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Resistance in animal pathogens

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Highlights

Surveillance of antimicrobial resistance in 2025 focused on pathogenic bacteria from acute mastitis in dairy cows and from various organs in pigs and included results obtained through antimicrobial susceptibility testing.

None of the **pathogenic bacteria from acute mastitis in dairy cows** displayed significant changes in phenotypic resistance between 2024 and 2025. Of note, 27.6% of *Streptococcus uberis* isolates displayed resistance to penicillin, which is noteworthy because beta-lactamase sensitive penicillins are the most commonly used drugs for treatment of adult cattle in Denmark. However, most of the isolates had a minimum inhibitory concentration value of 0.25 mg/L, which is just above the tentative epidemiological cut-off of 0.12 mg/L, and there is currently no clinical breakpoint available for penicillin in *S. uberis*. Thus, it remains unclear whether penicillin is active against these borderline resistant *S. uberis* isolates.

Most **pathogenic bacteria isolated from pigs** in 2025 displayed similar levels of phenotypic resistance as in 2024 (1-year period) and 2020 (5-year period). However, ten pathogen-drug combinations were associated with significantly increased resistance, whereas none were associated with significantly decreased resistance. The high level of neomycin resistance in haemolytic *Escherichia coli* (59.9%) is worrisome because it is one of only a few drugs recommended in Denmark as first choice for treating *E. coli*-associated post-weaning diarrhoea. The high level of gentamicin resistance in haemolytic *E. coli* (48.8%) is also worrisome because it is considered critically important for human medicine by the World Health Organization. It should also be noted that 6.8% of haemolytic *E. coli* isolates displayed resistance to 3rd generation cephalosporins (cefpodoxime).

9.1 Introduction

Surveillance of antimicrobial resistance in 2025 focused on pathogenic bacteria from mastitis in dairy cows and from various organs in pigs and included results obtained through antimicrobial susceptibility testing (AST).

9.2 Acute mastitis in dairy cows

9.2.1 Background

Milk samples for routine diagnosis of clinical mastitis in dairy cows are normally collected by and tested at the local veterinary clinics throughout Denmark. As part of the testing, veterinarians identify common pathogens using simple culture techniques and bacterial identification methods and sometimes perform AST to decide on therapeutic options. Normally, the milk samples and isolates are discarded after analysis.
In 2024, we established a surveillance program for mastitis pathogens by asking veterinarians specialised in cattle to send frozen milk samples from dairy cows with acute mastitis to Statens Serum Institut. In 2025, 441 milk samples were shipped by 15 veterinary clinics across Denmark. Isolates obtained from these milk samples were identified to the genus or species level using MALDI-TOF, and AST was performed by broth microdilution using customized Sensititre panels. Tables 9.1 and 9.2 show the results from 2025, while results from 2024 can be found on the homepage of the Danish Veterinary Consortium (https://www.vetssi.dk/). AST data were based on epidemiological cut-offs (ECOFFs) and clinical breakpoints when ECOFFs were unavailable (https://www.vetssi.dk/).

9.2.2 Results

Among the 441 milk samples tested, 90.5% were positive for one or more pathogenic bacteria, while the remaining milk samples were interpreted as negative, either because of lack of growth or unspecific growth suggestive of contamination. In total, 491 bacterial isolates were recovered, of which 80.9% belonged to well-known mastitis pathogens: *Streptococcus uberis* (25.1%), *Escherichia coli* (16.9%), *Staphylococcus aureus* (12.0%), *Streptococcus dysgalactiae* (11.2%), coagulase-negative staphylococci (CoNS) (6.1%), *Trueperella pyogenes* (3.7%), *Streptococcus agalactiae* (3.5%) and *Klebsiella pneumoniae* (2.4%). None of the remaining bacterial species were found in more than 2% of the milk samples. Table 9.1 provides an overview of the identified pathogenic bacteria.

AST was performed on 375 bacterial isolates representing well-known mastitis pathogens (Table 9.1). *T. pyogenes* isolates were not tested due to their relatively slow growth and specific methodological requirements for AST. Table 9.2 shows the proportions of resistant isolates in 2025.

We did not observe any significant changes in phenotypic resistance between 2024 and 2025.

