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NORM
NORM-VET

Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway

Norsk overvåkingssystem for antibiotikaresistens hos mikrober (NORM)

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CONTENTS

INTRODUCTION

Antimicrobial resistance is an emerging problem worldwide. It reduces the effectiveness of antimicrobial treatment of infectious diseases in humans and animals thereby leading to increased morbidity and mortality, as well as higher costs. It is well established that there is a strong association between the usage of antimicrobial agents and the occurrence of resistance. The selective pressure exerted following use of antimicrobial agents is a key issue in the epidemiology of resistance. In this report the term antimicrobial resistance is used synonymously with antibiotic resistance, although the term actually includes resistance in other microbes as well. Antimicrobial resistance can be disseminated through the spread of resistant pathogenic organisms themselves or by horizontal transfer of resistance genes from one type of organism to another. Such transfer is not limited to closely related organisms; it can also take place between organisms of different evolutionary origins and/or ecological niches. Thus, antimicrobial drug usage and resistance in one ecological compartment can have consequences for the occurrence of resistance in another compartment. When addressing antimicrobial resistance – the occurrences, causes, consequences and preventive measures – a holistic approach is needed, encompassing both data on usage and resistance in human and veterinary medicine, as well as organisms in the food production chain.

In response to the growing concern about antimicrobial resistance, the Norwegian Ministry of Health and Social Affairs issued the first national action plan against antimicrobial resistance in March 2000. The importance of monitoring the human and animal health sectors as well as food production, was emphasised. The action plan recognised the need for ongoing surveillance as a fundamental component of the strategy. The NORM and NORM-VET programmes were consequently established in order to provide and present data on the occurrence and distribution of antimicrobial resistance over time. The first national action plan formally expired by the end of 2004. However, the need for continued surveillance of both resistance and antimicrobial usage was emphasised at subsequent consultations and an integrated national strategy for prevention of infections in the health service and antibiotic resistance (2008-2012) was issued in the summer of 2008. A new national strategy (2015-2020) was launched by the Norwegian government in 2015 including an explicit target of 30% reduction in antibiotic consumption in human medicine by 2020 compared to 2012. For food-producing terrestrial animals and companion animals the targets were 10% and 30% reduction in the usage, respectively, by 2020, with 2013 as reference year. Additional specific targets in the food production chain were that livestock associated MRSA should not be established in the Norwegian pig population, and that ESC-resistant bacteria in the poultry production should be reduced to a minimum. Also, the action plan stated that the government would carry out mapping of reservoirs of antimicrobial resistant bacteria in humans, in food and in relevant animal populations and in sentinel environments. Due to the coronavirus pandemic, renewal of the national strategy was delayed until 2024 when a National One Health Strategy Against Antimicrobial Resistance (2024-2033) was launched. Sector specific action plans are presently under development.

The NORM surveillance programme for antimicrobial resistance in human pathogens is coordinated by the Department of Microbiology and Infection Control at the University Hospital of North Norway in Tromsø, while the NORM-VET monitoring programme for antimicrobial resistance in animals, food and feed is coordinated by the Norwegian Veterinary Institute commissioned by the Norwegian Food Safety Authority. Both programmes were established in 2000. The NORM/NORM-VET reports also present data on the usage of antimicrobial agents in humans and animals in Norway. The NORM and NORM-VET programmes are valuable tools for setting policies, assessing risks and evaluating interventions. This report, which is the twenty-sixth annual joint report from NORM and NORM-VET, presents data on resistance and usage for 2025. The editors would like to thank all those who contributed to data collection and the writing of this report, for excellent work.

Tromsø / Ås / Oslo, September 2026

SAMMENDRAG

Norsk overvåkingssystem for antibiotikaresistens hos mikrober (NORM) og Norsk overvåkingsprogram for antibiotikaresistens i mikrober fra fôr, dyr og næringsmidler (NORM-VET) utgir en felles årlig rapport. Årets rapport presenterer data om forekomst av antibiotikaresistens og forbruk av antibiotika til mennesker og dyr i 2025. Data fra relevante prosjekter som ikke er med i de kontinuerlige overvåkingsprogrammene, presenteres også. NORM og NORM-VET ble etablert som deler av Regjeringens tiltaksplan mot antibiotikaresistens offentliggjort i 2000. NORM koordineres av Avdeling for mikrobiologi og smittevern, Universitetssykehuset Nord-Norge i Tromsø. NORM-VET koordineres av Veterinærinstituttet.

Forbruk av antibiotika til dyr

I 2025 utgjorde salget av antibakterielle veterinærpreparater til landdyr totalt 4 272 kg aktiv substans, som er 68 kg lavere enn i 2024 (-2 %) og det laveste salget som er rapportert siden datainnsamlingen startet i 1993.

Salget av antibakterielle veterinærpreparater til matproduserende landdyr, inkludert hest, var på 3 905 kg. Data rapportert til Veterinært legemiddelregister (VetReg) viser at til storfe, gris og fjørfe ble det i all hovedsak brukt penicilliner, og av disse var det nesten utelukkende betalaktamaseømfindtlige penicilliner som ble benyttet. Estimert salg av antibakterielle veterinærpreparater som i hovedsak benyttes til de viktigste matproduserende artene (storfe, gris, sau, geit og fjørfe), var uendret (under én prosent endring) siden 2024, målt i mg aktivt stoff relatert til dyrepopulasjonen (mg/kg dyrebiomasse). Til hest ble det i hovedsak brukt trimetoprim-sulfa som oralpasta.

Salget av antibakterielle veterinærpreparater til flokkbehandling er fortsatt lavt; i 2025 representerte salg av slike preparater 3 % av totalsalget til matproduserende landdyr, inkludert hest.

Forbruket av veterinære antibakterielle midler til oppdrettsfisk (forbruk til rensefisk inkludert) var fortsatt lavt i 2025 og utgjorde 498 kg. Dette representerer en nedgang på 99 % sammenlignet med 1987 da forbruket var på sitt høyeste. I 2025 ble det foretatt behandling med antibiotika i 1 % av sjølokalitetene for laks og regnbueørret.

Til kjæledyr (hund og katt) ble det i 2025 solgt 367 kg veterinære antibakterielle midler. Det var en liten (3 %) økning sammenliknet med året før. Data rapportert (i kg) til VetReg for hund og katt for perioden 2015-2025 viser en reduksjon på totalt 37 % i forskrivningen av antibakterielle humanpreparater til hund og katt, noe som indikerer at redusert salg av veterinære antibakterielle midler i perioden ikke har blitt erstattet av forskrivning av antibakterielle humanpreparater.

Det europeiske legemiddelbyrået (EMA) har anbefalt å begrense bruken av enkelte antibakterielle midler til dyr, dvs. 3.-4. generasjon cefalosporiner, kinoloner (fluorokinoloner og andre kinoloner) og polymyksiner, på grunn av den potensielle risikoen for folkehelsa. Av disse antibakterielle midlene selges det kun kinoloner til matproduserende landdyr og oppdrettsfisk. Salget av kinoloner utgjorde en svært liten andel (0,3 %) av totalsalget av veterinære antibakterielle midler til dyr, inkludert fisk, i 2025.

Forbruk av antibiotika hos mennesker

Siden nittensyttitallet har vi hatt målemetoder for bruken av legemidler i Norge. Disse dataene har gjort det mulig å sette mål for riktig antibiotikabruk og å evaluere nasjonale tiltak. Totalt salg av antibakterielle midler til systemisk bruk (her benevnt som antibiotika, dvs. J01 unntatt metenamin) hos mennesker var 12,1 DDD/1000 innbyggere/døgn i 2025. Dette er en nedgang på 8 % sammenlignet med 2024. Siden 2012 har det vært en markant reduksjon i bruken av antibiotika. Under Covid-19-pandemien ble det observert en betydelig nedgang i antibiotikabruken, men forbruket har nå returnert til noenlunde samme nivå som før pandemien. Norge har et relativt lavt forbruk av antibiotika sammenlignet med andre land. Vi har også et fordelaktig forbruksmønster med en stor andel smalspektrede antibiotika, både i primærhelsetjenesten og i sykehussektoren. Rundt 83 % av den totale mengden DDD av antibakterielle midler brukes i primærhelsetjenesten, dvs. utenfor helseinstitusjoner. Sykehjem og tannpleie representerer henholdsvis 4,2 % og 4,8 %.

Penicilliner (J01C) er oftest forskrevet i primærhelsetjenesten. De to hyppigst foreskrevne antibiotikaene i primærhelsetjenesten i 2025 var metenamin og fenoksymetylpenicillin. I Norge er luftveisinfeksjoner den vanligste indikasjonen for smalspektret penicillin, og i 2025 utgjorde fenoksymetylpenicillin 19 % av all DDD, mens metenamin, et profylaktisk middel mot urinveisinfeksjoner, utgjorde 29 %.

Det har vært en økning i bruken i primærhelsetjenesten etter pandemien; bruken er litt lavere enn i 2019, samtidig, sett over det siste ti-året, har antibiotikabruk i primærhelsetjenesten hatt en generell jevn nedgang. Etter innføringen av regjeringens handlingsplan mot antimikrobiell resistens i 2016 har det vært økt oppmerksomhet om antimikrobiell resistens, både blant helsepersonell og befolkningen generelt. I primærhelsetjenesten har det vært fokus på oppdaterte retningslinjer for antibiotikaforskrivning. En stor andel av allmennlegene har gjennomført kvalitetsforbedringskurs om riktig antibiotikaforskrivning. Siden 2024 har det vært mulig for allmennleger å få automatiserte forskrivningsrapporter om egen praksis, noe som kan bidra til økt fokus på riktig antibiotikaforskrivning. Selv om mye er oppnådd, er det sannsynligvis fortsatt områder for forbedring i primærhelsetjenesten, f.eks. å unngå antibiotikaforskrivning for virusinfeksjoner, individualisering og riktig valg av type antibiotika, dose og behandlingsvarighet.

Antibiotikasalg (i DDD) til sykehus utgjorde 7,3 % av det totale salget av antibakterielle midler til mennesker i 2025. Salget er redusert med 5 % i DDD/1000 innbyggere/dag sammenlignet med 2019. I norske sykehus ble det gjennomsnittlig brukt 81 DDD/100 liggedøgn i 2025. Dette er en økning siden 2019, og en økning på 21 % siden 2012. I samme periode økte DDD/innleggelse med 4 %. Terapimønsteret for antibakterielle midler på sykehus endrer seg ikke mye fra ett år til et annet, men det er en klar trend mot mer bruk av antibiotika som er anbefalt i retningslinjene. Den proporsjonale bruken av bredspektrede antibiotika har sunket siden 2012. Denne gunstige utviklingen kan forklares med opprettelse av antibiotikastyringsprogram i

sykehus, kontinuerlig god oppfølging av antibiotika-teamene og oppdaterte retningslinjer. På sykehus var penicilliner (J01C) mest brukt (nesten halvparten av bruken målt i DDD), etterfulgt av cefalosporiner; 18 % av all DDD. Det er store variasjoner mellom sykehus, både målt i volum (i DDD/100 liggedøgn) av antibiotika som brukes og i terapiprofil. Variasjonene kan ikke forklares med forskjeller i aktivitet eller pasientgrunnlag alene.

I år har vi introdusert en ny metode for å estimere antibiotikabruk på sykehjem. Estimatet viser en synkende trend i bruk på nasjonalt nivå, og at de mest brukte antibakterielle midlene er smalspektrede antibakterielle midler.

Antibiotikaresistens i dyr og i mat

Resultatene fra 2025 bekrefter at situasjonen angående antibiotikaresistens hos bakterier fra dyr og mat i Norge er god. Forekomsten av multiresistens (MDR) og spesielle resistente bakterier/resistensmekanismer av særlig interesse, slik som ekstendert-spektrum cefalosporin (ESC) resistente *Escherichia coli*, er fremdeles lav.

NORM-VET følger kravene i EU-regelverket 2020/1729/EU for overvåking av AMR i indikatorbakterier og zoonotiske bakterier. I tillegg undersøkes det prøver av dyr og matvarer ut ifra nasjonale hensyn. *E. coli* og *Enterococcus* spp. benyttes som indikatorbakterier. *Staphylococcus* spp. er inkludert som en ekstra indikator på forekomsten av AMR hos hest og kjæledyr. Selektive metoder benyttes til overvåking av meldepliktige bakterier slik som ESC-resistente *E. coli*, karbapenem-resistente *Enterobacterales* (CRE), meticillinresistente *S. aureus* (MRSA) og meticillinresistente *S. pseudintermedius* (MRSP). Zoonotiske bakterier, det vil si *Salmonella spp.* og *Campylobacter* spp., er også inkludert og beskrevet under avsnittet om zoonotiske bakterier. MRSA i svinepopulasjonen er overvåket via et eget omfattende program, som har som mål å identifisere MRSA-positive besetninger. Resultatene fra dette programmet oppsummeres også i denne rapporten.

I 2025 ble følgende prøver fra friske dyr inkludert; blindtarmsprøver (cecum) fra storfe og slaktegris for sensitivitetsundersøkelse av indikatorbakteriene *E. coli* og *Enterococcus* spp., samt påvisning av ESC-resistente *E. coli* og CRE. Avføringsprøver (svaber) fra katt ble også inkludert for sensitivitetsundersøkelse av *E. coli*, og påvisning av *E. coli* resistente mot ESC og CRE. Svaberprøver fra munn/nese/perineum hos katt ble inkludert for isolering av *Staphylococcus felis*, MRSA og MRSP. Kliniske isolater omfattet *Actinobacillus pleuro-pneumoniae* og *E. coli* fra gris, og *S. felis* og *E. coli* fra katt. Næringsmidler som ble undersøkt, var prøver av storfekjøtt og svinekjøtt for påvisning av ESC-resistente *E. coli* og CRE, samt bær (dvs. blåbær, jordbær og bringebær) for sensitivitetsundersøkelse av *E. coli*, samt påvisning av ESC-resistente *E. coli*, CRE og MRSA.

Majoriteten av *E. coli* fra storfe (96,9 % av 292), gris (87,6 % av 299) og katt (83 % av 253) var fullt følsomme for alle antibakterielle substanser i testpanelet, og forekomsten av MDR var henholdsvis 0,3 %, 1,3 % og 2,0 %. Forekomsten av ESC-resistente *E. coli* i prøver fra storfe og gris var henholdsvis 3,6 % og 19,7 %. Denne resistensen var hovedsakelig knyttet til isolater med mutasjoner i kromosomalt lokaliserte gener, og kun i et fåtall tilfeller til overførbare resistensgener. Fra katteprøvene ble ESC-resistente *E. coli* påvist i kun én prøve, og var forårsaket av et overførbart resistensgen (0,4 %). Forekomsten av AMR, inkludert isolater klassifisert som MDR, hos indikatorbakteriene *Enterococcus* spp. fra gris er høyere enn hos *E. coli*; full følsomhet ble påvist hos henholdsvis 45,8 % av 24 *E. faecalis* og 31,7 % av 82 *E. faecium*. Blant de 162 *S. felis* isolatene fra katt var 74,5 % fullt følsomme.

Forekomsten av AMR er vanligvis høyere i kliniske isolater enn i indikatorbakterier som *E. coli* og *S. felis*. Henholdsvis 63,4 % av kliniske *E. coli* fra gris (n=71) og 72,4 % av kliniske *E. coli* fra katt (n=29) var fullt følsomme for alle de antibakterielle substansene i testpanelet. MDR ble påvist hos henholdsvis 5,6 % av isolatene fra gris og 13,8 % av isolatene fra katt. For kliniske *S. felis* ble det indikert en høyere forekomst av resistens mot benzylpenicillin enn hos indikatorbakteriene. *A. pleuropneumoniae* isolatene (n=70) var fullt følsomme for alle antimikrobielle substanser i testpanelet.

Forekomsten av ESC-resistente *E. coli* i mat var svært lav. Bakterien ble kun påvist i 0,9 % av 317 prøver av svine-kjøtt og ikke i noen av de 320 prøvene av storfekjøtt eller i de 945 bærprøvene (324 blåbær, 304 jordbær og 317 bringebær).

Samlet sett har forekomsten av AMR hos storfe og gris vært relativt stabil de siste ti årene, men med en økning i MDR hos *E. faecium* fra gris fra 2019 til 2021. AMR-resultatene fra katt er i samsvar med tidligere resultater fra 2022. Det ble ikke påvist CRE, MRSA eller MRSP i prøvene analysert i 2025, verken fra dyr eller mat. Forekomsten av MDR og ESC-resistens som skyldes overførbare resistensgener, er svært lav.

Resistens hos zoonotiske bakterier og andre enteropatogene bakterier

Zoonotiske bakterier fra dyr og mat

Salmonella spp. fra både dyre- og matprøver, samt *Campylobacter jejuni* og *Campylobacter coli* fra henholdsvis storfe og gris, var de zoonotiske bakteriene som ble inkludert i 2025. Totalt ble 23 *Salmonella* spp. isolater fra ulike dyre- og matkilder testet, hvorav alle unntatt tre isolater var fullt følsomme for alle antibakterielle substanser i testpanelet og ingen var MDR. Majoriteten, dvs. 81,3 % av 102 *C. jejuni* og 87,5 % av 239 *C. coli* isolater, var fullt følsomme for alle de antibakterielle substansene i testpanelet. MDR ble kun påvist i 2,9 % av *C. jejuni* isolatene.

Kliniske isolater av tarmpatogene bakterier fra mennesker

Referanselaboratoriet for enteropatogene bakterier (NRL) utfører årlig testing av antimikrobiell følsomhet for isolater av *Salmonella*, *Campylobacter*, *Yersinia* og *Shigella*. Siden 2020 har NRL også screenet alle *Enterobacterales* isolater for antimikrobielle resistensgener etter helgenom-sekvensering for å påvise genotypisk resistens. I 2020 og 2021 ble det innført reiserestriksjoner som en del av smitteverntiltakene under covid-19-pandemien, noe som førte til en betydelig nedgang i antallet reiseassosierte infeksjoner. Trender i antibiotikaresistens må derfor tolkes i lys av dette.

For *Salmonella* Typhimurium og den monofasiske varianten av *S.* Typhimurium var det totale resistensnivået høyere blant stammer fra reiseassosierte infeksjoner enn blant stammer fra innenlands smitte. Multiresistens (MDR) var et karakteristisk trekk ved en betydelig andel av de monofasiske *S.* Typhimurium isolatene (82,5 %). Totalt ble 18 isolater identifisert som ESBL-produserende, med følgende genotyper: $bla_{\text{CTX-M}}$ (n=15), $bla_{\text{SHV-12}}$ (n=1), $bla_{\text{CMY-1}}$ (n=1) og $bla_{\text{DHA-1}}$ (n=1).

Hos *Campylobacter jejuni* var det generelle resistensnivået mot ciprofloksacin og tetracyklin høyere blant stammer fra reiseassosierte infeksjoner enn blant stammer fra innenlands smitte. Antibiotikaresistensen i *Yersinia enterocolitica* forblir lav. Det ble observert en økende trend i resistens mot ciprofloksacin hos *Shigella flexneri*. Totalt ble 24 ESBL-produserende *S. sonnei* stammer og 5 *S. flexneri*-stammer identifisert med følgende resistensgener: $bla_{\text{CTX-M}}$ (n=27) og $bla_{\text{DHA-1}}$ (n=2). En høy andel av *Shigella* stammene (82,7 %) ble karakterisert som MDR.

Resistens hos kliniske isolater fra mennesker

Forekomsten av antibiotikaresistens hos bakterier i kliniske prøver fra mennesker var fortsatt lav i 2025. *Staphylococcus aureus* fra blodkultur og sårprøver var stort sett følsomme for alle relevante antibiotika. Det ble påvist 20 tilfeller av meticillinresistente *S. aureus* (MRSA) blant 1 678 blodkulturisolater (1,2 %). Resultatet samsvarer med tall fra laboratorienes datasystemer som rapporterte 33 MRSA isolater blant 2 382 *S. aureus* (1,4 %) fra blodkultur og spinalvæske i 2025. Dette er på samme nivå som i 2024 (1,1 %). Meldesystemet for infeksjonssykdommer (MSIS) registrerte 1 285 tilfeller av MRSA infeksjon i 2025. De fleste tilfellene var pasienter med overfladiske sår-infeksjoner og abscesser. MRSA utgjør fortsatt en svært liten andel av *S. aureus* isolater fra sårprøver (16 av 804; 2,0 %) slik de også har gjort i tidligere år (1,3 % i 2023; 1,9 % i 2024). MSIS registrerte videre 1 851 tilfeller av MRSA kolonisering i 2025. I alt ble det meldt funn av MRSA hos 3 153 personer i 2025 mot 2 942 i 2024 (+7 %). Dette utgjør en insidensrate på 57 per 100 000 personår sammenliknet med 46 i 2023 og 53 i 2024. Insidensen av MRSA er nå høyere enn den var før covid-19 pandemien (2 568 personer registrert i 2017). Det månedlige antall MRSA infeksjoner har ikke endret seg signifikant gjennom de siste ti årene, og insidensen av invasive infeksjoner har holdt seg stabil på et lavt nivå. En betydelig andel av tilfellene (19 %) ble smittet i utlandet, men for mange (61 %) var smittested ukjent. Det påvises svært få tilfeller av landbruksassosiert MRSA i Norge.

Blodkulturisolater av *E. coli* viste stabil forekomst av resistens mot bredspektrede antibiotika i 2025 sammenliknet med 2024. Andelen av gentamicinresistente *E. coli* isolater var 5,3 % i 2025 sammenliknet med 5,4 % i 2023 og 5,7 % i 2024, mens forekomsten av resistens mot ciprofloxacin var uendret på 9,9 % (9,7 % i 2024). *Klebsiella* spp. hadde lavere forekomst av resistens mot gentamicin (2,7 %) og ciprofloxacin (7,6 %) enn *E. coli*. Produksjon av ESBL er et utbredt problem i mange land, og forekomsten har også vært økende i Norge. Til sammen 154 av 2 424 (6,4 %) *E. coli* og 70 av 1 258 (5,6 %) *Klebsiella* spp. fra blodkultur ble rapportert som ESBL-positive i 2025. Forekomsten er stabil både for *E. coli* (5,8 % i 2023; 6,7 % i 2024) og *Klebsiella* spp. (5,5 % i 2023; 6,3 % i 2024). Andelen av ESBL-positive isolater er fortsatt høyere blant *E. coli* fra blodkulturer (6,4 %) enn fra urinprøver (4,0 %). Karbapenemaseproduserende *Enterobacterales* (CPE), *Pseudomonas aeruginosa* og *Acinetobacter* spp. har vært meldepliktige til MSIS siden 2012. Antall pasienter med CPE økte fra 265 i 2024 til 284 i 2025, mens antallet med karbapenemaseproduserende *P. aeruginosa* (n=24) og *Acinetobacter* spp. (n=30) var ganske stabilt (henholdvis n=24 og n=39 i 2024). Multiresistente Gram-negative bakterier kan ofte knyttes til import fra land med høy forekomst av slike mikrober. Isolater fra ukrainske pasienter ved norske sykehus utgjør en stadig synkende andel av totalen.

Antall systemiske isolater av *Haemophilus influenzae* og *Neisseria meningitidis* er på vei tilbake til samme nivå som før covid-19 pandemien. Det var en høyere andel systemiske *H. influenzae* isolater med produksjon av beta-laktamase i 2025 (18,2 %) enn i 2024 (11,6 %), men dette kan skyldes tilfeldig variasjon. Forekomsten av kromosomal beta-laktamresistens er stigende med 25,8 % i 2025 sammenliknet med 10,7 % i 2023 og 17,2 % i 2024. Det var noe færre *Neisseria gonorrhoeae* isolater i 2025 (1 341) enn i 2024 (1 471), og dette samsvarer med en reduksjon i antall kliniske tilfeller meldt til MSIS fra 3 148 i 2024 til 2 860 i 2025. Det var utbredt resistens mot penicillin G (25,3 %), og bare 4,9 % var følsomme for standard dosering av penicillin G svarende til villtype-populasjonen. Hele 69,4 % var resistente mot ciprofloxacin. Syv isolater (0,5 %) var resistente mot ceftriaxon og/eller det perorale cefalosporinet cefixim. Alle isolater var fullt følsomme for spectinomycin.

Det ble ikke påvist enterokokkisolater fra blodkultur med klinisk signifikant vankomycinresistens (VRE) i 2025. Forekomsten av resistens mot ampicillin i *E. faecium* var som tidligere rundt 70-80 %, mens høygradig gentamicin-resistens stort sett var uendret hos både *E. faecalis* (6,2 % i 2024; 4,9 % i 2025) og *E. faecium* (43,4 % i 2024; 43,1 % i 2025). Nesten alle *E. faecium* isolater med høygradig gentamicinresistens var også resistente mot ampicillin. Det ble funnet to *E. faecium* isolater med genetisk verifisert linezolidresistens (LRE). Både VRE og LRE er meldepliktige til MSIS. Nasjonalt senter for påvisning av antibiotikaresistens (K-res) kunne bekrefte funn av VRE hos 101 personer i 2025, en markant reduksjon fra 239 i 2024. Insidensraten har dermed sunket fra 4,4 per 100 000 personår i 2024 til 1,8 per 100 000 personår i 2025. Antallet LRE var derimot stabilt med 61 meldte tilfeller i 2025 sammenliknet med 66 i 2023 og 64 i 2024. Fem isolater var resistente mot både vankomycin og linezolid. Forekomsten av VRE varierer med utbrudd i sykehus fra år til år. Det var godt samsvar mellom funnene hos enterokokker fra blodkulturer og urinprøver.

Overvåkingen av *Streptococcus pneumoniae* (pneumokokker) viste at 0,8 % av isolatene fra blodkultur og spinalvæske var resistente mot penicillin G (1,1 % i 2024). I tillegg var 7,0 % bare følsomme for økt eksponering av dette middelet (5,6 % i 2024), og syv isolater (0,9 %) hadde nedsatt følsomhet for ett eller flere 3.-generasjon cefalosporiner. Forekomsten av makrolidresistens blant pneumokokker fra blodkultur var 5,5 % i 2025 (6,0 % i 2024), men betydelig høyere i isolater fra luftveisprøver (11,6 %). Alle systemiske isolater av *S. pyogenes* (beta-hemolytiske streptokokker gruppe A) var følsomme for penicillin G, men mange var resistente mot erytromycin (6,1 %) og tetracyklin (25,8 %). Systemiske isolater av

Streptococcus agalactiae (beta-hemolytiske streptokokker gruppe B) var også følsomme for penicillin G, men hadde utbredt resistens mot erytromycin (26,1 %) og tetracyklin (76,4 %). Subgrupper av viridansstreptokokker hadde varierende følsomhet for penicilliner og cefalosporiner.

I alt 155 pasienter med tuberkulose ble meldt til MSIS i 2025. Seks av 131 undersøkte isolater (4,6 %) ble definert som multiresistente (MDR) mot både rifampicin og isoniazid sammenliknet med 9,6 % i 2024. Pasientene var født i Norge (n=1), Europa utenom Norge (n=4) og i Asia (n=1).

Det ble utført resistensbestemmelse av 241 *Candida* blodkulturisolater fra 212 ulike pasienter. De vanligste artene var *C. albicans* (n=144), *C. glabrata* (n=36), *C. parapsilosis* (n=22) og *C. dubliniensis* (n=15). Alle *C. albicans* var følsomme for de undersøkte midlene, og det ble kun påvist enkelte non-*albicans* isolater med ervervet resistens. Nøyaktig speciesbestemmelse er nødvendig for å forutsi iboende resistens og velge effektiv behandling. Resultatene samsvarer med tidligere studier fra Norge.

Konklusjon

I Norge er forekomsten av antibiotikaresistens fortsatt lav i bakterier fra mennesker og dyr. Dette skyldes lavt forbruk av antibiotika, et fordelaktig forbruksmønster, og effektive tiltak mot spredning av resistente bakterier. Resultatene som presenteres i rapporten, viser at strategiene mot antibiotikaresistens har vært vellykkede både i husdyrholdet og i helsetjenesten. Det er imidlertid nødvendig med kontinuerlig innsats for å bevare den gunstige situasjonen slik at antibiotika også i fremtiden vil være effektive for de som trenger det. NORM/NORM-VET-rapporten er viktig for å dokumentere utviklingen av antibiotikaforbruk og resistens hos mennesker og dyr, og for å evaluere effekten av tiltak.

SUMMARY

This joint report from the surveillance programme for antimicrobial resistance in human pathogens (NORM) and the monitoring programme for antimicrobial resistance in bacteria from feed, food and animals (NORM-VET) presents data on the occurrence of antimicrobial resistance and the usage of antimicrobial agents in humans and animals for the year 2025. The NORM and NORM-VET programmes were established as part of the Norwegian Government's Action Plan against Antimicrobial Resistance issued in 2000. NORM is coordinated by the Department of Microbiology and Infection Control, University Hospital of North Norway, Tromsø. NORM-VET is coordinated by the Norwegian Veterinary Institute.

Usage of antimicrobial agents in animals

The total sales of antibacterial veterinary medicinal products (VMPs) for terrestrial animals in Norway were 4,272 kg antibacterial ingredients in 2025, which is 68 kg lower than in 2024 (-2%) and the lowest annual level reported (data available since 1993).

Sales of antibacterial VMPs for use in terrestrial food-producing animals, including horses, were 3,905 kg in 2025. Penicillins continued to be the most-selling antibacterial class for cattle, pigs and poultry - and were almost exclusively accounted for by beta-lactamase sensitive penicillins. Estimated sales of antibacterial VMPs for the largest food-producing species (cattle, pigs, sheep, goats and poultry) were unchanged (less than one percent difference) from 2024 when measured in mg related to population size (mg/kg animal biomass). For horses, the sales were mainly accounted for by trimethoprim-sulfa (oral paste).

The sales (kg) of antibacterial VMPs applicable for group treatment of terrestrial food-producing animals in Norway continued to be very low; in 2025 such products accounted for only 3% of the total sales.

In 2025, the sales (kg) of antibacterial VMPs for farmed fish (cleaner fish included) were 498 kg. This is a reduction of 99% compared to 1987, when the sales were at its highest. For Atlantic salmon and rainbow trout, fish at 1% of the on-growing locations were subjected to antibacterial treatment in 2025.

The sales (kg) of antibacterial VMPs marketed for companion animals were 367 kg in 2025; compared to 2024 a minor increase (3%) is observed. The prescription (in kg) for dogs and cats of human antibacterial medicinal products reported to the Veterinary Prescription Register declined by 37% from 2015 to 2025. This indicates that the decline in the sales of antibacterial VMPs for these species in the period has not been substituted by prescribing of human products.

The European Medicines Agency (EMA) has recommended restricting the use of some antibacterial classes in animals due to the potential risk to public health – i.e. 3rd and 4th generation cephalosporins, quinolones (fluoroquinolones and other quinolones) and polymyxins. In Norway, only quinolones are sold for use in food-producing terrestrial animals and farmed fish. The proportion sold of quinolones of the total sales of antibacterial VMPs was very low (0.3%) in 2025.

Usage of antimicrobial agents in humans

Since the nineteen-seventies we have been able to measure antimicrobial use in Norway. These data have allowed us to set targets and evaluate interventions for appropriate use of antimicrobials. Total sales of antibacterial agents for systemic use (here referred to as antibiotics, i.e. J01 excluding methenamine) in humans were 12.1 DDD/1,000 inhabitants/day in 2025. This is a reduction of 8% compared to 2024. Since 2012, there has been a marked decrease in total antibiotic use. During the Covid-19 pandemic, a significant fall in antibiotic use was observed, but consumption has now returned to roughly the same level as before the pandemic. Norway has a relatively low consumption of antibiotics compared to other countries. We also have an advantageous consumption pattern with a large proportion of narrow-spectrum antibiotics, both in primary health care and in the hospital sector. Around 83% of the total amount of DDD of antibacterial agents is used in primary health care, i.e. outside health institutions. Nursing homes and dental care represent 4.2% and 4.8%, respectively.

Penicillins (J01C) are most commonly prescribed in primary health care. The two most frequently prescribed antibiotics in primary care in 2025 were methenamine and phenoxymethylpenicillin. In Norway, respiratory tract infections are the most common indications for narrow-spectrum penicillin and in 2025, phenoxymethylpenicillin accounted for 19% of all DDD while methenamine, a prophylactic agent for urinary tract infections, accounted for 29%.

There has been an increase in use in primary care after the pandemic; use is slightly lower than in 2019, but over the past decade there has been a general and steady decline in antibiotic use in primary care. Following the introduction of the government's action plan against AMR in 2016, antimicrobial resistance has received increased attention, both among healthcare professionals and the general population. In primary health care, there has been a focus on updated guidelines for antibiotic prescribing, and a large proportion of general practitioners have completed quality improvement courses on correct antibiotic prescribing. Since 2024, it has been possible for general practitioners to obtain automated prescribing reports on their own practices, which could contribute to increased focus on correct antibiotic prescribing. Although much has been achieved, there are probably still areas for improvement in primary health care, e.g. avoiding antibiotic prescription for viral infections, individualisation and correct choice of type of antibiotic, dose and duration of treatment.

Antibiotic sales (in DDD) to hospitals accounted for 7.6% of total sales of antibacterial agents to humans in 2025. Sales have decreased by 5% in DDD/1,000 inhabitants/day compared to 2019. In Norwegian hospitals, antibiotics accounted for 81 DDD/100 bed days in 2025. This is an increase since 2019, and an increase of 21% since 2012. During the same period, DDD/admission increased by 4%. The therapy pattern for antibacterial agents in hospitals does not change much from one year to another, but there is a clear trend towards more use of antibiotics recommended in the guidelines. The proportional use of broad-

spectrum antibiotics has decreased since 2012. This favorable development can be explained by updated Guidelines, the establishment of antibiotic stewardship programmes in hospitals and continuously good follow-up of the Antibiotic stewardship teams. In hospitals, penicillins (J01C) were the most used (almost half of use measured in DDD) followed by the cephalosporins; 18% of all DDD. There are large variations between hospitals, both measured in volume (in DDD/100 bed days) of antibiotics used and in therapy profile. The variations cannot be explained by differences in activity or patient mix alone.

This year we have introduced a new method for estimating antibiotic use in nursing homes. The estimate shows a decreasing trend in use and that the most commonly used antibacterials are narrow-spectrum antibacterials.

Antimicrobial resistance in animals and food

The 2025 data confirm that the situation regarding antimicrobial resistance (AMR) in bacteria from animals and food in Norway is good. The occurrence of multi-drug resistance (MDR), and specific emerging resistant bacteria/ mechanisms, such as resistance to extended-spectrum cephalosporins (ESC), is low.

NORM-VET follows the requirements of Commission Implementing Decision 2020/1729/EU for monitoring AMR in zoonotic and commensal bacteria, while also including additional sources and bacteria in accordance with national priorities. *Escherichia coli* and *Enterococcus* spp. are used as indicator bacteria. *Staphylococcus* spp. is included as an additional indicator for the occurrence of AMR in horses and pets. Selective screening is applied to detect notifiable AMR bacteria such as ESC-resistant *E. coli*, carbapenem resistant *Enterobacterales* (CRE), methicillin resistant *S. aureus* (MRSA) and methicillin resistant *S. pseudintermedius* (MRSP). Zoonotic bacteria, i.e. *Salmonella* spp. and *Campylobacter* spp., are also covered and described under the section on zoonotic bacteria. MRSA in Norwegian pigs is monitored through a separate specifically designed surveillance programme aimed at identifying positive herds. The results from this separate MRSA programme are summarised in the NORM/NORM-VET report as well.

In 2025, samples from healthy animals included caecal samples from cattle and fattening pigs for susceptibility testing of indicator *E. coli* and *Enterococcus* spp., and detection of emerging resistant bacteria/resistance mechanisms such as ESC-resistant *E. coli* and CRE. Faecal swab samples from cats were also included for susceptibility testing of *E. coli*, and for detection of ESC-resistant *E. coli* and CRE. Oral/nasal/perineum swabs were included for isolation of *Staphylococcus felis*, MRSA and MRSP from cats. Clinical isolates included *Actinobacillus pleuropneumoniae* and *E. coli* from pigs, and *S. felis* and *E. coli* from cats. Food samples consisted of beef and pork for detection of ESC-resistant *E. coli* and CRE, and berries (i.e. blueberries, strawberries and raspberries) for susceptibility testing of *E. coli*, as well as for detection of ESC-resistant *E. coli*, CRE and MRSA.

The majority of the indicator *E. coli* from healthy cattle (96.9% of 292), pigs (87.6% of 299) and cats (83.0% of 253) were fully susceptible to all the antimicrobial agents in the test panel, and occurrence of MDR was 0.3%, 1.3% and 2.0% respectively. The occurrence of ESC-resistant *E. coli* in cattle and pig samples were 3.6% and 19.7%, respectively, and was mainly due to isolates with mutations in chromosomally located genes, and in only a few isolates due to plasmid encoded resistance genes. From the cat samples, *E. coli* resistant to ESC were detected in only one sample and was due to a plasmid encoded resistance gene (0.4%). The occurrence of AMR in indicator *Enterococcus* spp. from pigs, including isolates categorised as MDR, was higher than in the indicator *E. coli* with 45.8% of 24 *E. faecalis* and 31.7% of 82 *E. faecium* being fully susceptible. Among the 162 *S. felis* from cats, 74.5% were fully suscepible.

The occurrence of AMR in clinical isolates is usually higher than in indicator bacteria, i.e. in *E. coli* and in *S. felis*. A total of 63.4% of 71 and 72.4% of 29 clinical *E. coli* isolates from pigs and cats, respectively, were fully susceptible to the antimicrobial agents in the test panel, with 5.6% of the pig and 13.8% of the cat isolates being MDR. For clinical *S. felis*, a higher occurrence of resistance was indicated for benzylpenicillin. The *A. pleuropneumoniae* isolates (n=70) were fully susceptible to all the antimicrobial agents in the test panel.

The occurrence of ESC-resistant *E. coli* in food was very low, i.e. detected only in 0.9% of 317 pork samples, and in none of the 320 beef and 945 berry samples (324 blueberry, 304 strawberry and 317 raspberry). The resistance in the pig isolates was all due to mutations in a chromosomally located gene.

Overall, the occurrence of AMR in bacteria from cattle and pigs have been relatively stable over the last ten years, though with an increase in MDR for *E. faecium* from pigs from 2019 to 2021. The AMR results from cats are in concordance with previous results from 2022. No CRE, MRSA or MRSP was detected from the samples tested in 2025, neither from animals or food. The occurrence of MDR and ESC-resistance due to plasmid encoded resistance genes is very low.

Resistance in zoonotic bacteria and non-zoonotic enteropathogenic bacteria

Animal and meat isolates

Salmonella spp. from both animal and food sources, as well as *Campylobacter jejuni* and *Campylobacter coli* from cattle and pigs, respectively, were the zoonotic bacteria included in 2025. A total of 23 *Salmonella* spp. isolates from various animal and food sources were tested. All, but three isolates were fully susceptible to the antimicrobial agents included in the susceptibility test panel, and no MDR was detected. The majority, i.e. 81.3% of 102 *C. jejuni* and 87.5% of 239 *C. coli* isolates, were fully susceptible to all antimicrobial agents included in the test panel. MDR was only detected in 2.9% of the *C. jejuni* isolates.

Human clinical enteropathogenic isolates

The National Reference Laboratory for Enteropathogenic Bacteria (NRL) performs annual antimicrobial susceptibility testing of isolates of *Salmonella*, *Campylobacter*, *Yersinia*, and *Shigella*. Since 2020, the NRL has also screened all *Enterobacterales* isolates for antimicrobial resistance genes following whole-genome sequencing to detect genotypic resistance. In 2020 and 2021, travel restrictions were implemented as part of the infection control measures during the Covid-19 pandemic,

leading to a marked reduction in travel-associated infections. Trends in antibiotic resistance should therefore be interpreted in light of this.

For *Salmonella* Typhimurium and its monophasic variant, the overall level of resistance was higher among strains from travel-associated infections than among those acquired domestically. Multi-drug resistance (MDR) was a characteristic feature of a substantial proportion of the monophasic *S.* Typhimurium isolates (82.5%). In total, 18 isolates were identified as ESBL-producing, with the following genotypes: $bla_{\text{CTX-M}}$ (n=15), $bla_{\text{SHV-12}}$ (n=1), $bla_{\text{CMY-1}}$ (n=1), and $bla_{\text{DHA-1}}$ (n=1).

In *Campylobacter jejuni*, overall resistance to ciprofloxacin and tetracycline was higher among strains from travel-associated infections than among those acquired domestically. Antimicrobial resistance in *Yersinia enterocolitica* remains low. An increasing trend in resistance to ciprofloxacin was observed in *Shigella flexneri*. A total of 24 ESBL-producing *S. sonnei* strains and 5 *S. flexneri* strains were identified, carrying the following resistance genes: $bla_{\text{CTX-M}}$ (n=27) and $bla_{\text{DHA-1}}$ (n=2). A high proportion of *Shigella* strains (82.7%) were characterised as MDR.

Resistance in human clinical isolates

The prevalence of antimicrobial resistance in human clinical isolates was still low in Norway in 2025. *Staphylococcus aureus* from blood cultures and wound specimens were generally susceptible to all relevant antibiotics. Only 20 methicillin resistant *Staphylococcus aureus* (MRSA) blood culture isolates were detected among 1,687 strains included in NORM in 2025 (1.2%). This corresponds well with 33/2,382 (1.4%) blood culture and cerebrospinal fluid *S. aureus* isolates reported as MRSA from the laboratory information systems and is at the same level as in 2024 (1.1%). The Norwegian Surveillance System for Communicable Diseases (MSIS) registered 1,285 cases of MRSA infection in 2025. The majority of MRSA cases were reported as superficial wound infections and/or abscesses. The proportion of MRSA among non-invasive *S. aureus* isolates is still very low at 2.0% (16/804) and comparable to previous years (1.3% in 2023; 1.9% in 2024). Furthermore, MSIS registered 1,851 MRSA colonisations in 2025. A total of 3,153 persons were reported with MRSA in 2025 compared to 2,942 in 2024 (+7%). This corresponds to an incidence rate of 57 per 100,000 person-years compared to 46 in 2023 and 53 in 2024. The incidence of MRSA is now higher than before the Covid-19 pandemic (2,568 persons registered in 2017). The monthly number of MRSA infections has not changed significantly over the last ten years, and the incidence of invasive disease has remained stable at a low level. A large proportion of MRSA cases are still infected abroad (19%), but for many (61%) the location of acquisition was unknown. Very few cases of livestock-associated MRSA are detected in Norway.

The rates of resistance to broad-spectrum antimicrobials in *E. coli* blood culture isolates remained stable in 2025 compared to 2024. The prevalence of gentamicin resistance was 5.3% in 2025 compared to 5.4% in 2023 and 5.7% in 2024, while the prevalence of ciprofloxacin resistance remained unchanged at 9.9% (9.7% in 2024). *Klebsiella* spp. isolates demonstrated lower rates of resistance to gentamicin (2.7%) and ciprofloxacin (7.6%) than *E. coli*. Extended-spectrum beta-lactamases (ESBL) have emerged as a significant clinical problem in many countries, including Norway. A total of 154/2,424 (6.4%) *E. coli* and 70/1,258 (5.6%) *Klebsiella* spp. blood culture isolates were reported with this phenotype in 2025. The prevalence is stable for both *E. coli* (5.8% in 2023; 6.7% in 2024) and *Klebsiella* spp. (5.5% in 2023; 6.3% in 2024). The proportion of ESBL positive isolates is still higher among *E. coli* from blood cultures (6.4%) than from urine (4.0%). Carbapenemase-producing *Enterobacterales* (CPE), *P. aeruginosa* and *Acinetobacter* spp. have been notifiable to MSIS since 2012. The number of CPE patients increased from 265 in 2024 to 284 in 2025, whereas the number of patients with carbapenemase-producing *P. aeruginosa* (n=24) and *Acinetobacter* spp. (n=30) remained relatively stable (n=24 and n=39 in 2024, respectively). Many multi-drug resistant Gram-negative isolates were imported from countries with high prevalences of these organisms. Isolates from hospital patients transferred from Ukraine represent a decreasing proportion of the total.

The numbers of *Haemophilus influenzae* and *Neisseria meningitidis* isolates from blood cultures and cerebrospinal fluids is gradually returning to the same level as before the Covid-19 pandemic. The proportion of systemic *H. influenzae* demonstrating beta-lactamase production was higher in 2025 (18.2%) than in 2024 (11.6%), but this may be due to random variation. The rate of chromosomally encoded beta-lactam resistance has increased from 10.7% in 2023 and 17.2% in 2024, to 25.8% in 2025. The number of *Neisseria gonorrhoeae* isolates was lower in 2025 (n=1,341) than in 2024 (n=1,471), and this is in accordance with a decrease in the number of clinical cases reported to MSIS from 3,150 in 2024 to 2,860 in 2025. Many isolates displayed resistance to penicillin G (25.3%), and only 4.9% were susceptible to standard penicillin G dosage corresponding to the wild type population. Ciprofloxacin resistance was detected in 69.4% of isolates. Seven isolates (0.5%) were resistant to ceftriaxone and/or the oral cephalosporin cefixime. All isolates were susceptible to spectinomycin.

No enterococcal blood culture isolates with clinically relevant vancomycin resistance (VRE) were detected in 2025. The prevalence of ampicillin resistance in *E. faecium* has stabilised around 70-80%. High-level gentamicin resistance (HLGR) was essentially unchanged in both *E. faecalis* (6.2% in 2024; 6.9% in 2025) and *E. faecium* (43.4% in 2024; 43.1% in 2025). Almost all HLGR *E. faecium* isolates were also resistant to ampicillin. Two linezolid resistant *E. faecium* isolates (LRE) were genetically confirmed in the NORM surveillance programme in 2025. Both VRE and LRE should be reported to the national notification system (MSIS). The Norwegian Centre for Detection of Antimicrobial Resistance (K-res) confirmed the presence of VRE in 101 persons in 2025, which is a marked reduction from 239 persons in 2024. The incidence rate has thus decreased from 4.4 per 100,000 person-years in 2024 to 1.8 per 100,000 person-years in 2025. The number of LRE remained stable with 61 reported cases in 2025 compared to 64 in 2024. Five isolates were resistant to both vancomycin and linezolid. The VRE prevalence varies over time due to hospital outbreaks. There was good concordance between enterococcal resistance in isolates from blood culturers and the urinary tract.

Surveillance in *Streptococcus pneumoniae* (pneumococci) revealed penicillin G resistance in 0.8% of isolates from blood cultures and cerebrospinal fluids (1.1% in 2024). In addition, 7.0% would require increased exposure to this agent (5.5% in 2024). Seven isolates (0.9%) isolates displayed reduced susceptibility to one or more 3rd generation cephalosporins. The prevalence of macrolide resistance was 5.5% in 2025 compared to 6.0% in 2024 but was significantly higher in pneumococci from respiratory tract samples (11.6%). All systemic isolates of *S. pyogenes* (beta-haemolytic group A streptococci) were susceptible to penicillin G, but resistance to erythromycin (6.1%) and tetracycline (25.7%) was widespread. Systemic *Streptococcus agalactiae* (beta-haemolytic group B streptococci) isolates were also susceptible to penicillin G but had high rates of resistance to erythromycin (26.1%) and tetracycline (76.4%). Subgroups of viridans streptococci had variable susceptibility to penicillins and cephalosporins.

A total of 155 patients with tuberculosis were reported to MSIS in 2025. Six of 131 included isolates (4.6%) were defined as multi-drug resistant (MDR) to both rifampicin and isoniazid compared to 9.6 % in 2024. The patients were born in Norway (n=1), Europe outside Norway (n=4) and in Asia (n=1).

Susceptibility testing was performed on 241 *Candida* spp. blood culture isolates from 212 unique patients. The most common species were *C. albicans* (n=144), *C. glabrata* (n=36), *C. parapsilosis* complex (n=22), and *C. dubliniensis* (n=15). All *C. albicans* were susceptible to the substances examined. Only single non-*albicans* isolates with acquired resistance were detected. Precise species identification is essential to predict inherent resistance and select appropriate antifungal therapy.

Conclusion

Antimicrobial resistance is still a limited problem among humans and food-producing animals in Norway. This reflects the low usage of antimicrobial agents in human and veterinary medicine, a favourable usage pattern, as well as effective infection control measures. The data presented in this report show that strategies for containment of antimicrobial resistance have been successful both in the food-producing animal sector and in the healthcare sector. Continuous efforts and awareness rising are needed to preserve the favourable situation and ensure that antimicrobials are effective when needed. The NORM/ NORM-VET report is vital in order to document the trends in antibiotic usage and occurrence of resistance in humans and animals, and to evaluate the effectiveness of interventions.

POPULATION STATISTICS

Hege Salvesen Blix and Kari Olli Helgesen

Population statistics for humans and animals are data used for the analysis of antimicrobial sales and use. The population data can further be used for comparison of Norwegian data with corresponding figures from other countries. The data are collected by Norwegian authorities as shown in the tables below.

TABLE 1. Human population in Norway as of 25.02.2026. Data provided by Statistics Norway; Table 10211: Population by age, year and sex.

Age group	All	Males	Females
0 to 4 years	276,000	141,575	134,425
5 to 14 years	617,530	317,610	299,920
15 to 24 years	680,299	351,082	329,217
25 to 44 years	1,530,278	781,887	748,391
45 to 64 years	1,440,233	732,603	707,630
65 years and older	1,083,060	512,160	570,900
All age groups	5,627,400	2,836,917	2,790,483

TABLE 2. Animal population in Norway in 2025. All population categories are measured in heads, except finfish that are measured in tonnes. All data from the Register of Production Subsidies are from the counting date March 1. Data originate from Register of Production Subsidies (1, 5), Delivery Registry for Carcasses (2, 3A), EU's Trade Control and Expert System (3B), Directorate of Fisheries (4) and National Horse Registry (6).

Animal species	Population category	2025	Reference
Cattle	Dairy cow	208,064	1
	Slaughtered bullocks and bulls*	172,211	2
	Slaughtered calves and young cattle	15,424	2
	Slaughtered cow	103,242	2
Chickens	Slaughtered broilers	71,958,521	3A
Turkeys	Slaughtered turkeys	728,893	3A
Sheep	Live sheep	885,908	1
	Sheep for fattening – In	18	3B
	Slaughtered sheep and goat	1,089,225	2
Finfish (in tonnes)	Atlantic salmon	1,754,557	4
	Rainbow trout	103,546	4
	Other farmed fish produced	23,732	4
Pigs	Breeding sows > 50 kg	62,208	5
	Pigs for Fattening – Out	1,328	3B
	Slaughtered Pig	1,529,758	2
Horses	Living horses	78,528	6

* Aggregated data including slaughtered heifers, due to only aggregated data collected in Delivery register for carcasses.

References

1. Statistics Norway. https://www.ssb.no/statbank/table/03710/
2. Statistics Norway. https://www.ssb.no/statbank/table/05538/
3A and 3B. Norwegian Veterinary Institute. In-house data.
4. The Directorate of Fisheries. https://statistikkbanken.fiskeridir.no/PxWeb/pxweb/no/Fiskeridirektoratet/
5. Statistics Norway. https://www.ssb.no/statbank/table/03804/
6. Norwegian Veterinary Institute. https://www.vetinst.no/rapporter-og-publikasjoner/rapporter/2025/dyrehelserapporten-2024/_/attachment/inline/c0e27358-e672-4e3d-88aa-301ead53b706:231523db8f82cfc562515b8e1002a5f024ee7e39/2025_21_Dyrehelserapporten%202024%20KOMPLETT.pdf

ABBREVIATIONS

AMEG	Antimicrobial Advice Ad Hoc Expert Group
AMR	Antimicrobial resistance
ASP	Antibiotic Centre for Primary Care
AST	Antimicrobial susceptibility testing
ATC	Anatomical Therapeutic Chemical
ATCvet	Anatomical Therapeutic Chemical Veterinary
ATU	Area of technical uncertainty
AWaRe	Access, watch, reserve
cgMLST	Core genome multilocus sequence typing
CLSI	Clinical & Laboratory Standards Institute
CPE	Carbapenemase-producing *Enterobacterales*
CPO	Carbapenemase-producing organisms
CRE	Carbapenem resistant *Enterobacterales*
DDD	Defined daily doses
ECDC	European Centre for Disease Prevention and Control
ECOFF	Epidemiological cut-off values
EEA	European Economic Area
EFSA	European Food Safety Authority
EMA	European Medicine Agency
ESAC-Net	European Surveillance of Antimicrobial Consumption Network
ESBL	Extended-spectrum beta-lactamase
ESC	Extended-spectrum cephalosporin
ESCMID	European Society for Clinical Microbiology and Infectious Diseases
ESUAvet	European Sales and Use of Antimicrobials for Veterinary Medicine
ESVAC	European Surveillance of Veterinary Antimicrobial Consumption
EU	European Union
EUCAST	European Committee on Antimicrobial Susceptibility Testing
FEST	The Norwegian Prescription and Dispensing Support Database
GLASS	Global Antimicrobial Resistance and Use Surveillance System
GP	General practitioner
GR	Genotypic resistance
HMP	Human medicinal product
K-res	Norwegian Centre for Detection of Antimicrobial Resistance
LOS	Length of stay
LRE	Linezolid resistant enterococci
LVRE	Linezolid and vancomycin resistant enterococci
MDR	Multi-drug resistant
MIC	Minimum inhibitory concentration
MRL	Maximum residue level
MRSA	Methicillin resistant *Staphylococcus aureus*
MRSP	Methicillin resistant *Staphylococcus pseudintermedius*
MSIS	Norwegian Surveillance System for Communicable Disease
NDHRS	Norwegian Dairy Herd Recording System
NFSA	Norwegian Food Safety Authority
NSAS	National Centre for Antibiotic Use in Hospitals
NIPH	Norwegian Institute of Public Health
NorPD	Norwegian Prescribed Drug Registry
NRL	National reference laboratory
NVI	Norwegian Veterinary Institute
NWT	Non-wild type
OPAT	Outpatient parenteral antimicrobial therapy
PFAS	Per- and polyfluoroalkyl substances
PPS	Point prevalence survey
QRDR	Quinolone resistance-determining region
Rx	Prescription
ST	Sequence type
UDP	Union Product Database
VetReg	Veterinary Prescription Register
VMP	Veterinary medicinal product
VRE	Vancomycin resistant enterococci
WGS	Whole-genome sequence
WT	Wild type
XDR	Extensively drug resistant

USAGE OF ANTIMICROBIAL AGENTS

USAGE IN ANIMALS

Kari Olli Helgesen, Trishang Udhwani and Leif Lukas Löfling

Sales data for 1993-2025 of antibacterial veterinary medicinal products (VMP) for terrestrial animal species obtained at wholesaler's level, have been stratified into sales of antibacterial VMPs approved for terrestrial food-producing animals including horses and VMPs approved solely for companion animals, respectively. Further, sales data for food-producing animals have been stratified to reflect sales for the major food-producing species; terrestrial food-producing animals excluding horses (see Appendix 1 for methodology). The data are based on sales to Norwegian pharmacies from medicine wholesalers of VMPs. This includes all pharmaceutical formulations approved for food-producing terrestrial animals including horses, and for companion animals as well as VMPs used on special license (products approved in another European Economic Area (EEA) country). In addition, data obtained from the Veterinary Prescription Register (VetReg) have been used for some data analyses, including for supplementary information (see Appendix 1).

Calculation of kg active substance per VMP presentation follows the European Surveillance of Veterinary Antimicrobial Consumption (ESVAC) protocol for data up till 2022 and thereafter the European Sales and Use of Antimicrobials for Veterinary Medicine (ESUAvet) protocol from 2023 and onwards (see Appendix 1 and NORM/NORM-VET 2024).

Sales of veterinary antibacterial agents

All animals

Overall, the sales in Norway of antibacterial VMPs for therapeutic use in food producing terrestrial animals, including horses, and companion animals in 2025 were 4,272 kg active substance. A decline of the sales (kg) of such VMPs of 53% in the period 1993-2025 is observed (Figure 1).

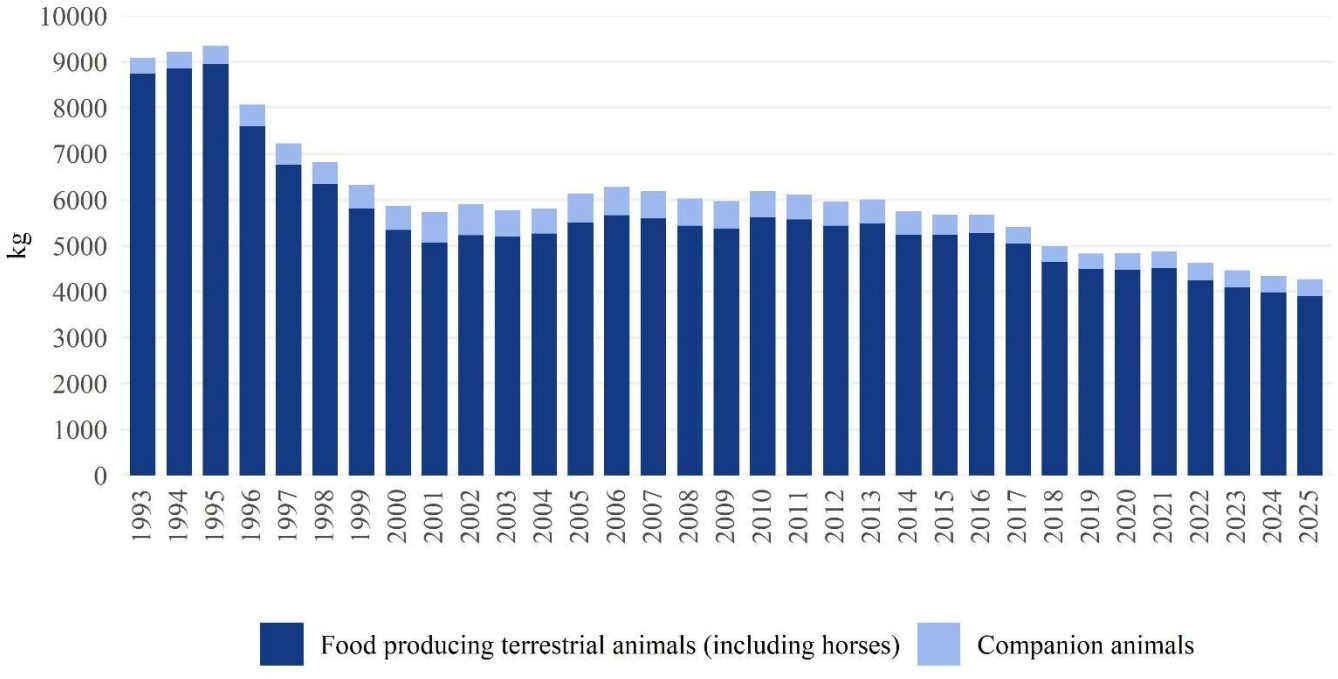

FIGURE 1. Total sales, in kg active substance, for food-producing terrestrial animals (including horses) and companion animals, of antibacterial veterinary medicinal products for therapeutic use in Norway in 1993–2025.

Food-producing terrestrial animals, including horses

In 2025 the sales, in kg active substance, of antibacterial VMPs sold for use in terrestrial food-producing animals, including horses, were 3,905 kg and compared to 1993 a decrease in the sales of such VMPs of 55% is observed (Figure 2). In total, 65% of the sales (kg) of antibacterial VMPs for this animal category in 2025 contained penicillins only, of which 95% was beta-lactamase sensitive penicillins. Of the total sales for use in terrestrial food producing animals in 2025, 26% was sales of oral paste containing trimethoprim + sulfa marketed for horses.

The proportion of sales of VMPs for terrestrial food-producing animals containing only penicillins increased from 18% to 65% during the period 1993-2025. This is mainly due to reduced sales of injectable and intramammary combination VMPs of penicillins and an aminoglycoside (dihydrostreptomycin) that has been gradually replaced by VMPs containing penicillins as the sole antibacterial agents.

