibiotic susceptibility patterns of meningococci do not reveal any imposing threats of resistance.

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### 8.3.9 *Shigella* spp.

**Introduction**

*Shigella* spp. is an enteroinvasive bacterium causing shigellosis, a gastrointestinal infection in humans characterized by diarrhea, abdominal pain and general malaise. The genus *Shigella* includes four species, *S. dysenteriae*, *S. flexneri*, *S. boydii*, and *S. sonnei*. The predominating Shigella species in Denmark are *S. sonnei* and *S. flexneri*. Infections occur through fecally contaminated food or drinking water and are therefore particularly associated with poor sanitation and poor food hygiene, but may also occur via direct contact, e.g. among children in day care or in adults through sexual contact. Shigellosis is usually a self-limiting infection that typically lasts five to seven days. In more severe cases or in case of prolonged diarrhea the recommended antimicrobial is azithromycin. Infections caused by *Shigella* or Enteroinvasive *Escherichia coli* (EIEC) are mandatory reportable in Denmark.

**Results**

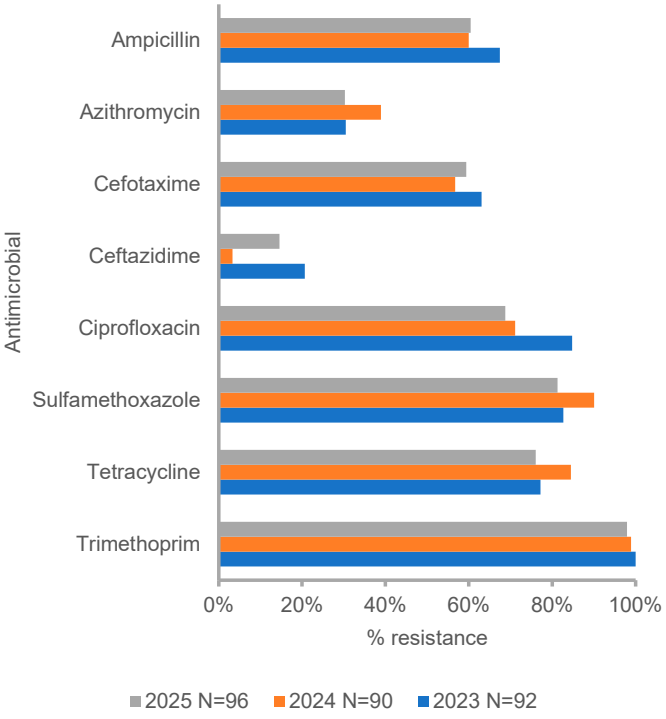
In 2025, 802 cases of shigellosis and EIEC were registered in Denmark. The primary PCR-based diagnostics do not distinguish between *Shigella* spp. and EIEC, but the species is determined for the subset of cases where an isolate is referred to the reference laboratory at SSI. The Danish cases consist of sporadic cases and small outbreak clusters, including outbreaks associated with sexual transmission within men who have sex with men (MSM).

This report presents antimicrobial resistance (AMR) data for the years 2023 to 2025 for *S. sonnei* and *S. flexneri*. In 2025, the reference laboratory at SSI tested 96 *S. sonnei* and 27 *S. flexneri* isolates from patients for AMR. Travelling abroad before onset of disease was recorded for 61% (59/96) of the *S. sonnei* and 63% (17/27) of the *S. flexneri* cases. The remaining cases were not travel related or lacked information about travel status. The number of isolates tested for susceptibility and the travel pattern of the patients were overall comparable in the years 2023 to 2025. The antimicrobial susceptibility was established by determination of the minimal inhibitory concentration (MIC) interpreted with epidemiological cut off values.

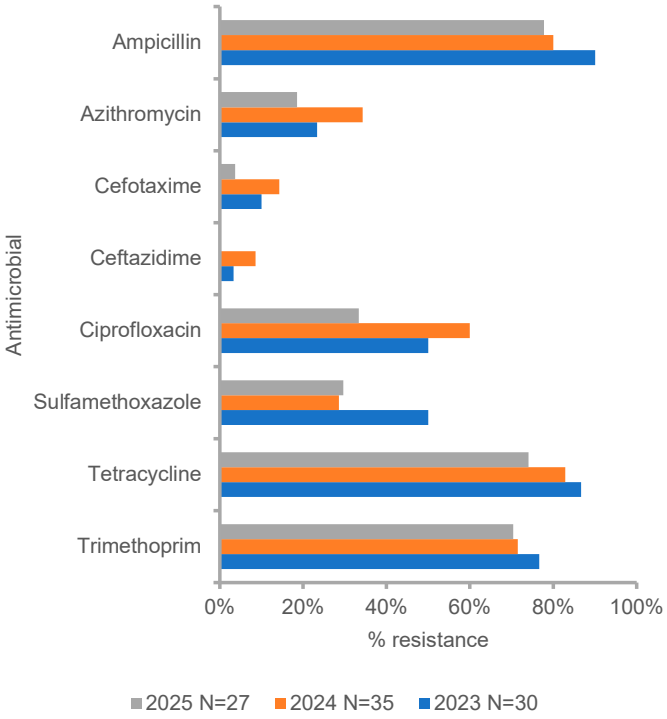
The levels of resistance in *S. sonnei* and *S. flexneri* isolated from patients isolated in 2023-2025 is presented in Figure 8.34. In 2025, 39% of *S. sonnei* and 19% of *S. flexneri*, respectively were resistant to azithromycin and the levels of resistance to the third-generation cephalosporin cefotaxime were 59% in *S. sonnei*, and and 4% in *S. flexneri*, respectively. In 2025 fluoroquinolone resistance was observed in 69% and 29% og *S. sonnei* and *S. flexneri*, respectively. Resistance to ampicillin, sulfamethoxazole, tetracycline and trimethoprim is widespread in both species, whereas resistance towards colistin, gentamicin and carbapenemase (meropenem) rarely is observed (data not shown). For *S. sonnei* there seem to be slightly lover resistance levels in travel associated isolates compared with domestic and isolates with no information of travel. No clear temporal trends in the levels of resistance were observed in the period from 2023 to 2026.

**Figure 8.34 Antimicrobial resistance in percent for *Shigella sonnei* (a) and *S. flexneri* (b) isolated from patients in Denmark, 2023-2025 and resistance in *S. sonnei* from travel associated cases (c)** DANMAP 2025

a)




b)




c)

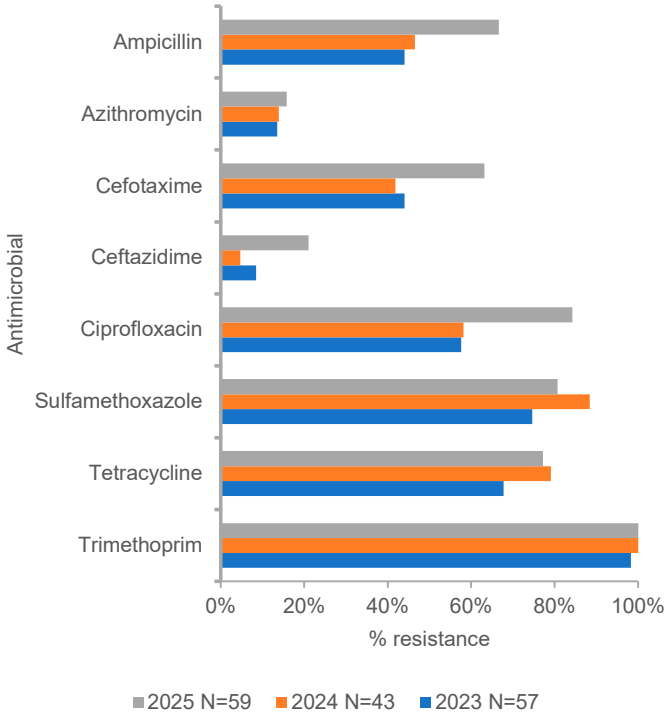


**Figure 8.35 Combinations of resistance in *Shigella sonnei* (a) and *Shigella flexneri* (b) isolates towards azithromycin (AZI), ceftazidime (CAZ), cefotaxime (CTX) and ciprofloxaxin (CIP), 2023-2025, from patients in Denmark** DANMAP 2025

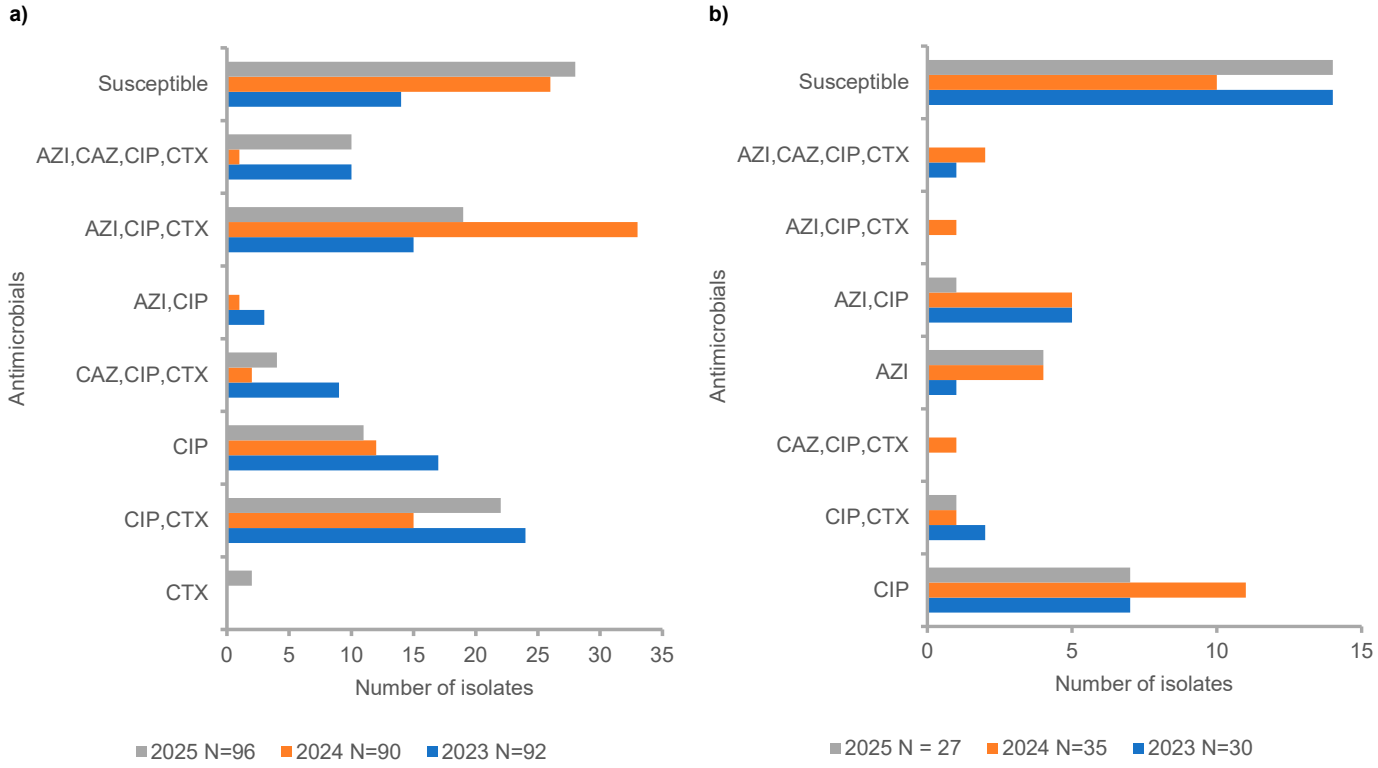



Figure 8.35 is a presentation of combinations of resistance in *Shigella sonnei* (a) and *Shigella flexneri* (b) isolates towards azithromycin (AZI), ceftazidime (CAZ), cefotaxime (CTX) and ciprofloxacin (CIP). It is notable that there is a high number of isolates that simultaneously are resistant towards azithromycin, third generation cephalosporins, and ciprofloxacin, in particular for *S. sonnei*.

**Conclusion**

The levels of resistance observed in the *Shigella* spp. isolates are generally in concordance with the levels that are reported internationally.

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## Textbox 8.1

# Long-term CPE outbreaks at Aalborg University Hospital: persistence in the hospital environment and risk factors for acquisition

A long-term outbreak of NDM-1-producing *Citrobacter freundii* ST18 was first detected at Aalborg University Hospital (AUH) in 2012. [1] The outbreak did subsequently spread to all five Danish regions and is the largest verified CPE outbreak in Denmark as of today (ID41). By the end of 2025, a total of 125 patients had been identified as part of the outbreak, including 12 new cases in 2025. In addition, an outbreak of NDM-1-producing *Klebsiella oxytoca* ST2 (ID1115) has been ongoing at the same hospital since 2022. By the end of 2025, this outbreak had affected 13 patients, including four identified in 2025. [2] Both outbreaks are classified as verified outbreaks in the national CPE surveillance programme.

The two outbreaks have persisted despite extensive infection prevention and control measures. A recent clinical study using data from 2012–2023 compared 69 cases with 552 matched controls and identified several factors associated with infection or colonisation of the *C. freundii* ST18 clone. Prolonged hospitalisation was strongly associated with infection or colonisation, with an odds ratio (OR) of 6.4 for stays exceeding 14 days compared with seven days or less. Intra-abdominal disease and biliary and pancreatic procedures were also strongly associated with infection or colonisation. In-hospital exposure to several antimicrobial classes was associated with increased odds of infection or colonisation, particularly vancomycin (OR 13.9), beta-lactam/beta-lactamase inhibitor combinations (OR 8.8), fluoroquinolones (OR 8.2) and systemic antifungals (OR 8.6). [3]

A root cause analysis investigated the *K. oxytoca* ST2 outbreak by combining repeated environmental sampling with weekly patient screening for more than 450 days. Specific NDM-1-producing *K. oxytoca* ST2 was repeatedly recovered from three toilets, with each toilet harbouring a distinct genomic sub-clade. Four patients hospitalised during the 450-day period were subsequently found to carry isolates closely related to isolates in two of the three sub-clades recovered from the toilets. Detailed hospitalisation data showed that these patients had not been hospitalised concurrently, providing no evidence for direct patient-to-patient transmission. The findings therefore support the contaminated toilets as the most plausible reservoirs for transmission to these patients. [2] Since publication of the study, a total of 13 patients have been associated with the outbreak by the end of 2025.

Several important questions remain unanswered. The precise route by which CPE is transferred from contaminated toilets or plumbing to patients is still unknown. Hypothesised transmission routes include direct contact with contaminated toilet water, transfer via surfaces, or aerosols generated during flushing. However, the available data do not allow these possibilities to be distinguished. The reason why certain CPE strains persist for years in toilets and drainage systems, and why eradication is difficult even when conventional cleaning and disinfection measures are intensified, remains unclear. Future investigations could examine the role of plumbing-associated biofilms, toilet and flushing system design, microbial and chemical conditions within the plumbing environment, and possible selective pressures that may favour long-term persistence. Understanding these factors may be important for developing more effective strategies to eliminate established environmental CPE reservoirs. [2,4]

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**References**

[1] Hammerum AM, Hansen F, Nielsen HL, et al. Use of WGS data for investigation of a long-term NDM-1-producing *Citrobacter freundii* outbreak and secondary in vivo spread of blaNDM-1 to *Escherichia coli*, *Klebsiella pneumoniae* and *Klebsiella oxytoca*. J Antimicrob Chemother. 2016;71(11):3117-3124.
[2] Eriksen HD, Porsbo LJ, Bang B, Ank N, Hasman H. New Delhi metallo-beta-lactamase-1-producing *Klebsiella oxytoca* sequence type 2 from toilets as the likely source of nosocomial transmission to patients - a root cause analysis. Infect Prev Pract. 2025;7(4):100487.
[3] Saarup LH, Andersen KV, Sogaard KK, et al. Risk and prognosis of infection and colonisation by carbapenemase-producing *Citrobacter freundii* in the North Denmark Region during 2012-2023: a matched case-control and cohort study. Infect Prev Pract. 2026;8:100529.
[4] Valzano F, Coda ARD, Liso A, Arena F. Multidrug-Resistant Bacteria Contaminating Plumbing Components and Sanitary Installations of Hospital Restrooms. Microorganisms. 2024;12(1):136.

## Textbox 8.2

# Infection Prevention and Control is a cornerstone in preventing the spread of antimicrobial resistance

In Denmark, there are numerous activities concerning infection prevention and control (IPC) and antimicrobial resistance (AMR) - both on the national, regional and local level as well as at 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, and not least communication about AMR at target group level.

**Danish IPC guidelines**

The Danish IPC guidelines have been in place for many years. All healthcare professionals are expected to be familiar with and act in compliance with local guidelines for IPC. These are based on the national IPC guidelines published by the National Centre for Infection Control at Statens Serum Institut (SSI). The standard infection control precautions, in Danish: "*NIR Generelle forholdsregler for sundhedssektoren*"[1] is the fundament. The transmission-based precautions include specific guidance on Vancomycin-resistant enterococci (VRE), Extended-spectrum beta-lactamases (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, in Danish: "*NIR Supplerende forholdsregler ved infektioner og bærertilstand i sundhedssektoren*"[2]. In case of an outbreak, it is necessary to supplement the standard precautions with transmission-based (isolation) precautions. SSI has in addition issued specific infection control guidance for hospitals, nursing homes and home care, in Danish; "*Infektionshygiejniske retningslinjer for MRSA*"[3] and "*Infektionshygiejniske retningslinjer for CPO*"[4]. 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. The national guidelines on preventing the spread of MRSA and CPO are to be found at the Danish Health Authority website www.sst.dk.

**Danish national action plan (NAP) on AMR**

In Denmark, IPC is for the first time part of the Danish national action plan (NAP) on AMR issued in 2025[5]. The NAP emphasizes the importance of strengthening cooperation between hospitals and municipalities, general practitioners, and practicing specialists to ensure access to IPC guidance and rational use of antibiotics. One out of four prioritized areas are dedicated to IPC with four concrete initiatives. IPC dedicated initiatives include development of e-learning material supporting the education of nursing assistants, revision of the CPO- and MRSA guidelines and a pilot project investigating antimicrobial stewardship and point of care testing (POCT) in Long Term Care Facilities (LTCFs) as an antibiotic saving initiative.

**Nordic collaboration**

In 2025, as part of a Nordic collaboration, Denmark (SSI) and Norway (FHI – Folkehelseinstituttet) have developed a joint report on the screening of resistant microorganisms: "*Helhetlige vurderinger av innkomstscreening for resistente mikrober I Norge og Danmark*"[6]. The main aim of this work has been to examine the evidence base for the screening of resistant microorganisms in order to update the recommendations, focusing on a generic approach to antimicrobial resistance in Denmark and Norway.

**Danish participation in European IPC initiatives**

In June 2023, the European Union recommended stepping up EU actions to combat AMR with a One Health approach. Improving infection prevention and control is one of the main priorities[7]. To support the countries in stepping up the AMR actions the European Commission has invested 50 million Euros in EU-JAMRAI 2 (European Joint Action on Antimicrobial Resistance and Healthcare-Associated Infections) which is a four-year-project (2024-2027)[8] under the EU4health programme[9].

In EU-JAMRAI 2, Denmark participates in work package (WP)5: National Action Plans, WP6: Antimicrobial Stewardship, WP7: Infection Prevention and Control, WP8: One Health Surveillance and WP9: Access to antibiotics. EU-JAMRAI 2 is progressing well, and results are being published on an ongoing basis in scientific literature and presented at the EU-JAMRAI webpage www.eu-jamrai.eu

The aim of WP7 is to improve the 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. Denmark leads the framework recommendations to support implementation of core competencies for IPC in the human sectors. The framework includes the develop-

**continued ... Textbox 8.2**

ment of a competency self-assessment tool (SAS) to support skills assessment and IPC development at individual health care provider level and in the organizations. Activities are carried out in close collaboration with European IPC peers, in addition to international bodies including ECDC, ESCMID/EUCIC, and WHO.

