

6.

Resistance in zoonotic bacteria

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

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

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

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

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

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

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

6. 1 Introduction

6.1.1 Introduction to resistance in zoonotic bacteria

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

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

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

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

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

6.2 *Campylobacter* spp.

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

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

6.2.1 Resistance in *Campylobacter jejuni*

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

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

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

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

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

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

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

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

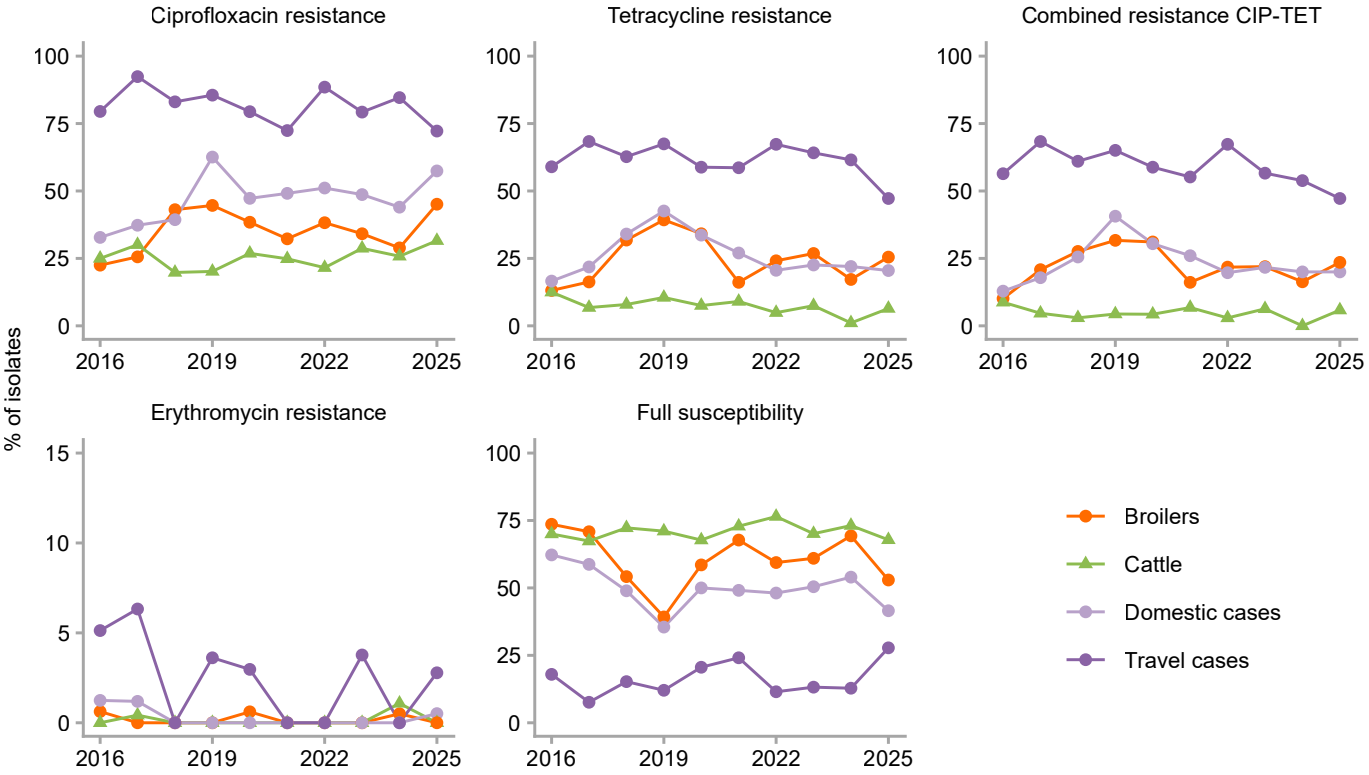
In 2025, macrolide (erythromycin) resistance was observed in two human isolates, one domestic and one travel-related, respectively, while no macrolide resistance was observed in broiler and cattle *C. jejuni* isolates. Resistance to macrolides is of concern since macrolides are frequently used for the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

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

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

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

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



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

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

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

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

6.2.2 Resistance in *Campylobacter coli*

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

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

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

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

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

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

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

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

6.3 *Salmonella* spp.

