

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 *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 *Acinetobacter* species *Enterococcus faecalis* *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 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

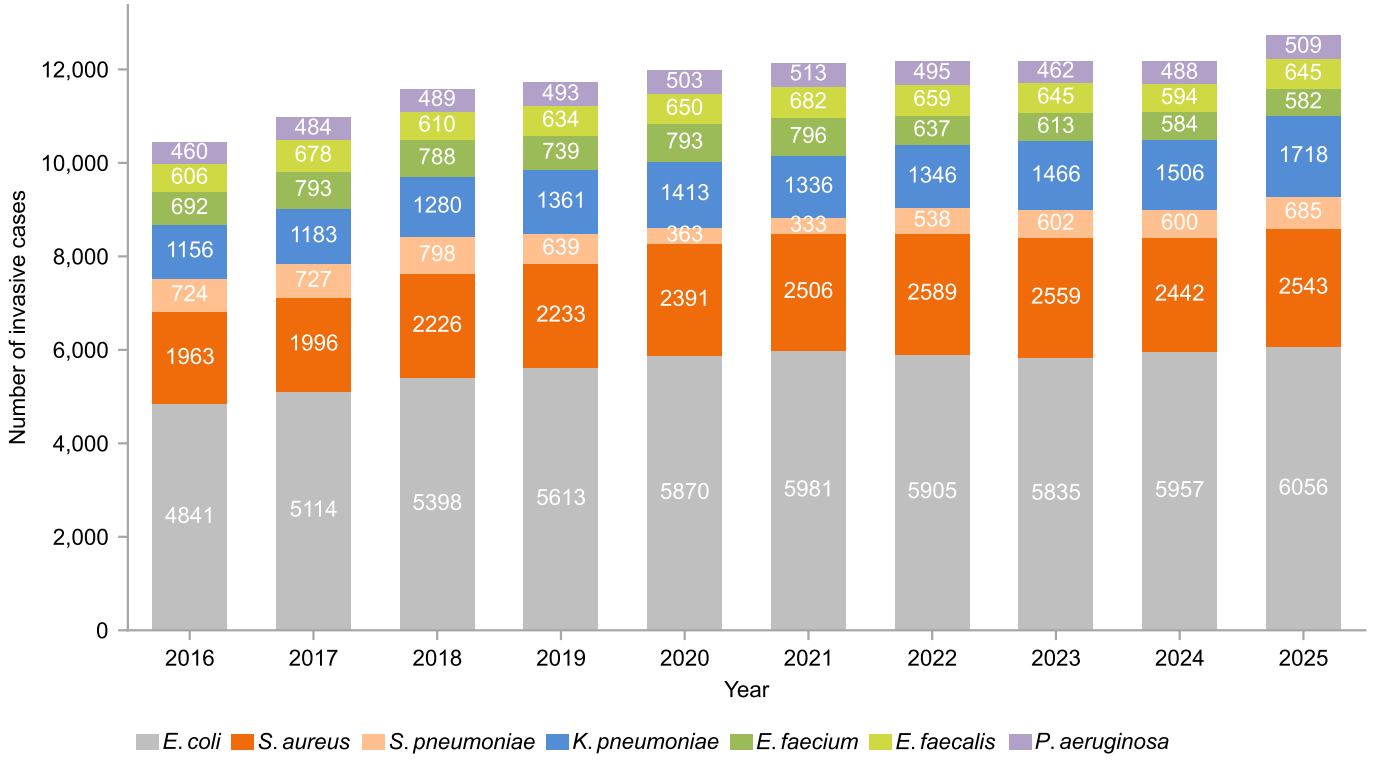
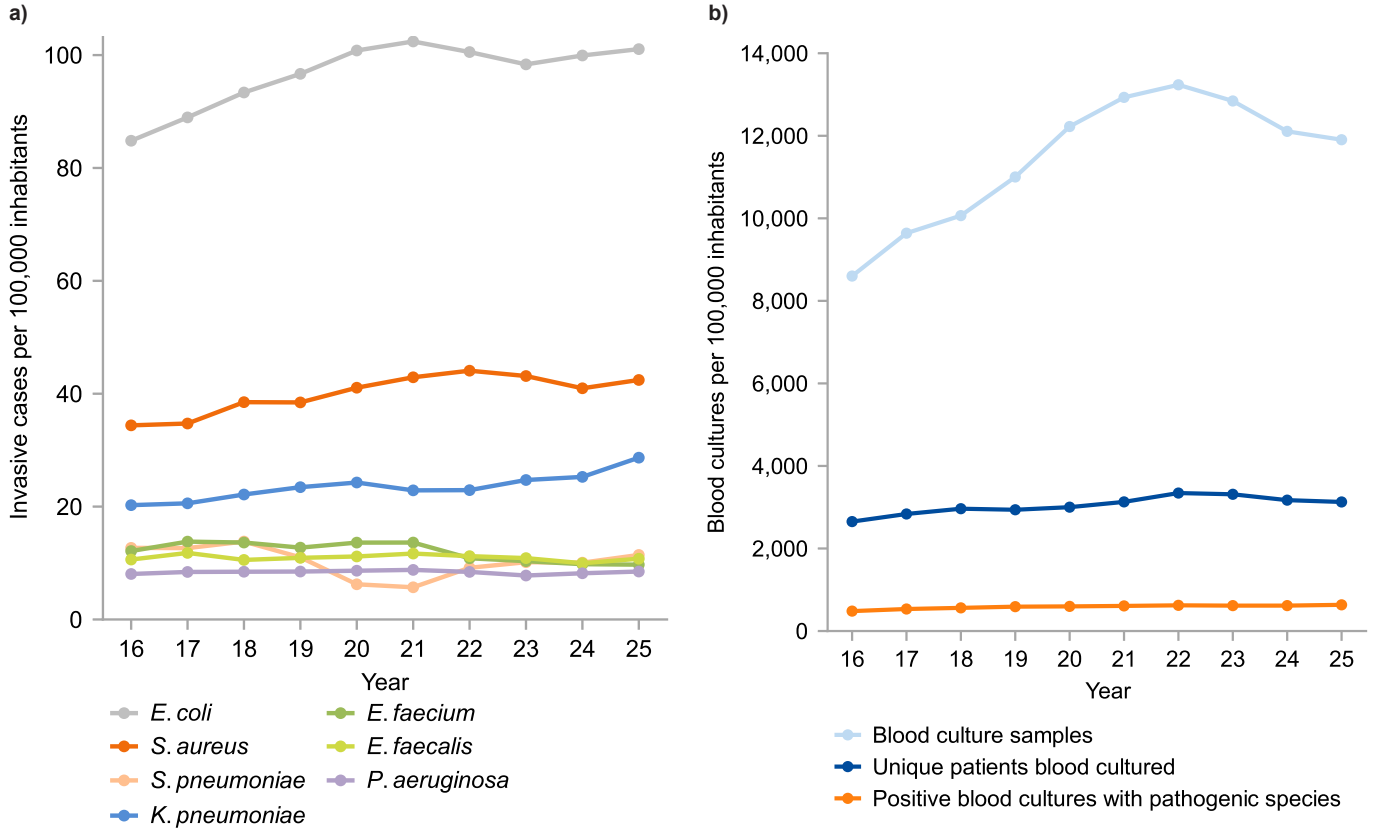


Figure 8.2 Incidence of a) Invasive cases and b) blood cultures taken per 100,000 inhabitants, Denmark, 2016-2025 DANMAP 2025



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

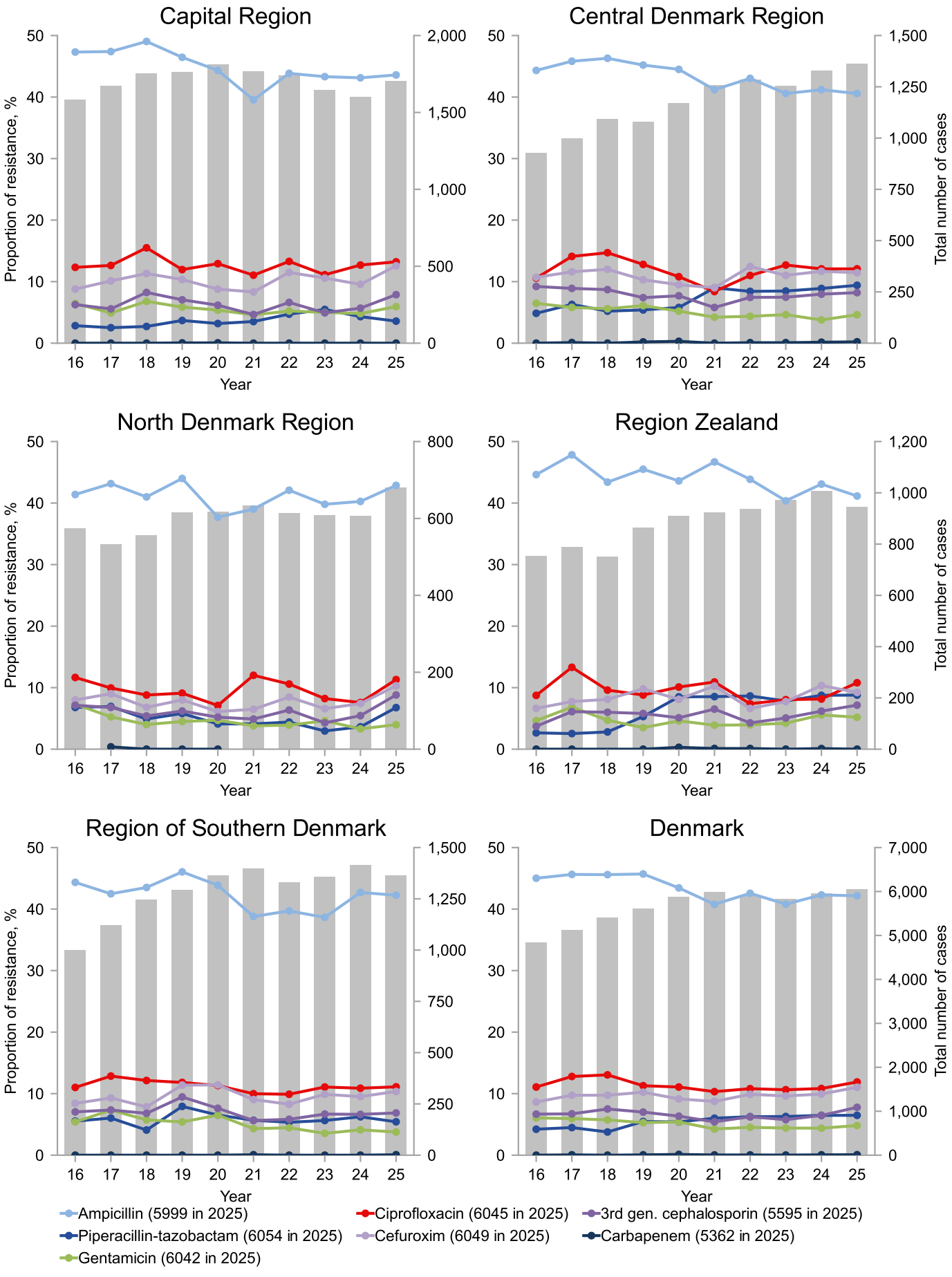
The number of invasive cases of *E. coli* appears to have reached a plateau. Resistance levels are generally stable for all specimen types, however, the slow rise in ciprofloxacin, cefuroxime, 3rd generation cephalosporins and piperacillin-tazobactam resistance in *E. coli* from invasive infections and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

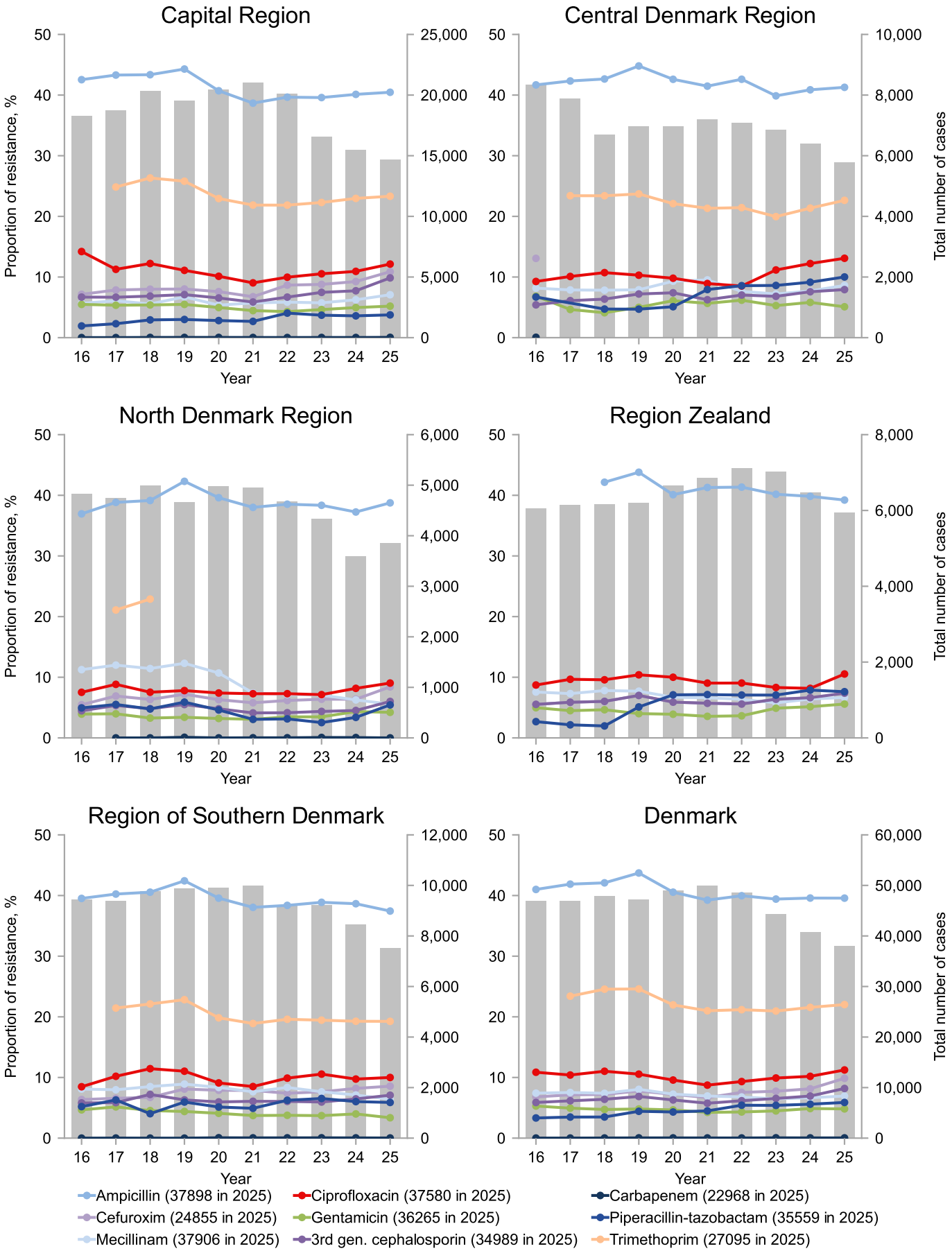
* Indicates less than 6 DCMs reported routine susceptibility testing.