In May 2026, ECDC issued a "Proposal for EU guidance on the establishment and implementation of infection prevention and control programmes in healthcare"[10] to further emphasize the importance of implementing IPC in the countries at all levels (national, hospitals, LTCFs) and including behavior change science in the effort. WP7 provided input to the guidance.

As part of the EU-JAMRAI 2 project, SSI follows a number of IPC implementation activities from around the country. Municipalities, regions, and projects across sectors are represented. SSI is participating in a behavior change implementation project focusing on the use of gloves in close collaboration with Bispebjerg Hospital. In spring 2026, SSI launched a new inspiration site for sharing of materials and tools among healthcare professionals working with IPC in Denmark. This inspiration site supports initiative 9 – strengthening training in IPC - in the Danish NAP on AMR. Read more about the Danish EU-JAMRAI 2 IPC activities at CEI (the Danish National Center for Infection Control) SSI subsite[11].

Denmark's involvement in the EU-JAMRAI 2 - project is well aligned and supports the objectives and indicators in the Danish NAP on AMR at national and international level.

EU-JAMRAI 2 receives funding from the European Union's EU4Health programme under grant agreement n°101127787.

EU-JAMRAI Joint Action Antimicrobial Resistance and Healthcare-Associated Infections

Funded by the European Union

Funded by the European Union. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or the European Health and Digital Executive Agency (HADEA). Neither the European Union nor the granting authority can be held responsible for them.

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**References**

1 https://hygiejne.ssi.dk/NIRgenerelle
2 https://hygiejne.ssi.dk/NIRsupplerende
3 https://hygiejne.ssi.dk/retningslinjer/infektionshygiejniske-retningslinjer-for-mrsa
4 https://hygiejne.ssi.dk/retningslinjer/infektionshygiejniske-retningslinjer-for-cpo
5 https://www.ism.dk/Media/638852182560099312/National%20handlingsplan%20for%20antimikrobiel%20resistens%20hos%20mennesker.pdf
6 https://hygiejne.ssi.dk/retningslinjer/andet-materiale
7 https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32023H0622(01)
8 https://eu-jamrai.eu/
9 https://health.ec.europa.eu/funding/eu4health-programme-2021-2027-vision-healthier-european-union_en
10 https://www.ecdc.europa.eu/en/publications-data/proposal-eu-guidance-infection-prevention-and-control
11 https://hygiejne.ssi.dk/formidling/eu-jamrai-2

## Textbox 8.3

# Fungemia surveillance in Denmark – Update from 2024-2025

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Bloodstream infections with fungi (fungaemia) are most often caused by *Candida* species (candidaemia). Candidaemia occurs predominantly in immunocompromised patients, patients with gastrointestinal surgical conditions and/or critically ill individuals and has a mortality of 35% (8.7-77.3%)[1,2]. Several *Candida* species have recently been formally reclassified but for recognizability, we retain the previous nomenclature[3].

Denmark has conducted fungemia surveillance since 2004, with Departments of Clinical Microbiology submitting fungal isolates to the Mycology Reference Laboratory at Statens Serum Institut. Here we present data from 2024-2025 and compare with preceding years[4-9].

In 2024-2025, we identified 987 isolates from 954 episodes in 886 individuals. The majority of isolates were *C. albicans* and *C. glabrata*, Figure 1. Over the last two years, the incidence declined slightly, from above 9/100,000 inhabitants in preceding years to 8.1 in 2024 and 7.8 in 2025. The highest incidence was observed in elderly men (Figure 2). The decline in incidence remains unexplained and is likely multifactorial.

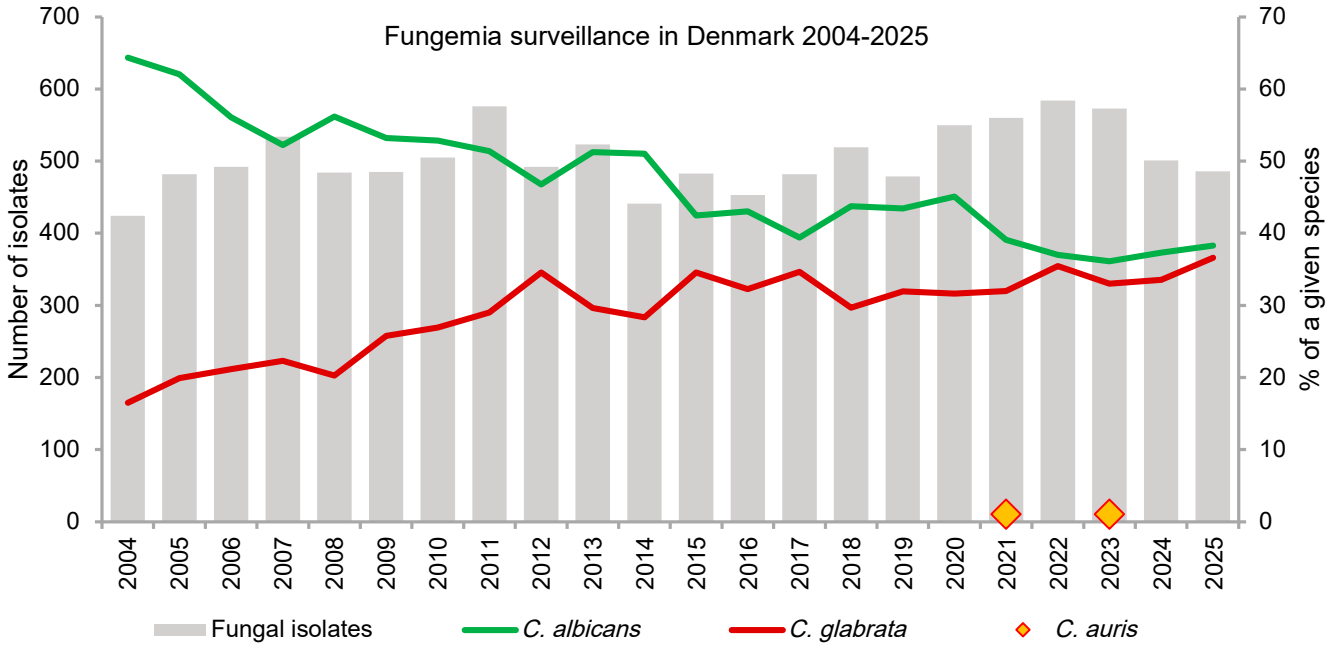
The overall fluconazole susceptibility rate has declined during the surveillance period, from 68.5% in 2004-2007 to 57.6% in 2024-2025[7]. These changes can largely be attributed to the change in species distribution over recent years from 64.4% *C. albicans* and 16.5% *C. glabrata* in 2004[6] to 38.3% *C. albicans* and 36.6% *C. glabrata* in 2024-2025 (Figure 1). Acquired antifungal resistance remain low; acquired fluconazole resistance were detected in 0.5% of *C. albicans*, 6.7% of *C. glabrata*, 6.2% of *C. tropicalis* and 0% in *C. dubliniensis*, *C. krusei* and *C. parapsilosis*. Acquired amphotericin B (AmB) resistance was not observed. However, although *C. lusitaniae* exhibits an AmB minimal inhibitory concentration (MIC) distribution similar to that of other *Candida* spp. (our 23 isolates were in the MIC range from 0.06 to 0.25), the species is not considered a good AmB target. Thus, the overall AmB coverage was 97.4% (950/975 isolates). Acquired echinocandin resistance for *C. glabrata* and *C. albicans* was 1.7% and 0.3% respectively. No bloodstream infections with *C. auris* - or azole-/echinocandin resistant *C. parapsilosis* - were observed in the two-year period.

No major changes in antifungal consumption were observed during 2024-2025, Figure 3. Fluconazole use has declined slowly over the past decade and continues that pattern - in 2025 fluconazole use was down by a third from its peak around 2013. One explanation for the species shift has been the extensive use of fluconazole compared with neighbouring countries[7], yet the beforementioned reduction in fluconazole use has, at least so far, not affected the species shift towards *C. glabrata*. Of note, the abrupt decline in overall use of mould active azoles in 2015, is largely an artifact due to the change in posaconazole DDD definition from 800 mg/day to 300 mg/day, which overinflate the earlier posaconazole use.

In conclusion, acquired antifungal resistance remains low, however, the species shift has increased the proportion of isolates with intrinsically reduced azole susceptibility. The fungemia incidence was slightly lower in 2024-25 compared to the previous years. Of note, *C. auris* candidaemia remains a rare event.

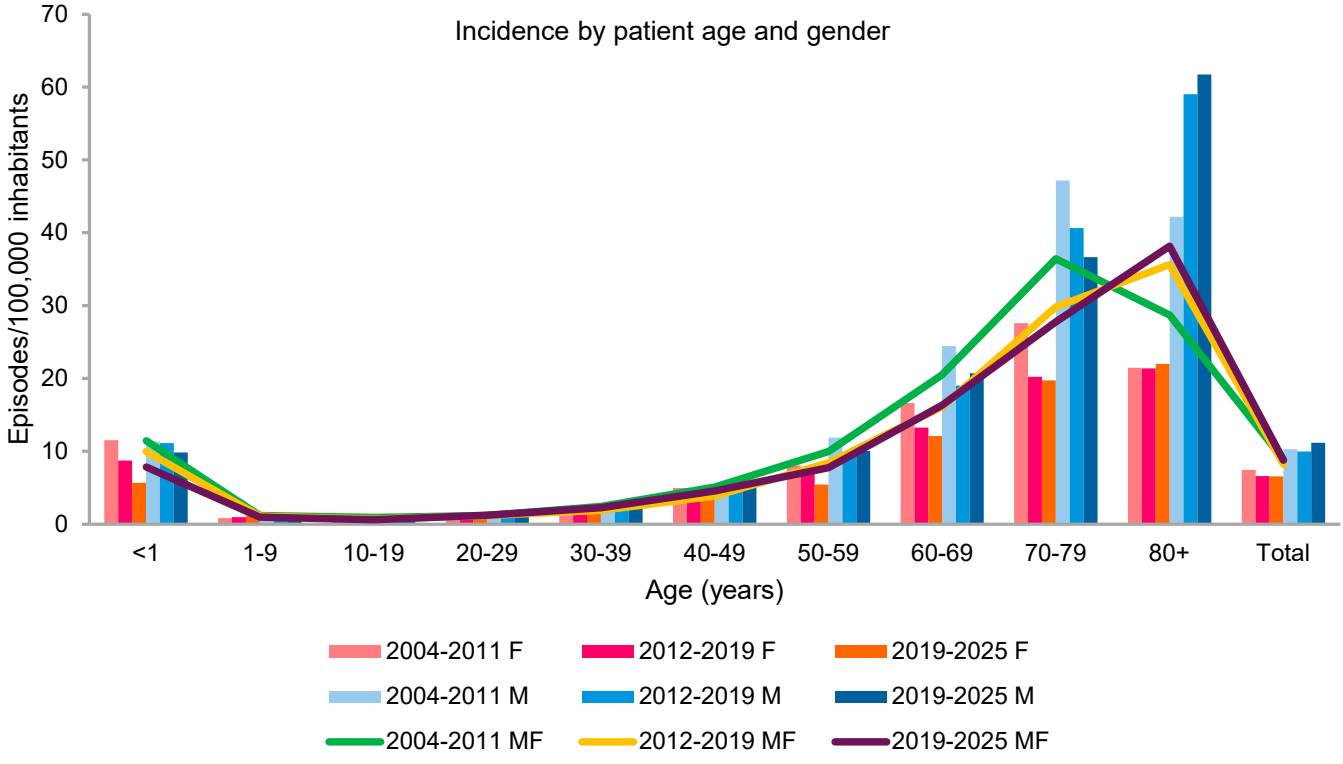
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**Figure 1 Number of yearly isolates (bars) and species distribution in percentage over the years (curves)** DANMAP 2025



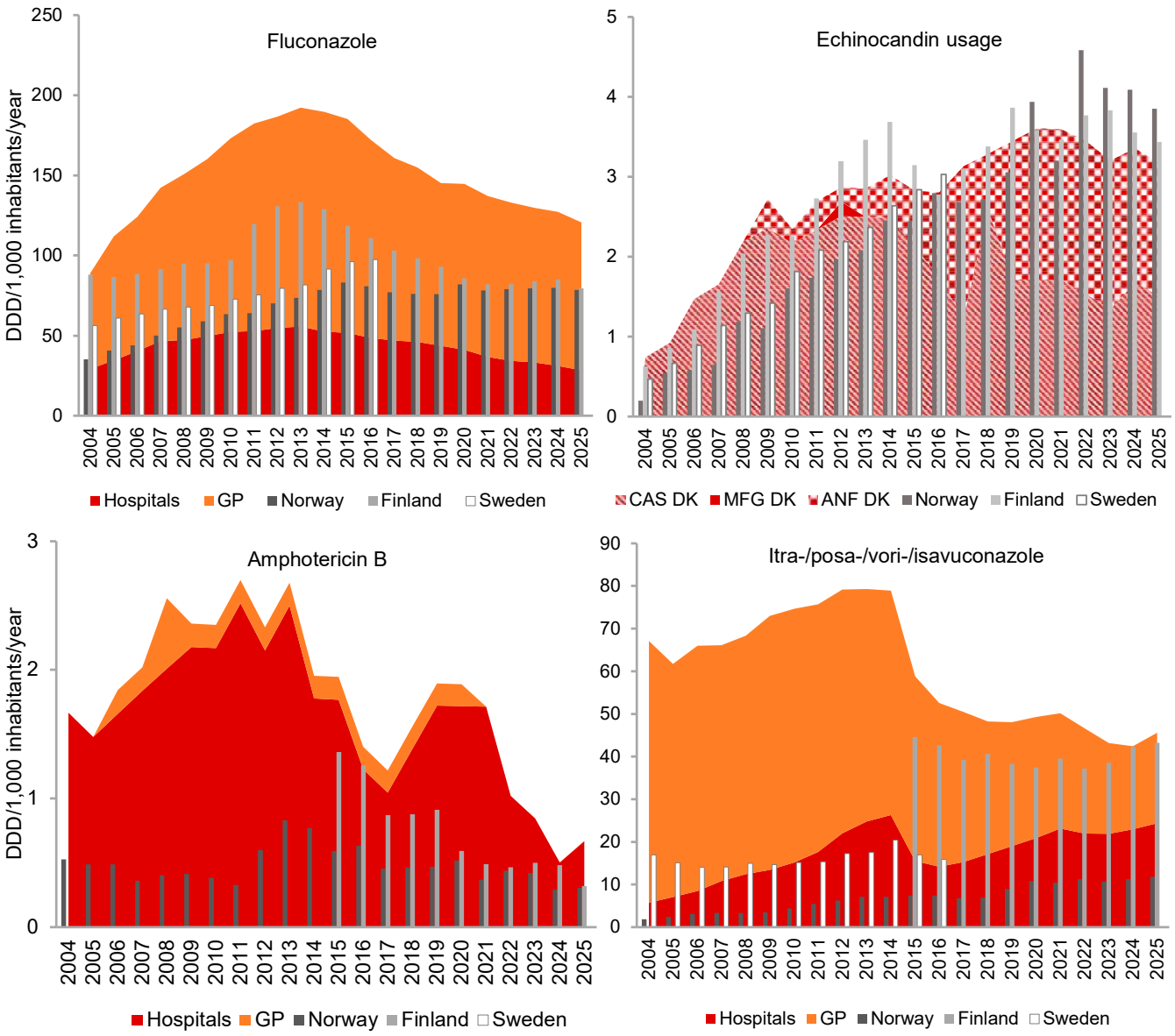

◆ Indicates one single *C. auris* episode in each of 2021 and 2023.

**Figure 2 Incidence by patient age in total (curves) and by gender (bars) across two 8-year periods and a 6-year period including 2024-2025** DANMAP 2025




F = female, M = male, FM = Female & Male.

**Figure 3 Systemic antifungal use in the Nordic countries. Danish data is shown for hospital and primary sector use** DANMAP 2025




Abbreviations: DDD = Defined Daily Dosis. GP = General Practice. CAS = Caspofungin. MFG = Micafungin. ANF = Anidulafungin.
Data from the figures above is calculated on data from Sundhedsdatastyrelsen (www.medstat.dk), Danmarks Statistik (www.dst.dk), Folkehelseinstituttet (www.fhi.no) and Finnish Medicines Agency (www.fimea.fi). Data from Sweden is not available after 2016.
The amphotericin B DDD has recently been changed to reflect the different dose depending on the formulation; updated DDDs were not available from Sweden or from Finland prior to 2015.
The abrupt decline in azole use after 2014 largely reflects a change in posaconazole DDD definition, not an actual drop in usage (see text).

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continued ... Textbox 8.3

**References**

[1] Cornely OA, Sprute R, Bassetti M, *et al.* Global guideline for the diagnosis and management of candidiasis: an initiative of the ECMM in cooperation with ISHAM and ASM. *The Lancet Infectious Diseases* 2025; **25**: e280-93.
[2] Denning DW. Global incidence and mortality of severe fungal disease. *The Lancet Infectious Diseases* 2024; **24**: e428-38.
[3] De Hoog S, Walsh TJ, Ahmed SA, *et al.* A conceptual framework for nomenclatural stability and validity of medically important fungi: a proposed global consensus guideline for fungal name changes supported by ABP, ASM, CLSI, ECMM, ESCMID-EFISG, EUCAST-AFST, FDLC, IDSA, ISHAM, MMSA, and MSGERC. J *Clin Microbiol* 2023; **61**: e00873-23.
[4] Arendrup MC, Fuursted K, Gahrn-Hansen B, *et al.* Seminational Surveillance of Fungemia in Denmark: Notably High Rates of Fungemia and Numbers of Isolates with Reduced Azole Susceptibility. *J Clin Microbiol* 2005; **43**: 4434-40.
[5] Arendrup MC, Fuursted K, Gahrn-Hansen B, *et al.* Semi-national surveillance of fungaemia in Denmark 2004-2006: increasing incidence of fungaemia and numbers of isolates with reduced azole susceptibility. *Clinical Microbiology and Infection* 2008; **14**: 487-94.
[6] Arendrup MC, Bruun B, Christensen JJ, *et al.* National Surveillance of Fungemia in Denmark (2004 to 2009). *J Clin Microbiol* 2011; **49**: 325-34.
[7] Risum M, Astvad K, Johansen HK, *et al.* Update 2016-2018 of the Nationwide Danish Fungaemia Surveillance Study: Epidemiologic Changes in a 15-Year Perspective. *JoF* 2021; **7**: 491.
[8] Arendrup MC, Dzajic E, Jensen RH, *et al.* Epidemiological changes with potential implication for antifungal prescription recommendations for fungaemia: data from a nationwide fungaemia surveillance programme. *Clinical Microbiology and Infection* 2013; **19**: e343-53.
[9] Astvad KMT, Johansen HK, Røder BL, *et al.* Update from a 12-Year Nationwide Fungemia Surveillance: Increasing Intrinsic and Acquired Resistance Causes Concern. *J Clin Microbiol* 2018; **56**: e01564-17.
[10] Bing J, Li S, Ji L, *et al.* Global emergence and rapid spread of *Candidozyma auris* (syn. *Candida auris*): epidemiology, biology, and antifungal resistance. *Clin Microbiol Rev* 2026; **39**: e00394-25.