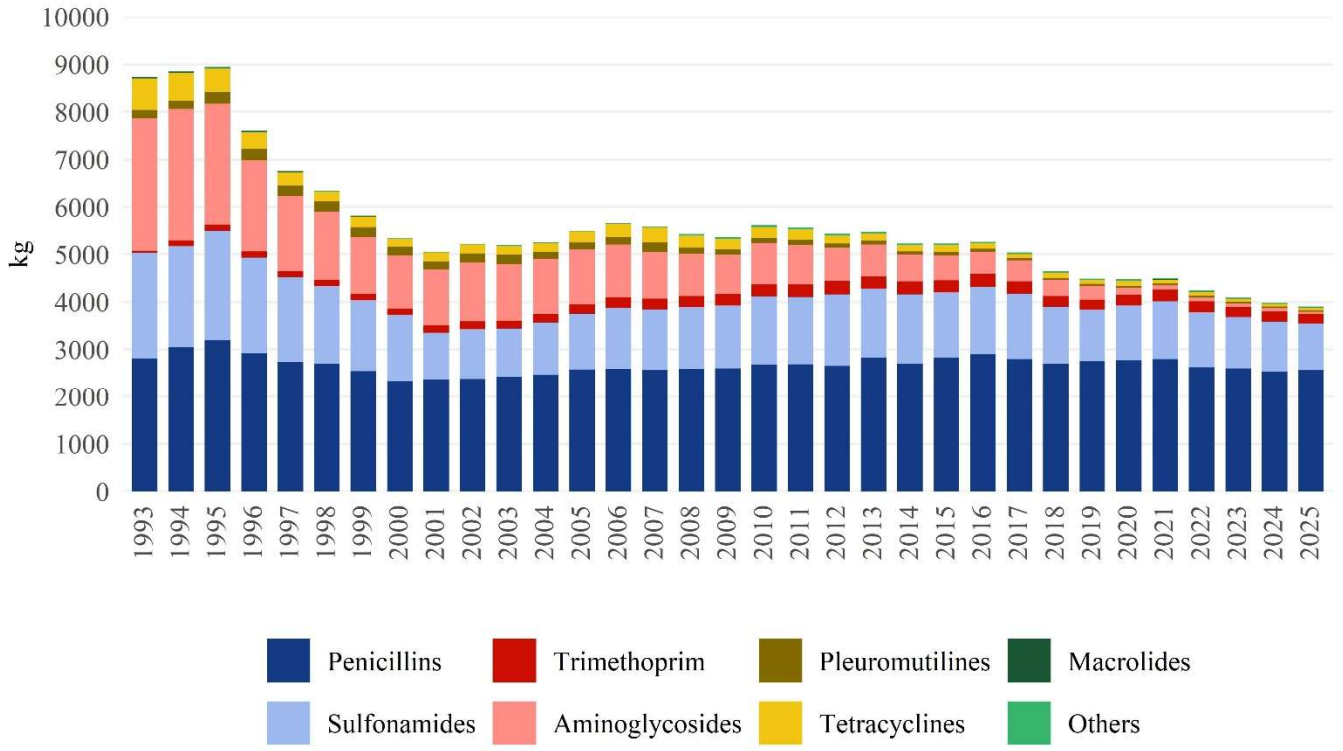

FIGURE 2. Sales, in kg active substance, of antibacterial veterinary medicinal products (VMPs) for therapeutic use in food-producing terrestrial animals (including horses) in Norway in 1993-2025. "Others" consists of minor sales of baquiloprim in 1994-2000 (range 0.2-1.8 kg), 3rd generation cephalosporines in 2012-2023 (range 0.001-0.07 kg), amphenicols in 2008-2025 (range 16-27 kg), and fluoroquinolones in 1993-2025 (range 6-19 kg).

Of the antibacterials for which restriction on use in animals is recommend at European Union (EU)/EEA level due to potential public health risks – i.e. 3rd and 4th generation cephalosporins, polymyxins and quinolones (fluoroquinolones and other quinolones) (1), only fluoro-quinolones are marketed in Norway for food-producing terrestrial animals. From 1993 to 2025, the proportion of sales of fluoroquinolones for food-producing terrestrial animals has been very low and stable varying between 0.1% and 0.3% of the total sales (Figure 2). During 1993-2025 no VMPs containing 3rd and higher generations of cephalosporins has been approved for food-producing animals in Norway via national procedures. Several 3rd generation cephalosporin VMPs have been approved via EU community procedures, but they are not marketed in Norway. Applications for special permits to use such VMPs marketed in other EEA countries for food-producing animals are normally not approved, and approval would only be given for specific animals if sensitivity testing precludes all other options. This is the case also for polymyxins (Knud Torjesen, Norwegian Medicinal Products Agency, personal communication). Glyco-peptides and carbapenems are not allowed to be used for food-producing animals in EU/EEA countries.

In Norway, sales of antibacterial VMPs for treatment of food-producing terrestrial animals are predominately pharmaceutical forms for treatment of individual animals (Figure 3) and primarily by injectables. This reflects that the livestock is characterised by small herds, but it can also partly be explained by type of infections and therapeutic traditions. In 2025, only 3% of the sales of antibacterial VMPs for food-producing terrestrial animals was for VMPs applicable for group treatment (oral treatment).

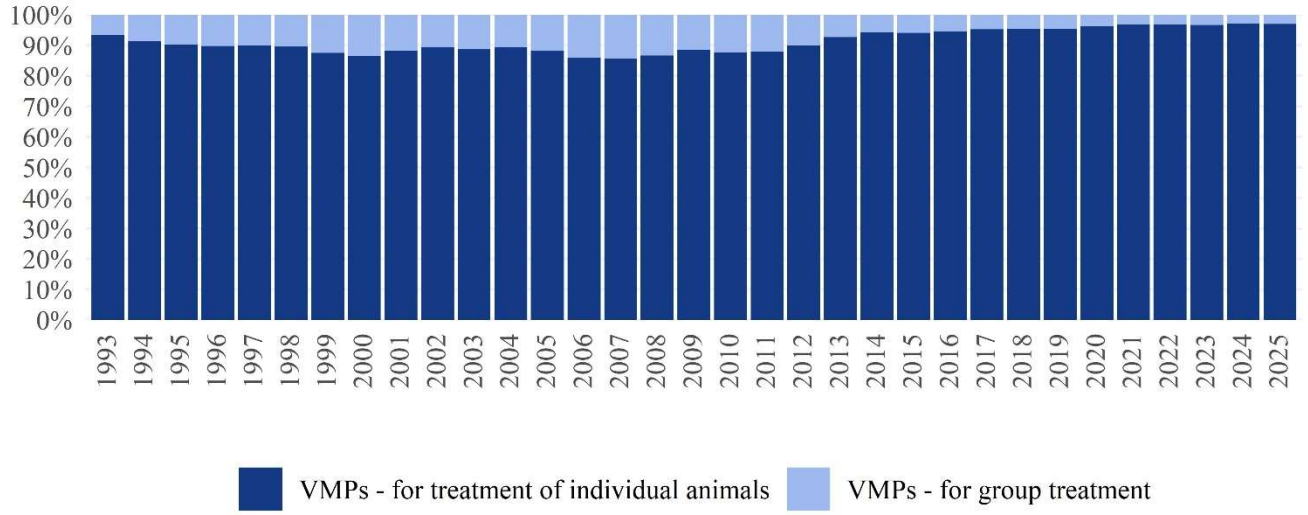

FIGURE 3. Proportion of sales in Norway, 1993-2025, (in kg active substance), of antibacterial veterinary medicinal products (VMPs) marketed for treatment of individual food-producing terrestrial animals, including horses (bolus, injectables, intramammary preparations, intrauterine preparations, oral paste and tablet VMP presentations – see Appendix 1) and applicable for group treatment through feed or drinking water (oral solution and oral powder). No premixes were sold for terrestrial food-producing animals.

Major food-producing terrestrial animal species

Antibacterial VMPs predominantly sold to food-producing terrestrial animals, excluding horses, are shown as mg per kg animal biomass in Figure 4. The methodology is described in Appendix 1. From 2013 to 2023 the sales for this group of species were reduced by 27%, based on mg/kg biomass values, while the sales were stable from 2023 to 2025 (1% change).

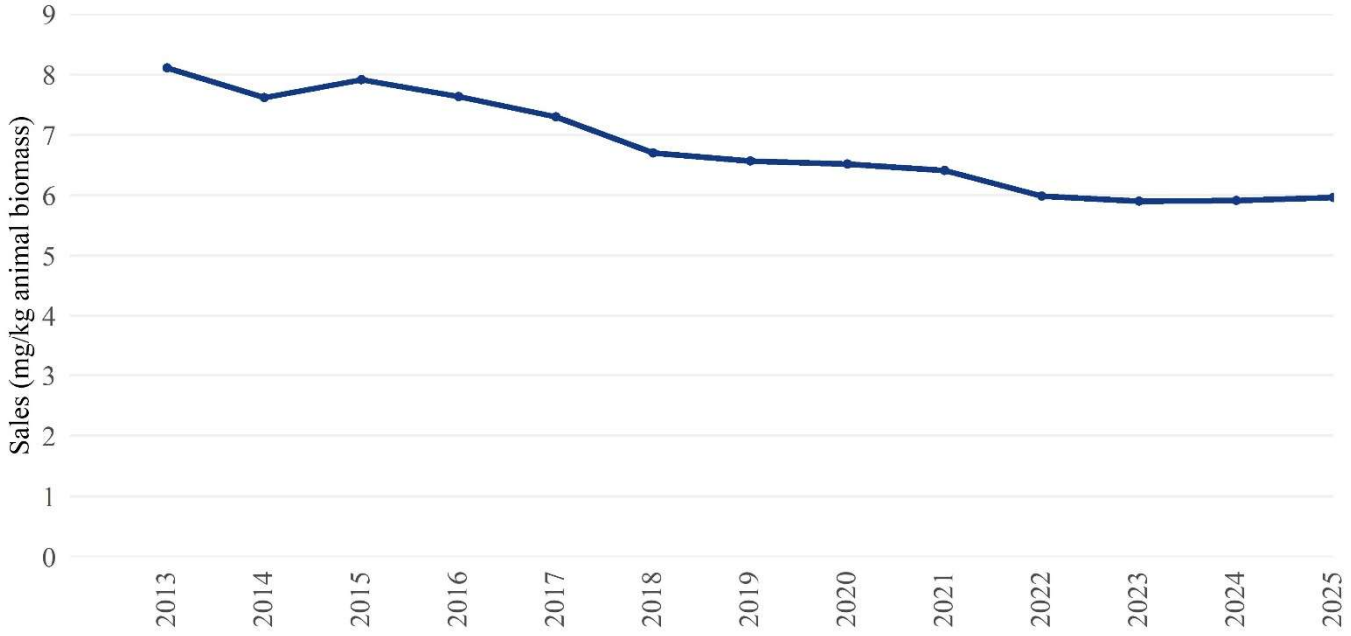

FIGURE 4. Annual sales in Norway, 2013-2025, in mg/kg animal biomass, of antibacterial veterinary medicinal products (VMPs) marketed for treatment of food-producing terrestrial animals, stratified to exclude sales for horses (all VMP presentations included, except oral pastes – see Appendix 1). The denominator is annual animal biomass using the European Surveillance of Veterinary Antimicrobial Consumption methodology for animal biomass calculation (see Appendix 1) for food-producing terrestrial animals, excluding the biomass for horses.

Farmed fish

In 2025, the total amounts of antibacterial VMPs dispensed for use in farmed fish in Norway was 498 kg (active substance) (Table 3); of this 0.93 kg were dispensed for use in cleaner fish. The data for farmed fish were extracted from VetReg 2nd February 2026.

Of the antibacterials for which restriction of use in animals is recommend in EU/EEA countries, advised due to potential public health risk (1), only other quinolones are used for farmed fish. From 2016 to 2025, the proportion of sales of quinolones has fluctuated; in 2025 this proportion was 0.5% (2.5 kg) (Table 3).

TABLE 3. Use, in kg of active substance, of antibacterial veterinary medicinal products (VMPs) for farmed fish in Norway in 2016-2025. Data represent dispensed prescriptions obtained from the Veterinary Prescription Register (see Appendix 1). Note that data include antibacterials for use in cleaner fish[1].

Active substance	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025
Tetracyclines										
Oxytetracycline	0	0	20	0	0.16	0	0	0	0.04	0
Amphenicols										
Florfenicol	134	264	857	152	113	531	397	516	703	496
Quinolones										
Oxolinic acid	66	343	54	66	107	57	28	32	6	2.5
Enrofloxacin	0.05	0.01	0	0.01	0.12	0.44	0.10	0.05	0.06	0.02
Total	**199**	**607**	**930**	**218**	**220**	**588**	**425**	**548**	**709**	**498**

[1]The total amounts (kg) given may be deviating due to rounding of each single value.

From 2016 to 2020 the major proportion of dispensed prescriptions of antibacterials was for fish in the pre-ongrowing phase. However, between 2021 (2022 for marine species) and 2024 this trend discontinued, while in 2025 the pre-ongrowing phase again dominated (Figure 5). The number of dispensed prescriptions of antibacterial VMPs for Atlantic salmon on-growers were, however, low during the period 2016-2025 (range 5-29 prescriptions), considering that Atlantic salmon production in this period varied between 1.3 and 1.9 million tonnes per year. This is a strong indication that the vaccines used in Atlantic salmon are efficient and that the coverage of vaccination of fingerlings is very high.

Of the antibiotics dispensed in 2025 for food-producing fish (136 prescriptions), 72% (98 prescriptions) were for marine species; 94 prescriptions for halibut and four prescriptions for cod. These 98 dispensed prescriptions accounted for 34% (170 of 498 kg) of all antibiotic use in farmed fish.

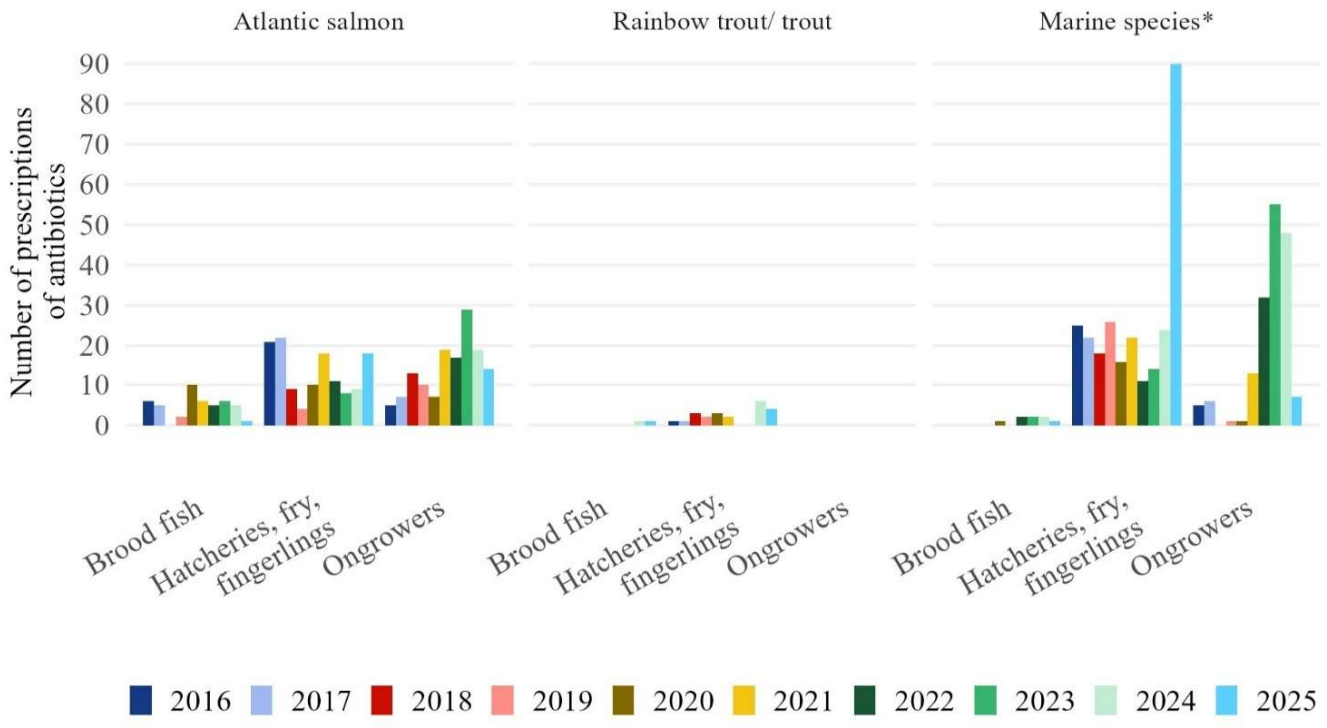

FIGURE 5. Number of dispensed prescriptions of antibiotic VMPs by fish species (aggregated for marine fish), split into production stages/types, in Norway in 2016-2025. Data were obtained from the Veterinary Prescription Register. *Arctic char, cod, halibut, pollack and/or wolfish. Note that cleaner fish are not included.

The annual sales of antibacterial VMPs for use in aquaculture peaked in 1987 when it amounted to 48 tonnes (Figure 6) – i.e. 876 mg/mg animal biomass; the corresponding figure in 2025 was 0.26 mg/kg animal biomass. Thus, the sales in mg/kg animal biomass have declined by more than 99.9%. The significant decrease in the sales of antibacterial agents in Norwegian aquaculture from 1987 is mainly attributed to the introduction of effective vaccines against bacterial diseases in Atlantic salmon and rainbow trout, but also prevention of bacterial diseases and their spread.

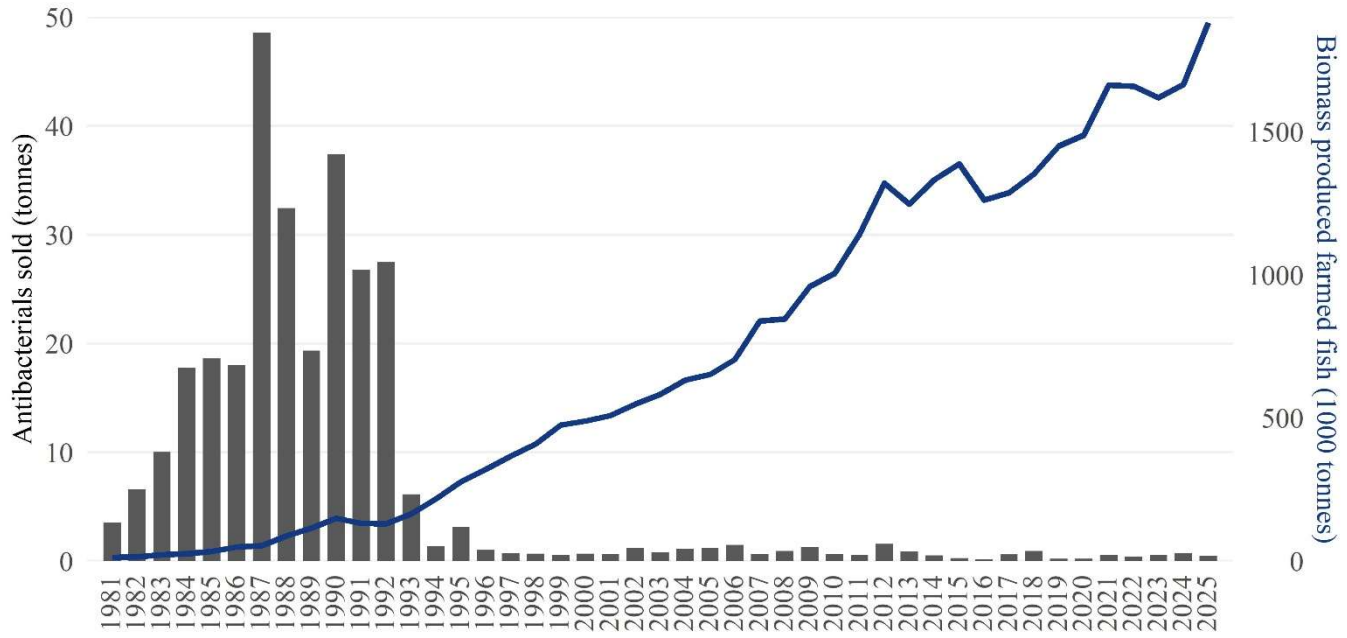

FIGURE 6. Sales, in tonnes of active substance, of antibacterial veterinary medicinal products for therapeutic use in farmed fish (including cleaner fish) in Norway in 1981-2025 versus tonnes produced (slaughtered) farmed fish. For the years 1981-2012 the data represent sales data provided by Norwegian Institute of Public Health; for 2013-2025 data represent prescription data obtained from the Veterinary Prescription Register. Data on slaughtered biomass farmed fish (Atlantic salmon, rainbow trout, other salmonid and marine species) were obtained from Norwegian Directorate of Fisheries. Note differences in the scales of the Y-axes.

In 2013-2017 only a low percentage of Atlantic salmon and rainbow trout on-growing farms were subjected to treatment with antibiotics (range 0.6%–1.5%) (2). This was also the case for the years 2018-2024, when this figure was between 0.8% and 3.3%. In 2025 this figure was 1%.

Companion animals (dogs and cats)

The sales in 2025 of antibacterial VMPs approved solely for companion animals (includes VMPs formulated as tablets, oral solution, injectable and oral paste) was 367 kg (active substance); in 2024 this figure was 357 kg. As shown in Figure 7, a steady increase in the sales from 1993 to 2001 was observed. This can in part be explained by an increase in the availability of antibacterial VMPs marketed for dogs and cats during that period. When the availability of VMPs for dogs and cats was lower, it is likely that antibacterial HMPs were prescribed for dogs and cats. In 1993, only eight antibacterial VMP presentations (name, pharmaceutical form, strength and pack size) were approved and sold in Norway for dogs and cats only, while in 2025 the corresponding number was 37.

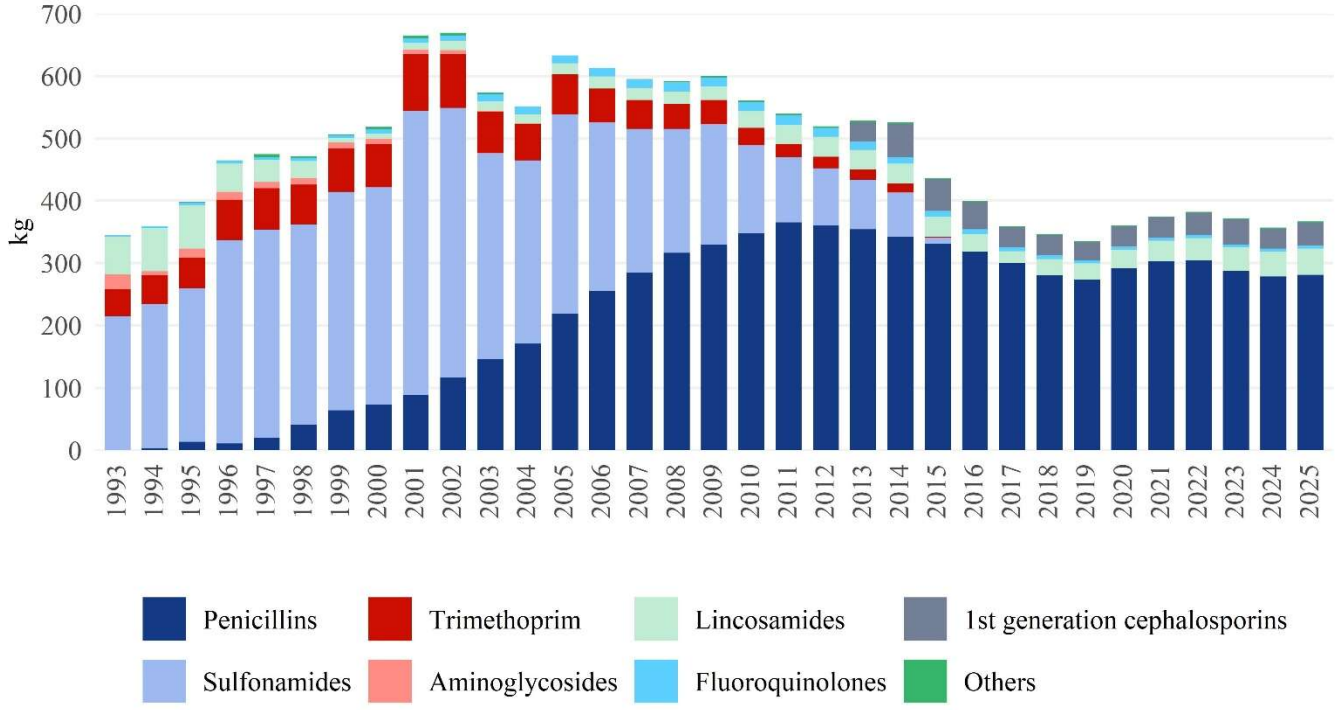

FIGURE 7. Sales, in kg active substance, of antibacterial veterinary medicinal products marketed solely for use in companion animals (see Appendix 1) in Norway for the period 1993-2025. "Others" includes minor annual sales of a 3rd generation cephalosporin injectable VMP (range 0.3-1.1 kg) during 2008-2025, tetracycline VMPs (range 0.05-2.3) during 1995-2025, macrolide VMPs (0.4-5 kg) during 1996-2003, and baquiloprim VMPs (0.2-0.4 kg) during 1995-1999.

The sales patterns of antibacterial VMPs marketed solely for companion animals (dogs and cats) have changed significantly during the period 1993-2025 (Figure 7). The first penicillin VMP as tablets – i.e. amoxicillin (an aminopenicillin), was marketed for dogs and cats in 1994; since then, the proportion belonging to the penicillins (only aminopenicillin VMPs marketed) sold of total sales of antibacterial VMPs approved for such animals has increased from 1% to 77% (Figure 7). Among penicillin VMPs, amoxicillin combined with clavulanic acid accounted for 78% of the sales in 2025 (Figure 8).

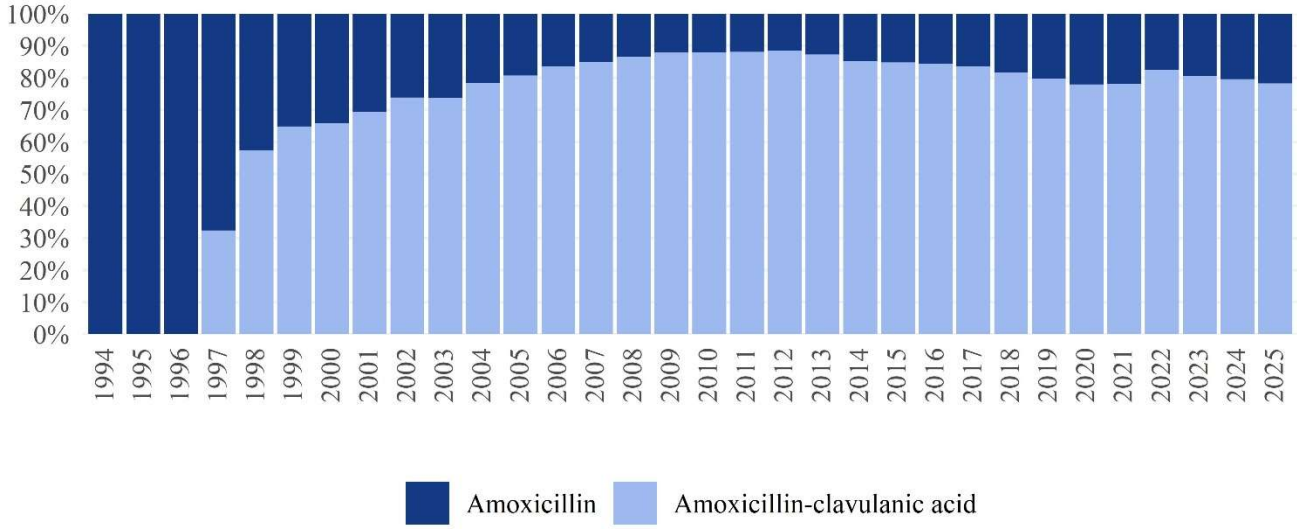

FIGURE 8. Proportions of sales (in kg active substance), of VMPs with amoxicillin combined with clavulanic acid versus amoxicillin for dogs and cats in Norway during 1994-2025.

From 1993 to 2023 the proportion of sales of fluoroquinolones have been very low, accounting for 0.5% of the total sales for this animal category in 1993, increasing marginally to 2.8% in 2011, and since then this proportion has decreased slightly to 1.2% in 2025 (Figure 7). The proportion of the total sales for dogs and cats of 3rd generation cephalosporins has been low since such VMPs were marketed in Norway in 2008; this figure was 0.2% in 2008 and 0.1% in 2025 (Figure 7).

Antibacterials for which use in animals is adviced to be restricted

In 2019, EMA's Antimicrobial Advice Ad Hoc Expert Group (AMEG) published a categorisation of antibiotics for use in animals for prudent and responsible use at EU/EEA level. This categorisation was adjusted in 2025 (1). AMEG category B contains certain classes – i.e. quinolones (fluoroquinolones and other quinolones), 3rd- and 4th-generation cephalosporins and polymyxins – where it is advised that the potential risk to public health resulting from veterinary use needs to be mitigated by specific restrictions. Figure 9 shows the amounts sold, in kg of the antibacterials belonging to AMEG category B compared to the total sales of antibacterial VMPs. In total, 0.3% of the total sales of antibacterial VMPs in 2025 belonged to the AMEG B category. For companion animals the VMPs represent 3rd generation cephalosporins and fluoroquinolones, for farmed fish other quinolones, and for food-producing animals fluoroquinolones (2). Of note is that apart from two VMPs for local ear treatment, other pharmaceutical forms of VMPs containing polymyxins are not marketed in Norway.

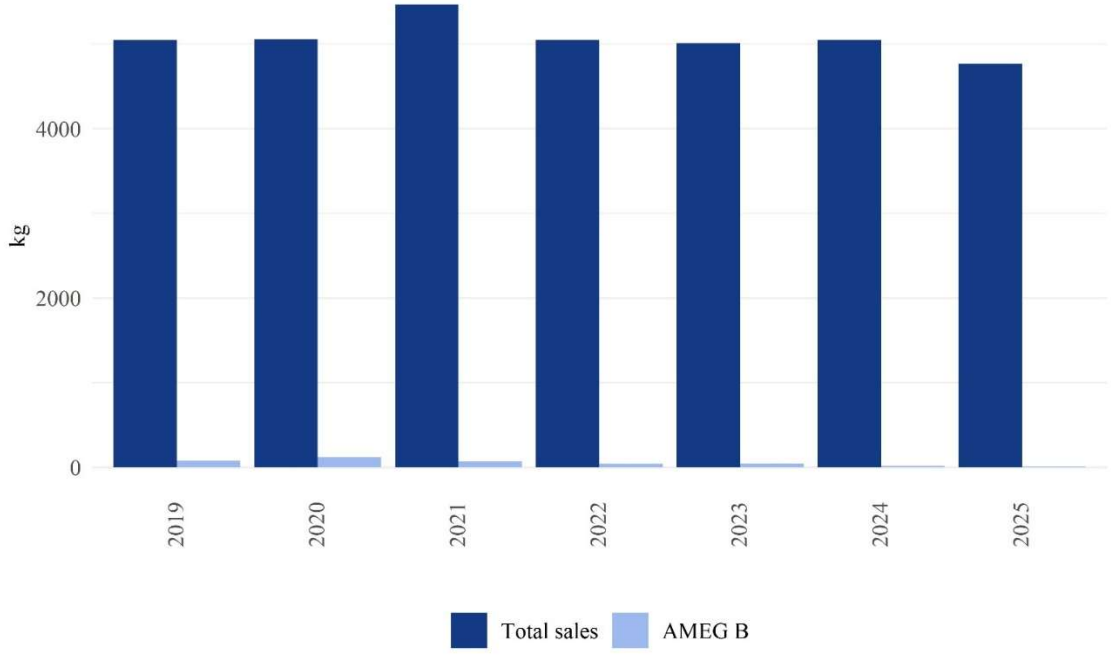

FIGURE 9. Total sales and sales of antibacterial veterinary medicinal products (VMPs) in Norway in 2019-2025, for which the Antimicrobial Advice Ad Hoc Expert Group (AMEG) of the European Medicines Agency advises restricting the use (AMEG category B) (1). Of note – VMPs for topical treatment are not included.

National Strategy against Antibiotic Resistance

Historic targets

All targets for antibiotic use set by the Norwegian livestock industry for the period 1996-2001 and in the National Strategy against Antibiotic Resistance (2015-2020) (3) were achieved and some of them also exceeded. For more details on evaluation of these targets see the NORM/NORM-VET 2023 report.

2024-2033: National One Health Strategy

In 2024, a new National One Health Strategy Against Antimicrobial Resistance 2024-2033 was agreed upon (4). The strategy did not include any targets for reduction of antibacterial use for animals in Norway. The need to ensure restrictive and prudent use is, however, highlighted. Moreover, surveillance of use of antimicrobials should improve as such data is the key basis for advice and management measures.

References

1. EMA. Categorisation of antibiotics for use in animals for prudent and responsible use. 2019. (https://www.ema.europa.eu/en/documents/report/infographic-categorisation-antibiotics-use-animals-prudent-responsible-use_en.pdf).
2. Kari Grave and Kari Olli Helgesen. Antibacterials for farmed fish – prescribing, usage and diagnoses 2013 - 2017 (In Norwegian: Antibakterielle midler til oppdrettsfisk – rekvirering, forbruk og diagnose 2013 - 2017). Report 5: Veterinærinstituttet, 2018. https://www.vetinst.no/rapporter-og-publikasjoner/rapporter/2018/antibakterielle-midler-til-oppdrettsfisk-og-rensefisk--rekvireringer-forbruk-og-diagnoser-2013-2017.
3. Norwegian ministries, 2015. National Strategy against Antibiotic Resistance 2015–2020 (https://www.regjeringen.no/contentassets/5eaf66ac392143b3b2054aed90b85210/antibiotic-resistance-engelsk-lavopploslig-versjon-for-nett-10-09-15.pdf).
4. The Government of Norway, 2024. National One Health Strategy Against Antimicrobial Resistance 2024–2033.(https://www.regjeringen.no/contentassets/7ae8eacec9cc4af085b5c113a98a0eb0/national-one-health-strategy-against-antimicrobial-resistance.pdf).

Use of antibacterial agents per species and data quality

In the NORM/NORM-VET reports for the years 2017-2024, use data from the Veterinary Prescription Register (VetReg) were presented per species for certain food-producing terrestrial animals, as proportion by class/subclass of antibiotics. The reason for not presenting use in kg was that the coverage – i.e. the proportion of data mandatory to be reported covered by the reported data – was relatively low and it was not known whether the data were representative (1, 2). For 2017-2023 prescription patterns were presented for cattle, pigs and sheep, while in 2024 data for turkeys and chicken were included instead of for sheep. Cattle, pigs, turkeys and chicken are the species for which use data currently are mandatory to report to the European Medicines Agency (EMA) according to the European Union Regulation on Veterinary Medicinal Products (Regulation (EU) 2019/6, Article 57).

The second European Sales and Use of Antimicrobials for Veterinary Medicine report (ESUAvet report), covering 2024 data, presented use data in kg per species per country (3). These data should be interpreted with great care for these three main reasons: 1) Use data coverage varies substantially between countries, 2) Use data coverage may vary between species, also within a country, and 3) The methodology for calculating coverage is not given in the ESUAvet report and may therefore differ between countries.

Importantly for Norway, for 2024 data a 109% coverage of use data (use data calculated as percent of sales data for the same veterinary medicinal products (VMPs)) was estimated for chicken and turkeys and an 80% coverage was estimated for cattle and pigs. For 2025 data these figures were 72% and 85%, respectively. The 2024 figures on use and coverage presented here deviate somewhat from what was reported in the second ESUAvet report due to updates in methodology (see Annex 1) and updated information on double reporting of VetReg data for 2024.

To present use data in NORM/NORM-VET harmonised with data in the ESUAvet report, use data for 2024 and 2025 are presented in Figure 10 as kg active substance used per species as reported to VetReg per 17.03.2026, subdivided per antibacterial class. The antibacterials included are the VMPs for which use is mandatory to be reported to EMA and where metadata (e.g. active substance and strength) are found in Union Product Database (see Annex 1). The prescription pattern is presented in Figure 11 as percent per antibacterial class per species.

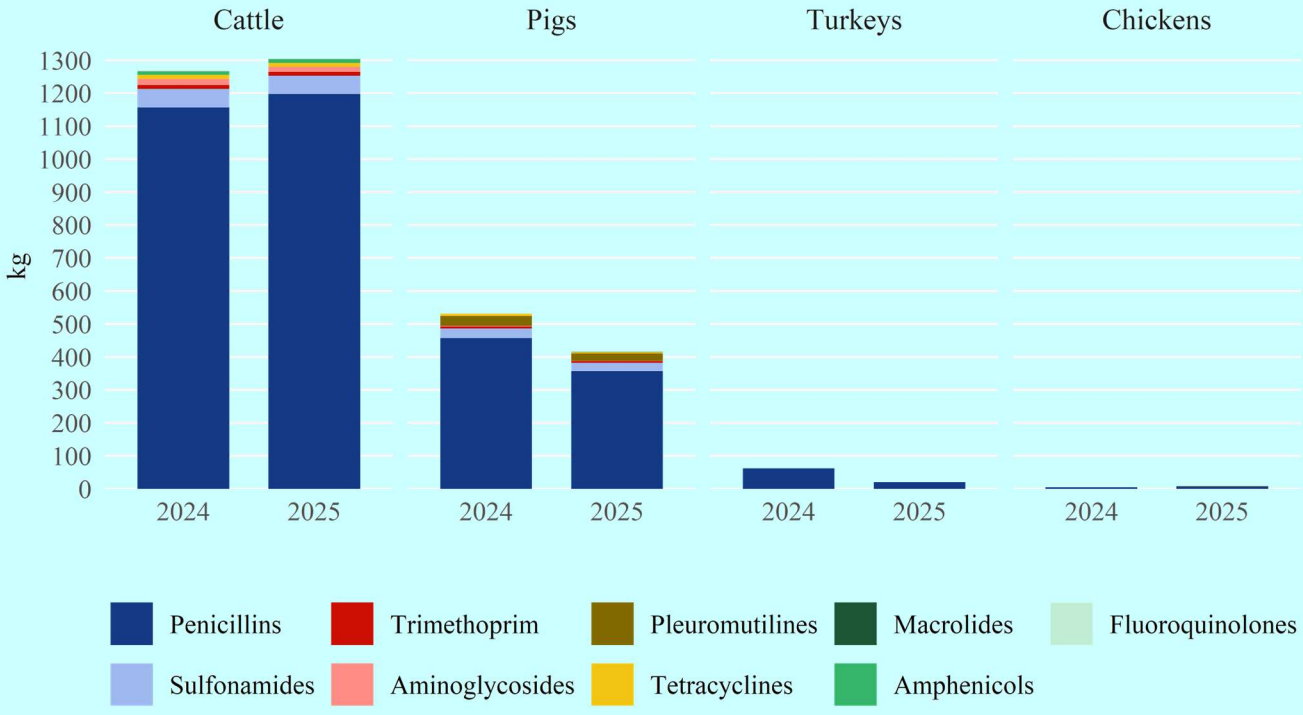

FIGURE 10. Use, in kg active substance per class/subclass of active substance, for cattle, pigs, turkeys and chickens, of antibacterial veterinary medicinal products (VMPs) for therapeutic use in Norway in 2024 and 2025. Data were obtained from the Veterinary Prescription Register and represent all use of VMPs for which use data are mandatory to be reported to the European Medicines Agency. In addition, minor amounts of human medicinal products (2.4 kg in 2024 and 1.9 kg in 2025) and of VMPs not included in Union Product Database (0.8 kg in 2024 and 0.5 kg in 2025) were prescribed for cattle, pigs, turkeys and chickens (not included in the figure).

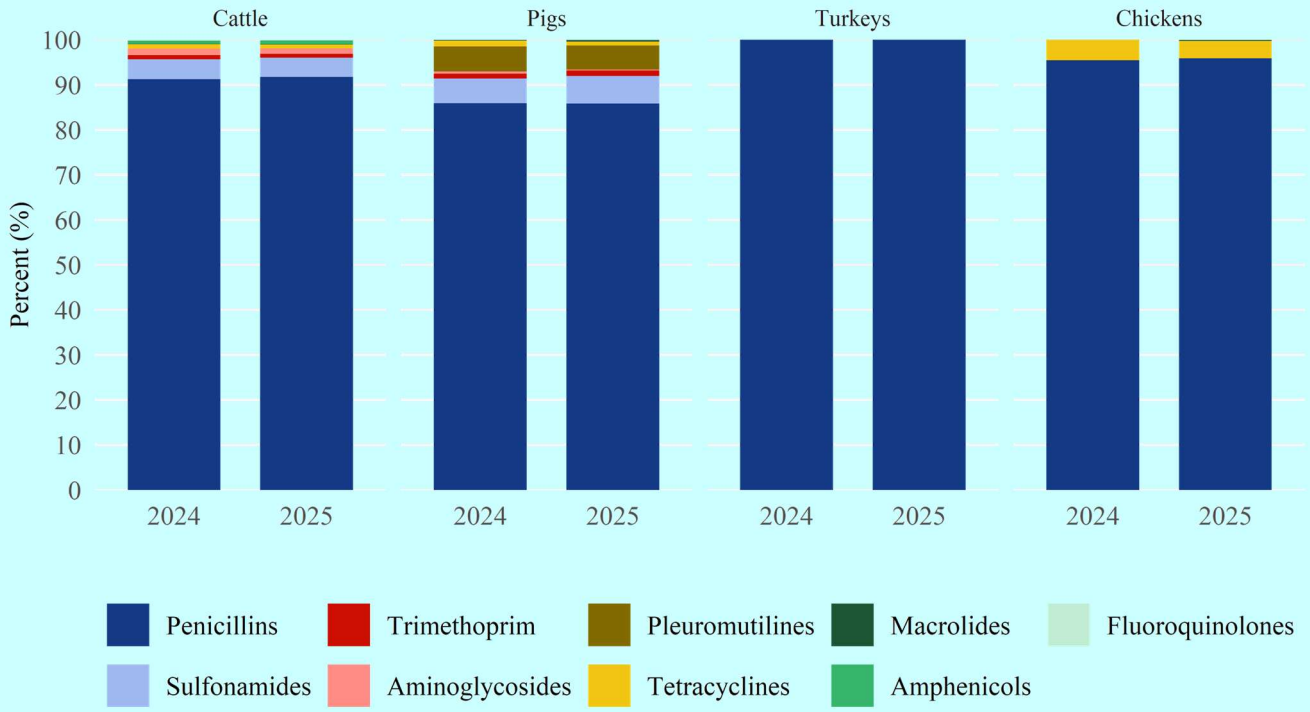

FIGURE 11. Prescribing patterns, in percentage of kg active substance, of antibacterial veterinary medicinal products (VMPs) per species in Norway in 2024 and 2025. Data were obtained from the Veterinary Prescription Register and represent all use of VMPs for which use data are mandatory to be reported to the European Medicines Agency. In addition, minor amounts of human medicinal products (0.12% of total use) and VMPs not included in the Union Product database (0.04% of total use) were prescribed for cattle, pigs, turkeys and chickens, respectively (not included in the figure).

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The role of agricultural azoles in food safety and security: Implications for antifungal resistance and human health

Azoles are highly effective fungicides widely used in human and veterinary medicine to treat and prevent fungal infections. They are also essential for the safe and sufficient production of food in agriculture, healthy plants in horticulture, and the wood industry. While residues of azoles in the environment are considered environmental contaminants, an equally important concern is their role in driving the development of antifungal resistance in human, animal and plant pathogens. Environmental exposure to azoles has been shown to promote cross-resistance in clinically important fungal pathogens, particularly *Aspergillus fumigatus*. This link between environmental azole use and resistance in human pathogens has been consistently demonstrated in multiple international studies. The clinical consequences are severe: the case fatality rate of culture-confirmed azole resistant invasive aspergillosis ranges from 50% to 100%. Urgent action is therefore needed to address antifungal resistance (AFR), to avoid a crisis similar to the global rise of antibiotic resistance. Despite its serious implications, awareness of fungal infections and antifungal resistance as global health threats remains limited. However, important steps have been taken in recent years. In 2013, the European Centre for Disease Prevention and Control (ECDC) published a risk assessment highlighting how environmental use of triazoles contributes to resistance in *Aspergillus* species[1]. This was followed in 2022 by the WHO Fungal Priority Pathogens List, which highlighted that the fungal species pose the greatest threat to public health and emphasises the urgency of addressing AFR[2].

Fungal pathogens also pose a direct food safety risk, if they remain untreated. Many plant-pathogenic fungi produce mycotoxins, which are harmful to human health. Dietary exposure to mycotoxins is considered too high for both animals and humans, especially children, in several countries[4,5,6,7]. Effective control of fungal diseases in agriculture is therefore essential not only to protect crop yields, but also to ensure food safety and human health.

Climate change is expected to create warmer, wetter, and more variable weather conditions, which are favourable for many fungal pathogens. As a result, both the diversity and incidence of fungal diseases in crops are likely to increase. This will intensify the need for effective disease control strategies in agriculture to reduce crop losses, close yield gaps, and secure sufficient and safe food supplies for a growing global population towards 2050.

Because azoles are extensively used across healthcare, agriculture, and industry, antifungal resistance represents a true One Health challenge. Surveillance studies indicate that in regions where azole resistance in *Aspergillus* is endemic, more than 90% of resistance mechanisms are driven by environmental selection pressures. Understanding how resistance develops and spreads in the environment is therefore crucial for designing effective mitigation strategies. Coordinated global surveillance efforts and revised regulations governing azole use across sectors are urgently needed.

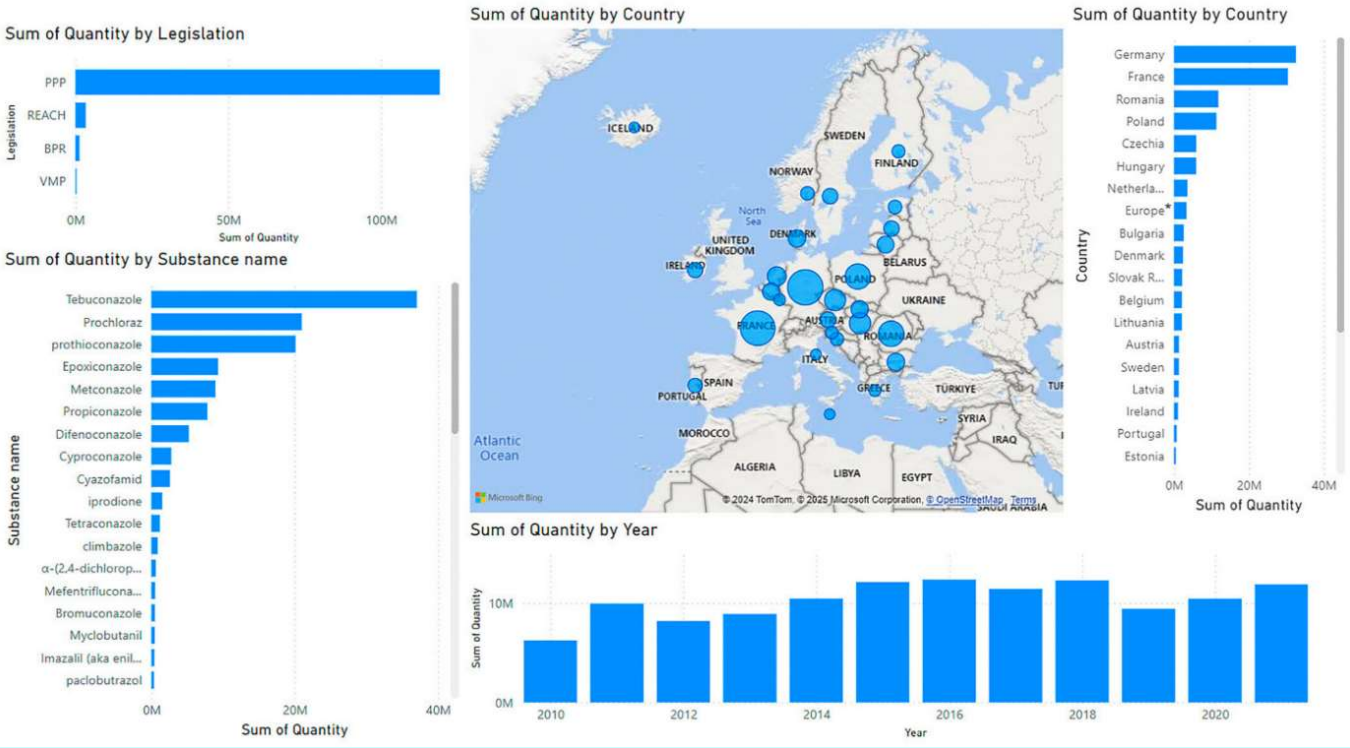
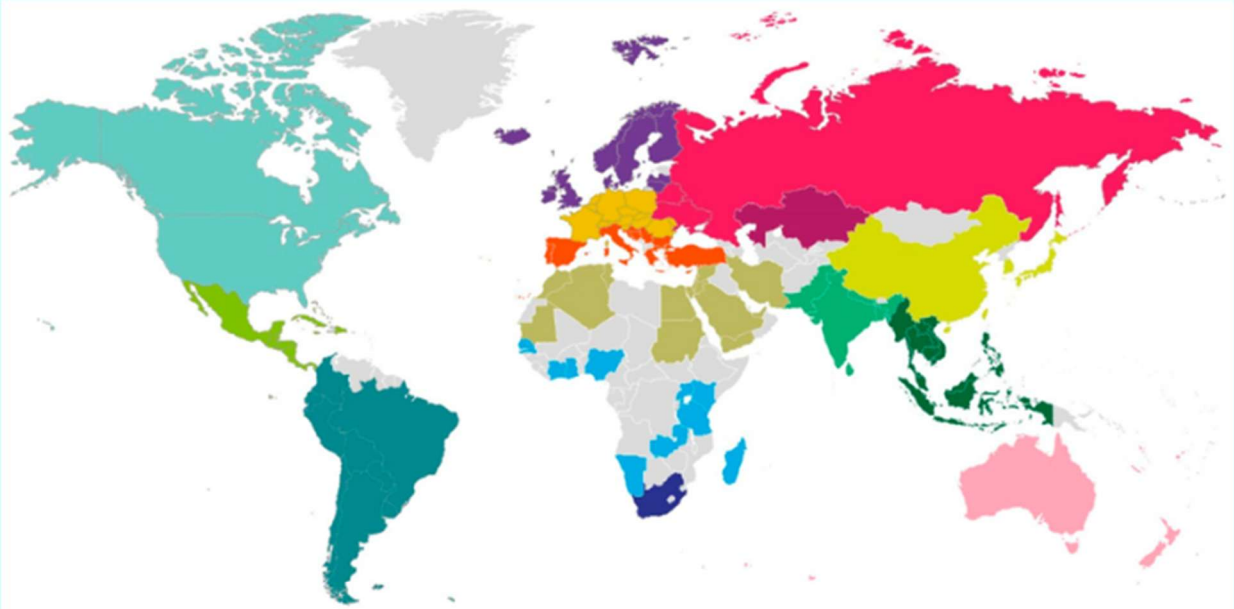


FIGURE 12. Overall sum of quantities of azoles reported as sold for 2010-2021 per Regulation (PPP, BPR, VMP, REACH), per substance, per country, per year and the geographical variation, please note the limitations of the submitted data. These data do not represent the complete situation in the EU/EEA (EFSA[3]).

Azoles in agriculture

Over the past four decades, azole fungicides have been one of the most important classes of compounds for managing fungal diseases in crops. Between 2010 and 2021, approximately 120,000 tonnes of azoles were sold in the EU/EEA for non-medical purposes, the vast majority being used as plant protection products (Figure 13)[3].

The first widely used systemic fungicides active within plants were introduced in the late 1960s. Over time, azole compounds became central to crop protection due to their specificity and effectiveness against fungal pathogens. However, only a few years after their widespread introduction, reduced sensitivity and resistance were observed in some fungal populations. Azoles are part of the sterol biosynthesis inhibitor fungicides (SBI) and practical recommendations to reduce the risk of resistance development are updated annually and implemented in the field[8].



	ABF1	FUM	ZEN	DON	OTA	T-2
Northern Europe (n = 1,958)	5.9% 3.1 µg/kg	22.4% 186 µg/kg	28.9% 35 µg/kg	74.2% 504 µg/kg	8.1% 1.9 µg/kg	30.3% 34 µg/kg
Central Europe (n = 21,036)	12.7% 1.6 µg/kg	43.2% 187 µg/kg	45% 40 µg/kg	69.8% 428 µg/kg	11.9% 2.8 µg/kg	30.7% 11 µg/kg
Southern Europe (n = 3,527)	28.9% 2.1 µg/kg	74.9% 607 µg/kg	36.3% 44 µg/kg	52.9% 324 µg/kg	21.2% 2.6 µg/kg	11.7% 25 µg/kg
Eastern Europe (n = 2,382)	17.0% 3.4 µg/kg	33.6% 87 µg/kg	42.5% 15 µg/kg	59.9% 153 µg/kg	36.4% 3.6 µg/kg	48.2% 21 µg/kg
North America (n = 5,471)	10.5% 8.7 µg/kg	47.7% 652 µg/kg	31.7% 102 µg/kg	64.1% 505 µg/kg	4.3% 2.4 µg/kg	3.9% 29 µg/kg
Central America (n = 367)	8.6% 3.9 µg/kg	81.8% 929 µg/kg	38.2% 60 µg/kg	70.0% 316 µg/kg	3.8% 2.5 µg/kg	4.1% 3.1 µg/kg
South America (n = 17,332)	23.5% 3.2 µg/kg	75.3% 1,390 µg/kg	46.9% 51 µg/kg	26.9% 344 µg/kg	4.9% 17 µg/kg	21.5% 31 µg/kg
Middle East/North Africa (n = 1,075)	22.2% 2.4 µg/kg	66.8% 347 µg/kg	44.8% 31 µg/kg	47.8% 236 µg/kg	20.3% 3.1 µg/kg	8.5% 14 µg/kg
Sub-Saharan Africa (n = 208)	76.0% 23 µg/kg	72.6% 789 µg/kg	52.2% 38 µg/kg	49.5% 352 µg/kg	31.9% 7.2 µg/kg	3.0% 3.0 µg/kg
South Africa (n = 1,077)	9.0% 2.2 µg/kg	62.6% 266 µg/kg	41.6% 30 µg/kg	63.2% 363 µg/kg	5.6% 2.2 µg/kg	1.2% 4.4 µg/kg
Oceania (n = 1,695)	11.3% 2.0 µg/kg	22.2% 106 µg/kg	21.5% 105 µg/kg	34.5% 158 µg/kg	7.5% 3.6 µg/kg	2.0% 16 µg/kg
South Asia (n = 1,136)	82.2% 20 µg/kg	69.0% 288 µg/kg	19.6% 37 µg/kg	23.1% 96 µg/kg	60.4% 4.6 µg/kg	0.9% 13 µg/kg
Southeast Asia (n = 4,310)	57.4% 10 µg/kg	69.6% 573 µg/kg	45.9% 43 µg/kg	42.5% 137 µg/kg	15.2% 3.0 µg/kg	2.7% 26 µg/kg
East Asia (n = 13,232)	17.1% 10 µg/kg	60.7% 810 µg/kg	58.2% 90 µg/kg	84.8% 418 µg/kg	14.1% 2.9 µg/kg	11.0% 16 µg/kg
Central Asia (n = 15)	7.7% 1.4 µg/kg	25.0% 13 µg/kg	23.1% 1.5 µg/kg	26.7% 28 µg/kg	13.3% 22 µg/kg	6.7% 25 µg/kg

FIGURE 13. Occurrence of mycotoxins in animal feed in 15 geographic regions of the world. For each region, countries of sample origin are labeled in the map using a distinct colour. The legend indicates percentage of positive samples and median of positive samples for each mycotoxin in each region. Each row represents one region and is labeled using the distinct colour corresponding to the respective region in the map. n=sample number; AFB1=aflatoxin B1; DON=deoxynivalenol; ZEN=zearalenone; FUM=fumonisins (sum of fumonisins B1, B2 and B3); OTA=ochratoxin A; T-2=T-2 toxin (Gruber-Dorninger et al.[7]).

Today, azole fungicides such as prothioconazole, remain widely used in crop production, including in Norway. Several active ingredients in fungicides are azoles, but they do not work in exactly the same way on the different target pathogens. Whether there is cross resistance between agricultural azoles and medical azoles in human pathogens needs to be clearly shown on a case-by-case basis. New legislation is being discussed to further reduce the number of azoles available for European and Norwegian agriculture because their break-down products include PFAS[9]. However, the extensive and repeated application of products containing the same active ingredient, can lead to strong selection pressure for resistance development, both in plant pathogens and in environmental fungi with relevance for human health.

Managing fungicide resistance requires integrated strategies. These include combining fungicides with different modes of action, using the lowest effective doses, deploying resistant crop varieties, and reducing inoculum sources through crop rotation and soil management. However, such approaches depend on access to fungicides with diverse mechanisms of action. In practice, crop protection often relies on a limited number of active compounds, increasing the risk of resistance. Importantly, the potential impact on medically important fungi must be considered when developing new plant protection strategies.

Azoles in industry

Azoles are also widely used in industrial applications, particularly as preservatives in wood, paints, and coatings. Growing concerns about the environmental and health impacts of heavy metal-based preservatives have led to increased use of azole-based alternatives such as propiconazole and tebuconazole.

Despite their widespread use, there is limited comprehensive data on the extent of azole application across different industrial sectors. Improving this knowledge base is essential to assess environmental exposure and its contribution to antifungal resistance.

References

1. ECDC (European Centre for Disease Prevention and Control). (2013). Risk assessment on the impact of environmental usage of triazoles on the development and spread of resistance to medical triazoles in Aspergillus species. https://www.ecdc.europa.eu/en/publications-data/risk-assessment-impact-environmental-usage-triazoles-development-and-spread
2. WHO fungal priority pathogens list to guide research, development and public health action (2022) https://www.who.int/publications/i/item/9789240060241
3. EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), ECHA (European Chemicals Agency), EEA (European Environment Agency), EMA (European Medicines Agency) & JRC (European Commission's Joint Research Centre). (2025). Impact of the use of azole fungicides, other than as human medicines, on the development of azole-resistant Aspergillus spp. EFSA Journal, 23(1), e9200. https://doi.org/10.2903/j.efsa.2025.9200
4. Martinez-Miranda, M. M., Rosero-Moreano, M., & Taborda-Ocampo, G. (2019). Occurrence, dietary exposure and risk assessment of aflatoxins in arepa, bread and rice. *Food control*, *98*, 359-366.
5. https://www.fao.org/fao-who-codexalimentarius/sh-proxy/zh/?lnk=1&url=https%253A%252F%252Fworkspace.fao.org%252Fsites%252Fcodex%252FMeetings%252FCX-735-11%252FWD%252Fcf11_INF01x.pdf
6. Eskola, M., Kos, G., Elliott, C. T., Hajšlová, J., Mayar, S., & Krska, R. (2020). Worldwide contamination of food-crops with mycotoxins: Validity of the widely cited 'FAO estimate'of 25%. *Critical reviews in food science and nutrition*, *60*(16), 2773-2789.
7. Gruber-Dorninger, Christiane & Jenkins, Timothy & Schatzmayr, Gerd. (2019). Global Mycotoxin Occurrence in Feed: A Ten-Year Survey. Toxins. 11. 375. 10.3390/toxins11070375.
8. https://www.frac.info/frac-teams/working-groups/sbi-fungicides/
9. PFAS-stoffet trifluoreddiksyre (TFA) | Mattilsynet

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USAGE IN HUMANS

Hege Salvesen Blix, Marion Neteland, Eli Leirdal Hoem, Sigurd Høye, Ragnhild Raastad, Petter Langlete

Overall antibiotic sales

In 2025, the total sales of antibacterials for systemic use in humans (J01, excl. methenamine) was reduced by 8% compared to 2024 and was 12.1 DDD/1,000 inhabitants/day (Table 4, Figure 14). Since 2012, there has been a stable decrease in the use of antibacterials. A marked decline (13%) was observed from 2019 to 2020, largely driven by reduced use of antibiotics for respiratory tract infections during the Covid-19 pandemic (Figure 15), due to lock-down measures. Antibiotic use has since returned to pre-pandemic levels.

In Norway, antibiotics are prescription-only drugs. Overall antibiotic consumption includes all sales of antibiotics to humans in Norway across primary care, hospitals and nursing homes. Approximately 88% of antibacterial use in humans occurs outside health institutions. In 2025, hospitals accounted for 7.6% of total DDDs of systemic antibiotics (ATC group J01), while nursing home care contributed with around 4%.