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

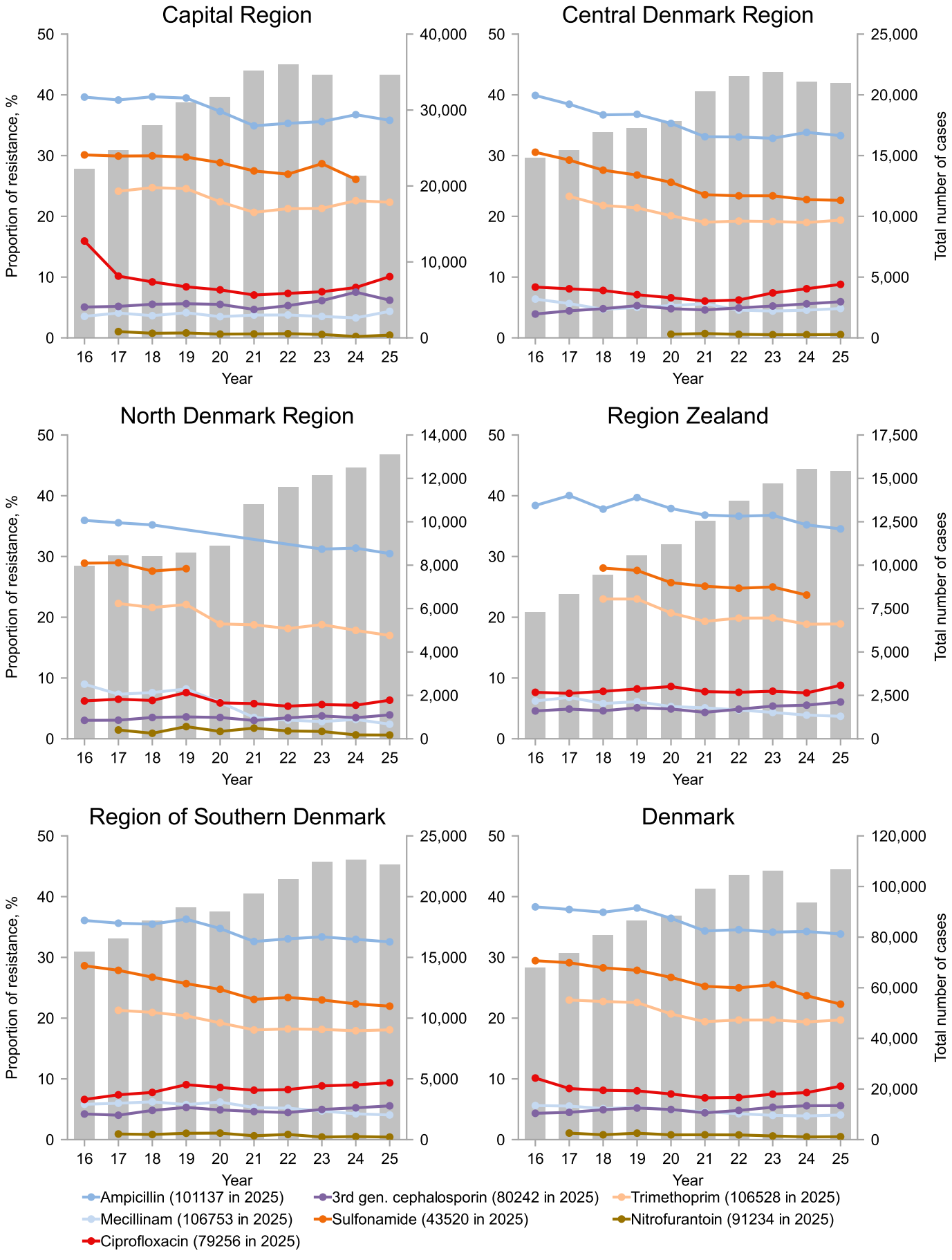
DANMAP 2025



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.

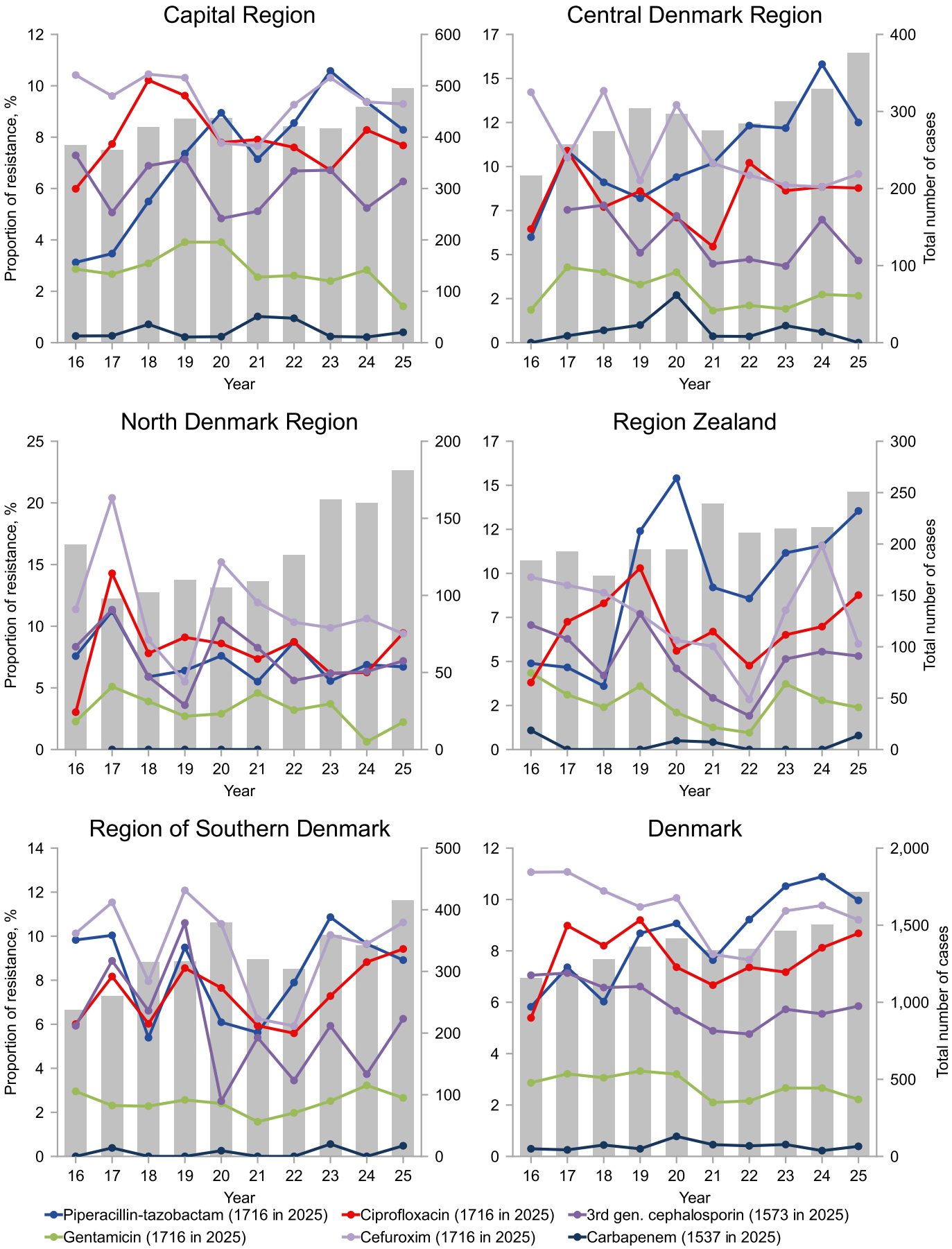
Table 8.7 *Klebsiella pneumoniae* complex. Resistance (%) in isolates from humans, Denmark, 2025 DANMAP 2025

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 % (N)	2017 % (N)	2018 % (N)	2019 % (N)	2020 % (N)	2021 % (N)	2022 % (N)	2023 % (N)	2024 % (N)	2025 %(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 (1,131)	95 (1,122)	93 (1,188)	94 (1,275)	93 (1,308)	93 (1,248)	94 (1,259)	92 (1,344)	92 (1,386)	91 (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

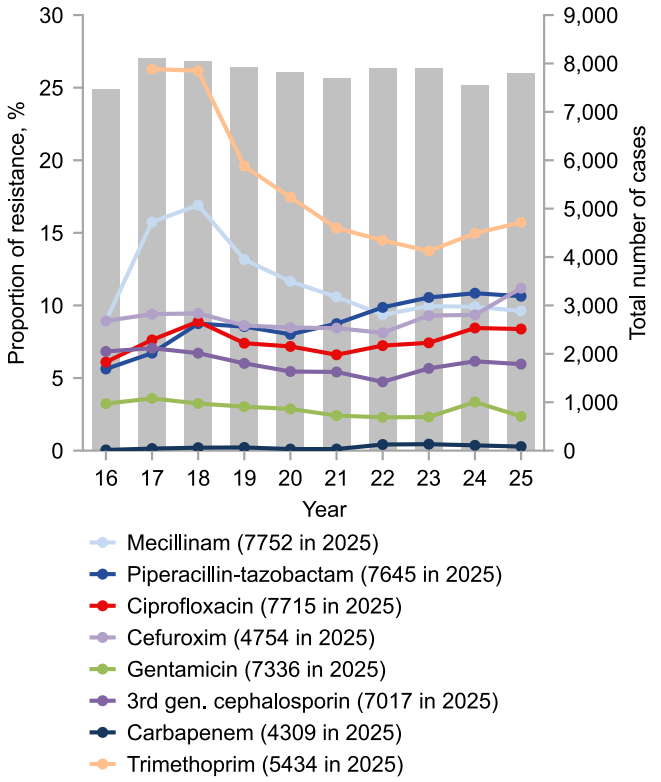
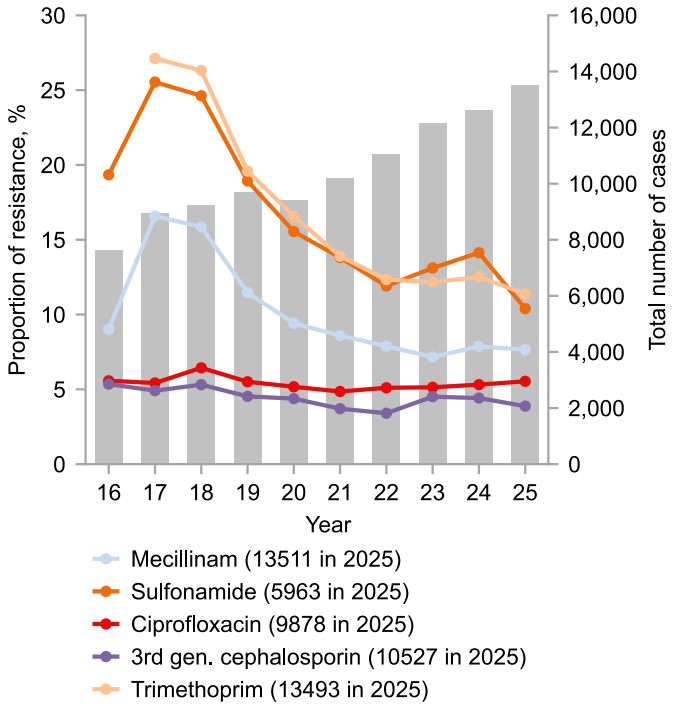


Figure 8.8 *Klebsiella pneumoniae* complex isolates from urines in humans (primary health care): proportion of resistant isolates and annual number of individual cases, Denmark, 2016-2025

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.

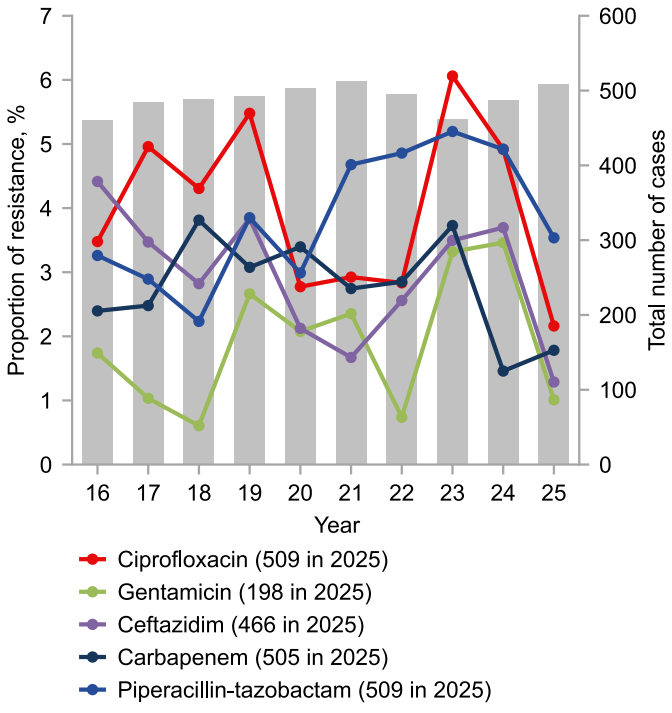
Invasive cases from hospital patients

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

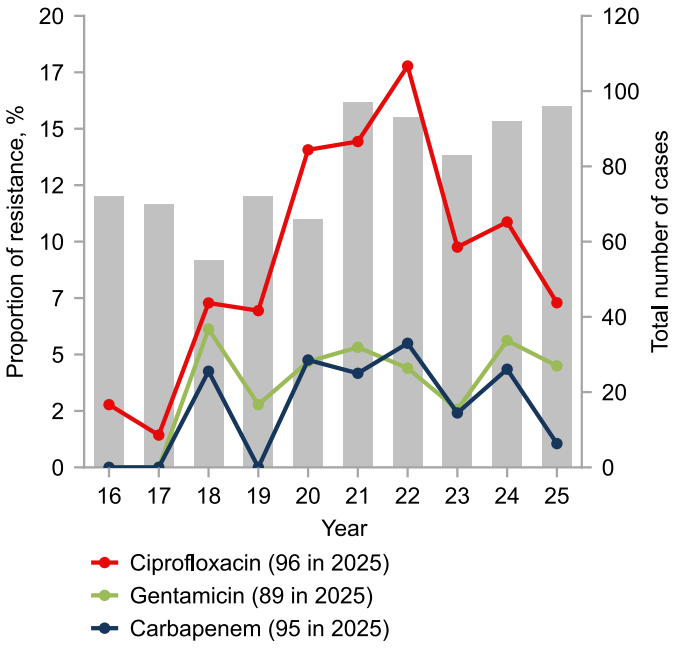


Table 8.12 *Acinetobacter* spp. tested and resistant invasive isolates, Denmark, 2016-2025 DANMAP 2025

	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

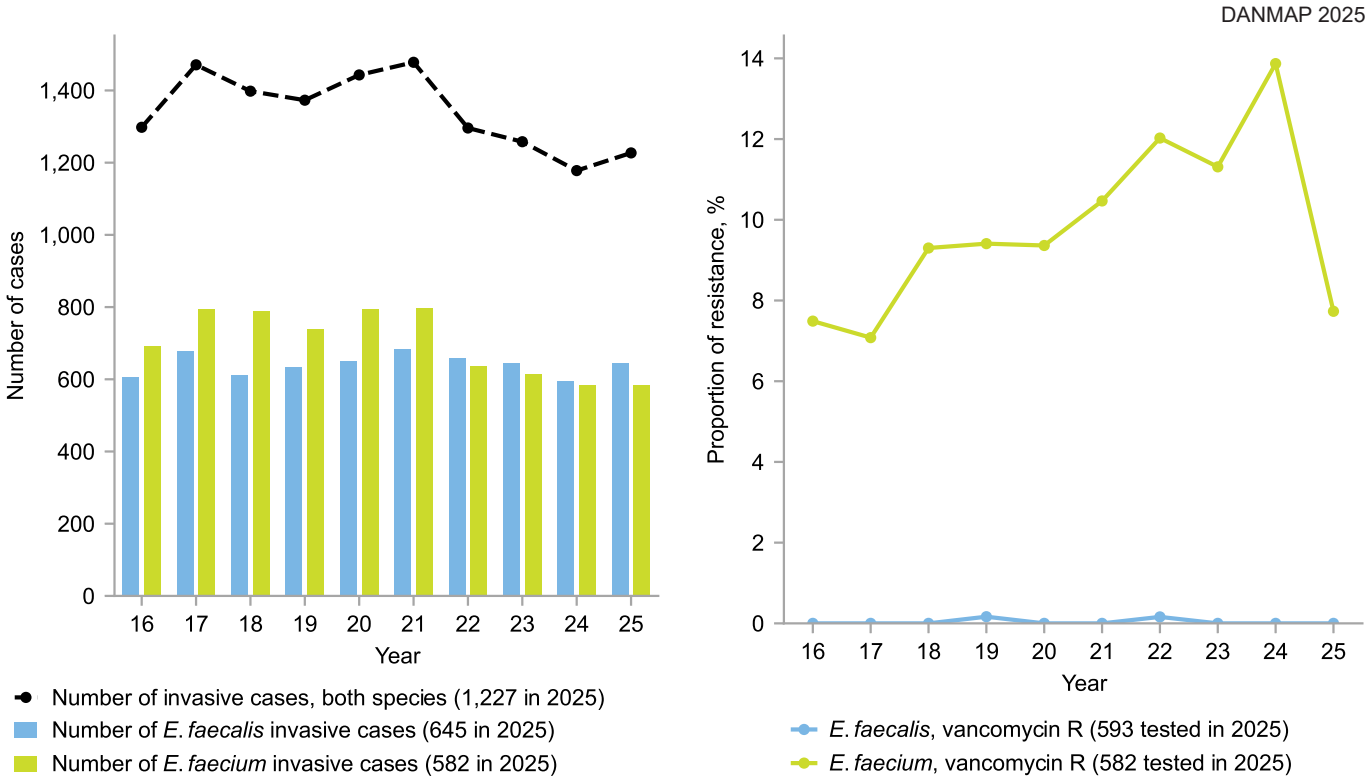
In 2025, a total of 645 and 582 individual patients were registered in Denmark with invasive *E. faecalis* and *E. faecium* isolates, respectively. Table 8.13 shows resistance percentages towards the most important antibiotics for both species for 2025 and Figure 8.11 shows the annual numbers of invasive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