Among streptococci, we observed that 27.6% of the *S. uberis* isolates displayed resistance to penicillin. It should be noted, however, that 33 of the 34 penicillin-resistant *S. uberis* isolates had a minimum inhibitory concentration (MIC) value of 0.25 mg/L, which is just above the tentative ECOFF for *S. uberis* and the ECOFF for *S. agalactiae* (both 0.12 mg/L), whereas the remaining isolate had a MIC value of 0.5 mg/L. Tetracycline resistance was observed in 16.3% of the *S. uberis* and 16.4% of the *S. dysgalactiae* isolates. Tetracycline resistance was also found in 70.6% of the *S. agalactiae* isolates, which is consistent with a high prevalence of tetracycline resistance genes in this bacterial species (Da Cuna *et al.* Nat Commun. 2014 Aug 4;5:4544. doi: 10.1038/ncomms5544). Moreover, 29.4% of the *S. agalactiae* isolates were resistant to clindamycin, while 17.6% were resistant to erythromycin.

The relatively high level of borderline resistance to penicillin in *S. uberis* is particularly noteworthy because beta-lactamase sensitive penicillins are the most commonly used drugs for treatment of adult cattle in Denmark (DANMAP 2024).

Among staphylococci, we found that 13.3% of the CoNS and 8.5% of the *S. aureus* isolates were resistant to penicillin. Of note, a single *S. aureus* isolate was resistant to cefoxitin, which is used as a surrogate for detection of *mecA*- and *mecC*-mediated methicillin resistance. The isolate was therefore further analysed with a multiplex polymerase chain reaction assay, which showed that it belongs to *spa* type t034 and clonal complex 398 and carries *mecA*.

E. coli isolates were resistant to ampicillin (15.2%), sulfamethoxazole (15.2%), tetracycline (5.1%) and trimethoprim (12.7%). As in 2024, a single *E. coli* isolate displayed an extended-spectrum beta-lactamase (ESBL) phenotype and was resistant to multiple drugs, including ampicillin, cefotaxime, ceftazidime, chloramphenicol, ciprofloxacin, sulphamethoxazole, tetracycline and trimethoprim. Due to the ESBL phenotype (resistance to cefotaxime and ceftazidime), this isolate was further analysed with extra disk diffusion tests and subjected to whole genome sequencing, which confirmed the ESBL phenotype and showed that it belongs to multilocus sequence type 58 and carries $bla_{\text{CTX-M-15}}$. In comparison, the ESBL-producing *E. coli* isolate from 2024 was resistant to the same antimicrobials (plus nalidixic acid) and also carried $bla_{\text{CTX-M-15}}$ but belonged to multilocus sequence type 46.

As in 2024, 91.7% of the *K. pneumoniae* isolates were resistant to ampicillin, reflecting that this bacterial species is intrinsically resistant to penicillins.

Finally, five bacterial species displayed low levels of phenotypic resistance to specific antimicrobials (<5.0%).

Table 9.1 Pathogenic bacteria from acute mastitis in dairy cows, Denmark, 2025 DANMAP 2025