## Textbox 8.4

# Azole resistance in clinical isolates of *A. fumigatus* (Oct 2023-Sept 2025)

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*A. fumigatus* is ubiquitous in the environment and can cause disease in patients with severely impaired lung function or an impaired immune system[1]. Azoles remain the most efficacious and the only orally available treatment. However, their efficacy has increasingly been challenged by resistance, which mainly arises in the environment following agri- and horticultural azole use. Environmentally selected resistance is typically characterised by specific *cyp51A* promoter tandem repeats and associated alterations, most commonly $TR_{34}$/L98H and $TR_{46}$/Y121F/T289A (with or without additional alterations), whereas various other cyp51A alterations have been observed in resistance emerging during long-term treatment. For environmentally acquired resistance, mortality may be high due to delayed appropriate treatment and the lower efficacy and poorer tolerability of second line agents[2]. An international expert guideline recommends alternative treatment when the local azole rate exceeds 10%, a threshold exceeded in the Netherlands and, more recently, in parts of Belgium[3,4]. A Danish voluntary surveillance of azole-resistant *A. fumigatus* (AR*Af*) from clinical samples was instituted in October 2018. All isolates underwent susceptibility testing using azole screening agar and/or EUCAST reference microdilution method, with *cyp51A* sequencing of resistant isolates[5]. Here, we report new data from surveillance years 6 (Oct 2023-Sept 2024) and 7 (Oct 2024-Sept 2025).

### Results

A total of 1,545 isolates from 1,253 patients were included over the two-year period (Oct 2023-Sept 2025). The majority of isolates were cultured from airway samples (81.9%; 1,265/1,545) and ear samples (15.5%; 239/1,545). After a decrease in annual number of isolates during years 1-5, the number of referred isolates before exclusion increased from 750 in year 6 to 795 isolates in year 7. This may represent random variation, changes in laboratory routines or increased awareness of isolate referral. Amphotericin B susceptibility remained high (99.9%; 1,332/1,334 isolates). Azole resistance (to any azole tested) was found in 6.2% isolates, with resistance for the individual azoles ranging from 5.2%-5.6% (Table 1). 59% of resistant isolates (3.7% of all isolates) harboured an environmentally driven resistance mechanism ($TR_{34}$ or $TR_{46}$, Figure 1). Patients with AR*Af* frequently had concurrent azole susceptible isolates during the same year (39%; 28/71 during the two years).

**Table 1 Susceptibility classifications and MIC distributions for *A. fumigatus* isolates included during the two years** DANMAP 2026

| Antifungal | S | Number of isolates that were azole screening susceptible/had the given MIC (mg/L) | | | | | | | | | | | | N tested | % R |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | **0.008** | **0.016** | **0.03** | **0.06** | **0.125** | **0.25** | **0.5** | **1** | **2** | **4** | **8 (>4)** | **>8** | | |
| AMB | | | | | | 14 | 342 | 808 | 168 | 2 | | | | 1334 | 0,1% |
| ITZ | 212 | | 2 | 9 | 19 | 198 | 855 | 154 | 8 | 4 | 3 | 80 | | 1544 | 5,6% |
| POS | 1138 | 3 | 9 | 25 | 175 | 99 | 13 | 45 | 23 | 11 | | 3 | | 1544 | 5,6% |
| VOR | 211 | | | | | 2 | 53 | 797 | 399 | 20 | 39 | 23 | | 1544 | 5,3% |
| ISCO* | 1141 | | | | 1 | | 8 | 150 | 153 | 20 | 31 | 20 | 21 | 1545 | 5,2% |

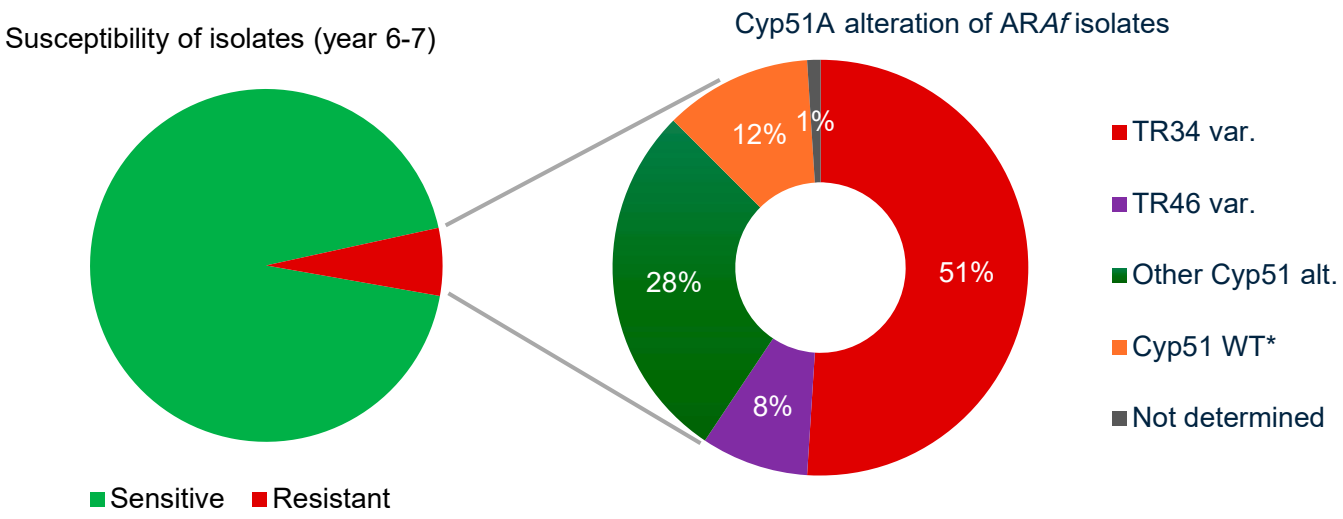
AMB: Amphotericin B. ITZ: Itraconazole. POS: Posaconazole. VOR: Voriconazole. ISA: Isavuconazole.
* All azole susceptible isolates without an ISA MIC were considered ISA susceptible.

### Conclusion

The AR*Af* rate remained stable during Oct 2023-Sept 2025 compared with previous years and below the 10% threshold for changing primary therapy. The risk of potentially unexpected (environmental) resistance upon culturing *A. fumigatus* was approximately 3.7%. A large environmental study conducted in 2020-2022 detected $TR_{46}$ only towards the end of the study period, and $TR_{46}$ was also detected more consistently in clinical isolates in recent years, suggesting that this mechanism, which confers high-level vori- and isavuconazole resistance, may be increasing in Denmark[6]. Dual use of azoles in the environment and human medicine has recently been assessed by five European Agencies[7]. New and upcoming antifungals such as olorofim

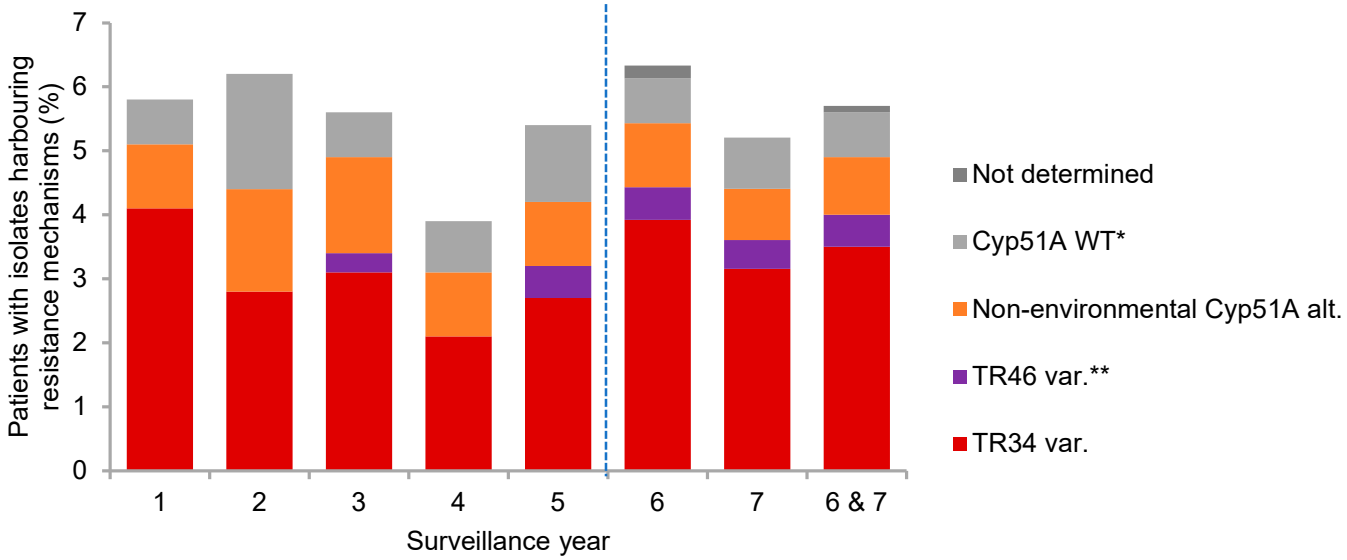
could warrant similar consideration. Ipflufenoquin shares its target with olorofim and has experimentally been shown to select for cross-resistance[8], yet is licensed for crop protection outside the EU. Resistance surveillance would therefore be advisable should ipflufenoquin be licensed in the EU, to monitor for potential emergence of olorofim resistance. ,

**Figure 1 Azole susceptibility of 1,545 isolates Oct 2023-Sept 2025 (left) and associated Cyp51A alterations in resistant isolates (right)** DANMAP 2025




Var: Variant. Alt: Alteration.
*) Cyp51A alterations not uniformly associated with azole resistance (e.g. F46Y/M172V/E427K) are considered as WT (wild-type) here.

**Figure 2 Cyp51A-mediated resistance mechanisms in AR*Af* isolates on a patient basis. The resistance profile was categorized as environmental if both environmentally associated and other Cyp51A mechanisms were detected in isolates from the same patient. Patients could also harbour susceptible/WT isolates within the same year as resistant isolates (not detailed here)** DANMAP 2025




Var: Variant. Alt: Alteration.
* Cyp51A alterations not uniformly associated with azole resistance (e.g. F46Y/M172V/E427K) are considered as WT (wild-type) here.
** One patient had AR*Af* isolates with TR34 and TR46 within the same year (grouped under TR46).

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**References**

[1] Ullmann AJ, Aguado JM, Arikan-Akdagli S, et al. Diagnosis and management of Aspergillus diseases: executive summary of the 2017 ESCMID-ECMM-ERS guideline. *Clin Microbiol Infect*. 2018;24:e1-e38. doi:10.1016/j.cmi.2018.01.002

[2] Resendiz-Sharpe A, Mercier T, Lestrade PPAA, et al. Prevalence of voriconazole-resistant invasive aspergillosis and its impact on mortality in haematology patients. *J Antimicrob Chemother*. 2019;74(9):2759-2766. doi:10.1093/jac/dkz258

[3] Lestrade PPA, Buil JB, van der Beek MT, et al. Paradoxal Trends in Azole-Resistant Aspergillus fumigatus in a National Multicenter Surveillance Program, the Netherlands, 2013-2018. Alspaugh JA, ed. *Emerg Infect Dis*. 2020;26(7):1447-1455. doi:10.3201/eid2607.200088

[4] Cuypers L, Aerts R, Van de gaer O, et al. Doubling of triazole resistance rates in invasive aspergillosis over a 10-year period, Belgium, 1 April 2022 to 31 March 2023. *Eurosurveillance*. 2025;30(18):1-12. doi:10.2807/1560-7917.ES.2025.30.18.2400559

[5] Risum M, Hare RK, Gertsen JB, et al. Azole resistance in Aspergillus fumigatus. The first 2-year's Data from the Danish National Surveillance Study, 2018-2020. *Mycoses*. 2022;65(4):419-428. doi:10.1111/myc.13426

[6] Arendrup MC, Hare RK, Jørgensen KM, et al. Environmental Hot Spots and Resistance-Associated Application Practices for Azole-Resistant Aspergillus fumigatus , Denmark, 2020-2023. *Emerg Infect Dis*. 2024;30(8). doi:10.3201/eid3008.240096

[7] EFSA (European Food Safety Agency), ECDC (European Centre for Disease Prevention and Control), ECHA (European Chemicals Agency), EEA (European Environment Agency), EMA (European Medicines Agency), JRC (European Commission's Joint Research Centre). Impact of the use of azole fungicides, other than as human medicines, on the development of azole-resistant Aspergillus spp. *EFSA* J. 2025;23(1):e9200. doi:10.2903/j.efsa.2025.9200

[8] van Rhijn N, Storer ISR, Birch M, Oliver JD, Bottery MJ, Bromley MJ. Aspergillus fumigatus strains that evolve resistance to the agrochemical fungicide ipflufenoquin in vitro are also resistant to olorofim. *Nat Microbiol*. 2024;9(1):29-34. doi:10.1038/s41564-023-01542-4

## Textbox 8.5

# Nontuberculous mycobacteria – an emerging challenge of antimicrobial resistance

**Background**

While the number of tuberculosis (TB) cases is decreasing in Denmark, the number of drug-resistant cases has remained stable for many years, with an average of approximately three cases annually (Fig. 1). MDR- and XDR-TB therefore represent a limited public health burden in Denmark, given their low prevalence and the absence of TB-related mortality among affected patients1. In contrast, the incidence of pulmonary nontuberculous mycobacterial disease (NTM) is increasing in Denmark2 as well as globally3. This increase has been attributed to several factors, particularly an ageing population, a higher prevalence of chronic and structural lung disease, and the increasing use of immunosuppressive treatment.

In Denmark, approximately 100–150 cases of NTM disease occur annually. Approximately three quarters are pulmonary infections, while the remaining cases mainly comprise infections of lymph nodes, skin and soft tissue. Disseminated NTM disease is rare and occurs predominantly in immunocompromised patients. The annual number of unique patients with NTM isolates is approaching the number of TB cases in Denmark (Fig. 1).

NTM comprise a heterogeneous group of more than 200 *Mycobacterium* species other than those causing TB and leprosy. NTM are widely distributed in the environment, including soil and water, and only a minority of species are associated with human disease. In contrast to *Mycobacterium tuberculosis*, NTM are generally not transmitted from person to person.

Treatment of NTM disease represents a particular antimicrobial challenge. NTM display substantial intrinsic resistance to many antimicrobial agents, and resistance profiles vary considerably between species. Treatment is therefore species-dependent and typically requires combinations of several antimicrobial agents administered for many months or even years. In addition, acquired resistance may develop during treatment, further reducing the number of effective treatment options.

**Diagnostic methods**

In Denmark, diagnostic testing for mycobacteria is performed at the International Reference Laboratory of Mycobacteria at Statens Serum Institut (SSI), which serves as the national reference and specialist laboratory for TB and NTM.

The standard examination for mycobacteria includes microscopy, one routine PCR for *M. tuberculosis* complex, and culture. When acid-fast bacilli are detected by microscopy but PCR for the *M. tuberculosis* complex is negative, additional molecular testing for NTM is performed. Culture-positive isolates are subsequently identified to species level and, when indicated, subjected to antimicrobial susceptibility testing using both genotype and fenotypic methods.

Interpretation of NTM findings differs from that of *M. tuberculosis*. Detection of NTM in a clinical specimen does not necessarily indicate disease, as NTM are ubiquitous in the environment and may represent contamination or colonisation. Repeated microbiological samples and correlation with clinical and radiological findings may therefore be required to establish clinically significant NTM disease. Overall, more than half of all newly identified patients with NTM isolates, excluding *M. gordonae*, meet criteria for NTM-disease.

**Antimicrobial resistance and clinical implications**

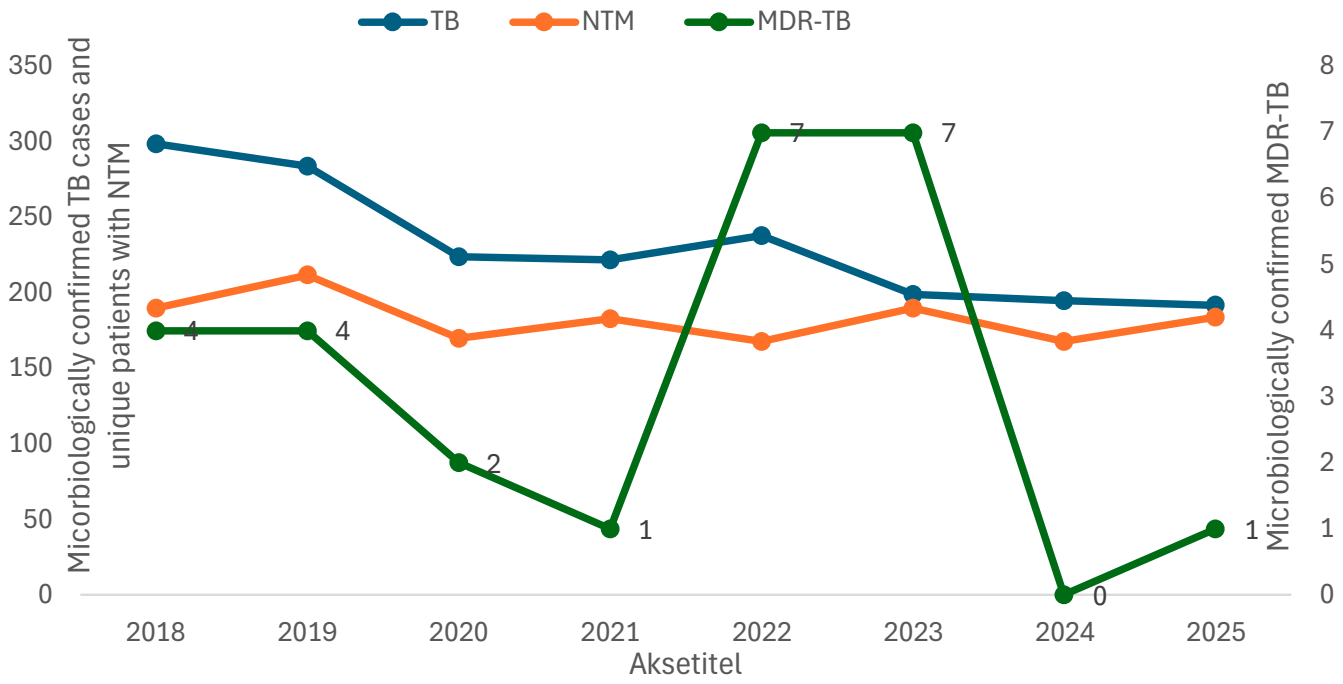
Antimicrobial susceptibility in NTM is complex. Different NTM species have markedly different intrinsic susceptibility patterns, and susceptibility testing does not predict clinical outcome equally well for all combinations of species and antimicrobial agents. Consequently, correct species identification is essential for selecting appropriate treatment and interpreting susceptibility results.

The substantial intrinsic resistance of NTM means that treatment generally is complex and requires multidrug regimens, often administered for prolonged periods and associated with substantial toxicity, drug interactions, and adverse effects. In addition, acquired resistance may develop during therapy, particularly when an effective combination of antimicrobial agents cannot be maintained.

The increasing occurrence of NTM disease, combined with intrinsic and acquired antimicrobial resistance, makes NTM an emerging challenge for clinical microbiology and antimicrobial treatment in Denmark. Continued surveillance of species distribution and antimicrobial resistance is important to monitor changes in the epidemiology of NTM and to support appropriate treatment of these often difficult-to-treat infections. Pulmonary NTM disease is associated with substantial mortality, with an overall five-year mortality of approximately 50% reported.

**Figure 1 Microbiologically confirmed TB and MDR-TB cases and unique patients with NTM isolated, Denmark 2018-2025**

DANMAP 2025




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**References**

[1] Holden, I. K., Lillebaek, T., Andersen, P. H., Wejse, C. & Johansen, I. S. Characteristics and predictors for tuberculosis related mortality in Denmark from 2009 through 2014: A retrospective cohort study. *PLoS One* **15**, 1-13 (2020).
[2] Dahl, V. N. *et al.* Relationship between age, sex, geography and incidence of nontuberculous mycobacteria in Denmark from 1991 to 2022. *ERJ Open Res.* **11**, (2025).
[3] Dahl, V. N. *et al.* Global trends of pulmonary infections with nontuberculous mycobacteria: a systematic review. *Int. J. Infect. Dis.* **125**, 120-131 (2022).