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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

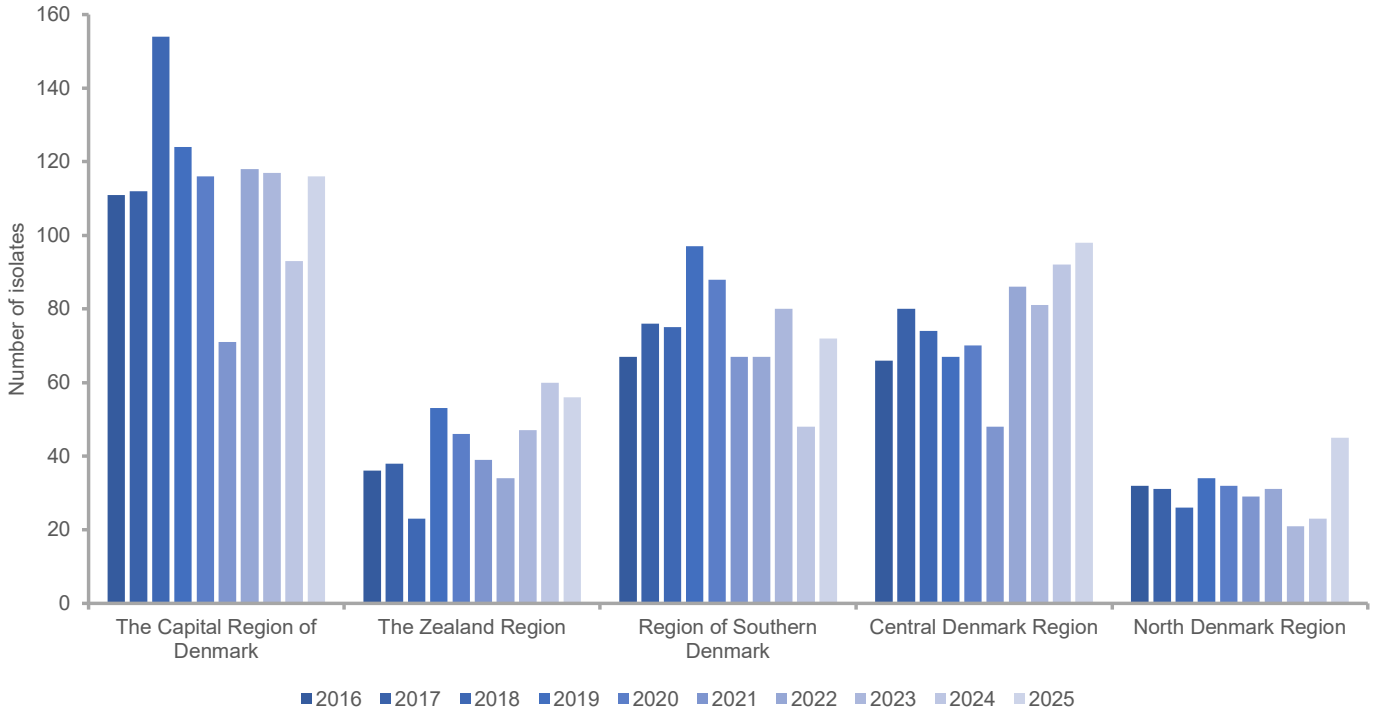
In 2025, a total of 387 *E. coli* blood isolates from unique patients, were identified by phenotypic testing as ESBL-, AmpC- and/or carbapenemase positive. This corresponds to a 22.5% relative increase compared to 2024, where 316 isolates were reported. Demographic data was available for all 387 *E. 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

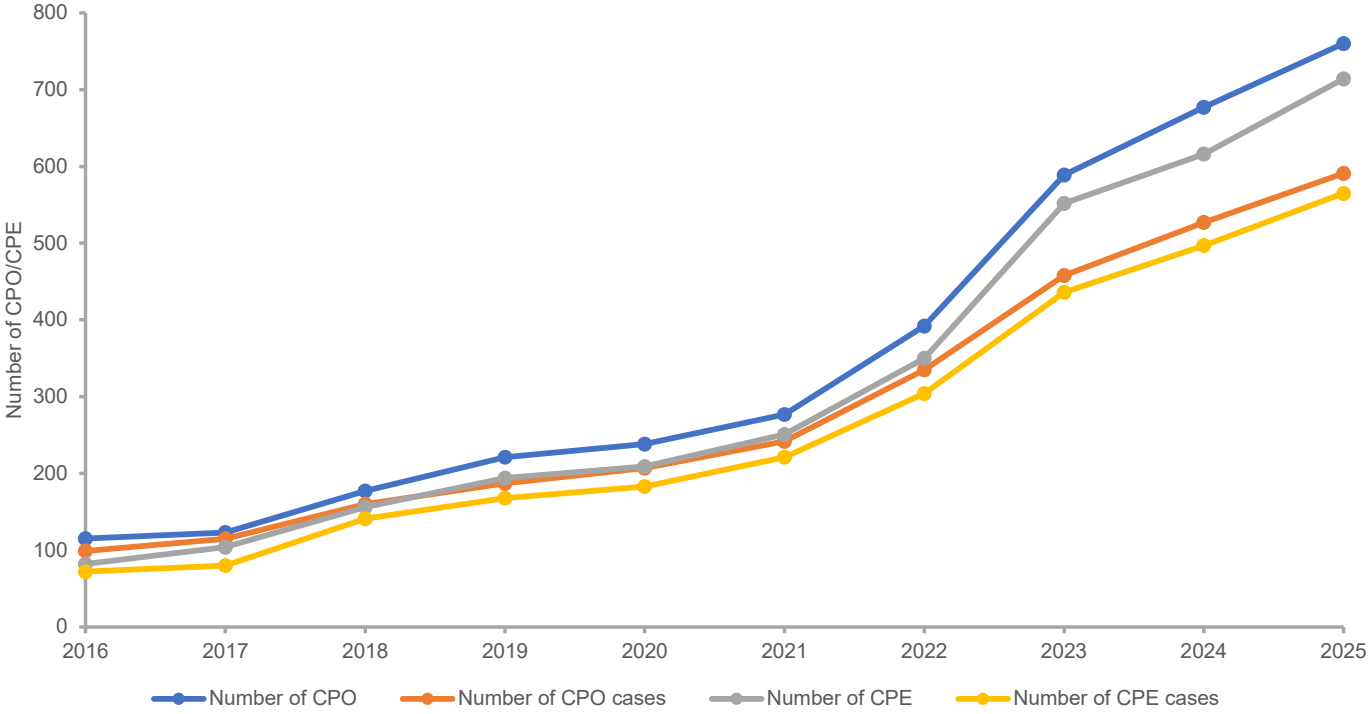
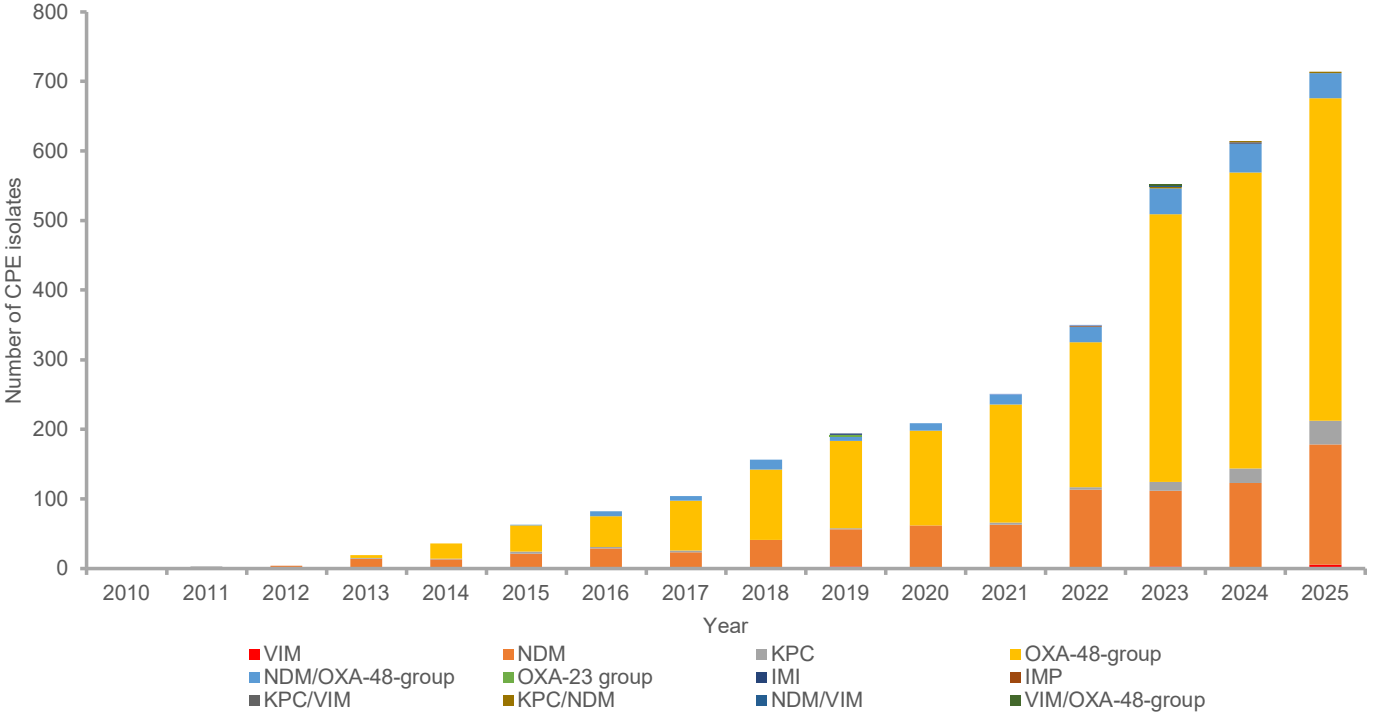


Table 8.17 Number of CPO/CPE isolates and cases in Denmark from 2016-2025 DANMAP 2025

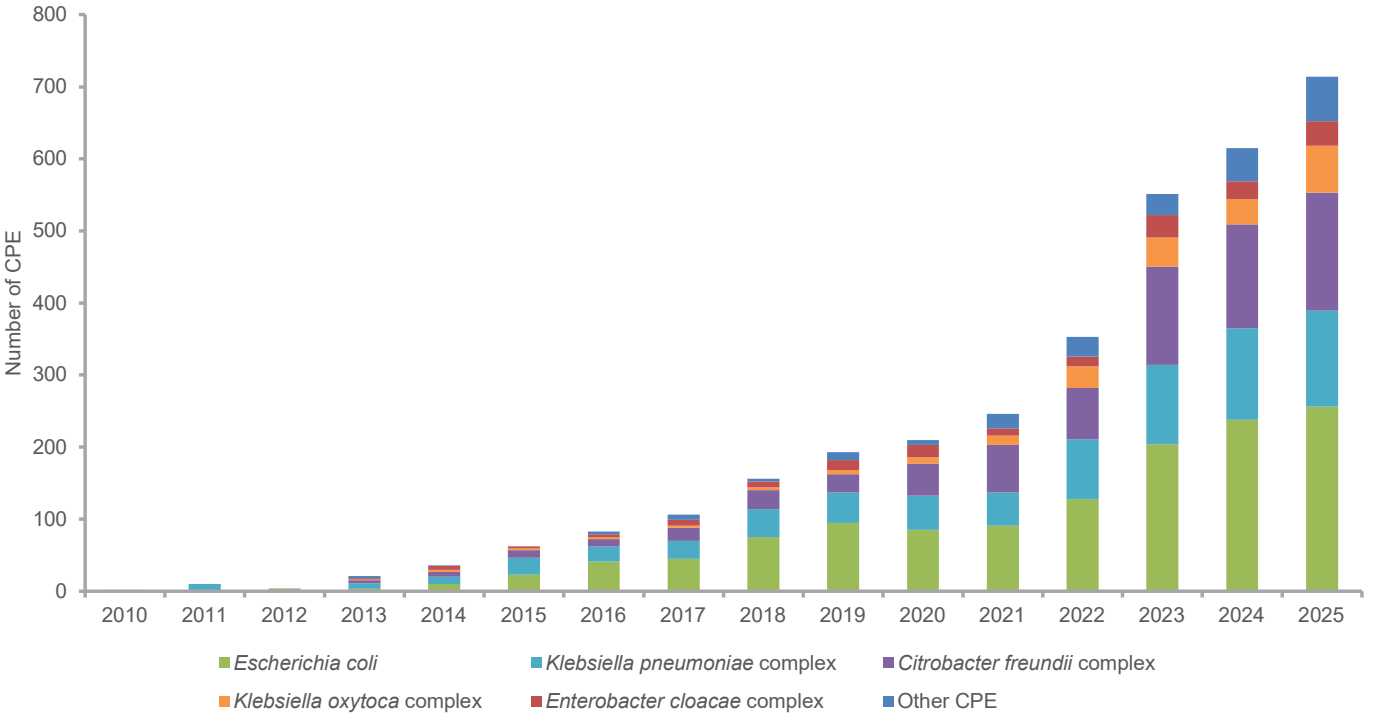
	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025
Number of CPO isolates	115	123	177	221	238	277	392	589	677	760
Number of CPO cases	99	115	160	187	207	242	335	458	527	591
Number of CPE isolates	82	104	156	194	209	251	350	552	616	714
Number of CPE cases	72	80	141	168	183	221	304	436	497	565

Figure 8.14a Genes identified in CPE DANMAP 2025



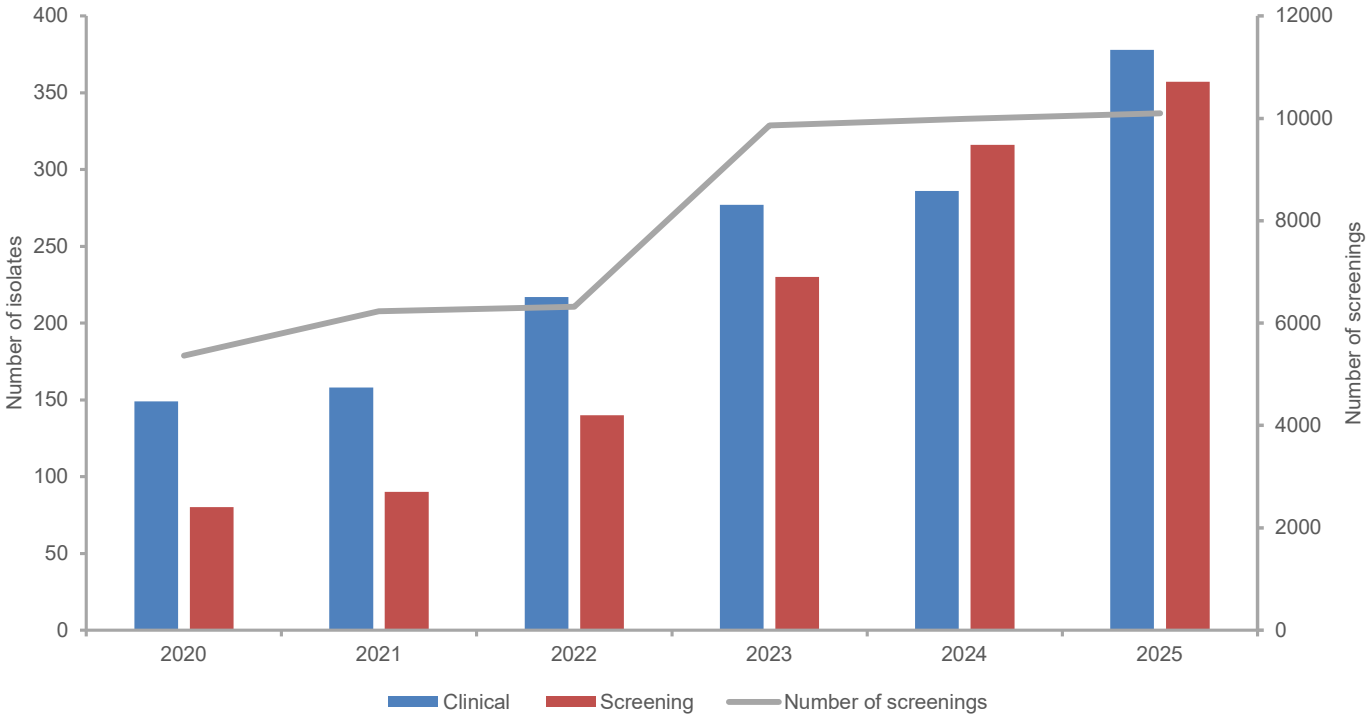
Isolates from the same patient were included if they belonged to different species or carried different carbapenemases.