Pathogen	Milk samples (n=441)		AST
	Positive (no.)	Positive (%)	Isolates (no.)
Streptococcus uberis	123	25.1%	123
Escherichia coli	83	16.9%	79
Staphylococcus aureus	59	12.0%	59
Streptococcus dysgalactiae	55	11.2%	55
Coagulase-negative staphylococci	30	6.1%	30
Coagulase-negative staphylococci in mixed cultures	29	5.9%	ND
Trueperella pyogenes	18	3.7%	ND
Streptococcus agalactiae	17	3.5%	17
Klebsiella pneumoniae	12	2.4%	12
Enterococcus faecium	4	0.8%	ND
Helcococcus ovis	4	0.8%	ND
Lactococcus garviae	4	0.8%	ND
Streptococcus equinus/Streptococcus infantarius	4	0.8%	ND
Serratia liquefaciens	3	0.6%	ND
Streptococcus gallolyticus	3	0.6%	ND
Streptococcus spp.	3	0.6%	ND
Corynebacterium bovis	2	0.4%	ND
Corynebacterium variabile	2	0.4%	ND
Empedobacter brevis	2	0.4%	ND
Enterococcus faecalis	2	0.4%	ND
Helcococcus kunzii	2	0.4%	ND
Klebsiella oxytoca	2	0.4%	ND
Mannheimia haemolytica	2	0.4%	ND
Micrococcus luteus	2	0.4%	ND
Pantoea agglomerans	2	0.4%	ND
Streptococcus canis	2	0.4%	ND
Streptococcus parauberis	2	0.4%	ND
Corynebacterium amycolatum	1	0.2%	ND
Corynebacterium testudinoris	1	0.2%	ND
Elizabethkingia miricola	1	0.2%	ND
Enterococcus cecorum	1	0.2%	ND
Klebsiella variicola	1	0.2%	ND
Proteus mirabilis	1	0.2%	ND
Pseudomonas aeruginosa	1	0.2%	ND
Pseudomonas spp.	1	0.2%	ND
Psychrobacter spp.	1	0.2%	ND
Raoultella ornithinolytica	1	0.2%	ND
Raoultella terrigena	1	0.2%	ND
Serratia marcescens	1	0.2%	ND
Serratia nematodiphila	1	0.2%	ND
Serratia proteamaculans	1	0.2%	ND
Streptococcus suis	1	0.2%	ND
Trueperella spp.	1	0.2%	ND
Vibrio fluvialis	1	0.2%	ND
Weissela thailandensis	1	0.2%	ND
Streptococcus suis	1	0.2%	ND
Trueperella spp.	1	0.2%	ND
Vibrio fluvialis	1	0.2%	ND
Weissela thailandensis	1	0.2%	ND

Isolates were identified to the genus or species level using MALDI-TOF.
Antimicrobial susceptibility testing was performed by broth microdilution using customized Sensititre panels.
Abbreviations: AST, antimicrobial susceptibility testing; ND, not determined.

Table 9.2 Phenotypic antimicrobial resistance among pathogenic bacteria from acute mastitis in dairy cows, Denmark, 2025

DANMAP 2025

Antimicrobial agent	Ec (n=79)	Kp (n=12)	Sau (n=59)	CoNS (n=30)	Sag (n=17)	Sd (n=55)	Su (n=123)
	R (%)	R (%)	R (%)	R (%)	R (%)	R (%)	R (%)
Amikacin	0.0%	0.0%*	ND	ND	ND	ND	ND
Ampicillin	15.2%	91.7%*	ND	ND	ND	ND	ND
Azithromycin	0.0%	ND	ND	ND	ND	ND	ND
Cefotaxime	1.3%	0.0%*	ND	ND	ND	ND	ND
Cefoxitin	ND	ND	1.7%	ND	ND	ND	ND
Ceftazidime	1.3%	0.0%*	ND	ND	ND	ND	ND
Chloramphenicol	2.5%	0.0%*	0.0%	3.3%	0.0%*	0.0%	0.0%
Clindamycin	ND	ND	1.7%	ND	29.4%*	0.0%	4.1%
Ciprofloxacin	1.3%	0.0%*	0.0%	ND	0.0%*	ND	ND
Colistin	0.0%	0.0%*	ND	ND	ND	ND	ND
Erythromycin	ND	ND	0.0%	3.3%	17.6%	1.8%	2.4%
Fusidate	ND	ND	0.0%	ND	ND	ND	ND
Gentamicin	1.3%	0.0%*	0.0%	0.0%	0.0%*	ND	ND
Kanamycin	ND	ND	0.0%	ND	ND	ND	ND
Linezolid	ND	ND	0.0%	0.0%	0.0%*	ND	ND
Meropenem	0.0%	0.0%*	ND	ND	ND	ND	ND
Mupirocin	ND	ND	0.0%	ND	ND	ND	ND
Nalidixic acid	0.0%	ND	ND	ND	ND	ND	ND
Penicillin	ND	ND	8.5%	13.3%	0.0%*	ND	27.6%
Quinopristin-dalfopristin	ND	ND	1.7%	ND	ND	ND	ND
Rifampin	ND	ND	0.0%	0.0%	ND	ND	ND
Streptomycin	ND	ND	0.0%	ND	ND	ND	ND
Sufamethoxazole	15.2%	ND	ND	ND	ND	ND	ND
Tetracycline	5.1%	0.0%*	1.7%	0.0%	70.6%*	16.4%	16.3%
Tiamulin	ND	ND	1.7%	ND	ND	ND	ND
Tigecycline	0.0%	0.0%*	ND	ND	ND	ND	ND
Trimethoprim	12.7%	0.0%*	1.7%	ND	ND	ND	ND
Vancomycin	ND	ND	0.0%	0.0%	0.0%*	0.0%	0.0%