# 9.

# Resistance in animal pathogens

# 9. Resistance in animal pathogens

## Highlights

Surveillance of antimicrobial resistance in 2025 focused on pathogenic bacteria from acute mastitis in dairy cows and from various organs in pigs and included results obtained through antimicrobial susceptibility testing.

None of the **pathogenic bacteria from acute mastitis in dairy cows** displayed significant changes in phenotypic resistance between 2024 and 2025. Of note, 27.6% of *Streptococcus uberis* isolates displayed resistance to penicillin, which is noteworthy because beta-lactamase sensitive penicillins are the most commonly used drugs for treatment of adult cattle in Denmark. However, most of the isolates had a minimum inhibitory concentration value of 0.25 mg/L, which is just above the tentative epidemiological cut-off of 0.12 mg/L, and there is currently no clinical breakpoint available for penicillin in *S. uberis*. Thus, it remains unclear whether penicillin is active against these borderline resistant *S. uberis* isolates.

Most **pathogenic bacteria isolated from pigs** in 2025 displayed similar levels of phenotypic resistance as in 2024 (1-year period) and 2020 (5-year period). However, ten pathogen-drug combinations were associated with significantly increased resistance, whereas none were associated with significantly decreased resistance. The high level of neomycin resistance in haemolytic *Escherichia coli* (59.9%) is worrisome because it is one of only a few drugs recommended in Denmark as first choice for treating *E. coli*-associated post-weaning diarrhoea. The high level of gentamicin resistance in haemolytic *E. coli* (48.8%) is also worrisome because it is considered critically important for human medicine by the World Health Organization. It should also be noted that 6.8% of haemolytic *E. coli* isolates displayed resistance to 3rd generation cephalosporins (cefpodoxime).

## 9.1 Introduction

Surveillance of antimicrobial resistance in 2025 focused on pathogenic bacteria from mastitis in dairy cows and from various organs in pigs and included results obtained through antimicrobial susceptibility testing (AST).

## 9.2 Acute mastitis in dairy cows

### 9.2.1 Background

Milk samples for routine diagnosis of clinical mastitis in dairy cows are normally collected by and tested at the local veterinary clinics throughout Denmark. As part of the testing, veterinarians identify common pathogens using simple culture techniques and bacterial identification methods and sometimes perform AST to decide on therapeutic options. Normally, the milk samples and isolates are discarded after analysis.
In 2024, we established a surveillance program for mastitis pathogens by asking veterinarians specialised in cattle to send frozen milk samples from dairy cows with acute mastitis to Statens Serum Institut. In 2025, 441 milk samples were shipped by 15 veterinary clinics across Denmark. Isolates obtained from these milk samples were identified to the genus or species level using MALDI-TOF, and AST was performed by broth microdilution using customized Sensititre panels. Tables 9.1 and 9.2 show the results from 2025, while results from 2024 can be found on the homepage of the Danish Veterinary Consortium (https://www.vetssi.dk/). AST data were based on epidemiological cut-offs (ECOFFs) and clinical breakpoints when ECOFFs were unavailable (https://www.vetssi.dk/).

### 9.2.2 Results

Among the 441 milk samples tested, 90.5% were positive for one or more pathogenic bacteria, while the remaining milk samples were interpreted as negative, either because of lack of growth or unspecific growth suggestive of contamination. In total, 491 bacterial isolates were recovered, of which 80.9% belonged to well-known mastitis pathogens: *Streptococcus uberis* (25.1%), *Escherichia coli* (16.9%), *Staphylococcus aureus* (12.0%), *Streptococcus dysgalactiae* (11.2%), coagulase-negative staphylococci (CoNS) (6.1%), *Trueperella pyogenes* (3.7%), *Streptococcus agalactiae* (3.5%) and *Klebsiella pneumoniae* (2.4%). None of the remaining bacterial species were found in more than 2% of the milk samples. Table 9.1 provides an overview of the identified pathogenic bacteria.

AST was performed on 375 bacterial isolates representing well-known mastitis pathogens (Table 9.1). *T. pyogenes* isolates were not tested due to their relatively slow growth and specific methodological requirements for AST. Table 9.2 shows the proportions of resistant isolates in 2025.

We did not observe any significant changes in phenotypic resistance between 2024 and 2025.

Among streptococci, we observed that 27.6% of the *S. uberis* isolates displayed resistance to penicillin. It should be noted, however, that 33 of the 34 penicillin-resistant *S. uberis* isolates had a minimum inhibitory concentration (MIC) value of 0.25 mg/L, which is just above the tentative ECOFF for *S. uberis* and the ECOFF for *S. agalactiae* (both 0.12 mg/L), whereas the remaining isolate had a MIC value of 0.5 mg/L. Tetracycline resistance was observed in 16.3% of the *S. uberis* and 16.4% of the *S. dysgalactiae* isolates. Tetracycline resistance was also found in 70.6% of the *S. agalactiae* isolates, which is consistent with a high prevalence of tetracycline resistance genes in this bacterial species (Da Cuna *et al.* Nat Commun. 2014 Aug 4;5:4544. doi: 10.1038/ncomms5544). Moreover, 29.4% of the *S. agalactiae* isolates were resistant to clindamycin, while 17.6% were resistant to erythromycin.

The relatively high level of borderline resistance to penicillin in *S. uberis* is particularly noteworthy because beta-lactamase sensitive penicillins are the most commonly used drugs for treatment of adult cattle in Denmark (DANMAP 2024).

Among staphylococci, we found that 13.3% of the CoNS and 8.5% of the *S. aureus* isolates were resistant to penicillin. Of note, a single *S. aureus* isolate was resistant to cefoxitin, which is used as a surrogate for detection of *mecA*- and *mecC*-mediated methicillin resistance. The isolate was therefore further analysed with a multiplex polymerase chain reaction assay, which showed that it belongs to *spa* type t034 and clonal complex 398 and carries *mecA*.

*E. coli* isolates were resistant to ampicillin (15.2%), sulfamethoxazole (15.2%), tetracycline (5.1%) and trimethoprim (12.7%). As in 2024, a single *E. coli* isolate displayed an extended-spectrum beta-lactamase (ESBL) phenotype and was resistant to multiple drugs, including ampicillin, cefotaxime, ceftazidime, chloramphenicol, ciprofloxacin, sulphamethoxazole, tetracycline and trimethoprim. Due to the ESBL phenotype (resistance to cefotaxime and ceftazidime), this isolate was further analysed with extra disk diffusion tests and subjected to whole genome sequencing, which confirmed the ESBL phenotype and showed that it belongs to multilocus sequence type 58 and carries $bla_{\text{CTX-M-15}}$. In comparison, the ESBL-producing *E. coli* isolate from 2024 was resistant to the same antimicrobials (plus nalidixic acid) and also carried $bla_{\text{CTX-M-15}}$ but belonged to multilocus sequence type 46.

As in 2024, 91.7% of the *K. pneumoniae* isolates were resistant to ampicillin, reflecting that this bacterial species is intrinsically resistant to penicillins.

Finally, five bacterial species displayed low levels of phenotypic resistance to specific antimicrobials (<5.0%).

**Table 9.1 Pathogenic bacteria from acute mastitis in dairy cows, Denmark, 2025** DANMAP 2025

| Pathogen | Milk samples (n=441) | | AST |
|---|---|---|---|
| | Positive (no.) | Positive (%) | Isolates (no.) |
| *Streptococcus uberis* | 123 | 25.1% | 123 |
| *Escherichia coli* | 83 | 16.9% | 79 |
| *Staphylococcus aureus* | 59 | 12.0% | 59 |
| *Streptococcus dysgalactiae* | 55 | 11.2% | 55 |
| Coagulase-negative staphylococci | 30 | 6.1% | 30 |
| Coagulase-negative staphylococci in mixed cultures | 29 | 5.9% | ND |
| *Trueperella pyogenes* | 18 | 3.7% | ND |
| *Streptococcus agalactiae* | 17 | 3.5% | 17 |
| *Klebsiella pneumoniae* | 12 | 2.4% | 12 |
| *Enterococcus faecium* | 4 | 0.8% | ND |
| *Helcococcus ovis* | 4 | 0.8% | ND |
| *Lactococcus garviae* | 4 | 0.8% | ND |
| *Streptococcus equinus/Streptococcus infantarius* | 4 | 0.8% | ND |
| *Serratia liquefaciens* | 3 | 0.6% | ND |
| *Streptococcus gallolyticus* | 3 | 0.6% | ND |
| *Streptococcus* spp. | 3 | 0.6% | ND |
| *Corynebacterium bovis* | 2 | 0.4% | ND |
| *Corynebacterium variabile* | 2 | 0.4% | ND |
| *Empedobacter brevis* | 2 | 0.4% | ND |
| *Enterococcus faecalis* | 2 | 0.4% | ND |
| *Helcococcus kunzii* | 2 | 0.4% | ND |
| *Klebsiella oxytoca* | 2 | 0.4% | ND |
| *Mannheimia haemolytica* | 2 | 0.4% | ND |
| *Micrococcus luteus* | 2 | 0.4% | ND |
| *Pantoea agglomerans* | 2 | 0.4% | ND |
| *Streptococcus canis* | 2 | 0.4% | ND |
| *Streptococcus parauberis* | 2 | 0.4% | ND |
| *Corynebacterium amycolatum* | 1 | 0.2% | ND |
| *Corynebacterium testudinoris* | 1 | 0.2% | ND |
| *Elizabethkingia miricola* | 1 | 0.2% | ND |
| *Enterococcus cecorum* | 1 | 0.2% | ND |
| *Klebsiella variicola* | 1 | 0.2% | ND |
| *Proteus mirabilis* | 1 | 0.2% | ND |
| *Pseudomonas aeruginosa* | 1 | 0.2% | ND |
| *Pseudomonas* spp. | 1 | 0.2% | ND |
| *Psychrobacter* spp. | 1 | 0.2% | ND |
| *Raoultella ornithinolytica* | 1 | 0.2% | ND |
| *Raoultella terrigena* | 1 | 0.2% | ND |
| *Serratia marcescens* | 1 | 0.2% | ND |
| *Serratia nematodiphila* | 1 | 0.2% | ND |
| *Serratia proteamaculans* | 1 | 0.2% | ND |
| *Streptococcus suis* | 1 | 0.2% | ND |
| *Trueperella* spp. | 1 | 0.2% | ND |
| *Vibrio fluvialis* | 1 | 0.2% | ND |
| *Weissela thailandensis* | 1 | 0.2% | ND |
| *Streptococcus suis* | 1 | 0.2% | ND |
| *Trueperella* spp. | 1 | 0.2% | ND |
| *Vibrio fluvialis* | 1 | 0.2% | ND |
| *Weissela thailandensis* | 1 | 0.2% | ND |

Isolates were identified to the genus or species level using MALDI-TOF.
Antimicrobial susceptibility testing was performed by broth microdilution using customized Sensititre panels.
Abbreviations: AST, antimicrobial susceptibility testing; ND, not determined.

**Table 9.2 Phenotypic antimicrobial resistance among pathogenic bacteria from acute mastitis in dairy cows, Denmark, 2025**

DANMAP 2025

| Antimicrobial agent | Ec (n=79) | Kp (n=12) | Sau (n=59) | CoNS (n=30) | Sag (n=17) | Sd (n=55) | Su (n=123) |
|---|---|---|---|---|---|---|---|
| | R (%) | R (%) | R (%) | R (%) | R (%) | R (%) | R (%) |
| Amikacin | 0.0% | 0.0%* | ND | ND | ND | ND | ND |
| Ampicillin | 15.2% | 91.7%* | ND | ND | ND | ND | ND |
| Azithromycin | 0.0% | ND | ND | ND | ND | ND | ND |
| Cefotaxime | 1.3% | 0.0%* | ND | ND | ND | ND | ND |
| Cefoxitin | ND | ND | 1.7% | ND | ND | ND | ND |
| Ceftazidime | 1.3% | 0.0%* | ND | ND | ND | ND | ND |
| Chloramphenicol | 2.5% | 0.0%* | 0.0% | 3.3% | 0.0%* | 0.0% | 0.0% |
| Clindamycin | ND | ND | 1.7% | ND | 29.4%* | 0.0% | 4.1% |
| Ciprofloxacin | 1.3% | 0.0%* | 0.0% | ND | 0.0%* | ND | ND |
| Colistin | 0.0% | 0.0%* | ND | ND | ND | ND | ND |
| Erythromycin | ND | ND | 0.0% | 3.3% | 17.6% | 1.8% | 2.4% |
| Fusidate | ND | ND | 0.0% | ND | ND | ND | ND |
| Gentamicin | 1.3% | 0.0%* | 0.0% | 0.0% | 0.0%* | ND | ND |
| Kanamycin | ND | ND | 0.0% | ND | ND | ND | ND |
| Linezolid | ND | ND | 0.0% | 0.0% | 0.0%* | ND | ND |
| Meropenem | 0.0% | 0.0%* | ND | ND | ND | ND | ND |
| Mupirocin | ND | ND | 0.0% | ND | ND | ND | ND |
| Nalidixic acid | 0.0% | ND | ND | ND | ND | ND | ND |
| Penicillin | ND | ND | 8.5% | 13.3% | 0.0%* | ND | 27.6% |
| Quinopristin-dalfopristin | ND | ND | 1.7% | ND | ND | ND | ND |
| Rifampin | ND | ND | 0.0% | 0.0% | ND | ND | ND |
| Streptomycin | ND | ND | 0.0% | ND | ND | ND | ND |
| Sufamethoxazole | 15.2% | ND | ND | ND | ND | ND | ND |
| Tetracycline | 5.1% | 0.0%* | 1.7% | 0.0% | 70.6%* | 16.4% | 16.3% |
| Tiamulin | ND | ND | 1.7% | ND | ND | ND | ND |
| Tigecycline | 0.0% | 0.0%* | ND | ND | ND | ND | ND |
| Trimethoprim | 12.7% | 0.0%* | 1.7% | ND | ND | ND | ND |
| Vancomycin | ND | ND | 0.0% | 0.0% | 0.0%* | 0.0% | 0.0% |

Data were based on epidemiological cut-offs (ECOFFs) or clinical breakpoints when ECOFFs were unavailable (https://www.vetssi.dk/).
Percentages based on small sample sizes (n<20) are indicated by asterices and should be interpreted with caution.
Abbreviations: Ec, *Escherichia coli*; Kp, *Klebsiella pneumoniae*; Sau, *Staphylococcus aureus*; CoNS, coagulase-negative staphylococci; Sag, *Streptococcus agalactiae*; Sd, *Streptococcus dysgalactiae*; Su, *Streptococcus uberis*; R, resistant; ND, not determined.

## 9.3 Pigs

### 9.3.1 Background

The Veterinary Laboratory, The Danish Agriculture and Food Council, performed AST of isolates belonging to *Actinobacillus pleuropneumoniae, Bordetella bronchiseptica*, haemolytic and non-haemolytic *E. coli, Klebsiella pneumoniae, Salmonella enterica, Staphylococcus hyicus* and *Streptococcus suis*. Table 9.3 shows the proportions of resistant isolates in 2025, while results from 2016-2024 can be found on the homepage of the Danish Veterinary Consortium (https://www.vetssi.dk/). AST data were based on ECOFFs and clinical breakpoints when ECOFFs were unavailable (https://www.vetssi.dk/).

### 9.3.2 Results

Most isolates displayed similar levels of phenotypic resistance as in 2024 (1-year period) and 2020 (5-year period). However, ten pathogen-drug combinations were associated with significantly increased resistance, whereas none were associated with significantly decreased resistance. Table 9.4 and Figure 9.1 show all significant changes in phenotypic resistance over a 1-year period (2025 vs. 2024) and a 5-year period (2025 vs. 2020).

*A. pleuropneumoniae* displayed significantly increased resistance to trimethoprim-sulfamethoxazol (2025 vs. 2020).

Haemolytic *E. coli* displayed significantly increased resistance to amoxicillin-clavulanic acid (2025 vs. 2024 and 2025 vs. 2020), florfenicol (2025 vs. 2020), gentamicin (2025 vs. 2020), neomycin (2025 vs. 2020), spectinomycin (2025 vs. 2020), streptomycin (2025 vs. 2020) and tetracycline (2025 vs. 2020).

**Table 9.3 Phenotypic antimicrobial resistance among pathogenic bacteria from pigs, Denmark, 2025** DANMAP 2025

| Antimicrobial agent | Ap (n=57) R (%) | Bb (n=28) R (%) | H-Ec (n=207) R (%) | NH-Ec (n=131) R (%) | Kp (n=11) R (%) | Se (n=20) R (%) | Sh (n=8) R (%) | Ss (n=109) R (%) |
|---|---|---|---|---|---|---|---|---|
| Amoxicillin | 0.0% | ND | 75.4% | 84.2% | ND | 80.0% | 100.0%* | ND |
| Ampicillin | ND | ND | ND | ND | ND | ND | ND | ND |
| Amoxicillin-clavulanic acid | ND | ND | 38.6% | 35.3% | 0.0%* | 20.0% | ND | ND |
| Cefotaxime | ND | ND | ND | ND | ND | ND | ND | ND |
| Cefpodoxime | ND | ND | 6.8% | 0.8% | ND | ND | ND | ND |
| Cefquinome | ND | ND | ND | ND | 0.0%* | ND | ND | ND |
| Ceftiofur | 0.0% | ND | ND | ND | ND | ND | ND | ND |
| Chloramphenicol | ND | ND | ND | ND | ND | ND | ND | ND |
| Ciprofloxacin | ND | ND | ND | ND | ND | ND | ND | ND |
| Colistin | ND | ND | 0.0% | 0.0% | 0.0%* | ND | ND | ND |
| Doxycyclin | 0.0% | ND | 71.0% | 66.2% | 36.4%* | 70.0% | ND | 40.4% |
| Enrofloxacin | 7.0% | ND | 11.6% | 6.0% | ND | ND | 0.0%* | 0.0% |
| Erythromycin | ND | ND | ND | ND | ND | ND | ND | ND |
| Florfenicol | 0.0% | 7.1% | 23.7% | 21.8% | 27.3%* | 20.0% | 25.0%* | 0.9% |
| Gentamicin | ND | ND | 48.8% | 13.5% | 10.0%* | 5.0% | ND | ND |
| Lincomycin | ND | ND | ND | ND | ND | ND | 75.0%* | ND |
| Nalidixan | ND | ND | ND | ND | ND | ND | ND | ND |
| Neomycin | ND | ND | 59.9% | 25.6% | 0.0%* | ND | ND | ND |
| Penicillin | 1.8% | ND | ND | ND | ND | ND | 100.0%* | 5.5% |
| Spectinomycin | ND | ND | 64.3% | 45.9% | ND | 50.0% | ND | ND |
| Streptomycin | ND | ND | 87.9% | 83.5% | ND | 90.0% | ND | ND |
| Sulfamethoxazole | ND | ND | ND | ND | ND | ND | ND | ND |
| Tetracycline | ND | ND | 72.0% | 66.2% | 40.0%* | 75.0% | ND | ND |
| Tiamulin | 0.0% | ND | ND | ND | ND | ND | 37.5%* | ND |
| Tildipirosin | 0.0% | 0.0% | ND | ND | ND | ND | ND | ND |
| Tilmicosin | 0.0% | ND | ND | ND | ND | ND | 37.5%* | ND |
| Trimethoprim | ND | ND | ND | ND | ND | ND | ND | ND |
| Trimethoprim-sulfamethoxazole | 19.3% | ND | 66.7% | 77.4% | 54.5%* | 35.0% | 37.5%* | 18.3% |
| Tulathromycin | ND | 0.0% | ND | ND | ND | ND | ND | ND |
| Tylosin | ND | ND | ND | ND | ND | ND | 37.5%* | ND |