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



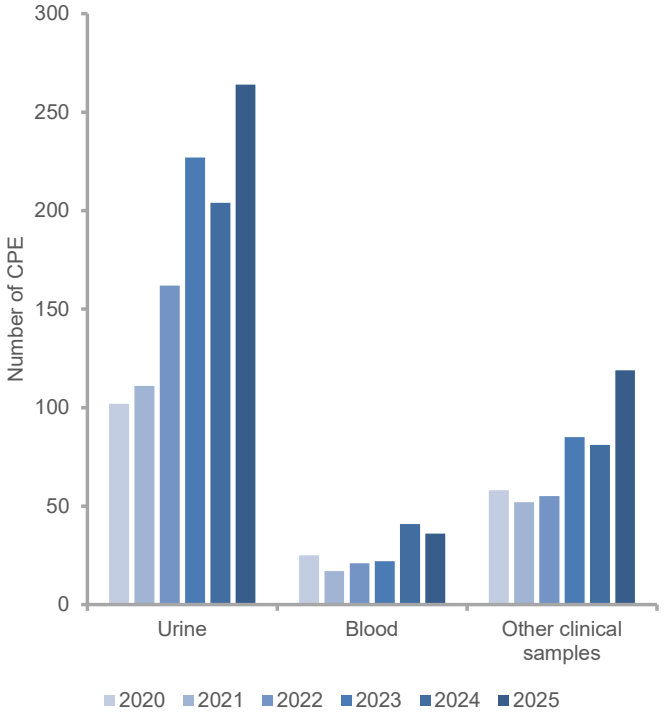
In this DANMAP report CPE-surveillance was supplemented with data from MiBa, which includes all microbiology reports from all ten Danish Departments of Clinical Microbiology. Data was extracted from MiBa for 2020-2025.

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

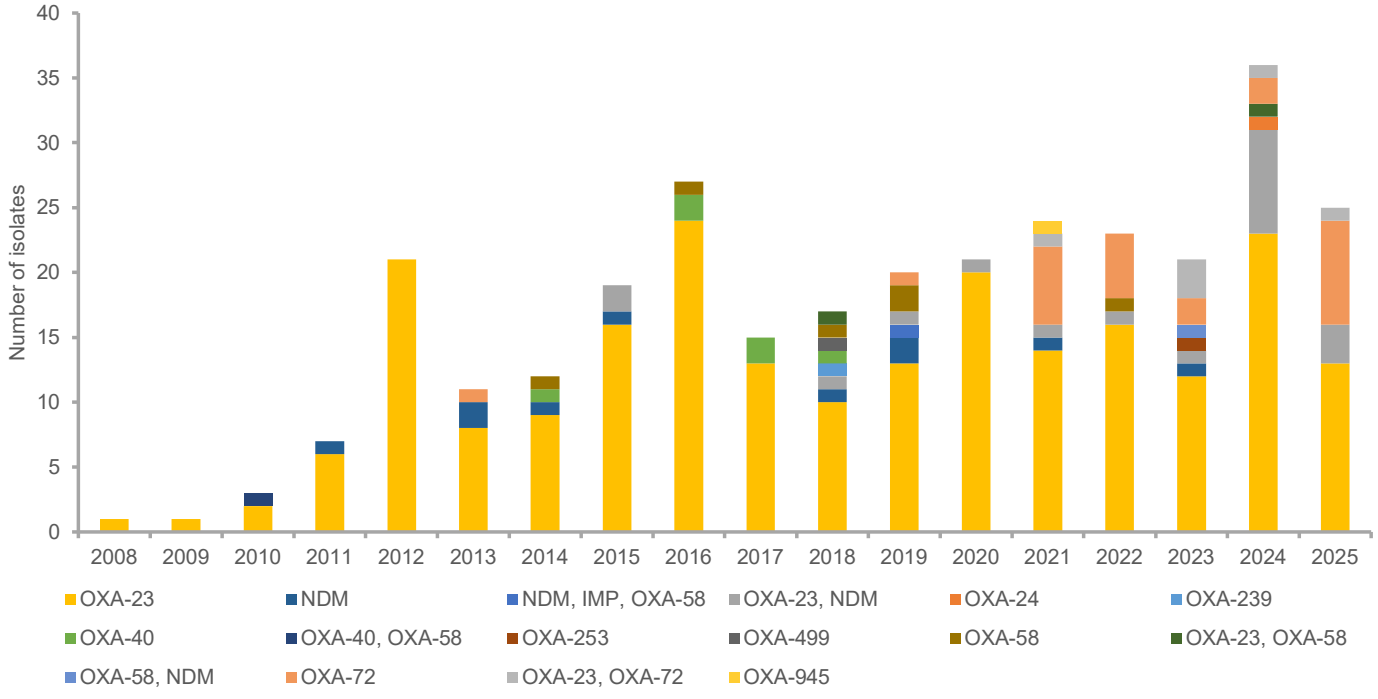


Figure 8.18 Carbapenemase-producing *Pseudomonas* spp. and enzymes identified, Denmark, 2010-2025 DANMAP 2025

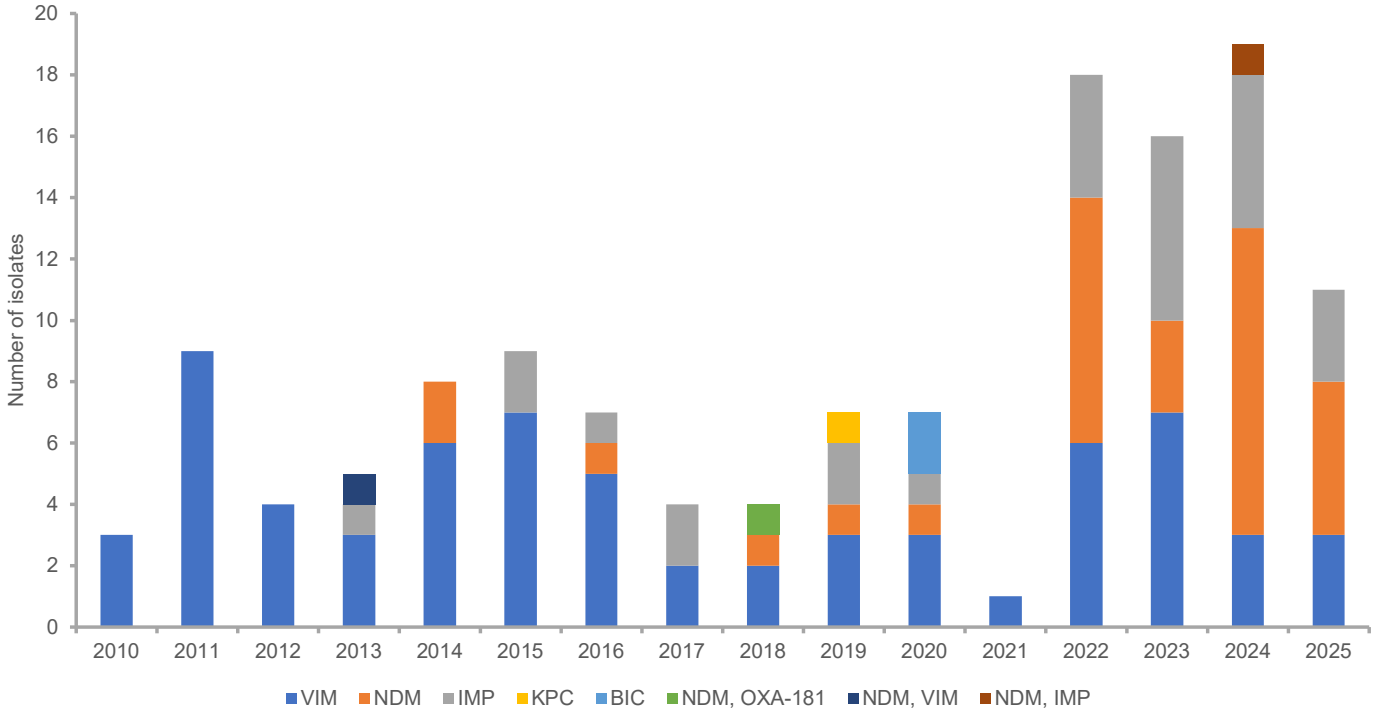
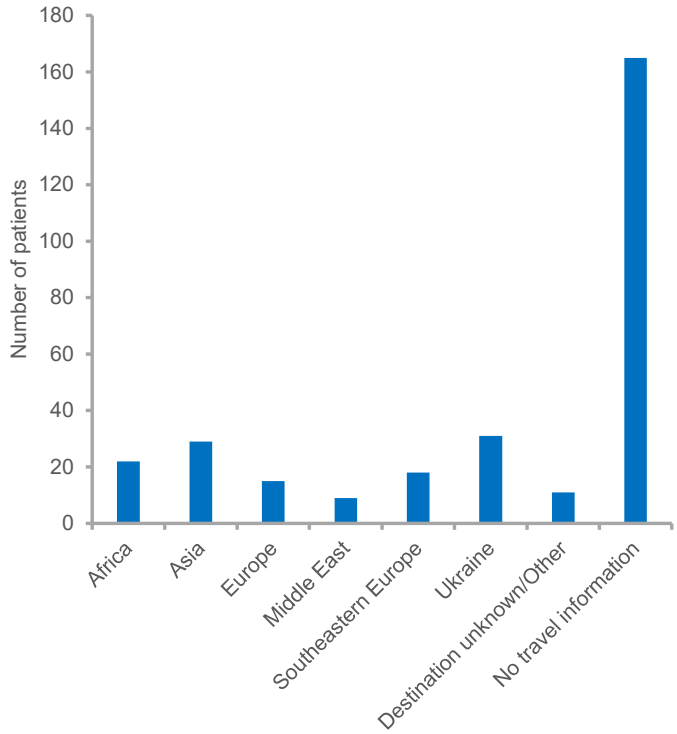


Figure 8.19 Place of origin of CPO, 2019-2025 DANMAP 2025



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 $bla_{OXA-244}$ 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

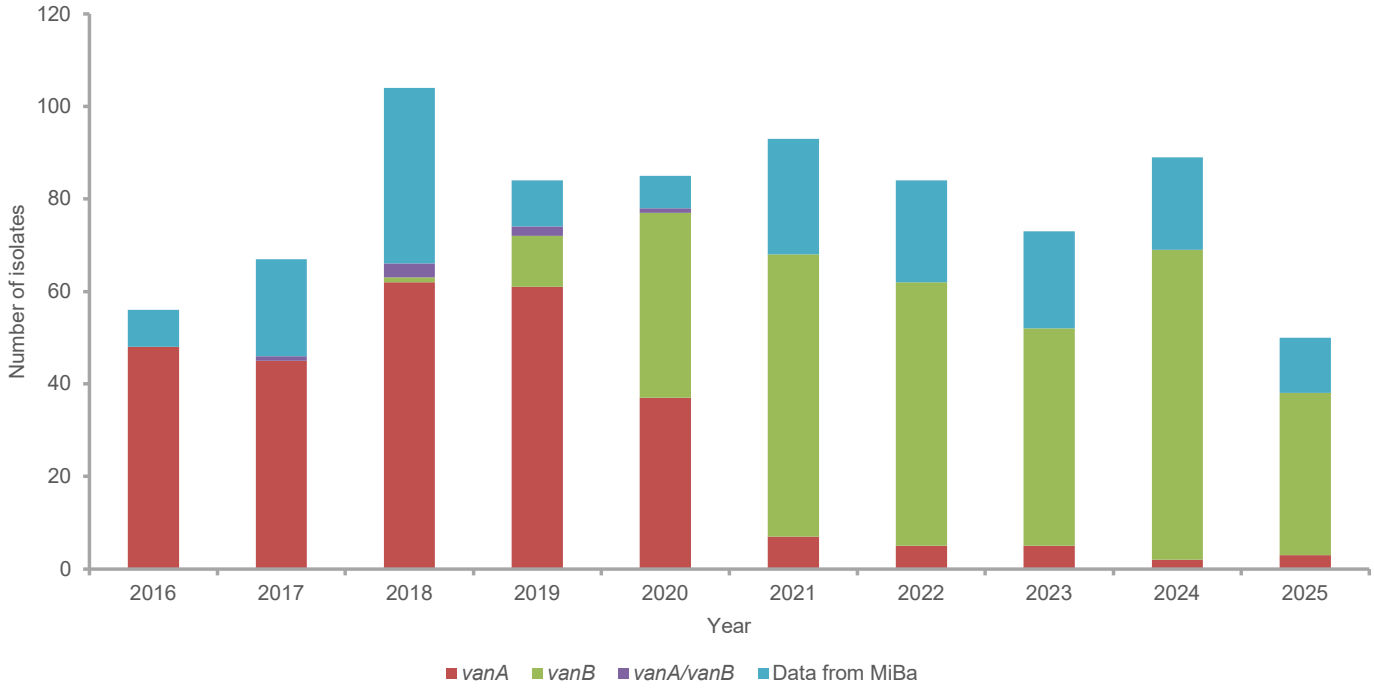


Table 8.19 Description of the types of *vanA* or *vanB* Enterococcus faecium according to MLST and cgMLST, Denmark, 2025

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

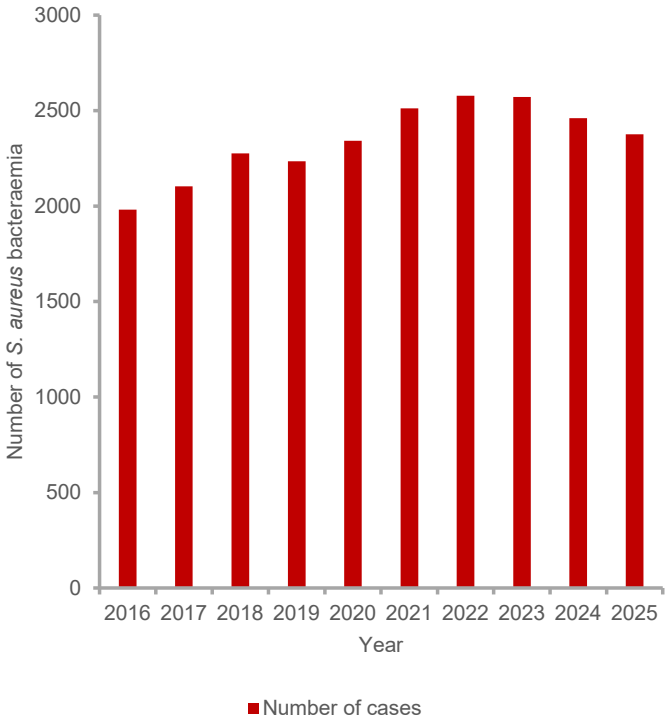


Table 8.20 Resistance (%) in isolates from *Staphylococcus aureus* bacteraemia cases, Denmark, 2016-2025 DANMAP 2025