In Norway, narrow-spectrum penicillins are first-line treatment when antibiotics are warranted for respiratory tract infections. Over years the proportion of narrow-spectrum penicillins (J01CE) of the total antibiotic sales (J01, excl. methenamine) has remained relatively stable at around 26-27%, with a small drop during the pandemic. In 2024 and 2025, the proportion was 25%. The proportion of phenoxymethylpenicillin among antibiotics used for respiratory tract infections (RTI-AB) increased, reaching 50% in 2025. This may indicate a shift towards reduced overall antibiotic use for respiratory tract infections and greater reliance on narrow-spectrum agents when treatment is initiated. However, phenoxymethylpenicillin is also used for other indications, and this interpretation should therefore be made with caution.

Recent national and international shortage situations have led to fluctuations in sales from wholesalers. However, these have not appeared to significantly affect antibiotic use patterns. During shortage periods, generic alternatives were available, mitigating potential impacts. Across Europe, supply challenges are increasing, often driven by production or distribution issues, or higher-than-expected demand. If shortages are expected to pose sustained health risks, the Norwegian Medical Products Agency (DMP) may implement rationing to ensure equitable distribution, assessed on a case-by-case basis.

TABLE 4. Human usage of antibacterial agents in Norway 2012, 2015, 2018, 2021, 2024 and 2025 by ATC groups. The usage is presented as DDD (Defined Daily Doses)/1,000 inhabitants/day and in % change 2024-2025 and 2015-2025. Data from the Norwegian Drug Wholesales Statistics Database. Methodology for collection of data on human usage of antimicrobial agents is described in Appendix 2.

		Year						Change (%)	
ATC	Groups of substances	2012	2015	2018	2021	2024	2025	2024-2025	2015-2025
J01A	Tetracyclines	3.87	3.39	2.86	2.68	3.41	2.89	-15	-14
J01B	Amphenicols	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	-	-
J01CA	Penicillins with extended spectrum	2.79	2.73	2.46	2.19	2.31	2.24	-3	-18
J01CE	Beta-lactamase sensitive penicillins	4.31	3.88	3.43	2.70	3.31	3.08	-7	-21
J01CF	Beta-lactamase resistant penicillins	0.90	0.89	0.90	0.95	1.10	1.08	-2	+21
J01CR	Combination of penicillins, incl. beta-lactamase inhibitors	0.04	0.08	0.08	0.13	0.17	0.18	+6	+117
J01D	Cephalosporins, monobactams, carbapenems	0.53	0.43	0.39	0.34	0.34	0.35	+1	-20
J01E	Sulfonamides and trimethoprim	0.87	0.88	0.88	0.90	0.92	0.92	0	+5
J01F	Macrolides, lincosamides and streptogramins	2.26	1.51	1.05	0.67	0.81	0.65	-21	-57
J01G	Aminoglycosides	0.08	0.08	0.09	0.07	0.09	0.09	-2	+20
J01M	Quinolones	0.74	0.60	0.42	0.27	0.24	0.23	-5	-62
J01X*	Other antibacterials	0.47	0.41	0.32	0.31	0.40	0.41	+1	-2
J01	**Total excluding methenamine**	**16.9**	**14.9**	**12.9**	**11.2**	**13.1**	**12.1**	**-8**	**-19**
J01XX05	Methenamine	3.57	3.99	4.08	3.94	4.21	4.43	+5	+11
J01	**Total all antimicrobial agents**	**20.4**	**18.9**	**16.9**	**15.2**	**17.3**	**16.5**	**-5**	**-12**

*J01X incl. glycopeptides, colistin, fusidic acid, metronidazole (i.v.), nitrofurantoin, fosfomycin, linezolid, daptomycin and tedizolid. Methenamine is excluded.

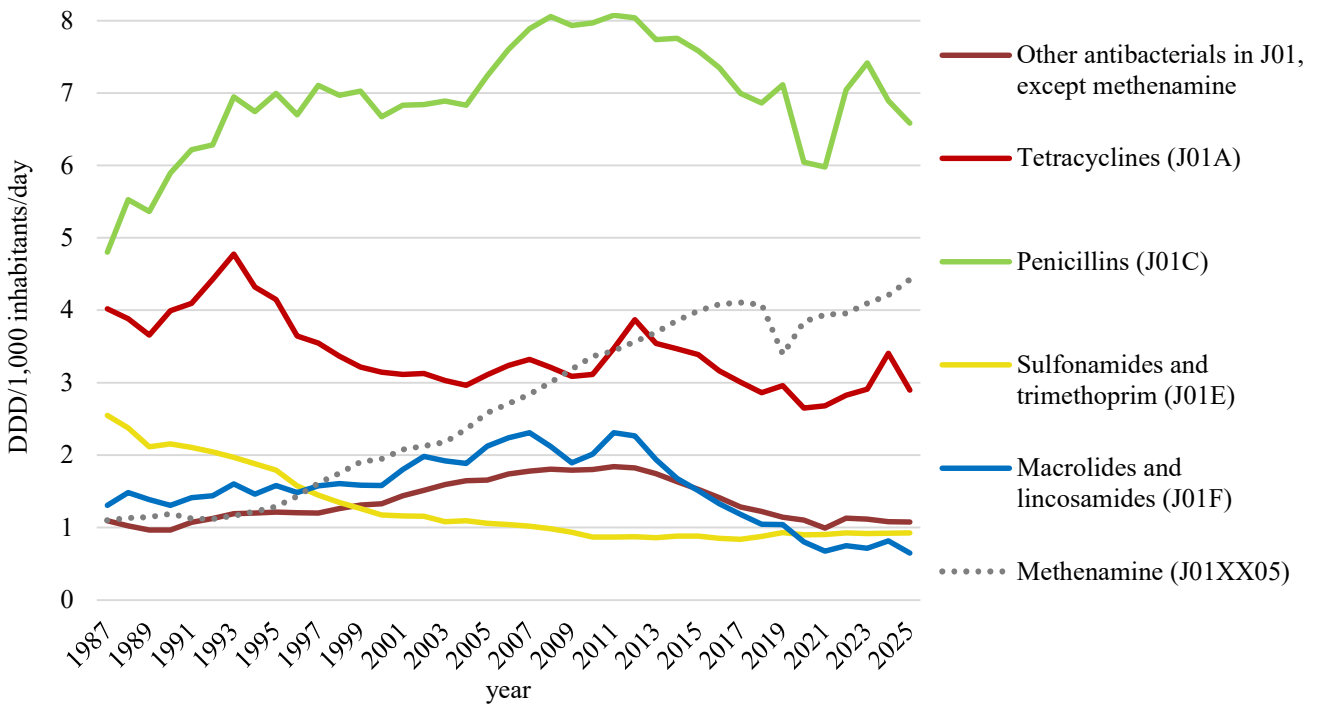

FIGURE 14. Sales of penicillins (J01C), tetracyclines (J01A), macrolides, lincosamides and streptogramines (J01F), sulfonamides and trimethoprim (J01E), methenamine and other antibacterials in Norway 1987-2025. Other types of antibacterials include all other antibacterials in ATC group J01, except methenamine (J01XX05). Data from the Norwegian Drug Wholesales Statistics Database.

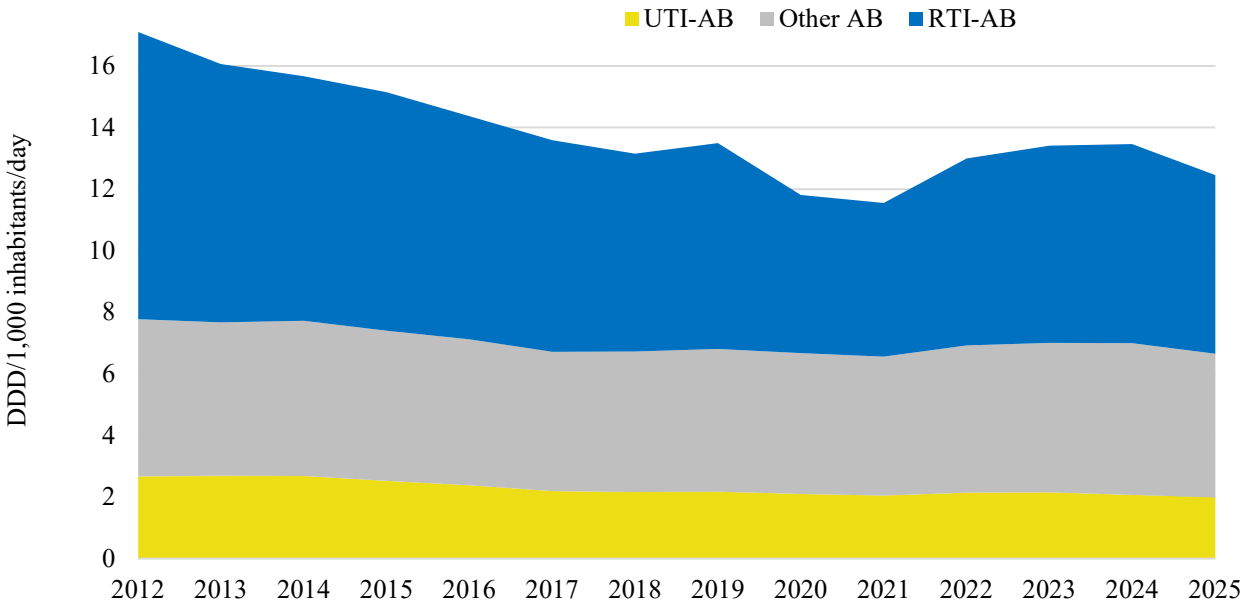

FIGURE 15. Sales of antibiotics in 2012-2025 as measured in DDD/1,000 inhabitants/day. Sales of antibiotics for respiratory tract infections (RTI-AB) are defined as amoxicillin, phenoxymethylpenicillin, macrolides and doxycycline. Antibiotics for urinary tract infections (UTI-AB) is defined as pivmecillinam, trimethoprim and nitrofurantoin. Other antibiotics (AB) is defined as all other antibiotics in ATC group J01, excl. methenamine. Data from the Norwegian Drug Wholesales Statistics Database.

In 2025, the three most used antibacterial groups in Norway were beta-lactamase sensitive penicillins (J01CE), tetracyclines (J01A), and penicillins with extended spectrum (J01CA) (Table 4). Methenamine, a urinary prophylactic agent, accounts for the highest number of defined daily doses (DDDs) among antibacterial agents in Norway, largely due to continuous daily use. During a major shortage in spring 2019, its use declined markedly but increased again thereafter. In 2024 and 2025, new evidence indicating that methenamine may reduce the frequency of UTIs in older women was published (see page 107), likely contributing to the steeper increase observed in these years (Figure 14, Table 4). In 2025, methenamine accounted for 26% of total antibacterial use as measured in DDDs (Figure 16).

Among the tetracyclines (J01A), doxycycline is the most frequently used, followed by lymecycline, which is primarily used for acne treatment (Table 5).

In 2025, penicillins (ATC group J01C) accounted for 40% of the total antibacterial use in Norway (Figure 16). Over time, there has been a shift towards increased use of broader-spectrum penicillins. In 2025, beta-lactamase sensitive penicillins represented 47% of total penicillin use (measured in DDDs), while extended-spectrum penicillins (J01CA) accounted for 34%. Beta-lactamase resistant penicillins (J01CF) made up 16% of use, up from 12% ten years earlier. Use of penicillins with beta-lactamase inhibitors (J01CR) has also increased in recent years (Table 4). Since the introduction of oral co-amoxiclav in Norway in May 2017, its use has risen markedly, despite being recommended only for limited number of indications in Norwegian primary care guidelines.

Antibiotic use for urinary tract infections (UTI-AB) has declined by 17% since 2015 (Figure 15). Recommendations for shorter treatment courses explain some of the decrease. Pivmecillinam remains the most commonly used agent, although pivmecillinam, trimethoprim, and nitrofurantoin are all equally recommended for acute cystitis in primary care. Use of trimethoprim has decreased over time, possibly reflecting increasing awareness among general practitioners of relatively high resistance levels and a preference for alternative agents. However, overall use of the sulfonamides and trimethoprim subgroup has increased, driven by a rise in use of the combination product co-trimoxazole (Figures 14 and 16, Table 5).

Macrolide use has declined markedly since 2012 (Tables 4 and 5; Figures 14 and 16). Overall use of the J01F group (macrolides, lincosamides, and streptogramins) has shown a fluctuating pattern over time. These variations may partly reflect recurrent epidemics of *Mycoplasma pneumoniae in* Norway, which tend to occur every four to six years, the most recent outbreak occurred in 2023-2024. Although recent *M. pneumoniae* epidemics may contribute to short-term fluctuations in macrolide use, the overall trend has been downward, and current use is comparable to levels observed in the 1970s.

In recent years, sales of ATC group J01D (cephalosporins, monobactams, and carbapenems) have remained relatively stable (Tables 4 and 5; Figure 16).

In 2025, quinolones accounted for only 1% of total antibacterial sales (Tables 4 and 5; Figure 16), and their use has declined steadily since 2012. This reduction likely reflects increased awareness of their potential to drive antimicrobial resistance, as well as concerns about serious adverse effects associated with fluoroquinolones. In 2025, ciprofloxacin was the predominant agent in this group, accounting for 93% of quinolone use.

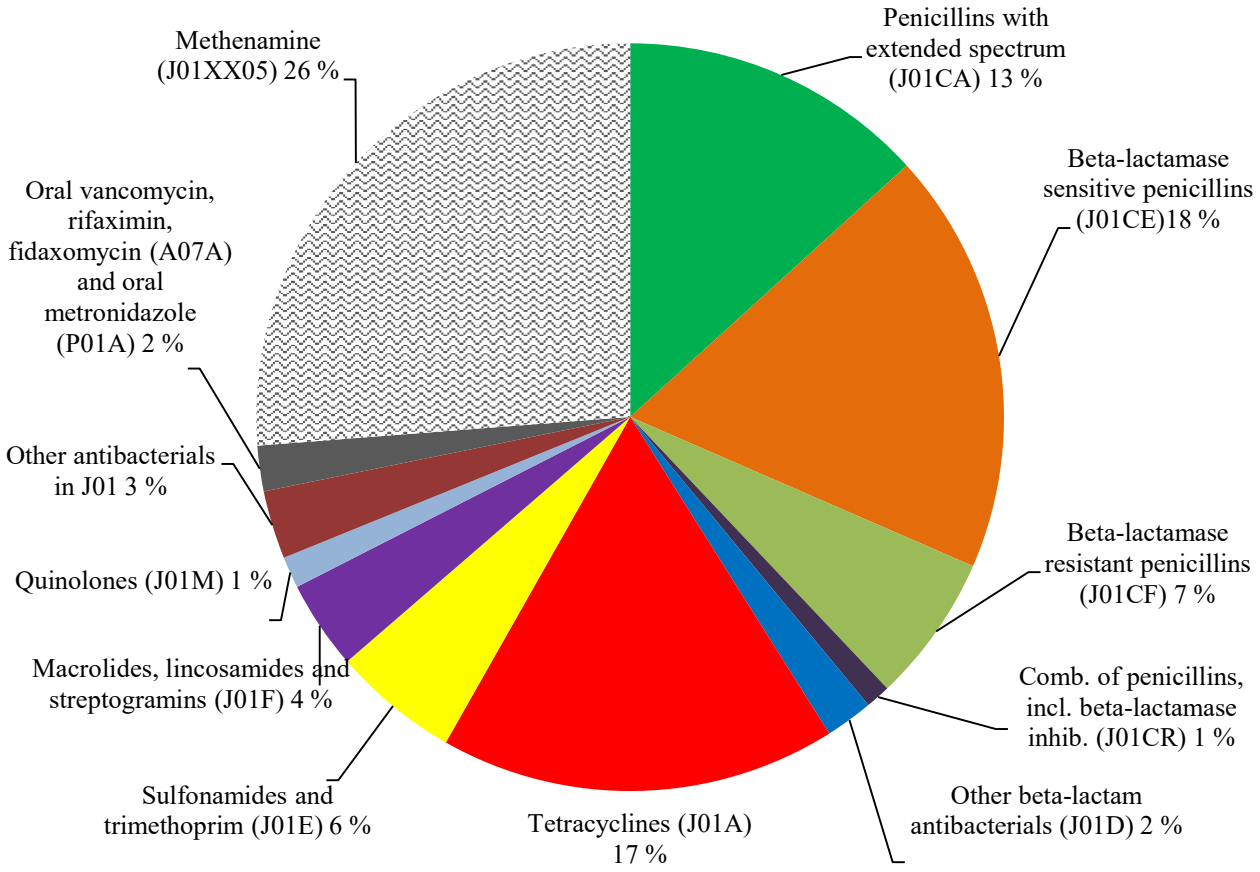

FIGURE 16. Relative amounts of antibacterial agents for systemic use in 2025 in Defined Daily Doses (DDD) (total sales in the country). Data from the Norwegian Drug Wholesales Statistics Database.

TABLE 5. Total human usage of single antibacterial agents for systemic use in Norway. Sales for overall use are given in DDD/1,000 inhabitants/day. Data from the Norwegian Drug Wholesales Statistics Database. ATC-version 2026 is used. The methodology for collection of data on human usage of antibacterial agents is described in Appendix 2.

ATC group	ATC code	Substance	2012	2015	2018	2021	2024	2025
J01A - Tetracyclines	J01A A02	Doxycycline	2.35	1.97	1.61	1.30	1.96	1.66
	J01A A04	Lymecycline	0.90	0.97	0.93	1.11	1.26	1.12
	J01A A06*	Oxytetracycline	-	<0.001	<0.001	<0.001	<0.001	<0.001
	J01A A07	Tetracycline	0.62	0.45	0.32	0.27	0.18	0.11
	J01A A08*	Minocycline	0.006	0.002	0.001	0.001	0.001	0.001
	J01A A12	Tigecycline	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
J01B - Amphenicols	J01B A01*	Chloramphenicol	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
J01CA - Penicillins with extended spectrum	J01C A01	Ampicillin	0.03	0.04	0.05	0.03	0.06	0.07
	J01C A04	Amoxicillin	0.97	0.93	0.84	0.67	0.76	0.76
	J01C A08	Pivmecillinam	1.78	1.76	1.57	1.49	1.49	1.42
	J01C A11	Mecillinam	0.008	0.006	0.002	-	-	-
	J01C A17	Temocillin	-	-	-	-	-	<0.001
J01CE - Beta-lactamase sensitive penicillins	J01C E01	Benzylpenicillin	0.24	0.22	0.24	0.14	0.17	0.16
	J01C E02	Phenoxymethyl-penicillin	4.07	3.66	3.18	2.56	3.14	2.92
	J01C E08*	Benzathine benzylpenicillin	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
J01CF - Beta-lactamase resistant penicillins	J01C F01	Dicloxacillin	0.76	0.73	0.74	0.79	0.88	0.87
	J01C F02	Cloxacillin	0.14	0.16	0.16	0.17	0.22	0.21
	J01C F05*	Flucloxacillin	<0.001	<0.001	0.001	<0.001	<0.001	<0.001
J01CR - Combination of penicillins, incl. beta-lactamase inhibitors	J01C R01*	Ampicillin and enzyme inhibitor	-	-	-	-	<0.001	-
	J01C R02	Amoxicillin and enzyme inhibitor	0.002	0.009	0.03	0.07	0.11	0.11
	J01C R05	Piperacillin and enzyme inhibitor	0.03	0.08	0.05	0.06	0.07	0.07
J01DB – 1st generation cephalosporins	J01D B01	Cefalexin	0.18	0.12	0.09	0.06	0.06	0.05
	J01D B03	Cefalotin	0.08	0.09	0.07	0.02	0.02	0.01
	J01D B04	Cefazolin	-	-	0.03	0.09	0.09	0.11
J01DC – 2nd generation cephalosporins	J01D C02	Cefuroxime	0.08	0.04	0.03	0.01	0.01	0.01
J01DD – 3rd generation cephalosporins	J01D D01	Cefotaxime	0.12	0.12	0.13	0.11	0.12	0.12
	J01D D02	Ceftazidime	0.009	0.008	0.006	0.005	0.003	0.003
	J01D D04	Ceftriaxone	0.03	0.02	0.02	0.02	0.03	0.02
	J01D D08*	Cefixime	-	-	<0.001	<0.001	-	<0.001
	J01D D52	Ceftazidime and avibactam	-	-	<0.001	0.001	0.001	<0.001
J01DF - Monobactams	J01D F01	Aztreonam	<0.001	0.001	<0.001	<0.001	0.003	0.002
	J01D F51	Aztreonam and avibactam	-	-	-	-	-	<0.001
J01DH - Carbapenems	J01D H02	Meropenem	0.03	0.03	0.02	0.02	0.02	0.02
	J01D H03	Ertapenem	0.002	0.003	0.002	0.002	0.002	0.003
	J01D H51	Imipenem and enzyme inhibitor	0.002	0.002	0.002	0.002	<0.001	<0.001
	J01D H52*	Meropenem and vaborbactam	-	-	-	-	<0.001	<0.001
	J01D H56	Imipenem, cila-statin, relebactam	-	-	-	-	<0.001	<0.001

ATC group	ATC code	Substance	2012	2015	2018	2021	2024	2025
J01DI – Other cephalo-sporins and penems	J01D I02	Ceftaroline fosamil	-	<0.001	<0.001	<0.001	<0.001	<0.001
	J01D I04	Cefiderocol	-	-	-	-	<0.001	<0.001
	J01DI54	Ceftolozane and enzyme inhibitor	-	-	<0.001	<0.001	<0.001	<0.001
J01E - Sulfonamides and trimethoprim	J01E A01	Trimethoprim	0.51	0.42	0.34	0.31	0.26	0.25
	J01E B02*	Sulfamethizole	-	-	-	<0.001	-	-
	J01E C02*	Sulfadiazine	-	-	<0.001	0.002	<0.001	<0.001
	J01E E01	Sulfamethoxazole and trimethoprim	0.36	0.46	0.53	0.59	0.66	0.68
J01F - Macrolides, lincosamides and streptogramins	J01F A01	Erythromycin	1.06	0.68	0.44	0.17	0.25	0.16
	J01F A02	Spiramycin	0.007	0.004	0.002	<0.001	<0.001	<0.001
	J01F A06*	Roxithromycin	-	<0.001	<0.001	<0.001	<0.001	<0.001
	J01F A09	Clarithromycin	0.39	0.18	0.11	0.10	0.12	0.10
	J01F A10	Azithromycin	0.48	0.33	0.24	0.19	0.23	0.20
	J01FS15	Telithromycin	<0.001	<0.001	-	-	-	-
	J01F F01	Clindamycin	0.33	0.31	0.25	0.22	0.22	0.19
	J01F G01*	Pristinamycin	-	-	-	<0.001	<0.001	<0.001
J01G - Aminoglycosides	J01GA01*	Streptomycin	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
	J01G B01	Tobramycin	0.03	0.02	0.01	0.01	0.01	0.01
	J01G B03	Gentamicin	0.05	0.06	0.08	0.06	0.08	0.08
	J01G B06	Amikacin	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
J01M - Quinolones	J01M A01*	Ofloxacin	0.024	0.014	0.009	0.006	<0.001	<0.001
	J01M A02	Ciprofloxacin	0.71	0.58	0.39	0.25	0.22	0.21
	J01MA12	Levofloxacin	0.002	0.002	0.004	0.006	0.008	0.006
	J01MA14*	Moxifloxacin	0.004	0.008	0.011	0.009	0.010	0.010
J01X - Other antibacterials	J01X A01	Vancomycin	0.01	0.02	0.02	0.01	0.02	0.02
	J01X A02*	Teicoplanin	<0.001	<0.001	<0.001	-	<0.001	-
	J01X A04	Dalbavancin	-	-	-	-	<0.001	<0.001
	J01X B01	Colistin	0.004	0.005	0.006	0.008	0.008	0.008
	J01X C01	Fusidic acid	0.005	0.004	0.003	<0.001	<0.001	<0.001
	J01X D01	Metronidazole	0.07	0.04	0.04	0.03	0.04	0.04
	J01X E01	Nitrofurantoin	0.37	0.34	0.25	0.24	0.32	0.33
	J01XX01	Fosfomycin	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
	J01X X05	Methenamine	3.57	4.00	4.08	3.94	4.21	4.43
	J01XX08	Linezolid	0.009	0.009	0.009	0.009	0.009	0.008
	J01XX09	Daptomycin	<0.001	<0.001	0.001	0.001	0.001	<0.001
	J01X X11	Tedizolid	-	-	<0.001	0.002	0.003	0.002
Antibiotics in other ATC groups	A07A A09	Vancomycin	0.002	0.002	0.002	0.003	0.005	0.005
	A07AA11	Rifaximin	0.004	0.03	0.08	0.12	0.14	0.15
	A07A A12	Fidaxomicin	<0.001	<0.001	<0.001	<0.001	0.002	0.002
	P01A B01	Metronidazole	0.23	0.24	0.21	0.21	0.19	0.18
	J04A B02	Rifampicin	0.046	0.044	0.043	0.036	0.046	0.042
	D06A X09/ R01A X06	Mupirocin**	145	226	247	256	429	471

* Substances used but not licensed in the Norwegian marked in 2025. ** Given as the total amount grams (g) mupirocin per year.

Antibiotic use in primary care

Approximately 88% of the total human sales of antibacterials, measured in DDDs, is dispensed as prescriptions from pharmacies. This mainly reflects antibiotics prescribed to persons in ambulatory care, most of whom live at home. The data in this chapter is derived from the Norwegian Prescribed Drug Registry (NorPD), which includes all antibacterial prescriptions dispensed to persons living in Norway. The data also include antibiotics prescribed to discharged patients and outpatients by hospital doctors, see Appendix 2.

The overall reduction in antibacterial use during the Covid-19 pandemic was mainly driven by decreased use in primary care. In 2025, the use of antibacterials (J01 excl. methenamine) in primary care was 10.0 DDD/1,000 inhabitants/day. Of the whole group of antibacterials (J01) in primary care, penicillins (J01C) was the most commonly used antibiotic group, accounting for 38% of total DDDs within ATC group J01. Tetracyclines (J01A) was the second most used group at 20%, and sulfonamides and trimethoprim (J01E) made up 5% of all DDDs in primary care. The six antibiotic substances most often prescribed as measured in DDDs for outpatients in 2025 were methenamine, phenoxymethylpenicillin, doxycycline, pivmecillinam, lymecycline, and dicloxacillin (Table 6). Together, these six antibiotics accounted for 81% of all DDDs of the antibacterial group J01. Phenoxymethyl-penicillin represented 19% while methenamine covered 29% of the DDDs.

Antibiotic use in primary care remains relatively low in Norway. When excluding methenamine from the count, Norway is among the countries with lowest use in primary care. Antibacterial use in primary care, measured in DDDs, is now slightly lower than in 2019; the year before the Covid-19 pandemic. Between 2012 and 2019 there was a substantial reduction in the proportion of the population having dispensed at least one prescription of antibacterials (-22%) and number of prescriptions dispensed per 1,000 inhabitants (-27%) per year. From 2019 to 2025, the corresponding reductions are lower, -2% and -3%, respectively (Figure 17).

Antibiotics should be used when clinically indicated, and insufficient access or underuse may cause harm. The level of antibiotic use required in a population is not fixed, but varies with ongoing epidemics, the burden of antimicrobial resistance, population structure, and the risk profile of the patient groups being treated. In Norway, antimicrobial resistance has received sustained attention among both the public and health care personnel. Since the launch of the previous National Action Plan against AMR in 2016, a large proportion of general practitioners (GPs) have completed quality improvement courses targeting antibiotic prescribing. Additionally, since 2024, automated feedback reports on individual prescribing practices have been made available to all GPs, further supporting effort to promote appropriate antibiotic use.

The usage of antibacterials varies among the Norwegian regions, Table 6. However, the ranking of the antibacterial substances with the highest DDD volume was broadly similar across regions. Lymecycline, which is mainly used for acne, ranked fifth in all regions. Nitrofurantoin has increased in rank since 2022 while trimethoprim use has declined. Together with pivmecillinam, nitrofurantoin and trimethoprim are recommended first-line treatment for urinary tract infections. None of the regions have reached target set in the previous National Strategy against Antibiotic Resistance of 250 prescriptions/1,000 inhabitants/year when excluding methenamine (Figure 18). The North Region has the lowest number of prescriptions/ 1,000 inhabitants/year (297 Rx/1,000 inhabitant/day) and the lowest use measured as DDD/1,000 inhabitants/day i.e. 9 DDD/1,000 inhabitants/day, Figure 18. The South-East region had the highest proportion of phenoxymethyl-penicillin use in 2025, accounting for 19.8% of all DDDs, while the North region had the lowest proportion at 15.6%. Conversely, the North region had the highest proportion of urinary tract antibiotics (pivmecillinam, trimethoprim and nitrofurantoin) at 13.8% of all DDDs. The corresponding proportion was lowest in South-East (11.5%). These regional differences may reflect variations in patient demographics, infection burden, prescribing practices, and the case mix of conditions managed in ambulatory care.

Females use more antibiotics than males; in 2025, 22.6% of the females purchased at least one antibiotic prescription (methenamine is excluded) compared to 15.4% of the males (Figure 19). Except for the years of the pandemic, the prevalence is the lowest seen among women since measuring started in 2004, while for men we have seen lower prevalences e.g. in 2022. Young children, young women and the elderly are high users of antibiotics (Figure 19). Between 2012 and 2019, there was a reduced prevalence of use in all age groups. In 2023 and 2024 there was increased use in children while in 2025 the prevalence of use was lower in all age-groups except for the 10-19-year-old, Figure 20. However, compared to 2019 also in the older age-groups the prevalence is decreased. The dramatic reduction during the pandemic in 2020 for all age groups was mainly due to lower prescribing of antibiotics for respiratory tract infections, Figure 20. The prevalence varies somewhat from one year to another according to the burden of infection. The increase in 2023 and 2024 may be explained by the increased reporting of *Bordetella pertussis* and *Mycoplasma pneumoniae* from autumn 2023. The pertussis epidemic peaked in 2024 and appeared to subside during spring 2025. The highest number of reported cases was among older children.

Among those who are prescribed antibacterials, the elderly population are prescribed more frequently compared to younger age groups; for those above 75 years; 2.2 prescriptions/user for females and 2.1 prescriptions/user for males are dispensed every year compared to around 1.5 prescriptions/user for younger persons (men and women together), Figure 21. This has been stable over years. The mean number of antibacterial prescriptions delivered from pharmacies is reduced between 2019 and 2025 for men and women, and in all age groups - the largest reduction was in age group 15-29 years and for women, Figure 22. It is difficult to predict future antibiotic consumption, but optimising use requires continuous reminders to both the public and prescribers that antibiotics should be used only when necessary and with caution. The observed differences by age and gender suggest that targeted interventions for specific population groups may promote more appropriate and effective antibiotic use.

Over the years there are differences in the therapy patters according to recommendations in guidelines. In Norway, narrow-spectrum antibiotics are first-line antibiotics. Figure 23 shows variation in use of antibiotics (as measured in DDD/1,000 inhabitants/day), recommended as first-line versus not first-line treatment, and the figure is indicating a higher prescribing of the recommended antibiotics in recent years. This could be caused by increased attention towards AMR, quality improvement programmes and increased adherence to guidelines by health care workers in the period

TABLE 6. Human usage of the 15 antibacterial agents for systemic use with the highest volume in primary care in the four health regions in Norway in 2025. Sales are given in DDD/1,000 inhabitants/day. Data from the Norwegian Prescribed Drug Registry (NorPD).

	Health region				Norway
	Mid	North	South-East	West	
Methenamine	4.78	4.32	3.95	3.99	4.11
Phenoxymethylpenicillin	2.57	2.07	2.76	2.69	2.69
Doxycycline	1.52	1.39	1.52	1.49	1.51
Pivmecillinam	1.35	1.21	1.17	1.21	1.21
Lymecycline	1.06	0.95	1.09	1.29	1.12
Dicloxacillin	0.74	0.72	0.79	0.72	0.77
Amoxicillin	0.57	0.55	0.63	0.52	0.60
Sulfamethoxazole and trimethoprim	0.55	0.60	0.52	0.53	0.54
Nitrofurantoin	0.36	0.37	0.26	0.33	0.30
Trimethoprim	0.27	0.26	0.19	0.19	0.20
Azithromycin	0.15	0.14	0.18	0.20	0.18
Ciprofloxacin	0.16	0.16	0.16	0.16	0.16
Erythromycin	0.14	0.11	0.16	0.15	0.15
Clindamycin	0.13	0.13	0.16	0.14	0.15
Tetracycline	0.13	0.11	0.14	0.12	0.13

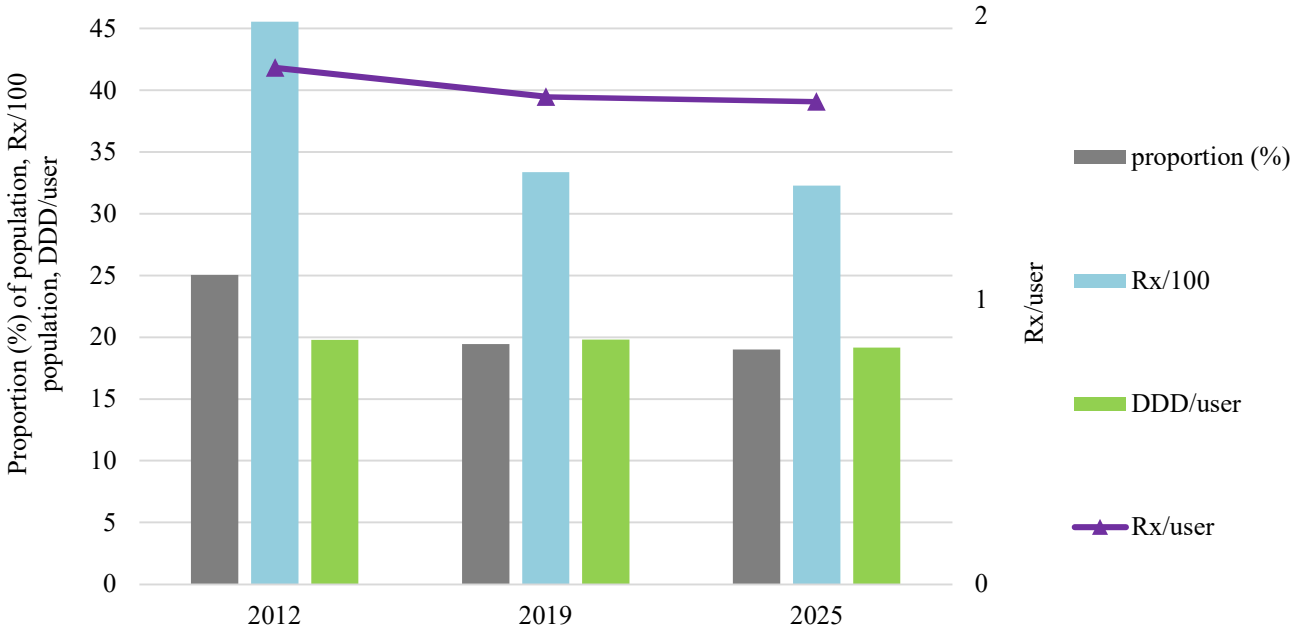

FIGURE 17. The proportion of the population having dispensed at least one prescription of antibacterials (one-year prevalence), number of prescriptions (Rx) per 100 inhabitants, number of DDDs/user and number of Rx/user in primary care in Norway, 2012, 2019 and 2025. Antibiotics included are antibacterials for systemic use (ATC group J01, excl. methenamine). Data from the Norwegian Prescribed Drug Registry (NorPD).

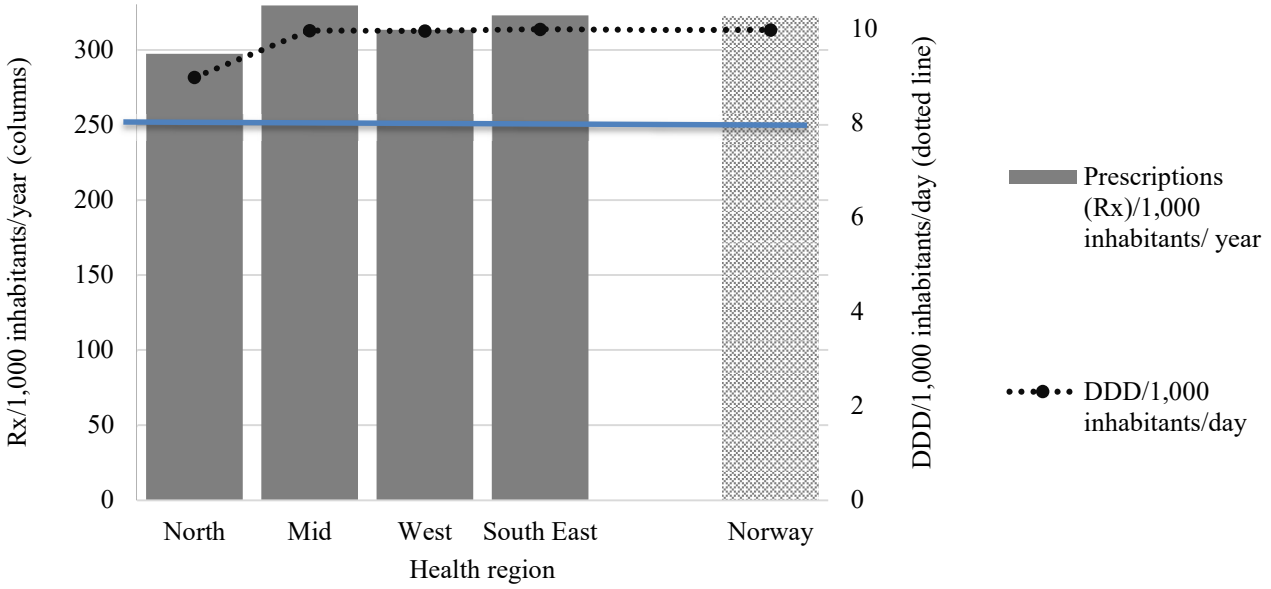

FIGURE 18. Consumption of antibacterial agents for systemic use (ATC group J01, excl. methenamine) in primary care in the different health regions of Norway in 2025. Measured as number of prescriptions (Rx)/1,000 inhabitants/year and in DDD/1,000 inhabitants/day. Prescription target set in National Strategy against Antibiotic Resistance is 250 Rx/1,000 inhabitants/year (blue line). Data from the Norwegian Prescribed Drug Registry (NorPD).

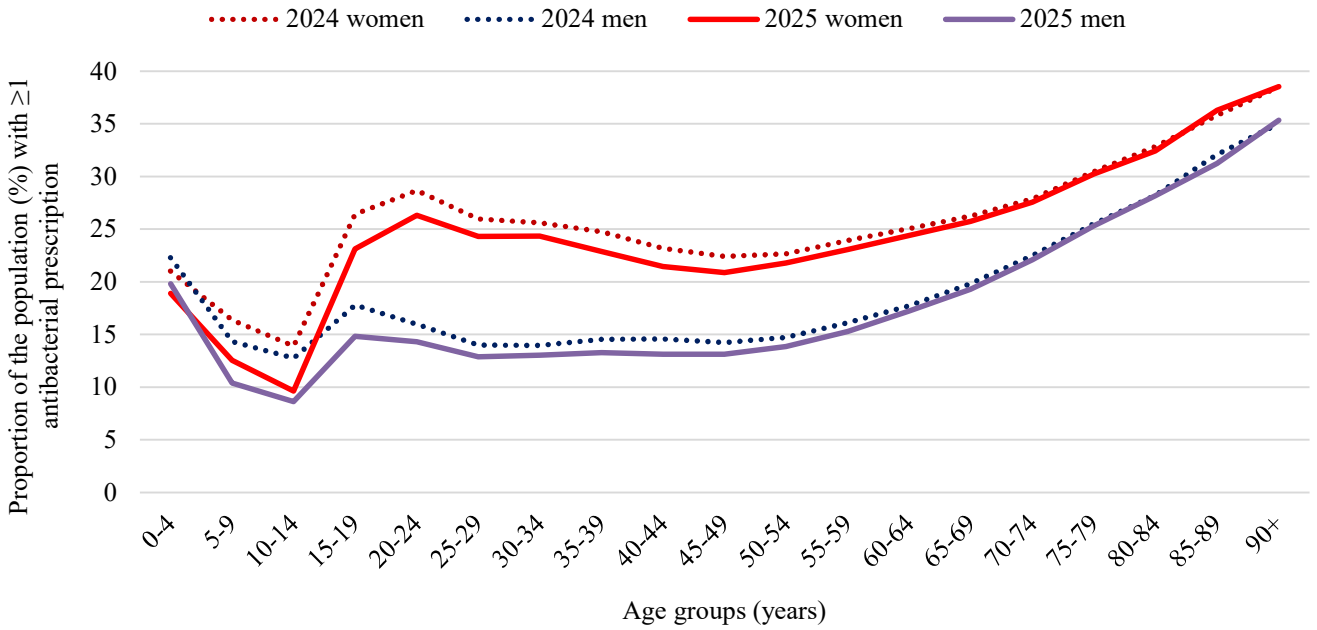

FIGURE 19. Proportion (%) of the population with at least one dispensed antibacterial prescription (one-year prevalence) in primary care, by gender and age group in Norway, 2024 (dotted line) and 2025 (whole line). Antibacterials include antibacterials for systemic use (ATC group J01, excl methenamine), vancomycin (A07AA09), fidaxomicin (A07AA12) and metronidazole (P01AB01). For age groups above 65+ figures are adjusted according to persons from these age groups living in long-term care institutions. Data from the Norwegian Prescribed Drug Registry (NorPD).

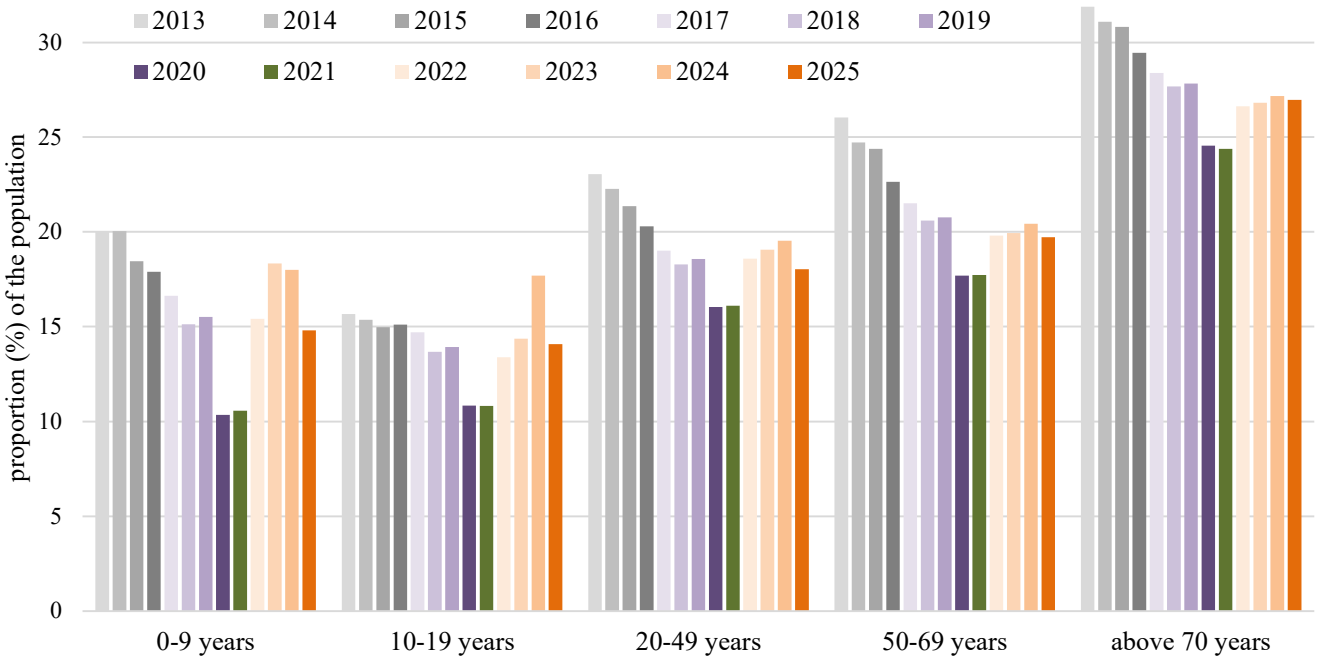

FIGURE 20. Proportion (%) of the population having dispensed at least one prescription of antibacterials (one-year prevalence) in primary care in Norway, 2013-2025. Antibiotics included are antibacterials for systemic use (ATC group J01, excl. methenamine). Data from the Norwegian Prescribed Drug Registry (NorPD).

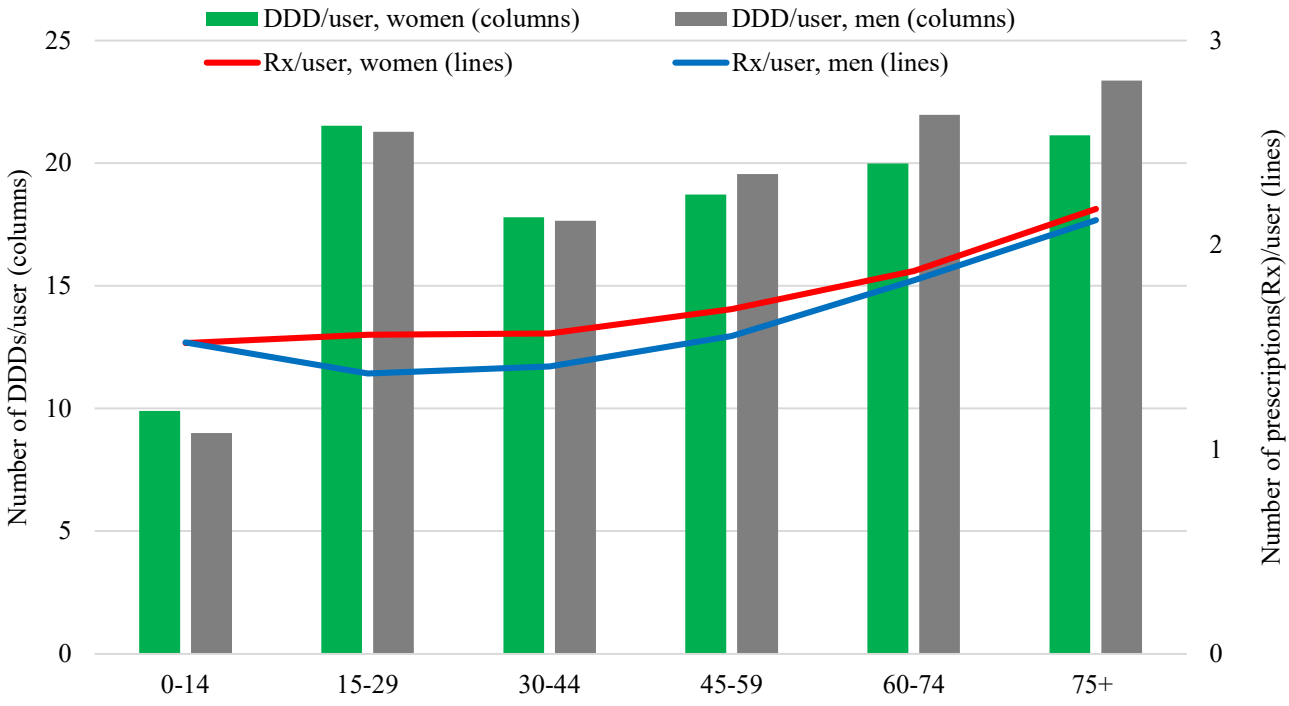

FIGURE 21. Mean number of DDDs per user and mean number of prescriptions (Rx) per user among users of antibacterials in ambulatory care by gender and age in Norway, 2025. Antibacterials included are antibacterials for systemic use (ATC group J01, excl. methenamine). Data from the Norwegian Prescribed Drug Registry (NorPD).

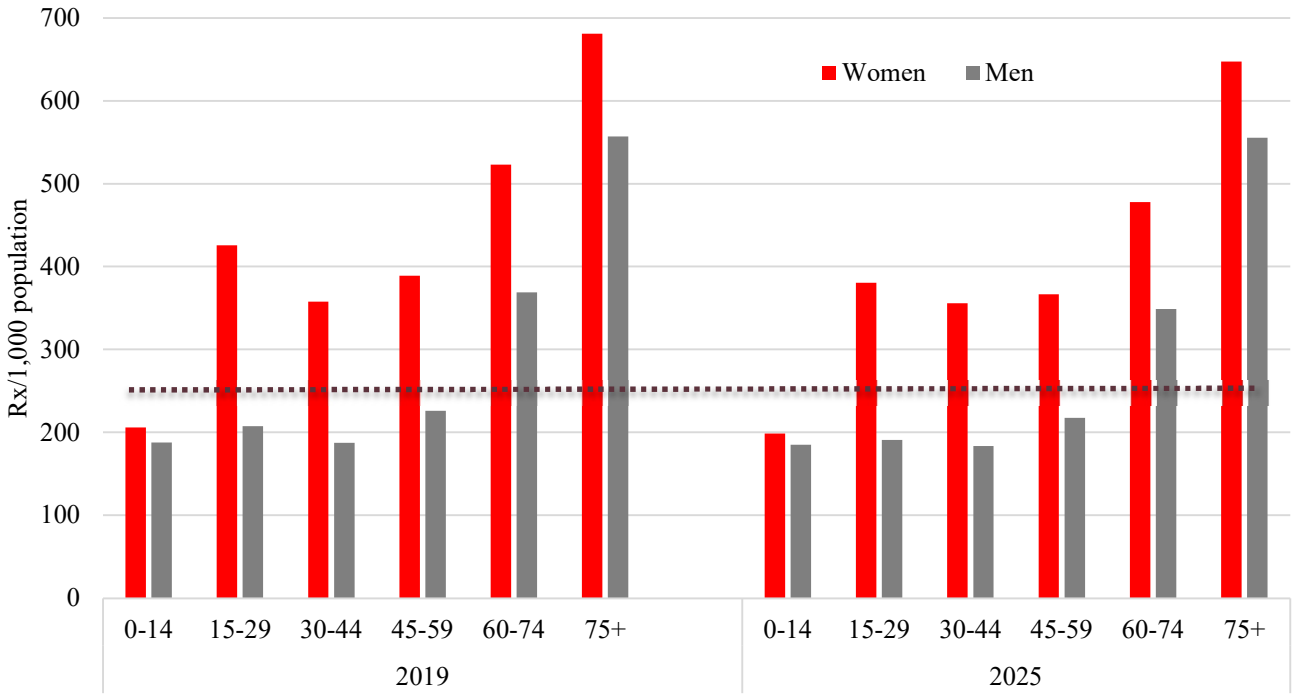

FIGURE 22. Mean number of prescriptions (Rx)/1,000 population of antibacterials (J01, excluding methenamine in ambulatory care by gender and age groups; 2019 and 2025. The dotted black line indicates the target of 250 prescription/1,000 population/ year. Data from the Norwegian Prescribed Drug Registry (NorPD).

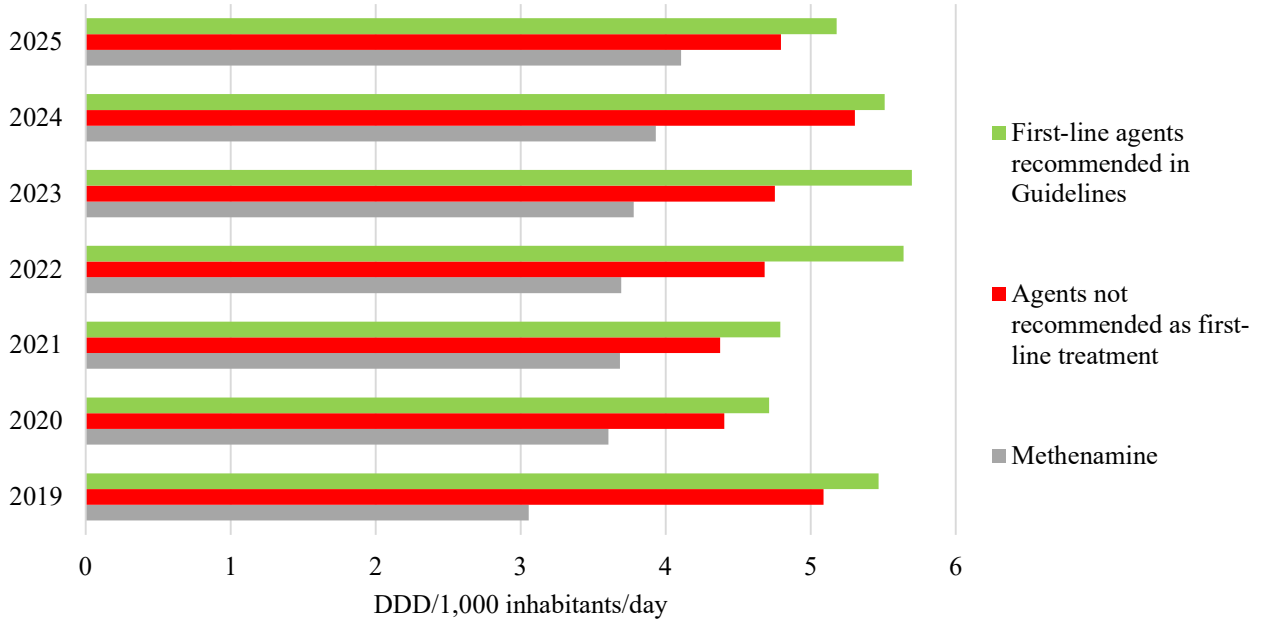

FIGURE 23. Consumption of antibacterial agents for systemic use (ATC group J01) in outpatients. Aggregated in three groups; a) Recommended as first-line treatment in the guidelines for primary care (phenoxymethylpenicillin for respiratory tract infections, pivmecillinam, trimethoprim and nitrofurantoin for urinary tract infections and dicloxacillin for skin infections), b) Not first-line treatment includes all other antibiotics in J01, excluding methenamine, and c) Methenamine. Measured as number of DDD/1,000 inhabitants/day. Data from the Norwegian Prescribed Drug Registry (NorPD) (i.e. sales to health institutions and prescribers' own practice not included).

Antibiotic prescribing in dentistry

Dentists accounted for 5.6%, as measured in DDDs, of all antibiotics prescribed in outpatient care in 2025. Antibiotic use associated with dental prescribing, measured as DDD/1,000 inhabitants/day, was 4% lower in 2025 than in 2012, but 16% higher than in 2019 (Figure 24). Phenoxymethylpenicillin accounted for the largest share of DDDs, followed by amoxicillin, oral metronidazole, and clindamycin. In 2025, these substances accounted for 80%, 9%, 5% and 4%, respectively, of all DDDs of antibiotics prescribed by dentists. The proportion of phenoxymethylpenicillin increased from around 75% in 2019 to 80 % in 2025. This may reflect increased adherence to national guidelines.

The one-year prevalence of use has remained stable. Around 2.3% of the population had at least one antibiotic dispensed from a dental prescription during 2025. This corresponds to approximately 128,000 unique persons.

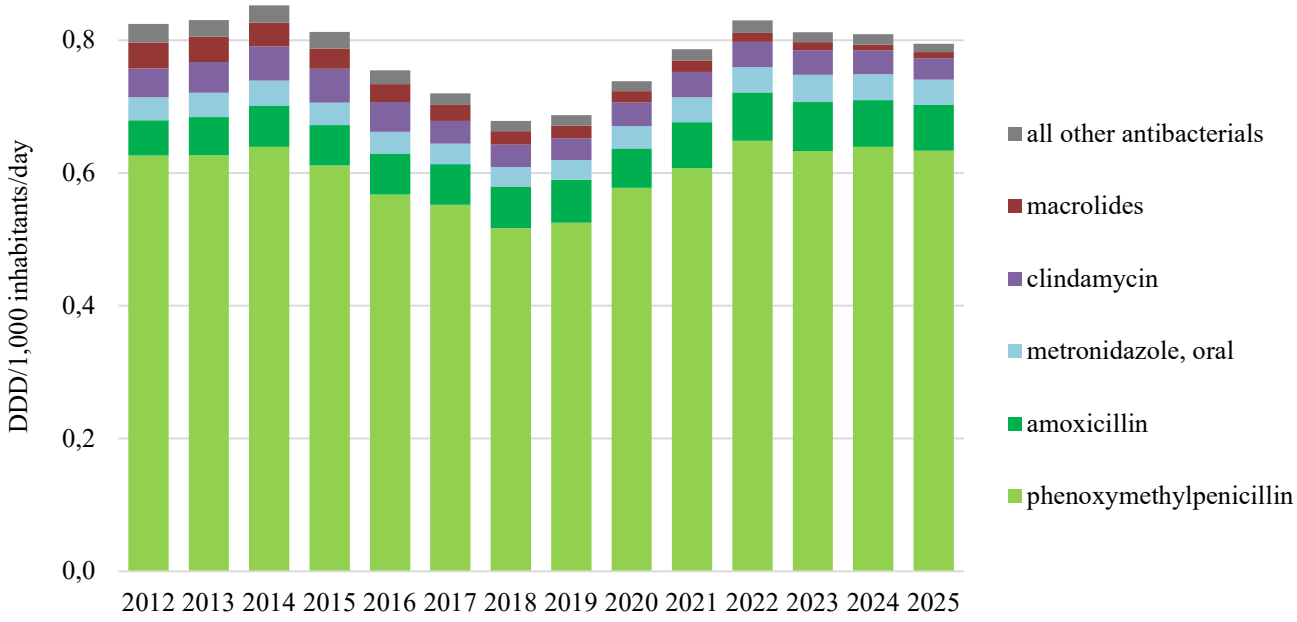

FIGURE 24. Antibiotics (J01 and oral metronidazole (P01AB01), prescribed by dentists in Norway for the years 2012-2025, measured in DDDs per 1,000 inhabitants per day. Data from the Norwegian Prescribed Drug Registry (NorPD).

Antibiotic consumption in nursing homes

Antibiotic use in nursing homes has not been included in the national monitoring program, except through point prevalence studies, due to difficulties in collecting national data. Consequently, only estimated antimicrobial consumption in nursing homes (long-term care facilities) is available. The estimation method has been improved and is described in Appendix 2 and in a thematic box (page 47).

The nursing home share of total antibiotic use has decreased over time and is estimated to be around 4% of total use, which is lower than the corresponding share for dental care. The initiation of an antibiotic stewardship programme targeting nursing homes in 2016, RASK (Riktig antibiotikabruk i sykehjem/kommunale helseinstitusjoner) together with updated guidelines for antibiotic use in nursing homes, may have contributed to this reduction (Figure 25).

In 2025, the five substances most used in nursing homes, as measured in DDDs, were pivmecillinam, phenoxymethylpenicillin, co-trimoxazole, amoxicillin and dicloxacillin. Their combined share of total (J01, excluding methenamine) DDDs in nursing homes increased from 61% in 2014 to approximately 70% in 2025. In 2025, the urinary antiseptic agent, methenamine, accounted for 30% of all DDDs sold to nursing homes.

Antibiotic consumption in hospital care

In 2025, hospitals accounted for approximately 7.6% of total human antibacterial sales in Norway, measured in DDDs (J01 excl. methenamine, A07AA09, A07AA12 and P01AB01). The hospital share of total antibacterial use has increased slightly over time (Figure 25). Antibiotic use in hospitals (measured in DDDs/1,000 inhabitants/day) decreased by 5% compared with 2019 and was 9% lower than in 2012 (Figure 26). The temporary decrease in 2020-2021 was due to the Covid-19 pandemic, when elective surgeries were postponed, leading to fewer admissions and hospital bed days. Hospital antibiotic use patterns are generally stable from year to year, but use of selected broad-spectrum “indicator” antibiotics has declined since 2012. In 2025, these agents (defined as J01CR/DC/DD/DI/DF/DH/MA) accounted for 20% of total use, down from 26% in 2012. Beta-lactamase sensitive penicillins (J01CE) represented 14% of total use in 2025, the lowest share observed during the 2012-2025 period (Figure 26).

Overall, penicillins (J01C) accounted for 48% of hospital antibiotic use in 2025, measured in DDDs (J01CE 14%,

J01CA 12%, J01CF 17%, and J01CR 6%). Cephalosporins were the second-largest group, accounting for 18% of use, the dominant subgroup being 3rd generation cephalosporins (J01DD). In 2025, twelve antibiotics accounted for 75% of all DDDs for systemic antibiotic use in hospitals (i.e. J01, A07AA09, A07AA12 and P01AB01). These were cloxacillin, benzylpenicillin, cefotaxime, cefazolin, gentamicin, piperacillin/tazobactam, doxycycline, co-trimoxazole, ampicillin, pivmecillinam, phenoxymethylpenicillin and amoxicillin.