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

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

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

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

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

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

6.3.1 Resistance in human *Salmonella* spp. isolates

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

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

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

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

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

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

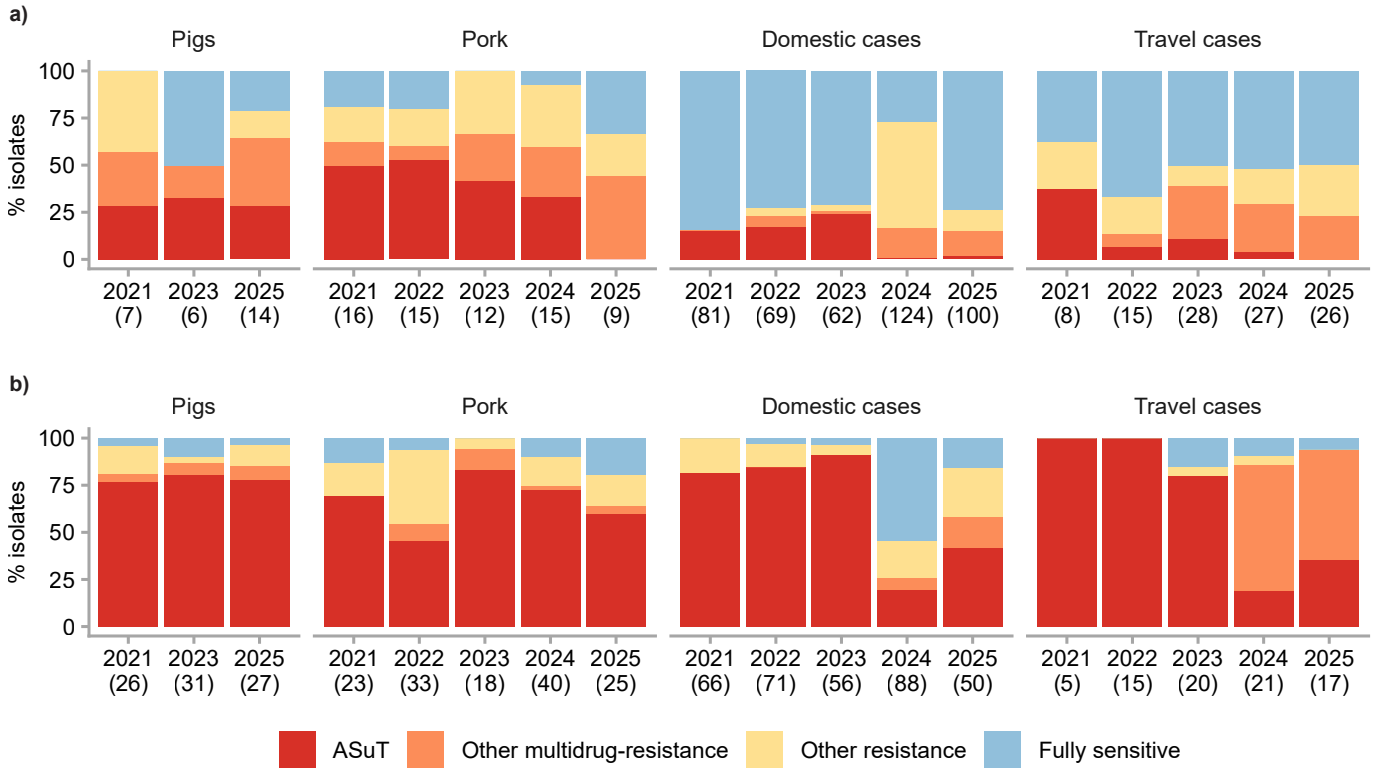
6.3.2 Resistance in *S.* Typhimurium and monophasic *S.* Typhimurium