Data were based on epidemiological cut-offs (ECOFFs) or clinical breakpoints when ECOFFs were unavailable (https://www.vetssi.dk/).
Percentages based on small sample sizes (n<20) are indicated by asterices and should be interpreted with caution.
Abbreviations: Ec, *Escherichia coli*; Kp, *Klebsiella pneumoniae*; Sau, *Staphylococcus aureus*; CoNS, coagulase-negative staphylococci; Sag, *Streptococcus agalactiae*; Sd, *Streptococcus dysgalactiae*; Su, *Streptococcus uberis*; R, resistant; ND, not determined.

9.3 Pigs

9.3.1 Background

The Veterinary Laboratory, The Danish Agriculture and Food Council, performed AST of isolates belonging to *Actinobacillus pleuropneumoniae, Bordetella bronchiseptica*, haemolytic and non-haemolytic *E. coli, Klebsiella pneumoniae, Salmonella enterica, Staphylococcus hyicus* and *Streptococcus suis*. Table 9.3 shows the proportions of resistant isolates in 2025, while results from 2016-2024 can be found on the homepage of the Danish Veterinary Consortium (https://www.vetssi.dk/). AST data were based on ECOFFs and clinical breakpoints when ECOFFs were unavailable (https://www.vetssi.dk/).

9.3.2 Results

Most isolates displayed similar levels of phenotypic resistance as in 2024 (1-year period) and 2020 (5-year period). However, ten pathogen-drug combinations were associated with significantly increased resistance, whereas none were associated with significantly decreased resistance. Table 9.4 and Figure 9.1 show all significant changes in phenotypic resistance over a 1-year period (2025 vs. 2024) and a 5-year period (2025 vs. 2020).

A. pleuropneumoniae displayed significantly increased resistance to trimethoprim-sulfamethoxazol (2025 vs. 2020).

Haemolytic *E. coli* displayed significantly increased resistance to amoxicillin-clavulanic acid (2025 vs. 2024 and 2025 vs. 2020), florfenicol (2025 vs. 2020), gentamicin (2025 vs. 2020), neomycin (2025 vs. 2020), spectinomycin (2025 vs. 2020), streptomycin (2025 vs. 2020) and tetracycline (2025 vs. 2020).

Table 9.3 Phenotypic antimicrobial resistance among pathogenic bacteria from pigs, Denmark, 2025 DANMAP 2025

Antimicrobial agent	Ap (n=57) R (%)	Bb (n=28) R (%)	H-Ec (n=207) R (%)	NH-Ec (n=131) R (%)	Kp (n=11) R (%)	Se (n=20) R (%)	Sh (n=8) R (%)	Ss (n=109) R (%)
Amoxicillin	0.0%	ND	75.4%	84.2%	ND	80.0%	100.0%*	ND
Ampicillin	ND	ND	ND	ND	ND	ND	ND	ND
Amoxicillin-clavulanic acid	ND	ND	38.6%	35.3%	0.0%*	20.0%	ND	ND
Cefotaxime	ND	ND	ND	ND	ND	ND	ND	ND
Cefpodoxime	ND	ND	6.8%	0.8%	ND	ND	ND	ND
Cefquinome	ND	ND	ND	ND	0.0%*	ND	ND	ND
Ceftiofur	0.0%	ND	ND	ND	ND	ND	ND	ND
Chloramphenicol	ND	ND	ND	ND	ND	ND	ND	ND
Ciprofloxacin	ND	ND	ND	ND	ND	ND	ND	ND
Colistin	ND	ND	0.0%	0.0%	0.0%*	ND	ND	ND
Doxycyclin	0.0%	ND	71.0%	66.2%	36.4%*	70.0%	ND	40.4%
Enrofloxacin	7.0%	ND	11.6%	6.0%	ND	ND	0.0%*	0.0%
Erythromycin	ND	ND	ND	ND	ND	ND	ND	ND
Florfenicol	0.0%	7.1%	23.7%	21.8%	27.3%*	20.0%	25.0%*	0.9%
Gentamicin	ND	ND	48.8%	13.5%	10.0%*	5.0%	ND	ND
Lincomycin	ND	ND	ND	ND	ND	ND	75.0%*	ND
Nalidixan	ND	ND	ND	ND	ND	ND	ND	ND
Neomycin	ND	ND	59.9%	25.6%	0.0%*	ND	ND	ND
Penicillin	1.8%	ND	ND	ND	ND	ND	100.0%*	5.5%
Spectinomycin	ND	ND	64.3%	45.9%	ND	50.0%	ND	ND
Streptomycin	ND	ND	87.9%	83.5%	ND	90.0%	ND	ND
Sulfamethoxazole	ND	ND	ND	ND	ND	ND	ND	ND
Tetracycline	ND	ND	72.0%	66.2%	40.0%*	75.0%	ND	ND
Tiamulin	0.0%	ND	ND	ND	ND	ND	37.5%*	ND
Tildipirosin	0.0%	0.0%	ND	ND	ND	ND	ND	ND
Tilmicosin	0.0%	ND	ND	ND	ND	ND	37.5%*	ND
Trimethoprim	ND	ND	ND	ND	ND	ND	ND	ND
Trimethoprim-sulfamethoxazole	19.3%	ND	66.7%	77.4%	54.5%*	35.0%	37.5%*	18.3%
Tulathromycin	ND	0.0%	ND	ND	ND	ND	ND	ND
Tylosin	ND	ND	ND	ND	ND	ND	37.5%*	ND