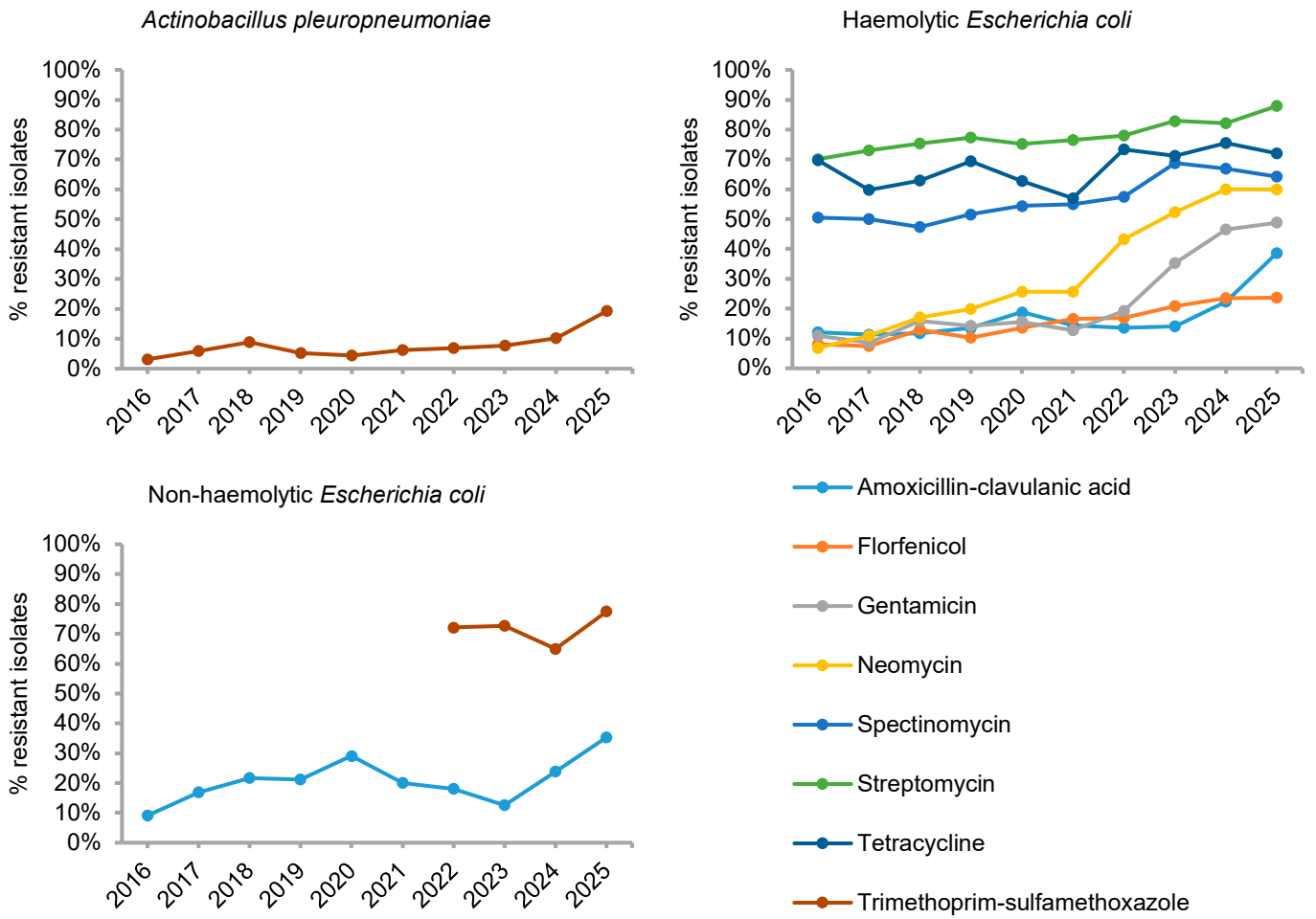
Data were based on epidemiological cut-offs (ECOFFs) or clinical breakpoints when ECOFFs were unavailable (https://www.vetssi.dk/).
Percentages based on small sample sizes (n<20) are indicated by asterices and should be interpreted with caution.
Abbreviations: Ap, *Actinobacillus pleuropneumoniae*; Bb, *Bordetella bronchiseptica*; H-Ec, haemolytic *Escherichia coli*; NH-Ec, non-haemolytic *Escherichia coli*; Kp, *Klebsiella pneumoniae*; Se, *Salmonella enterica*; Sh, *Staphylococcus hyicus*; Ss, *Streptococcus suis*; R, resistant; ND, not determined.

**Table 9.4 Statistically significant temporal changes in antimicrobial resistance phenotypes among pathogenic bacteria from pigs, Denmark, 2025 vs. 2024 and 2025 vs. 2020** DANMAP 2025

| Patho-gen | Antimicrobial agent | 2016 R (%) | 2017 R (%) | 2018 R (%) | 2019 R (%) | 2020 R (%) | 2021 R (%) | 2022 R (%) | 2023 R (%) | 2024 R (%) | 2025 R (%) | 2025 vs. 2024 Trend (p value) | 2025 vs. 2020 Trend (p value) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Ap | Trimethoprim-sulfamethoxazole | 3.1% | 6.0% | 8.8% | 5.2% | 4.3% | 6.3% | 6.9% | 7.7% | 10.5% | 19.3% | → (0.3897) | ↗ (0.0016) |
| H-Ec | Amoxicillin-clavulanic acid | 12.1% | 11.3% | 11.7% | 13.5% | 18.8% | 14.5% | 13.5% | 14.1% | 22.4% | 38.6% | ↗ (0.0002) | ↗ (0.0000) |
| H-Ec | Florfenicol | 8.1% | 7.4% | 12.9% | 10.3% | 13.6% | 16.5% | 16.9% | 20.8% | 23.6% | 23.7% | → (1.0000) | ↗ (0.0071) |
| H-Ec | Gentamicin | 10.9% | 8.6% | 15.9% | 14.3% | 15.6% | 12.8% | 19.3% | 35.2% | 46.5% | 48.8% | → (0.6378) | ↗ (0.0000) |
| H-Ec | Neomycin | 6.9% | 10.9% | 17.0% | 19.8% | 25.6% | 25.6% | 43.2% | 52.3% | 60.0% | 59.9% | → (1.0000) | ↗ (0.0000) |
| H-Ec | Spectinomycin | 50.5% | 50.0% | 47.3% | 51.6% | 54.4% | 55.0% | 57.4% | 68.8% | 66.9% | 64.3% | → (0.5526) | ↗ (0.0359) |
| H-Ec | Streptomycin | 70.1% | 73.0% | 75.4% | 77.4% | 75.2% | 76.4% | 78.0% | 82.9% | 82.1% | 87.9% | → (0.0899) | ↗ (0.0007) |
| H-Ec | Tetracycline | 69.8% | 59.8% | 62.9% | 69.4% | 62.8% | 57.0% | 73.3% | 71.1% | 75.5% | 72.0% | → (0.4520) | ↗ (0.0456) |
| NH-Ec | Amoxicillin-clavulanic acid | 9.1% | 16.8% | 21.7% | 21.1% | 29.1% | 20.0% | 18.0% | 12.6% | 23.9% | 35.3% | ↗ (0.0235) | → (0.2076) |
| NH-Ec | Trimethoprim-sulfamethoxazole | ND | ND | ND | ND | ND | ND | 72.1% | 72.6% | 65.0% | 77.4% | ↗ (0.0313) | ND |

Antimicrobial resistance phenotypes that remained at the same level during 2024-2025 and 2020-2025 were excluded (https://www.vetssi.dk/).
Abbreviations: Ap, *Actinobacillus pleuropneumoniae*; H-Ec, haemolytic *Escherichia coli*; NH-Ec, non-haemolytic *Escherichia coli*; R, resistant; ND, not determined.

**Figure 9.1 Statistically significant temporal changes in antimicrobial resistance phenotypes among pathogenic bacteria from pigs, Denmark, 2025 vs. 2024 and 2025 vs. 2020** DANMAP 2025



The continued high level of neomycin resistance in haemolytic *E. coli* (59.9%) is worrisome because it is one of only a few drugs recommended in Denmark as first choice for treating *E. coli*-associated post-weaning diarrhoea. Furthermore, haemolytic *E. coli* also displayed medium to high levels of resistance to the other first-choice drugs, including amoxicillin-clavulanic acid (38.6%), spectinomycin (64.3%), trimethoprim-sulfamethoxazole (66.7%) and streptomycin (87.9%). *E. coli* isolates from 2023, 2024 and 2025 were not tested for susceptibility to the remaining first-choice drug ampicillin as it is currently not available for treatment of pigs in Denmark. However, it should be noted that we observed a high level of ampicillin resistance in haemolytic *E. coli* from 2022 (60.9%) (DANMAP 2022), and resistance against amoxicillin without clavulanic acid was high in 2025 (75.4%). The rapid increase in neomycin resistance coincided with increased use of neomycin in weaners (DANMAP 2024) following two recent decisions to restrict the use of alternative drugs in pigs: 1) the Danish Yellow Card initiative to reduce the use of specific antibiotics in 2016 and 2) the European Union-wide ban of medicinal zinc in 2022.

The continued high level of gentamicin resistance in haemolytic *E. coli* (48.8%) is also worrisome because it is considered critically important for human medicine by the World Health Organization. We have previously shown that most of the gentamicin resistance genes found in haemolytic *E. coli* also confer resistance to apramycin, which is increasingly used in weaners (DANMAP 2024). In contrast, the use of gentamicin in pigs is negligible and cannot explain the rapidly increasing resistance to this drug (DANMAP 2024). Together, these observations suggest a causal relationship between increased use of apramycin and increased resistance to gentamicin in haemolytic *E. coli*.

It should also be noted that 6.8% of haemolytic *E. coli* isolates displayed resistance to 3rd generation cephalosporins (cefpodoxime). This subclass of antimicrobials is not used in pig production in Denmark, and the level of cefpodoxime resistance in haemolytic *E. coli* isolates has been relatively stable since testing started in 2022.

As observed for neomycin and apramycin, the use of amoxicillin in combination with a beta-lactamase inhibitor (e.g., clavulanic acid) in weaners has increased in recent years (DANMAP 2024), which might have contributed to the increasing level of resistance to amoxicillin-clavulanic acid and the occurrence of cefpodoxime resistance in haemolytic *E. coli*.

Finally, non-haemolytic *E. coli* displayed significantly increased resistance to amoxicillin-clavulanic acid (2025 vs. 2024) and trimethoprim-sulfamethoxazole (2025 vs. 2024).

## 9.4 Conclusions and perspectives

Pathogenic bacteria from acute mastitis in dairy cows generally displayed similar levels of phenotypic resistance as in 2024.

In haemolytic *E. coli* from pigs, the continued high level of resistance to first-choice drugs for treating *E. coli*-associated post-weaning diarrhoea and to drugs that are critically important for human medicine is worrisome and should be monitored closely in the coming years.

Interpretation of resistance to antimicrobial agents of veterinary importance are often based on tentative ECOFFs and ECOFFs as animal-specific clinical breakpoints for many drugs are currently lacking (e.g., penicillin resistance in *S. uberis* and neomycin resistance in *E. coli*). ECOFFs are based on microbiological studies and do not necessarily indicate whether a drug will be clinically active. Future studies should therefore seek to establish clinical breakpoints in animals by considering what happens to the drug within a specific animal and body site (pharmacokinetics).

It should be noted that the pathogenic bacteria isolated from pigs originate from outbreaks. As they are not randomly selected, the levels of resistance reported above do not necessarily reflect the national levels.

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# 10.

# Materials and methods

# 10. Materials and methods

## 10.1 General information

For the DANMAP 2024 report, population sizes and geographical data were obtained from Statistics Denmark [www.dst.dk] and data on the number of general practitioners from the Danish Medical Association [www.laeger.dk].

The epidemiological unit for pigs and cattle was defined at the individual farm level, meaning that only one isolate per bacterial species per farm was included in the report. The individual flock of broilers was defined as the epidemiological unit, and for food, the epidemiological unit was defined as the individual meat sample.

For humans, the epidemiological unit was defined as the individual patient and the first isolate per species per patient per year was included for analyses of AMR trends. An overview of all antimicrobial agents registered for humans and animals in Denmark is presented in Table 2.4.

## 10.2 Data on antimicrobial consumption in animals

### 10.2.1 Data

In Denmark, all antimicrobial agents used for treatment are available on prescription only. Until 2007, antimicrobial agents were exclusively sold by pharmacies or as medicated feed from the feed mills. This monopoly was suspended in April 2007, and since then private companies have been able to obtain license to sell prescribed veterinary medicinal products for animals, if they adhere to the same guidelines that apply to pharmacies. A pharmacy or licensed company either sells the medicine to veterinarians for use in their practice or for resale to farmers or sells the medicine directly to the animal owner upon presentation of a prescription.

Data on all sales of veterinary prescription medicine from pharmacies, private companies, feed mills and veterinarians are sent electronically to a central database, VetStat, which is hosted by the Danish Veterinary and Food Administration. Veterinarians are required by law to report all use of antibiotics and prescriptions for production animals to VetStat monthly.

For most veterinarians, the registration of data is linked to their invoice system. Electronic registration of the sales at pharmacies is linked to the billing process and stock accounts at the pharmacy. This ensure a very detailed data of high quality. Data are transferred daily from pharmacies to The Register of Medicinal Product Statistics at The Danish Health Authority and to VetStat.

In addition, data on coccidiostatics as feed additives (non-prescription) and antimicrobial growth promoters (not used since 2000) are also collected by VetStat, providing an almost complete register of all antimicrobial agents used for animals in Denmark since 2000. In very rare instances, medicine is prescribed on special license, i.e. medicines not approved for marketing in Denmark. These are not included in VetStat data.

VetStat contains detailed information about source (veterinarian/pharmacy/feed mill) and consumption for each prescription item: date of sale, identity of prescribing veterinarian, source ID (identity of the pharmacy, feed mill, or veterinarian practice reporting), package identity code and amount, animal species, age group, disease category and code for farm-identity (CHR Danish Central Husbandry Register). The package code is a unique identifier, relating to all information on the medicinal product, such as active ingredient, content as number of unit doses (e.g. number of tablets), package size, and code of the antimicrobial agent in the Veterinary Anatomical Therapeutic Chemical (ATCvet) classification system.

Knowledge of the target animal species enables the presentation of consumption data in "defined animal daily doses" (DADD) a national veterinary equivalent to the international defined daily doses (DDDs) system applied in the human sector [www.whocc.no]. The data presented in DANMAP 2025 were extracted from VetStat on 31 July 2026.

### 10.2.2 Methods

In DANMAP, we report use of antimicrobials in different animal populations. As a first step, the amount of antimicrobial agents used in animals is measured in kg active compound. This enables an overall crude comparison of consumption among different animal species and between the veterinary and human sectors.

Furthermore, a more detailed comparison of antimicrobial use is performed, taking into account potency, formulation, route of administration and the age of the animals (where relevant), by generating defined animal daily doses (DADDs). For these calculations, we select data with relevant animal and age group codes and relevant codes for dispensation. For example, when calculating the antimicrobial use for systemic treatment in pigs, we select consumption data where the age groups are defined as finishers, weaners, and sows (including piglets and boars) and exclude antimicrobials dispensed as tablets, products for topical use, intramammaries and gynaecologicals.

***Numerator - DADD***

Defined animal daily dose (DADD) is the average maintenance dose per day for a drug used for its main indication in the appropriate animal species. The DADD is not defined at product level but as mg active compound per kg live animal for each antimicrobial agent, administration route and animal species.

DADD has been specifically defined for use in DANMAP and does not always completely match the "prescribed daily dose" or the recommended dosage in the Summaries of Product Characteristics (SPC).

The following principles are applied when setting the DADDs:

1. Minor inconsistencies are corrected (e.g. due to rounding of numbers);
2. Approved dosage for the most widely used antimicrobial products is given priority above dosage for products that are rarely used;
3. Approved dosage for older products within the group is maintained as the common DADD even if a new product is approved with a higher dosage;
4. If the dosage for a group shows large variation in approved dosages of the products, the dosages provided by "The Veterinary Formulary" [British Veterinary Association 2005, 6th edition] are applied;
5. Dosages may vary within active compound and administration route, if different dosages have been approved for different age groups, indications or formulations.

When principles 3 and 4 are conflicting, principle 5 is applied.

**Denominator - live biomass**

The number of animals in a population (in epidemiological terms: the population at risk) is represented by their live biomass. The biomass of a species is calculated, taking into account average live bodyweight and the average lifespan in each age group. The estimation of live biomass and thus the number of standard animals at risk per day depends on the available data sources for each species. For DANMAP 2024, only the live biomass for pigs and cattle were updated. Pig production: The estimation was based on the number of pigs produced, including exports at different ages, productivity data for each year [Statistics Denmark; Danish Agriculture and Food Council] and census data for breeding animals [Statistics Denmark]. The average weight and life span for the growing animals (piglets, weaners and finishers) was estimated from the annual productivity numbers [Danish Agriculture and Food Council]. The size of the breeding animals (sows and boars) has probably increased over the last decade, but this was not accounted for.

Cattle production: The live biomass of the cattle population is estimated from census data [Statistics Denmark] and the average live weight of the different age groups. The Danish cattle population is mainly dairy, particularly Holstein Friesian, but also other breeds such as Jersey and a small population of beef cattle. Most of the cattle slaughtered are dairy cows and bull calves of dairy origin. The average live weight was estimated for 10 different age-gender categories.

**Treatment proportion - DAPD**

The treatment proportion is a statistical measure for AMU in animal populations, calculated as the annual number of DADDs administered in the population, divided by the estimated total population live biomass. For a single animal, the mg active compound (e.g. the number of DADDs) given in a daily treatment depends on the body weight. The treatment proportions, therefore, also represents the proportion of animals treated daily with an average maintenance- dose of a particular antimicrobial agent. These are reported as Defined animal daily dose per 1,000 animals per day (DAPD).

For example, 10 DAPDs indicate that an estimated 1% of the population, on average, receives a certain treatment on a given day. In principle, the metric DAPD is parallel to the metric DID, defined daily dose per 1,000 inhabitants per day (DID), used in pharmaco-epidemiology for the human sector, see Section 10.8.2.

In 2024, DAPD calculations were carried out for pigs and cattle.

For example, the antimicrobial use per pig produced is calculated as:

$$DAPD = \frac{DADD_{sows} + DADD_{weaners} + DADD_{finishers}}{\Sigma biomassdays}$$

Where DADDs, DADDw, and DADDf are amounts of antimicrobial agents used in finishers, weaners, and sows (including piglets and boars).

## 10.3 Collection of bacterial isolates from animals and meat

In DANMAP, samples originate both from the EU harmonised monitoring of antimicrobial resistance in zoonotic and commensal bacteria, and the national *Salmonella* surveillance programs. Since 2014, most isolates available for DANMAP have been collected in accordance with the EU harmonised monitoring, according to Decision 2013/652/EU. This Decision was repealed by Decision 2020/1729/EU, applied from 1 January 2021. With the aim to ensure continuity in assessing future trends in antimicrobial resistance, the new Implementing Decision includes adaptations of food categories to be sampled, sampling design to be followed, bacterial species to be tested and the analytical methods to be used.