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

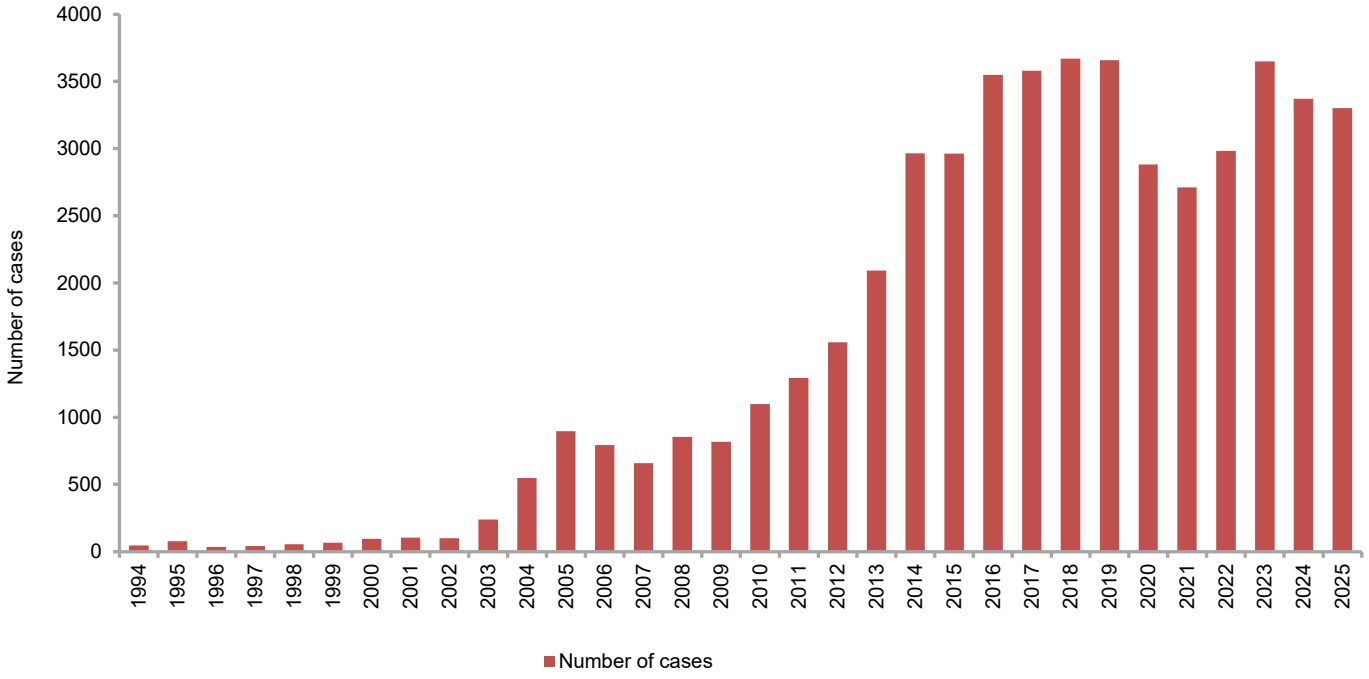
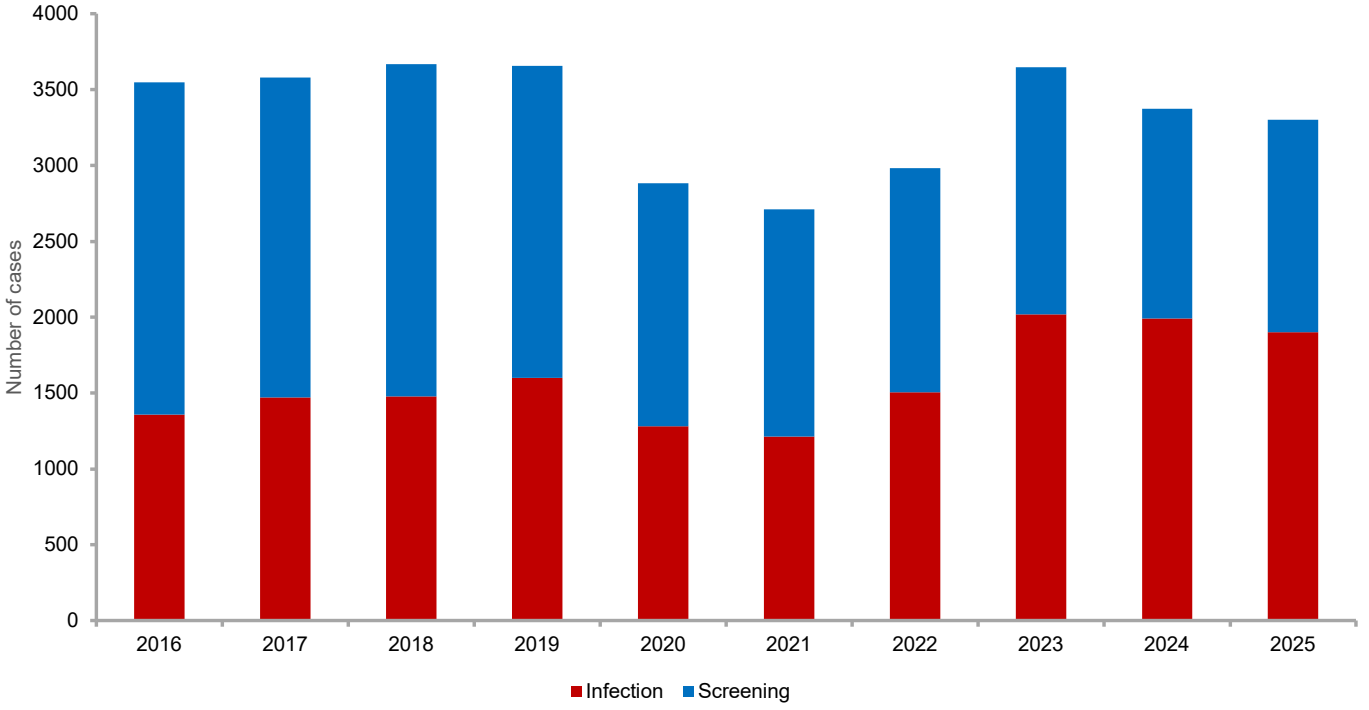


Figure 8.22b Number of new MRSA cases divided in infection and screening samples, Denmark, 2016-2025 DANMAP 2025



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

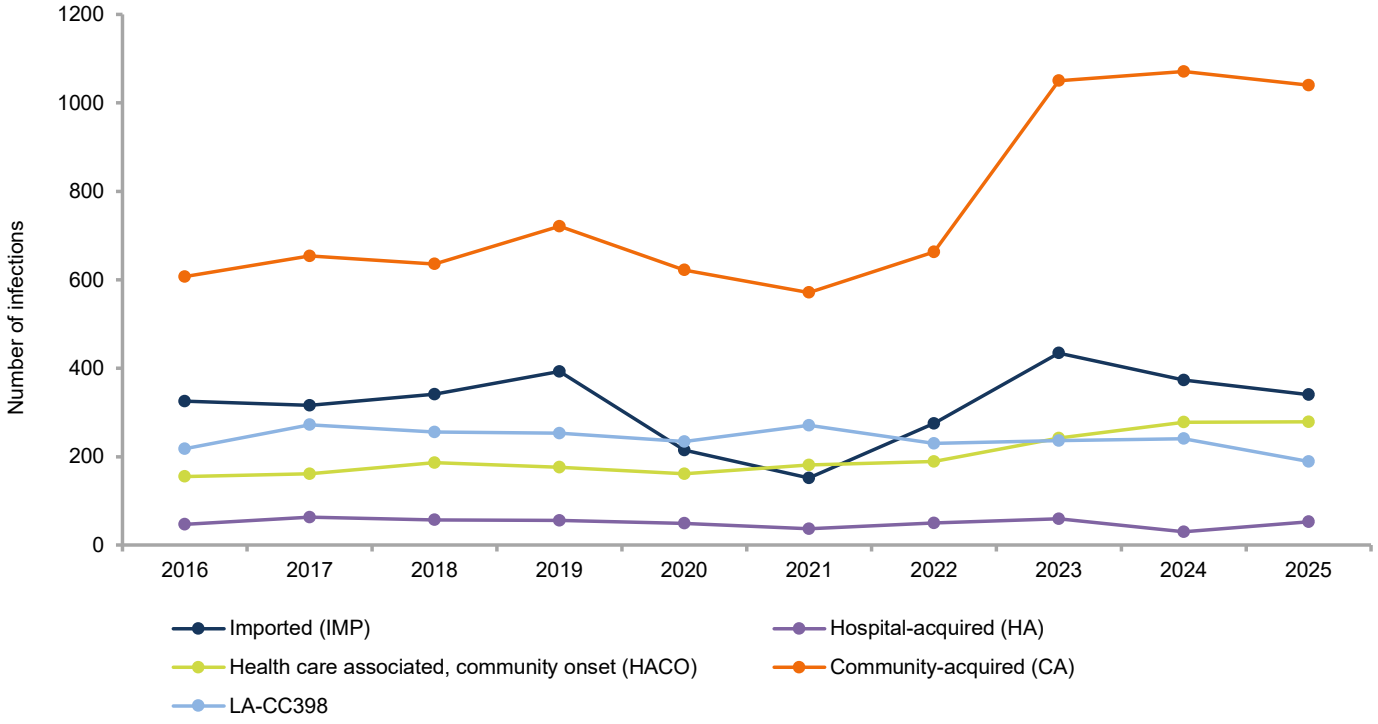


Table 8.25 Resistance (%) in non-livestock-associated CC398 MRSA isolates, Denmark, 2016-2025 DANMAP 2025

	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

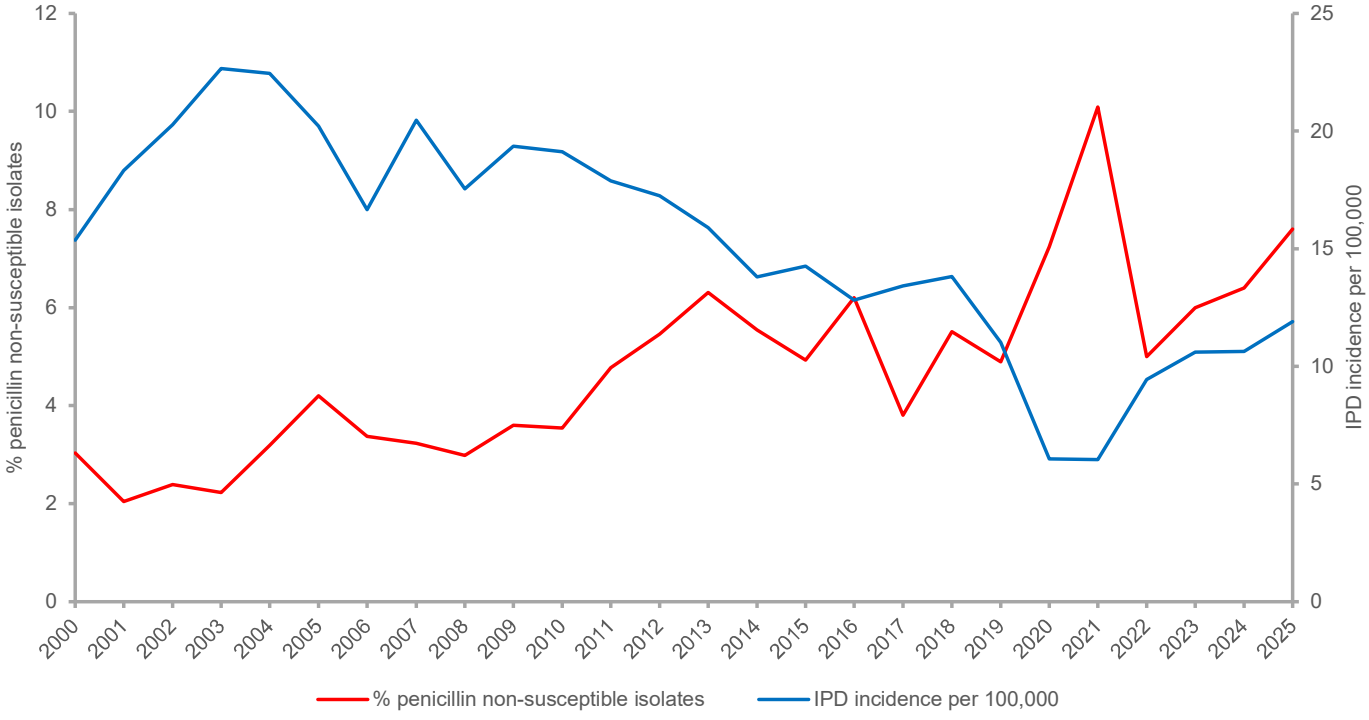


Table 8.28 All IPD cases for which information on penicillin susceptibility was available, in order of serotype distribution, Denmark, 2025

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 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

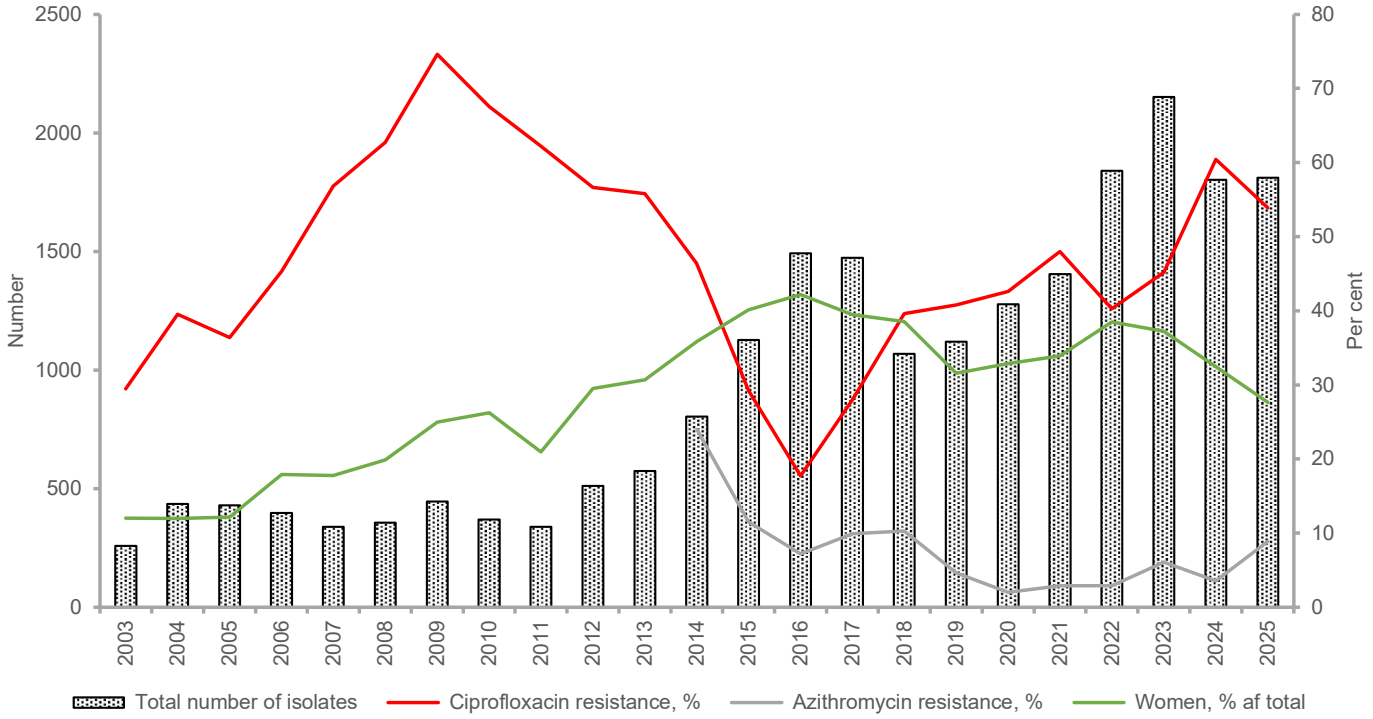
Females:
1. Pharyngeal
2. Cervical
3. Other anogenital (high vaginal swab/rectal/urethral)
4. Other

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.