When data from national point prevalence surveys (PPS) are extrapolated to sales data, prophylactic use is estimated to account for approximately 8% of hospital antibiotic consumption in 2015, increasing to 11% in 2025 (Figure 27). These estimates should be interpreted with caution, as they combine indication data from PPS with aggregated sales data.

Hospital antibiotic use is often presented as DDD/1,000 inhabitants/day, but activity-adjusted metrics such as DDD/100 bed days and DDD/100 admissions are more informative for comparisons between hospitals (Figure 28). While length of stay (LOS) in Norwegian hospitals has remained stable in recent years, the number of admissions and bed days has declined. This likely reflects a shift towards day-care and outpatient treatment, rather than reduced overall hospital activity. Proportional change will vary according to the measures used. Figure 29 illustrates how reduction in bed days influences antibiotic use statistics.

Figure 30 shows trends for seven antibiotic groups primarily used in hospitals. Piperacillin/tazobactam use has increased over several years but declined markedly in 2017 and 2018 due to a nationwide shortage, followed by an increase in 2020 and 2021. In 2025, use of penicillins with beta-lactamase inhibitors, 3rd generation cephalosporins, and aminoglycosides increased compared with 2024. Since 2016, aminoglycoside use has increased by 64%, in line with guideline recommendations. Glycopeptide use has also increased by 32%. Carbapenem use peaked in 2014 and again in 2022 but has since decreased. This may partly reflect updated guidelines and the implementation of antibiotic stewardship programmes in Norwegian hospitals from 2016.

Over the past three years, an increase in patients with infections caused by carbapenemase-producing organisms (CPO) in Norway may have contributed to increased use of antibiotics targeting carbapenemase-producing Gram-negative bacteria in Norwegian hospitals. Figure 31 illustrates the increased use of last-resort antibiotics.

The WHO AWaRe classification of antibacterials into Access-, Watch- or Reserve-antibiotics is a useful tool for promoting responsible antibiotic use. WHO recommends that Access group antibiotics should account for at least 60% of total national antibiotic consumption. In Norwegian hospitals, the proportion of Access antibiotics increased from 70% in 2012 to 75% in 2025. During the same period, the share of Reserve antibiotics, while still low, increased from 0.4% to 0.7%. Within this group, linezolid was the most frequently used agent, representing 46% of total DDDs, followed by aztreonam (28%), Figure 32.

In Norway, mainly parenteral formulations of 2nd, 3rd and higher generation cephalosporins and carbapenems are licensed, and these are primarily used in hospitals. However, few antibiotics are used exclusively in the hospital setting. Figure 33 illustrates the hospital share of selected ATC 4th level antibiotic groups. Antibiotics with a high proportion of hospital use are typically reserved for severe infections and are therefore particularly important from an antibiotic stewardship perspective, including outside hospitals. For aminoglycosides, colistin and aztreonam, inhalation therapy is used for a small number of patients in ambulatory care. However, the inhalation part accounts for a high share of total DDD for the substance. Among antibiotics used outside hospitals, inhalation therapy accounted for 99% of colistin, 90% of aminoglycoside, and 84% of aztreonam DDDs. As stewardship efforts primarily focus on systemic use, only parenteral DDDs of these agents are included in Figure 33. One explanation for parenteral use outside hospitals is the increasing use of outpatient parenteral antimicrobial therapy (OPAT) - the administration of intravenous (IV) antibiotics outside the hospital setting, e.g. at home or an outpatient clinic. While this represents a positive development, it remains important that OPAT is delivered by personnel with appropriate expertise in antibiotic stewardship.

Figure 34 shows the distribution between “preferred antibiotics”, largely reflecting standard treatment regimens in national guidelines, and antibiotics considered to drive antimicrobial resistance, across Norwegian hospitals. The proportion of preferred antibiotics varies between hospitals, from 57% to 79%. There are substantial variations between hospitals in both the volume of antibiotic use (measured in DDD/100 bed days), and the types of antibiotics prescribed.

The five groups of broad-spectrum antibiotics targeted in the former National Action Plan have been used as quality indicators in antibiotic stewardship programmes in Norwegian hospitals/health trusts, Figures 35 and 36. Overall use of these agents in 2025 was 3% lower than in 2016. The decline observed in 2017-2021 was largely related to the piperacillin/tazobactam shortage, during which hospitals used more beta-lactamase sensitive and resistant penicillins (J01CE and J01CF) instead. The low levels in 2020 and 2021 were influenced by the Covid-19 pandemic and case-mix changes. The reasons for the low use observed in 2019 remain speculative but may reflect improved adherence to established guidelines. The variations observed between hospitals cannot be explained by differences in activity or patient mix alone, and are likely influenced by local prescribing practices, Figure 36. Prior to the Covid-19 pandemic, total hospital antibiotic use remained stable (DDD/1,000 inhabitants/day), but prescribing patterns shifted towards increased use of narrow-spectrum agents - a trend that has continued after the pandemic. Narrow-spectrum penicillins, recommended in national guidelines, are widely used.

DDD-metrics should be interpreted with caution. For several narrow-spectrum penicillins, the WHO-defined DDD is lower than the doses commonly prescribed in Norway, meaning DDD-based metrics may underestimate actual use. In addition, combination therapy with narrow-spectrum penicillins and aminoglycosides may generate higher total DDDs than broad-spectrum monotherapy with cephalosporins or carbapenems. This may give a misleading impression of excessive use despite reflecting guideline-adherent prescribing

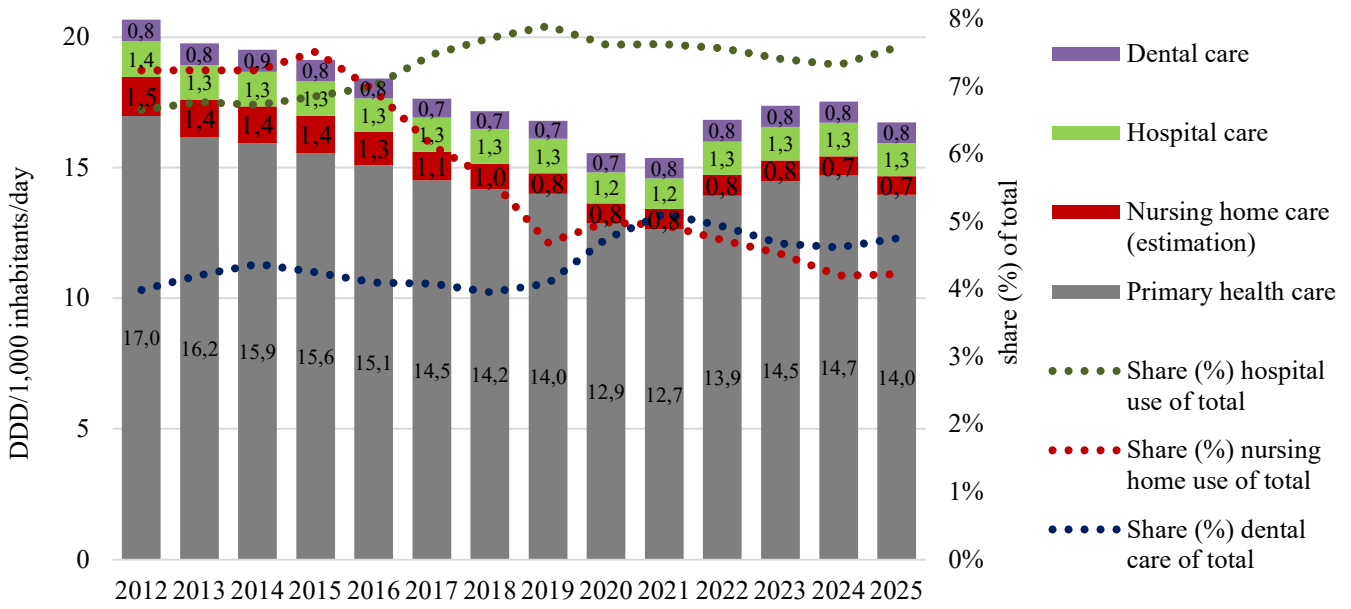

FIGURE 25. Consumption of antibacterial agents for systemic use (J01, A07AA09, A07AA12 and P01AB01) in Norway in primary care, nursing homes, hospitals and dental care 2012-2025, measured in DDD/1,000 inhabitants/day. Total use in nursing homes is estimated, as consumption in nursing homes is not trackable through a single national data source. For each year, total consumption is estimated by extrapolating from wholesales data on the amount of antibacterial agents purchased by the nursing homes covered by the Norwegian drug wholesales statistics database, based on the proportion of nursing homes represented in the data. In 2025, the sales data covered approximately 55% of Norwegian nursing homes. Data from Norwegian Drug Wholesales Statistics Database, Norwegian Prescribed Drug Registry (NorPD) and Hospital Pharmacies Drug Statistics Database.

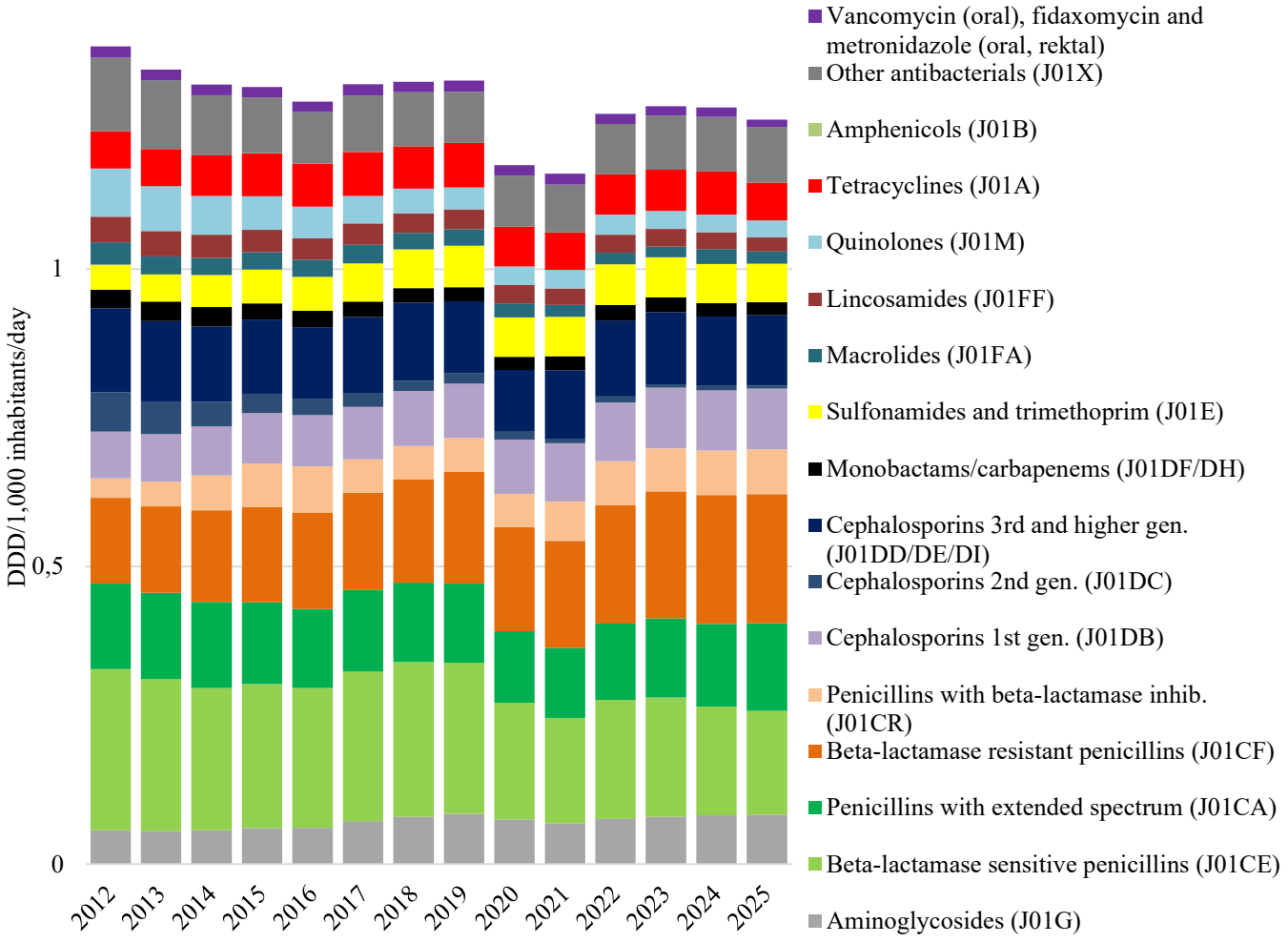

FIGURE 26. Use of antibacterial agents for systemic use (J01), vancomycin (A07AA09), fidaxomicin and oral metronidazole (P01AB01) in Norwegian hospitals 2012-2025, measured as DDD/1,000 inhabitants/day. Data from Hospital Pharmacies Drug Statistics Database.

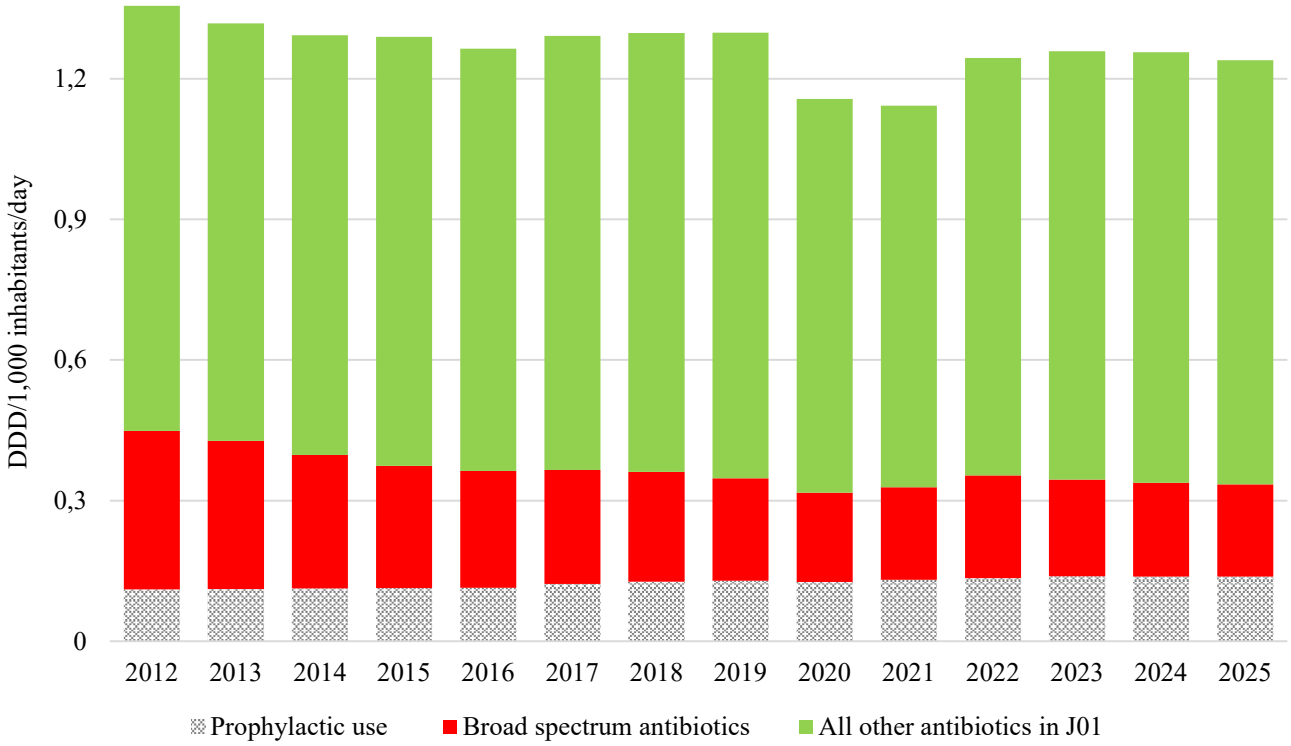

FIGURE 27. Proportions of prophylactic antibacterial agents for systemic use, broad-spectrum and other antibiotics in Norwegian somatic hospitals 2012-2025, measured as DDD/1,000 inhabitants/day. The volume of antibiotics for prophylactic use is estimated. Information on prescribing indications from the national point prevalence surveys were used to recalculate the sales data. Included in prophylactic use are all DDDs of the 1st gen cephalosporins cefazolin and cefalotin and 40% of the DDDs from metronidazole i.v. and co-trimoxazole, respectively. Broad-spectrum antibiotics are defined as J01CR, J01DC/DD/DI/DH), J01M, J01XA, J01XX-08, -09, -11, and J01AA12. Data source; Hospital Pharmacies Drug Statistics Database.

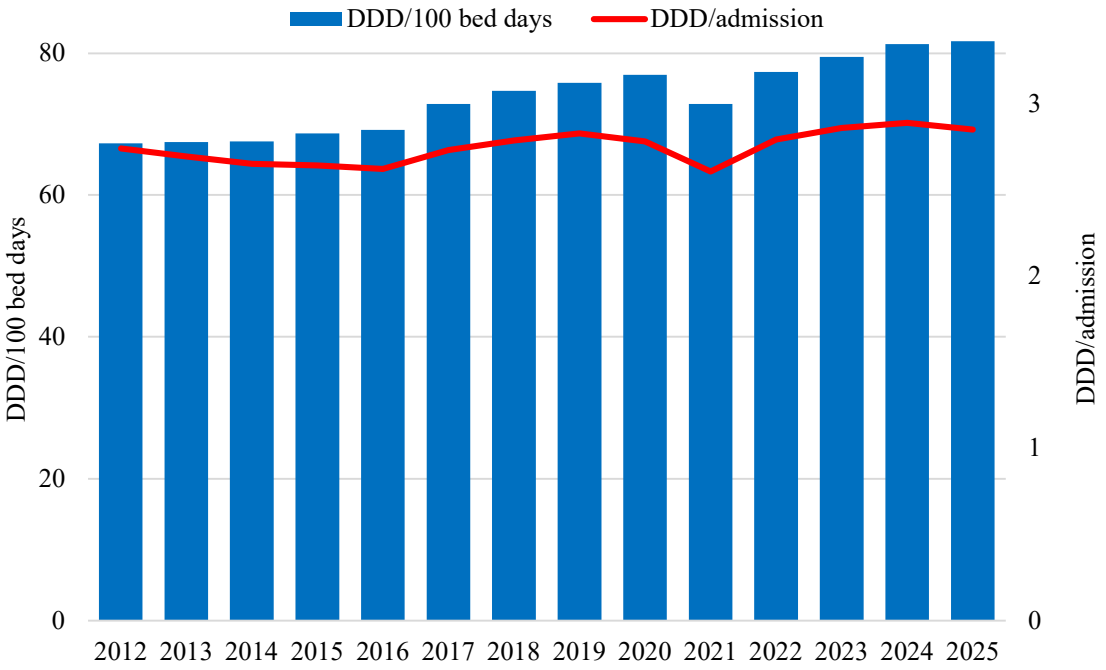

FIGURE 28. Total use of antibiotics in Norwegian hospitals (somatic) 2012-2025, in DDD/100 bed days and in DDD/admission. Antibiotics are defined as J01 antibacterials for systemic use, A07AA09 vancomycin (oral), A07AA12 fidaxomycin and P01AB01 metronidazole (oral and rectal). Data source; Hospital Pharmacies Drug Statistics Database and the Norwegian Patient Register.

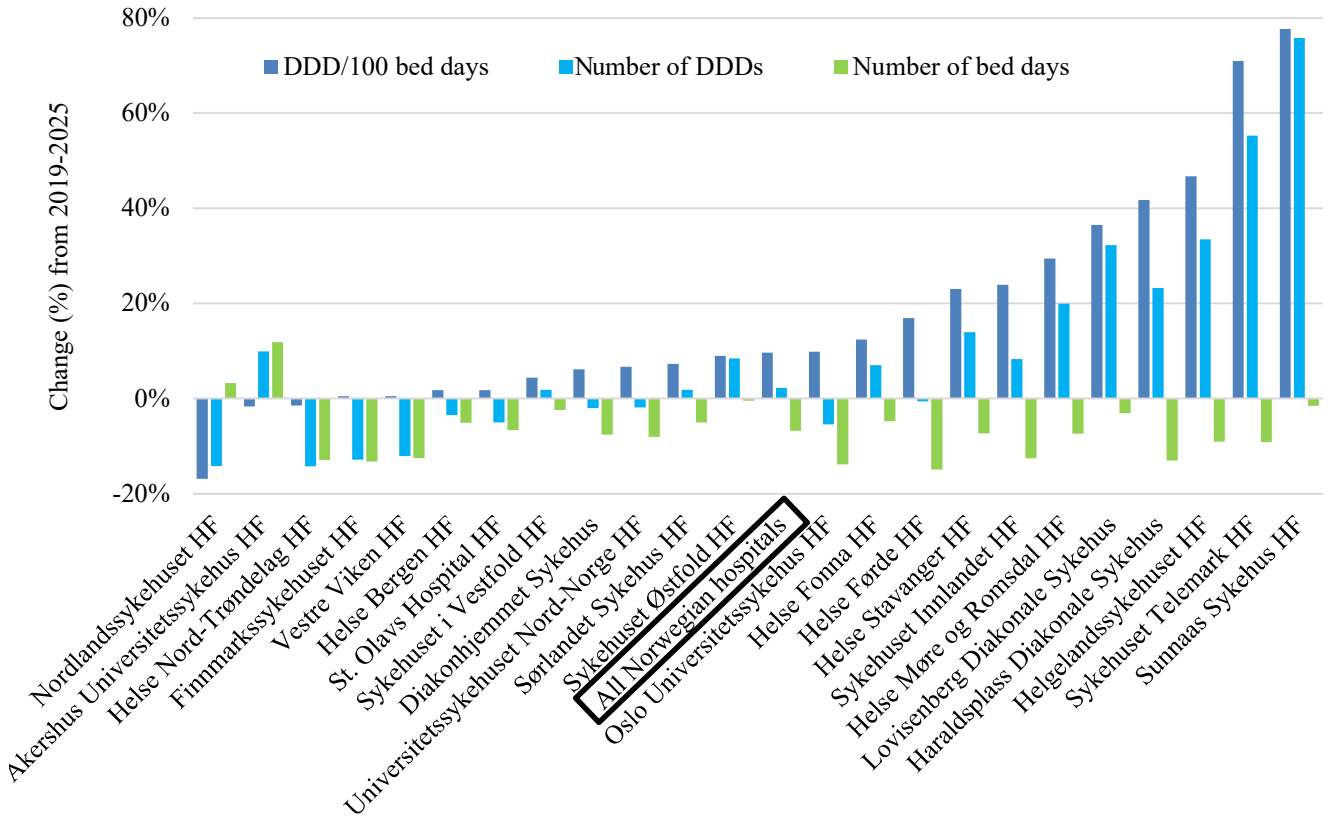

FIGURE 29. Proportional change will vary according to the measures used. Antibiotic usage in hospitals is often presented as DDD/100 bed days, but total number of DDDs may also be used as a measure. The number of bed days in Norwegian hospitals has been reduced by 7% since 2019. The figure visualises the impact of the reduction in bed days on antibiotic consumption statistics for five broad-spectrum antibiotic ATC-groups (J01CR, J01DC, J01DD, J01DH and J01M) in Norwegian hospitals 2019-2025. Data source; Hospital Pharmacies Drug Statistics Database and the Norwegian Patient Register.

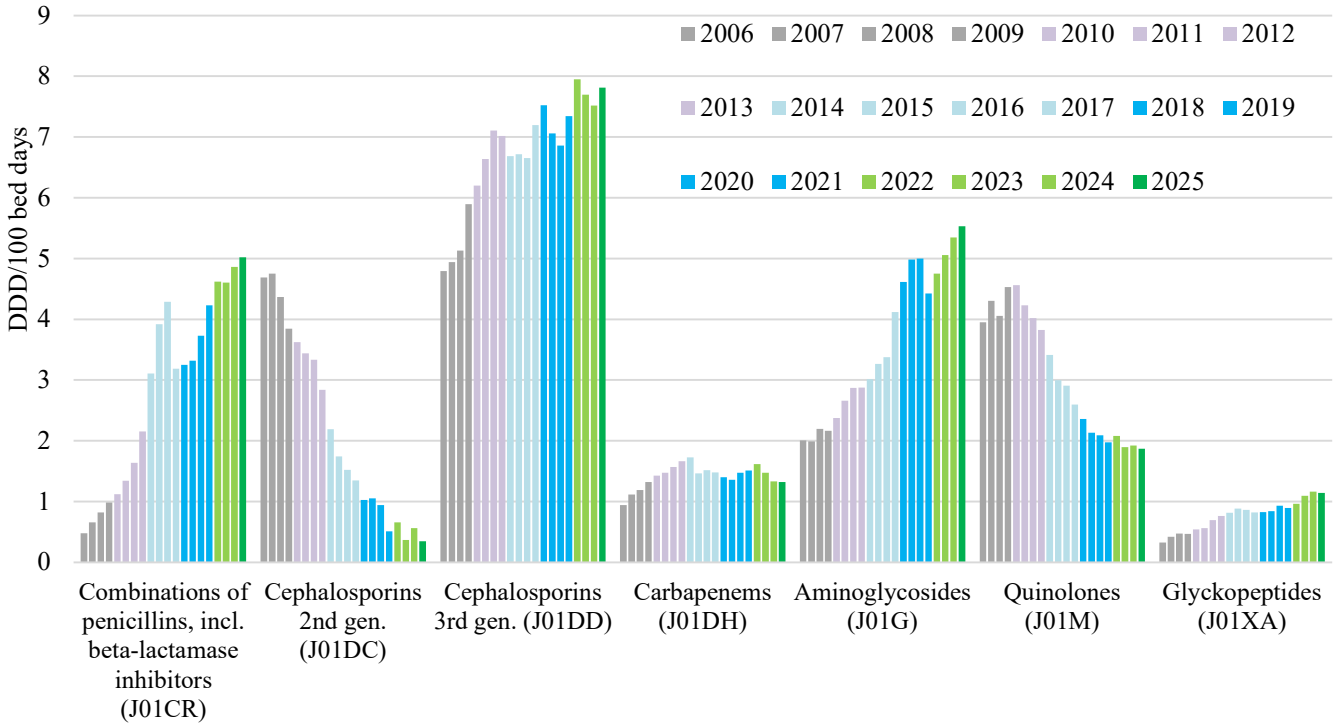

FIGURE 30. Consumption of seven antibacterial agents for systemic use (ATC J01CR, ATC group J01DC, J01DD, J01DH, J01G, J01M and J01XA) in Norwegian hospitals 2006-2025, measured in DDD/100 bed days. Data source; hospital pharmacies drug statistics database and the Norwegian Patient Register.

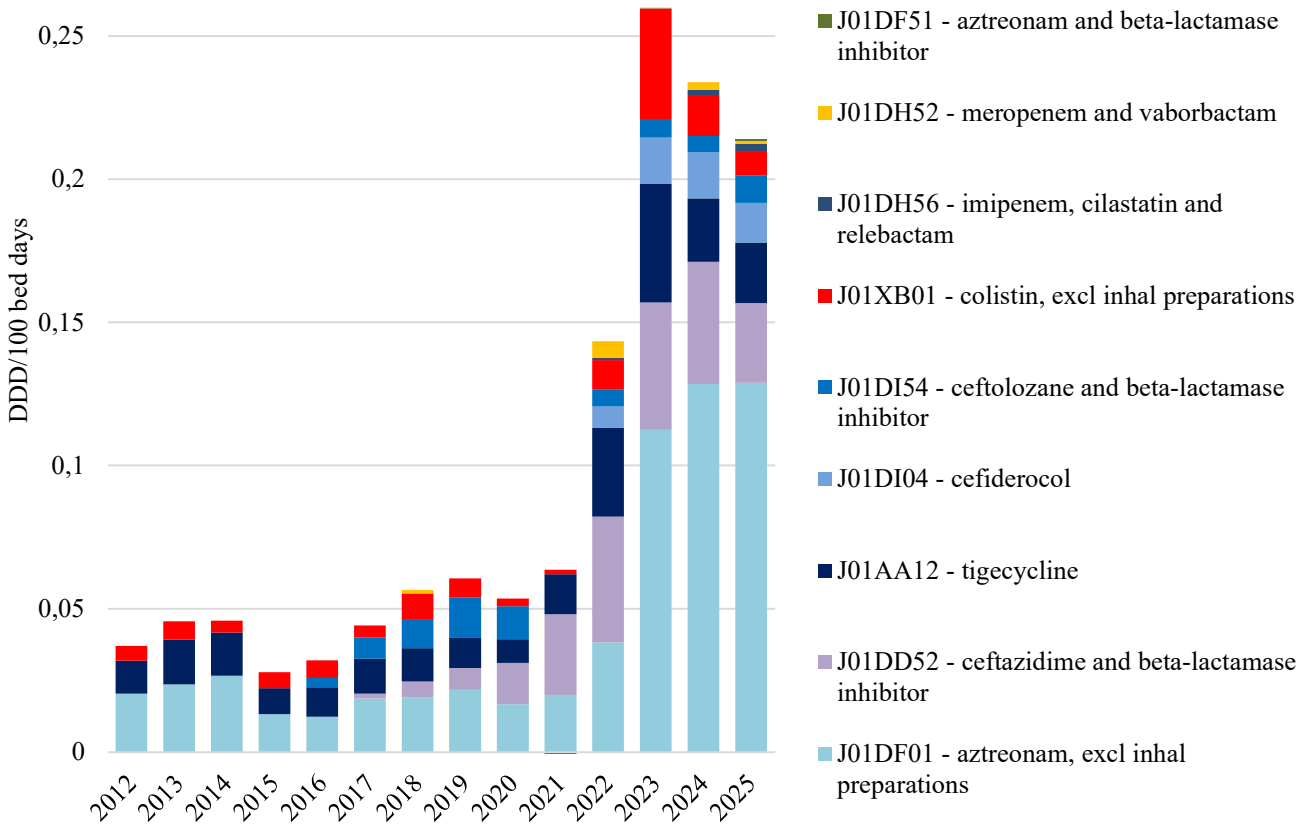

FIGURE 31. Antibiotics that are indicated for carbapenemase-producing Gram-negative bacteria in Norwegian hospitals (somatic) 2012-2025, measured in DDD/100 bed-days. Antibiotics in ATC group J01 are included. Inhalation formulations containing aztreonam and colistin are not included in the count. Data source; Hospital Pharmacies Drug Statistics Database and the Norwegian Patient Register.

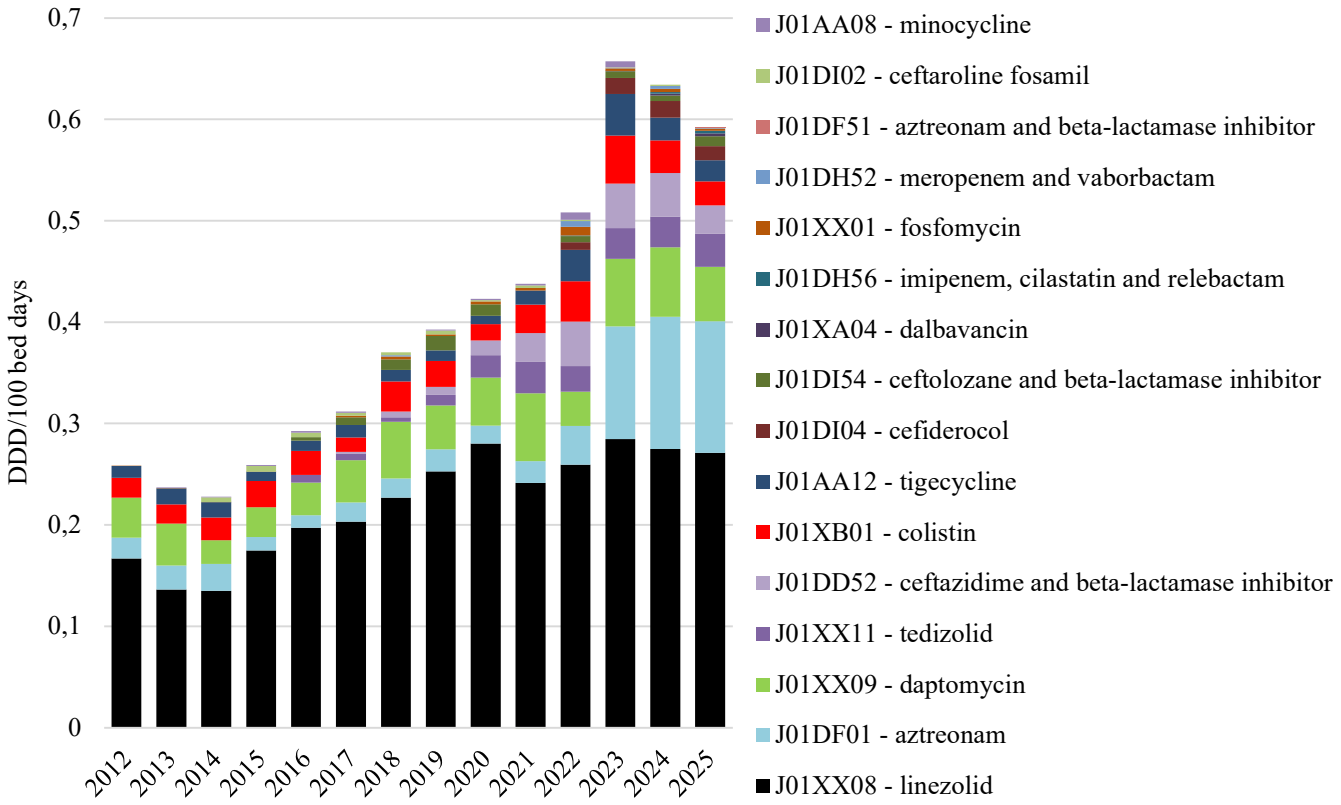

FIGURE 32. Reserve antibiotics (as defined according to the WHO AWaRe 2025 classification) used in Norwegian hospitals (somatic) 2012-2025, in DDD/100 bed days. Only antibiotics in ATC group J01 are included. Inhalation formulations containing aztreonam and colistin are included in the count. Data source; Hospital Pharmacies Drug Statistics Database and the Norwegian Patient Register.

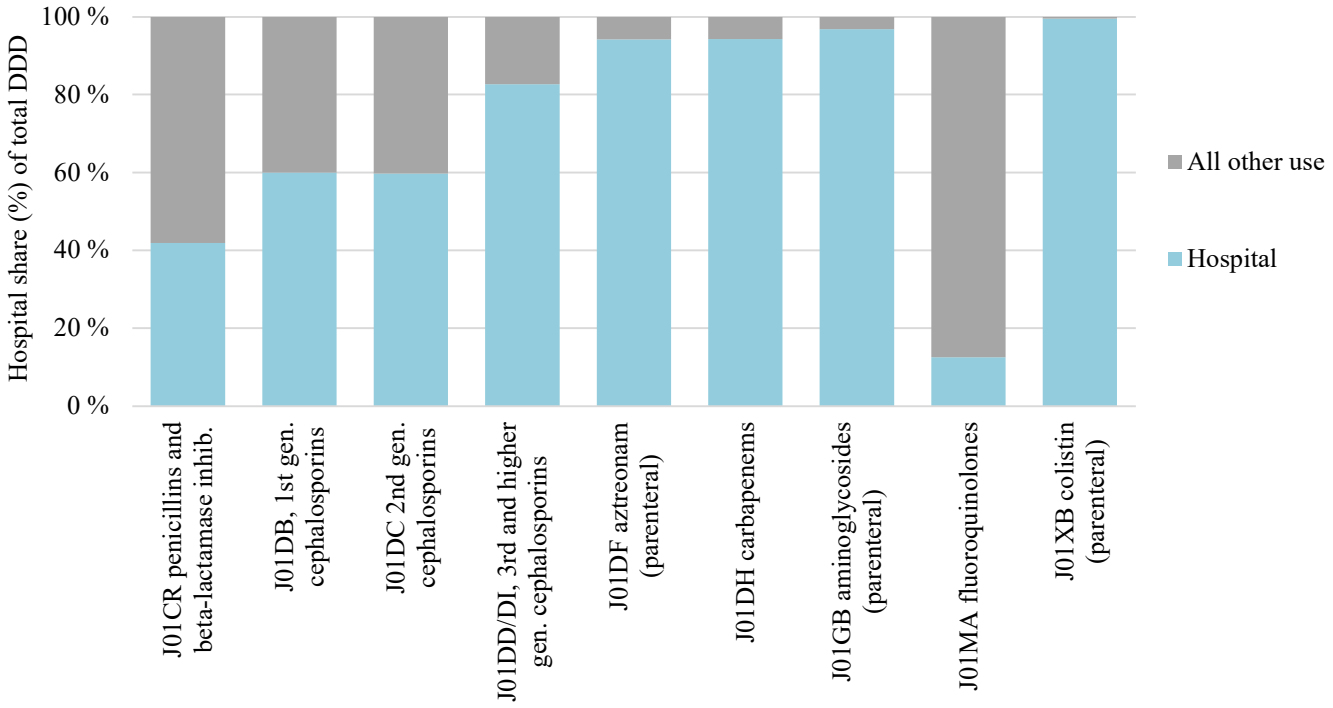

FIGURE 33. Proportion (%) of total sales as measured in defined daily doses (DDD) attributable to hospitals in 2025 shown for selected antibiotic groups; the five groups defined as broad-spectrum antibiotics in Norway (J01CR, J01DC, J01DD/DI, J01DH and J01M), in addition J01DB, J01DF, J01GB and J01XB. For ATC groups J01DF, J01GB and J01XB only parenteral forms are included. Data source; Norwegian Drug Wholesales Statistics Database and the Hospital Pharmacies Drug Statistics Database.

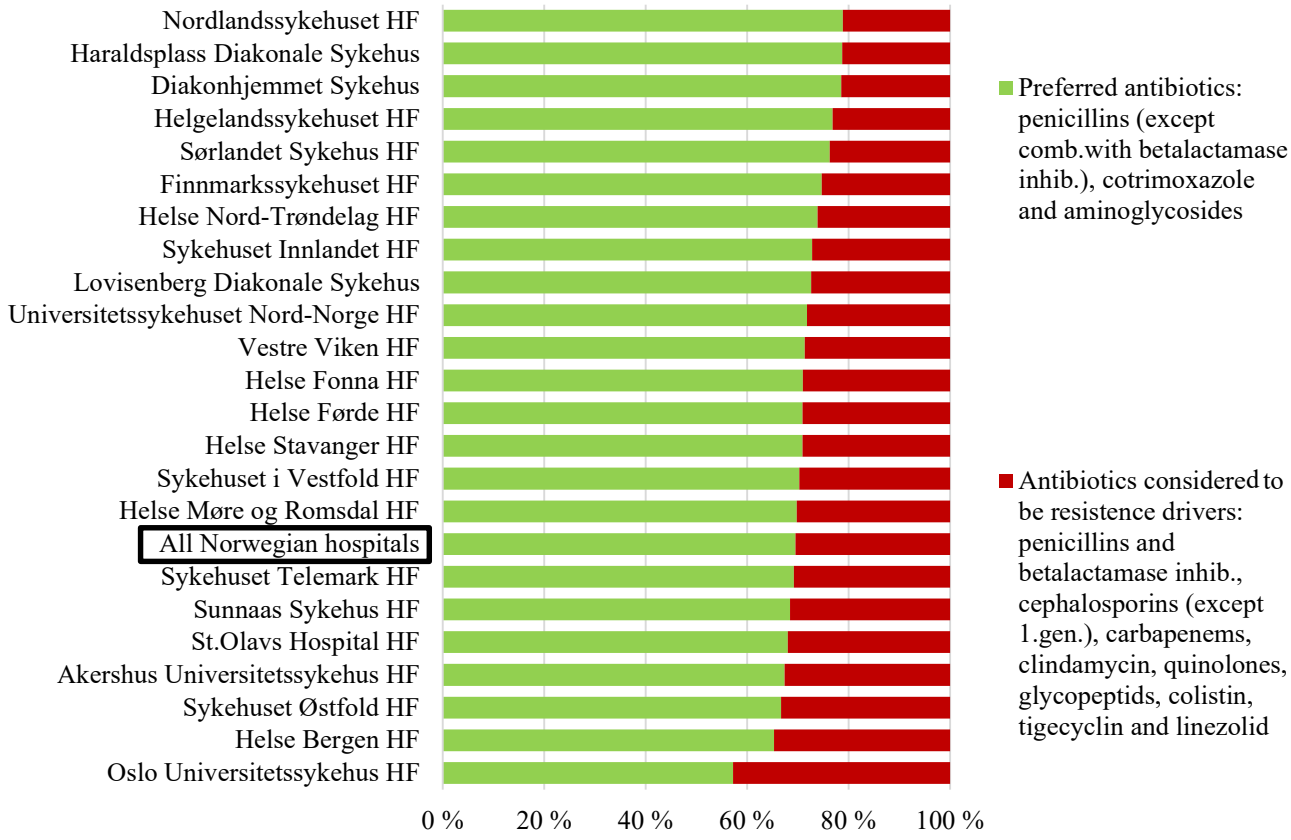

FIGURE 34. Proportions (% of DDDs) of preferred antibiotics (green part of the column) and antibiotics that are considered to be drivers of antibiotic resistance (red part i.e. belonging to ATC groups J01CR, J01DC, J01DD, J01DE, J01DI, J01DH, J01M, J01XA, J01XB, J01AA12, J01FF01 and J01XX08) in Norway, presented per hospital/health trust in 2025. 1st gen. cephalosporins and tetracyclines are not included as they in hospitals mainly are used for surgical prophylaxis. Metronidazole is also excluded from the figure because it does not readily fit either of the descriptions "preferred" or "resistance driver", and there are no alternative drugs mainly targeting anaerobic bacteria. Data source; Hospital Pharmacies Drug Statistics Database.

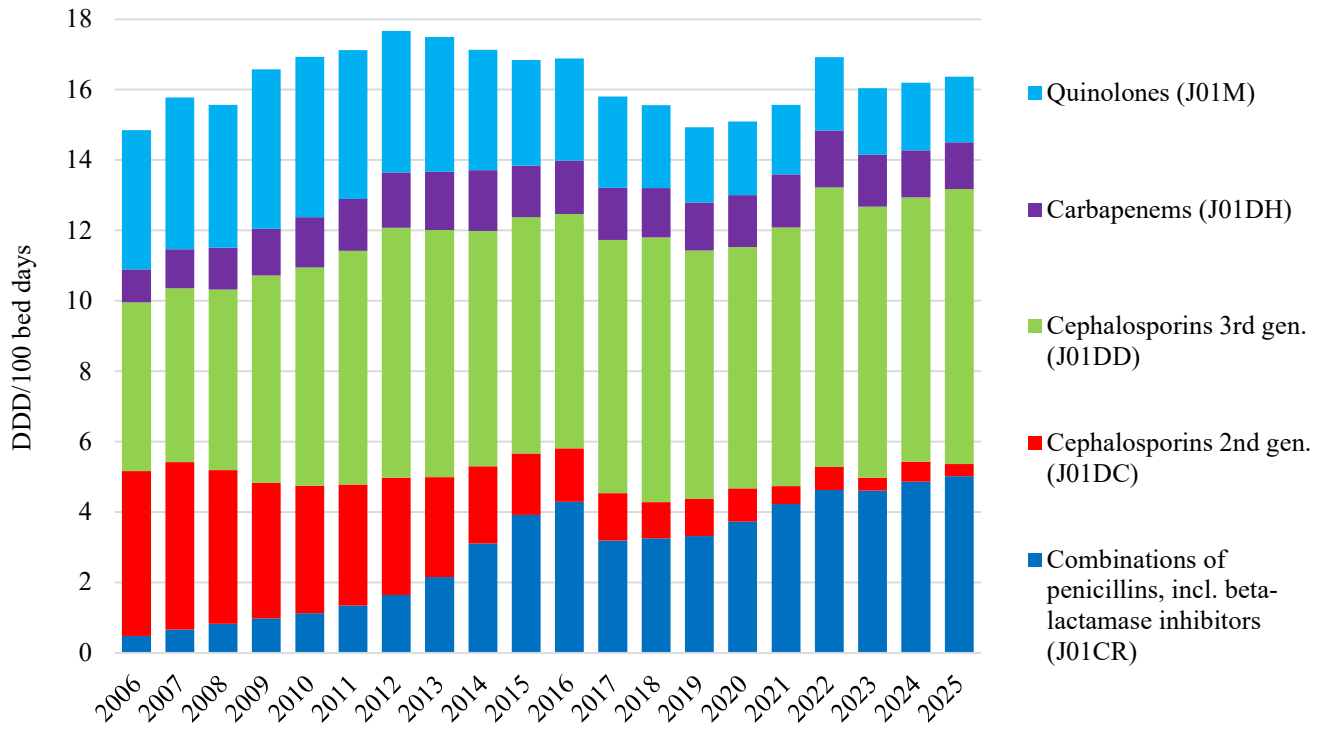

FIGURE 35. Consumption of selected antibacterial agents for systemic use (belonging to ATC-groups J01CR, J01DC, J01DD, J01DH and J01M) in Norwegian hospitals 2006-2025, in DDD/100 bed days. Data source; Hospital Pharmacies Drug Statistics Database and the Norwegian Patient Register.

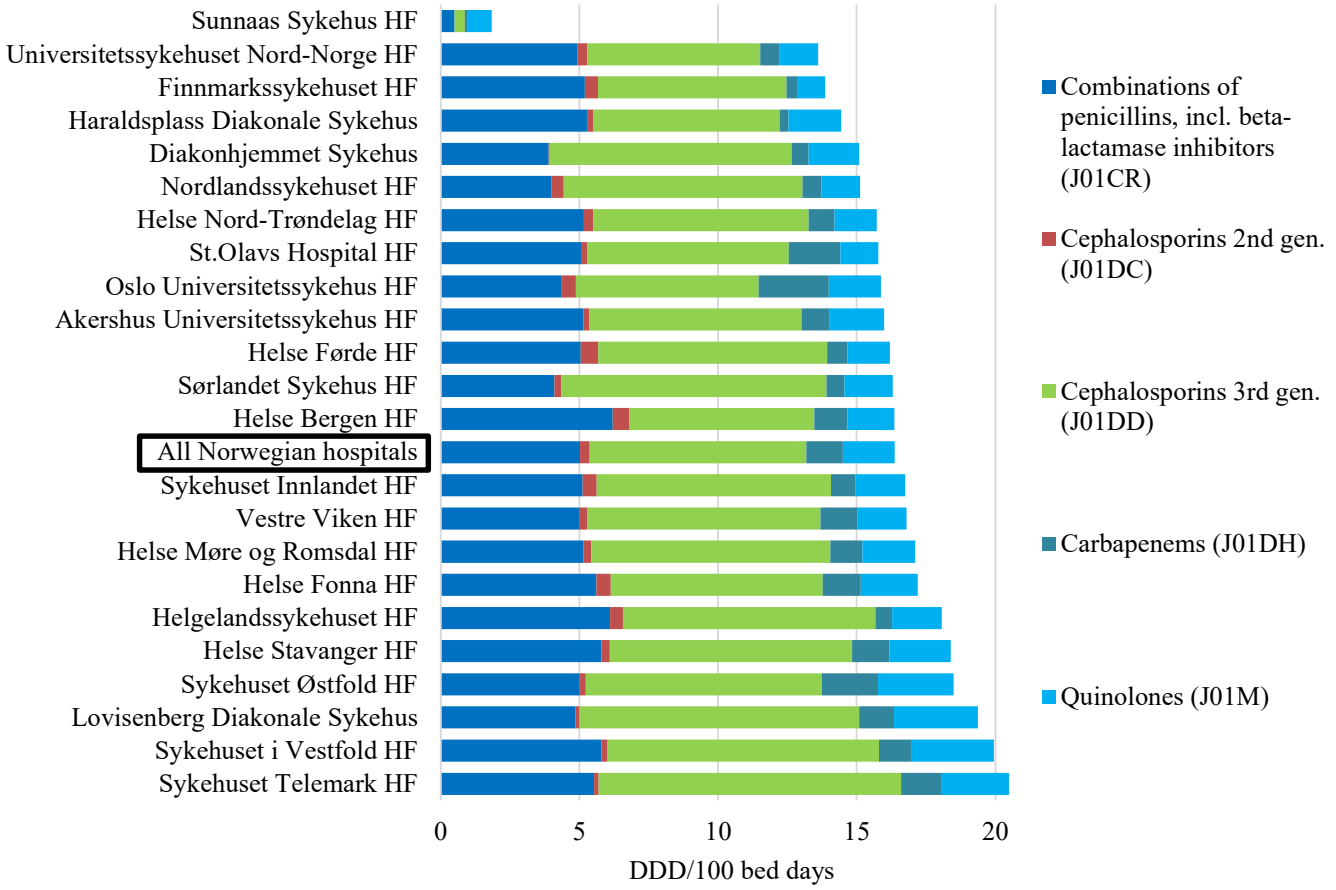

FIGURE 36. Consumption of selected antibacterial agents for systemic use (belonging to ATC groups J01CR, J01DC, J01DD, J01DH and J01M) in Norway, presented per hospital/health trust, in 2025, measured in DDD/100 bed days. All hospitals, except Sunnaas Sykehus, are acute care hospitals. Data source; Hospital Pharmacies Drug Statistics Database and the Norwegian Patient Register.

Antibiotic use patterns in Norwegian nursing homes – A new method for collecting data on antibiotic usage in nursing homes

Over years, very rough estimates of antibiotic use in Norwegian nursing homes have been available. The former AMR strategy and National Action Plan addressed the lack of antibiotic usage data and antibiotic stewardship programmes (AMS) in nursing homes. The intervention RASK (Riktigere bruk av antibiotika i sykehjem/kommunale helseinstitusjoner) was initiated by The Antibiotic Centre for Primary Care, utilising antibiotic sales data from wholesalers in an AMS programme developed for nursing homes. There is no unique nursing home identifier that must be used when purchasing antibiotics. This has made it particularly resource-intensive to produce antibiotic reports for each nursing home. Moreover, we are still not able to produce a trustworthy national overview on the use of antibiotics in Norwegian nursing homes. This obvious lack of data is hampering the ability to evaluate effect of campaigns and national programmes and further development of effective national AMS programmes in the nursing home sector.

Antibiotic usage data is essential for AMS programmes. For individual nursing homes there are two national programmes tracking antibiotic use; NOIS-PIAH – national point prevalence surveys, available since 2016, and the mentioned quality improvement programme RASK, initiated in 2016, aiming to promote appropriate antibiotic prescribing.

RASK has been shown to be a successful tool (1). Drug use data from RASK is only available for the participating nursing homes (approximately 30% of all Norwegian nursing homes), and no national overview is available. Moreover, the harvesting of antibiotic data for the programme has been shown to be time-consuming and cumbersome. Around 50% of Norwegian nursing homes participate in the NOIS-PIAH programme (2), but it is not known how they use the automated feedback report as the effect from the PPS surveys has not been assessed.

By legislation nursing homes may procure drugs directly from drug wholesalers or directly from local pharmacies (3). Data on direct sales from drug wholesalers to nursing homes is included in the Norwegian Drug Wholesales Statistics Database while medicines procured through local pharmacies are included in the NorPD.

As national data for nursing homes is urgently needed, we aimed to explore whether the Norwegian Drug Wholesales Statistics Database (4) may be used to estimate antibiotic use in nursing homes. Not all nursing homes procure medicines from wholesalers, but when a substantial number of nursing homes are included, estimates from this new method could give us a trustworthy overview and thereby provide possibilities for better national estimates. In addition, this method could ease the data collection for RASK.

The aim of this project was to explore whether information in the Norwegian Drug Wholesales Statistics Database is sufficient to provide good estimates for antibiotic use in nursing homes. If the data quality is good, our aim was to present estimates of national usage data for the nursing home sector.

Methods

We identified nursing homes in the Norwegian Drug Wholesales Statistics Database and captured antibiotic sales data measured in DDDs for antibiotics in ATC group J01 antibacterials for systemic use, A07AA09 oral vancomycin, A07AA12 fidaxomycin and P01AB01 oral metronidazole for the years 2015-2025.

To be able to compare by population, we collected the number of bed-days in order to present DDDs used per bed day. The number of bed-days for individual nursing homes were collected from KOSTRA (mandatory report from all Norwegian municipalities), including 865 nursing homes in their list (5). The number of bed-days reported were compared to bed-days reported through RASK participation. The KOSTRA data reported for 2025 were used as a standard, but if KOSTRA data were not available (e.g. in private nursing homes), the RASK information on bed-days was used. To validate the quality of data in the database, we compared the calculated DDD/100 bed-days for a specified period with similar data from RASK. The number of bed-days were used for comparisons, while for proportions all DDDs procured by nursing homes to the Drug Wholesales Statistics Database were included.

Results

The number of nursing homes purchasing medicines directly from wholesalers and included in the Norwegian Drug Wholesales Statistics Database has increased from 408 nursing homes in 2015 to 511 in 2025. Information on KOSTRA- or RASK-reported bed-days was available for 322 nursing homes in 2015, increasing to 437 in 2025. The database includes both public and private nursing homes that are geographically well distributed, except in Northern Norway, where very few nursing homes were included.

Data from selected individual nursing homes was compared in the Norwegian Drug Wholesales Statistics Database and in the RASK database. For the nursing homes compared, the number of DDDs included for individual nursing homes was equal for the compared time period.

The volume of use of antibiotics in Norwegian nursing homes has decreased over the years from 9.4 DDD/100 bed days in 2015 to 6.4 DDD/100 bed-days in 2025, Figure 37. Nine antibiotics represent the majority of use, Table 7. These are mainly narrow-spectrum antibiotics. Antibiotics for urinary tract infections (UTI-AB) dominate the pattern. Use of ciprofloxacin has been reduced over years, and use seems to be shifted to co-trimoxazole.

TABLE 7. The nine most commonly used antibiotics in Norwegian nursing homes shown as proportion of total DDDs of antibacterials for systemic use, oral vancomycin, fidaxomicin and metronidazole. Methenamine is excluded from the count. Antibiotics recommended as first-line antibiotics for urinary tract infections are compiled in the upper row.

	% of total DDD (excl. methenamine)			
	2015	2019	2023	2025
Pivmecillinam/trimethoprim/nitrofurantoin	33	30	30	30
Phenoxymetylpenicillin	16	19	18	16
Amoxicillin	10	10	10	11
Co-trimoxazole	7	10	11	11
Dicloxacillin	6	6	8	8
Doxycycline	6	6	5	5
Ciprofloxacin	8	5	4	3
Nine most commonly used antibiotics	**85**	**85**	**85**	**86**

The use of methenamine in nursing homes has decreased since 2015 when methenamine represented 40% of all DDDs purchased to nursing homes. In 2019, a large fall in utilisation was observed due to a 4-month drug shortage, Figure 37. Interestingly, the use of methenamine has been low since then. Since methenamine is used for prophylaxis of UTI and is used every day it still covers a large proportion of DDD utilised for infections in nursing homes, 29% in 2025.

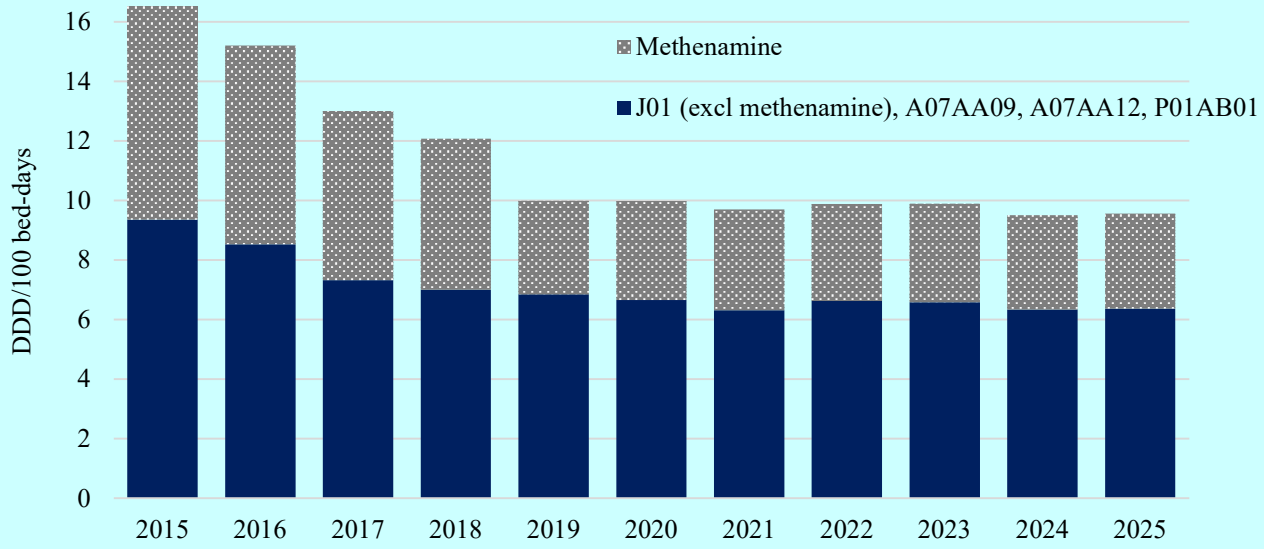

FIGURE 37. Sales of antibiotics in 2015-2025 as measured in DDD/100 bed-days. Antibacterials for systemic use, oral vancomycin and fidaxomicin, and oral metronidazole are included. The urinary antiseptic methenamine is shown separately. Data from the Norwegian Drug Wholesales Statistics Database.

Conclusions

Given the large number of nursing homes included in the Norwegian Drug Wholesales Statistics Database, we may today achieve good estimates for national use, estimates that likely will be close to real use. The quality of data seems good, and the majority of antibiotics purchased to a nursing home is likely to be included in the database. There are still several quality issues to address e.g. with regard to private versus public nursing homes, changes in bed-days over time, and the lack of data from Northern Norway. However, patterns of use fit with the information we have from earlier studies, RASK and NOIS-PIAH. Moreover, the therapy patterns are fairly stable over time, indicating that such estimates of use may give a good picture of national average use in nursing homes over time. Until individual-level antibiotic consumption data based on medical records are included in the NorPD, this may be an adequate method for estimating antibiotic use in nursing homes.

References

1. Harbin NJ, Haug JB, Lindbæk M, Akselsen PE, Romøren M. A Multifaceted Intervention and Its Effects on Antibiotic Usage in Norwegian Nursing Homes. Antibiotics (Basel). 2023 Aug 27;12(9):1372. doi: 10.3390/antibiotics12091372..
2. Årsrapport 2024: Norsk overvåkingssystem for antibiotikabruk og helsetjenesteassosierte infeksjoner, NOIS. Folkehelseinstituttet. 978-82-8406-533-5
3. Regulations on wholesale activities in pharmaceuticals https://lovdata.no/dokument/SF/forskrift/1993-12-21-1219/KAPITTEL_4#KAPITTEL_4 (30 June 2026)
4. Norwegian drug wholesales statistics database https://www.fhi.no/he/legemidler/om-den-grossistbaserte-legemiddelfo/ (30 June 2026)
5. Statistics on Care services, Statistics Norway.

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National action plans and targets for antibiotic use in healthcare

The former National Strategy against Antibiotic Resistance was agreed upon in 2015, and set an overarching goal of reducing the total volume of antibiotics used in Norway by 30%, by the end of 2020, compared to the baseline year of 2012. In September 2024, a new policy document, *National One Health Strategy against Antimicrobial Resistance 2024–2033*, was published. The corresponding National Action Plan for the human health sector is expected to be finalised by autumn 2026.

Norway has established two national advisory units dedicated to antibiotic use and stewardship in humans; The Antibiotic Centre for Primary Care (ASP), founded in 2006, focuses on primary care, while the National Centre for Antibiotic Use in Hospitals (NSAS), established in 2011, serves the hospital and specialist healthcare services. The Directorate of Health, in collaboration with the national advisory units, issues updated, evidence-based National Antibiotic Treatment Guidelines for antibiotic use in ambulatory care, nursing homes, dental practices and hospitals. Norwegian antibiotic consumption data are shared through European Surveillance of Antimicrobial Consumption Network (ESAC-Net) at the European Centre for Disease Prevention and Control (https://www.ecdc.europa.eu) and through the Global Antimicrobial Resistance and Use Surveillance System (GLASS) in WHO (https://www.who.int/initiatives/glass).