EU harmonized monitoring from 2021 to 2027 shall cover *Salmonella* spp., *Campylobacter coli*, *Campylobacter jejuni*, indicator commensal *Escherichia coli*, ESBL-, AmpC- or carbapenemase- producing *Salmonella* spp. and *E. coli*, and may cover *Enterococcus faecalis* and *Enterococcus faecium*. Previously, monitoring of *Campylobacter coli* was voluntary. For the monitoring of *Salmonella* in poultry, it is now possible to report only samples collected within the national control programme in poultry farms, while the monitoring of *Salmonella* in fattening pigs at slaughter is still required for most countries, including Denmark, due to the inexistence of an implemented national surveillance programme which has been approved at EU level.

Additionally to monitoring of fresh meat at retail, the present EU legislation requires monitoring of indicator *E. coli* and ESBL-, AmpC- and CP-producing *E. coli* on fresh imported meat sampled at border control posts, and the fresh meat categories to be monitored include turkey, both at retail and at the border.

Decision 2020/1729/EU further allows the use of whole genome sequencing as an alternative method for the specific monitoring of ESBL-, AmpC- or CP-producing *E. coli* or for further testing of indicator *E. coli* and *Salmonella* showing resistance to cefotaxime, ceftazidime or meropenem.

The legislation continues to require mandatory sampling of broilers and fattening turkeys and meat thereof in even years (2022, 2024, 2026), and sampling of fattening pigs and cattle <1 year, and meat thereof in odd years (2021, 2023, 2025, 2027). In Denmark, fattening turkeys are not sampled at slaughter as part of the EU harmonised monitoring, because the national production of turkey meat is below 10.000 tonnes per year.

### 10.3.1 Animals

In 2024, most of the sampling for DANMAP was allocated to the mandatory sampling of caeca from at slaughter, and additional sampling of caeca from broilers fattening pigs and cattle <1 year was also carried out.

Caecal samples from healthy broilers, cattle (<1 year) and pigs were collected by meat inspection staff at the slaughterhouses. Samples were collected throughout the year, in major Danish slaughterhouses slaughtering conventionally produced broilers, pigs and cattle.

Sampling was stratified per slaughterhouse by allocating the number of samples from domestically produced animals per slaughterhouse, proportionally to the annual throughput of the slaughterhouse. For broiler flocks, ten intact caeca were pooled into one sample. For pigs and cattle, samples contained 30-100 g caecal material from a single animal.

All samples were processed by the Danish Veterinary and Food Administration's (DVFA) laboratory in Ringsted or by a DVFA-approved private laboratory. Samples from all three animal species were examined for indicator *E. coli*, and samples from broilers and cattle were examined for *Campylobacter jejuni* and *C. coli.*

Furthermore, pig and cattle samples were also examined for ESBL/AmpC/carbapenemase-producing *E. coli*, and pig samples for *Enterococcus faecalis and Enterococcus faecium* (Table 10.1).

Pathogenic bacteria from pigs reported in 2025 comprised *Actinobacillus pleuropneumoniae*, *Bordetella bronchiseptica*, haemolytic and non-haemolytic *Escherichia coli*, *Klebsiella pneumoniae*, *Salmonella enterica*, *Staphylococcus hyicus*, and *Streptococcus suis* isolates identified in clinical samples submitted by veterinarians to the Veterinary Laboratory, The Danish Agriculture and Food Council. Pathogenic bacteria from acute mastitis in dairy cows reported in 2025 were isolated from milk samples submitted to Statens Serum Institut by veterinarians.

### 10.3.2 Meat

In 2025, ESBL/AmpC/carbapenemase-producing *E. coli* were isolated from packages of fresh, chilled pork and beef meat collected in Danish wholesale and retail outlets. These samples were collected throughout the year by DVFA officers (Table 10.1). Products with added saltwater or other types of marinade as well as minced meat were not included. Packages of meat were selected without pre-selecting by country of origin, as requested for the harmonised EU monitoring.

The number of establishments and samples selected by each regional DVFA control unit was proportional to the number of establishments in the region in relation to the total number of establishments in the country. One unit of meat (minimum of 200 g) was collected and all samples were processed at the DVFA laboratory.

*Salmonella* isolates from domestically produced pork originated from the national control programme at the slaughterhouses (Table 10.1). Carcasses were swabbed in four designated areas (covering 4 x 100 $cm^2$) after min. 12 hours of chilling. All samples were processed at DVFA-approved Industry laboratories and isolates were sent to the DVFA laboratory.

**Table 10.1 Legislative and voluntary sampling plans under national control programmes and EU harmonised monitoring that contributed with isolates to DANMAP 2025** DANMAP 2025

| Bacteria | Origin of isolates | Legislative reporting frequency (2020/1729/EU) | Number of tested and positive samples in 2025 |
|---|---|---|---|
| *Campylobacter* spp. | Caecal samples from broilers[a]<br>Caecal samples from cattle <1 yr[a]<br>Caecal samples from fattening pigs[a] | Even years<br>Odd years<br>Odd years | 175 flocks (69 positive)<br>215 animals (193 positive)<br>414 animals (204 positive) |
| *Enterococcus* spp. | Caecal samples from fattening pigs[b] | Odd years | 490 animals (204 positive) |
| Indicator *E. coli* | Caecal samples from broilers<br>Caecal samples from fattening pigs<br>Caecal samples from cattle <1 yr | Even years<br>Odd years<br>Odd years | 137 flocks (130 positive)<br>179 animals (173 positive)<br>184 animals (177 positive) |
| Specific monitoring of ESBL/AmpC and carbapenemase-producing *E. coli* | Caecal samples from fattening pigs<br>Fresh pork meat at retail (Danish)<br>Fresh pork meat at retail (Imported)<br>Caecal samples from cattle <1 yr<br>Fresh beef meat at retail (Danish)<br>Fresh beef meat at retail (Imported)<br>WGS data for collected ESBL/AmpC isolates | Odd years<br>Odd years<br>Odd years<br>Odd years<br>Odd years<br>Odd years<br>Odd years | 409 animals (88 positive)[c]<br>240 units (3 positive)[c]<br>83 units (8 positive)[c]<br>308 animals (15 positive)[c]<br>144 units (1 positive)[c]<br>149 units (4 positive)[c]<br>117 isolates[d] |
| *Salmonella* spp. | Carcase swabs from fattening pigs[e]<br>Caecal samples from fattening pigs | Odd years<br>Odd years | 15,024 units (89 positive)[f]<br>888 animals (116 positive)[g] |

a) Broilers: *C. jejuni* (n=51), *C. coli* (n=11), unspecified (n=7) ; Cattle <1 yr: *C. jejuni* (n=173), *C. coli* (n=5), unspecified (n=15); Fattening pigs: *C. jejuni* (n=8), *C. coli* (n= 166), unspecified (n=30).
b) Fattening pigs: *E. faecalis* (n=122), *E. faecium* (n=80).
c) Positive for ESBL/AmpC-producing *E. coli* and negative for carbapenemase-producing *E. coli.*
d) 117 isolates from the positive samples were sequenced (15 from cattle, 1 from Danish beef meat, 4 from imported beef meat, 87 from pigs, 3 from Danish pork meat, and 7 from imported pork meat).
e) Carcass swab samples are part of the national *Salmonella* surveillance program and are classified in DANMAP as meat of domestic origin. Samples collected at slaughterhouses slaughtering more than 30,000 pigs are analysed in pools of 5 individual samples. The total number of animals tested and the total number of positives refer to individual pooled samples.
f) Pork meat (carcass): S. 4,[5],12:i:- (n=25), *S.* Derby (n=40), *S.* Typhimurium (n=9), other serotypes or unspecified (n=15)
g) Caecal samples from fattening pigs: S. 4,[5],12:i:- (n=27), *S.* Derby (n=63), *S.* Typhimurium (n=14), other serotypes or unspecified (n=12)

## 10.4 Microbiological methods – isolates from animals and meat

### 10.4.1 *Salmonella*

*Salmonella* from pork not originating from the national *Salmonella* surveillance program were isolated at DVFA in accordance with the methods issued by the NMKL [NMKL No. 187, 2007] and in accordance with Annex D, ISO 6579-1 [ISO6579-1:2017]. Serotyping of those isolates was performed at DVFA by whole genome sequencing using the Illumina MiSeq platform, paired-end sequencing 2x250 cycles. For bioinformatics, a CGE service (Centre for Genomic Epidemiology, DTU) for *Salmonella* serotyping was applied based on the genetic background for antigenic formulas given by the White-Kauffmann-Le Minor scheme.

*Salmonella* from carcasses originating from the national *Salmonella* surveillance program were isolated and serotyped according to the White-Kauffmann-Le Minor scheme at DVFA-approved Industry laboratories.

### 10.4.2 *Campylobacter*

*Campylobacter* from broilers, pigs and cattle was isolated and identified according to the methods issued by the NMKL [NMKL No. 119, 2007] with modifications, with pre-enrichment in Bolton broth, and followed by species-determination by BAX® rtPCR assay (Hygiena, BAX® System PCR Assays for Campylobacter). Only one *Campylobacter* isolate per flock or herd was selected for antimicrobial susceptibility testing.

### 10.4.3 *Escherichia coli*

Indicator *E. coli* from broilers, pigs and cattle was isolated by direct spread onto violet red bile agar incubated for 24h at 44 °C. Presumptive *E. coli* was identified on TBX agar incubated at 44 °C o/n. Only one indicator *E. coli* isolate per flock or herd was selected. The specific isolation of ESBL/AmpC or carbapenemase-producing *E. coli* from broiler and turkey meat and caecal samples from broilers occurred within 96 h after sample collection, applying the current EURL-AR laboratory protocol [https://www.eurl-ar.eu/protocols.aspx]. Carbapenemase-producing *E. coli* screening was done with ChromID CARBA and ChromID OXA-48 plates. ESBL/AmpC-producing *E. coli* screening was done with MCA cefotaxime plates. All presumptive ESBL/AmpC or carbapenemase producing *E. coli* isolates were sequenced by WGS using the Illumina MiSeq platform (paired-end sequencing 2x250). Only one ESBL/AmpC-producing *E. coli* isolate per herd and meat sample was selected for antimicrobial susceptibility testing.

### 10.4.4 Enterococci

Indicator enterococci were isolated from pig caeca by adding 2 ml buffered peptone water to the content of a cotton swab, after which 100 µl were inoculated onto Slanetz agar and incubated for 48 h at 41,5 °C. Presumptive *E. faecium/E. faecalis* were identified by real-time PCR assay. When present, only one *E. faecalis or E. faecium* isolate per herd was selected for antimicrobial susceptibility testing.

## 10.5 Susceptibility testing – isolates from animals and meat

Antimicrobial susceptibility testing of *Salmonella, Campylobacter* and *E. coli* was carried out by Minimum Inhibitory Concentration (MIC) determination, using broth microdilution by Sensititre (Trek Diagnostic Systems Ltd.). Inoculation and incubation procedures were performed in accordance with the CLSI guidelines [Clinical and Laboratory Standards Institute, USA] and the European standard [ISO 20776-1:2020]. The isolates were tested for antimicrobial susceptibility in accordance with the Decision 2020/1729/EU about the EU harmonised monitoring of antimicrobial resistance.

The quality control strains used were: *E. coli* ATCC 25922, *E. faecalis* ATCC 29212, *C. jejuni* ATCC 33560 and *P. aeruginosa* ATCC 27853. Isolates from animals and meat were tested for antimicrobial susceptibility at the DVFA laboratory in Ringsted, which is accredited by DANAK (the national body for accreditation).

Antimicrobial susceptibility testing of pathogenic bacteria from pigs was performed at the Veterinary Laboratory, The Danish Agriculture and Food Council. In brief, MICs were determined by broth microdilution using customised Sensititre panels according to CLSI standards. The analysis is accredited by DANAK.

**Table 10.2 Interpretation criteriae for MIC-testing by EUCAST- and EFSA-provided epidemiological cut-off values (ECOFFs)**

DANMAP 2025

| Antimicrobial agent | *Salmonella* | *E. coli* | *E. faecalis* | *C. jejuni* | *C. coli* |
|---|---|---|---|---|---|
| | ECOFF µg/ml | ECOFF µg/ml | ECOFF µg/ml | ECOFF µg/ml | ECOFF µg/ml |
| Amikacin | >4 | >8 | Not tested | Not tested | Not tested |
| Ampicillin | >8 | >8 | >4 | Not tested | Not tested |
| Azithromycin | >16 | >16 [a] | Not tested | Not tested | Not tested |
| Cefepime | >0.125 [a] | >0.125 [a] | Not tested | Not tested | Not tested |
| Cefotaxime | >0.5 | >0.25 | Not tested | Not tested | Not tested |
| Cefotaxime-clavulanic acid | >0.5 [a] | >0.25 | Not tested | Not tested | Not tested |
| Cefoxitin | >8 | >8 | Not tested | Not tested | Not tested |
| Ceftazidime | >2 | >0.5 | Not tested | Not tested | Not tested |
| Ceftazidime-clavulanic acid | >2 [a] | >0.5 | Not tested | Not tested | Not tested |
| Chloramphenicol | >16 | >16 | >32 | >16 [d] | >16 [d] |
| Ciprofloxacin | >0.064 | >0.064 | >4 | >0.5 | >0.5 |
| Colistin | >2 [a] [b] | >2 | Not tested | Not tested | Not tested |
| Daptomycin | Not tested | Not tested | >4 | Not tested | Not tested |
| Ertapenem | >0.064 [a] | >0.064 [a] | Not tested | >0.5 [a] [d] | >0.5 [a] [d] |
| Erythromycin | Not tested | Not tested | >4 | >4 | >8 |
| Gentamicin | >2 | >2 | >64 | >2 [a] | >2 [a] |
| Imipenem | >1 | >0.5 | Not tested | Not tested | Not tested |
| Linezolid | Not tested | Not tested | >4 | Not tested | Not tested |
| Meropenem | >0.125 [a] | >0.125 | Not tested | Not tested | Not tested |
| Nalidixic acid | >8 | >8 | Not tested | Not tested | Not tested |
| Quinopristin-dalfopristin | Not tested | Not tested | >1 [a] [c] | Not tested | Not tested |
| Sulfamethoxazole | >256 [a] | >64 [a] | Not tested | Not tested | Not tested |
| Teicoplanin | Not tested | Not tested | >2 | Not tested | Not tested |
| Temocillin | >16 [a] | >16 | Not tested | Not tested | Not tested |
| Tetracycline | >8 | >8 | >4 | >1 | >2 |
| Tigecycline | >0.5 [a] | >0.5 | >0.25 | Not tested | Not tested |
| Trimethoprim | >2 | >2 | Not tested | Not tested | Not tested |
| Vancomycin | Not tested | Not tested | >4 | Not tested | Not tested |

EUCAST epidemiological cut-off values (ECOFFs) and ECOFFs provided by EFSA for EU harmonized reporting.
a) ECOFF as provided by EFSA [EFSA Supporting publication 2023:EN-7826].
b) For colistin, a tentative ECOFF of 16 µg/ml for *Salmonella* Dublin is established by EUCAST. The same ECOFF is used in DANMAP to interpret results of *Salmonella* Enteritidis. Both serotypes belong to the O-group (O:1, 9,12), which has been associated with increased MIC for colistin [https://www.doi.org/10.1089/fpd.2011.1015].
c) For quinopristin-dalfopristin, ECOFF only applies for *E. faecium*. ECOFF >1 for *E. faecalis* (intrinsically resistant to quinopristin-dalfopristin) is used only for the purpose of EU harmonized reporting.
d) In 2021, chloramphenicol and ertapenem were introduced in the test panel for *Campylobacter* spp..

Milk samples from dairy cows with acute mastitis were collected by veterinarians at clinics across Denmark and submitted to Statens Serum Institut. Pathogens were isolated using standard culture techniques and identified to genus or species level by MALDI-TOF. Antimicrobial susceptibility testing was performed by broth microdilution using organism-specific Sensititre panels according to CLSI standards.

## 10.6 Whole genome sequencing - isolates from animals and meat

Whole genome sequencing (WGS) and in silico bioinformatics tools were used to detect the genetic background of the ESBL/AmpC and carbapenemase-producing *E. coli*. At the DVFA laboratory in Ringsted, strains were sequenced using the Illumina MiSeq platform and the bioinformatics analysis was conducted at DTU National Food Institute using the ResFinder application v. 4.5.0 and the ResFinder database v. 2.2.1.

Whole genome sequences of all sequenced *S.* Typhimurium and monophasic *S.* Typhimurium isolates from Danish pork were analysed for AMR determinants using the AMRFinderPlus tool (v. 4.2.7) with the AMRFinderPlus database (v. 2026-01-21.1). Detection parameters were set a minimum length coverage of 0.5 and the sequence identity threshold of 0.9. From the identified AMR proteins, only core resistance proteins were included in the analysis.

## 10.7 Data handling - isolates from animals and meat

For the samples processed at the DVFA laboratory, sampling details and laboratory results were stored in the DVFA Laboratory system. Following validation by DVFA, data were sent to DTU National Food Institute (Excel sheets). At the DTU National Food Institute, data were harmonised and one isolate per epidemiological unit was selected for reporting.

For the samples processed at the Veterinary Laboratory, The Danish Agriculture and Food Council, sampling details and laboratory results were stored in the information management system used at the Veterinary Laboratory. Following internal validation and anonymisation, data were sent to DK-VET (Excel sheets). At DK-VET, data were harmonised and one isolate per epidemiological unit was selected for reporting.

### 10.7.1 Interpretation of MIC values

MIC values were retained as continuous variables, from which binary variables (resistant/sensitive) were created using the relevant cut-off. Since 2007, MIC results have been interpreted using EUCAST epidemiological cut-off (ECOFF) values, with a few exceptions, as described in Table 10.2. An isolate is considered multidrug-resistant if resistant to three or more of the antimicrobial classes defined in Table 10.3 and fully sensitive if susceptible to all antimicrobial agents included in the test panel.

**Table 10.3 Definitions of antimicrobial classes for calculation of multidrug-resistance in *Salmonella* and indicator *E. coli***

DANMAP 2025

| Antimicrobial classes | *Salmonella* and *E. coli* |
|---|---|
| Beta-lactam penicillins | Ampicillin |
| Macrolides | Azithromycin |
| Cephalosporins | Cefotaxime and/or ceftazidime |
| Phenicols | Chloramphenicol |
| Quinolones | Ciprofloxacin and/or nalidixic acid |
| Polymyxins | Colistin |
| Aminoglycosides | Gentamicin and/or amikacin |
| Carbapenems | Meropenem |
| Sulfonamides | Sulfamethoxazole |
| Tetracyclines | Tetracycline |
| Glycylcyclines | Tigecycline |
| Trimethoprim | Trimethoprim |

An isolate is considered multidrug-resistant if resistant to three or more of the defined antimicrobial classes and fully susceptible if sensitive to all antimicrobial agents included in the test panel; The aminoglycoside antimicrobial amikacin has been introduced in the test panel in 2021.

For pathogenic bacteria from pigs, MIC values were interpreted with ECOFFs (1st choice) or tentative ECOFFs (2nd choice) established by EUCAST. When ECOFFs were unavailable, interpretation was based on CLSI-approved animal-specific or human clinical breakpoints (3rd and 4th choice, respectively) (available at https://www.vetssi.dk/).

### 10.7.2 ESBL/AmpC phenotypes

Classification of CP-, ESBL- or AmpC-producing phenotypes was done according to the scheme provided by EFSA. [EFSA 2023. EFSA Journal 21(3):7867].

1. ESBL phenotype if cefotaxime and/or ceftazidime MIC >1 µg/ml and meropenem MIC <=0.12 µg/ml and cefoxitin MIC <=8 µg/ml and synergy (clavulanic acid and cefotaxime/ceftazidime);
2. AmpC phenotype if cefotaxime and/or ceftazidime MIC >1 µg/ml and meropenem MIC <=0.12 µg/ml and cefoxitin MIC >8 µg/ ml and no synergy (clavulanic acid and cefotaxime/ceftazidime);
3. ESBL-AmpC phenotype if cefotaxime and/or ceftazidime MIC >1 µg/ml and meropenem MIC <=0.12 µg/ml and cefoxitin MIC >8 µg/ml and synergy (clavulanic acid and cefotaxime/ ceftazidime);
4. CP phenotype if meropenem MIC >0.12 µg/ml;
5. Other phenotype if not in 1-4.