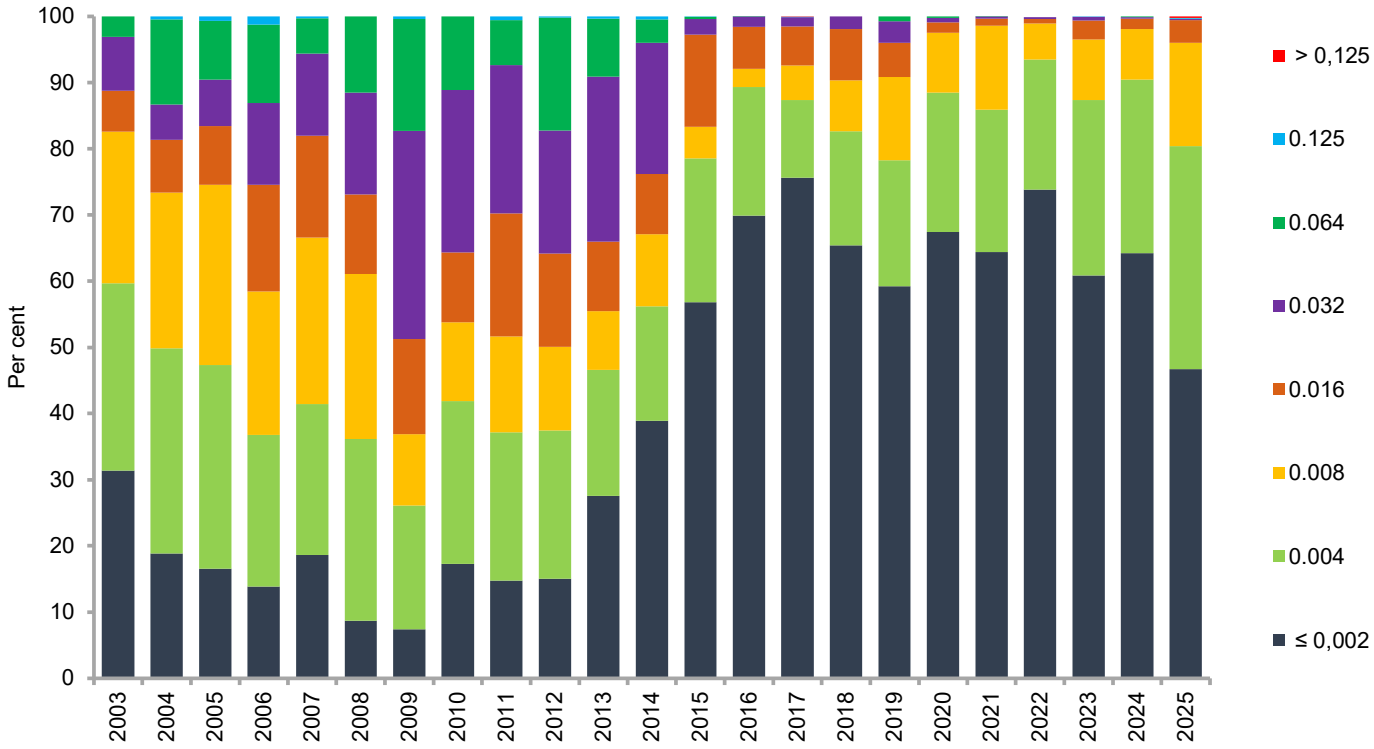
The Danish National Board of Health issued guidelines in 2015 for the diagnosis and treatment of sexually transmitted infections. A combination of high dose ceftriaxone (500 mg i.m.) and azithromycin (2 g p.o.) was recommended for the empiric treatment of gonorrhoea. This therapeutic regimen has gradually 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

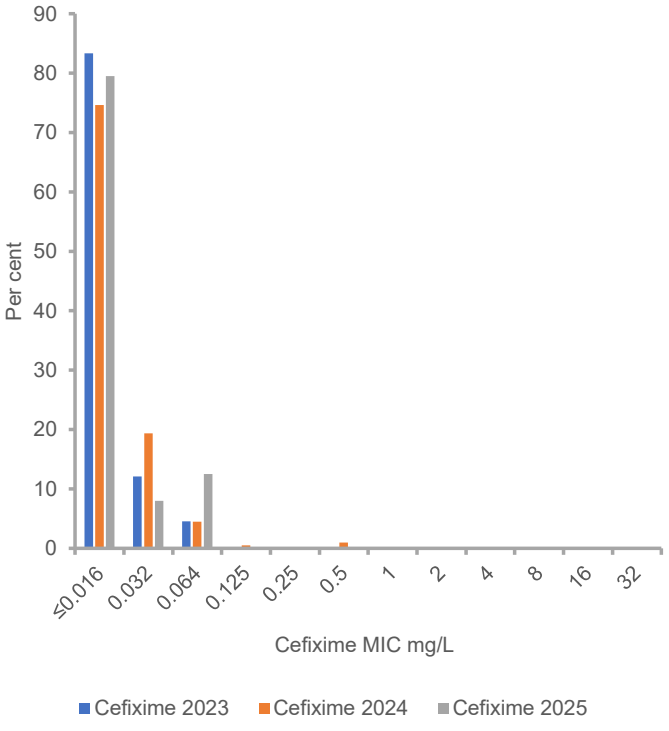


Figure 8.28 Distribution of gonococcal isolates according to MIC values for tetracycline; number of isolates (total number: 132 in 2023, 201 in 2024 and 200 in 2025). Breakpoint for susceptibility to tetracycline, 0.5 mg/L DANMAP 2025

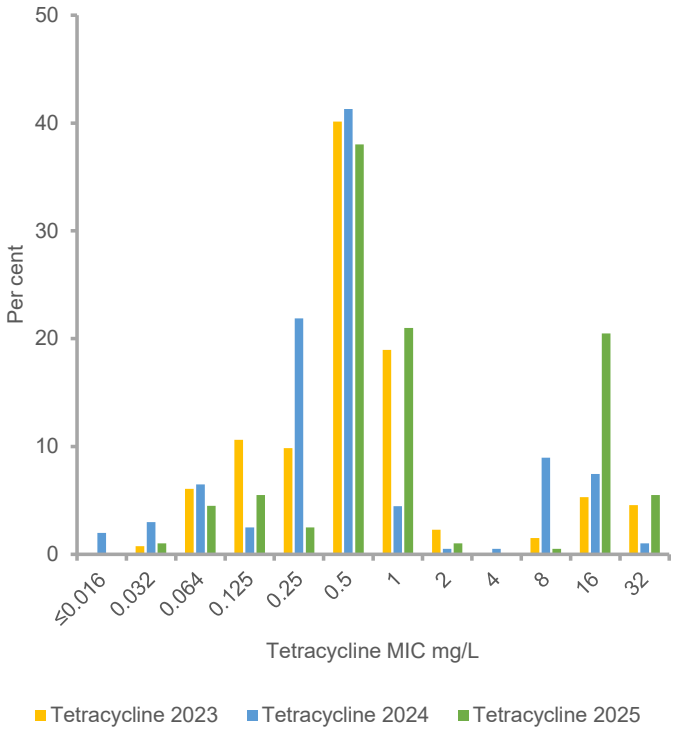


Table 8.32 Ciprofloxacin resistance rates by gender and anatomical origin of the isolates, 2025 DANMAP 2025

	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.

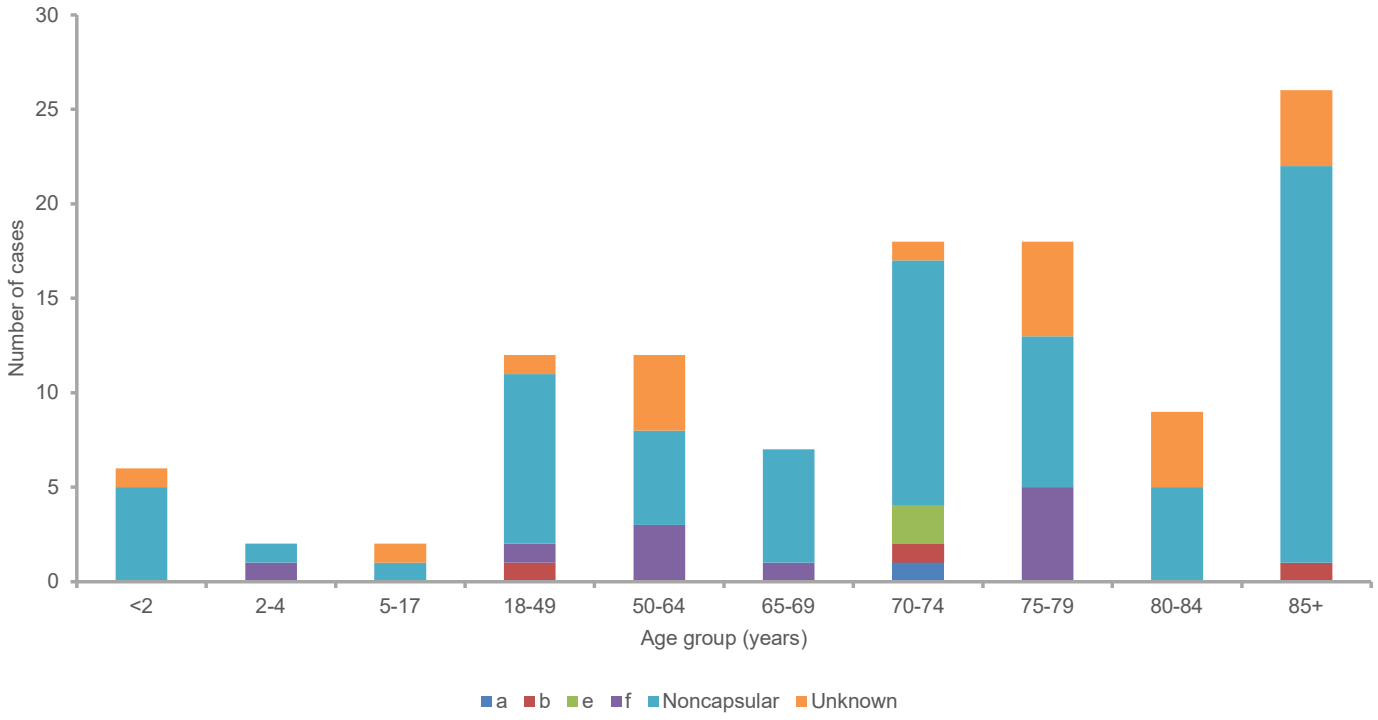
Surveillance of *Haemophilus influenzae*

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

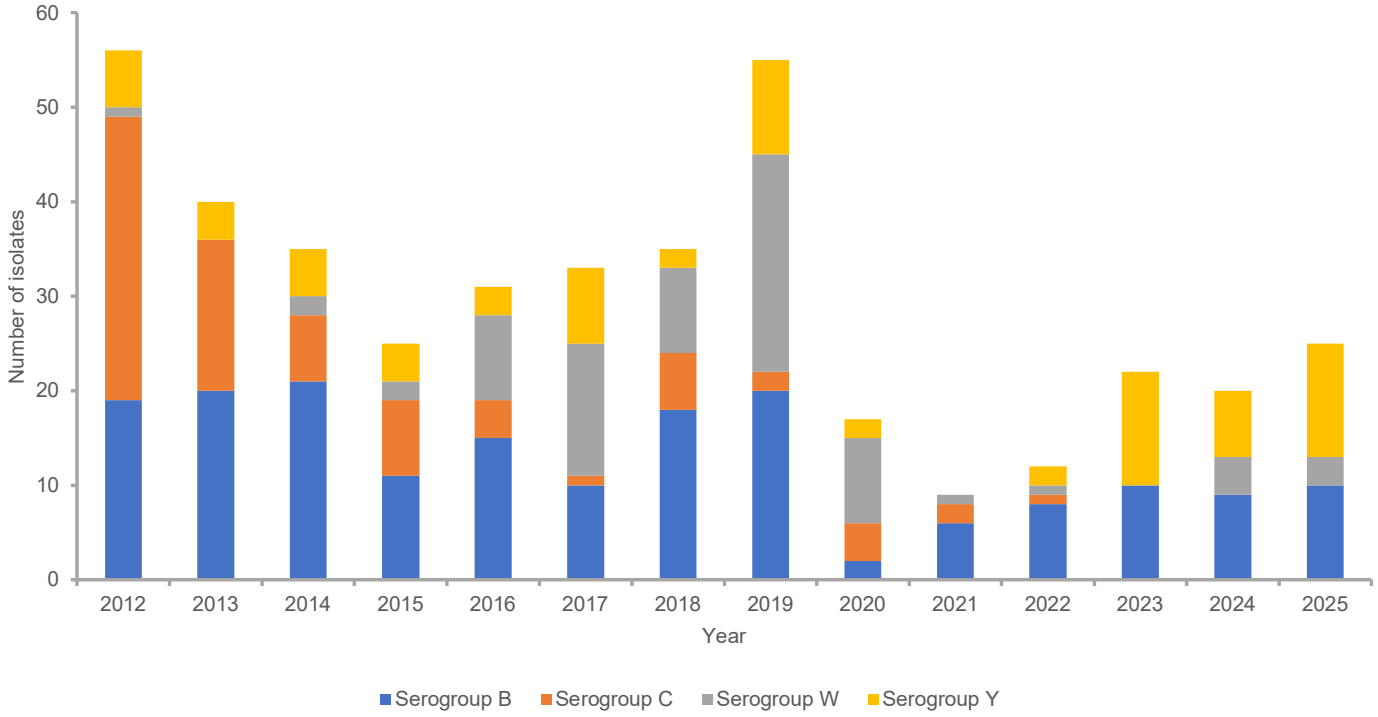


Figure 8.31 Distribution of ceftriaxone MIC values (mg/L) by serogroup, 2012-2025 DANMAP 2025

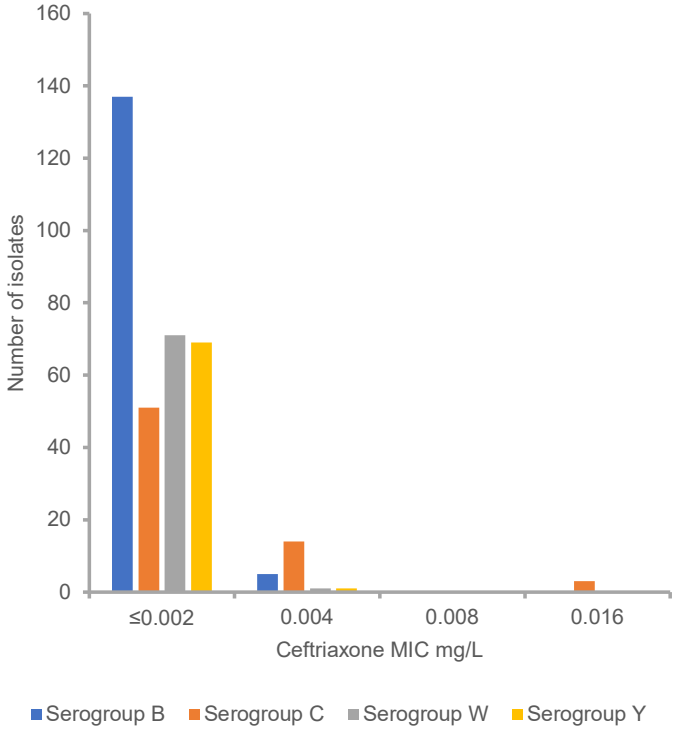


Figure 8.32 Distribution of ciprofloxacin MIC values (mg/L) by serogroup, 201-2025 DANMAP 2025

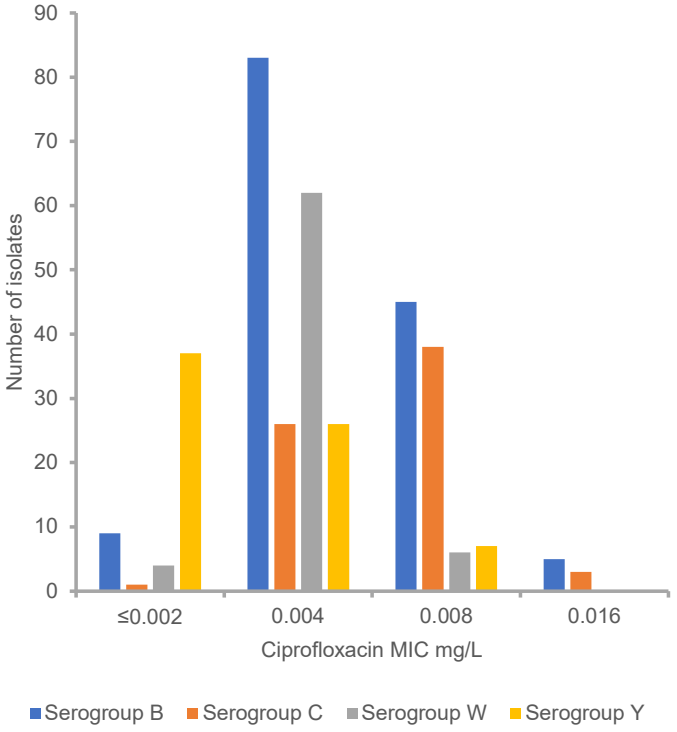


Figure 8.33 Distribution of penicillin MIC values (mg/L) by serogroup, 2012-2025 DANMAP 2025