Data were based on epidemiological cut-offs (ECOFFs) or clinical breakpoints when ECOFFs were unavailable (https://www.vetssi.dk/).
Percentages based on small sample sizes (n<20) are indicated by asterices and should be interpreted with caution.
Abbreviations: Ap, *Actinobacillus pleuropneumoniae*; Bb, *Bordetella bronchiseptica*; H-Ec, haemolytic *Escherichia coli*; NH-Ec, non-haemolytic *Escherichia coli*; Kp, *Klebsiella pneumoniae*; Se, *Salmonella enterica*; Sh, *Staphylococcus hyicus*; Ss, *Streptococcus suis*; R, resistant; ND, not determined.

Table 9.4 Statistically significant temporal changes in antimicrobial resistance phenotypes among pathogenic bacteria from pigs, Denmark, 2025 vs. 2024 and 2025 vs. 2020

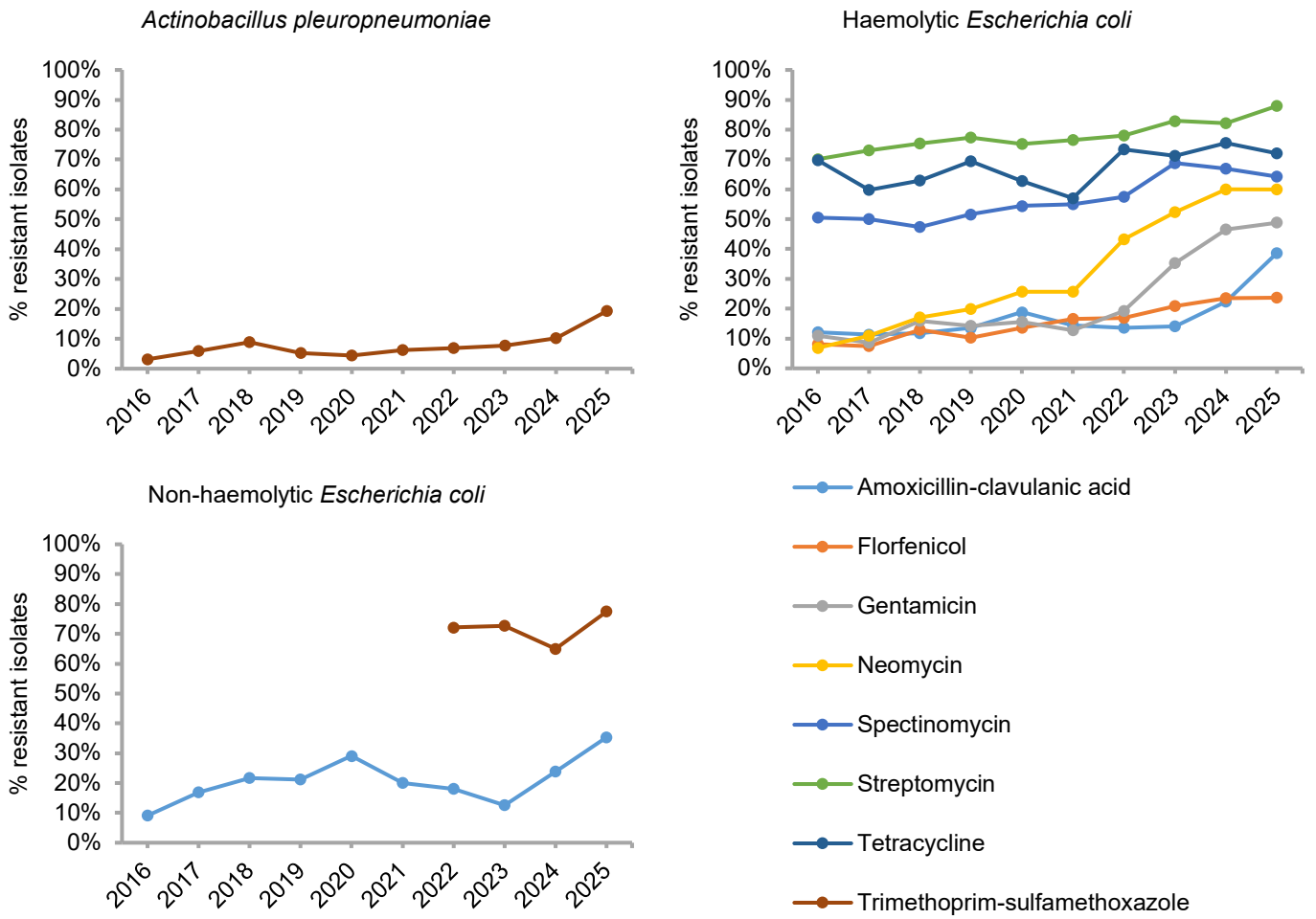
DANMAP 2025

Patho-gen	Antimicrobial agent	2016 R (%)	2017 R (%)	2018 R (%)	2019 R (%)	2020 R (%)	2021 R (%)	2022 R (%)	2023 R (%)	2024 R (%)	2025 R (%)	2025 vs. 2024 Trend (p value)	2025 vs. 2020 Trend (p value)
Ap	Trimethoprim-sulfamethoxazole	3.1%	6.0%	8.8%	5.2%	4.3%	6.3%	6.9%	7.7%	10.5%	19.3%	→ (0.3897)	↗ (0.0016)
H-Ec	Amoxicillin-clavulanic acid	12.1%	11.3%	11.7%	13.5%	18.8%	14.5%	13.5%	14.1%	22.4%	38.6%	↗ (0.0002)	↗ (0.0000)