Norway has a beneficial pattern of antibacterial use compared to other countries and we belong to the low-use countries in Europe. Since the nineteen-seventies we have been able to measure antimicrobial use, both in human and animal sector. These data allow us to set targets and evaluate interventions for appropriate use of antimicrobials. Figure 38 shows the change in consumption of human antibiotics (J01, excl methenamine) and antibiotics for respiratory tract infections (amoxicillin, phenoxymethylpenicillin, macrolides and doxycycline) in Norway since 2012. In the former National Action Plan, two sector specific objectives were established for ambulatory care; a reduction in the average number of prescriptions to 250 prescriptions per 1,000 inhabitants per year, and a 20% reduction in the use of antibiotics for respiratory tract infections, measured in DDD/1,000 inhabitants/day. The first target was not achieved (in 2025; 323 prescriptions per 1,000 inhabitants), the latter was achieved in 2015. For hospitals, the work was focused on reducing the combined use of five specific groups of antibiotics by 30% compared with 2012. To support this goal, the National Action Plan mandated the implementation of antibiotic stewardship programmes in all Norwegian hospitals. Figure 39 shows the change of total hospital use of these targeted groups from 2019 to 2025 according to the national target. Between 2019 and 2025, Norwegian hospitals achieved a 10% reduction in use of the five selected groups of broad-spectrum antibiotics when adjusting for activity using bed-days. However, this indicator has limitations, as the number of bed days has declined steadily over time while outpatient consultations have increased considerably. Relying solely on bed-days to measure clinical activity may obscure actual trends in antibiotic use, and alternative indicators could contribute to different interpretations of the data.

The World Health Organization (WHO) has established a target for 2025-2030, encouraging countries to have at least 70% of their total antibiotic consumption come from the "Access" group. Figure 40 shows the proportion of Access antibiotics in different health care settings in Norway: hospital care, primary care, and total.

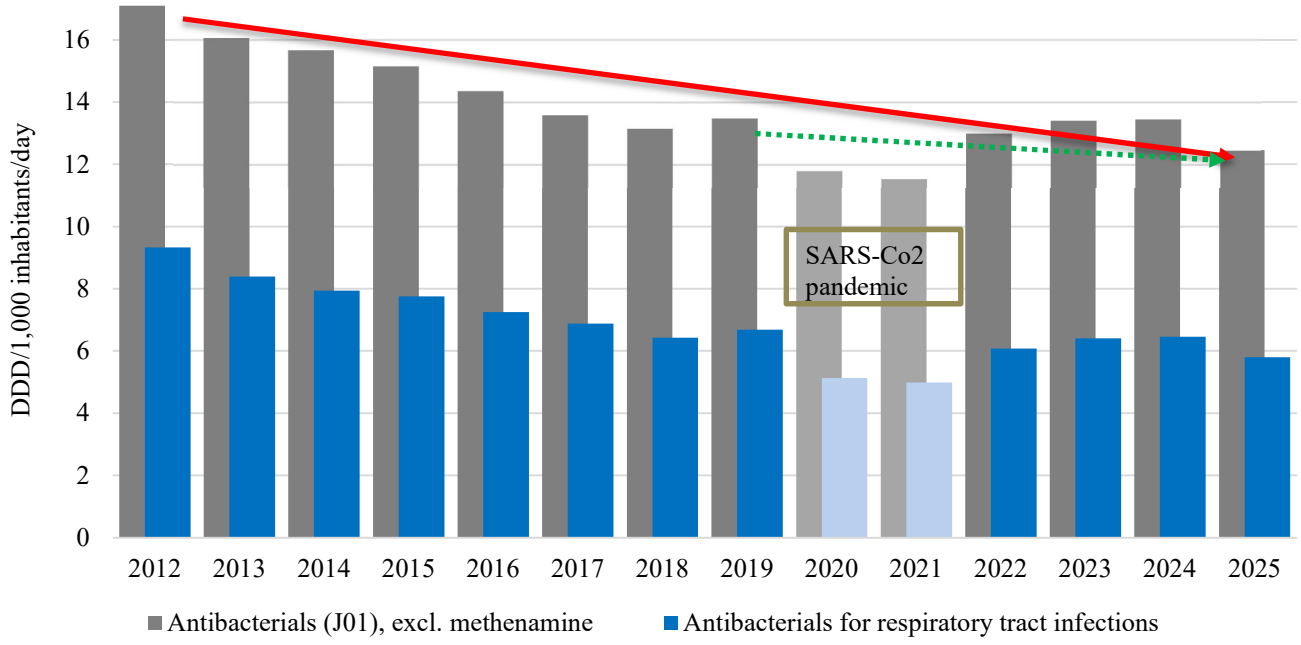

FIGURE 38. Total human sales of antibacterial agents for systemic use (ATC group J01, excl methenamine) and sales of antibiotics for respiratory tract infections (amoxicillin, phenoxymethylpenicillin, macrolides (J01FA01, J01FA02, J01FA06, J01FA09, J01FA10), and doxycycline) in Norway in 2012-2025 measured in DDD/1,000 inhabitants/day. Reduction of total use, excl. methenamine since 2012, measured in DDDs (end of red line) was 27% and since 2019 was 8% (end of green line), and for antibacterials for respiratory tract infections the reduced use was 38% since 2012 and 13% since 2019. Bars show measured use 2012-2025 (grey; J01, excl. methenamine blue; antibiotics for respiratory tract infections). Data from the Norwegian Drug Wholesales Statistics Database.

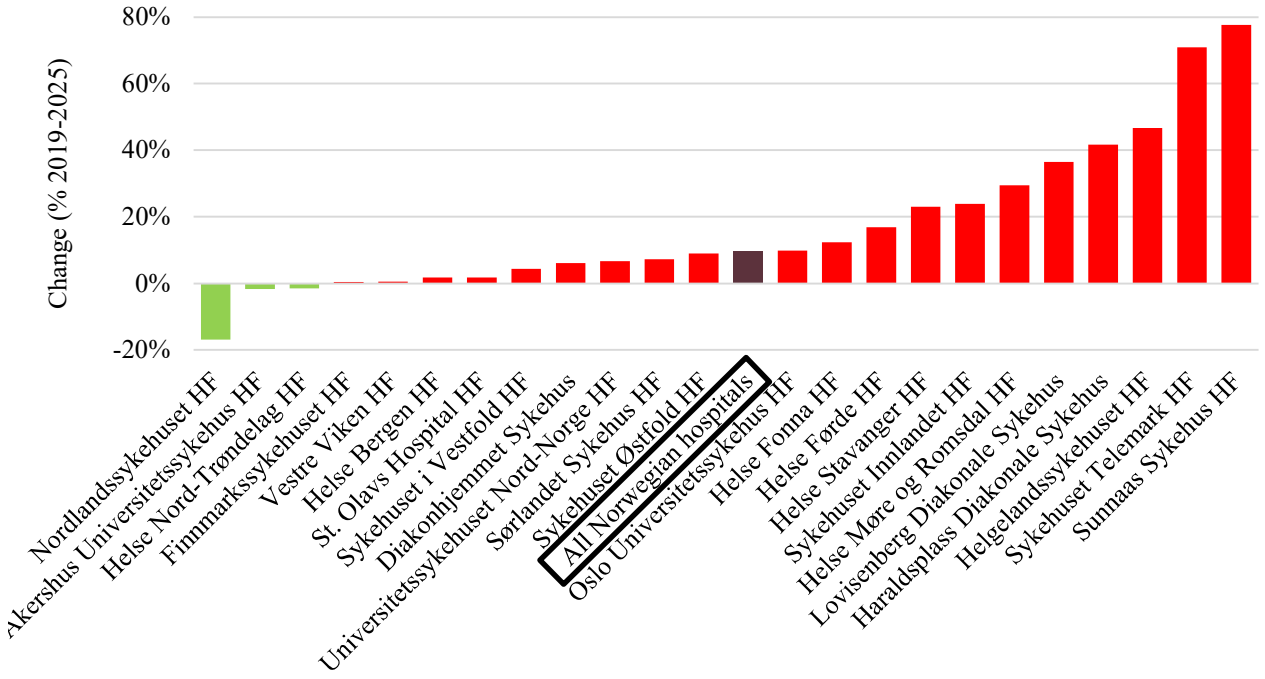

FIGURE 39. Changes in the use of selected antibacterials for systemic use (ATC-groups J01CR, J01DC, J01DD, J01DH and J01M) in Norwegian hospitals, 2019-2025. The data are presented per hospital/health trust as DDD/100 bed-days. Red columns; increase, green column; decrease and average for all Norwegian hospitals shown in black. Data source; Hospital Pharmacies Drug Statistics Database.

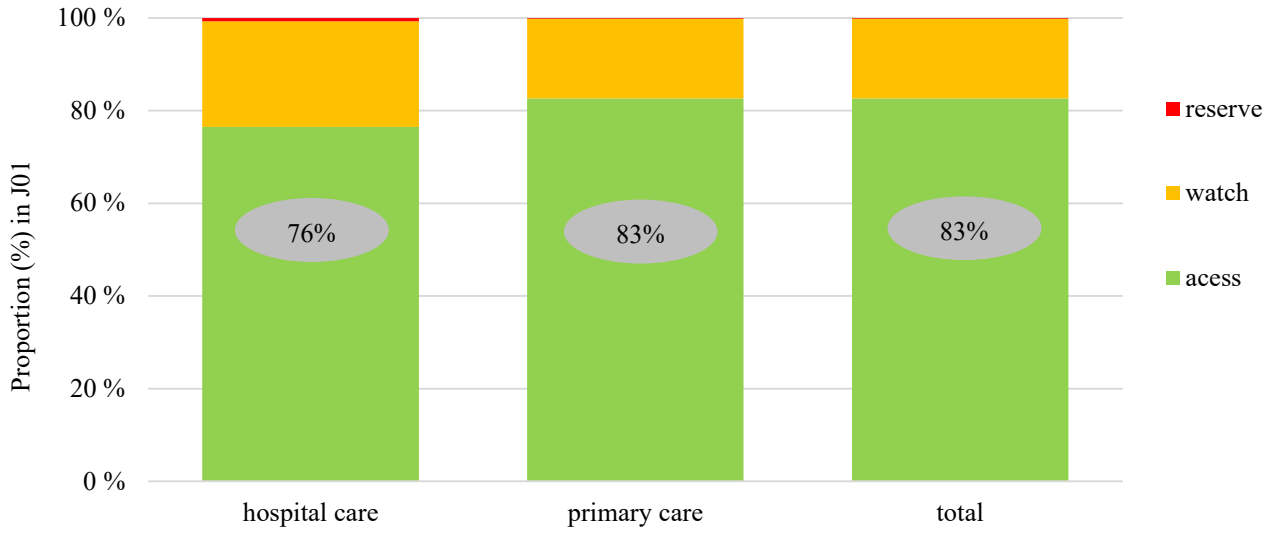

FIGURE 40. Relative consumption as measured in DDDs of Access, Watch and Reserve antibiotics in hospital care, ambulatory care, and in total use in Norway, 2025. Included are antibiotics at the WHO AWaRe list (version 2025) i.e. ATC group J01, antibiotics in A07AA, J04AB02/04, and P01AB01. Data source: Norwegian Drug Wholesales Statistics Database (total use); Hospital Pharmacies Drug Statistics Database (hospitals); Norwegian Prescribed Drug Registry (NorPD) (primary care).

Antimycotic use in hospitals and ambulatory care in Norway

The use of systemic antimycotics (ATC group J02) has increased in ambulatory care in Norway, while the use has decreased in hospitals (Figure 41). In 2018, hospital use accounted for 18% of total antimycotic consumption measured in DDDs; by 2025 this proportion had decreased to 14%. Fluconazole remains the most commonly used agent in both settings. In July 2013, a safety warning was issued for oral ketoconazole due to an increased risk of hepatotoxicity. This led to a marked reduction in its use in ambulatory care. Although oral ketoconazole remains available for endogenous Cushing's syndrome, its use is minimal, and it is therefore not included in the figure. Oral formulations accounted for 93% of total DDDs in 2025, an increase from 88% in 2012. Oral antimycotics are more frequently used in ambulatory care, whereas 50% of antimycotic use in hospitals was parenteral. It should be noted that nystatin oral suspension is not included in these data. This formulation is mainly used in young children. In 2025, 2.4% of children aged 0-4 years were prescribed nystatin mixture.

Over the last two decades, treatment patterns for invasive fungal infections in Norwegian hospitals have changed. In earlier guidelines, fluconazole was recommended as first-line therapy for candidemia, while echinocandins were reserved for critically ill patients and for infections caused by *Candida* species with reduced susceptibility to fluconazole. Following updates in international recommendations - most notably the ESCMID guidelines published in 2012 and the IDSA guidelines from 2016, which increasingly recommended echinocandins as the preferred initial therapy for candidemia - clinical practice in Norway gradually shifted towards increased use of echinocandins. The Norwegian national guidelines were updated in 2020, aligning with these recommendations by endorsing echinocandins as first-line therapy for all patients with candidemia. These changes are reflected in antifungal consumption patterns in Norwegian hospitals. Although fluconazole remains the most frequently used antifungal agent, its use has declined over time. In contrast, echinocandin use increased steadily until around 2022, after which it appears to have stabilised. The use of posaconazole has increased over time, likely reflecting expanded use for antifungal prophylaxis in high-risk populations, particularly patients with haematological malignancies and prolonged neutropenia, who are at increased risk of invasive fungal infections. In 2025, fluconazole accounted for 49% of total antifungal use in hospitals, compared with 30% for echinocandins and 15% for posaconazole (Figures 42-43). Figure 44 illustrates the distribution of antifungal classes across Norwegian hospitals. The proportion of fluconazole varies considerably between hospitals, ranging from 36% to 93%, while the corresponding share for echinocandins ranges from 0% to 43%, probably reflecting differences in patient mix and perhaps local implementation of treatment recommendations. Procurement practices also influence drug utilisation. Hospital drug procurement is coordinated through large-scale national tenders. As the echinocandins are considered clinically equivalent, these processes largely determine which specific agent is most widely used at any given time.

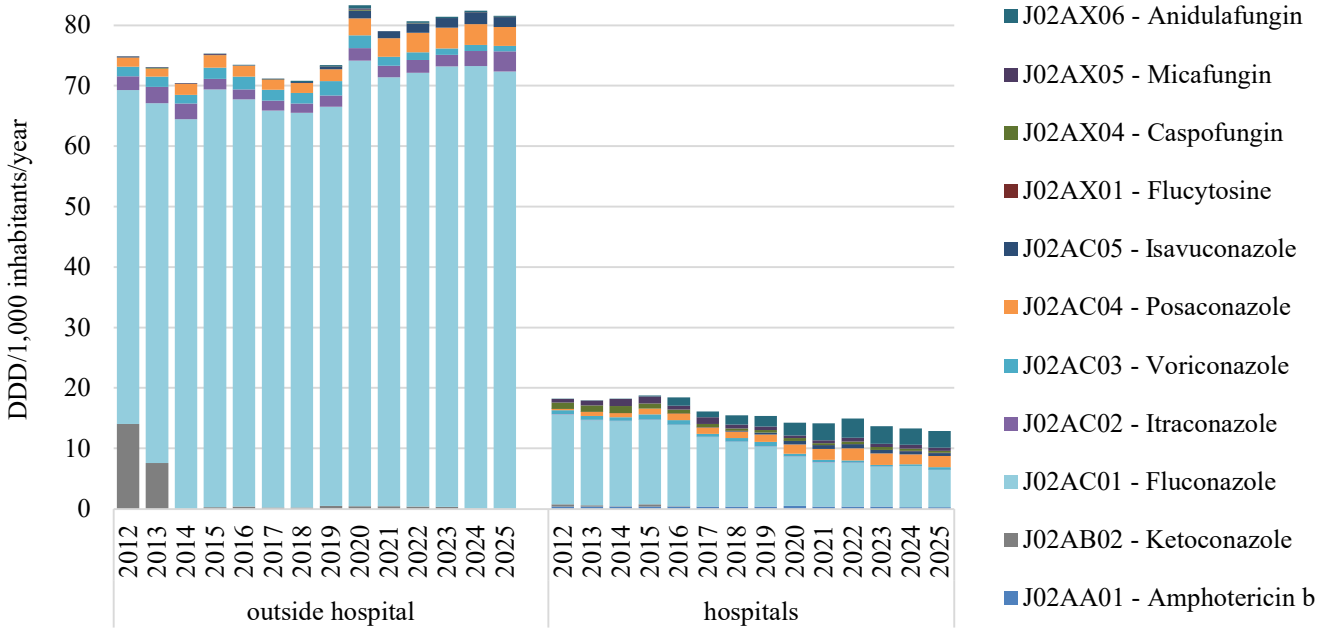

FIGURE 41. Sales of antimycotics for systemic use (ATC group J02) in Norway for ambulatory care and somatic hospitals 2012-2025, measured in DDD/1,000 inhabitants/year. Ambulatory care includes all use outside hospitals. Data source; Norwegian Drug Wholesales Statistics Database and the Hospital Pharmacies Drug Statistics Database.

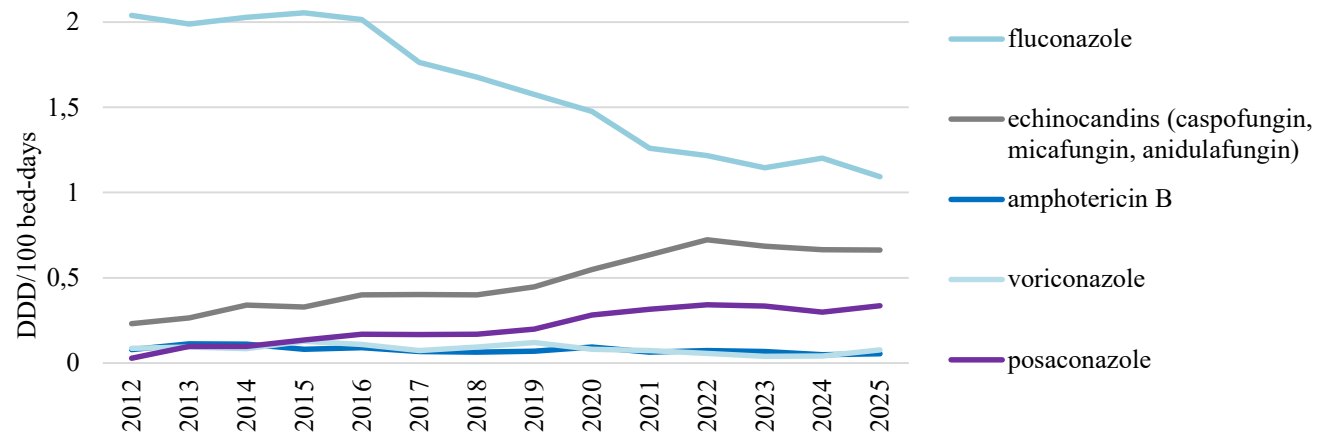

FIGURE 42. Sales of antimycotics for systemic use (ATC group J02) in Norwegian somatic hospitals 2012-2025, measured in DDD/100 bed-days. Data source; Hospital Pharmacies Drug Statistics Database and the Norwegian Patient Register.

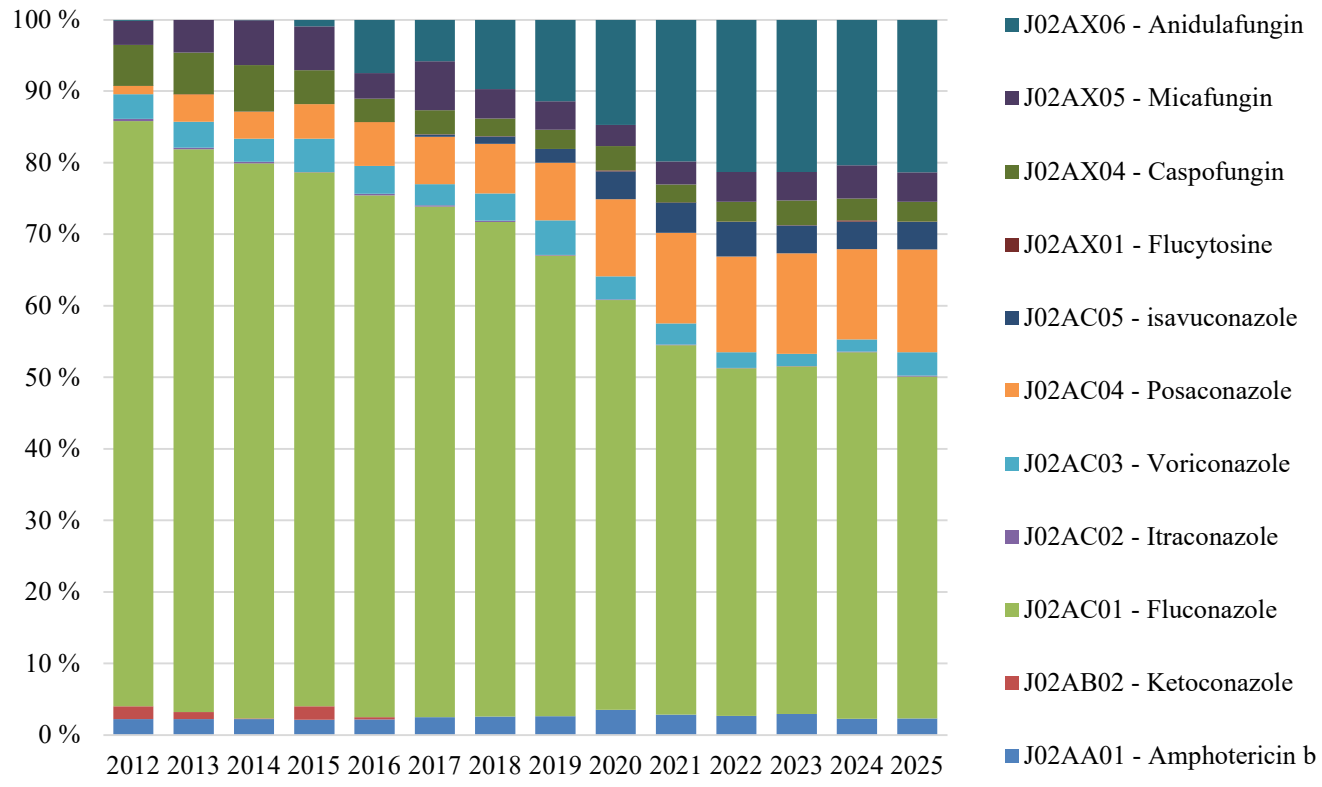

FIGURE 43. Sales of antimycotics for systemic use (ATC group J02) in Norway for ambulatory care and somatic hospitals 2012-2025, measured in DDD/1,000 inhabitants/year. Ambulatory care includes all use outside hospitals. Data source; Norwegian Drug Wholesales Statistics Database and the Hospital Pharmacies Drug Statistics Database.

FIGURE 44. Sales of antimycotics for systemic use (ATC group J02), presented per hospital/health trust (somatic), in 2025, measured in DDD/100 bed-days. All hospitals, except Sunnaas Sykehus, are acute care hospitals. Data source; Hospital Pharmacies Drug Statistics Database and the Norwegian Patient Register.

ANTIMICROBIAL RESISTANCE IN ANIMALS AND FOOD

ANIMAL CLINICAL ISOLATES

Madelaine Norström, Jannice Schau Slettemeås, Marianne Sunde and Anne Margrete Urdahl

The clinical isolates included in NORM-VET 2025 were *Actinobacillus pleuropneumoniae* and *Escherichia coli* from pigs, and *Staphylococcus felis* and *E. coli* from cats. Sampling, laboratory methods and data processing are described in Appendix 3.

Actinobacillus pleuropneumoniae from pigs

A total of 70 isolates of *A. pleuropneumoniae* from infections in pigs were susceptibility tested. The isolates were collected through the years 2021-2025. The results are presented in Table 8 and in the text.

TABLE 8. Antimicrobial resistance in *Actinobacillus pleuropneumoniae* from infections in pigs (n=70) in 2021-2025.

			Distribution (%) of MIC values (mg/L)*												
Substance	Resistance (%)	[95% CI]	0.015	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64
Doxycycline	0.0	[0.0-5.1]					1.4	10	88.6						
Tetracycline	0.0	[0.0-5.1]					1.4	14.3	81.4	2.9					
Florfenicol	0.0	[0.0-5.1]							100						
Ampicillin	0.0	[0.0-5.1]			5.7	65.7	28.6								
Benzylpenicillin	0.0	[0.0-5.1]			5.7	42.9	42.9	7.1	1.4						
Amoxicillin-clavulanic acid	0.0	[0.0-5.1]					25.7	74.3							
Trimethoprim-sulfamethoxazole	8.6	[3.2-17.7]		81.4	10.0	8.6									
Enrofloxacin	0.0	[0.0-5.1]	4.3	40.0	54.3	1.4									

*Bold vertical lines denote epidemiological cut-off values for resistance. CI = confidence interval. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested. Clinical breakpoints are marked in blue vertical lines. Only ECOFF is shown in cases where clinical breakpoints are identical to the ECOFF, though all the clinical breakpoints are defined as ≥. Clinical breakpoint for doxycycline, benzylpenicillin, amoxicillin-calvulanic acid and trimethoprim-sulfamethoxazole were ND.

RESULTS AND COMMENTS

The majority of the 70 *A. pleuropneumoniae* isolates were fully susceptible to the antimicrobial agents included in the susceptibility testing as shown in Table 8. Six of the isolates showed reduced susceptibility to trimethoprim-sulfamethoxazole. Previously, *A. pleuropneumoniae*, collected through the years 2004-2020, were tested and included in the 2020 NORM-VET report. However, any comparisons of results have to take into consideration changes made in the panel of antimicrobial agents tested. Though, for enrofloxacin and florfenicol, there has been a significant decrease in resistance occurrence from 12% to 0% for enrofloxacin (p=0.003) and from 8.4% to 0% for florfenicol (p=0.015) (NORM/NORM-VET 2020). The national recommendations for antimicrobial treatment of *A. pleuropneumoniae* infections in pigs list benzyl-penicillinprocain as the first-choice drug. None of the tested isolates were resistant to benzylpenicillin.

Escherichia coli from pigs

A total of 71 isolates of *E. coli* from intestinal infections in pigs were susceptibility tested. The isolates were collected through the years 2021-2025. The most common serotypes were as follows: F4 O149 (n=21), O139 (n=20), O141 (n=8), O138 (n=6), O149 (n=5), O45 (n=1), F4 O138 (n=1), O138 O141 (n=1), O139 O141 (n=1), F4 (n=1). For six isolates the serotype was not determined. The results are presented in Table 9, Figures 45-46 and in the text.

TABLE 9. Antimicrobial resistance in *Escherichia coli* from intestinal infections in pigs (n=71) in 2021-2025.

			Distribution (%) of MIC values (mg/L)*												
Substance	Resistance (%)	[95% CI]	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128
Tetracycline	23.9	[14.6-35.5]							71.8	4.2			23.9		
Ampicillin	14.1	[7.0-24.4]							38.0	46.5	1.4	1.4	12.7		
Amoxicillin-clavulanic acid	2.8	[0.3-9.8]								81.7	15.5	2.8			
Cefalexin	2.8	[0.3-9.8]								9.9	77.5	7.0	2.8	2.8	
Cefotaxime	0.0	[0.0-5.1]				100									
Meropenem	0.0	[0.0-5.1]		100											
Trimethoprim-sulfamethoxazole	9.9	[4.1-19.3]					90.1	1.4			8.5				
Gentamicin	1.4	[0.0-7.6]							98.6	1.4					
Neomycin	2.8	[0.3-9.8]								97.2				2.8	
Enrofloxacin	1.4	[0.0-7.6]			98.6	1.4									
Colistin	0.0	[0.0-5.1]						100							
Nitrofurantoin	0.0	[0.0-5.1]											100		

*Bold vertical lines denote epidemiological cut-off values for resistance. CI = confidence interval. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested. Clinical breakpoints are marked in blue vertical lines. Only ECOFF is shown in cases where clinical breakpoints are identical to the ECOFF. Clinical cut-off for neomycin is not defined.

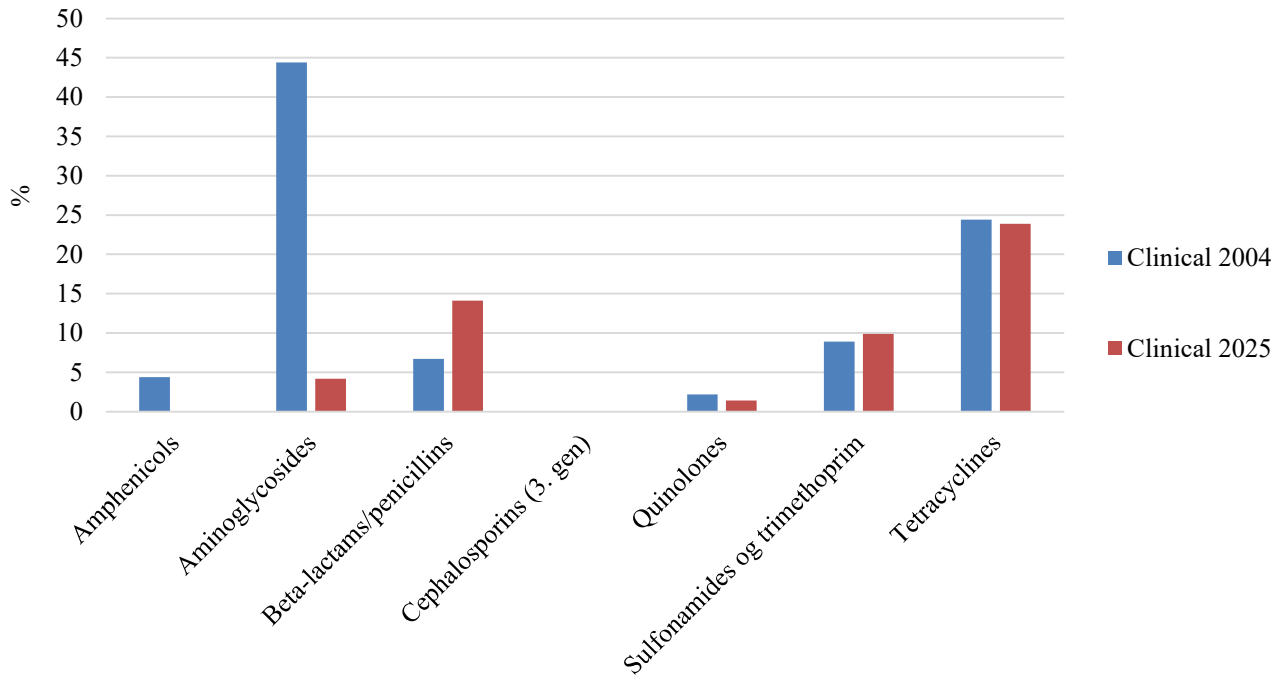

FIGURE 45. Prevalence of resistance to various antimicrobial classes in *Escherichia coli* from intestinal infections in pigs in 2004 and 2025. The epidemiological cut-off values used in NORM-VET 2025 were applied. For aminoglycosides, streptomycin was included only in 2004 (see text for further explanation).

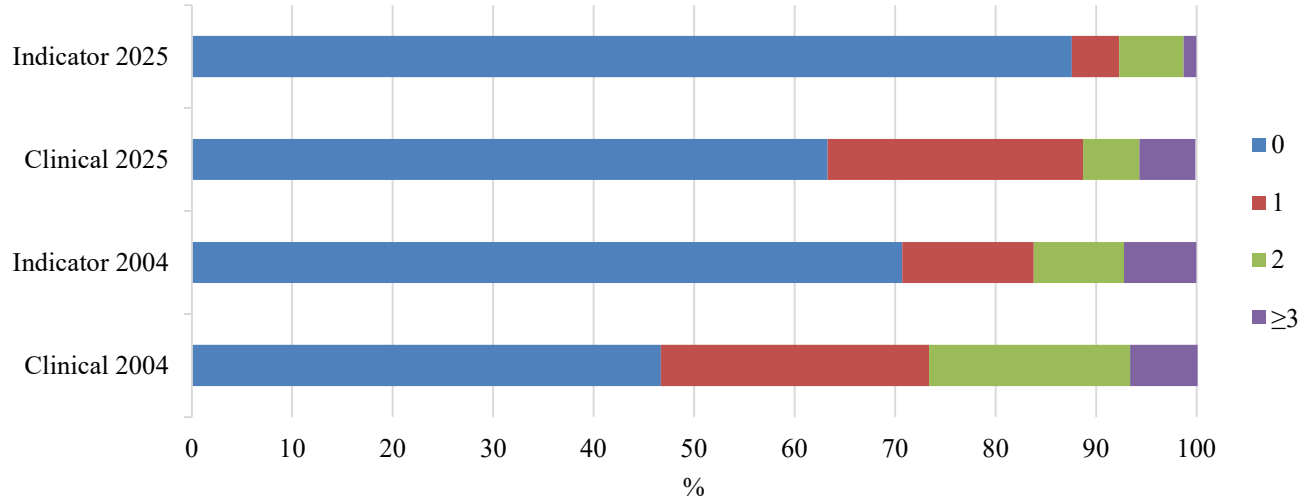

FIGURE 46. Antimicrobial resistance profile for *Escherichia coli* from clinical infections and from healthy pigs in 2004 and 2025. Percentage of isolates susceptible to all (0) or resistant to one (1), two (2), and three or more (≥3) antimicrobial classes. The epidemiological cut-off values used in NORM-VET 2025 were applied.

RESULTS AND COMMENTS

In total, 63.4% of the isolates were susceptible to all antimicrobial agents included in the susceptibility testing. The following proportions of isolates were resistant to one or more antimicrobial classes: 25.4% were resistant to one, 5.6% to two and 5.6% to three or more antimicrobial classes. Resistance towards tetracycline, ampicillin, and trimethoprim-sulfamethoxazole was most common as shown in Table 9 and Figure 45.

None of the isolates displayed resistance to the third generation extended-spectrum cephalosporin (ESC) cefotaxime, nor to meropenem, the preferred carbapenem used for detecting carbapenem resistance.

The last time *E. coli* from clinical infections in pigs were included was back in 2004. However, any comparisons of results have to take into consideration changes made in the panel of antimicrobial agents tested for. Resistance to the amoniglycoside streptomycin, which is not part of the 2025 panel, was most commonly detected in 2004 with 44.4% streptomycin resistant isolates, and 46.7% of the isolates being fully susceptible (NORM/NORM-VET 2004). Figure 45 shows this difference in resistance occurrence to aminoglycosides between the two years. This difference is also reflected in Figure 46, showing a higher occurrence of fully susceptible isolates in 2025 compared to 2004. These differences are probably due to differences in treatment regimes. In 2004, streptomycin, together with tetracycline, were among the most commonly used antimicrobial agents for therapy in swine production. In 2025, the national recommendations for antimicrobial treatment of *E. coli* diarrhoea in pig lists trimethoprim-sulfamethoxazole and amoxicillin as first-choice drugs. There has been a substantial reduction in occurrence of streptomycin resistance in indicator *E. coli* these years (see textbox page 70 in the NORM/NORM-VET 2023 report) that probably also to some degree is reflected in the figure.

Epidemiological cut-off values were used for the classification of resistance in these clinical *E. coli* isolates, facilitating comparison to surveillance results for indicator *E. coli*. However, due to differences in antimicrobial susceptibility testing panels, comparisons have to be made with caution. The occurrences in clinical isolates are usually higher than in indicator isolates as shown in Figure 46. This difference in resistance was observed for tetracycline resistance that was 23.9% in clinical isolates and 4.3% in indicator isolates, and for ampicillin resistance that was 14.1% in clinical isolates and 5.7% in indicator isolates (indicator *E. coli* page 61).

Escherichia coli from cats

A total of 29 isolates of *E. coli* from clinical submissions in cats, mainly with urinary tract infections, were collected between 2018 and 2025. The results are presented in Table 10, Figure 47 and in the text.

TABLE 10. Antimicrobial resistance in *Escherichia coli* from clinical infections in cats (n=29) from 2018-2025.

		Distribution (n) of MIC values (mg/L)*												
Substance	Resistance (n)	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128
Tetracycline	1							27	1			1		
Ampicillin	8							5	16			8		
Amoxicillin-clavulanic acid	3								20	6		3		
Cefalexin	2								4	22	1		2	
Cefotaxime	2				27	2								
Meropenem	1		28	1										
Trimethoprim-sulfamethoxazole	2					27				2				
Gentamicin	0							29						
Neomycin	0								29					
Enrofloxacin	2			27	2									
Colistin	0						29							
Nitrofurantoin	0											29		

*Bold vertical lines denote epidemiological cut-off values for resistance. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested. Clinical breakpoints are marked in blue vertical lines. Only ECOFF is shown in cases where clinical breakpoints are identical to the ECOFF. Clinical cut-off for neomycin is not defined.

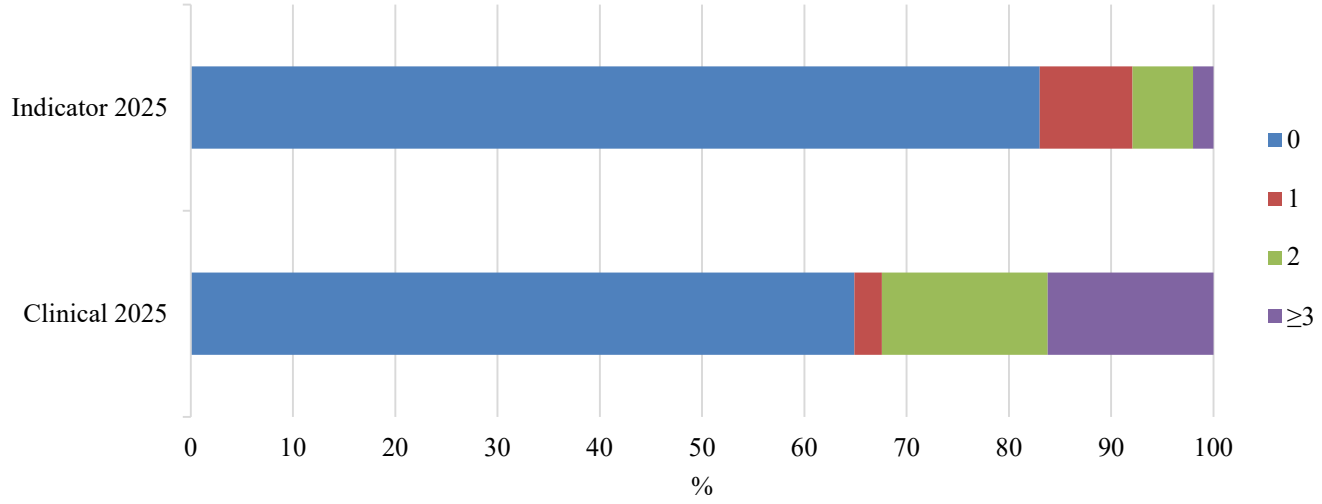

FIGURE 47. Antimicrobial resistance profile for *Escherichia coli* from clinical infections and healthy cats in 2025. Percentage of isolates susceptible to all (0) or resistant to one (1), two (2), and three or more (≥3) antimicrobial classes are illustrated. The epidemiological cut-offs used in NORM-VET 2025 were applied.

RESULTS AND COMMENTS

In total, 21 of the 29 isolates (72.4%) were susceptible to all antimicrobial agents included in the susceptibility testing. The following proportions of isolates were resistant to one or more antimicrobial classes: two (6.9%) were resistant to one, two (6.9%) to two, and four (13.8%) to three or more antimicrobial classes. Resistance towards ampicillin was most common as shown in Table 10.

Two isolates displayed reduced susceptibility to the ESC cefotaxime (6.9% [95% CI: 0.8-22.8]). These isolates displayed an AmpC beta-lactamase phenotype and both had the point mutation at n.-32T>A in the chromosomally located *ampC* gene causing upregulation of this gene. One of the isolates displayed resistance to meropenem, the preferred carbapenem used for detecting carbapenem resistance, with a MIC value just above the ECOFF. This isolate was retested on the EUVSEC2 panel which is specific for isolates resistant to ESCs and/or carbapenems and was susceptible to all substances in the panel. Using the broth microdilution method, a one two-fold dilution difference in MIC values for the same strain is acceptable due to methodological limitations.

This is the first time clinical *E. coli* from cats have been included in NORM-VET. Epidemiological cut-off values were used for the classification of resistance in these

clinical *E. coli* isolates, facilitating comparison to surveillance results for indicator *E. coli*. However, due to a low number of clinical isolates and differences in the antimicrobial susceptibility testing panels, comparisons have to be made with caution. The occurrence of resistance in clinical isolates are usually higher than in indicator isolates, as also indicated by the resistance to ampicillin (eight out of 29) in these clinical isolates versus 13.4% in the indicators. Also, there is a higher proportion of overall antimicrobial resistance in these clinical *E. coli* isolates compared to antimicrobial resistance in indicator *E. coli* from cats as presented in Figure 47.

Clinical breakpoints are shown in dotted blue lines in Table 10. However, these clinical breakpoints are defined in order to indicate if treatment of a specific pathogen is likely to succeed or not, and factors like dosage, formulations and host species will affect the clinical result. The national recommendations for antimicrobial treatment in uncomplicated bacterial cystitis list amoxicillin as first-choice drug. Amoxicillin is included in the test panel in combination with clavulanic acid. Ampicillin, however, is included and eight of the 29 isolates were resistant, emphasising the importance of performing bacteriological analysis with antimicrobial susceptibility testing.

Staphylococcus felis from cats

A total of 34 *S. felis* isolates from clinical infections in cats were included. Of these, 15 were from local skin/ear infections, while 19 were from other infections. The isolates were collected through the years 2018 and 2025. The results are presented in Tables 11-12 and in the text.

TABLE 11. Antimicrobial resistance in *Staphylococcus felis* (n=15) from local skin/ear infections in cats in 2018-2025.

		Distribution (n) of MIC values (mg/L)*												
Substance	Resistance (n)	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128
Tetracycline	0						15							
Chloramphenicol	0								15					
Florfenicol	0							15						
Oxacillin	0				15									
Cefoxitin	0								15					
Tobramycin	0						15							
Gentamicin	0						15							
Neomycin	15							15						
Enrofloxacin	ND			14	1									
Fusidic acid	0				15									

*Bold vertical lines denote epidemiological cut-off values for resistance, i.e. for *Staphylococcus aureus*. ND = not defined. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested. Clinical breakpoints are marked in blue vertical lines. Only ECOFF is shown in cases where clinical breakpoints are identical to the ECOFF. Clinical cut-offs for *S. aureus* are used for oxacillin and cefoxitin, and *Staphylococcus hyicus* cut-off for enrofloxacin. Clinical cut-off for florfenicol is ND.

TABLE 12. Antimicrobial resistance in *Staphylococcus felis* (n=19) from other infections in cats in 2018-2025.

		Distribution (n) of MIC values (mg/L)*												
Substance	Resistance (n)	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128
Tetracycline	1				18					1				
Benzylpenicillin	7	12				1		6						
Oxacillin	0				19									
Cefalexin	ND						2	17						
Cefoxitin	0							19						
Trimethoprim-sulfamethoxazole	0				19									
Erythromycin	3				10	6			3					
Clindamycin	3				16				3					
Gentamicin	0						19							
Enrofloxacin	ND				18	1								
Fusidic acid	0					19								
Nitrofurantoin	0										19			

*Bold vertical lines denote epidemiological cut-off values for resistance, i.e. for *Staphylococcus aureus*. ND = not defined. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested. Clinical breakpoints are marked in blue vertical lines. Only ECOFF is shown in cases where clinical breakpoints are identical to the ECOFF. Clinical cut-offs for *S. aureus* are used for oxacillin, cefotoxin and nitrofurantoin, and *Staphylococcus hyicus* cut-off for enrofloxacin.

RESULTS AND COMMENTS

As shown in Table 11, the 15 *S. felis* isolates from local infections were regarded susceptible to all substances but neomycin. However, since there are no ECOFFs determined for *S. felis*, ECOFFs for *Staphylococcus aureus* were used in this report and it could be argued that this reduced susceptibility to neomycin is a consequence of this.

In total, 12 of 19 isolates (63.2%) from the other infections, were susceptible to all antimicrobial classes included in the susceptibility testing. The following proportions of isolates were resistant to one or more antimicrobial classes: three isolates (15.8%) were resistant to one and four isolates (21.1%) to two antimicrobial classes. Resistance towards benzylpenicillin was most common as shown in Table 12. This is the first time clinical *S. felis* from cats have been included in NORM-VET. Epidemiological cut-off values for *S. aureus* were used for the classification of resistance in these clinical isolates, facilitating comparison to surveillance results for indicator *S. felis*. However, due to differences in the antimicrobial susceptibility testing panels and low number of clinical isolates, comparisons have to be made with caution. The occurrence of resistance in clinical isolates is usually higher than in indicator isolates. This difference in resistance was indicated for benzylpenicillin.

Clinical breakpoints are shown in dotted blue lines in the tables. However, these clinical breakpoints are defined in order to indicate if treatment of a specific pathogen is likely to succeed or not, and factors like dosage, formulations and host species will affect the clinical result.

Antimicrobial susceptibility testing in routine mastitis diagnostics in Norway 2025

Background

TINE SA, the Norwegian dairy co-operative, runs the TINE Mastitis Laboratory in Molde. This lab conducts all bacteriological testing related to mastitis control throughout Norway and analysed about 75,000 quarter milk samples from dairy cows in 2025. The laboratory also performs antimicrobial susceptibility testing on selected isolates, supporting surveillance of antimicrobial resistance in milk-producing animals. The results are reported to the Norwegian Dairy Herd Recording System (NDHRS) (1, 2). Statistical data from mastitis diagnostics in dairy cows are published annually in the TINE udder health report (3). *Staphylococcus aureus* is identified as the main cause of mastitis in Norwegian dairy cows (3, 4). Because benzylpenicillin procaine is the preferred treatment for mastitis in Norwegian dairy cows (5), testing for beta-lactamase production in *S. aureus* is the primary focus of antimicrobial susceptibility testing in mastitis diagnostics.

Methods

Results from susceptibility testing of isolates from dairy cows in 2025 were retrieved from the NDHRS. *S. aureus* are routinely tested for beta-lactamase production by the clover leaf assay (6). Penicillin resistant *S. aureus* and *Enterobacteriaceae* from clinical mastitis are tested by disc diffusion for amoxicillin-clavulanic acid, ampicillin, cefoxitin (*S. aureus*) and trimethoprim-sulfamethoxazole (*Enterobacteriaceae*). Other bacterial species from clinical mastitis may also be tested. Streptococci are considered sensitive to penicillin (7) and are therefore not routinely tested.

A total of 7,784 isolates from cow milk were tested in 2025. The tested isolates were *S. aureus* (n=6,325, 81%), *Enterobacteriaceae* (n=966, 12%), non-aureus staphylococci (n=430, 6%) and other bacteria (n=63, 1%). The isolates were from 5,383 cows from 2,214 farms. The results for *S. aureus* and *E. coli* are presented here.

Results and discussion

Among the *S. aureus* from cows, 142 of 6,325 (2.2%) isolates were resistant by the clover leaf test, whilst 6 isolates were susceptible with increased exposure. Hence, 97.7% of *S. aureus* from bovine mastitis in Norway were sensitive to penicillin. The proportion of penicillin resistant *S. aureus* in milk samples from Norwegian dairy cows has been low the last 20 years, ranging from 1.5-3.5% (2). Results from disk diffusion for amoxicillin-clavulanic acid were available for 139 *S. aureus* isolates, whereof all were sensitive. For ampicillin, results were available for 139 *S. aureus* isolates, all of which were resistant. Methicillin resistant *S. aureus*, i.e. MRSA, were not detected in milk samples from cows in 2025.

Table 13 shows the results of the susceptibility testing for amoxicillin-clavulanic acid and trimethoprim-sulfamethoxazole of *E. coli* in 2025. The majority of the isolates were susceptible to trimethoprim-sulfamethoxazole. In the routine mastitis diagnostics, susceptible *E. coli* is reported as “susceptible with increased exposure (I)” to amoxicillin-clavulanic acid and ampicillin because the response to treatment is expected to be low. According to the Norwegian antimicrobial stewardship guidelines (5), cases of *E. coli* clinical mastitis do not benefit from antimicrobial treatment and should be treated with supportive therapy only.

TABLE 13. Susceptibility testing of *E. coli* from mastitis in Norwegian dairy cows in 2025. Number of isolates (%) is given for each category susceptible (S), susceptible with increased exposure (I), and resistant (R).

Species	Amoxicillin-clavulanic acid (n=953)		Trimethoprim/sulfamethoxazole (n=953)			Ampicillin (n =952)	
	I	R	S	I	R	I	R
E. coli	870 (91%)	83 (9%)	852 (89%)	1 (0.1%)	100 (10%)	797 (84%)	155 (16%)

In conclusion, *S. aureus* remains the most common cause of mastitis in Norwegian dairy cows. The level of penicillin resistance of *S. aureus* from mastitis samples is very low in dairy cows (2.2%). *E. coli* is an important cause of severe clinical mastitis in Norway but do not benefit from antimicrobials and could, if identified at the time of clinical examination, be treated with supportive therapy. The routine diagnostics performed by TINE are crucial for national surveillance of both mastitis pathogens and their antimicrobial resistance occurrences, contributing to targeted treatment and improved animal health.

References

1. TINE. Årsrapport Kukontrollen og Geitekontrollen. https://medlem.tine.no/aktuelt-fra-tine/statistikksamling-for-ku-og-geitekontrollen-2023, 2023 Accessed May 20th, 2024.
2. Smistad M, Bakka HC, Sølverød L, Jørgensen HJ, Wolff C. Prevalence of udder pathogens in milk samples from Norwegian dairy cows recorded in a national database in 2019 and 2020. Acta Veterinaria Scandinavica. 2023;65(1):19.
3. TINE. TINE Jurhelserapport 2025 [TINE udder health report 2025] (In Norwegian). Available at: https://medlem.tine.no/fag-og-forskning/statistikksamling-for-ku-og-geitekontrollen-2025 Accessed June 10th 2026.
4. Smistad M, Sølverød L, Inglingstad R, Østerås O. Distribution of somatic cell count and udder pathogens in Norwegian dairy goats. Journal of Dairy Science. 2021;104(11):11878-88.
5. Norwegian medicines agency. Terapianbefaling - bruk av antibakterielle midler til matproduserende dyr. https://www.dmp.no/veterinermedisin/terapianbefalinger/bruk-av-antibakterielle-midler-til-matproduserende-dyr . 2022. Accessed May 25th, 2024.
6. Bryan L. β-lactam antibiotics. Mode of action and bacterial resistance. Antibiotics in laboratory medicine 3rd ed. 1991:599-644.
7. Jensen VF, Damborg P, Norström M, Nonnemann B, Slettemeås JS, Smistad M, et al. Estimation of epidemiological cut-off values for eight antibiotics used for treatment of bovine mastitis caused by Streptococcus uberis and Streptococcus dysgalactiae subsp. dysgalactiae. Veterinary Microbiology. 2024;290:109994.

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European Antimicrobial Resistance Surveillance Network in Veterinary Medicine (EARS-Vet)

The European Antimicrobial Resistance Surveillance Network in Veterinary Medicine (EARS-Vet) is a part of the EU-funded project EU-JAMRAI2 (Joint Action Antimicrobial Resistance and Healthcare-Associated Infections) where the Norwegian Veterinary Institute (NVI) is one of many international partners. Currently, the network includes 38 partners from 19 European countries. EARS-Vet is the equivalent to EARS-Net established in the human sector and was first established as part of the EU-JAMRAI project (2017-2021). EARS-Vet aims to fill a gap in AMR surveillance in bacterial pathogens of animals in Europe (1). This is done by complementing the existing AMR and antimicrobial consumption (AMC) surveillance systems by covering animal species, bacterial pathogens and antimicrobials of relevance to both veterinary and human medicine, which are currently not included in EARS-Net and the harmonised EFSA monitoring (2). Close collaboration with other institutions, such as European Food Safety Authority (EFSA), European Centre for Disease Prevention and Control (ECDC), the European Commission, World Organization for Animal Health (WOAH), Food and Agriculture Organization (FAO), World Health Organization (WHO), and Federation of Veterinarians of Europe (FVE) has been established.

NVI have so far contributed with available AMR data from pathogenic bacteria matching the scope of EARS-Vet (Table 14), although data were not available for several of the included combinations of animal species, infection type and bacterial species. This is likely due to a combination of a favorable situation regarding certain infectious diseases among both food-producing and companion animals in Norway, but also due to lack of clinical sampling and clinical samples being sent to private laboratories, mainly abroad, for analysis.

TABLE 14. Combination of animal species, type of infections and bacterial species currently included in the EARS-Vet scope.

Animal species	Infection type	Bacterial species
Cattle	digestive, septicemia or mastitis	*Escherichia coli*
	mastitis	*Klebsiella pneumoniae*
		Staphylococcus aureus
		Streptococcus uberis
		Streptococcus dysgalactiae
	respiratory	*Mannheimia haemolytica*
		Pasteurella multocida
Swine	digestive	*Escherichia coli*
	cutaneous, septicemia or arthritis	*Staphylococcus hyicus*
	cutaneous, septicemia, arthritis or respiratory	*Streptococcus suis*
	respiratory or septicemia	*Pasteurella multocida*
		Actinobacillus pleuropneumoniae
Chicken	septicemia or arthritis	*Escherichia coli*
		Staphylococcus aureus
Dog	urinary	*Escherichia coli*
	cutaneous, otitis or respiratory	*Pasteurella multocida*
	cutaneous or otitis	*Staphylococcus pseudintermedius*
		Staphylococcus aureus
Cat	urinary	*Escherichia coli*
	cutaneous, otitis or urinary	*Staphylococcus felis*
	cutaneous or otitis	*Staphylococcus aureus*
	respiratory or septicemia	*Pasteurella multocida*
Horse	cutaneous	*Staphylococcus aureus*
	reproductive	*Escherichia coli*
	reproductive or respiratory	*Streptococcus equi* subsp. *zooepidemicus*
Sheep and goat	mastitis, septicemia or digestive	*Escherichia coli*
	respiratory	*Mannheimia haemolytica*
	respiratory or septicemia	*Pasteurella multocida*
	mastitis	*Staphylococcus aureus*

The first report, including results from partner countries, will be finalised during 2026, and a summary of the main findings will be presented in the next NORM-VET report.

References

1. Mader, R. et al. Building the European Antimicrobial Resistance Surveillance network in veterinary medicine (EARS-Vet). Euro Surveill. 2021;26(4):pii=2001359. https://doi.org/10.2807/1560-7917.ES.2021.26.4.2001359
2. Mader, R. et al. Defining the scope of the European Antimicrobial Resistance Surveillance network in Veterinary medicine (EARS-Vet): a bottom-up and One Health approach. J Antimicrob Chemother 2022; 77: 816–826 https://doi.org/10.1093/jac/dkab462.

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INDICATOR BACTERIA FROM ANIMALS

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The prevalence of antimicrobial resistance among certain bacteria of the normal microbiota can be used as an indicator of the selective pressure from use of antimicrobial agents. These bacteria may form a reservoir of transferrable resistance genes enabling the spread of antimicrobial resistance to other bacteria, including those responsible for infections in animals or humans. Thus, resistance monitoring of indicator bacteria from the microbiota of healthy animals is of importance in a One Health perspective, and to detect trends and evaluate effects of interventions.

Escherichia coli, *Enterococcus faecalis* and *Enterococcus faecium* are used as indicator bacteria for antimicrobial resistance surveillance in animals. In addition, *Staphylococcus* spp. is included as an indicator in horses and pets.

In 2025, samples from animals included caecal samples from pigs and cattle, and faecal swabs from cats for isolation of indicator bacteria. In addition, oral/nasal/perineum swabs from cats were included for detection of *Staphylococcus felis*. Selective screening methods for detection of some notifiable resistance bacteria were implemented on the same sample material (see chapter on notifiable antimicrobial resistance, page 70).

Only data retrieved following the requirements set in decision 2013/652/EU and 2020/1729/EU are shown for cattle and pigs. For previous data, please see the respective annual reports. Sampling, laboratory methods and data processing are described in Appendix 3.

PRODUCTION ANIMALS

Escherichia coli from cattle and pigs

Caecal samples from a total of 308 cattle and 299 fattening pigs were examined. *E. coli* isolates were obtained from 292 (94.8%) of the cattle and 299 (100%) of the pig samples. One isolate per positive sample was susceptibility tested. The results are presented in Table 15 and Figures 48-50, and in the text.

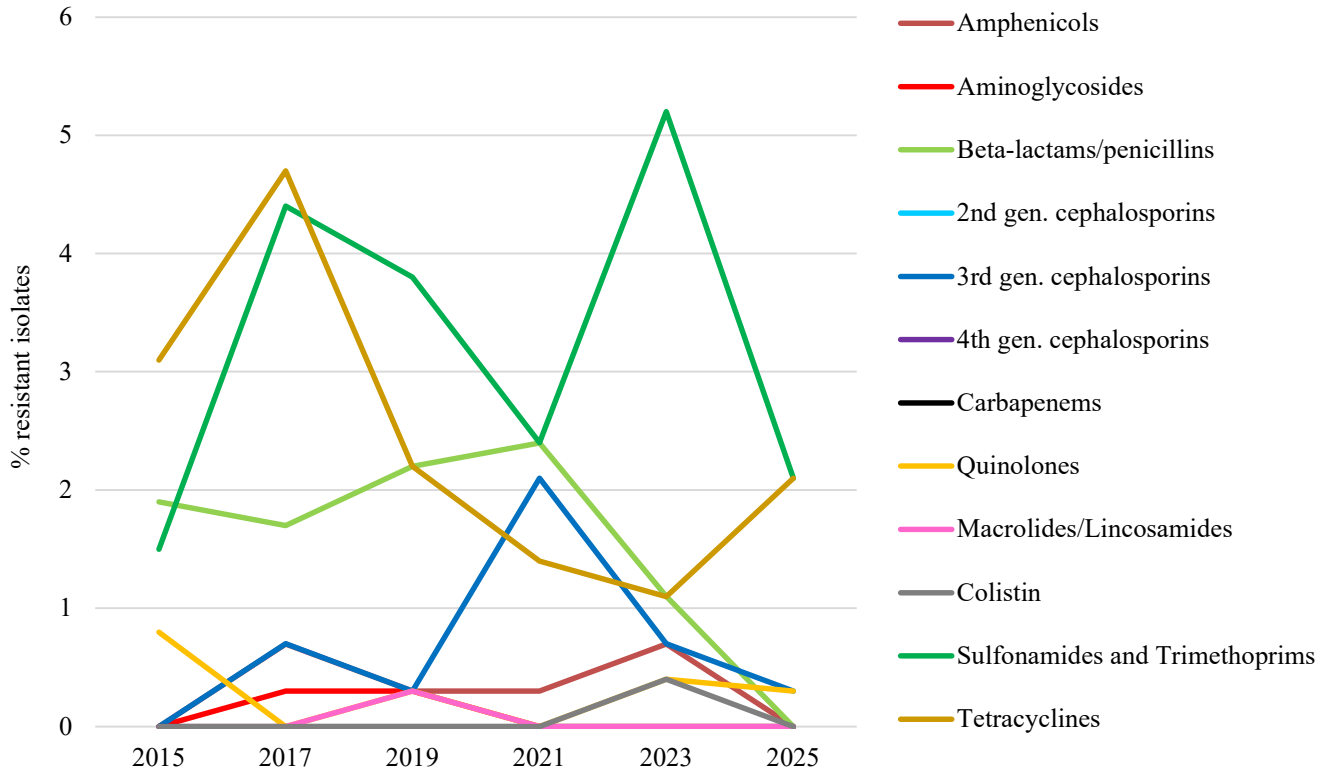

FIGURE 48. Prevalence of resistance to various antimicrobial classes in *Escherichia coli* from cattle in 2015-2025. The epidemiological cut-off values used in NORM-VET 2025 were applied.

TABLE 15. Antimicrobial resistance in *E. coli* from caecal samples of cattle (n=292) and fattening pigs (n=299) in 2025.