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

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

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

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



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

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

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

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

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

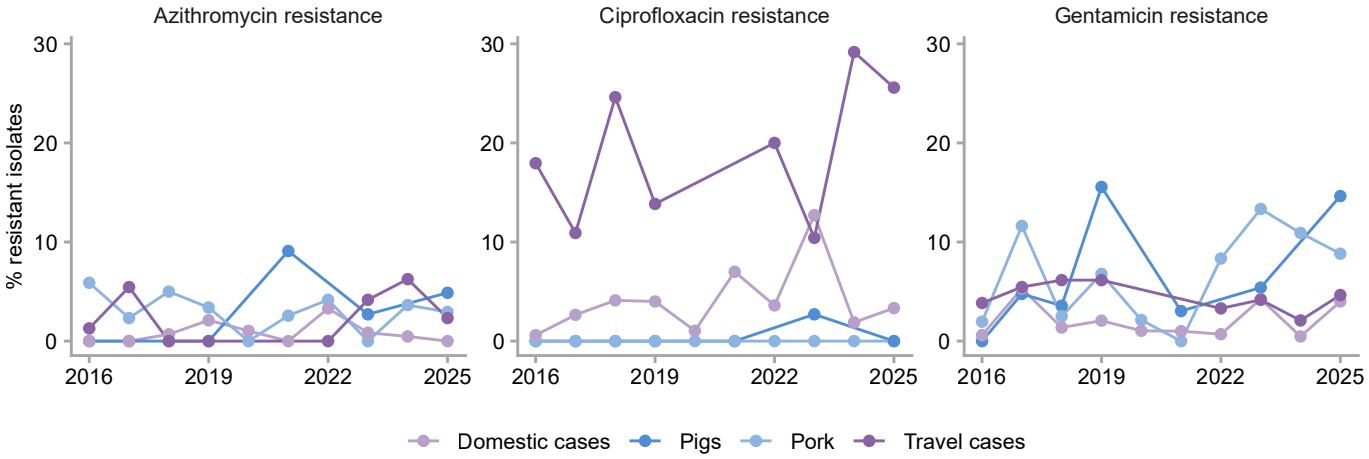
As in previous years, the occurrence of resistance in *S.* Typhimurium and monophasic *S.* Typhimurium continued to be overall higher in isolates from domestic pigs and pork than in isolates from humans.

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

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

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

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



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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

DANMAP 2025



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

Resistance determinants in human monophasic *S.* Typhimurium isolates

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

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

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

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

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

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

Resistance determinants in pork monophasic *S.* Typhimurium isolates

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

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

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

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

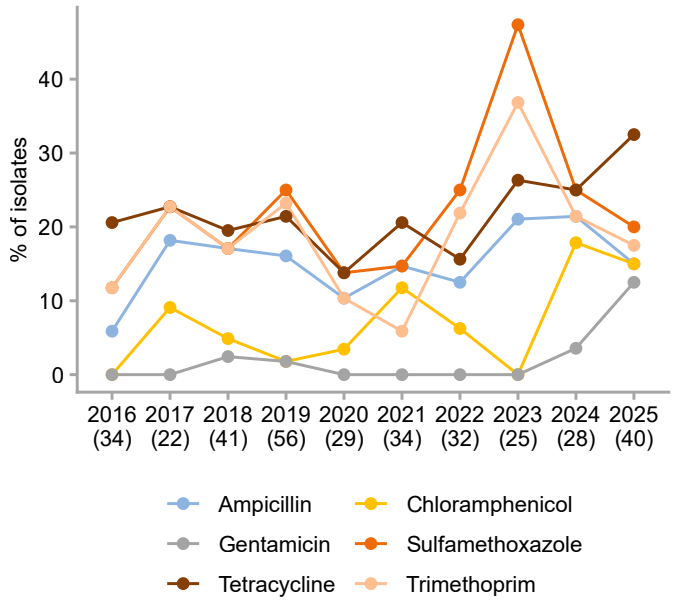
6.3.4 Resistance in other *Salmonella* serotypes from domestic pigs and pork