Synergy is defined as ≥3 twofold concentration decrease in MIC for clavulanic acid combined with cefotaxime/ceftazidime vs the MIC of cefotaxime/ceftazidime alone.

### 10.7.3 Statistical tests

When performed, significance tests of differences between proportions of resistant isolates were calculated using Chi-square, or Fisher's Exact Tests as appropriate depending on sample size. Significance tests for trends in rates of resistance were performed by applying the Cochran-Armitage test, using the DescTools R package. One-sided tests were chosen because of preliminary expected trend directions. A significance level of 0.05 was considered in all significance tests.

Analyses were done using R statistical software [R Core Team (2019). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. https://www.R-project.org].

## 10.8 Data on antimicrobial consumption in humans

### 10.8.1 Data registration

Annual data on antimicrobial consumption in Denmark has been provided to DANMAP by the Register of Medicinal Product Statistics at the Danish Health Data Authority every year since 1997. Since 2020, DANMAP also reports monthly antimicrobial consumption data to allow analysis of the impact of the Covid-19 pandemic on antimicrobial consumption in humans since 2020.

Until 2012, data from hospitals on certain infusion substances such as cephalosporins, carbapenems and trimethoprim were obtained by DANMAP directly from hospital pharmacies. Since 2013, all data from hospitals are reported to and provided to DANMAP by The Register of Medicinal Product Statistics at the Danish Health Data Authority.

Reports of human antimicrobial consumption in Denmark existed already before 1997. These were prepared by the Association of Medicine Importers (Medicinimportørforeningen, MEDIF) and the Association of Danish Medicinal Factories (Foreningen af danske Medicinfabrikker, MEFA) based on whole sales data to pharmacies. These reports became less reliable over time since there was an increasing amount of parallel imported drugs from the late 1980s, which were not covered by MEDIF/MEFA.

In the primary sector, all antibacterial agents for human use are prescription-only medicines. Sales are reported by pharmacies using a code relating to the defined package. The code includes information on the active drug, the brand name of the product, formulation, size and number of packages. The report also includes age, gender and regional residence of the patient. Since 2004, the sales registration has included a code for indication of the prescription as well. However, clinical indications provided for the treatment of infectious diseases were often quite unspecific ("against infection"). Since 2016, the use of more specific indication codes has increased following the implementation of electronic prescribing via the "common medicine card" (fælles medicinkortet, FMK), a digital pharmacy platform which is mandatory to be used by all medical doctors. In 2023, indication codes were available for 94% of prescriptions, but specific indication codes still only accounted for 75%.

For hospitals, reporting is based on deliveries from the hospital pharmacies to the different clinical departments and includes all generic products that are supplied through general trade agreements between different medical suppliers and Amgros, a private company under agreement with the five Danish Regions. Amgros is responsible for harmonisation of prices and for ensuring deliveries to all hospitals and works closely together with the Regions' Joint Procurement. Detailed information is given on the different drugs delivered on ATC5 level. For surveillance purposes, it has to be assumed that the amount of delivered antimicrobials is similar to the consumption at the different departments. In reality, antimicrobials may be exchanged between different specialties and departments belonging to the same hospital making precise calculations of the consumption on specialty level difficult. In DANMAP, reporting of data on hospital consumption is therefore kept at national and regional level. In case of production failures and shortages in delivery of specific products, the hospitals have to apply for special delivery through the Danish Medicines Agency (Figure A5.2 in web annex). These special deliveries are reported separately to DANMAP through the hospital pharmacies. An example is the shortages in delivery of piperacillin with tazobactam and pivmecillinam as well as mecillinam in 2017. The shortage in piperacillin with tazobactam had significant impact on the amount used, while the shortage in (piv)mecillinam could not be clearly tracked in changes in consumption. In 2023, 126.490 DDD (3%) of the total antimicrobial consumption were special deliveries. Data on consumption at patient level are available at some hospitals and have so far been used in local quality assurance only but have not been available to DANMAP.

### 10.8.2 Method

Primarily somatic hospitals were included in the DANMAP reporting. Data from private hospitals and clinics, psychiatric hospitals, specialised non-acute care clinics, rehabilitation centres and hospices were excluded from DANMAP in most calculations since their activity and functions are not comparable to public, somatic hospitals and therefor may skew the data. Their consumption accounts for approximately 3% of the antimicrobial consumption at hospitals in Denmark.

The present report includes data on the consumption of "antibacterials for systemic use", or group J01, of the 2023 update of the Anatomical Therapeutic Chemical (ATC) classification, in primary healthcare and in hospitals as well as consumption of oral and rectal preparations of metronidazole (P01AB01) and for hospitals oral preparations of vancomycin (A07AA09). As recommended by the World Health Organization (WHO), consumption of antibacterial agents in primary healthcare is expressed as DIDs, i.e. the number of DDDs per 1,000 inhabitants per day.

The consumption in hospital healthcare is expressed as the number of DDDs per 100 occupied beds per day (DDD/100 occupied bed-days or DBD). Since reporting in DBD does not necessarily reflect changes in hospital activity and production, consumption at hospitals is also presented as DAD (the number of DDDs per 100 admissions) and crude DDD. Finally, the consumption of antibacterial agents at hospitals has also been calculated in DIDs, primarily for comparison with primary healthcare.

### 10.8.3 DDD

Defined daily dose is the assumed average maintenance dose per day for a drug used for it's main indication in adults. DDDs provide a fixed unit of measurement independent of price and formulation, enabling the assessment of trends in drug consumption and to perform comparisons between population groups. The DDDs are defined and revised yearly by the WHO Collaborating Centre for Drug Statistics and Methodology [https://www.whocc.no/atc_ddd_index/].

Per January 2019 the WHO updated the DDDs for seven main antimicrobial agents, based on recommendations from an expert working group in collaboration with the European Center for Disease Control (ECDC) (Table 10.5). From DANMAP 2018, the new DDD values were applied and all tables and figures were updated ten years back.

### 10.8.4 DBD

DDD/100 occupied bed-days. The number of occupied bed-days are calculated as the exact duration of a hospital stay in hours divided by 24 hours. Number of bed-days was extracted from the National Patient Registry at the Danish Health Data Authority [www.sundhedsdatastyrelsen.dk].

The National Patient Registry was upgraded in 2019 and data are still being validated and may be adjusted in the future. This has to be kept in mind when data are interpreted.

### 10.8.5 DAD

DDD/100 admissions. One admission is registered whenever a patient is admitted to a specific hospital for ≥12 hours. If a patient is transferred between wards within 4 hours, it will not count as a new admission. The admissions were extracted from the National Patient Registry at the Danish Health Data Authority [www.sundhedsdatastyrelsen.dk].

The National Patient Registry was upgraded in 2019 and data are still being validated and may be adjusted in the future. This has to be kept in mind when data are interpreted.

### 10.8.6 Antimicrobial consumption for older inhabitants living in long care facilities

Data from the Care Home Register were combined with data from the Danish Civil Registration System (CPR) and with data from the Register of Medicinal Product Statistics in order to determine the antimicrobial consumption for older people living in care homes and for people living in their own homes.

## 10.9 *Salmonella* and *Campylobacter* isolates from humans

### 10.9.1 Data source

Antimicrobial susceptibility was performed on human clinical isolates submitted to Statens Serum Institut (SSI). *Salmonella* isolates were submitted from all clinical microbiology laboratories in Denmark and *Campylobacter* isolates were submitted from clinical microbiology laboratories representing the island of Zealand excluding the Capital Region, Funen, and Northern Jutland. As in previous years, SSI collected information on travel history from the patients. Cases were categorised as "domestically acquired" if the patients had not travelled abroad within the week prior to the onset of disease. Data on *Salmonella* and *Campylobacter* infections are stored in the Danish Registry of Enteric Pathogens (SQL database) that is maintained by SSI. This register includes only one isolate per patient within a window of six months and includes the recorded data on susceptibility testing of *Salmonella* and *Campylobacter*.

**Table 10.4 New DDDs assigned by WHO Collaborating Centre per January 2019** DANMAP 2025

| ATC5 code | ATC level name | Previous DDD | | | New DDD | | |
|---|---|---|---|---|---|---|---|
| | | Weight | Unit | Route of administration | Weight | Unit | Route of administration |
| J01CA01 | Ampicillin | 2.0 | g | Parenteral | 6.0 | g | Parenteral |
| J01CA04 | Amoxicillin | 1.0 | g | Oral | 1.5 | g | Oral |
| J01CA04 | Amoxicillin | 1.0 | g | Parenteral | 3.0 | g | Parenteral |
| J01CA17 | Temocillin | 2.0 | g | Parenteral | 4.0 | g | Parenteral |
| J01CR02 | Amoxicillin and beta-lactamase inhibitor | 1.0 | g | Oral | 1.5 | g | Oral |
| J01DE01 | Cefepime | 2.0 | g | Parenteral | 4.0 | g | Parenteral |
| J01DH02 | Meropenem | 2.0 | g | Parenteral | 3.0 | g | Parenteral |
| J01MA02 | Ciprofloxacin | 0.5 | g | Parenteral | 0.8 | g | Parenteral |
| J01XB01 | Colistin | 3.0 | MU | Parenteral | 9.0 | MU | Parenteral |

### 10.9.2 Serotype and species identification

*Salmonella* isolates were analysed by whole genome sequencing and the serotypes were derived from the DNA sequences. In a few cases, the DNA information was supplemented with slide agglutination according to the Kauffman-White Scheme. *Campylobacter* species identification was performed by the use of MALDI-TOF.

### 10.9.3 Susceptibility testing

Antimicrobial susceptibility testing of *Salmonella* and *Campylobacter* was performed as Minimum Inhibitory Concentration (MIC) determination using the Sensititre broth microdilution system (ThermoFisher Scientific). Inoculation and incubation procedures were in accordance with the EU protocol for harmonised monitoring of antimicrobial resistance in human *Salmonella* and *Campylobacter* isolates – June 2016, see "http://www.ecdc.europa.eu/en". The interpretation criteria for MIC testing were done using ECOFFs, see Table 10.2.

### 10.9.4 Identification of AMR determinants in *Salmonella* isolates

Whole genome sequences of all sequenced *S.* Typhimurium and monophasic *S.* Typhimurium were analysed for AMR determinant using the AMRFinderPlus tool (v. 4.2.7) with the AMRFinderPlus database (v. 2026-01-21.1). Detection parameters were set a minimum length coverage of 0.5 and the sequence identity threshold of 0.9. From the identified AMR proteins, only core resistance proteins were included in the analysis. The occurrence of each AMR determinant was calculated as the proportion of all *S.* Typhimurium and *S.* Typhimurium monophasic variant isolates within the respective year and travel-status category. Isolates with unknown travel status were excluded from comparisons between domestic and travel-associated isolates

## 10.10 *Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Acinetobacter* species, *Enterococcus faecium* and *Enterococcus faecalis* isolates from humans

### 10.10.1 Data source

The surveillance of invasive isolates of *E. coli, K. pneumoniae, E. faecalis* and *faecium, P. aeruginosa* and A. spp. and urine isolates of *E. coli* and *K. pneumoniae* are all based on data from routine diagnostics at the ten Departments of Clinical Microbiology (DCMs) in Denmark. All data were extracted directly from the Danish Microbiology Database (MiBa) [https://miba.ssi.dk]. Before 2018, data were reported by the individual DCM to SSI. A description of MiBa and the usage and validation of MiBa-data is given in Textbox 8.1 in DANMAP 2018 [www.danmap.org].

### 10.10.2 Microbiological methods

All microbiological analyses including species identification, susceptibility testing and interpretation of test results, were performed by the DCM. Since November 2015, all Danish DCMs used the EUCAST terminology with the EUCAST clinical breakpoints and the EUCAST methods for roughly all species. Few exceptions exist at some DCMs where local rules were applied to the susceptibility interpretations in specific cases - e.g. susceptibility to mecillinam in invasive cases. In 2019 EUCAST introduced the Area of Technical Uncertainty (ATU) for some combinations of species and agents reflecting problematic areas regarding variations and uncertainty of susceptibility categorisation. Piperacillin-tazobactam, ciprofloxacin and amoxicillin-clavulanic acid (in systemic breakpoints) and Enterobacterales are examples where ATUs were applied. ATUs can be handled differently by individual DCMs and may influence interpretation results. This was commented on when necessary in the affected sections.

To be included in resistance surveillance more than 75% of respective isolates need to be antimicrobial susceptibility tested for a given antibiotic, if not stated otherwise. Data of antimicrobial susceptibility testing was mainly performed by disc diffusion. The presented data consist of the registered interpretation results, performed by the respective DCM, based on the S-I-R system. In addition, zone diameters have also been registered since 2015 and will be commented upon in specific cases.

Urine specimen taken in primary health care are also being tested at DCMs except for some samples taken by GPs in the Capital Region of Denmark that are being tested at a private laboratory.

All enterococci isolates reported as VRE in MiBa (based on PCR results for *vanA/B* genes) were reported as vancomycin-resistant independent of the actual zone/MIC result. It was not distinguished between VRE and VVE (vancomycin-variable enterococci). High-level resistance to gentamicin was defined using EUCAST break points (MIC >128 mg/L and/or zone diameters <8 mm) for MIC and/or zone diameters reported in MiBa. Gentamicin MIC and/or zone diameters were routinely reported by three DCMs in 2020.

### 10.10.3 Data handling

Cases and susceptibility results were extracted from MiBa and analysed in Python 3.8.10.

The case definition has been harmonised with the definition used by the European Antimicrobial Resistance Surveillance Network (EARS-Net): The first sample, by date of sample collection, of each given bacterial species per unique patient per year of observation. Duplicates from the same patient, within the year of observation, were removed. Thereby only resistance data on the first isolate per patient per specimen per year were included. Resistance data from DCMs were excluded if not tested or registered in MiBa routinely (minimum 75% of the specific species/antimicrobial agent combination). Samples were either invasive (including blood cultures or cerebrospinal fluid) or urinary samples from patients at hospitals or primary healthcare settings.

## 10.11 ESBL-producing bacterial isolates from humans

### 10.11.1 Data source

Since 2014, the Danish DCMs have on a voluntary basis submitted 3rd generation cephalosporin-resistant *Escherichia coli* isolates from bloodstream infections for verification and genotyping at the Antimicrobial Resistance Reference Laboratory, Statens Serum Institut.

### 10.11.2 Microbiological methods of isolates from patients

Since 2014, whole genome sequencing (WGS) and in silico bioinformatics analysis have been applied for isolates predicted to carry ESBL and/or AmpC genes based on initial phenotypic tests, to characterize the genetic background of the ESBL and/or AmpC phenotypes. Only one isolate from each patient was included if less than 12 months were between isolation of the two isolates.

### 10.11.3 Data handling

The quality of the raw sequencing and assembly data was ensured using the analytical tool BIFROST [https://github.com/ssi-dk/bifrost/]. An in-house bacterial analysis pipeline, building on a weekly update of the ResFinder database [https://bitbucket.org/genomicepidemiology/resfinder/src/master/] was used for the in silico detection of acquired ESBL genes, pAmpCs, carbapenemase genes and MLST from assembled WGS data. For isolates with no ESBL-, pAmpC-, or carbapenemase-encoding genes detected, the sequences were investigated for promotor mutations presumed to up-regulate chromosomal AmpC by the use of myDb-Finder version 1.2 [https://cge.food.dtu.dk/]. Possible clonal clusters were detected using the SeqSphere+ (Ridom) software to call cgMLST types (*E. coli* scheme).

## 10.12 CPO isolates from humans

### 10.12.1 Data source

Historically, Danish DCMs have submitted carbapenem-resistant isolates for verification and genotyping on a voluntary basis to the Antimicrobial Resistance Reference Laboratory at the Statens Serum Institut. Since 5 September 2018, notification of CPO has been mandatory in Denmark. For outbreak investi-gation Data from The National Patient Register (LPR), informa-tion gathered at the hospitals and information of residence from the Danish Civil Registration System (CPR) has been included in the analysis for this report.

### 10.12.2 Microbiological methods

All submitted isolates (originating both from screening and clinical samples) predicted to carry a carbapenemase based on initial phenotypic tests were analysed using WGS. More than one isolate from the same patient was only included in the dataset if the isolates belonged to different bacterial species and/or if isolates within the same species harboured different carbapenemases.

### 10.12.3 Data handling

The quality of the raw sequencing and assembly data was ensured using the analytical tool BIFROST [https://github.com/ssi-dk/bifrost/]. An in-house bacterial analysis pipeline, building on a weekly update of the ResFinder database [https://bitbucket.org/genomicepidemiology/resfinder], was used for the in silico detection of acquired CPO genes and MLST from assembled WGS data. Possible clonal clusters were detected using the SeqSphere+ (Ridom) software to call cgMLST types where such schemes are available (*E. coli*, *Klebsiella pneumoniae* and *Acinetobacter baumannii*). For outbreak investigations, identified clonal clusters were linked with patient data like time and place of hospitalization and place of residence. Identification of isolates from two or more persons (cases) sharing the same unique genotype was defined as an outbreak. An outbreak was defined as a verified outbreak if an epidemiological link could be established between two or more cases in the cluster, e.g. the patients had been at the same hospital ward at the same time or lived at the same geographical location such as a nursing home. When no epidemiological link could be establish between cases with the same unique genotype, the outbreak was classified as a possible outbreak. A possible outbreak can be reclassified as a verified outbreak if new cases or information providing an epidemiological link between two or more of the cases becomes available. Both, possible and verified outbreaks, are registered in the CPO-outbreak database KURS (coordinated outbreak registration).

Outbreak investigations of a cluster of cases are closed when no new cases have been reported within 6 months after the last reported case, but can be reopened, if new cases are being detected.

## 10.13 VRE isolates from humans

### 10.13.1 Data source

Danish DCMs are submitting VRE for species identification, genotyping and surveillance on a voluntary basis to the Antimicrobial Resistance Reference Laboratory at Statens Serum Institut.

### 10.13.2 Microbiological methods

All clinical VRE isolates have been whole-genome sequenced. Only one isolate from each patient was included if less than 12 months were between isolation of the two isolates.

### 10.13.3 Data handling

The quality of the raw sequencing and assembly data was ensured using the analytical tool BIFROST [https://github.com/ssi-dk/bifrost/]. An in-house bacterial analysis pipeline, building on a weekly update of the ResFinder database [https://bitbucket.org/genomicepidemiology/resfinder], was used for the in silico detection of genes related to vancomycin resistance in enterococci and MLST from assembled WGS data. Possible clonal clusters were detected using the SeqSphere+ (Ridom) software to call cgMLST types.

## 10.14 Invasive *Streptococcus pneumoniae* isolates from humans

### 10.14.1 Data source

Invasive pneumococcal disease is a notifiable disease in Denmark and it is mandatory to submit all invasive isolates of *S. pneumoniae* for serotyping and susceptibility testing to the Neisseria and Streptococci Reference Laboratory at Statens Serum Institut. For cases of invasive pneumococcal disease, where isolates from blood/spinal fluid could not be submitted, identification and registration of cases is conducted by extracting the required information from the Danish Microbiology Database (MiBa).

### 10.14.2 Microbiological methods

Identification or confirmation of the species *S. pneumoniae* was based on: visual evaluation of colonies, positive optochin test and test with either latex omni test (ImmuLex™ *S. pneumoniae* Omni, SSI Diagnostica, Denmark) or Neufeld based Omni serum (SSI Diagnostica, Denmark). If challenging results occurred, MALDI-TOF, bile solubility test, or whole genome sequencing were performed to further confirm the correct species identification. For non-viable isolates, species identification was based on the detection of the lytA and Ply gene by the use of PCR.