				Distribution (%) of MIC values (mg/L)*														
Substance	Animal	Resistance (%)	[95% CI]	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128	256	≥512
Tetracycline	Cattle	2.1	[0.8-4.4]								83.6	14.4				2.1			
	Pig	4.3	[2.3-7.3]								81.3	14.4			0.7	3.7			
Tigecycline	Cattle	0.0	[0.0-1.3]					100											
	Pig	0.0	[0.0-1.2]					99.7	0.3										
Chloramphenicol	Cattle	0.0	[0.0-1.3]										97.6	2.4					
	Pig	0.7	[0.1-2.4]										97.3	2.0	0.7				
Ampicillin	Cattle	1.0	[0.2-3.0]							1.0	28.8	60.3	80.9			1.0			
	Pig	5.7	[3.3-8.9]							5.0	38,5	47.5	3.3	0.3		5.4			
Cefotaxime	Cattle	0.3	[0.0-1.9]					99.7		0.3									
	Pig	0.0	[0.0-1.2]					100											
Ceftazidime	Cattle	0.3	[0.0-1.9]					96.6	3.1		0.3								
	Pig	0.0	[0.0-1.2]					96.7	3.3										
Meropenem	Cattle	0.0	[0.0-1.3]		99.7	0.3													
	Pig	0.3	[0.1-2.4]		99.3	0.3	0.3												
Trimethoprim	Cattle	1.0	[0.2-3.0]					74.7	23.6	0.7					1.0				
	Pig	5.4	[3.1-8.5]					66.9	26.4	1.0	0.3				5.4				
Sulfamethoxazole	Cattle	1.7	[0.6-4.0]										45.2	44.2	7.9	1			1.7
	Pig	7.7	[4.9-11.3]										46.8	36.8	7.4	1.3		0.3	7.4
Azithromycin	Cattle	0.0	[0.0-1.3]								15.4	66.8	17.8						
	Pig	0.0	[0.0-1.2]								18.4	61.9	19.7						
Gentamicin	Cattle	0.0	[0.0-1.3]						65.4	32.5	2.1								
	Pig	0.3	[0.0-1.8]						63.5	33.8	2.3	0.3							
Amikacin	Cattle	0.0	[0.0-1.3]									97.6	2.4						
	Pig	0.7	[0.1-2.4]									95.0	4.3	0.7					
Ciprofloxacin	Cattle	0.3	[0.0-1.9]	91.1	8.6			0.3											
	Pig	0.7	[0.1-2.4]	94.6	4.7			0.3	0.3										
Nalidixic acid	Cattle	0.0	[0.0-1.3]									100							
	Pig	0.3	[0.0-1.8]									99.3	0.3				0.3		
Colistin	Cattle	0.0	[0.0-1.3]							100									
	Pig	0.0	[0.0-1.2]							99.7	0.3								

*Bold vertical lines denote epidemiological cut-off values for resistance. CI = confidence interval. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested.

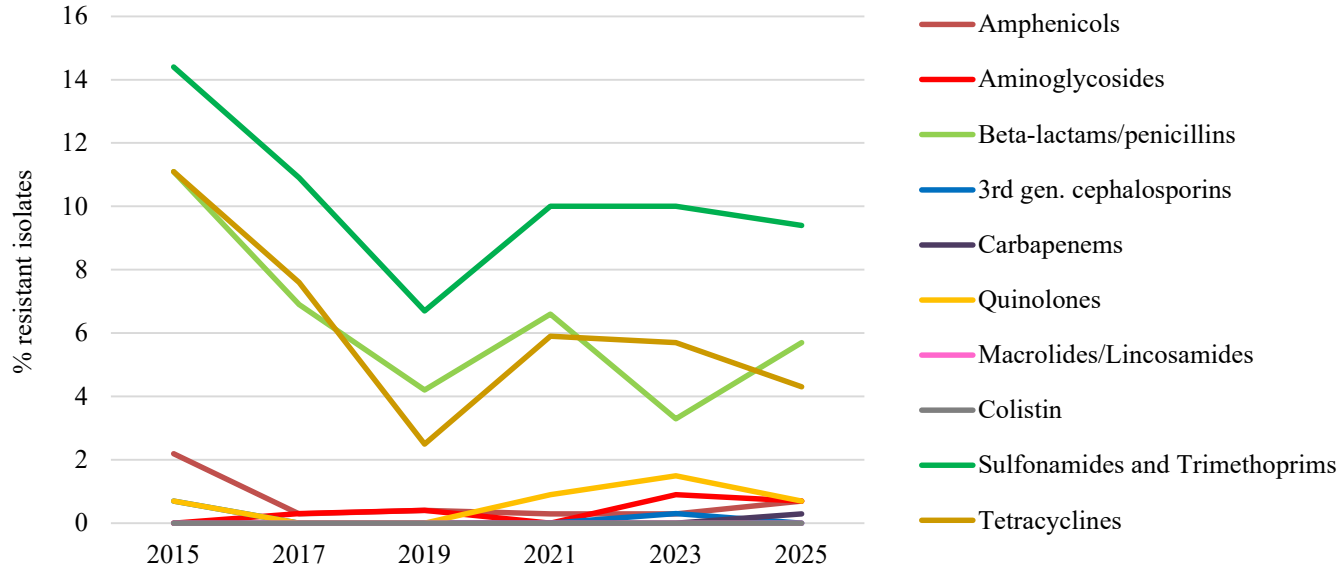

FIGURE 49. Prevalence of resistance to various antimicrobial classes in *Escherichia coli* from fattening pigs in 2015-2025. The epidemiological cut-off values used in NORM-VET 2025 were applied.

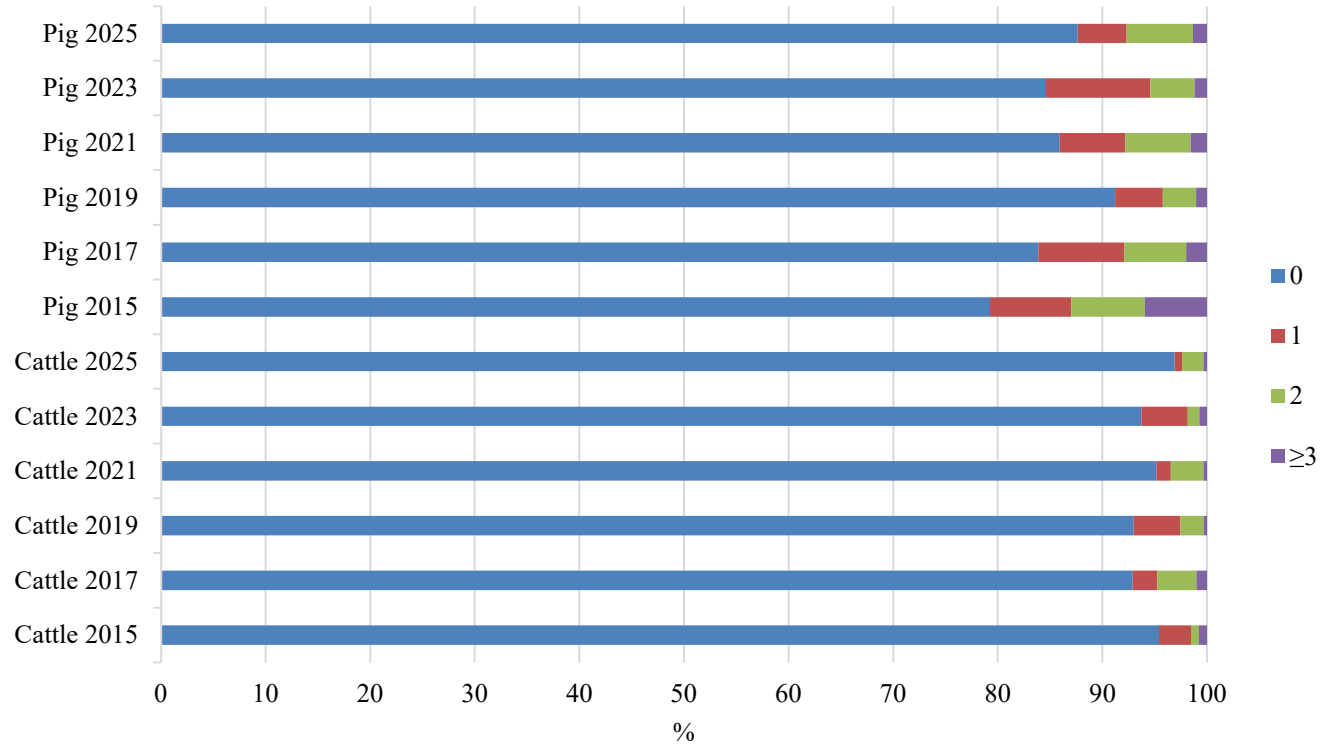

FIGURE 50. Antimicrobial resistance profile for *Escherichia coli* from fattening pigs and cattle in 2015-2025. Percentage of isolates susceptible to all (0) or resistant to one (1), two (2), and three or more (≥3) antimicrobial classes are illustrated. The epidemiological cut-off values used in NORM-VET 2025 were applied.

RESULTS AND COMMENTS

CATTLE

A total of 96.9% of the *E. coli* isolates from cattle caecal samples were susceptible to all antimicrobial agents included in the test panel. Altogether, 0.7% of the isolates were resistant to one antimicrobial class, 2.1% to two and 0.3% to three or more antimicrobial classes. Resistance to sulfamethoxazole and tetracyclines were the most frequently identified resistance phenotypes (Figure 48). A total of 3.1% of the isolates were resistant which indicates a low occurrence of resistance among *E. coli* from cattle caecal samples according to the EFSA classification described in Appendix 6. The low detected occurrence is in concordance with the results from previous years, i.e. 2015-2023 as shown in Figure 50, i.e. the number of isolates being fully susceptible has been relatively stable > 90% over the years 2015-2025.

One isolate displayed resistance to the extended-spectrum cephalosporins (ESC) cefotaxime and ceftazidime (0.3% [95% CI: 0.0-1.9]). The isolate displayed an AmpC beta-lactamase phenotype and the resistance was due to mutations in the promoter and attenuator region of the chromosomally located *ampC* gene (p.C-42T) causing an upregulation. None of the isolates displayed resistance to meropenem, the preferred carbapenem used for detecting carbapenem resistance. Selective methods were applied on the same sample material to investigate the occurrence of *E. coli* resistant to ESC and carbapenem resistant *Enterobacterales* (CRE) in cattle (see page 72).

In a European perspective, the occurrence of resistance among *E. coli* from cattle in Norway is among the lowest of the countries reporting to EFSA (EFSA and ECDC Summary Report 2023-2024). This situation corresponds to the low use of antimicrobials in the Norwegian cattle production.

PIGS

A total of 87.6% of the *E. coli* isolates from pig caecal samples were susceptible to all antimicrobial agents tested, indicating a moderate occurrence of resistance among *E. coli* from caecal samples of fattening pigs according to the EFSA classification described in Appendix 6. Resistance to sulfamethoxazole, followed by resistance to betalactams (i.e. penicillin) and tetracycline, were the most frequently identified resistance phenotypes (Figure 49). Altogether, 4.7% of the isolates were resistant to one antimicrobial class, 6.4% to two, and 1.3% to three or more antimicrobial classes (Figure 50).

None of the isolates displayed resistance to the ESCs cefotaxime and ceftazidime [95% CI: 0.0-1.2]. One of the isolates displayed resistance to meropenem with a MIC value just over ECOFF, the preferred carbapenem used for detecting carbapenem resistance. However, a one two-fold dilution difference in MIC values for the same strain is acceptable due to methodological limitations, and no known resistance genes coding for meropenem resistance were detected by whole genome sequencing (WGS). Moreover, selective methods were applied on the same sample material to investigate the occurrence of both *E. coli* resistant to ESC and CRE in fattening pigs without detecting any CRE from this sample (see page 72).

As shown in Figure 50, the number of isolates being fully susceptible has been relatively stable between 80-90% over the years 2015-2025. Comparisons to data from years before 2015 have to take into consideration changes made in the panel of antimicrobial agents tested. Resistance to streptomycin, which is no longer part of the panel, has historically been most frequently identified in isolates from pigs with 17.2% resistant isolates in 2011 (NORM/NORM-VET 2011). See textbox page 70 in the 2023 NORM/NORM-VET report for further investigation on streptomycin resistance (NORM/NORM-VET 2023). After the changes made to the test panel, resistance to sulfamethoxazole has been most frequently identified. Resistance to sulfamethoxazole was previously the second most frequently identified resistance determinant.

In a European perspective, the occurrence of resistance among *E. coli* from fattening pigs in Norway is among the lowest (EFSA and ECDC Summary Report 2023-2024). The occurrence varies markedly between countries reporting to EFSA, ranging from very few susceptible isolates and up to nearly 80% fully susceptible, with the levels of full susceptibility decreasing in a north to south gradient. This favourable Norwegian situation corresponds to the low use of antimicrobials in the Norwegian pig production.

Enterococcus spp. from pigs

Caecal samples from a total of 299 fattening pigs were examined. *E. faecalis* was obtained from 24 (8.0%) and *E. faecium* from 82 (27.4%) of the samples. One isolate of *E. faecalis* and/or *E. faecium* per positive sample was susceptibility tested. The results are presented in the text, in Tables 16-17 and Figures 51-52.

TABLE 16. Antimicrobial resistance in *Enterococcus faecalis* from caecal samples of fattening pigs (n=24) in 2025.

		Distribution (n) of MIC values (mg/L)*															
Substance	Resistance (n)	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128	256	≥512
Tetracycline	13							11					4	6	3		
Tigecycline	0			1	11	12											
Chloramphenicol	0									24							
Ampicillin	0						3	4	16	1							
Erythromycin	0							12	12								
Quinupristin-dalfopristin	0										2	22					
Gentamicin	0										12	12					
Ciprofloxacin	0						1	19	4								
Vancomycin	0							6	10	8							
Teicoplanin	0						24										
Linezolid	0								23	1							
Daptomycin	0							2	20	2							

*Bold vertical lines denote epidemiological cut-off values for resistance. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested.

TABLE 17. Antimicrobial resistance in *Enterococcus faecium* from caecal samples of fattening pigs (n=83) in 2025.

			Distribution (%) of MIC values (mg/L)*															
Substance	Resistance (%)	[95% CI]	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128	256	≥512
Tetracycline	31.7	[21.9-42.9]							68.3						31.7			
Tigecycline	0.0	[0.0-4.4]		3.7	42.7	52.4	1.2											
Chloramphenicol	0.0	[0.0-4.4]									25.6	74.4						
Ampicillin	26.8	[17.6-37.8]						9.8	13.4	24.4	25.6	25.6	1.2					
Erythromycin	4.9	[1.3-12.0]							22.0	69.5	3.7	2.4					2.4	
Quinupristin-dalfopristin	62.2	[50.8-72.7]						8.5	25.6	3.7	53.7	8.5						
Gentamicin	0.0	[0.0-4.4]										95.1	4.9					
Ciprofloxacin	0.0	[0.0-4.4]					2.4	34.1	32.9	15.9	9.8	4.9						
Vancomycin	0.0	[0.0-4.4]							90.2	9.8								
Teicoplanin	0.0	[0.0-4.4]						97.6	2.4									
Linezolid	0.0	[0.0-4.4]							6.1	90.2	3.7							
Daptomycin	0.0	[0.0-4.4]					3.7	3.7	24.4	51.2	15.9	1.2						

*Bold vertical lines denote epidemiological cut-off values for resistance. CI = confidence interval. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested.

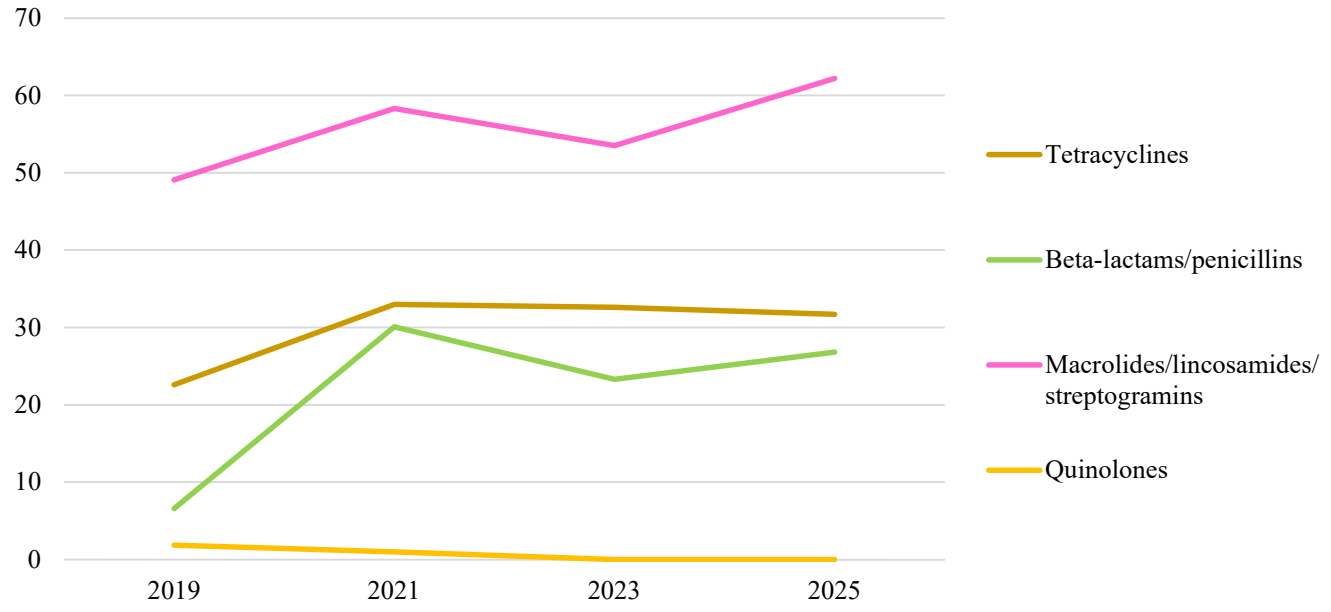

FIGURE 51. Prevalence of resistance to various antimicrobial classes in *Enterococcus faecium* from fattening pigs in 2019-2025. The epidemiological cut-off values used in NORM-VET 2025 were applied.

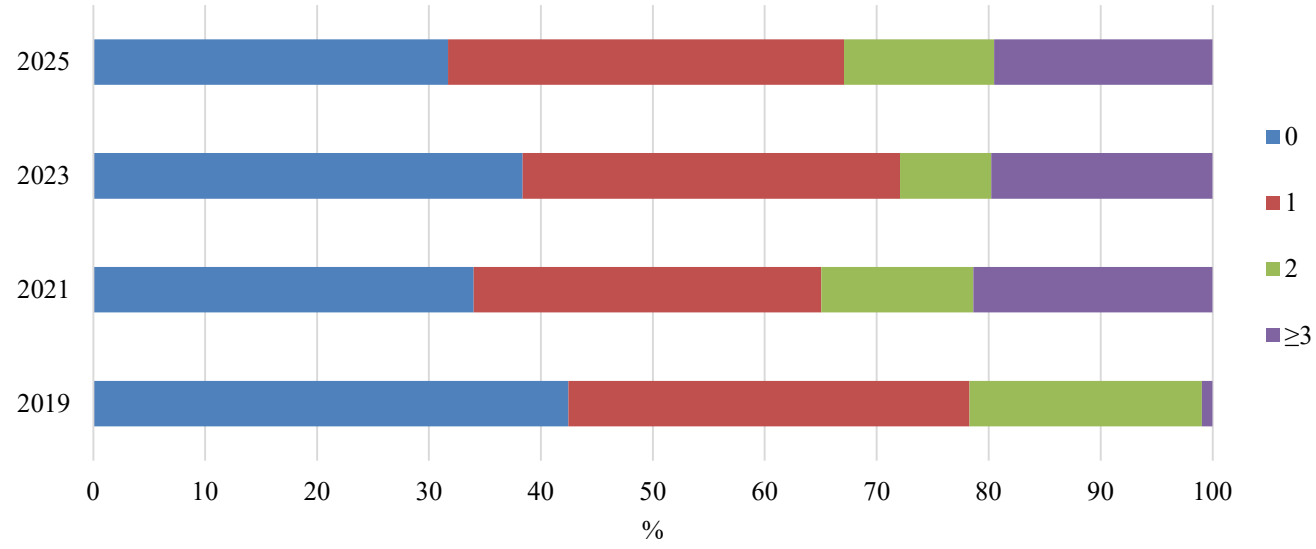

FIGURE 52. Antimicrobial resistance profile for *Enterococcus faecium* from fattening pigs in 2019-2025. Percentage of isolates susceptible to all (0) or resistant to one (1), two (2), and three or more (≥3) antimicrobial classes are illustrated. The epidemiological cut-off values used in NORM-VET 2025 were applied.

RESULTS AND COMMENTS

PIGS

The 2025 data showed that 45.8% of the 24 *E. faecalis* isolates from pig caecal samples were susceptible to all antimicrobial agents included in the test panel. The remaining *E. faecalis* isolates, i.e. 54.2% were resistant to one antimicrobial class (tetracyclines), indicating a very high occurrence of resistance in *E. faecalis* according to the EFSA classification described in Appendix 6.

Among the 82 *E. faecium* isolates, 31.7% were fully susceptible while 35.4% were resistant to one antimicrobial class, 13.4% were resistant to two (tetracyclines and macrolides/lincosamides) and 19.5% were resistant to three antimicrobial classes (Figure 52). Resistance to the streptogramin quinupristin-dalfopristin was the most frequently identified resistance determinant, followed by resistance to tetracycline (Figure 51). In total, 68.3% of the *E. faecium* isolates were resistant to at least one antimicrobial agent, indicating a very high occurrence of resistance according to the EFSA classification described in Appendix 6.

The 2025 results are in concordance with the results from 2021 and 2023 (NORM/NORM-VET 2021, NORM/NORM-VET 2023). Compared to the results from 2019 (NORM/NORM-VET 2019), however, there has been an increase in resistance to several antimicrobial classes, especially to the beta-lactam ampicillin, shown in Figure 51, i.e. from 6.6% in 2019 to 26.8% in 2025 (p=0.002). This increase in ampicillin resistance has affected the occurrence of MDR isolates, with an increase in MDR from 0.9% in 2019 to 19.5% in 2025. It has also resulted in a slight decrease in totally susceptible *E. faecium* isolates from 42.5% in 2019 to between 34-40% in 2021-2025 (Figure 52).

SPORTS AND FAMILY ANIMALS

Escherichia coli from cats

Faecal swab samples from a total of 291 cats were examined. The majority of these cats had no symptoms from the intestines, as only 15 cats were reported to have such symptoms. Although a total of 26 cats were reported to have received antimicrobial treatment the last 12 months, the 15 cats with symptoms from the intestines were not among these. *E. coli* isolates were obtained from 253 samples (86.9%) and were further susceptibility tested (one isolate per positive sample). The results are presented in Table 18, Figure 53-54, and in the text.

TABLE 18. Antimicrobial resistance in *Escherichia coli* (n=253) from faecal swab samples from cats in 2025.

			Distribution (%) of MIC values (mg/L)*															
Substance	Resistance (%)	[95% CI]	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128	256	≥512
Tetracycline	3.6	[1.6-6.6]								86.2	10.3				3.6			
Tigecycline	0.0	[0.0-1.4]					99.2	0.8										
Chloramphenicol	0.4	[0.0-2.2]										98.4	1.2	0.4				
Ampicillin	13.4	[9.5-18.3]							2.0	36.2	45.3	2.8		1.2	12.3			
Cefotaxime	1.2	[0.2-3.4]					98.8	0.8				0.4						
Ceftazidime	0.0	[0.0-1.4]					97.2	2.4	0.4									
Meropenem	0.0	[0.0-1.4]		98.8	1.2													
Trimethoprim	2.4	[0.9-5.1]					65.2	31.3	1.2					2.4				
Sulfamethoxazole	5.9	[3.4-9.6]										34.4	43.9	12.6	3.2	0.4	0.4	5.1
Azithromycin	0.0	[0.0-1.4]								34.0	56.5	9.5						
Gentamicin	0.4	[0.0-2.2]						58.1	39.1	2.4				0.4				
Amikacin	0.4	[0.0-2.2]									94.9	4.7	0.4					
Ciprofloxacin	3.2	[1.4-6.1]	87.4	9.5		0.4	2.0	0.8										
Nalidixic acid	2.8	[1.1-5.6]									96.0	1.2	0.4		0.8	1.6		
Colistin	0.0	[0.0-1.4]							100									

*Bold vertical lines denote epidemiological cut-off values for resistance. CI = confidence interval. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested.

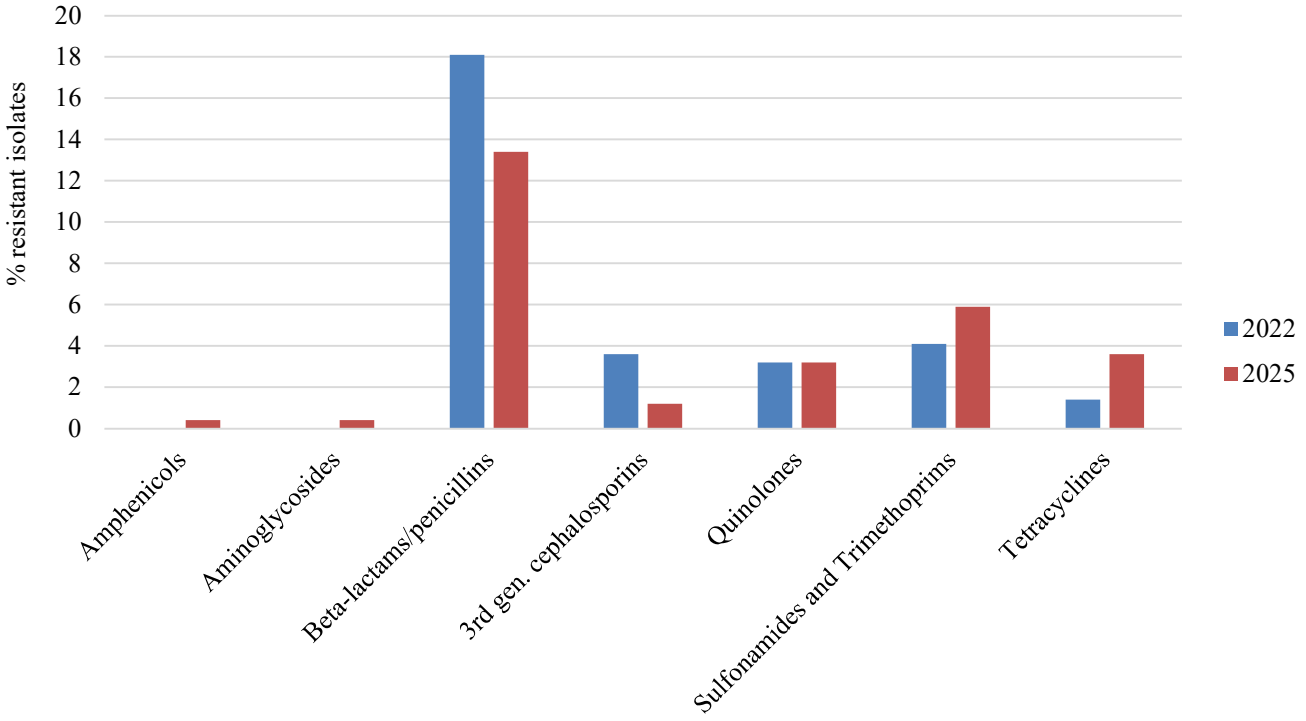

FIGURE 53. Prevalence of resistance to various antimicrobial classes in *Escherichia coli* from cats in 2022 and 2025. The epidemiological cut-off values used in NORM-VET 2025 were applied.

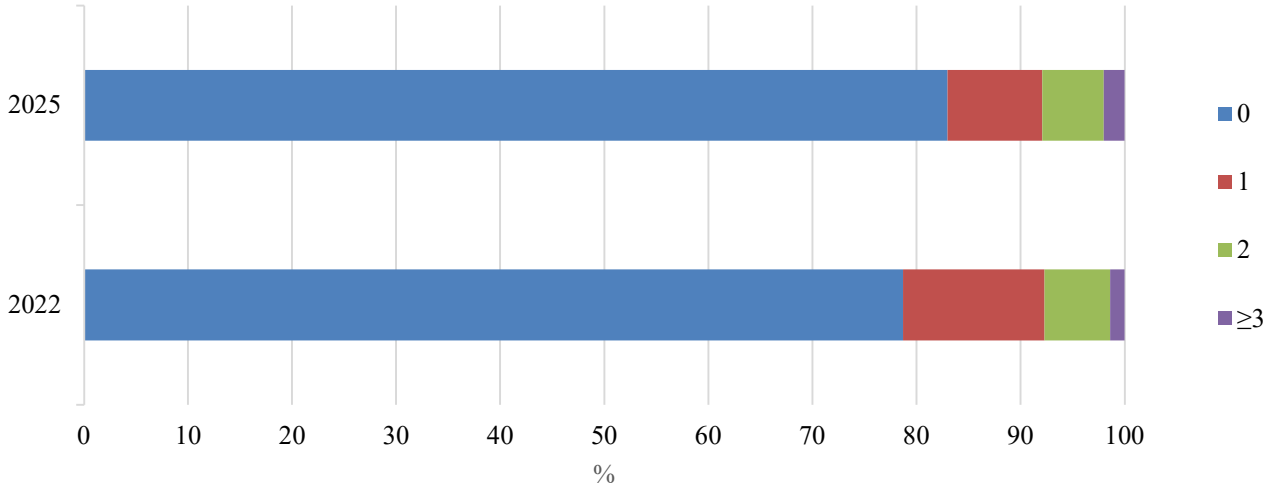

FIGURE 54. Antimicrobial resistance profile for *Escherichia coli* from cats in 2022 and 2025. Percentage of isolates susceptible to all (0) or resistant to one (1), two (2), and three or more (≥3) antimicrobial classes are illustrated. The epidemiological cut-off values used in NORM-VET 2025 were applied.

RESULTS AND COMMENTS

In total, 83.0% of the isolates were susceptible to all antimicrobial agents included. Altogether, 9.1% of the isolates were resistant to one antimicrobial class (predominantly ampicillin, Figure 53), 5.9% to two, and 2.0% to three or more antimicrobial classes (Figure 54). In total, 17% of the isolates were resistant to at least one of the tested antimicrobial agents, indicating a moderate occurrence of resistance among *E. coli* from faecal samples of cats according to the EFSA classification described in Appendix 6.

Two of the isolates displayed resistance to the ESC cefotaxime, though not to ceftazidime. One of these displayed an ESBL phenotype and carried the *bla*$_{\text{CTX-M-14}}$ gene. The other displayed an AmpC beta-lactamase phenotype due to mutations in the chromosomally located *ampC* gene (n.-32T>A). Selective methods were applied to screen the same sample material for the occurrence of ESC resistant *E. coli* and of CRE.

Samples from cats have been included in NORM-VET on only one previous occasion, in 2022 (NORM/NORM-VET 2022). The 2025 results are in concordance with the results from 2022 as shown in Figures 53-54.

Staphylococcus felis from cats

A total of 291 oral/nasal/perineum swab samples from cats were investigated for the presence of *S. felis*. Among these, only 20 were reported to have clinical symptoms from skin or ears, of which two had received treatment with antimicrobials the last 12 months. In total, 26 cats had received antimicrobial treatment last 12 months. *S. felis* was detected from 162 of these samples (55.7%). One isolate per cat was susceptibility tested. The results are presented in Table 19, Figures 55-56 and in the text.

TABLE 19. Antimicrobial resistance in *Staphylococcus felis* (n=162) from oral/nasal/perineum swab samples from cats in 2025.

			Distribution (%) of MIC values (mg/L)*															
Substance	Resistance (%)	[95% CI]	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128	256	≥512
Tetracycline	0.6	[0.0-3.4]						99.4						0.6				
Chloramphenicol	0.0	[0.0-2.3]									95.7	4.3						
Benzylpenicillin	13.0	[8.2-19.1]			85.8	1.2	1.9		0.6	10.5								
Cefoxitin	0.0	[0.0-2.3]						99.4		0.6								
Trimethoprim	0.6	[0.0-3.4]							74.1	25.3	0.6							
Sulfamethoxazole	ND	ND													68.5	21.6	4.9	5.0
Erythromycin	8.0	[4.3-13.3]					79.6	12.3					8.0					
Clindamycin	8.6	[4.8-14.1]				75.9	15.4	0.6	0.6			7.4						
Quinupristin-dalfopristin	0.0	[0.0-2.3]						99.4	0.6									
Streptomycin	0.0	[0.0-2.3]									92.0	8.0						
Gentamicin	0.0	[0.0-2.3]						100										
Kanamycin	0.0	[0.0-2.3]									100							
Ciprofloxacin	0.0	[0.0-2.3]					100											
Vancomycin	0.0	[0.0-2.3]							100									
Fusidic acid	0.6	[0.0-3.4]					98.8	0.6			0.6							
Tiamulin	0.6	[0.0-3.4]						94.4	4.9			0.6						
Linezolid	0.0	[0.0-2.3]							100									
Rifampicin	0.0	[0.0-2.3]	100															
Mupirocin	0.0	[0.0-2.3]						100										

*Bold vertical lines denote epidemiological cut-off values for resistance. CI = confidence interval. ND = not defined. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested. ECOFFs used are those for *Staphylococcus aureus*.

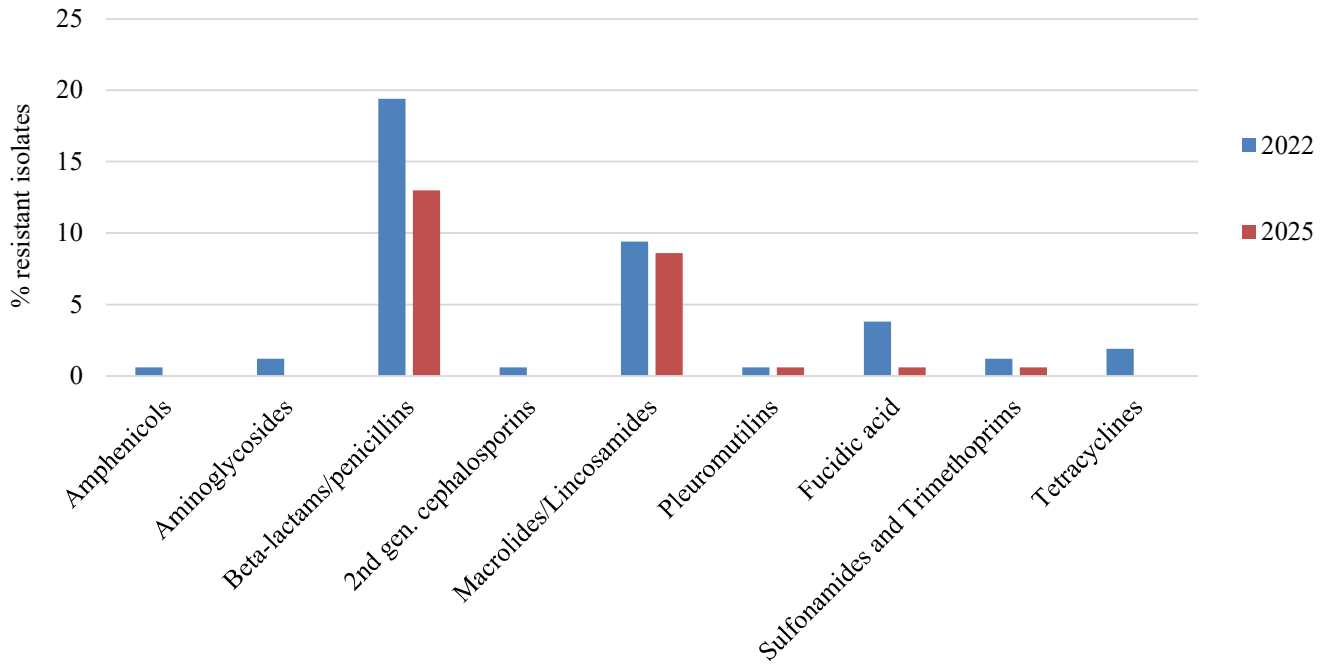

FIGURE 55. Prevalence of resistance to various antimicrobial classes in *Staphylococcus felis* from cats in 2022 and 2025. The epidemiological cut-off values used in NORM-VET 2025 were applied.

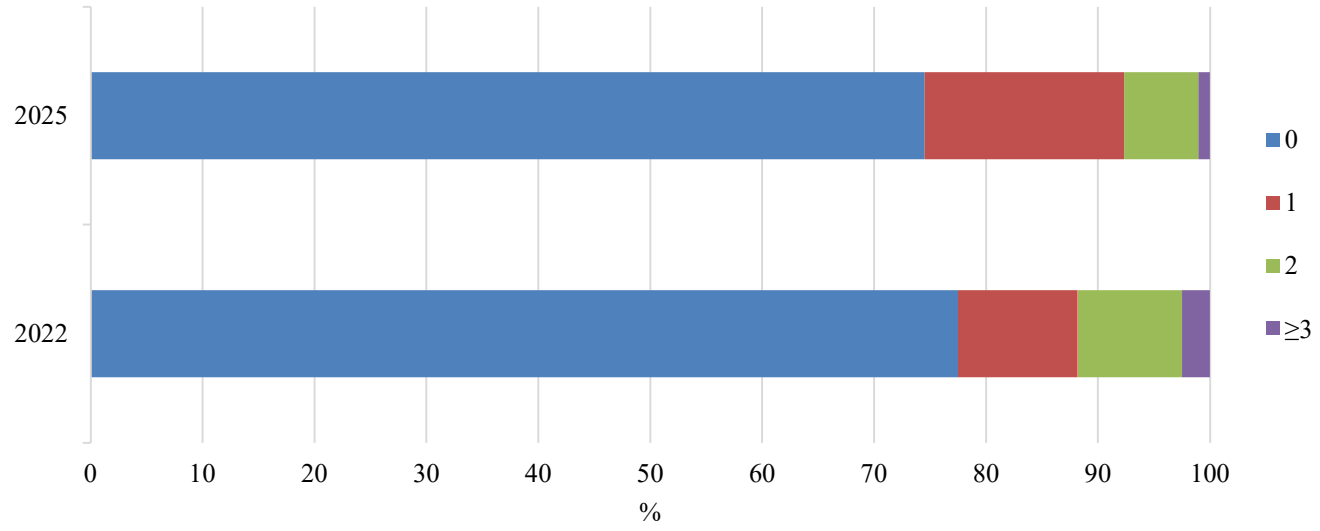

FIGURE 56. Antimicrobial resistance profile for *Staphylococcus felis* from cats in 2022 and 2025. Percentage of isolates susceptible to all (0) or resistant to one (1), two (2), and three or more (≥3) antimicrobial classes are illustrated. The epidemiological cut-off values used in NORM-VET 2025 were applied.

RESULTS AND COMMENTS

In total, 74.5% of the *S. felis* isolates were susceptible to all antimicrobial agents included in the test panel. Altogether, 17.8% of the isolates were resistant to one antimicrobial class, 6.6% to two, and 1.0% to three or more antimicrobial classes (Figure 56). Resistance to benzylpenicillin was the most frequently identified resistance determinant, followed by resistance to the macrolides erythromycin and clindamycin (Figure 55).

All isolates were subjected to the clover leaf test for detection of beta-lactamase production. The majority of isolates with a positive beta-lactamase test had penicillin MIC values > 0.125 mg/L, and the majority of beta-lactamase negative isolates had penicillin MIC-values ≤ 0.125 mg/L, overall confirming the results from the susceptibility testing.

The *S. felis* isolates were also subjected to oxacillin susceptibility testing using disk diffusion to identify possible methicillin resistant isolates. All the isolates were susceptible.

Isolation and susceptibility testing of carrier *S. felis* have been included in NORM-VET on only one previous occasion, in 2022 (NORM/NORM-VET 2022). The 2025 results are in concordance with the results from 2022 (Figures 55-56).

NOTIFIABLE ANTIMICROBIAL RESISTANCE IN ANIMALS

Madelaine Norström, Jannice Schau Slettemeås and Anne Margrete Urdahl

Resistance to some important antimicrobials, such as extended-spectrum cephalosporins (ESC) and carbapenems are defined by the WHO as critically important for antimicrobial treatment of human infections (WHO 2019). A reservoir of such resistant bacteria in food production animals and the food chain is of concern as they may have an impact on resistance development in human bacterial populations.

In 2019, some antimicrobial resistant bacteria were made notifiable to the Norwegian Food Safety Authority by the Animal Health Regulations. This was implemented to monitor the occurrence and to follow trends of these in the animal populations. The resistant bacteria included in the regulation largely corresponds to those that are notifiable in humans.

In NORM-VET, selective screening methods are used for detection of *E. coli/Enterobacterales* resistant to ESC, carbapenem resistant *Enterobacterales* (CRE), vancomycin resistant *Enterococcus* spp. (VRE), linezolid resistant *Enterococcus* spp. (LRE), methicillin resistant *Staphylococcus aureus* (MRSA) and methicillin resistant *Staphylococcus pseudintermedius* (MRSP).

In 2025, samples from animals included caecal samples from cattle and pigs, and faecal swabs from cats for isolation of ESC-resistant *E. coli* and CRE. In addition, swabs from oral/nasal mucosa of cats were included for detecting MRSA/MRSP. Results from the surveillance programme for MRSA in pigs are described as well (see page 72).

Extended-spectrum cephalosporin resistant *Escherichia coli* from cattle, pigs and cats

A total of 308 cattle and 299 pig caecal samples, as well as 288 faecal swab samples from cats, were examined for the presence of *E. coli* resistant to extended-spectrum cephalosporins (ESC) by selective methods. One isolate per positive sample was susceptibility tested. Results are presented in Figures 57-58 and in the text.

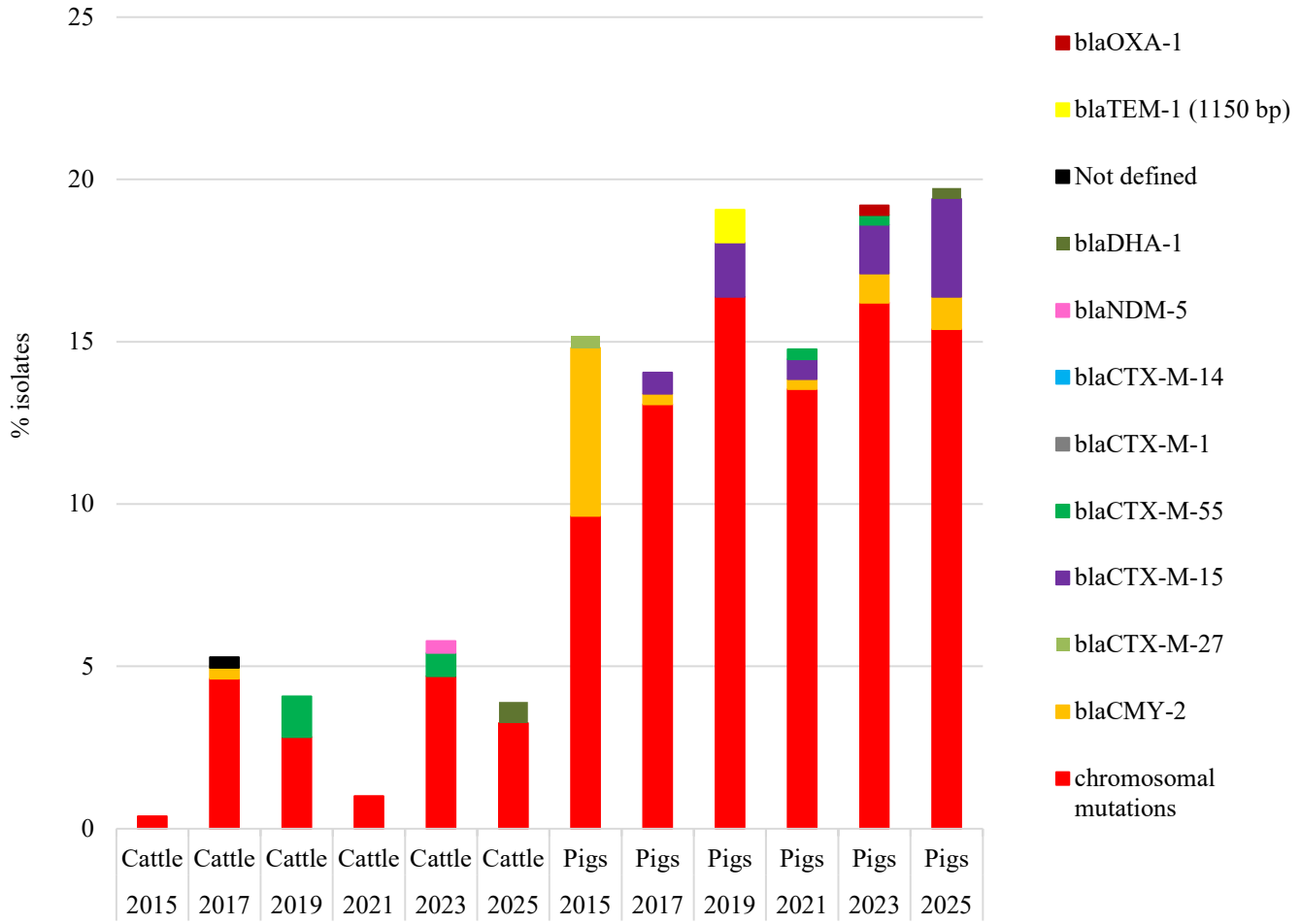

FIGURE 57. Occurrence (%) of different ESC-resistant *Escherichia coli* from fattening pigs and cattle in 2015-2025.

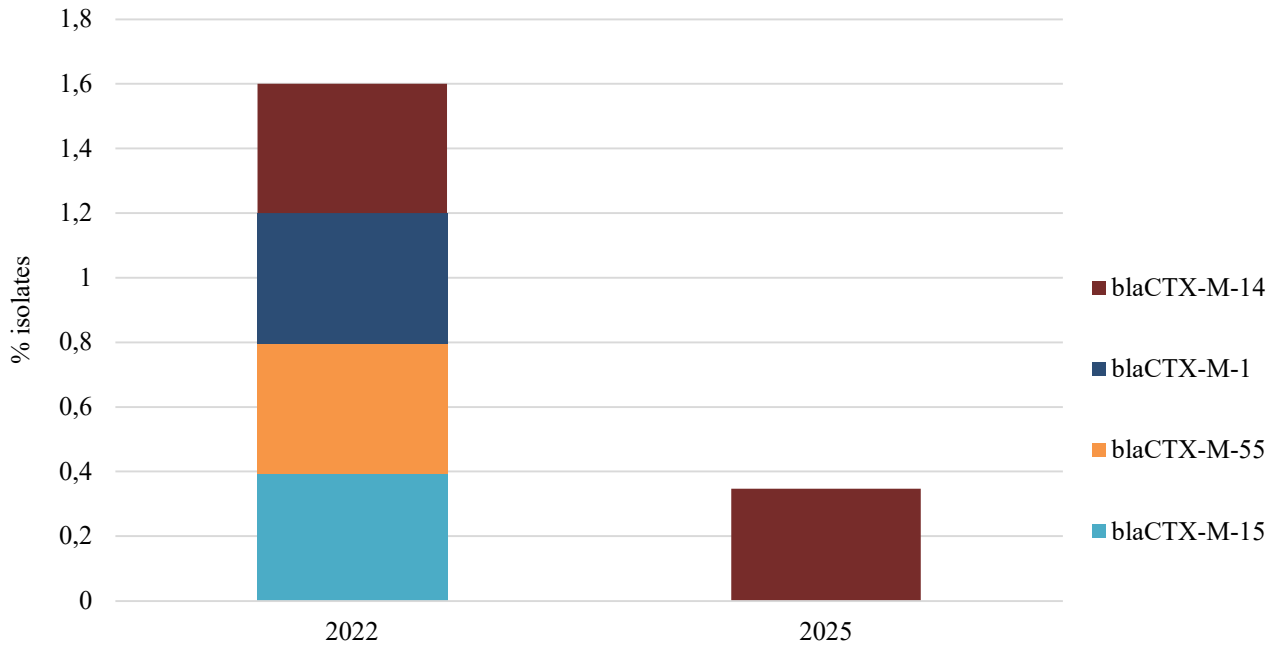

FIGURE 58. Occurrence (%) of different ESC-resistant *Escherichia coli* from cats in 2022 and 2025.

RESULTS AND COMMENTS

CATTLE AND PIGS

ESC-resistant *E. coli* was detected from eleven of the cattle (3.6% [95% CI: 1.8-6.3]) and 59 of the pig (19.7% [95% CI: 15.4-24.7]) samples. In addition to being resistant to beta-lactams, i.e. ampicillin and the ESCs cefotaxime and ceftazidime, resistance to sulfamethoxazole, trimethoprim, tetracycline and quinolones were most commonly detected.

All eleven cattle isolates displayed an AmpC beta-lactamase phenotype. For nine of these isolates the resistance was due to mutations in the promoter and attenuator region of the chromosomally located *ampC* gene (p.C-42T) causing an upregulation. The two last isolates were genotyped as $bla_{\text{DHA-1}}$.

Of the 59 pig isolates, 50 displayed an AmpC beta-lactamase phenotype where three were genotyped as $bla_{\text{CMY-2}}$ and one as $bla_{\text{DHA-1}}$. The $bla_{\text{DHA-1}}$ isolate also carried multiple resistance genes like *qnrB4* and *mph*(A). In the remaining 46 isolates, the AmpC phenotype was due to mutations in the promoter and attenuator region of the chromosomally located *ampC* gene (p.C-42T) causing an upregulation. Nine isolates displayed an ESBL phenotype and were genotyped as $bla_{\text{CTX-M-15}}$, where one isolate in addition carried the *qnrS1* gene encoding quinolone resistance.

The overall occurrence of all genotypes of ESC-resistant *E. coli* in cattle is similar to the results from 2017, 2019 and 2023, while the occurrences were slightly lower in 2015 and 2021 (Figure 57). This is mainly due to variation in the resistance determined by chromosomal mutations. In pigs, the overall occurrence of all genotypes is in concordance with previous years. The occurrence of *E. coli* resistant to ESC is in both cattle and pigs mainly due to isolates with mutations in the chromosomally located *ampC* gene. Additionally, there were some ESC-resistant *E. coli* isolated from pig in 2015 due to occurrence of $bla_{\text{CMY-2}}$. A few *E. coli* displaying an ESBL phenotype due to plasmid encoded genes have been detected as well through the years (Figure 57). The source of introduction of plasmid encoded resistance in *E. coli* to cattle and pigs in Norway, as well as their ability to disseminate further, is currently unknown. There is negligible numbers of import of live cattle and pigs to Norway, which is a preventive measure for importing *E. coli* resistant to ESC from areas/countries with higher prevalence.

In a European perspective, the occurrence in Norwegian cattle and fattening pigs of *E. coli* resistant to ESC that are not due to chromosmal mutations, are among the lowest, though the occurrences varies markedly between countries reporting to EFSA (EFSA and ECDC Summary Report 2021-2022). A continued awareness of animal bacterial reservoirs resistant to ESC is of importance to be able to implement control measures if needed.

CATS

E. coli resistant to ESC were detected in only one of the cat samples (0.4% [95% CI: 0.009-1.9]). The isolate displayed an ESBL phenotype and carried the $bla_{\text{CTX-M-14}}$ gene.

This is in concordance with the results from 2022 where ESC resistant *E. coli* was detected from 1.6% of the samples. The different genotypes identified from cats in 2022 and 2025 are shown in Figure 58.

Carbapenem resistant *Enterobacterales* from cattle, pigs and cats

Selective method for detection of carbapenem resistant *Enterobacterales* (CRE) was performed on a total of 308 and 299 caecal samples from cattle and pigs, respectively. In addition, 288 faecal swab samples from cats were screened. CRE was not detected in any of the samples (cattle [95% CI: 0.0-1.1], pigs [95% CI: 0.0-1.2], cats [95% CI: 0.0-1.3]). To date, CRE has not been detected from pigs, nor from cats in Norway. However, CR *E. coli* was detected in a caecal sample from a dairy herd in 2023 (NORM-VET 2023), and CR *Klebsiella pneumoniae* from a dog with chronic skin and ear infections in 2025 (Sunde and Urdahl 2025). Carbapenems are not approved for use in food-producing animals in EU and EEA countries. Nevertheless, resistance to these critically important antimicrobial agents has increasingly been reported from animals in some of the EU/EEA countries, and further monitoring is recommended to follow the situation in the years to come.

Methicillin resistant *Staphylococcus aureus* (MRSA) and methicillin resistant *Staphylococcus pseudintermedius* (MRSP) from cats

A total of 291 samples from cats were investigated for the presence of methicillin resistant *S. aureus* (MRSA) and methicillin resistant *S. pseudintermedius* (MRSP). Neither MRSA nor MRSP were detected from the samples [95% CI: 0.0-1.3]. This is in concordance with the screening results from 2022.

Surveillance of methicillin resistant *Staphylococcus aureus* (MRSA) in pigs

Methicillin resistant *S. aureus* (MRSA) associated with animals, i.e. livestock associated MRSA (LA-MRSA) have become widespread in pig populations around the world, thereby representing a risk for dissemination to the human population. As the only country in the world, Norway implemented a control strategy from 2013 including measures to eradicate MRSA in pigs as described in Grøntvedt *et al.* 2016 (1). The rationale behind this strategy was to prevent the pig population from becoming a domestic reservoir of MRSA with the potential of zoonotic transmission, as MRSA is not a significant cause of disease in pig.

As part of this strategy, an extensive yearly surveillance programme was implemented from 2014. The aim of the programme is to identify MRSA positive pig herds. Each year the nucleus and multiplier herds, as well as central units of sow pool herds and the 20 biggest sow herds are sampled twice, while the remaining sow herds are sampled once. Every third year finisher pig herds are sampled instead of the sow herds. In 2025, 524 herds were investigated, of which 58 were genetic nucleus or multiplier herds, 11 herds were central units of the sow pool herds, 19 were of the largest farrow to grower or farrow to finish herds, and the remaining 436 were herds with more than 10 sows. The surveillance programme did not detect any pig herds with MRSA in 2025. Further details can be found in the report "The surveillance programme for methicillin resistant *Staphylococcus aureus* in pig in Norway 2025" (2). Figure 59 shows the number of pig herds positive for MRSA in 2013-2025, including clonal complex (CC) and *spa*-types.

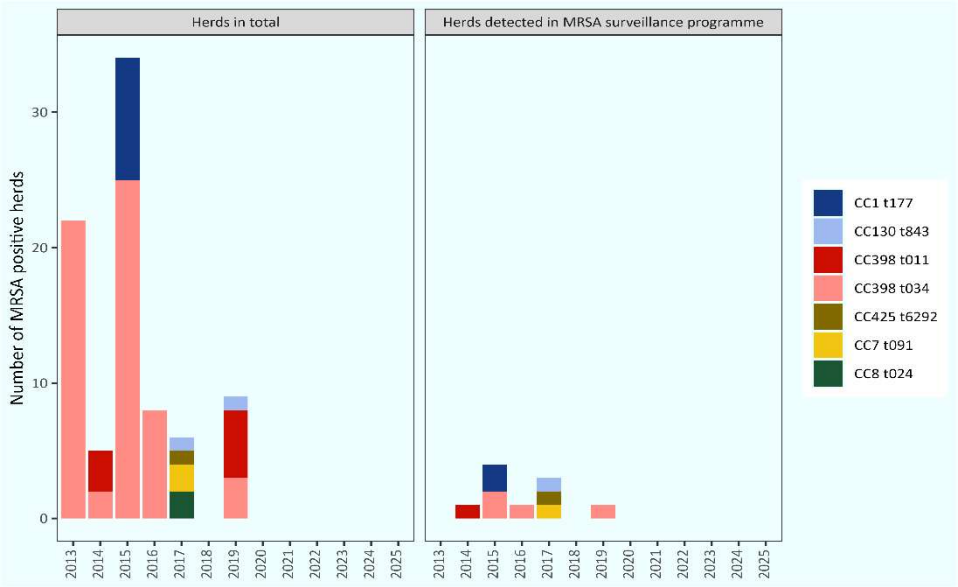

FIGURE 59. Number of pig herds positive for methicillin resistant *Staphylococcus aureus* (MRSA) in Norway in 2013-2025. The herds detected by the MRSA surveillance programme in pigs are shown on the right, while the figure on the left also includes herds detected through contact-tracing. There have been no findings since 2019. Colours of bars refer to the clonal complex (CC) and *spa*-type of the isolates, *mecC* gene detected for CC130 and CC425, *mecA* gene for the others.

References

1. Grøntvedt. C.A., Elstrøm. P., Stegger. M., Skov. R.L., Skytt Andersen. P., Larssen. K.W., Urdahl. A.M., Angen. Ø., Larsen. J., Åmdal. S., Løtvedt. S.M., Sunde. M., Bjørnholt. J.V. Methicillin-Resistant *Staphylococcus aureus* CC398 in Humans and Pigs in Norway: A "One Health" Perspective on Introduction and Transmission. Clin Infect Dis. 2016 Dec 1;63(11):1431-1438.
2. Urdahl AM, Norström M, Welde H, Bergsjø B, Grøntvedt CA. The surveillance programme for methicillin resistant *Staphylococcus aureus* in pigs in Norway 2025. *Surveillance programmes for terrestrial and aquatic animals in Norway. Annual report 2025.* Norwegian Veterinary Institute 2026.

Anne Margrete Urdahl, Madelaine Norström, Marianne Sunde and Carl Andreas Grøntvedt, Norwegian Veterinary Institute.

Notifiable antimicrobial resistant bacteria in animals

In 2019, some antimicrobial resistant bacteria were made notifiable to the Norwegian Food Safety Authority (NFSA) by the Animal Health Regulations. This was implemented to monitor the occurrence and follow trends in the animal populations. The resistant bacteria included in the regulations largely correspond to those that are notifiable in humans (Table 20).

TABLE 20. Overview of antimicrobial resistant bacteria notifiable according to the Norwegian Animal Health Regulations.

Resistant bacteria	Explanations with MIC and zone diameters
Colistin resistant *Enterobacterales*, *Acinetobacter* spp. and *Pseudomonas* spp.	*Enterobacterales* (e.g. *Escherichia coli* and *Klebsiella* spp.), *Acinetobacter* spp. and *Pseudomonas* spp. resistant to colistin (MIC ECOFF > 2 mg/L, 2 mg/L and 4 mg/L, respectively, or by detected *mcr* genes). Exempt from notification are *Enterobacterale*s that are naturally resistant to colistin: *Proteus* spp., *Morganella morganii*, *Serratia* spp. and *Providencia* spp.
Enterobacterales and *Pseudomonas* spp. resistant to extended-spectrum cephalosporins (ESC)	*Enterobacterales* (e.g. *Escherichia coli* and *Klebsiella* spp.) and *Pseudomonas* spp. resistant to 3. and 4. generations cephalosporins. *E. coli*; MIC (zone diameter): • Cefotaxime MIC > 0.25 mg/L (< 21 mm) • Ceftazidime MIC > 0.5 mg/L (< 20 mm) *Salmonella* spp.; MIC (zone diameter): • Cefotaxime MIC > 0.5 mg/L (< 20 mm) • Ceftazidime MIC > 2 mg/L (< 20 mm) *K. aerogenes*; MIC (zone diameter): • Cefotaxime MIC > 0.5 mg/L (-) • Ceftazidime MIC > 1 mg/L (-) *K. oxytoca*; MIC (zone diameter): • Cefotaxime MIC > 0.125 mg/L (-) • Ceftazidime MIC > 0.5 mg/L (-) *K. pneumoniae*; MIC (zone diameter): • Cefotaxime MIC > 0.25 mg/L (< 21 mm) • Ceftazidime MIC > 0.5 mg/L (< 19 mm) *Pseudomonas aeruginosa*; MIC (zone diameter): • Ceftazidime MIC > 8 mg/L (< 16 mm) Exempt from the notification obligation are the detection of inherent/natural resistance, e.g. resistance to cefotaxime in *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Stenotrophomonas maltophilia*
Carbapenemase producing/carbapenem resistant *Enterobacterales* (CPE/CRE), *Acinetobacter* spp. and *Pseudomonas* spp.	*Enterobacterales* (e.g. *Escherichia coli*, *Klebsiella* spp., *Enterobacter* spp.), *Acinetobacter* spp. and *Pseudomonas* spp. resistant to carbapenems. *Enterobacterales*; MIC (zone diameter): • Meropenem MIC > 0.125 mg/L (< 25 mm) *Acinetobacter baumannii* and *Pseudomonas aeruginosa*; MIC (zone diameter for *P. aeruginosa*): • Meropenem MIC > 2 mg/L (< 24 mm) Exempt from the notification obligation are *Enterobacterales* that are naturally resistant to carbapenems such as *Stenotrophomonas maltophilia*
Linezolid resistant *Enterococcus* spp. (LRE)	*Enterococcus* spp. resistant to linezolid (MIC > 4 mg/L, zone diameter < 19 mm), and/or isolates with detected transferable linezolid resistance genes
Methicillin resistant *Staphylococcus aureus* (MRSA)	*Staphylococcus aureus* resistant to cefoxitin (MIC > 4 mg/L, zone diameter < 22 mm), and/or isolates with detected *mecA* or *mecC* genes
Methicillin resistant *Staphylococcus pseudintermedius* (MRSP)	*Staphylococcus pseudintermedius* resistant to cefoxitin (MIC > 4 mg/L, zone diameter < 22 mm), and/or isolates with detected *mecA* or *mecC* genes
Linezolid resistant *Staphylococcus* spp.	*Staphylococcus* spp. resistant to linezolid (MIC > 4 mg/L, zone diameter < 19 mm), and/or isolates with detected transferable linezolid resistance genes
Vancomycin resistant *Enterococcus* spp.	*Enterococcus* spp. resistant to vancomycin (MIC > 4 mg/L, zone diameter < 12 mm). Exempt from the notification requirement are *Enterococcus gallinarum* and *Enterococcus casseliflavus*, which are naturally resistant
Fluoroquinolone resistant *Campylobacter* spp.	Thermophile *Campylobacter* spp. (e.g. *C. jejuni* and *C. coli*) resistant to fluoroquinolones: • Ciprofloxacin MIC > 0.5 mg/L (zone diameter < 26 mm)

Since the implementation of the notification requirement, there has been some notifications made every year. However, several reported cases had to be rejected for further analysis, as the reporting was incomplete or unclear. Part of the reason for this may be explained by a poorly designed reporting system during the first years. However, the last couple of years a new and better system for reporting these has been implemented at the NFSA website (Melding om resistente bakterier) though this has not led to an increase in reported cases.