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

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

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

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



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

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

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

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

6.4 Conclusions and future perspectives

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

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

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

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

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

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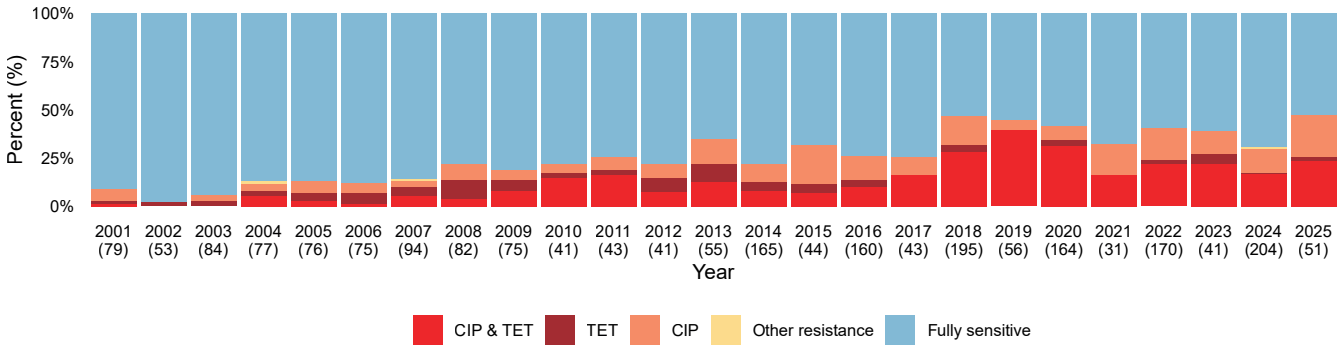
Textbox 6.1

30 years of *Campylobacter jejuni* surveillance in Denmark

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

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

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



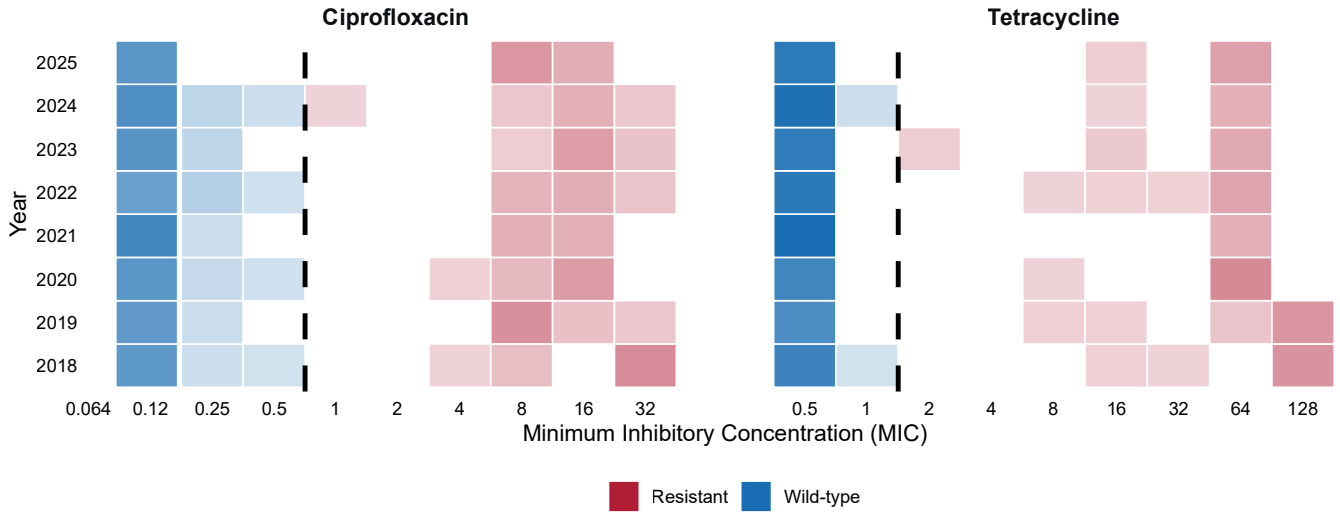
The bars show the percentage of isolates classified as having resistance to ciprofloxacin (CIP), tetracycline (TET), both CIP and TET, other resistance or being fully sensitive (sensitivity to all antimicrobial substances tested). The number of isolates included for each year is given in parentheses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