Serotype identification of invasive *S. pneumoniae* was performed by the use of latex agglutination (ImmuLex™ Pneumotest Kit, SSI Diagnostica, Denmark) and serotype specific antisera by the Neufeld test (SSI Diagnostica, Denmark). For non-viable isolates, serotyping was often possible by the use of PCR.

### 10.14.3 Susceptibility testing

Screening for penicillin- and erythromycin-resistant *S. pneumoniae* was performed with 1 µg oxacillin discs and 15 µg erythromycin discs (Oxoid, Roskilde, Denmark), respectively, on Mueller-Hinton agar (Mueller-Hinton plate, 5% blood, SSI Diagnostica, Denmark). Breakpoints were according to EUCAST Clinical Breakpoint Tables v. 11.0. Isolates, that were found non-susceptible by screening were further analysed for penicillin and erythromycin MICs by broth microdilution using the STP6F plate, Sensititre (Trek Diagnostic Systems, Thermo Scientific) as recommended by the manufacturer. All breakpoints used were as defined by EUCAST (Eucast Clinical Breakpoint Tables v.11.0). For cases, where an isolate was not received at the reference laboratory, susceptibility data could often be found in MiBa.

### 10.14.4 Data handling

Only cases with isolates from blood or spinal fluid were included in the DANMAP report. Repeated samples within a 30 days window were classified as duplicates and were omitted from the analysis.

## 10.15 Isolates of beta-haemolytic streptococci of groups A, B, C, and G from invasive infections in humans

### 10.15.1 Data source

All invasive isolates of beta-haemolytic streptococci (BHS) (e.g., blood, cerebrospinal fluid, synovial fluid, pleural fluid, ascites, and tissue obtained during surgery) were submitted to SSI from the departments of clinical microbiology on a voluntary basis.10.15.2 Microbiological methods

Identification of streptococcal group was performed by latex agglutination (Streptococcal Grouping Reagent, Oxoid, Denmark). Genomic DNA was extracted using an enzymatic pre-lysis step before automated purification on MagNA Pure 96 DNA Small Volume Kit (Roche Diagnostics). Fragment libraries were constructed using the Nextera XT DNA Library Preparation Kit (Illumina, San Diego, CA), followed by 150-bp paired-end sequencing on a NextSeq (Il- lumina) according to manufacturer's instructions. The sequencing reads were assembled using SKESA [https://github.com/ncbi/SKESA]. The isolates were species typed using Kraken [https://ccb.jhu.edu], and MLST typed using https://github.com/tseemann/mlst.

For Group A Streptococcus (GAS), isolates were *emm* typed by performing a BLAST search to all published *emm* types by CDC [https://www.cdc.gov/streplab/protocol-emm-type.html]. For Group B Streptococcus (GBS), all isolates were serotyped by latex agglutination test and, if needed, confirmed using Lancefield tests. In addition, blasting of capsular sequencing was used for identification of genotypes. No additional identification tests were performed for isolates from Group C or G.

### 10.15.3 Susceptibility testing

Screening for penicillin, erythromycin and clindamycin resistance was performed with 1 unit penicillin G discs, 15 µg erythromycin discs and 2 µg clindamycin discs (Oxoid, Denmark) on Mueller-Hinton agar (Mueller-Hinton plate, 5% blood, SSI Diagnostica, Denmark). Isolates were also tested for inducible clindamycin resistance. For non-susceptible streptococci the MIC was determined with ETEST (Biomérieux), with erythromycin or clindamycin on Mueller-Hinton agar. The breakpoints used were as defined by the EUCAST (EUCAST v. 14.0 Breakpoint Tables).

Isolates that were either resistant or susceptible to increased exposure were categorised together as resistant.

### 10.15.4 Data handling

A case of invasive BHS disease was defined as the isolation of BHS from a normally sterile site (e.g., blood, cerebrospinal fluid, synovial fluid, pleural fluid, ascites, and tissue obtained during surgery). A new case was defined as an invasive isolate with a different Lancefield group within 30 days from the first one or an invasive isolate of any Lancefield group more than 30 days after the first episode, or the isolation of a new type (*emm*-type or GBS serotype) if the group was identical on both occasions.

Only one isolate from each unique case of BHS infection was included in the DANMAP report.

## 10.16 Invasive *Haemophilus influenzae* isolates from humans

### 10.16.1 Data source

Invasive infections with *Haemophilus influenzae* type b (Hib) is a notifiable disease in Denmark and all invasive isolates nationwide are sent to the reference laboratory at SSI. By tradition, invasive isolates of other serotypes have also been submitted on a voluntary basis, and thus a broader picture of invasive *H. influenzae* in Denmark can be obtained. All cases were identified through MiBa and registered in the surveil-lance database at SSI. Cases, where isolates were not submit-ted to the reference laboratory were registered as "unknown serotype".

### 10.16.2 Microbiological methods

At SSI, the received isolates were analysed by whole-genome sequencing, from which serotype and biotype were extracted.

### 10.16.3 Susceptibility testing

Susceptibility data for the 2024 isolates were retrieved from MiBa. In cases where a series of isolates from the same episode developed non-susceptibility over time, the most non-susceptible profile was used for the analysis in DANMAP. In addition, for isolates received at SSI, whole-genome sequencing data was analysed for the presence of beta-lactamase encoding plasmids TEM-1 and ROB-1 as well as for the presence of mutations in the *ftsI* gene that encodes for penicillin-binding protein 3 (PBP3).

### 10.16.4 Data handling

A case was defined as isolation of *H. influenzae* from normally sterile sites (e.g. blood, spinal fluid, pleura, joint). Repeated samples within a 30 days window were classified as duplicates and were omitted from the analysis.

## 10.17 *Staphylococcus aureus* including MRSA isolates from humans

### 10.17.1 Data source

Blood isolates were referred on a voluntary basis by all DCMs to the National reference laboratory for antimicrobial resistance at SSI. Detection of methicillin-resistant *Staphylococcus aureus* (MRSA) is a notifiable condition in Denmark and therefore all MRSA isolates from all sample types were sent to the reference laboratory.

### 10.17.2 Microbiological methods

At SSI, all isolates were initially tested using a multiplex PCR detecting the *spa, mecA, hsd, scn* and *pvl* (LukF-PV) genes [Larsen *et al.* 2008. Clin Microbiol Infect. 14: 611-614; Stegger *et al.* 2012. Clin Microbiol Infect. 18: 395-400]. *spa* was used as *S. aureus* specific marker and for subsequent typing by Sanger sequencing [Harmsen *et al.* 2003. J Clin Microbiol. 41: 5442-5448], mecA to determine MRSA status, and scn and *hsd* as markers for human adaptation and relation to CC398, respectively. All bacteremia cases and *mecA* negative presumed MRSA were tested for presence of the *mecC* gene. *spa*-negative isolates were confirmed as *S. aureus* by MALDI-TOF. Based on the *spa* type and known association with MLST typing, each isolate was assigned to a clonal complex (CC).

### 10.17.3 Susceptibility testing

Data on antimicrobial susceptibility was extracted from MiBa.

### 10.17.4 Data handling

For blood isolates, a case was defined as a patient with a positive blood culture. Subsequent isolates from the same patient was only included if the positive blood cultures were obtained at least one month apart (new episode).

For MRSA, data on the characteristics of the isolates and the clinical/epidemiological information were obtained from the Danish MRSA register at SSI (mandatory reportable). Patients were registered, regardless of colonisation or clinical infection, the first time they were diagnosed with MRSA or when a new subtype was demonstrated. Based on the reported information, MRSA cases were classified as colonisation/active screening (i.e. surveillance samples to detect nasal, throat, gut or skin colonisation), imported infection (i.e. acquired outside Denmark), infection acquired in a Danish hospital, defined as diagnosed >48 hours after hospitalisation with no sign of infection at admittance (HA-MRSA) or infection diagnosed outside hospitals (community onset). MRSA cases with community onset were further classified according to risk factors during the previous 6 months as either health-care associated with community onset (HACO) or community-acquired (CA). Health-care associated risk factors included prior hospitalisations, stay in long-term care facilities and being a health-care worker. Community risk factors included known MRSA-positive household members or other close contacts. Due to the increasing numbers of cases belonging to CC398, this type was treated separately as both epidemiology and relevant exposure are different from other CA cases.

## 10.18 Gonococcal isolates

### 10.18.1 Data source

Isolates of gonococci (*Neisseria gonorrhoeae*) were submitted from the departments of clinical microbiology to SSI on a voluntary basis. The isolates were obtained by culture of specimens from a variety of anatomical locations, most often urethra, cervix, rectum, throat, and rarely from other sites, e.g. eyes, joint fluid, and blood.

### 10.18.2 Microbiological methods

The bacteriological identification of the received isolates was performed by MALDI-TOF.

### 10.18.3 Susceptibility testing

For all isolates the MICs of azithromycin, ceftriaxon and ciprofloxacin were determined with ETEST (Biomérieux) on chocolate agar incubated at 35 °C in 5% $CO_2$. The breakpoints used were those defined by EUCAST (EUCAST v. 14.0 Breakpoint Tables). A cefinase disc technique was used to examine the isolates for beta-lactamase production.

The breakpoints for azithromycin were changed as of January 1, 2019 (EUCAST version 9.0) (S: MIC ≤1 mg/L; R: MIC >1 mg/L) and it was advised that azithromycin should only be used in conjunction with another efficient agent. Until January 1, 2019, S was defined by MIC ≤0.25 mg/L and R by MIC >0.5 mg/L.

In addition to the above, the MIC of cefixime was determined for 117 consecutive isolates as part of an ECDC project on gonococcal antimicrobial resistance (Euro-GASP). The breakpoints used were those defined by EUCAST (EUCAST v. 14.0 Breakpoint Tables).

### 10.18.4 Data handling

Only one isolate from each unique case of gonorrhoea were included in the DANMAP report. Laboratory demonstration of gonococci in repetitive specimens was considered to represent a new case of gonorrhoea if the specimens were obtained with an interval of more than 21 days.



# 11.

# Terminology

# List of abbreviations

| | |
|---|---|
| AGP | Antimicrobial growth promoter |
| AMU | Antimicrobial use |
| AMR | Antimicrobial resistance |
| ATC | Anatomical Therapeutic Chemical Classification System |
| ATCvet | Anatomical Therapeutic Chemical Classification System for veterinary medicines |
| CA | Community-acquired |
| CC | Clonal complex |
| CHR | Central Husbandry Register |
| CPE | Carbapenemase producing Enterobacterales/Enterobacteriaceae |
| CPO | Carbapenemase producing organisms |
| CPR | Danish Civil Registry, register for social security numbers |
| DAD | Defined Daily Doses per 100 admissions |
| DADD | Defined Animal Daily Dose |
| DAPD | Defined Animal Daily Dose per 1,000 animals per day |
| DBD | Defined Daily Doses per 100 occupied bed-days |
| DCM | Department of clinical microbiology |
| DDD | Defined Daily Dose |
| DID | Defined Daily Doses per 1,000 inhabitants per day (DDD/1,000 inhabitants/day) |
| DTU | Technical University of Denmark |
| DVFA | Danish Veterinary and Food Administration |
| EARS-Net | The European Antimicrobial Resistance Surveillance Network |
| ECDC | European Centre for Disease Prevention and Control |
| EFSA | European Food Safety Authority |
| ESC | Extended Spectrum cephalosporinase |
| EUCAST | European Committee on Antimicrobial Susceptibility Testing |
| GP | General Practitioner |
| HACO | Health care associated community onset |
| MiBa | The Danish Microbiology Database |
| MIC | Minimum inhibitory concentration |
| MDR | Multidrug-resistant |
| MRSA | Methicillin-resistant *Staphylococcus aureus* |
| PCR | Polymerase chain reaction |
| SPC | Summaries of Product Characteristics |
| SSI | Statens Serum Institut |
| ST | Serotype/Sequence type |
| VASC | Veterinary advisory service contracts |
| VMPs | Veterinary medicinal products |
| VetStat | Danish Register of Veterinary Medicines |
| VRE | Vancomycin-resistant enterococci |
| VVE | Vancomycin-variable enterococci |
| WGS | Whole-genome sequencing |
| WHO | World Health Organization |

# Glossary

**Anatomical Therapeutic Chemical (ATC) classification:** An international classification system for drug consumption studies. The ATC code identifies the therapeutic ingredient(s) of each drug for human use according to the organ or system on which it acts and its chemical, pharmacological and therapeutic properties. Antibacterials for systemic use are known as ATC group J01. The ATC classification is maintained by the WHO Collaborating Centre for Drug Statistics and Methodology (Oslo, Norway) [www.whocc.no/atcddd/indexdatabase/]. The ATC classification for veterinary medicinal products, ATCvet, is based on the same main principles as the ATC classification system for medicines for human use and is also maintained by the WHO Collaborating Centre for Drug Statistics and Methodology [www.whocc.no/atcvet/database/].

**Antibacterial agents:** Synthetic (chemotherapeutics) or natural (antibiotics) substances that destroy bacteria or suppress bacterial growth or reproduction [Source: Dorland's Illustrated Medical Dictionary]. In the section on human consumption, 'antibacterial agents' are referred to as 'antimicrobial agents' (see below).

**Antimicrobial agents:** The term 'antimicrobial agents' covers antibacterial, antiviral, coccidiostatic and antimycotic agents. In the section on veterinary consumption, the broad term 'antimicrobial agents' is generally used because coccidiostats are included. Antiviral substances are not used in veterinary medicine, and antimycotics are only registered for topical veterinary use and used mainly in companion animals. Antimycobacterial agents are not included. The term 'antibacterial agents' is only used in the veterinary section for precision, to distinguish from use of coccidiostats as feed additives (poultry only). In the chapter on human consumption, the term 'antimicrobial agents' refers to all antibacterial agents for systemic use (J01 in the ATC system) including metronidazole and vancomycin, which are used for systemic treatment but registered under the ATC code P01AB01 and A07AA09, respectively.

**Broiler:** A type of chicken raised specifically for meat production. In Denmark, the average weight after slaughter is 1.51 kg.

**Central Husbandry Register (CHR):** This is a register of all Danish farms defined as geographical sites housing production animals. It contains information concerning ownership, farm size, animal species, age groups, number of animals and production type. Each farm has a unique farm identity number (CHR-number).

**Defined Daily Dose (DDD):** This is the assumed average maintenance dose per day for a drug used for its main indication in adults. It should be emphasised that the Defined Daily Dose is a unit of measurement and does not necessarily reflect the recommended or prescribed daily dose. DDDs provide a fixed unit of measurement independent of price and formulation, enabling the assessment of trends in drug consumption and to perform comparisons between population groups. The DDDs are defined and revised yearly by the WHO Collaborating Centre for Drug Statistics and Methodology [https://www.whocc.no/atc_ddd_index/].

**Defined Daily Dose per 100 admissions (DAD):** DAD measures the amount of daily doses consumed per 100 admitted patients at hospitals during a given timeframe (one year). It is used for benchmarking consumption related to the hospital activity and will typically be compared to the consumption measured in DBD (see below). DAD and DBD will generally be applied to comparing individual hospitals and consumption of individual drug classes over time. In DANMAP DAD covers all patients attended at somatic hospitals only. Admission-days are extracted from the National Patient Registry (Landspatientregistret, LPR).

**Defined animal daily dose (DADD):** DADD is the average maintenance dose per day for a drug used for its main indication in the appropriate animal species. DADD has been specifically defined for use in DANMAP and does not always completely match the "prescribed daily dose" or the recommended dosage in the Summaries of Product Characteristics (SPC). The DADD is defined as mg active compound per kg live biomass for each antimicrobial agent, administration route and animal species. In DANMAP 2012, the DADD replaced the ADD (as defined in VetStat and assigned at product level). For more details, see section 9.2, Materials and Methods and the applied DADD's are listed in the web annex.

**DADD per 1,000 animals per day (DAPD):** Trends in veterinary consumption, both within and across species, are presented in DAPD, which allows for comparison between sectors and adjustment for changes in live biomass. The estimated live biomass is expressed as the number of standard animals with an estimated average weight and lifetime. This may also be referred to as the 'standard-animals-at-risk' and takes into account species differences in body-mass and lifespan. The DAPD is a statistical measure, providing an estimate of the proportion of animals (in thousands) treated daily with a particular antimicrobial agent. For example, 10 DAPDs indicate that an estimated 1% of the population, on average, receives a certain treatment on a given day (see section 9.2, Materials and Methods).

**Defined Daily Doses per 100 occupied bed-days (DBD):** DBD is the consumption calculated in defined daily doses at hospitals, divided through the number of bed-days. This allows comparison of hospitals related to the length of patient stays. The number of bed-days is extracted from The National Patient Registry (Landspatientregistret, LPR). Time of reporting

differs between hospitals and closing time for reporting is later than extraction time for the DANMAP report. Every patient admitted to a hospital accounts for the exact length of the hospital stay. This corresponds to the actual hours at hospital divided by 24 hours.

**DDD per 1,000 inhabitants per day (DID):** Consumption in both primary health care, hospital care and the overall total consumption is presented in DID, allowing for comparison between sectors and for illustration of the consumption in hospital care without taking hospital activity (discharges and length of stays) into account. Data presented in DID provide a rough estimate of the proportion of the population within a defined area treated daily with certain drugs. For example, 10 DIDs indicate that 1% of the population on average gets a certain treatment daily. In figures presented as DDD/1,000 inhabitants/day.

**Finishers:** Pigs from 30-100 kg live weight from after the weaner stage to time of slaughter.

**Fully susceptible:** An isolate will be referred to as fully susceptible if sensitive to all antimicrobial agents included in the test panel for the specific bacteria.

**Human clinical samples/isolates:** In the DANMAP report, human clinical samples and/or isolates refers to the sample being taken in a clinical situation, meaning in the course of diagnosing and treating a possible infection in a patient.

**Human screening samples/isolates:** In the DANMAP report, human screening samples and/or isolates refers to sampling being performed for monitoring purposes in a defined group of asymptomatic individuals. Examples are rectal swaps to determine carriage of multidrug-resistant bacteria in the intestine or swaps from the throat, nostrils or perineum to determine carriage of methicillin-resistant *Staphylococcus areus* (MRSA).

**Intramammaries:** Antimicrobial agents for local application in the mammary gland (udder) to treat mastitis.

**Layer:** A hen raised to produce eggs for consumption.

**Minimum inhibitory concentration (MIC):** This is the lowest concentration of antimicrobial agent in a given culture medium, e.g. broth or agar, below which growth of the bacteria is not inhibited.

**Multidrug-resistant:** A *Salmonella*, *Campylobacter*, *Enterococcus* or *E. coli* isolate is assumed multidrug-resistant if it is resistant to three or more of the main antimicrobial classes. The number of antimicrobial classes and antimicrobial agents included in this definition depends on the test panel for each bacterium.

**Pets or pet animals:** Dogs, cats, birds, mice, Guinea pigs and more exotic species kept at home for pleasure, rather than kept for work or food. Horses are not included as pet animals. The live biomasses of Danish pets used for estimating veterinary consumption only include dogs and cat.

**Piglet:** The new-born pig is called a piglet from birth till they are permanently separated from the sow at 3-4 weeks of age. The weight of the piglet at weaning is approximately 7 kg.

**Poultry:** The major production species are fowl *Gallus gallus* (broilers, layers, including breeding and rearing) and turkey. Regarding antimicrobial consumption, 'poultry' also includes domesticated ducks, geese, game birds and pigeons.

**Sow:** Any breeding female pig on the farm.

**Weaner:** Any pig of 7–30 kg live weight after it has been weaned (dry diet and water only).



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