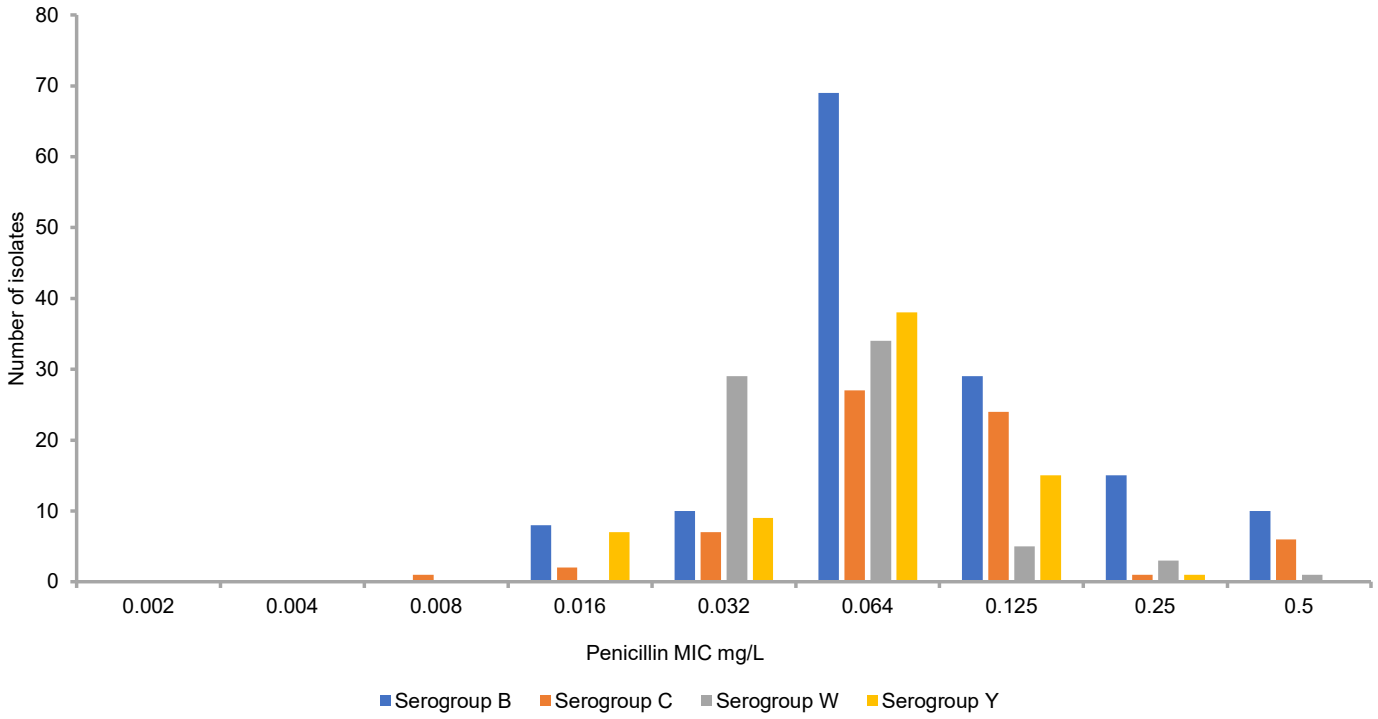


Table 8.36 Number of penicillin-resistant meningococcal isolates (MIC >0.25 mg/L), serogroups B, C, and W, 2013-2025 DANMAP 2025

	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

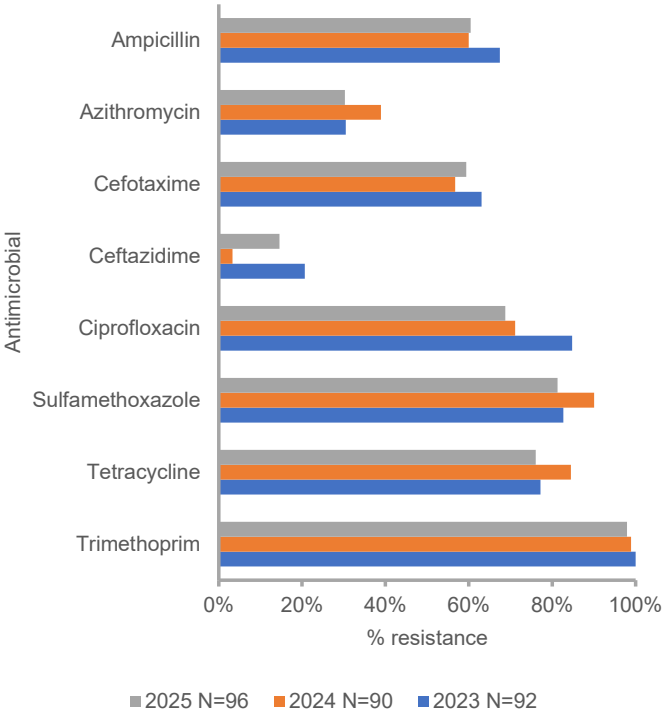
In 2025, 802 cases of shigellosis and EIEC were registered in Denmark. The primary PCR-based diagnostics do not distinguish between *Shigella* spp. and EIEC, but the species is determined for the subset of cases where an isolate is referred to the reference laboratory at SSI. The Danish cases consist 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.

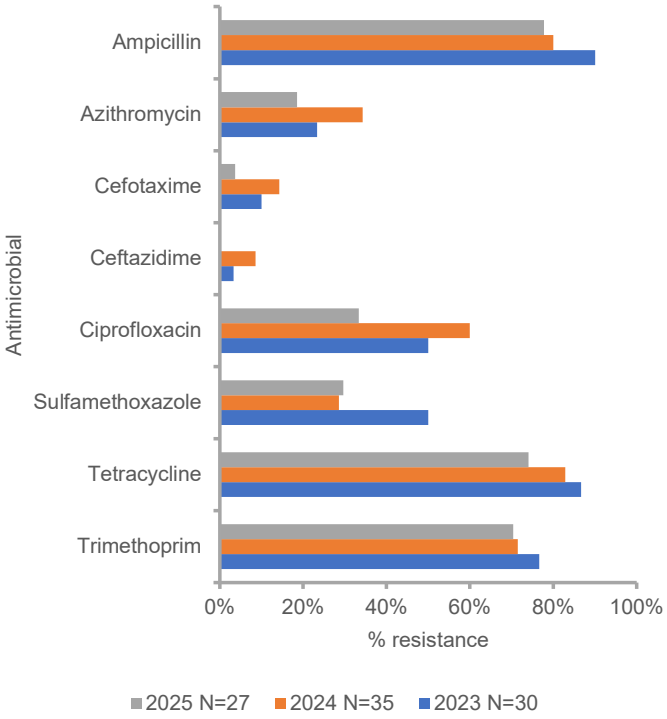
The levels of resistance in *S. sonnei* and *S. flexneri* isolated from patients isolated in 2023-2025 is presented in Figure 8.34. In 2025, 39% of *S. sonnei* and 19% of *S. flexneri*, respectively were resistant to azithromycin and the levels of resistance to the third-generation cephalosporin cefotaxime 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)

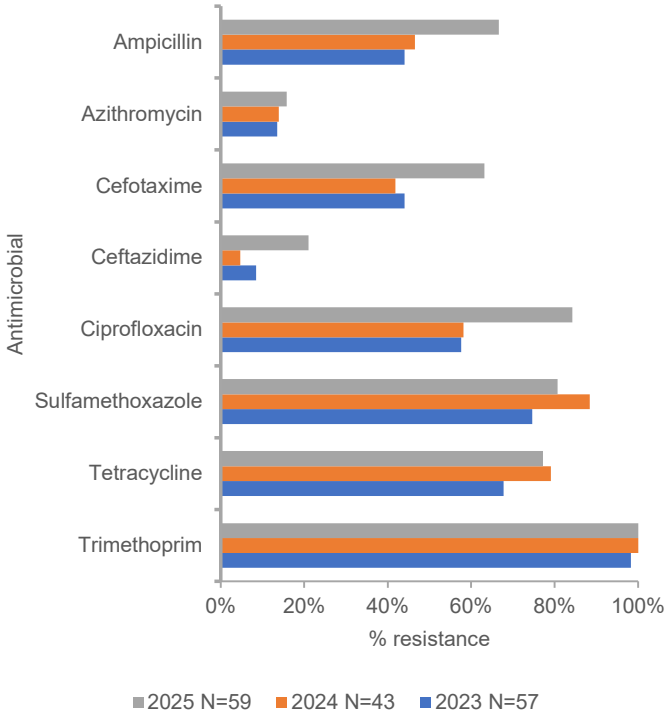


Figure 8.35 Combinations of resistance in *Shigella sonnei* (a) and *Shigella flexneri* (b) isolates towards azithromycin (AZI), ceftazidime (CAZ), cefotaxime (CTX) and ciprofloxaxin (CIP), 2023-2025, from patients in Denmark DANMAP 2025

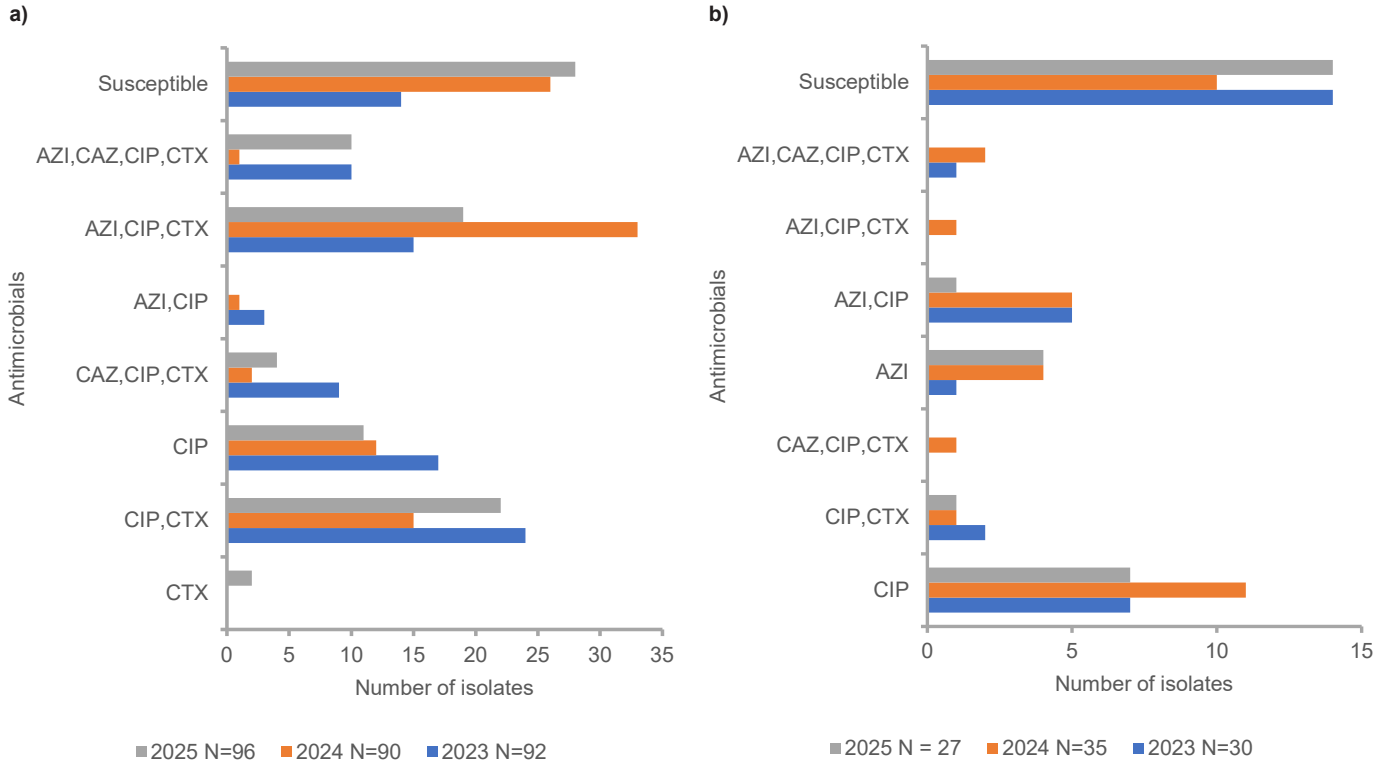


Figure 8.35 is a presentation of combinations of resistance in *Shigella sonnei* (a) and *Shigella flexneri* (b) isolates towards azithromycin (AZI), ceftazidime (CAZ), cefotaxime (CTX) and ciprofloxacin (CIP). It is notable that there is a high number of isolates that simultaneously are resistant towards 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]

Hanne Donskov Eriksen, Lone Jannok Porsbo, Nina Ank, Lukas Holm Saarup, Kasper Vium Andersen, Anette M. Hammerum, Hans Linde Nielsen and Henrik Hasman
For further information: Henrik Hasman, henh@ssi.dk

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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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For further information: Asja Kunøe, asku@ssi.dk

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8 https://eu-jamrai.eu/
9 https://health.ec.europa.eu/funding/eu4health-programme-2021-2027-vision-healthier-european-union_en
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Textbox 8.3

Fungemia surveillance in Denmark – Update from 2024-2025

Patrick Offendal, Nissrine Abou-Chakra, Lise Kristensen, Jan B. Gertsen, Valeria Antsupova, Helle K. Johansen, Sofia Sulim, Marianne E. Clausen, Michael Pedersen, Flemming S. Rosenvinge, Lisbeth Lützen, Esad Dzajic, Turid S. Søndergaard, Maiken C. Arendrup, Karen M.T. Astvad.

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.

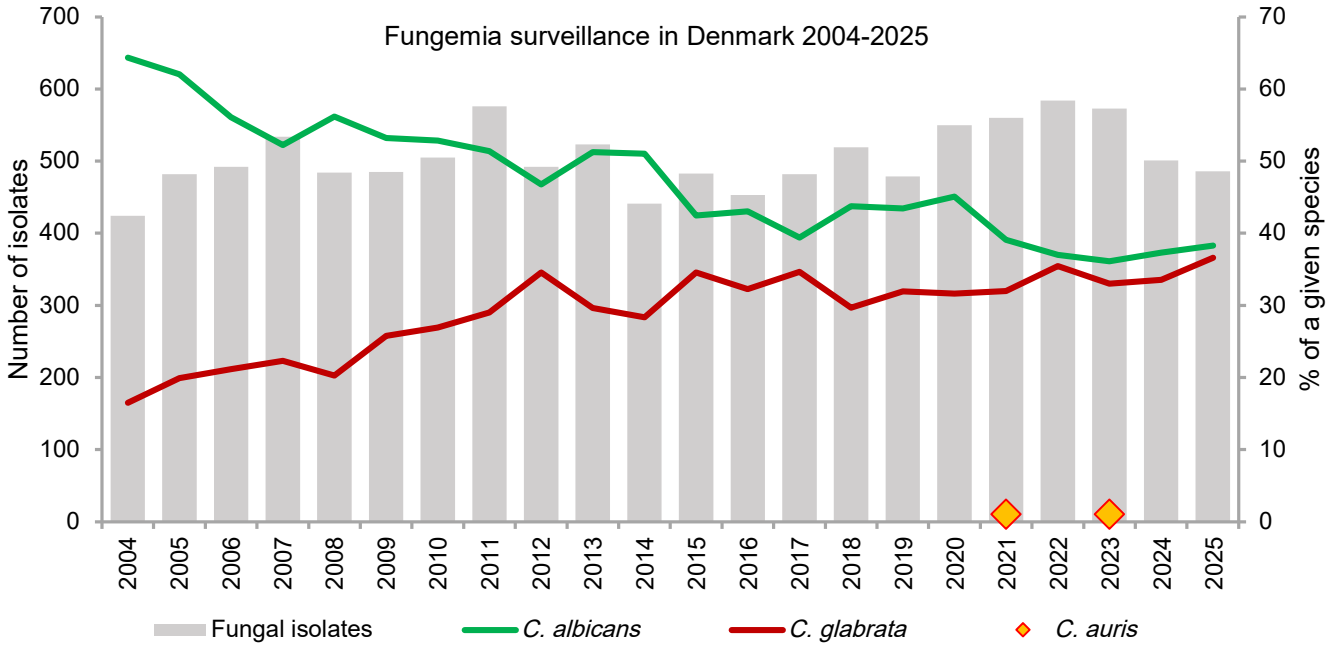
The overall fluconazole susceptibility rate has declined during the surveillance period, from 68.5% in 2004-2007 to 57.6% in 2024-2025[7]. These changes can largely be attributed to the change in species distribution over recent years from 64.4% *C. albicans* and 16.5% *C. glabrata* in 2004[6] to 38.3% *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.