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

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

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

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



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

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

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

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

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Textbox 6.2

30 years of *Salmonella* surveillance in Denmark

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

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

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

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

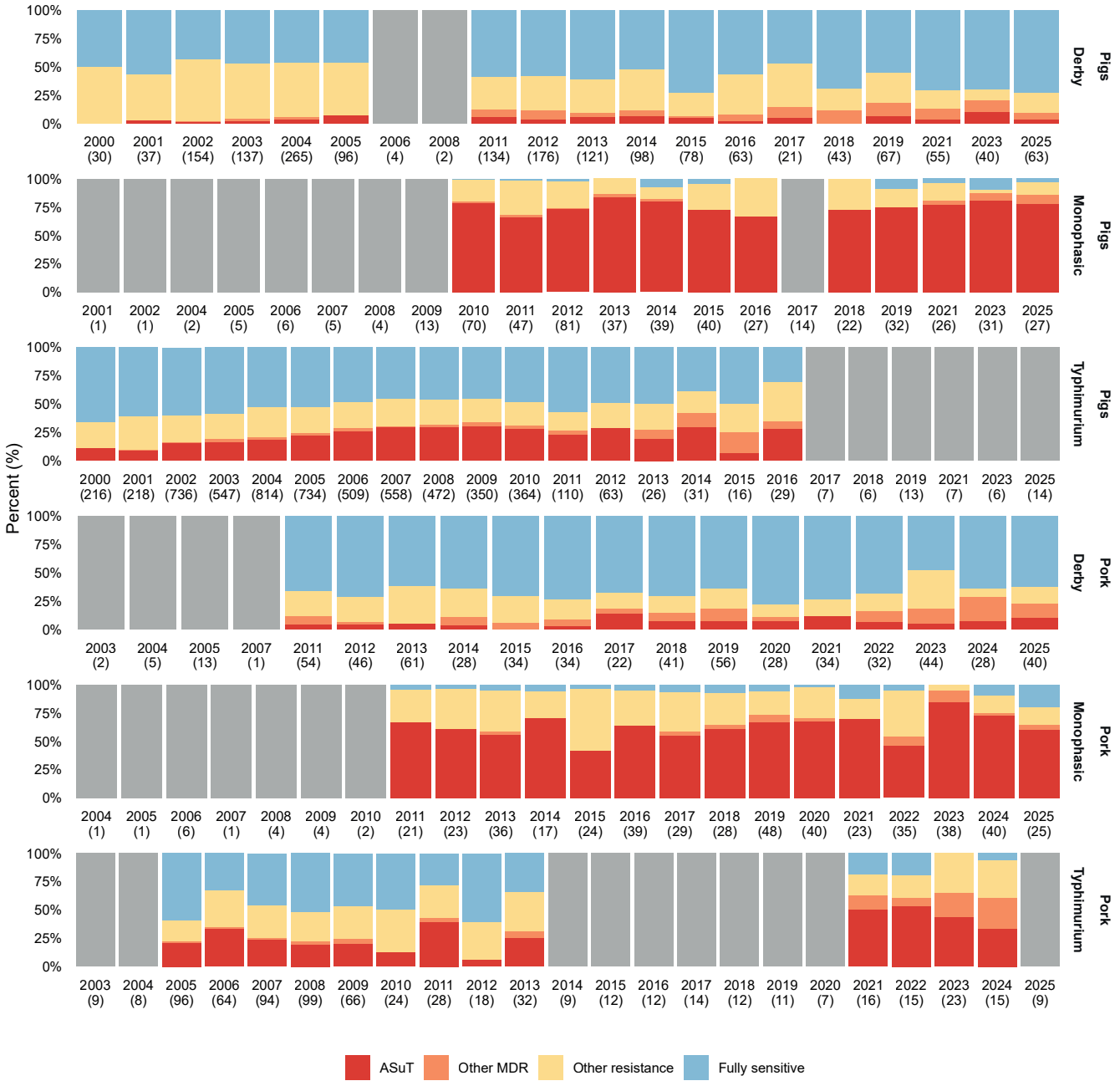
Among monophasic *S.* Typhimurium from pigs, ASuT remained the predominant resistance profile across all years, with proportions accounting for 66–84% of isolates, and the highest value observed in 2013. Among isolates from pork, ASuT accounted for 55–71% of isolates during 2011–2021, except in 2015,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