H-Ec	Florfenicol	8.1%	7.4%	12.9%	10.3%	13.6%	16.5%	16.9%	20.8%	23.6%	23.7%	→ (1.0000)	↗ (0.0071)
H-Ec	Gentamicin	10.9%	8.6%	15.9%	14.3%	15.6%	12.8%	19.3%	35.2%	46.5%	48.8%	→ (0.6378)	↗ (0.0000)
H-Ec	Neomycin	6.9%	10.9%	17.0%	19.8%	25.6%	25.6%	43.2%	52.3%	60.0%	59.9%	→ (1.0000)	↗ (0.0000)
H-Ec	Spectinomycin	50.5%	50.0%	47.3%	51.6%	54.4%	55.0%	57.4%	68.8%	66.9%	64.3%	→ (0.5526)	↗ (0.0359)
H-Ec	Streptomycin	70.1%	73.0%	75.4%	77.4%	75.2%	76.4%	78.0%	82.9%	82.1%	87.9%	→ (0.0899)	↗ (0.0007)
H-Ec	Tetracycline	69.8%	59.8%	62.9%	69.4%	62.8%	57.0%	73.3%	71.1%	75.5%	72.0%	→ (0.4520)	↗ (0.0456)
NH-Ec	Amoxicillin-clavulanic acid	9.1%	16.8%	21.7%	21.1%	29.1%	20.0%	18.0%	12.6%	23.9%	35.3%	↗ (0.0235)	→ (0.2076)
NH-Ec	Trimethoprim-sulfamethoxazole	ND	ND	ND	ND	ND	ND	72.1%	72.6%	65.0%	77.4%	↗ (0.0313)	ND

Antimicrobial resistance phenotypes that remained at the same level during 2024-2025 and 2020-2025 were excluded (https://www.vetssi.dk/).
Abbreviations: Ap, *Actinobacillus pleuropneumoniae*; H-Ec, haemolytic *Escherichia coli*; NH-Ec, non-haemolytic *Escherichia coli*; R, resistant; ND, not determined.