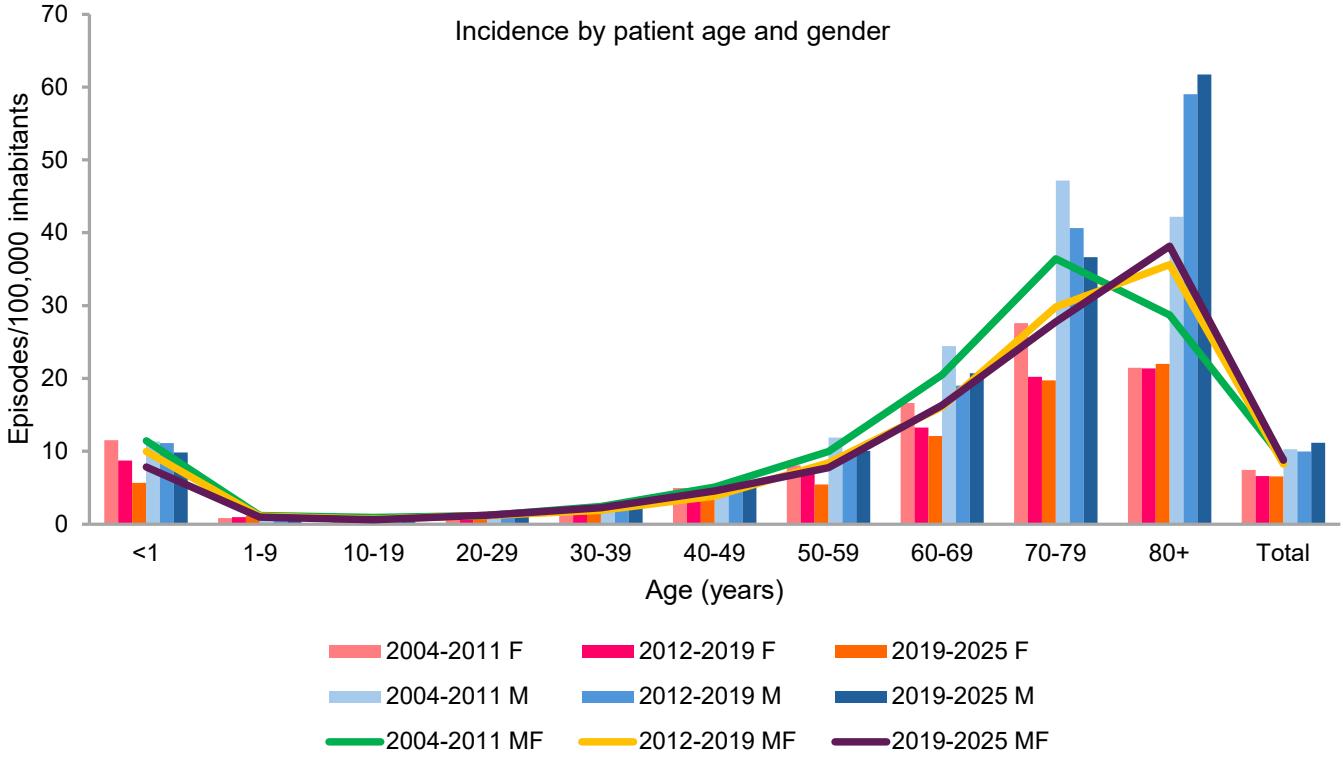
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Figure 1 Number of yearly isolates (bars) and species distribution in percentage over the years (curves) DANMAP 2025



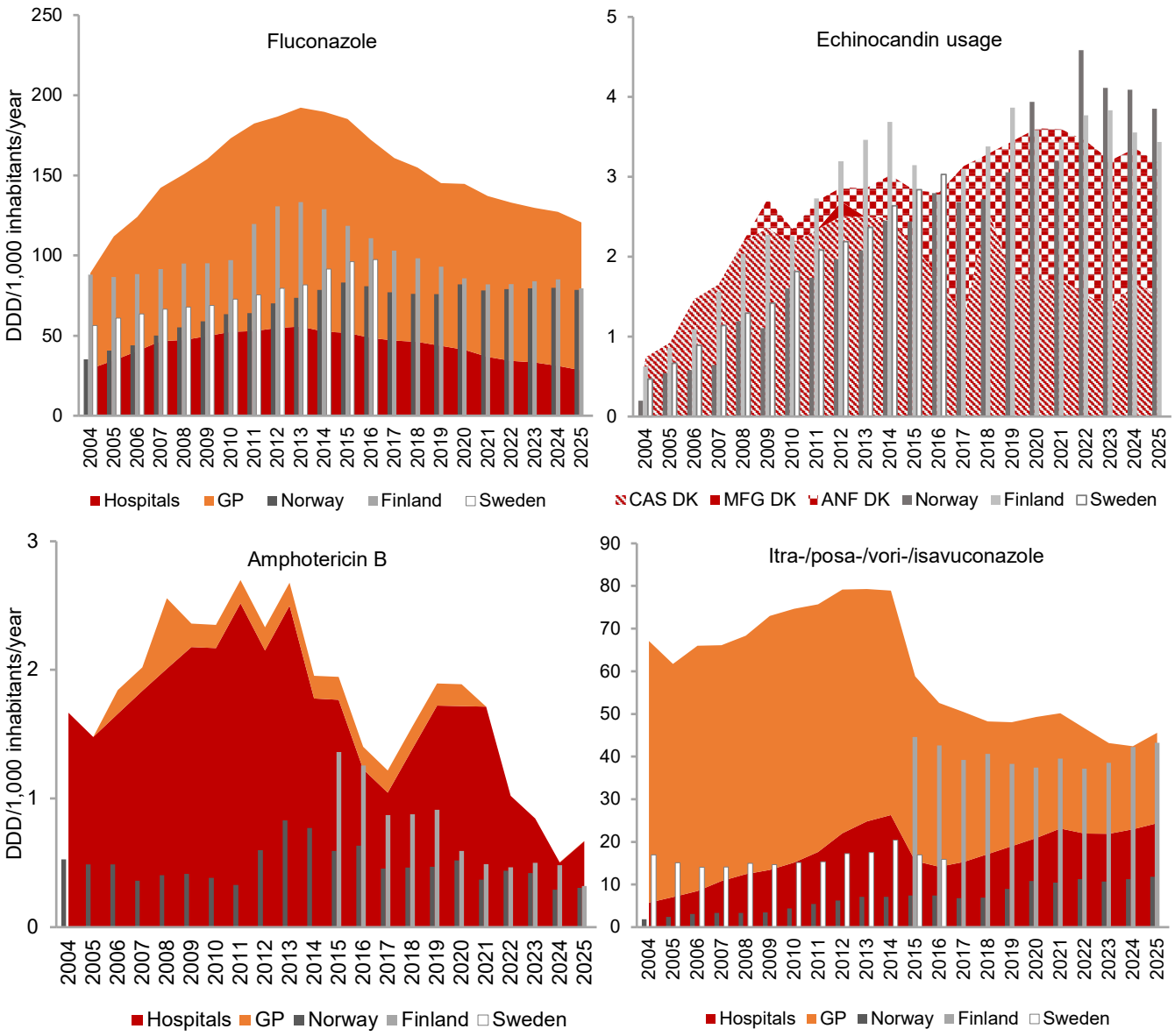
◆ Indicates one single *C. auris* episode in each of 2021 and 2023.

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

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Textbox 8.4

Azole resistance in clinical isolates of *A. fumigatus* (Oct 2023-Sept 2025)

Karen MT ASTVAD, Nissrine ABOU-CHAKRA, Jan B GERTSEN, Lise KRISTENSEN, Flemming S ROSENVINGE, Lisbeth LÜTZEN, Kristina Melbardis JØRGENSEN, Michael PEDERSEN, Marianne Engell CLAUSEN, Sofia SULIM, Marc TK Nielsen, Turid S SØNDERGAARD, Maiken C ARENDRUP.

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%

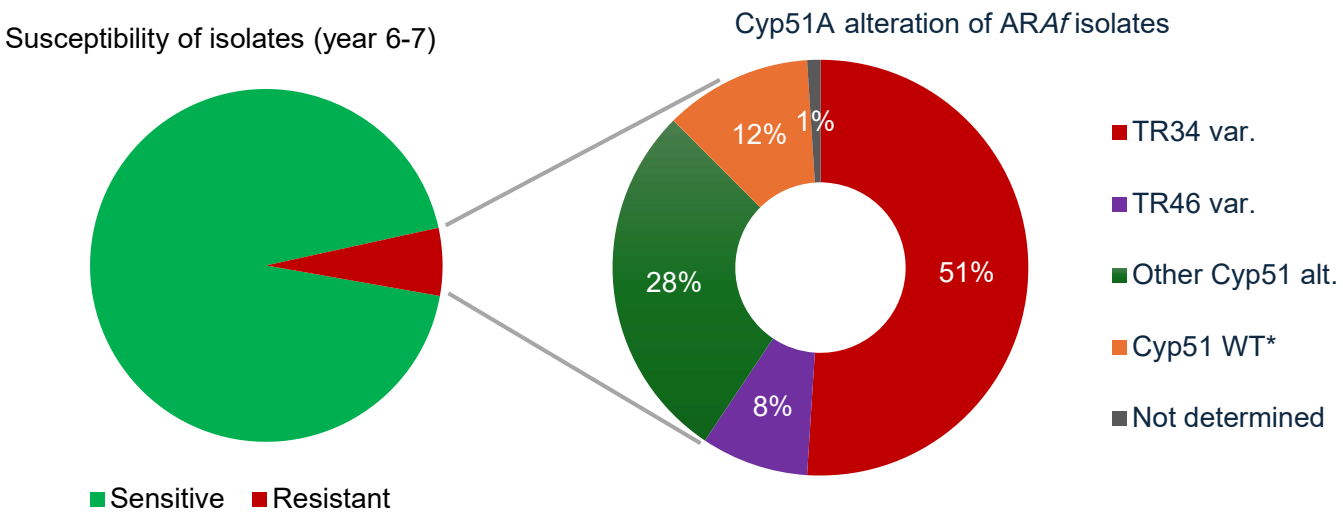
AMB: Amphotericin B. ITZ: Itraconazole. POS: Posaconazole. VOR: Voriconazole. ISA: Isavuconazole.
* All azole susceptible isolates without an ISA MIC were considered ISA susceptible.

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

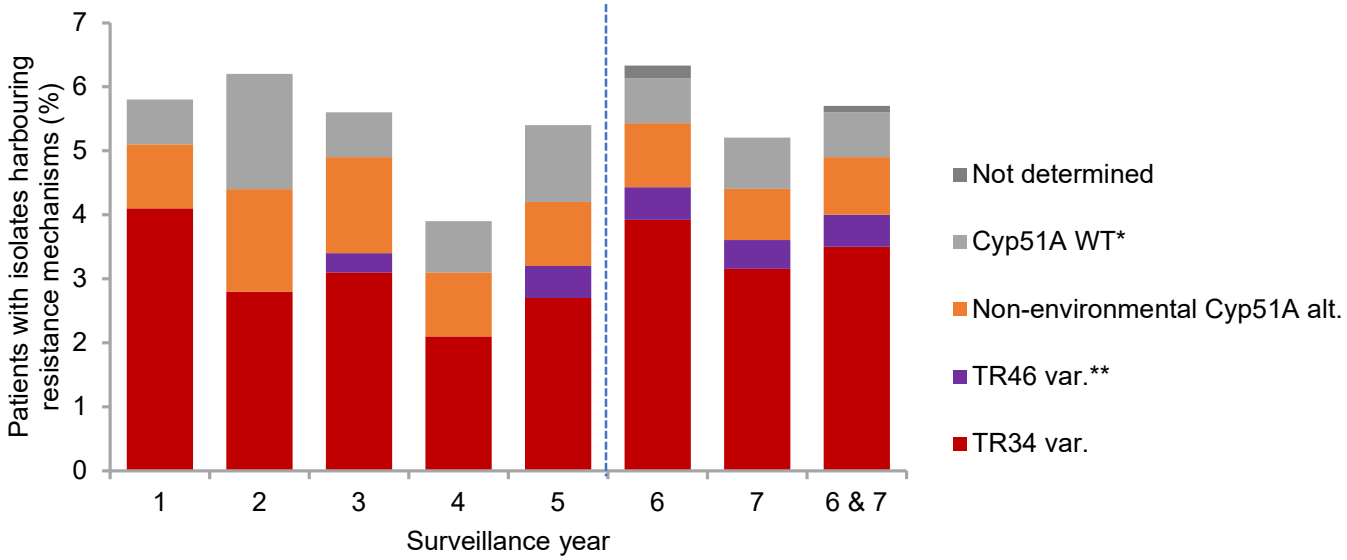
could warrant similar consideration. Ipflufenoquin shares its target with olorofim and has experimentally been shown to select for cross-resistance[8], yet is licensed for crop protection outside the EU. Resistance surveillance would therefore be advisable should ipflufenoquin be licensed in the EU, 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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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

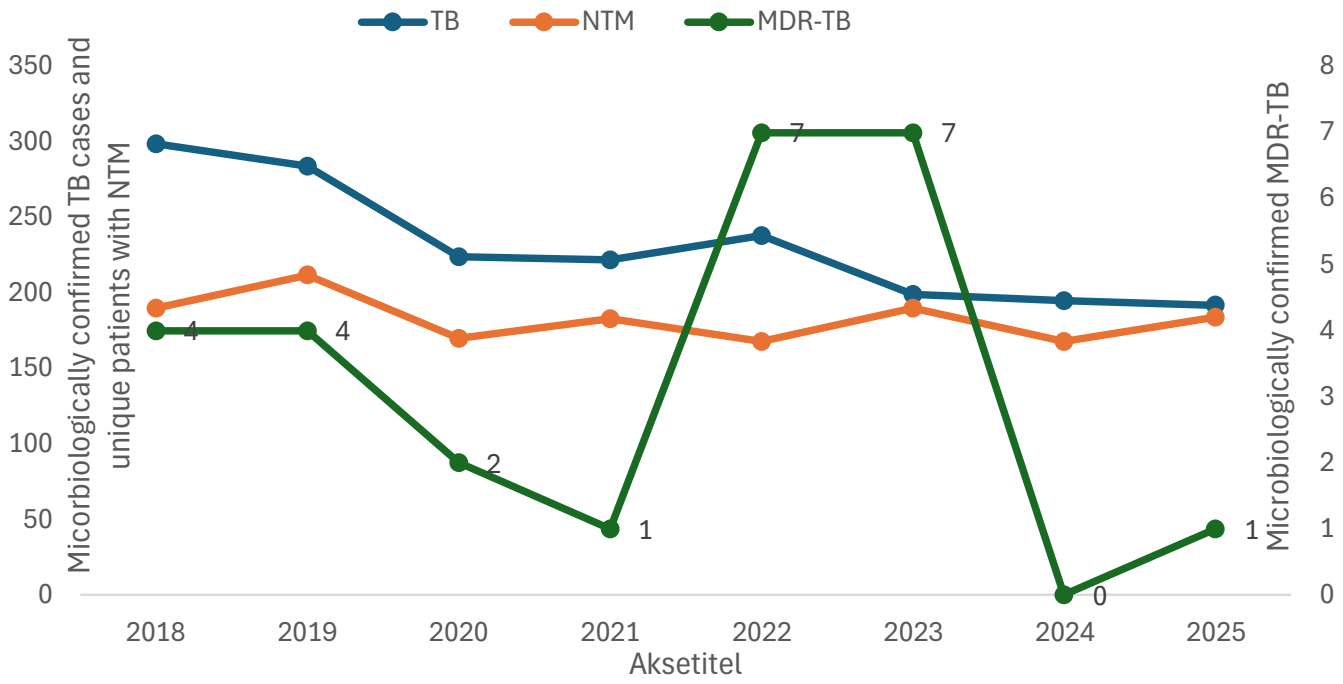
Antimicrobial susceptibility in NTM is complex. Different NTM species have markedly different intrinsic susceptibility patterns, and susceptibility testing does not predict clinical outcome equally well for all combinations of species and antimicrobial agents. Consequently, correct species identification 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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