Underreporting of antimicrobial resistant bacteria to the NFSA is suspected, particularly for bacteria resistant to extended-spectrum cephalosporins (ESC), as well as MRSA and MRSP. This may be partly attributable to a substantial proportion of samples from animals being analysed by laboratories abroad, which may not be aware of national notification requirements. In such cases, the responsibility for reporting rests with the submitting veterinarians; however, incomplete awareness of these reporting obligations likely contributes further to underreporting. The table below (Table 21) summarises the number of cases reported to the NFSA through these years.

TABLE 21. Number of notifiable antimicrobial resistant bacteria reported to the Norwegian Food Safety Authority in 2019-2025.

Notifiable resistant bacteria*	**2019**	**2020**	**2021**	**2022**	**2023**	**2024**	**2025**	**Total**
Carbapenem resistant						**1**	**1**	**2**
Escherichia coli						1		1
Klebsiella pneumoniae							1	1
ESC resistant	**17**	**3**		**4**	**7**	**6**	**3**	**40**
Acinetobacter baumannii							1	1
Enterobacter cloacae	1				1	1		3
Enterobacterales							1	1
Escherichia coli	16			1	1	1	1	20
Klebsiella pneumoniae				1				1
Pseudomonas aeruginosa					3	3		6
Pseudomonas spp.				1	2	1		4
unknown		3		1				4
Methicillin resistant	**7**	**3**	**3**	**2**	**4**	**5**	**3**	**26**
Staphylococcus aureus			1	1	3	1	2	8
Staphylococcus pseudintermedius	5	3	2	1		4	1	16
unknown	2							2
Colistin resistant							**1**	**1**
Escherichia coli							1	1

*Animal of origin (year): unknown ESC resistant bacteria from a bird (2020); two and 14 ESC resistant *E. coli* (2019) were from broiler parent and broiler flocks, respectively; one ESC resistant *E. cloacae* (2019), one ESC resistant *A. baumannii* (2025) and one MRSP (2019) from cats; three MRSA (2022, 2024 and 2025) and one carbapenem resistant *E. coli* from cattle; one ESC resistant *P. aeruginosa* (2024) from sheep; one ESC resistant *E. coli* from a turkey flock in 2024, the remaining reported notifiable AMR bacteria were from dogs.

Anne Margrete Urdahl, Norwegian Veterinary Institute; and Solfrid Åmdal, Norwegian Food Safety Authority.

ANTIMICROBIAL RESISTANCE IN FOOD

Gro Johannessen, Madelaine Norström, Jannice Schau Slettemeås and Anne Margrete Urdahl

In 2025, food samples included beef, pork and berries (i.e. blueberries, strawberries and raspberries). One isolate per positive sample was susceptibility tested. Some of the cut-off values defining resistance applied in NORM-VET have changed over the years. To facilitate comparisons in this report, data on prevalence of resistance presented in earlier reports have been recalculated using the cut-off values applied in 2025. Sampling, laboratory methods and data processing are described in Appendix 3.

MEAT

Extended-spectrum cephalosporin resistant *Escherichia coli* from beef and pork

In total, 320 beef and 317 pork samples were examined for the presence of *E. coli* resistant to extended-spectrum cephalosporins (ESC), i.e. cefotaxime and/or ceftazidime. Results are presented in the text and in Figure 60.

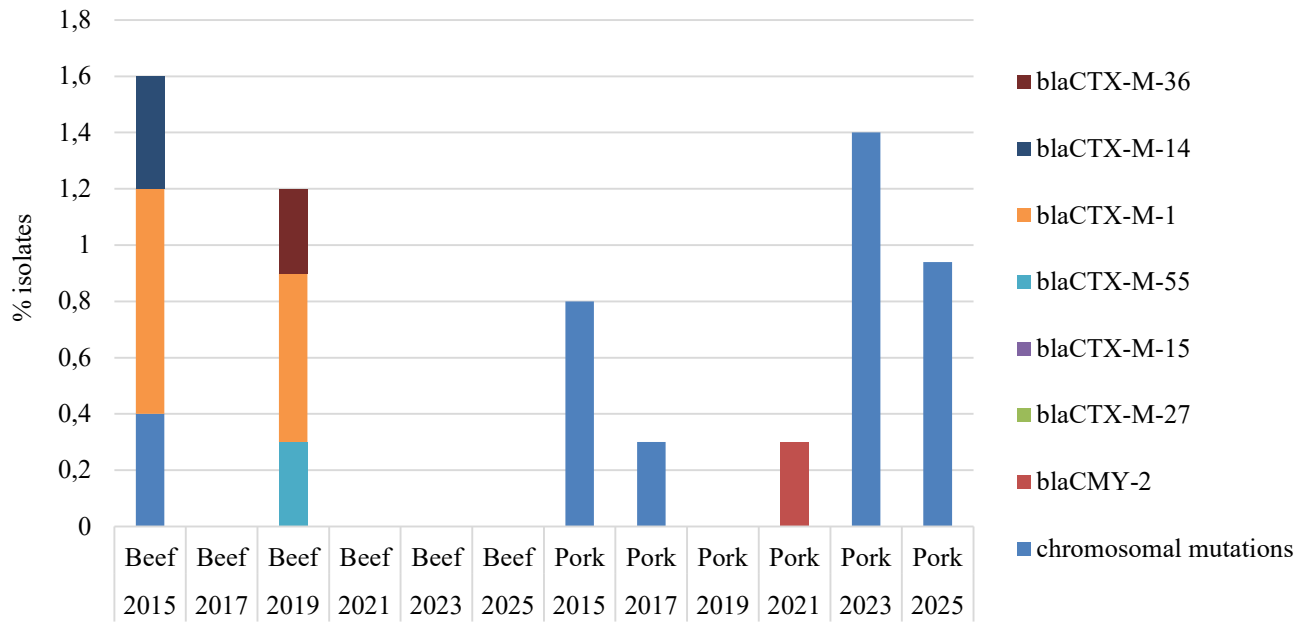

FIGURE 60. Occurrence of ESC resistant *Escherichia coli* isolates from beef and pork from 2015-2025.

RESULTS AND COMMENTS

ESC resistant *E. coli* was detected in three of the 317 pork samples (0,94% [95% CI: 0.2-2.7]). All isolates displayed an AmpC phenotype and the resistance was due to the n.-42C>T point mutation in the chromosomally located *ampC* gene. ESC-resistant *E. coli* were not detected in any of the 320 beef samples [95% CI: 0.0-1.1]. The occurrence is in concordance with previous results, though with some variations in detected resistance genes over the years as shown in Figure 60.

In a European perspective, the occurrence of *E. coli* resistant to ESC in Norwegian beef and pork continues to be among the lowest reported to EFSA (EFSA and ECDC Summary Report 2023-2024).

Transmission of bacteria, including *E. coli* resistant to ESC, between food-producing animals and meat thereof to humans may occur. However, several studies indicate that there is only a small proportion of bacteria resistant to ESC in humans that may have animals and meat thereof as a source of infection (Day et al. 2019, Dorado-Garcia et al. 2018). Such studies reflect the situation at the time of the study, and prevalence changes in animals may lead to an increase in this proportion in humans. A continued awareness of animal/food bacterial reservoirs resistant to ESC is important in order to be able to implement control measures if needed.

Carbapenem resistant *Enterobacterales* from beef and pork

A total of 320 beef and 317 pork samples were examined for the presence of carbapenem resistant *Enterobacterales* (CRE). No CRE were detected in beef [95% CI: 0.0-1.1], nor in pork samples [95% CI: 0.0-1.1]. This is in concordance with the results from previous years.

Carbapenems are not approved for use in food-producing animals in the EU and EEA countries. Nevertheless, resistance to these antimicrobial agents has increasingly been reported from animals in the EU/EEA countries. Carbapenems are defined by the WHO as critically important for treatment of human infections, and a possible development of a significant reservoir of carbapenem resistant bacteria in animals and food is therefore of concern. Further monitoring is recommended to follow the situation in the years to come.

OTHER FOOD CATEGORIES

Escherichia coli from berries

A total of 324 blueberry, 304 strawberry and 317 raspberry samples were examined. *E. coli* isolates were obtained from five of the strawberry and five of the raspberry samples, respectively. One isolate per positive sample was susceptibility tested. The 10 *E. coli* isolates were fully susceptible to all antimicrobial agents included in the test panel. In addition, selective methods were used to investigate the occurrence of ESC resistant *E. coli*, carbapenem resistant *Enterobacterales* (CRE), and methicillin resistant *Staphylococcus aureus* (MRSA) (see below). Berries have not previously been tested in NORM-VET.

Extended-spectrum cephalosporin resistant *Escherichia coli* from berries

In total, 324 blueberry, 304 strawberry and 317 raspberry samples were examined for the presence of *E. coli* resistant to extended-spectrum cephalosporins (ESC), i.e. cefotaxime and/or ceftazidime. No ESC resistant *E. coli* were detected (blueberry [95% CI: 0.0-1.1], strawberry [95% CI: 0.0-1.2], raspberry [95% CI: 0.0-1.2]).

Carbapenem resistant *Enterobacterales* from berries

A total of 324 blueberry, 304 strawberry and 317 raspberry samples were examined for the presence of carbapenem resistant *Enterobacterales* (CRE). One presumptive CRE was detected from strawberry and two from raspberry. The presumptive CR *Enterobacter ludwigii* isolated from strawberry was susceptible to the carbapenems ertapenem, imipenem and meropenem included in the testing panel. Presumptive CR *E. ludwigii* and *Enterobacter hormaechei* were isolated from raspberry. The *E. ludwigii* isolate was only resistant to the carbapenem ertapenem in the testing panel, while the *E. hormaechei* was resistant to all three carbapenems included. However, the carbapenemase inactivation test showed that none of these three produced carbapenemase enzymes, suggesting that the carbapenem resistance could be due to intrinsic resistance rather than acquired resistance (van der Zwaluw K *et al*, 2015). These findings will be followed up.

Methicillin resistant *Staphylococcus aureus* from berries

A total of 324 blueberry, 304 strawberry and 317 raspberry samples were examined for the presence of methicillin resistant *Staphylococcus aureus* (MRSA). None of the samples were positive for MRSA (blueberry [95% CI: 0.0-1.1], strawberry [95% CI: 0.0-1.2], raspberry [95% CI: 0.0-1.2]).

However, *Mammaliicoccus sciuri* was detected from one strawberry sample. *M. sciuri* (formerly *Staphylococcus sciuri*) is a gram-positive, coagulase-negative bacterium that acts as an environmental and animal commensal, though it is emerging as an opportunistic pathogen capable of carrying and spreading methicillin resistance. The isolate was not further characterised.

ZOONOTIC AND NON-ZOONOTIC ENTEROPATHOGENIC BACTERIA

Umaer Naseer, Madelaine Norström, Jannice Schau Slettemeås and Anne Margrete Urdahl

Zoonotic and non-zoonotic enteropathogenic bacteria represent a considerable public health problem. The presence of acquired antimicrobial resistance in these bacteria represents a further concern. Therefore, it is of great importance to monitor the occurrence of antimicrobial resistance in zoonotic and other enteropathogenic bacteria at relevant stages in the farm-to-fork continuum.

Included from animals and food are *Salmonella* spp., *Campylobacter coli,* and *Campylobacter jejuni* isolates. From human cases, all *Salmonella*, *Shigella,* and *Yersinia enterocolitica* isolates are included, as well as a representative number of *Campylobacter* isolates. Sampling, laboratory methods, and data processing are described in Appendix 4. One isolate of each serovar per incident was included for susceptibility testing.

SALMONELLA SPP.

Salmonella from animals and food

The situation regarding occurrence of *Salmonella* spp. in food-producing animals in Norway is very favourable, and such animal populations are considered virtually free from *Salmonella* spp.. To document and maintain this favourable situation, Norway has extensive surveillance programmes covering live animals and meat of pigs and cattle, and live poultry, poultry meat and eggs.

The *Salmonella* isolates examined in NORM-VET 2025 included those that were detected in the *Salmonella* surveillance programmes, as well as isolates obtained from submissions to the National Reference Laboratory for *Salmonella* (including isolates from non-domestic meat or other food products) and from clinical submissions or necropsies at the Norwegian Veterinary Institute. The data are presented in Table 22 and in the text.

TABLE 22. Antimicrobial resistance in *Salmonella* spp. (n=23) from animals (n=10); *S.* Typhimurium (4), *S.* Enteritidis, *S. enterica* subsp. *diarizonae* serovar 61 : k : 1,5,7 (3), *S.* Infantis and one unknown, and from food (n=13); *S.* Give (3), *S.* Bredeney, *S.* Mbandaka, *S.* Telaviv, *S.* Enteritidis, *S.* Dublin (3), *S.* Havana, *S. enterica* subsp. *diarizonae* serovar 38 : r : z, unknown (1).

		Distribution (n) of MIC values (mg/L)*															
Substance	Resistance (n)	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128	256	≥512
Tetracycline	3								20					3			
Tigecycline	ND					21	2										
Chloramphenicol	0										22	1					
Ampicillin	0							17	5								
Cefotaxime	0					23											
Ceftazidime	0					19	4										
Meropenem	ND		18	5													
Trimethoprim	0					19	3	1									
Sulfamethoxazole	ND											6	10	15	2		
Azithromycin	0								1	19	3						
Gentamicin	0						20	3									
Amikacin	0									23							
Ciprofloxacin	1	15	6	1	1												
Nalidixic acid	1									22				1			
Colistin	ND							14	4	3	2						

*Bold vertical lines denote epidemiological cut-off values for resistance. ND = not defined. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested.

RESULTS AND COMMENTS

In total, 23 *Salmonella* spp. from animals and food were susceptibility tested. Of these, there were four *S.* Typhimurium, three *S. enterica* subsp. *diarizonae* serovar 61 : k : 1,5,7, and one each of *S.* Enteritidis, *S.* Infantis and unknown from animals (i.e. four chickens, two cats, two alpaca, one cattle and one dog). The 13 food isolates were three *S.* Give, three *S.* Dublin, and one each of *S.* Bredeney, *S.* Mbandaka, *S.* Telaviv, *S.* Enteritidis, *S.* Havana, *S. enterica* subsp. *diarizonae* serovar 38 : r : z, and unknown. These were from imported meat products (n=9), alfalfa (*Medicago sativa*) (1), chia sage (*Salvia hispanica*) (1), cereal dust (1), and sprouts (1). Three isolates were resistant to tetracycline, whereof one was in addition resistant to quinolones.

Salmonella from human clinical specimens

In 2025, 861 human cases of nontyphoidal salmonellosis and 14 cases of typhoid fever were notified to the Norwegian Surveillance System for Communicable Disease (MSIS). Most cases with a known place of acquisition were travel-associated (62.2%). The National Reference Laboratory (NRL) for Enteropathogenic Bacteria at the Norwegian Institute of Public Health (NIPH) received 808 *Salmonella* isolates from primary diagnostic laboratories for further characterisation. Of these, 125 isolates were linked to 20 clusters, and 700 unique isolates were screened for antimicrobial resistance determinants following whole-genome sequencing. Antimicrobial susceptibility testing was performed on 498 isolates, including all unique isolates of *Salmonella* Typhi, *Salmonella* Paratyphi A, *Salmonella* Typhimurium, and the monophasic variant of *Salmonella* Typhimurium, as well as 92% of unique isolates of *Salmonella* Enteritidis, and 97% of isolates from other serovars (Table 23). Isolates were tested for susceptibility to six antibiotic classes: penicillins (ampicillin), extended-spectrum cephalosporins (cefotaxime and ceftazidime), carbapenems (meropenem), fluoroquinolones (ciprofloxacin/pefloxacin), phenicols (chloramphenicol), and tetracyclines (tetracycline).

TABLE 23. Number of *Salmonella* isolates tested for phenotypic antimicrobial susceptibility (AST) and screened for predicted genotypic resistance (GR) recovered from human clinical specimens in Norway 2025, by serovar and place of acquisition.

Salmonella serovars	No. of isolates tested in 2025		Place of acquisition					
			Norway		Abroad		Unknown	
	Phenotypic AST	Predicted GR	Phenotypic AST	Predicted GR	Phenotypic AST	Predicted GR	Phenotypic AST	Predicted GR
S. Typhimurium	93	93	53	53	23	23	17	17
S. Typhimurium monophasic	40	40	8	8	27	27	5	5
S. Enteritidis	99	174	45	49	44	115	10	10
S. Typhi	9	9	-	-	5	5	4	4
S. Paratyphi A	4	4	-	-	4	4	-	-
Other *Salmonella*	253	380	111	114	86	209	56	57
Total	**498**	**700**	**217**	**224**	**189**	**383**	**92**	**93**

ANTIMICROBIAL RESISTANCE IN SALMONELLA TYPHIMURIUM

TABLE 24. Percentage distributions of antimicrobial susceptibility categories in domestically acquired *Salmonella* Typhimurium (n=53) from human clinical specimens in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	90.6	-	9.4
Cefotaxime	≤ 1	> 2	100.0	0.0	0.0
Ceftazidime	≤ 1	> 4	100.0	0.0	0.0
Meropenem	≤ 2	> 8	100.0	0.0	0.0
Pefloxacin[1]	≥ 24 mm	< 24 mm	96.2	-	3.8
Tetracycline[2]	≥ 17 mm	< 17 mm	94.3	-	5.7
Chloramphenicol	≤ 8	> 8	98.1	-	1.9

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. [1]Low-level resistance against ciprofloxacin is underestimated using breakpoints based on ciprofloxacin disk diffusion. Susceptibility to ciprofloxacin is inferred from pefloxacin disk diffusion according to EUCAST clinical breakpoints (v.16.0). [2]Breakpoints according to national zone distributions.

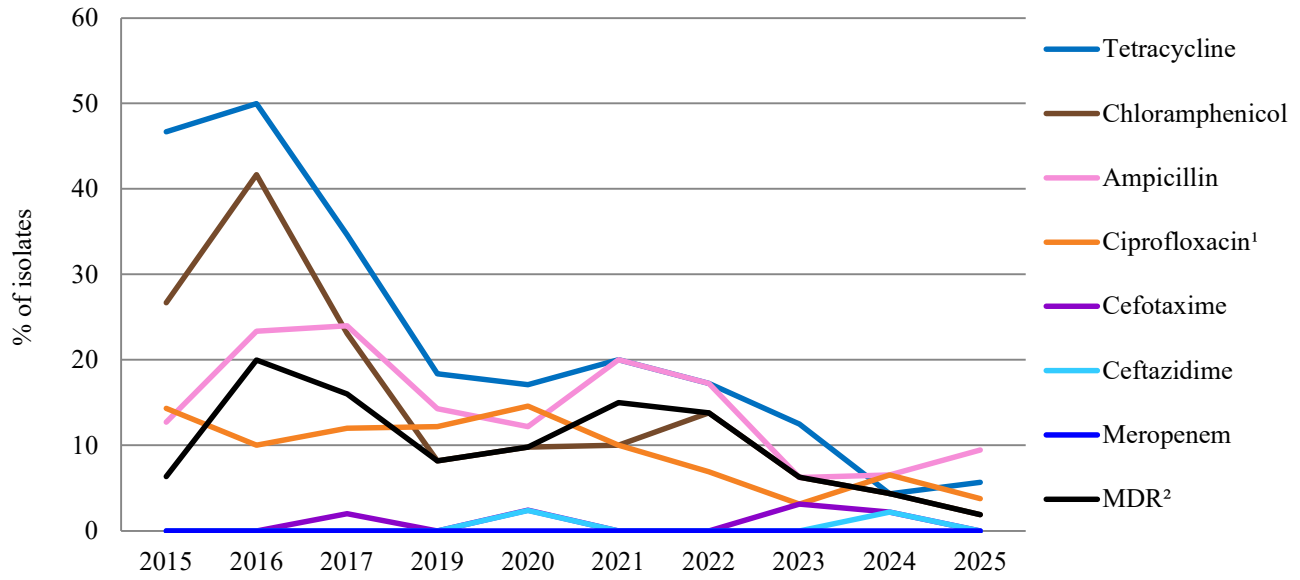

FIGURE 61. Trend 2015-2025. Percentage of domestically acquired *Salmonella* Typhimurium resistant to selected antimicrobial agents in Norway. [1]Resistance to ciprofloxacin is inferred from pefloxacin disk diffusion 2016 onwards. [2]MDR is defined as acquired non-susceptibility to antimicrobials from three or more categories.

TABLE 25. Percentage distributions of predicted genotypic resistance in domestically acquired *Salmonella* Typhimurium (n=53) compared to phenotypic wild type/non-wild type distribution (n=53) from human clinical specimens in Norway 2025.

	Phenotype[1] (%)		Predicted genotype[2] (%)	
Antibiotic	Wild type	Non-wild type	S	R
Gentamicin	-	-	100.0	0.0
Streptomycin	-	-	88.7	11.3
Ampicillin	88.7	11.3	90.6	9.4
Meropenem	100.0	0.0	100.0	0.0
Cefotaxime[3]	100.0	0.0	100.0	0.0
Ceftazidime[3]	100.0	0.0		
Colistin	-	-	100.0	0.0
Chloramphenicol	98.1	1.9	98.1	1.9
Ciprofloxacin	96.2	3.8	98.1	1.9
Sulfonamide	-	-	90.6	9.4
Tetracycline	94.3	5.7	94.3	5.7
Trimethoprim	-	-	90.6	9.4

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Salmonella enterica* (v.16.0). [2]R and S categorisation based on presence or absence of resistance determinants. [3]Predicted genotypic resistance to cefotaxime and ceftazidime is combined to predict genotypic resistance against extended-spectrum cephalosporins.

TABLE 26. Percentage distributions of antimicrobial susceptibility categories in travel-associated *Salmonella* Typhimurium (n=23) from human clinical specimens in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	65.2	-	34.8
Cefotaxime	≤ 1	> 2	95.7	0.0	4.3
Ceftazidime	≤ 1	> 4	95.7	4.3	0.0
Meropenem	≤ 2	> 8	100.0	0.0	0.0
Pefloxacin[1]	≥ 24 mm	< 24 mm	56.5	-	43.5
Tetracycline[2]	≥ 17 mm	< 17 mm	47.8	-	52.2
Chloramphenicol	≤ 8	> 8	78.3	-	21.7

[1] Low-level resistance against ciprofloxacin is underestimated using breakpoints based on ciprofloxacin disk diffusion. Susceptibility to ciprofloxacin is inferred from pefloxacin disk diffusion according to EUCAST clinical breakpoints (v.16.0). [2]Breakpoints according to national zone distributions.

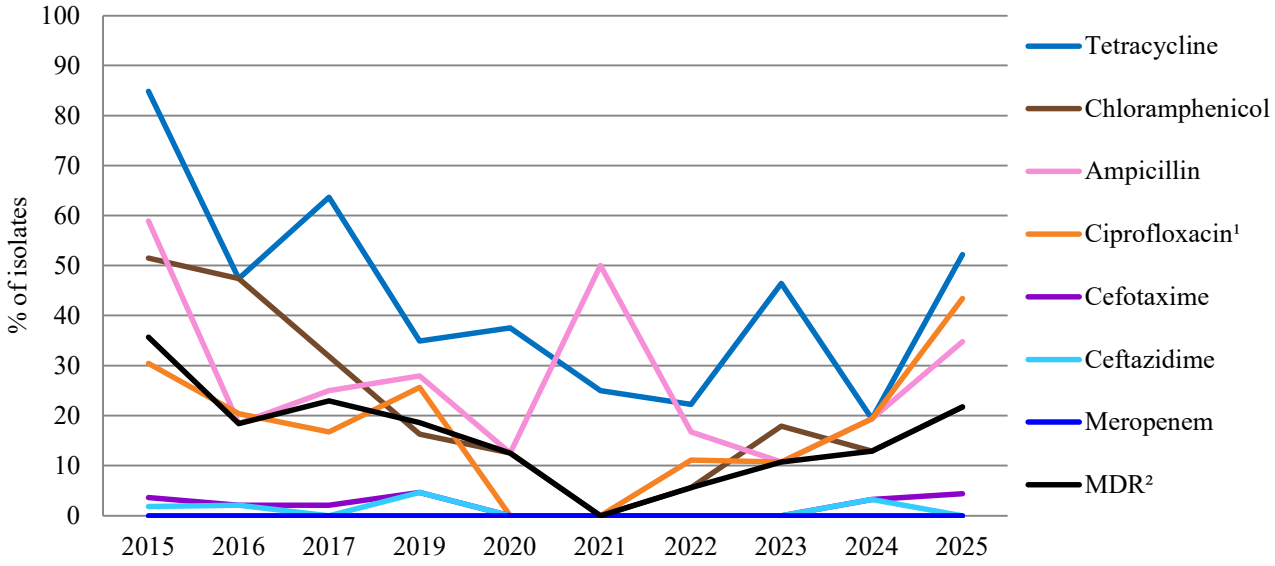

FIGURE 62. Trend 2015-2025. Percentage of travel-associated *Salmonella* Typhimurium resistant to selected antimicrobial agents in Norway. [1]Resistance to ciprofloxacin is inferred from pefloxacin disk diffusion 2016 onwards. [2]MDR is defined as acquired non-susceptibility to antimicrobials from three or more categories.

TABLE 27. Percentage distributions of predicted genotypic resistance in travel-associated *Salmonella* Typhimurium (n=23) compared to phenotypic wild type/non-wild type distribution (n=23) from human clinical specimens in Norway 2025.

	Phenotype[1] (%)		Predicted genotype[2] (%)	
Antibiotic	Wild type	Non-wild type	S	R
Gentamicin	-	-	95.7	4.3
Streptomycin	-	-	60.9	39.1
Ampicillin	60.9	39.1	60.9	39.1
Meropenem	100.0	0.0	100.0	0.0
Cefotaxime[3]	95.7	4.3	95.7	4.3
Ceftazidime[3]	100.0	0.0		
Colistin	-	-	100.0	0.0
Chloramphenicol	78.3	21.7	73.9	26.1
Ciprofloxacin	56.5	43.5	60.9	39.1
Sulfonamide	-	-	78.3	21.7
Tetracycline	47.8	52.2	47.8	52.2
Trimethoprim	-	-	95.7	4.3

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Salmonella enterica* (v.16.0). [2]R and S categorisation based on presence or absence of resistance determinants. [3]Predicted genotypic resistance to cefotaxime and ceftazidime is combined to predict genotypic resistance against extended-spectrum cephalosporins.

ANTIMICROBIAL RESISTANCE IN MONOPHASIC SALMONELLA TYPHIMURIUM

TABLE 28. Percentage distributions of antimicrobial susceptibility categories in domestically acquired monophasic *Salmonella* Typhimurium (n=8) from human clinical specimens in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	12.5	-	87.5
Cefotaxime	≤ 1	> 2	100.0	0.0	0.0
Ceftazidime	≤ 1	> 4	100.0	0.0	0.0
Meropenem	≤ 2	> 8	100.0	0.0	0.0
Pefloxacin[1]	≥ 24 mm	< 24 mm	87.5	-	12.5
Tetracycline[2]	≥ 17 mm	< 17 mm	12.5	-	87.5
Chloramphenicol	≤ 8	> 8	87.5	-	12.5

[1]Low-level resistance against ciprofloxacin is underestimated using breakpoints based on ciprofloxacin disk diffusion. Susceptibility to ciprofloxacin is inferred from pefloxacin disk diffusion according to EUCAST clinical breakpoints (v.16.0). [2]Breakpoints according to national zone distributions.

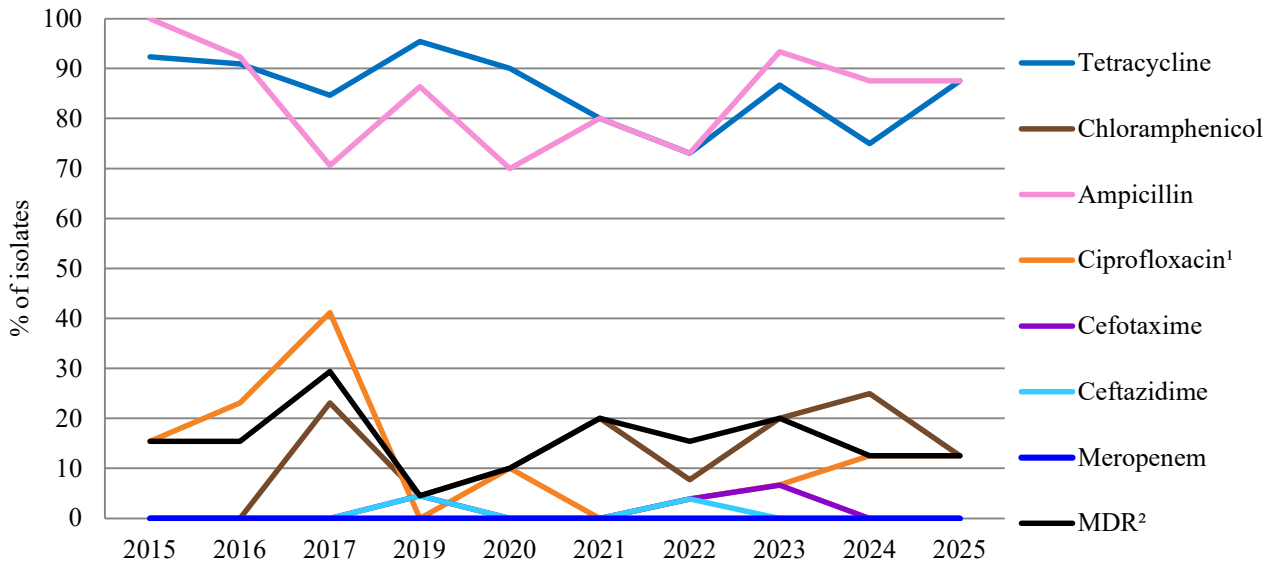

FIGURE 63. Trend 2015-2025. Percentage of domestically acquired monophasic *Salmonella* Typhimurium resistant to selected antimicrobial agents in Norway. [1]Resistance to ciprofloxacin is inferred from pefloxacin disk diffusion 2016 onwards. [2]MDR is defined as acquired non-susceptibility to antimicrobials from three or more categories.

TABLE 29. Percentage distributions of predicted genotypic resistance in domestically acquired monophasic *Salmonella* Typhimurium (n=8) compared to phenotypic wild type/non-wild type distribution (n=8) from human clinical specimens in Norway 2025.

	Phenotype[1] (%)		Predicted genotype[2] (%)	
Antibiotic	Wild type	Non-wild type	S	R
Gentamicin	-	-	100.0	0.0
Streptomycin	-	-	12.5	87.5
Ampicillin	12.5	87.5	25.0	75.0
Meropenem	100.0	0.0	100.0	0.0
Cefotaxime[3]	100.0	0.0	100.0	0.0
Ceftazidime[3]	100.0	0.0		
Colistin	-	-	100.0	0.0
Chloramphenicol	87.5	12.5	87.5	12.5
Ciprofloxacin	87.5	12.5	87.5	12.5
Sulfonamide	-	-	12.5	87.5
Tetracycline	12.5	87.5	12.5	87.5
Trimethoprim	-	-	87.5	12.5

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Salmonella enterica* (v.16.0). [2]R and S categorisation based on presence or absence of resistance determinants. [3]Predicted genotypic resistance to cefotaxime and ceftazidime is combined to predict genotypic resistance against extended-spectrum cephalosporins.

TABLE 30. Percentage distributions of antimicrobial susceptibility categories in travel-associated monophasic *Salmonella* Typhimurium (n=27) from human clinical specimens in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	3.7	-	96.3
Cefotaxime	≤ 1	> 2	88.9	0.0	11.1
Ceftazidime	≤ 1	> 4	88.9	3.7	7.4
Meropenem	≤ 2	> 8	100.0	0.0	0.0
Pefloxacin[1]	≥ 24 mm	< 24 mm	81.5	-	18.5
Tetracycline[2]	≥ 17 mm	< 17 mm	14.8	-	85.2
Chloramphenicol	≤ 8	> 8	85.2	-	14.8

[1]Low-level resistance against ciprofloxacin is underestimated using breakpoints based on ciprofloxacin disk diffusion. Susceptibility to ciprofloxacin is inferred from pefloxacin disk diffusion according to EUCAST clinical breakpoints (v.16.0). [2]Breakpoints according to national zone distributions.

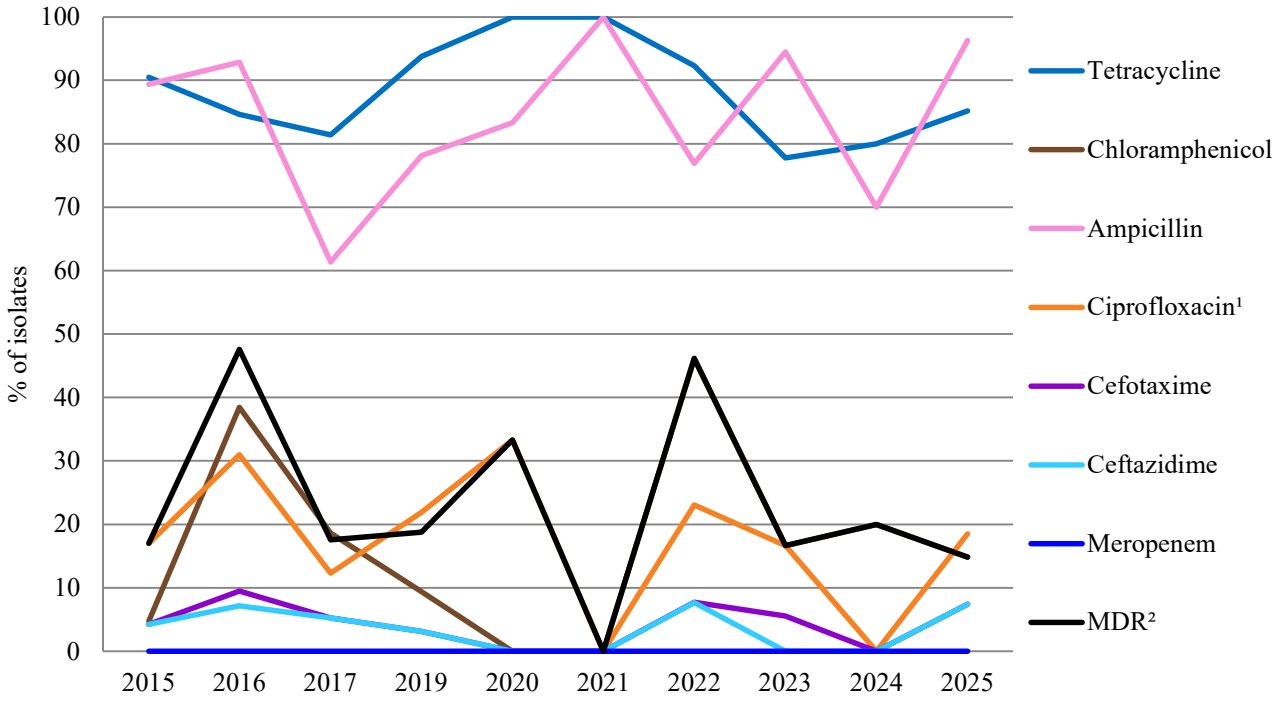

FIGURE 64. Trend 2015-2025. Percentage of travel-associated monophasic *Salmonella* Typhimurium resistant to selected antimicrobial agents in Norway.[1]Resistance to ciprofloxacin is inferred from pefloxacin disk diffusion 2016 onwards. [2]MDR is defined as acquired non-susceptibility to antimicrobials from three or more categories.

TABLE 31. Percentage distributions of predicted genotypic resistance in travel-associated monophasic *Salmonella* Typhimurium (n=27) compared to phenotypic wild type/non-wild type distribution (n=27) from human clinical specimens in Norway 2025.

	Phenotype[1] (%)		Predicted genotype[2] (%)	
Antibiotic	Wild type	Non-wild type	S	R
Gentamicin	-	-	85.2	14.8
Streptomycin	-	-	22.2	77.8
Ampicillin	3.7	96.3	7.4	92.6
Meropenem	100.0	0.0	100.0	0.0
Cefotaxime[3]	88.9	11.1	88.9	11.1
Ceftazidime[3]	92.6	7.4		
Colistin[3]	-	-	100.0	0.0
Chloramphenicol	85.2	14.8	85.2	14.8
Ciprofloxacin	81.5	18.5	77.8	22.2
Sulfonamide	-	-	25.9	74.1
Tetracycline	14.8	85.2	22.2	77.8
Trimethoprim	-	-	81.5	18.5

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Salmonella enterica* (v.16.0). [2]R and S categorisation based on presence or absence of resistance determinants. [3]Predicted genotypic resistance to cefotaxime and ceftazidime is combined to predict genotypic resistance against extended-spectrum cephalosporins.

ANTIMICROBIAL RESISTANCE IN SALMONELLA ENTERITIDIS

TABLE 32. Percentage distributions of antimicrobial susceptibility categories in *Salmonella* Enteritidis (n=99) from human clinical specimens irrespective of place of acquisition in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	90.9	-	9.1
Cefotaxime	≤ 1	> 2	99.0	0.0	1.0
Ceftazidime	≤ 1	> 4	99.0	0.0	1.0
Meropenem	≤ 2	> 8	100.0	0.0	0.0
Pefloxacin[1]	≥ 24 mm	< 24 mm	66.7	-	33.3
Tetracycline[2]	≥ 17 mm	< 17 mm	91.9	-	8.1
Chloramphenicol	≤ 8	> 8	99.0	-	1.0

[1]Low-level resistance against ciprofloxacin is underestimated using breakpoints based on ciprofloxacin disk diffusion. Susceptibility to ciprofloxacin is inferred from pefloxacin disk diffusion according to EUCAST clinical breakpoints (v.16.0). [2]Breakpoints according to national zone distributions.

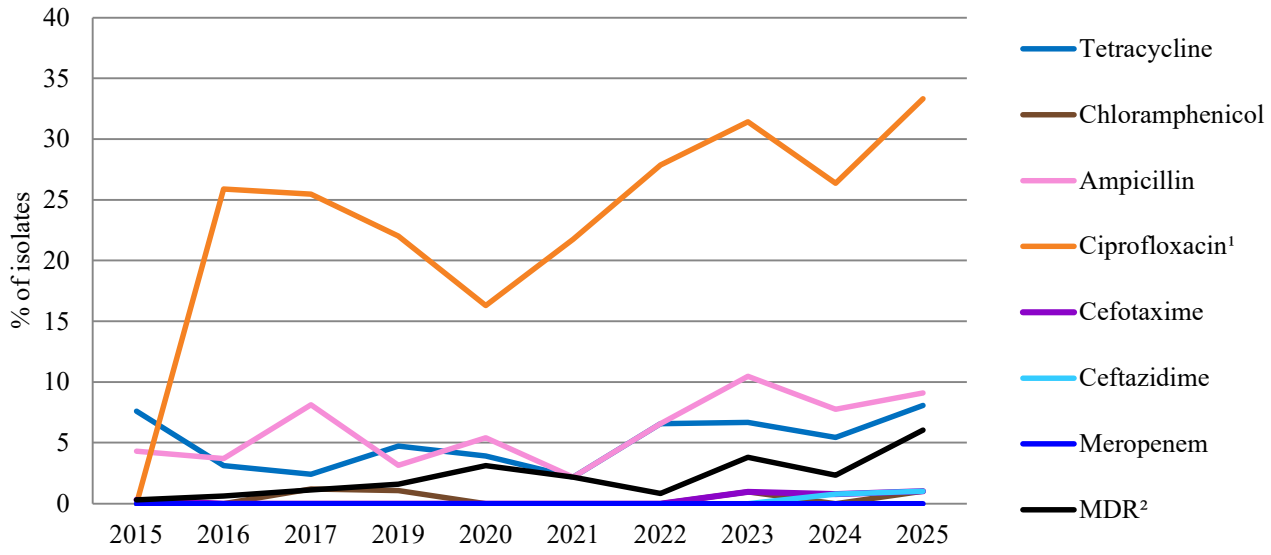

FIGURE 65. Trend 2015-2025. Percentage of *Salmonella* Enteritidis resistant to selected antimicrobial agents irrespective of place of acquisition in Norway. [1]Resistance to ciprofloxacin is inferred from pefloxacin disk diffusion 2016 onwards. [2]MDR is defined as acquired non-susceptibility to antimicrobials from three or more categories.

TABLE 33. Percentage distributions of predicted genotypic resistance in *Salmonella* Enteritidis (n=174) compared to phenotypic wild type/non-wild type distribution (n=99) from human clinical specimens in Norway 2025.

	Phenotype[1] (%)		Predicted genotype[2] (%)	
Antibiotic	Wild type	Non-wild type	S	R
Gentamicin	-	-	99.4	0.6
Streptomycin	-	-	97.7	2.3
Ampicillin	89.9	10.1	91.4	8.6
Meropenem	100.0	0.0	100.0	0.0
Cefotaxime[3]	99.0	1.0	99.4	0.6
Ceftazidime[3]	99.0	1.0		
Colistin	-	-	100.0	0.0
Chloramphenicol	99.0	1.0	99.4	0.6
Ciprofloxacin	67.7	32.3	64.9	35.1
Sulfonamide	-	-	98.3	1.7
Tetracycline	91.9	8.1	93.1	6.9
Trimethoprim	-	-	99.4	0.6

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Salmonella enterica* (v.16.0). [2]R and S categorisation based on presence or absence of resistance determinants. [3]Predicted genotypic resistance to cefotaxime and ceftazidime is combined to predict genotypic resistance against extended-spectrum cephalosporins.

ANTIMICROBIAL RESISTANCE IN SALMONELLA TYPHI

TABLE 34. Percentage distributions of antimicrobial susceptibility categories in *Salmonella* Typhi (n=9) from human clinical specimens irrespective of place of acquisition in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	66.7	-	33.3
Cefotaxime	≤ 1	> 2	88.9	0.0	11.1
Ceftazidime	≤ 1	> 4	88.9	0.0	11.1
Meropenem	≤ 2	> 8	100.0	0.0	0.0
Pefloxacin[1]	≥ 24 mm	< 24 mm	0.0	-	100.0
Tetracycline[2]	≥ 17 mm	< 17 mm	100.0	-	0.0
Chloramphenicol	≤ 8	> 8	55.6	-	44.4

[1]Low-level resistance against ciprofloxacin is underestimated using breakpoints based on ciprofloxacin disk diffusion. Susceptibility to ciprofloxacin is inferred from pefloxacin disk diffusion according to EUCAST clinical breakpoints (v.16.0). [2]Breakpoints according to national zone distributions.

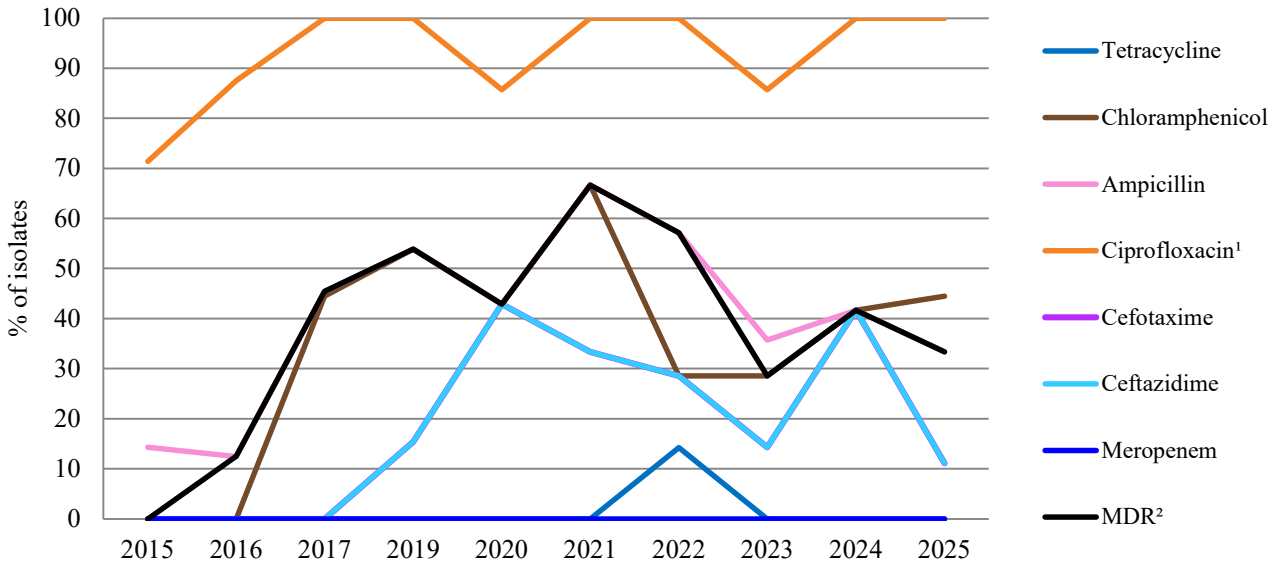

FIGURE 66. Trend 2015-2025. Percentage of *Salmonella* Typhi resistant to selected antimicrobial agents irrespective of place of acquisition in Norway.[1]Resistance to ciprofloxacin is inferred from pefloxacin disk diffusion 2016 onwards. [2]MDR is defined as acquired non-susceptibility to antimicrobials from three or more categories.

TABLE 35. Percentage distributions of predicted genotypic resistance in *Salmonella* Typhi (n=9) compared to phenotypic wild type/non-wild type distribution (n=9) from human clinical specimens in Norway 2025.

	Phenotype[1] (%)		Predicted genotype[2] (%)	
Antibiotic	Wild type	Non-wild type	S	R
Gentamicin	-	-	100.0	0.0
Streptomycin	-	-	66.7	33.3
Ampicillin	66.7	33.3	66.7	33.3
Meropenem	100.0	0.0	100.0	0.0
Cefotaxime[3]	88.9	11.1	88.9	11.1
Ceftazidime[3]	88.9	11.1		
Colistin	-	-	100.0	0.0
Chloramphenicol	55.6	44.4	55.6	44.4
Ciprofloxacin	0.0	100.0	0.0	100.0
Sulfonamide	-	-	55.6	44.4
Tetracycline	100.0	0.0	100.0	0.0
Trimethoprim	-	-	55.6	44.4

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Salmonella enterica* (v.16.0). [2]R and S categorisation based on presence or absence of resistance determinants. [3]Predicted genotypic resistance to cefotaxime and ceftazidime is combined to predict genotypic resistance against extended-spectrum cephalosporins.

ANTIMICROBIAL RESISTANCE IN OTHER SALMONELLA SEROTYPES

TABLE 36. Percentage distributions of predicted genotypic resistance in other *Salmonella* serotypes (n=380) to phenotypic wild type/non-wild type distribution (n=253) from human clinical specimens in Norway 2025.

	Phenotype[1] (%)		Predicted genotype[2] (%)	
Antibiotic	Wild type	Non-wild type	S	R
Gentamicin	-	-	96.8	3.2
Streptomycin	-	-	89.2	10.8
Ampicillin	88.5	11.5	89.7	10.3
Meropenem	100.0	0.0	100.0	0.0
Cefotaxime[3]	98.4	1.6	96.8	3.2
Ceftazidime[3]	98.4	1.6		
Colistin	-	-	100.0	0.0
Chloramphenicol	94.1	5.9	95.0	5.0
Ciprofloxacin	83.4	16.6	82.6	17.4
Sulfonamide	-	-	88.9	11.1
Tetracycline	90.1	9.9	87.4	12.6
Trimethoprim	-	-	93.9	6.1

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Salmonella enterica* (v.16.0). [2]R and S categorisation based on presence or absence of resistance determinants. [3]Predicted genotypic resistance to cefotaxime and ceftazidime is combined to predict genotypic resistance against extended-spectrum cephalosporins.

MULTI-DRUG RESISTANCE IN SALMONELLA

TABLE 37. Number of predicted genotypic multi-drug resistant (MDR) *Salmonella* isolates identified in Norway 2025, stratified according to serotype and resistance to different antibiotic categories.

Salmonella serotypes	MDR[1]	Antibiotic categories[2]							
		STR	AMP	ESC	CHL	CIP	SUL	TET	TMP
monophasic *Salmonella* Typhimurium	33	32	31	2	6	8	31	28	6
Salmonella Typhimurium	19	17	14	1	8	7	11	14	5
Salmonella Typhi	4	3	3	1	4	4	4	0	4
Salmonella Enteritidis	9	4	8	0	1	6	3	8	1
Other *Salmonella*	48	36	32	12	19	42	38	42	23
Total no. of MDR isolates	**112**	**92**	**88**	**16**	**38**	**67**	**87**	**92**	**39**

[1]Multi-drug resistance (MDR) defined as predicted genotypic resistance to 3 ≥ antibiotic categories. [2]Antibiotic category: STR: Streptomycin, AMP; Ampicillin, ESC; Extended-Spectrum Cephalosporin, CHL; Chloramphenicol, CIP; Ciprofloxacin, SUL; Sulfonamide, TET; Tetracycline, TMP; Trimethoprim.

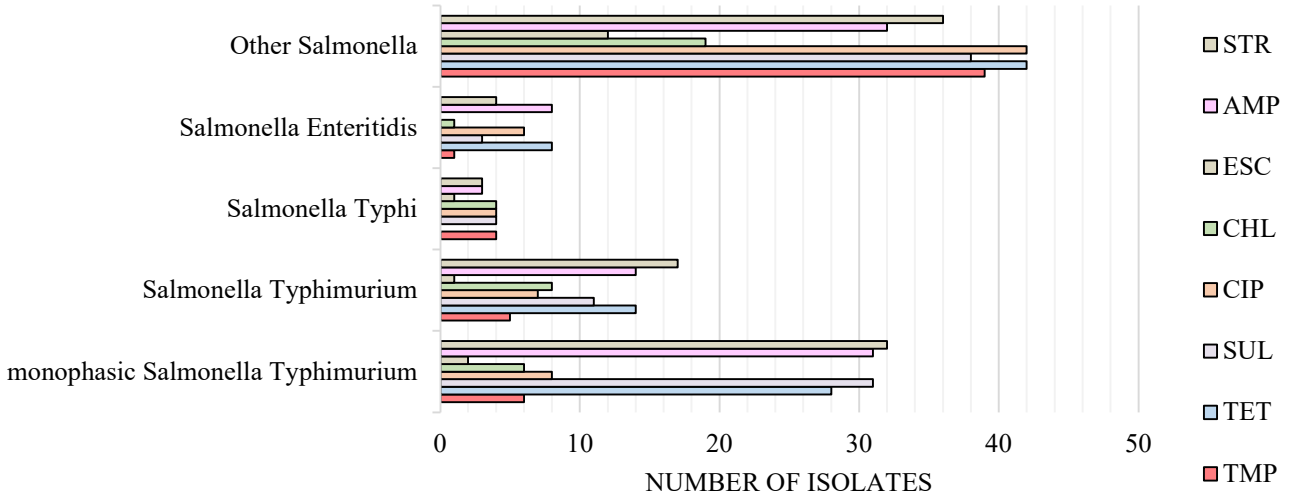

FIGURE 67. Number of predicted genotypic multi-drug resistant (MDR) *Salmonella* isolates (n=113) identified in Norway 2025, stratified according to serotype and resistance to different antibiotic categories; STR: Streptomycin, AMP; Ampicillin, ESC; Extended-Spectrum Cephalosporin, CHL; Chloramphenicol, CIP; Ciprofloxacin, SUL; Sulfonamide, TET; Tetracycline, TMP; Trimethoprim.

CORRELATION BETWEEN PHENOTYPIC AND PREDICTED GENOTYPIC RESISTANCE IN SALMONELLA

TABLE 38. Concordance between phenotypic and predicted genotypic resistance to selected antibiotic categories in *Salmonella* isolates identified in Norway 2025.

Antibiotic categories	Tested	Phenotype WT[1]		Phenotype NWT[1]		Sensitivity (%)	Spesificity (%)
		Genotype R	Genotype S	Genotype R	Genotype S		
Penicillins	498	0	401	85	12	100.0	97.1
ESC[2]	498	0	488	10	0	100.0	100.0
Carbapenems	498	0	498	0	0	-	100.0
Fluoroquinolones	498	2	387	100	10	99.0	97.5
Tetracycline	498	3	410	81	4	96.4	99.0
Phenicols	498	1	463	31	3	96.9	99.4

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in abscense of ECOFF for *Salmonella enterica* (v.16.0). [2]Predicted genotypic resistance to cefotaxime and ceftazidime is combined as predicted genotypic resistance against extended-spectrum cephalosporin (ESC).

RESULTS AND COMMENTS

The NRL annually performs antimicrobial susceptibility testing on a selected subset of received *Salmonella* isolates. Selection criteria are designed to ensure inclusion of the most important *Salmonella* serovars and antibiotics relevant for monitoring the emergence and spread of antimicrobial resistance in Norway. In addition, from 2020 onwards, the NRL has screened all *Salmonella* isolates for antimicrobial resistance determinants following whole-genome sequencing to predict genotypic resistance. In 2020 and 2021, during the Covid-19 pandemic, the government implemented infection control measures, including travel restrictions, which substantially reduced travel-associated *Salmonella* infections. Trends in antimicrobial resistance should therefore be interpreted accordingly.

In 2025, the NRL identified a total of 20 clusters, including 7 international clusters. Of the 13 domestic clusters, four were *S.* Typhimurium (n=12, n=5, n=3, and n=3), while the remainder comprised various serotypes ranging from 5 to 9 isolates. Antimicrobial resistance results from only a single strain from each of these clusters are included in this report.

Overall resistance in *S.* Typhimurium was higher in travel-associated strains than in strains from domestically acquired infections. We observed a stable, low-level resistance trend for most tested antibiotics in strains from domestically acquired infections. However, resistance to tetracycline and ciprofloxacin increased among travel-associated infections. A single strain was identified as an ESBL producer encoding $bla_{\text{CTX-M-65}}$. Variants of the plasmid-mediated quinolone resistance gene *qnr* were identified as the probable mediators of the observed ciprofloxacin resistance in 9 of 10 strains. An MDR genotype was assigned to 20.4% of the strains.

The overall resistance level in the monophasic variant of *S.* Typhimurium was higher than that observed in *S.* Typhimurium. We observed a stable resistance trend over the past five years for all tested antibiotics. High levels of resistance were observed for ampicillin and tetracycline in strains from both domestically acquired and travel-associated infections. Three ESBL-producing strains were identified from travel-associated infections, encoding $bla_{\text{CTX-M-15}}$, $bla_{\text{CTX-M-14}}$, and $bla_{\text{DHA-1}}$. An MDR genotype was identified in 82.5% of the strains.

Antibiotic resistance in *S.* Enteritidis is generally low. An apparent sudden emergence of ciprofloxacin resistance in 2016 was linked to the change in the antibiotic used to test fluoroquinolone resistance, from ciprofloxacin to pefloxacin. Screening for genotypic resistance determinants confirmed the presence of various mutations in the quinolone resistance-determining regions (QRDRs) of *gyrA* (n=58), as well as the presence of *qnr* (n=3). Two ESBL-producing strains were identified, encoding $bla_{\text{CTX-M-55}}$ and bla_{DHA}. An MDR genotype was identified in 5.2% of the strains.

The overall level of antibiotic resistance in *S.* Typhi was high. All isolates (n=9) were resistant to ciprofloxacin and carried various mutations in the QRDRs of *gyrA*. One strain was identified as an ESBL producer encoding $bla_{\text{CTX-M-15}}$. An MDR genotype was identified in 44.4% of the strains.

Among other *Salmonella* serotypes (n=380), the most common were *S.* Paratyphi B variant Java (n=29), *S.* Saintpaul (n=21), *S.* Newport (n=19), *S.* Stanley (n=19), *S.* Chester (n=15), *S.* Agona (n=13), *S.* Oranienburg (n=13), *S.* Infantis (n=12), *S.* Bovismorbificans (n=11), and *S.* Paratyphi B var. Java monophasic variant (n=11). Overall predicted genotypic resistance was low (<12%) across all screened antibiotics, except for quinolones (17.4%) and tetracycline (12.6%). Twelve ESBL-producing strains were identified, encoding $bla_{\text{CTX-M}}$ (n=10), $bla_{\text{SHV-12}}$ (n=1), and $bla_{\text{CMY-2}}$ (n=1). Various mutations in the QRDRs of *gyrA* and variants of *qnr* were predicted to confer resistance to quinolones (n=66). An MDR genotype was identified in 12.6% of the strains

In total, 18 strains were predicted to be genotypically resistant to extended-spectrum cephalosporins: mono-phasic variant of *S.* Typhimurium (n=3), *S.* Infantis (n=3), *S.* Kentucky (n=3), *S.* Agona (n=2), *S.* Enteritidis (n=1), and one strain each of *S.* Chester, *S.* Muenster, *S.* Saintpaul, *S.* Schwarzengrund, *S.* Typhi, and *S.* Typhimurium. Resistance was mediated by different variants of $bla_{\text{CTX-M}}$ (n=15), $bla_{\text{SHV-12}}$ (n=1), $bla_{\text{CMY-2}}$ (n=1) and $bla_{\text{DHA-1}}$ (n=1). The overall correlation between phenotypic resistance and predicted genotypic resistance was high, and both sensitivity and specificity were generally above 95% for all tested and screened antibiotics.

CAMPYLOBACTER SPP.

Campylobacter jejuni and *Campylobacter coli* from cattle and pigs

Caecal samples from 308 cattle and 299 fattening pigs were examined. *Campylobacter jejuni* was detected from 106 (33.1%) of the cattle samples and from 20 (6.7%) of the pig samples, respectively. *Campylobacter coli* isolates were obtained from 247 (82.6%) of the pig samples. Of these, 102 *C. jejuni* isolates from cattle and 239 *C. coli* isolates from fattening pigs were susceptibility tested. The results are presented in Tables 39-40, Figures 68-71, and in the text.

TABLE 39. Antimicrobial resistance in *Campylobacter jejuni* isolates (n=102) from caecal samples of cattle in 2025.

			Distribution (%) of MIC values (mg/L)*															
Substance	Resistance (%)	[95% CI]	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128	256	512	≥1024
Tetracycline	4.9	[1.6-11.1]						94.1	1.0					2.0	2.9				
Chloramphenicol	0.0	[0.0-3.6]								100									
Ertapenem	4.9	[1.6-11.1]				95.1	2.9		2.0										
Erythromycin	0.0	[0.0-3.6]							100										
Gentamicin	0.0	[0.0-3.6]					17.6	82.4											
Ciprofloxacin	15.7	[9.2-24.2]				82.4	2.0					4.9	10.8						

*Bold vertical lines denote epidemiological cut-off values for resistance. CI = confidence interval. ND = not defined. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested.

TABLE 40. Antimicrobial resistance in *Campylobacter coli* isolates (n=239) from caecal samples of fattening pigs in 2025.