Figure 9.1 Statistically significant temporal changes in antimicrobial resistance phenotypes among pathogenic bacteria from pigs, Denmark, 2025 vs. 2024 and 2025 vs. 2020

DANMAP 2025



The continued high level of neomycin resistance in haemolytic *E. coli* (59.9%) is worrisome because it is one of only a few drugs recommended in Denmark as first choice for treating *E. coli*-associated post-weaning diarrhoea. Furthermore, haemolytic *E. coli* also displayed medium to high levels of resistance to the other first-choice drugs, including amoxicillin-clavulanic acid (38.6%), spectinomycin (64.3%), trimethoprim-sulfamethoxazole (66.7%) and streptomycin (87.9%). *E. coli* isolates from 2023, 2024 and 2025 were not tested for susceptibility to the remaining first-choice drug ampicillin as it is currently not available for treatment of pigs in Denmark. However, it should be noted that we observed a high level of ampicillin resistance in haemolytic *E. coli* from 2022 (60.9%) (DANMAP 2022), and resistance against amoxicillin without clavulanic acid was high in 2025 (75.4%). The rapid increase in neomycin resistance coincided with increased use of neomycin in weaners (DANMAP 2024) following two recent decisions to restrict the use of alternative drugs in pigs: 1) the Danish Yellow Card initiative to reduce the use of specific antibiotics in 2016 and 2) the European Union-wide ban of medicinal zinc in 2022.

The continued high level of gentamicin resistance in haemolytic *E. coli* (48.8%) is also worrisome because it is considered critically important for human medicine by the World Health Organization. We have previously shown that most of the gentamicin resistance genes found in haemolytic *E. coli* also confer resistance to apramycin, which is increasingly used in weaners (DANMAP 2024). In contrast, the use of gentamicin in pigs is negligible and cannot explain the rapidly increasing resistance to this drug (DANMAP 2024). Together, these observations suggest a causal relationship between increased use of apramycin and increased resistance to gentamicin in haemolytic *E. coli*.

It should also be noted that 6.8% of haemolytic *E. coli* isolates displayed resistance to 3rd generation cephalosporins (cefpodoxime). This subclass of antimicrobials is not used in pig production in Denmark, and the level of cefpodoxime resistance in haemolytic *E. coli* isolates has been relatively stable since testing started in 2022.

As observed for neomycin and apramycin, the use of amoxicillin in combination with a beta-lactamase inhibitor (e.g., clavulanic acid) in weaners has increased in recent years (DANMAP 2024), which might have contributed to the increasing level of resistance to amoxicillin-clavulanic acid and the occurrence of cefpodoxime resistance in haemolytic *E. coli*.

Finally, non-haemolytic *E. coli* displayed significantly increased resistance to amoxicillin-clavulanic acid (2025 vs. 2024) and trimethoprim-sulfamethoxazole (2025 vs. 2024).

9.4 Conclusions and perspectives

Pathogenic bacteria from acute mastitis in dairy cows generally displayed similar levels of phenotypic resistance as in 2024.

In haemolytic *E. coli* from pigs, the continued high level of resistance to first-choice drugs for treating *E. coli*-associated post-weaning diarrhoea and to drugs that are critically important for human medicine is worrisome and should be monitored closely in the coming years.

Interpretation of resistance to antimicrobial agents of veterinary importance are often based on tentative ECOFFs and ECOFFs as animal-specific clinical breakpoints for many drugs are currently lacking (e.g., penicillin resistance in *S. uberis* and neomycin resistance in *E. coli*). ECOFFs are based on microbiological studies and do not necessarily indicate whether a drug will be clinically active. Future studies should therefore seek to establish clinical breakpoints in animals by considering what happens to the drug within a specific animal and body site (pharmacokinetics).

It should be noted that the pathogenic bacteria isolated from pigs originate from outbreaks. As they are not randomly selected, the levels of resistance reported above do not necessarily reflect the national levels.

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