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

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

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

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

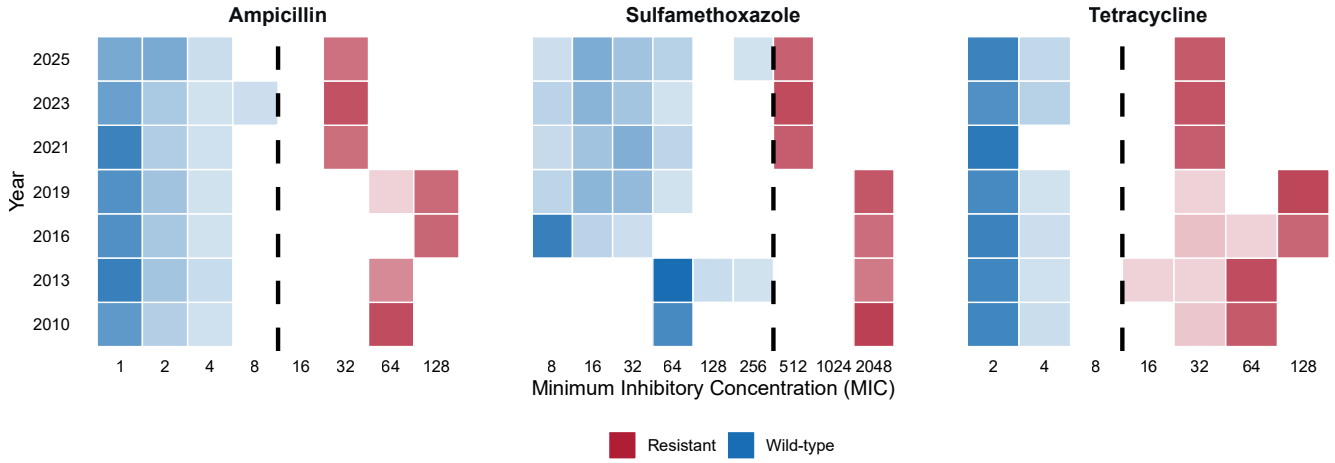


The bars show the percentage of isolates classified as ASuT (resistant to at least ampicillin, sulfamethoxazole and tetracycline), other MDR (other multidrug resistance profiles than ASuT), other resistance (resistance to one or two antimicrobial classes), or fully sensitive (sensitivity to all antimicrobial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

continued ... Textbox 6.2

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

DANMAP 2025



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

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

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

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

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