			Distribution (%) of MIC values (mg/L)*																
Substance	Resistance (%)	[95% CI]	0.015	0.03	0.06	0.12	0.25	0.5	1	2	4	8	16	32	64	128	256	512	≥1024
Tetracycline	0.8	[0.1-3.0]						99.2			0.4			0.4					
Chloramphenicol	0.0	[0.0-1.5]								92.5	7.5								
Ertapenem	ND	ND				90.4	6.7	2.1		0.8									
Erythromycin	0.0	[0.0-1.5]							99.6	0.4									
Gentamicin	0.0	[0.0-1.5]					5.4	49.4	45.2										
Ciprofloxacin	12.1	[8.3-17.0]				87.9						3.8	8.4						

*Bold vertical lines denote epidemiological cut-off values for resistance. CI = confidence interval. White fields denote range of dilutions tested for each antimicrobial agent. MIC values higher than the highest concentration tested are given as the lowest MIC value above the range. MIC values equal to or lower than the lowest concentration tested are given as the lowest concentration tested.

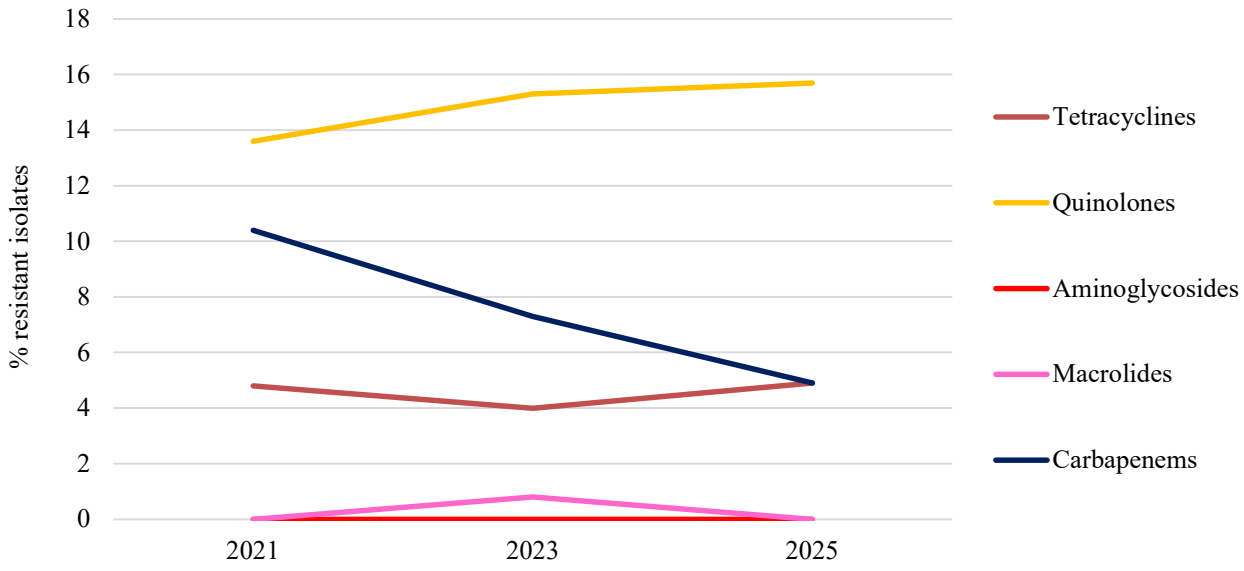

FIGURE 68. Prevalence of resistance to various antimicrobial classes in *Campylobacter jejuni* from cattle in 2021-2025. The epidemiological cut-offs used in NORM-VET 2025 were applied.

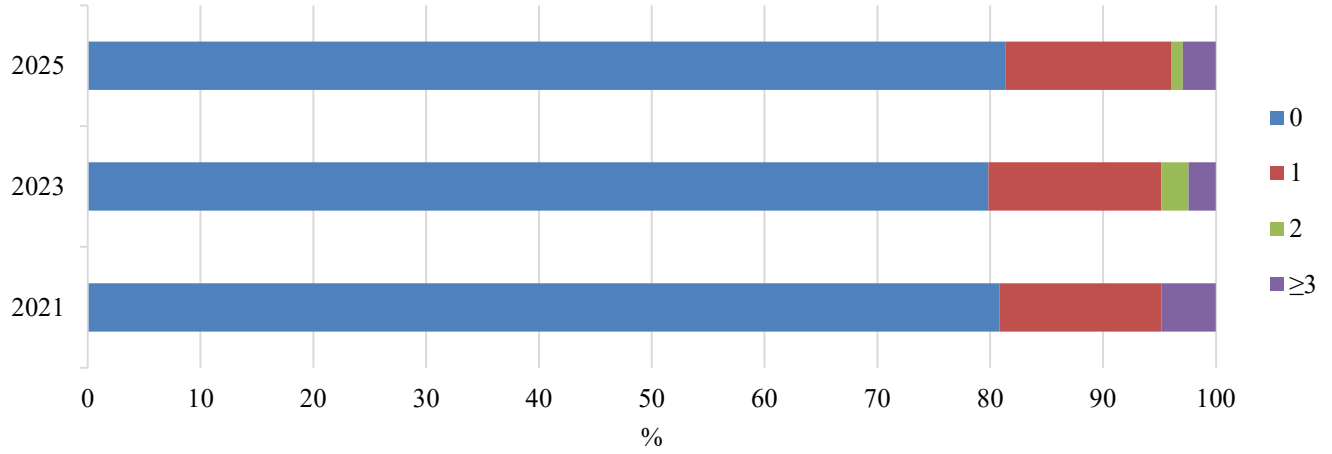

FIGURE 69. Antimicrobial resistance profile for *Campylobacter jejuni* from cattle in 2021-2025. Percentage of isolates susceptible to all (0) or resistant to one (1), two (2), and three or more (≥3) antimicrobial classes are illustrated. The epidemiological cut-offs used in NORM-VET 2025 were applied.

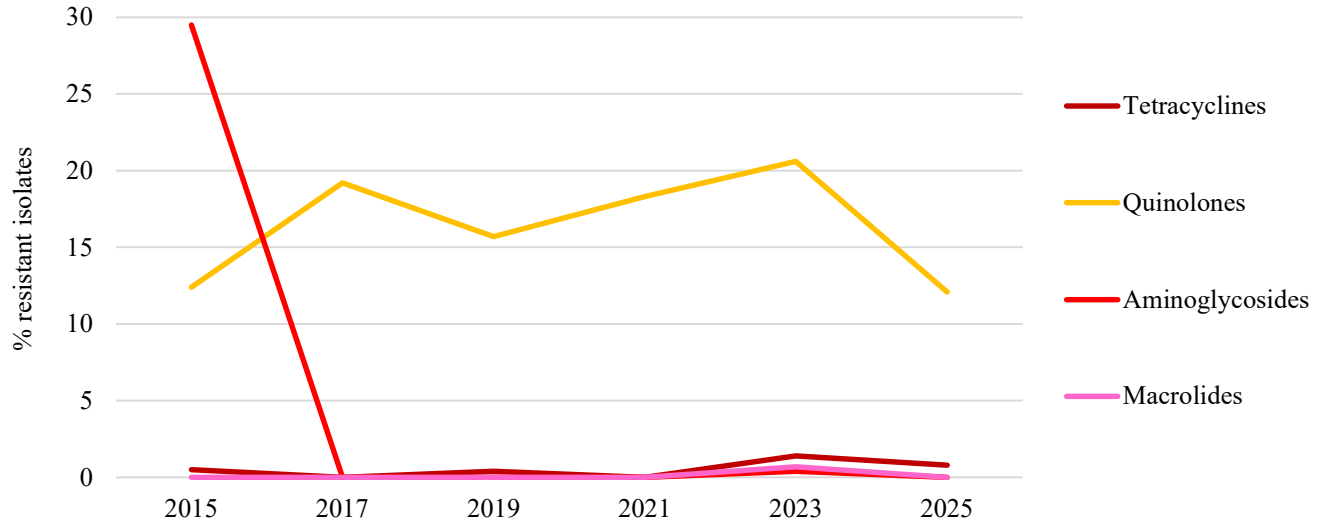

FIGURE 70. Prevalence of resistance to various antimicrobial classes in *Campylobacter coli* from fattening pigs in 2015-2025. Please note that resistance to streptomycin is included for the years 2015-2019, but not for 2021-2025. The epidemiological cut-offs used in NORM-VET 2025 were applied.

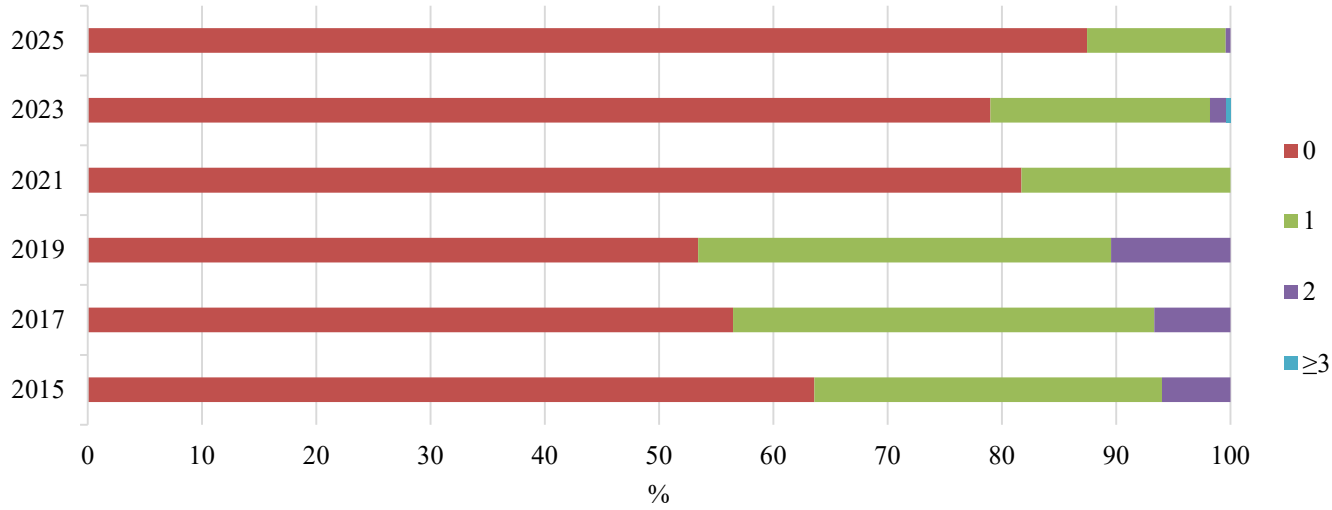

FIGURE 71. Antimicrobial resistance profile for *Campylobacter coli* from fattening pigs in 2015-2025. Percentage of isolates susceptible to all (0) or resistant to one (1), two (2), and three or more (≥3) antimicrobial classes are illustrated. Please note that resistance to streptomycin is included for the years 2015-2019, but not for 2021-2025. See text for further explanation and assessment of results. The epidemiological cut-offs used in NORM-VET 2025 were applied.

RESULTS AND COMMENTS

CATTLE

A total of 81.3% [95% CI: 72.4-88.4] of the *C. jejuni* isolates from cattle were fully susceptible to all antimicrobial agents included in the test panel. Altogether, 14.7% [95% CI: 8.5-23.1] were resistant to one, 1.0% [95% CI: 0.02-5.3] to two and 2.9% [95% CI: 0.6-8.4] to three or more of the antimicrobial classes, respectively. Resistance to quinolones was the most frequently identified resistance phenotype (Figure 68). A total of 18.7% of the isolates were resistant, indicating a moderate occurrence of resistance among *C. jejuni* from cattle according to the EFSA classification described in Appendix 6. As shown in Figure 69, the number of isolates being fully susceptible has been relatively stable ~80% over the years 2021-2025.

C. jejuni from cattle has previously been investigated in 2010, 2021 and 2023. However, comparisons to 2010 are difficult due to differences in methodology as well as the fact that a very low number of isolates was investigated in 2010. The results from 2025 are in concordance with the results from 2021 and 2023 with the exception of resistance to the carbapenem ertapenem (Figure 68). Resistance to ertapenem has decreased from 10.4% in 2021 to 4.9% in 2025 (p=0.24). This was, however, not a significant change in resistance. Combined resistance to ciprofloxacin and erythromycin was not detected.

The occurrence of resistance in *C. jejuni* from Norwegian cattle is lower than from the other countries reporting to EFSA. However, the data in the EFSA reports are from cattle under one year of age, and the majority of cattle slaughtered in Norway are older. In the EFSA and ECDC Summary Report from 2023 and 2024, resistance to tetracyclines and ciprofloxacin were the most commonly detected resistance determinantes among *C. jejuni* from cattle, i.e. 62.7% and 57.3%, respectively (EFSA and ECDC Summary Report 2023-2024). This was based on data from 12 countries. Only 0.7% of these isolates showed combined resistance to ciprofloxacin and erythromycin. The occurrence of *Campylobacter* spp. isolates displaying combined resistance to ciprofloxacin and erythromycin is of great importance to public health, since both compounds are recognised as critically important antimicrobials for the treatment of *Campylobacter* infections in humans (WHO, 2019).

PIGS

A total of 87.5% [95% CI: 82.6-91.4] of the *C. coli* isolates from fattening pigs were susceptible to all antimicrobial agents included in the test panel. Altogether, 12.1% [95% CI: 8.3-17.0] were resistant to one of the antimicrobial classes tested, and 0.4% [95% CI: 0.01-2.3] to two antimicrobial classes (Figure 71). According to the EFSA classification described in Appendix 6, this corresponds to a moderate occurrence of resistance among *C. coli* from fattening pigs. Combined resistance to ciprofloxacin and erythromycin was not detected.

C. coli has previously been investigated in 2009, 2015, 2017, 2019, 2021 and 2023. There has, however, been changes to the antimicrobial susceptibility testing panel for *Campylobacter* spp., and thereby comparison to the years before 2021 has to be done with caution. Resistance to the aminoglycoside streptomycin was previously the most common in *C. coli* isolates from pigs as shown in Figure 70, but streptomycin is no longer part of the test panel. In 2019, 41% [95% CI: 34.8-47.4] of the isolates were streptomycin resistant. Streptomycin is rarely used in Norwegian pig production, and streptomycin resistance in *C. coli* is therefore difficult to explain.

The quinolone ciprofloxacin has been included in the test panel all these years, and as shown in Figure 70 there has been an increasing trend in resistance to quinolones over the years, with 4.5% [95% CI: 1.2-13.4] in 2009 to 20.6% [95% CI: 16.0-25.9] in 2023 being resistant to ciprofloxacin. In 2025, however, the occurrence of ciprofloxacin resistance has decreased and is now 12.1% and similar to the 2015 results.

In the EFSA and ECDC Summary Report from 2023 and 2024, resistance to tetracyclines and ciprofloxacin were the most commonly detected resistance determinants among *C. coli* from pigs, i.e. 68.4% and 54.3%, respectively (EFSA and ECDC Summary Report 2023-2024). This was based on data from 27 countries. The occurrence of resistance among *C. coli* varies between the reporting countries. The results from Norway are still among the lowest reported. This situation is most likely due to the rather limited use of antimicrobials in the Norwegian pig production. Among the European isolates, 9.2% showed combined resistance to ciprofloxacin and erythromycin. The occurrence of *Campylobacter* spp. isolates displaying combined resistance to ciprofloxacin and erythromycin is of great importance to public health, since both compounds are recognised as critically important antimicrobials for the treatment of *Campylobacter* infections in humans (WHO, 2019).

Campylobacter spp. from human clinical cases

In 2025, 3,308 human cases of campylobacteriosis were notified to MSIS. Most cases with a known place of acquisition were infected abroad (53%). Surveillance data suggested that most cases were sporadic, and no outbreak clusters were reported. The first ten *Campylobacter* isolates each month from two sentinel regional laboratories and the first five isolates each month from two additional sentinel regional laboratories were submitted to the NRL for Enteropathogenic Bacteria at NIPH. In addition, isolates recovered from blood cultures were submitted to the NRL for surveillance purposes. A total of 449 isolates were received at the NRL. Antimicrobial susceptibility testing was performed on 419 unique *Campylobacter jejuni* isolates and 24 *Campylobacter coli* isolates (Table 41) against four antibiotic groups: macrolides (erythromycin), aminoglycosides (gentamicin), fluoroquinolones (ciprofloxacin), and tetracycline. The results of antimicrobial susceptibility testing are presented in Tables 42-44, Figures 72-74, and the accompanying text.

TABLE 41. Number of antimicrobial susceptibility-tested *Campylobacter* spp. isolates recoved from human clinical specimens in Norway 2025, by species and place of acquisition.

Campylobacter spp.	No. of isolates tested in 2025	Place of acquistion		
		Norway	Abroad	Unknown
Campylobacter jejuni	419	199	172	48
Campylobacter coli	24	2	21	1
Total	**443**	**201**	**193**	**49**

ANTIMICROBIAL RESISTANCE IN CAMPYLOBACTER JEJUNI

TABLE 42. Percentage distributions of antimicrobial susceptibility categories in domestically acquired *Campylobacter jejuni* (n=199) from human clinical specimens in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	Susceptible	Resistant	S	I	R
Tetracycline	≤ 2	> 2	89.9	-	10.1
Erythromycin	≤ 4	> 4	100.0	-	0.0
Gentamicin[1]	≤ 2	> 2	99.5	-	0.5
Ciprofloxacin[2]	≤ 0.001	> 0.5	0.0	82.4	17.6

[1]Breakpoints according to ECOFF. [2]Breakpoints for ciprofloxacin adjusted according to EUCAST in keeping with the new I-definition and current dosing practice for infections (v.16.0).

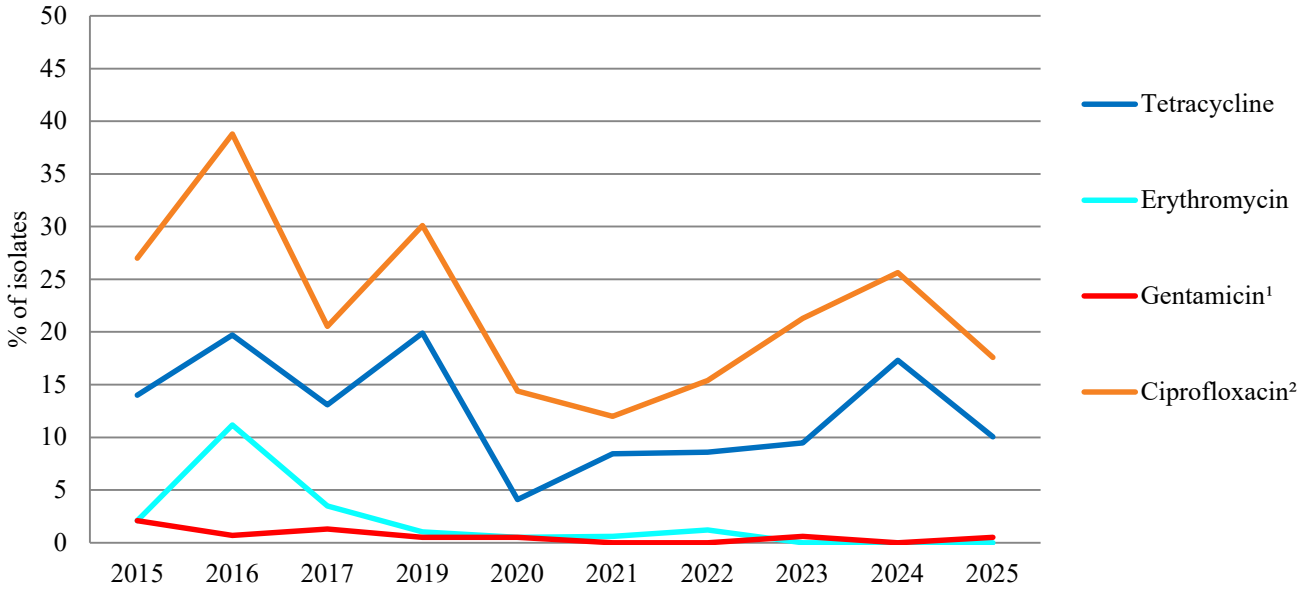

FIGURE 72. Trend 2015-2025. Percentage of domestically acquired *Campylobacter jejuni* resistant to selected antimicrobial agents in Norway. [1]Breakpoints according to ECOFF. [2]Breakpoints for ciprofloxacin adjusted 2020 onwards according to EUCAST in keeping with the new I-definition and current dosing practice for infections (v.16.0).

TABLE 43. Percentage distributions of antimicrobial susceptibility categories in travel-associated *Campylobacter jejuni* (n=172) from human clinical specimens in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	Susceptible	Resistant	S	I	R
Tetracycline	≤ 2	> 2	37.2	-	62.8
Erythromycin	≤ 4	> 4	99.4	-	0.6
Gentamicin[1]	≤ 2	> 2	100.0	-	0.0
Ciprofloxacin[2]	≤ 0.001	> 0.5	0.0	15.7	84.3

[1]Breakpoints according to ECOFF. [2]Breakpoints for ciprofloxacin adjusted according to EUCAST in keeping with the new I-definition and current dosing practice for infections (v.16.0).

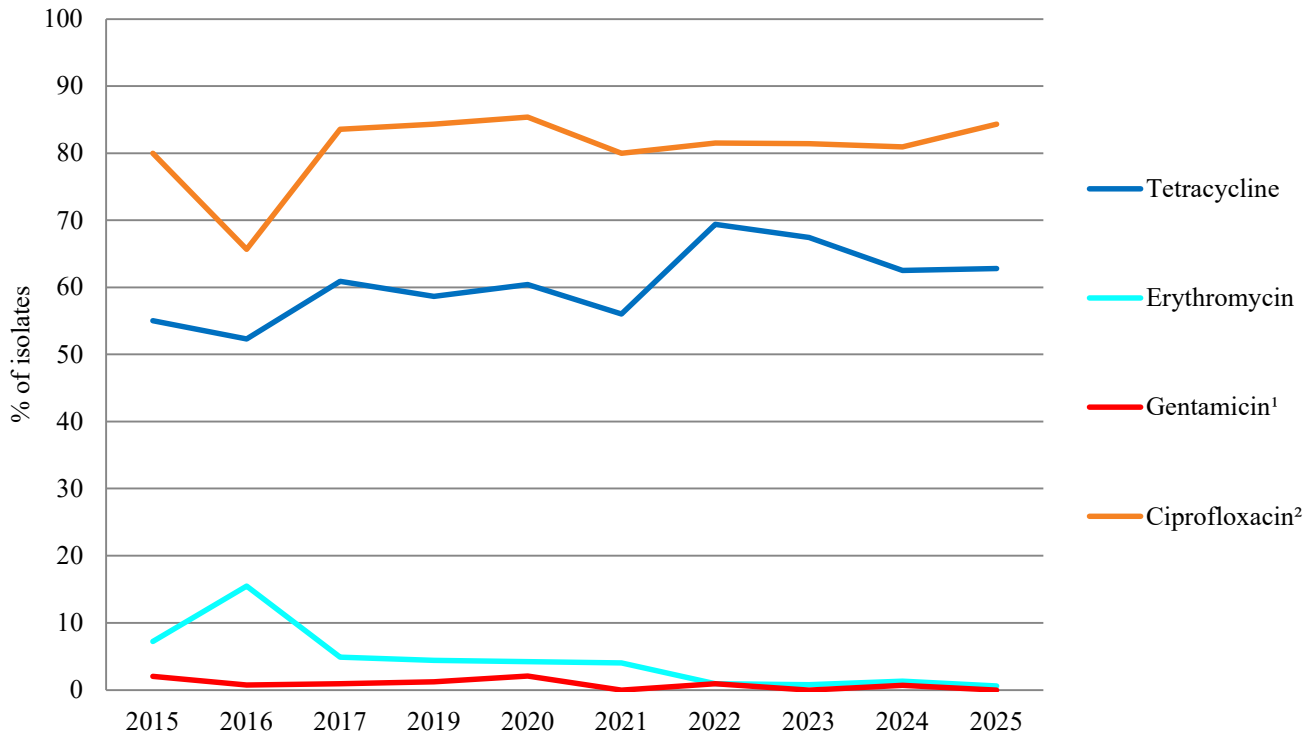

FIGURE 73. Trend 2015-2025. Percentage of travel-associated *Campylobacter jejuni* resistant to selected antimicrobial agents in Norway. [1]Breakpoints according to ECOFF. [2]Breakpoints for ciprofloxacin adjusted 2020 onwards according to EUCAST in keeping with the new I-definition and current dosing practice for infections (v.16.0).

ANTIMICROBIAL RESISTANCE IN CAMPYLOBACTER COLI

TABLE 44. Percentage distributions of antimicrobial susceptibility categories in *Campylobacter coli* (n=24) from human clinical specimens irrespective of place of acquisition in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	Susceptible	Resistant	S	I	R
Tetracycline	≤ 2	> 2	33.3	-	66.7
Erythromycin	≤ 8	> 8	87.5	-	12.5
Gentamicin[1]	≤ 2	> 2	95.8	-	4.2
Ciprofloxacin[2]	≤ 0.001	> 0.5	0.0	16.7	83.3

[1]Breakpoints according to ECOFF. [2]Breakpoints for ciprofloxacin adjusted according to EUCAST in keeping with the new I-definition and current dosing practice for infections (v.16.0).

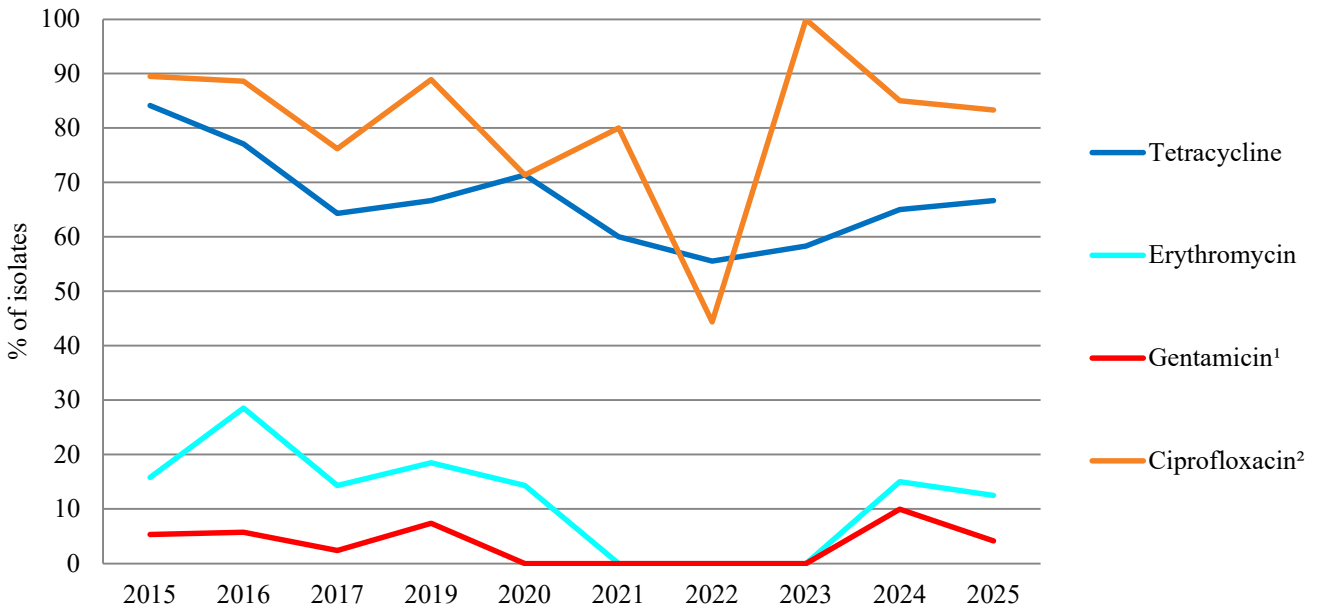

FIGURE 74. Trend 2015-2025. Percentage of *Campylobacter coli* resistant to selected antimicrobial agents irrespective of place of acquisition in Norway. [1]Breakpoints according to ECOFF. [2]Breakpoints for ciprofloxacin adjusted according to EUCAST in keeping with the new I-definition and current dosing practice for infections (v.16.0).

RESULTS AND COMMENTS

The NRL annually performs antimicrobial susceptibility testing on all *C. jejuni* and *C. coli* isolates received as part of the sentinel surveillance system. On 31st October 2020, the EUCAST Scientific Committee revised the breakpoints for fluoroquinolone susceptible isolates of both *C. jejuni* and *C. coli* from ≤0.5 mg/L to ≤0.001 mg/L, introducing a new intermediate category between susceptible and resistant isolates. In this report, data from 2020 onwards have been retrospectively adjusted to reclassify isolates that fall within this new category as intermediate.

For *C. jejuni*, we observed a stable resistance trend for all tested antibiotics. Resistance to tetracycline and ciprofloxacin was higher in strains from travel-associated infections than in strains from domestically acquired infections.

For *C. coli*, we observed a stable resistance trend for all tested antibiotics. Most strains were resistant to ciprofloxacin irrespective of place of acquisition. We identified an MDR phenotype in three travel-associated *C. coli* strains, with resistance to ciprofloxacin, tetracycline, and erythromycin.

Yersinia enterocolitica from human clinical specimens

In 2025, 94 human cases of yersiniosis were notified to MSIS. Most cases with a known place of acquisition were domestically acquired (71.8%). The National Reference Laboratory (NRL) for Enteropathogenic Bacteria at the Norwegian Institute of Public Health (NIPH) received 98 pathogenic *Yersinia* isolates from primary diagnostic laboratories. Three outbreak clusters were identified, and 84 unique isolates were screened for antimicrobial resistance determinants following whole-genome sequencing. Antimicrobial susceptibility testing was performed on 79 isolates (Table 45) against four antibiotic groups: beta-lactams (ampicillin, cefotaxime, ceftazidime, and meropenem), fluoroquinolones (ciprofloxacin), tetracycline, and chloramphenicol. The results of antimicrobial susceptibility testing are presented in Tables 46-48, Figure 75, and the accompanying text.

TABLE 45. Number of *Yersinia enterocolitica* isolates tested for phenotypic antimicrobial susceptibility (AST) and predicted genotypic resistance (GR) recovered from human clinical specimens in Norway 2025, by serotype and place of acquisition.

Yersinia enterocolitica	No. of isolates tested in 2025		Place of acquisition					
			Norway		Abroad		Unknown	
	Phenotypic AST	Predicted GR	Phenotypic AST	Predicted GR	Phenotypic AST	Predicted GR	Phenotypic AST	Predicted GR
Y. enterocolitica O:3	66	69	31	33	17	18	18	18
Y. enterocolitica O:9	7	7	5	5	1	1	1	1
Y. entericolitica (other serotypes)	6	8	3	5	-	-	3	3
Total	**79**	**84**	**39**	**43**	**18**	**19**	**22**	**22**

ANTIMICROBIAL RESISTANCE IN YERSINIA ENTEROCOLITICA SEROTYPE O:3 AND O:9

TABLE 46. Percentage distributions of antimicrobial susceptibility categories in *Yersinia enterocolitica* O:3 and O:9 (n=73) from human clinical specimens irrespective of place of acquisition in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	0.0	-	100.0
Cefotaxime	≤ 1	> 2	100.0	0.0	0.0
Ceftazidime	≤ 1	> 4	100.0	0.0	0.0
Meropenem	≤ 2	> 8	100.0	0.0	0.0
Ciprofloxacin	≤ 0.25	> 0.5	98.6	1.4	0.0
Tetracycline[1]	≥ 17 mm	< 17 mm	100.0	-	0.0
Chloramphenicol	≤ 8	> 8	90.4	-	9.6

[1]Breakpoints according to national zone distributions.

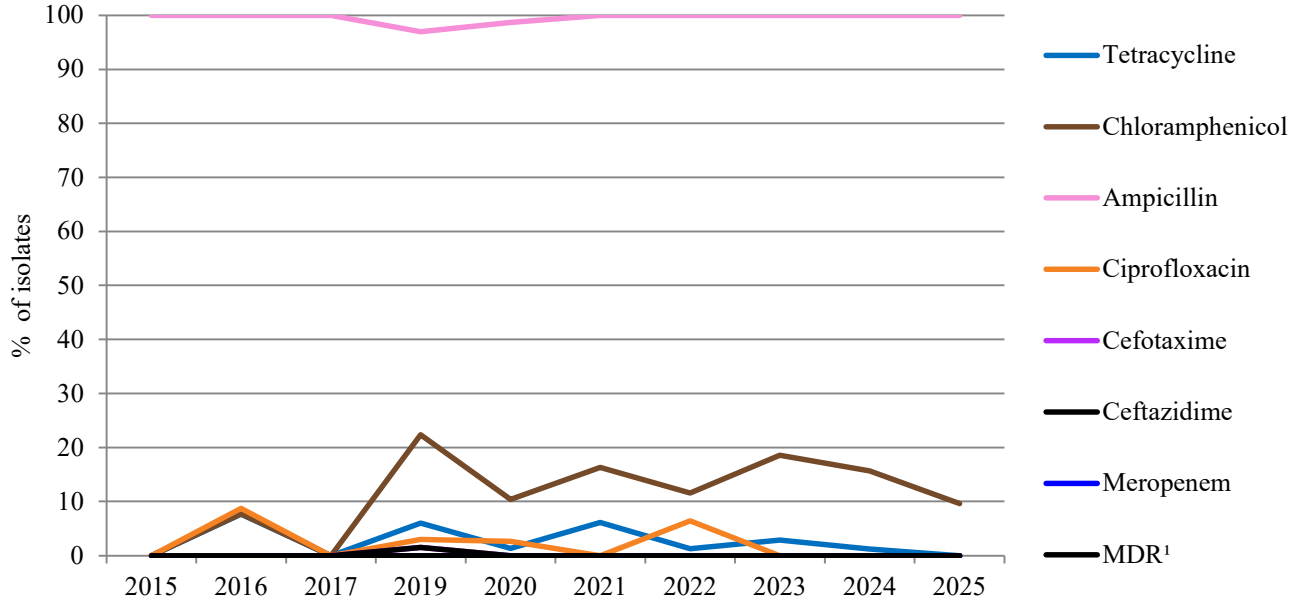

FIGURE 75. Trend 2015-2025. Percentage of *Yersinia enterocolitica* O:3 and O:9 resistant to selected antimicrobial agents irrespective of place of acquisition in Norway.

TABLE 47. Percentage distributions of genotypic resistance in *Yersinia enterocolitica* O:3 and O:9 (n=76) compared to phenotypic wild type/non-wild type distribution (n=73) from human clinical specimens in Norway 2025.

	Phenotype[1] (%)		Predicted genotype[2] (%)	
Antibiotic	Wild type	Non-wild type	S	R
Gentamicin	-	-	100.0	0.0
Streptomycin	-	-	86.8	13.2
Ampicillin	100.0	0.0	100.0	0.0
Meropenem	100.0	0.0	100.0	0.0
Cefotaxime[3]	100.0	0.0	100.0	0.0
Ceftazidime[3]	100.0	0.0		
Colistin	-	-	100.0	0.0
Chloramphenicol	90.4	9.6	88.2	11.8
Ciprofloxacin	98.6	1.4	100.0	0.0
Sulfonamide	-	-	86.8	13.2
Tetracycline	100.0	0.0	100.0	0.0
Trimethoprim	-	-	100.0	0.0

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Yersinia enterocolitica* (v.16.0). [2]R and S categorisation based on presence or absence of resistance determinants. [3]Predicted genotypic resistance to cefotaxime and ceftazidime is combined to predict genotypic resistance against extended-spectrum cephalosporins.

CORRELATION BETWEEN PHENOTYPIC AND PREDICTED GENOTYPIC RESISTANCE IN YERSINIA

TABLE 48. Concordance between phenotypic and predicted genotypic resistance to selected antibiotic categories in *Yersinia enterocolitica* O:3 and O:9 isolates identified in Norway 2025.

Antibiotic categories	Tested	Phenotype WT[1]		Phenotype NWT[1]		Sensitivity (%)	Specificity (%)
		Genotype R	Genotype S	Genotype R	Genotype S		
Penicillins	73	73	0	0	73	-	-
ESC[2]	73	0	73	0	73	-	100.0
Carbapenems	73	0	73	0	73	-	100.0
Fluoroquinolones	73	0	72	1	73	-	98.6
Tetracycline	73	0	73	0	73	-	100.0
Phenicols	73	0	66	7	73	100.0	100.0

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Yersinia enterocolitica* (v.16.0). [2]Predicted genotypic resistance to cefotaxime and ceftazidime is combined as predicted genotypic resistance against extended-spectrum cephalosporins (ESC).

RESULTS AND COMMENTS

The NRL annually performs antimicrobial susceptibility testing on all pathogenic *Yersinia enterocolitica* isolates. In addition, from 2020 onwards, the NRL has screened all isolates for antimicrobial resistance determinants following whole-genome sequencing to predict genotypic resistance.

Antimicrobial resistance in *Y. enterocolitica* serotypes O:3 and O:9 has been combined and presented without distinction by place of acquisition. We observed a stable resistance trend for all tested antibiotics. All isolates expressed intrinsic resistance to ampicillin, attributed to the *blaA* gene. In addition, an MDR genotype was identified in nine *Y. enterocolitica* O:3 isolates.

The overall correlation between phenotypic and predicted genotypic resistance was high, with both sensitivity and specificity above 98% for the tested and screened antibiotics.

Shigella spp. from human clinical specimens

In 2025, 126 human cases of shigellosis were notified to MSIS. Most cases with a known place of acquisition were infected abroad (70.6%). The National Reference Laboratory (NRL) for Enteropathogenic Bacteria at the Norwegian Institute of Public Health (NIPH) received 121 *Shigella* isolates from primary diagnostic laboratories. A total of 110 unique isolates were screened for antimicrobial resistance determinants following whole-genome sequencing. Antimicrobial susceptibility testing was performed on 110 *Shigella* isolates (Table 49) against four antibiotic groups: beta-lactams (ampicillin, cefotaxime, ceftazidime, and meropenem), fluoroquinolones (ciprofloxacin), tetracycline, and chloramphenicol. The results are presented in Tables 50–55, Figures 76-78, and the accompanying text.

TABLE 49. Number of *Shigella* spp. isolates tested for phenotypic antimicrobial susceptibility (AST) and predicted genotypic resistance (GR) recovered from human clinical specimens in Norway 2025, by species and place of acquisition.

Shigella spp.	No. of isolates tested in 2025		Place of acquisition					
			Norway		Abroad		Unknown	
	Phenotypic AST	Predicted GR	Phenotypic AST	Predicted GR	Phenotypic AST	Predicted GR	Phenotypic AST	Predicted GR
S. sonnei	67	67	12	12	52	52	3	3
S. flexneri	40	40	11	11	22	22	7	7
S. boydii	3	3	-	-	3	3	-	-
S. dysenteriae	-	-	-	-	-	-	-	-
Total	**110**	**110**	**23**	**23**	**77**	**77**	**10**	**10**

ANTIMICROBIAL RESISTANCE IN SHIGELLA SONNEI

TABLE 50. Percentage distributions of antimicrobial susceptibility categories in *Shigella sonnei* (n=67) from human clinical specimens irrespective of place of acquisition in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	61.2	-	38.8
Cefotaxime	≤ 1	> 2	67.2	0.0	32.8
Ceftazidime	≤ 1	> 4	95.5	4.5	0.0
Meropenem	≤ 2	> 8	100.0	0.0	0.0
Pefloxacin[1]	≥ 24 mm	< 24 mm	56.7	-	43.3
Tetracycline[2]	≥ 17 mm	< 17 mm	25.4	-	74.6
Chloramphenicol	≤ 8	> 8	98.5	-	1.5

[1]Low-level resistance against ciprofloxacin is underestimated using breakpoints based on ciprofloxacin disk diffusion. Susceptibility to ciprofloxacin is inferred from pefloxacin disk diffusion according to EUCAST clinical breakpoints (v.16.0). [2]Breakpoints according to national zone distributions.

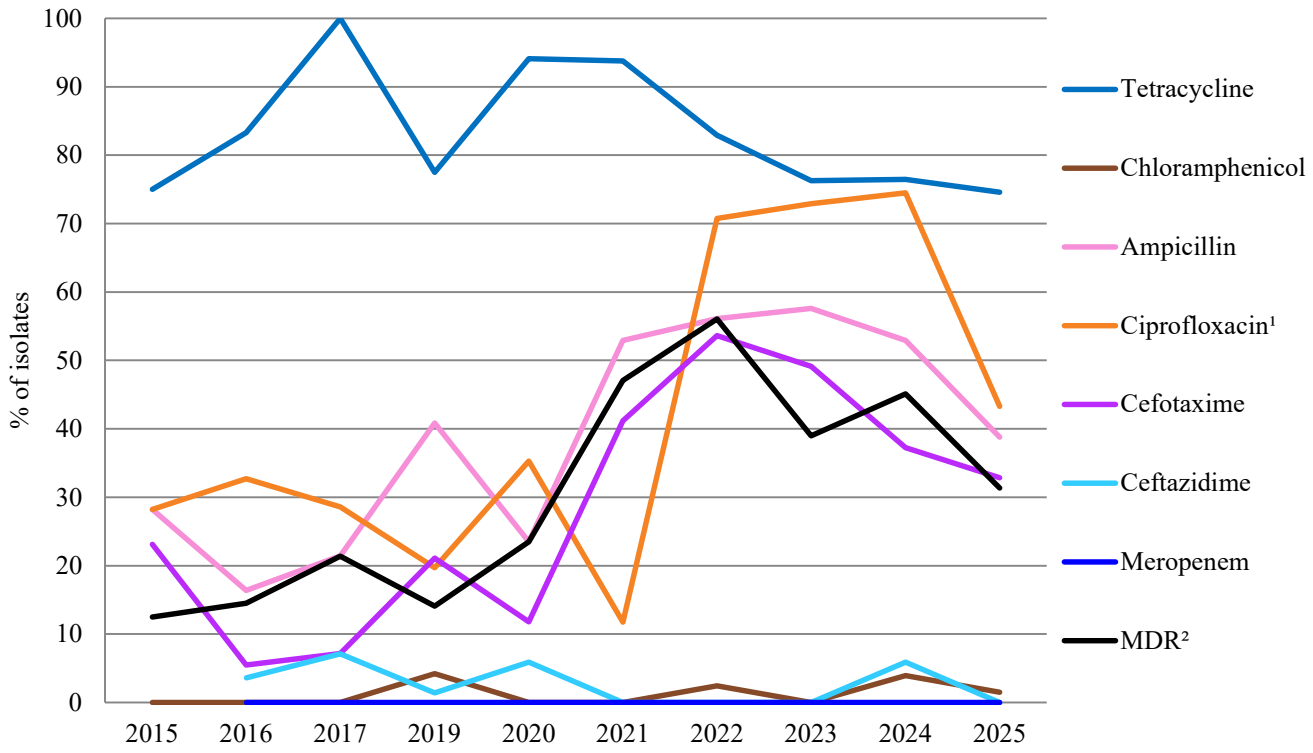

FIGURE 76. Trend 2015-2025. Percentage of *Shigella sonnei* resistant to selected antimicrobial agents irrespective of place of acquisition in Norway. [1]Resistance to ciprofloxacin is inferred from pefloxacin disk diffusion 2022 onwards to better align with observed genotypic resistance. [2]MDR is defined as acquired non-susceptibility to antimicrobials from three or more categories.

TABLE 51. Percentage distributions of genotypic resistant *Shigella sonnei* (n=67) compared to phenotypic wild type/non-wild type distribution (n=67) from human clinical specimens in Norway 2025.

	Phenotype[1] (%)		Predicted genotype[2] (%)	
Antibiotic	Wild type	Non-wild type	S	R
Gentamicin	-	-	100.0	0.0
Streptomycin	-	-	9.0	91.0
Ampicillin	61.2	38.8	61.2	38.8
Meropenem	100.0	0.0	100.0	0.0
Cefotaxime[3]	67.2	32.8	64.2	35.8
Ceftazidime[3]	95.5	4.5		
Colistin	-	-	100.0	0.0
Chloramphenicol	98.5	1.5	98.5	1.5
Ciprofloxacin	56.7	43.3	56.7	43.3
Sulfonamide	-	-	19.4	80.6
Tetracycline	25.4	74.6	28.4	71.6
Trimethoprim	-	-	4.5	95.5

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Shigella sonnei* (v.16.0). [2]R and S categorisation based on presence or absence of resistance determinants. [3]Predicted genotypic resistance to cefotaxime and ceftazidime is combined to predict genotypic resistance against extended-spectrum cephalosporins.

ANTIMICROBIAL RESISTANCE IN SHIGELLA FLEXNERI

TABLE 52. Percentage distributions of antimicrobial susceptibility categories in *Shigella flexneri* (n=40) from human clinical specimens irrespective of place of acquisition in Norway 2025.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	20.0	-	80.0
Cefotaxime	≤ 1	> 2	87.5	0.0	12.5
Ceftazidime	≤ 1	> 4	97.5	2.5	0.0
Meropenem	≤ 2	> 8	100.0	0.0	0.0
Pefloxacin[1]	≥ 24 mm	< 24 mm	55.0	-	45.0
Tetracycline[2]	≥ 17 mm	< 17 mm	22.5	-	77.5
Chloramphenicol	≤ 8	> 8	42.5	-	57.5

[1]Low-level resistance against ciprofloxacin is underestimated using breakpoints based on ciprofloxacin disk diffusion. Susceptibility to ciprofloxacin is inferred from pefloxacin disk diffusion according to EUCAST clinical breakpoints (v.16.0). [2]Breakpoints according to national zone distributions.

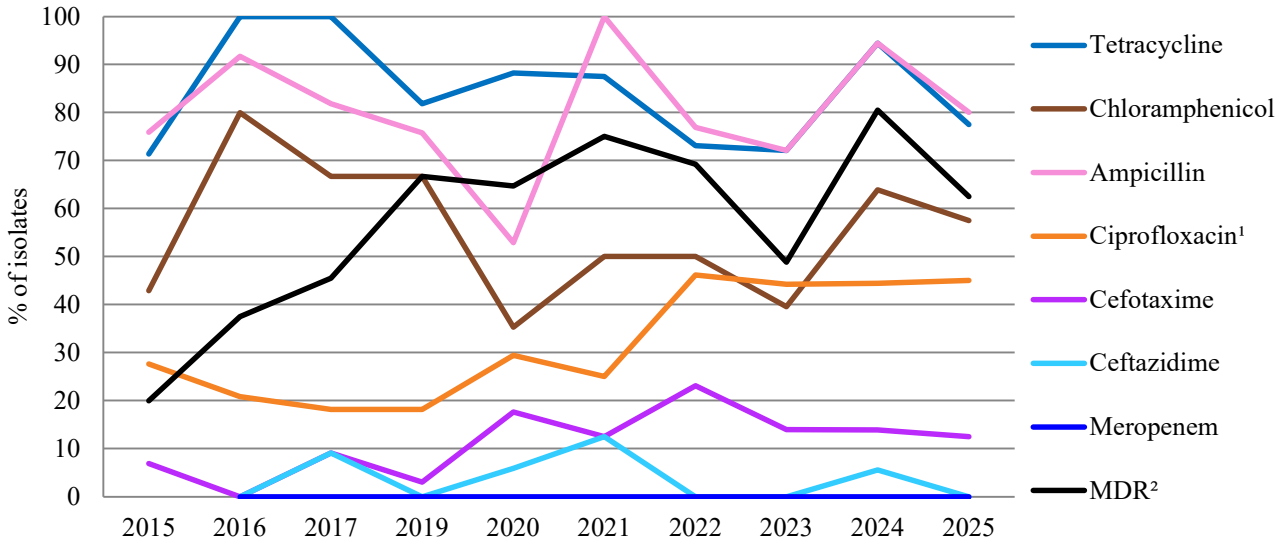

FIGURE 77. Percentage of *Shigella flexneri* resistant to selected antimicrobial agents irrespective of place of acquisition in Norway, trend 2015-2025. [1]Resistance to ciprofloxacin is inferred from pefloxacin disk diffusion 2022 onwards to better align with observed genotypic resistance. [2]MDR is defined as acquired non-susceptibility to antimicrobials from three or more categories.

TABLE 53. Percentage distributions of genotypic resistance in *Shigella flexneri* (n=40) compared to phenotypic wild type/non-wild type distribution (n=40) from human clinical specimens in Norway 2025.

	Phenotype[1] (%)		Predicted genotype[2] (%)	
Antibiotic	Wild type	Non-wild type	S	R
Gentamicin	-	-	100.0	0.0
Streptomycin	-	-	45.0	55.0
Ampicillin	20.0	80.0	20.0	80.0
Meropenem	100.0	0.0	100.0	0.0
Cefotaxime[3]	87.5	12.5	87.5	12.5
Ceftazidime[3]	97.5	2.5		
Colistin	-	-	100.0	0.0
Chloramphenicol	42.5	57.5	42.5	57.5
Ciprofloxacin	55.0	45.0	55.0	45.0
Sulfonamide	-	-	57.5	42.5
Tetracycline	22.5	77.5	22.5	77.5
Trimethoprim	-	-	17.5	82.5

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in absence of ECOFF for *Shigella flexneri* (v.16.0). [2]R and S categorisation based on presence or absence of resistance determinants. [3]Predicted genotypic resistance to cefotaxime and ceftazidime is combined to predict genotypic resistance against extended-spectrum cephalosporins.

MULTI-DRUG RESISTANCE IN SHIGELLA

TABLE 54. Number of predicted genotypic multi-drug resistance in (MDR) *Shigella* spp. isolates identified in Norway 2025, stratified according to species and resistance to different antibiotic categories.

Shigella spp.	MDR[1]	Antibiotic categories[2]							
		STR	AMP	ESC	CHL	CIP	SUL	TET	TMP
Shigella sonnei	56	53	25	24	1	28	54	48	54
Shigella flexneri	34	20	32	5	23	18	17	30	31
Shigella boydii	1	1	1	0	1	0	1	1	1
Total no. of MDR isolates	**91**	**74**	**58**	**29**	**25**	**46**	**72**	**79**	**86**

[1]Multi-drug resistance (MDR) defined as predicted genotypic resistance to 3 ≥ antibiotic categories. [2]Antibiotic category: STR: Streptomycin, AMP; Ampicillin, ESC; Extended-Spectrum Cephalosporin, CHL; Chloramphenicol, CIP; Ciprofloxacin, SUL; Sulfonamide, TET; Tetracycline, TMP; Trimethoprim.

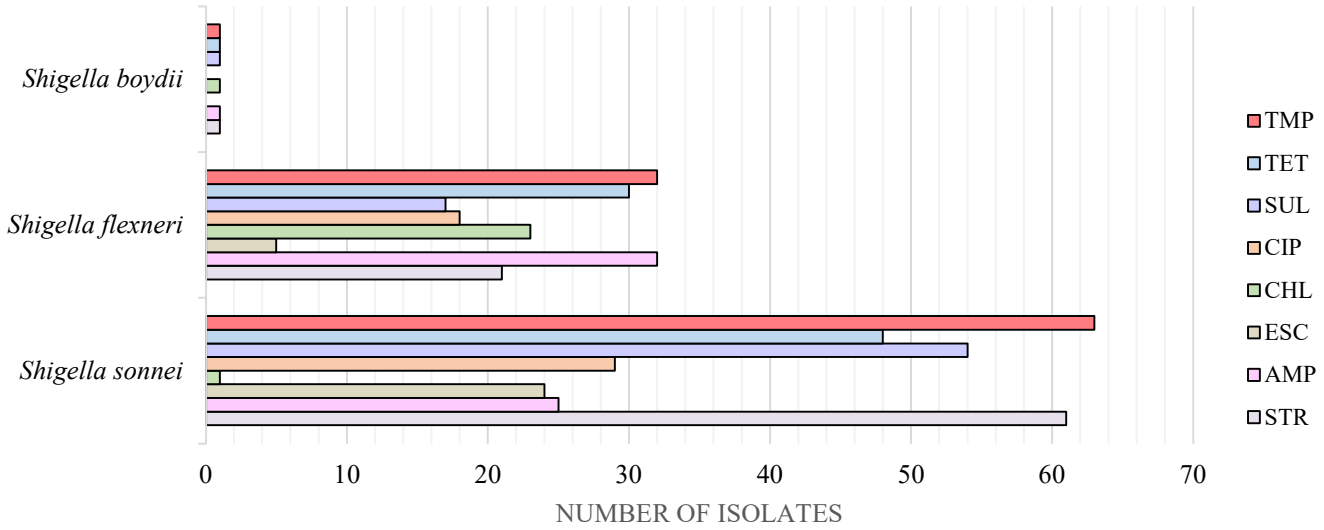

FIGURE 78. Number of predicted genotypically multi-drug resistant (MDR) *Shigella* spp. isolates (n=91) identified in Norway 2025, stratified according to species and resistance to different antibiotic categories; STR: Streptomycin, AMP; Ampicillin, ESC; Extended-Spectrum Cephalosporin, CHL; Chloramphenicol, CIP; Ciprofloxacin, SUL; Sulfonamide, TET; Tetracycline, TMP; Trimethoprim.

CORRELATION BETWEEN PHENOTYPIC AND PREDICTED GENOTYPIC RESISTANCE IN SHIGELLA

TABLE 55. Concordance between phenotypic and predicted genotypic resistance to selected antibiotic categories in *Shigella spp*. (n=110) isolates identified in Norway 2025.

		Phenotype WT[1]		Phenotype NWT[1]			
Antibiotic categories	Tested	Genotype R	Genotype S	Genotype R	Genotype S	Sensitivity (%)	Specificity (%)
Penicillins	110	0	51	59	0	100.0	100.0
ESC[2]	110	0	81	29	0	100.0	100.0
Carbapenems	110	0	110	0	0	-	100.0
Fluoroquinolones	110	0	63	47	0	100.0	100.0
Tetracycline	110	0	27	81	2	100.0	93.1
Phenicols	110	0	85	25	0	100.0	100.0

[1]Wild type (WT) and non-wild type (NWT) categorisation according to EUCAST epidemiological cut-off values (ECOFF), and clinical breakpoints in abscense of ECOFF for *Shigella spp.* (v.16.0). [2]Predicted genotypic resistance to cefotaxime and ceftazidime is combined as predicted genotypic resistance against extended-spectrum cephalosporins (ESC).

RESULTS AND COMMENTS

The NRL annually performs antimicrobial susceptibility testing on all *Shigella* isolates. Since 2020, the NRL has screened all isolates for antimicrobial resistance determinants following whole-genome sequencing to predict genotypic resistance. From 2022 onwards, ciprofloxacin resistance has been inferred from susceptibility to pefloxacin, as low-level ciprofloxacin resistance is underestimated when using breakpoints based on ciprofloxacin disk diffusion, thereby improving alignment between phenotypic resistance and predicted genotypic resistance.

A large and stable proportion of *S. sonnei* isolates have been resistant to tetracycline over the past decade. In addition, since 2020, an increasing trend in resistance to ciprofloxacin and extended-spectrum cephalosporins has been observed. Resistance to ciprofloxacin was 43.3% in 2025, representing a reduction from 74.5% in 2024. Screening for genotypic resistance determinants confirmed the presence of various mutations in the quinolone resistance-determining regions (QRDRs) of *gyrA* and *parC*, as well as different *qnr* variants. A total of 24 ESBL-producing strains (35.8%) were identified, of which 20 encoded $bla_{\text{CTX-M}}$ genes, and 2 encoded $bla_{\text{DHA-1}}$. An MDR genotype was identified in 83.6% of the strains.

For *S. flexneri*, a large proportion of strains have been resistant to tetracycline and ampicillin over the past decade. In addition, an increasing trend in resistance to ciprofloxacin and chloramphenicol has been observed. Resistance to ciprofloxacin was 45.0% in 2025, representing a slight increase from 44.4% in 2024. Screening for genotypic resistance determinants confirmed the presence of various mutations in QRDRs of *gyrA* and *parC*, as well as different *qnr* variants. A total of 5 ESBL-producing strains (12.5%) were identified, all of which encoded the $bla_{\text{CTX-M-15}}$ gene. An MDR genotype was identified in 85% of the strains.

The overall correlation between phenotypic and predicted genotypic resistance was high, with both sensitivity and specificity above 93% for the tested and screened antibiotics.

HUMAN CLINICAL ISOLATES

Gunnar Skov Simonsen, Jan Egil Afset, Cecilie Torp Andersen, Bente Børud, Caroline V. Knudsen, Anne Torunn Mengshoel, Karine Nordstrand and Carina Merethe Thilesen

Distribution of bacterial species in blood cultures

Surveillance of antimicrobial resistance is usually based on prevalences of reduced susceptibility and resistance to certain combinations of antimicrobials and bacterial species in clinical samples. The NORM surveillance programme generally follows this approach. However, there is a serious limitation to the model because a transition in the distribution from susceptible bacterial species to inherently more resistant ones will represent de facto emergence of resistance which is not easily detected. In order to complement the surveillance of individual species, NORM collects data on all positive blood cultures from the laboratory information systems of the participating institutions. A patient with a given microbial isolate was excluded from registration with a new isolate of the same species within a month from the first entry. This rule was applied irrespective of changes in the organism´s susceptibility pattern. Isolates of a different species from the same patient were included in the surveillance. It proved difficult to systematically evaluate the clinical significance of species which are commonly part of the normal skin flora. In Table 56, proportions are therefore estimated for all isolates and for all isolates excluding species considered to be common skin contaminants such as coagulase negative staphylococci, *Micrococcus* spp., *Bacillus* spp., *Corynebacterium* spp. and *Cutibacterium* spp.. This does not imply that such isolates cannot cause infections, but only that it was not possible to enforce a standardised protocol for inclusion of the clinically significant isolates. Similarly, all isolates were registered as individual findings although polymicrobial bloodstream infections are regularly detected in some patients. Limitations in the data extraction procedure prohibited in-depth analysis of these parameters.

TABLE 56. Number of blood culture isolates in 2025, proportion of all isolates, and proportion of isolates excluding possible skin contaminants (coagulase negative staphylococci, *Micrococcus* spp., *Bacillus* spp., *Corynebacterium* spp. and *Cutibacterium* spp.) 2021-2025. The table is based on data from all laboratories in Norway analysing blood cultures (n=19).

Species	No. of isolates 2025	% of all isolates					% of all isolates excluding skin flora				
		2021	2022	2023	2024	2025	2021	2022	2023	2024	2025
Staphylococcus aureus	2,345	10.5	10.7	10.2	10.1	10.0	13.8	14.1	13.4	13.4	13.3
Coagulase negative staphylococci	4,971	21.1	21.3	21.6	21.0	21.2	-	-	-	-	-
Streptococcus pneumoniae	754	1.6	2.5	2.6	2.8	3.2	2.1	3.4	3.5	3.7	4.3
Streptococcus pyogenes	202	0.4	0.6	1.8	1.5	0.9	0.5	0.8	2.3	2.0	1.1
Streptococcus agalactiae	310	1.6	1.5	1.2	1.3	1.3	2.0	2.0	1.6	1.7	1.8
Beta-haemolytic streptococci group C and G	536	2.4	2.0	2.1	2.1	2.3	3.1	2.6	2.8	2.7	3.0
Viridans- and non-haemolytic streptococci	1,244	5.1	5.8	5.2	5.0	5.3	6.7	7.7	6.8	6.6	7.0
Enterococcus faecalis	736	3.7	3.5	3.3	3.3	3.1	4.9	4.7	4.3	4.3	4.2
Enterococcus faecium	286	1.4	1.4	1.4	1.3	1.1	1.8	1.8	1.8	1.7	1.6
Other Gram-positive aerobic and facultative anaerobic bacteria	1,074	4.2	4.3	4.2	4.9	4.6	2.7	2.5	2.7	2.9	2.7
Escherichia coli	5,038	23.2	21.7	21.8	21.3	21.6	30.7	28.4	28.8	28.2	28.4
Klebsiella spp.	1,849	7.7	7.8	7.4	7.8	7.9	10.1	10.3	9.8	10.2	10.4
Enterobacter spp.	403	1.9	1.7	1.6	1.8	1.7	2.4	2.3	2.2	2.4	2.3
Proteus spp.	320	1.4	1.3	1.3	1.3	1.4	1.8	1.7	1.7	1.7	1.8
Other *Enterobacterales*	553	1.9	2.4	2.4	2.7	2.4	2.5	3.2	3.2	3.6	3.1
Pseudomonas spp.	363	1.9	1.9	1.7	1.6	1.6	2.5	2.5	2.3	2.1	2.1
Other Gram-negative aerobic and facultative anaerobic bacteria	566	2.0	2.1	2.4	2.5	2.4	2.6	2.8	3.2	3.3	3.2
Bacteroides spp.	474	2.3	2.0	2.1	1.9	2.0	3.0	2.6	2.8	2.5	2.7
Other anaerobic bacteria	1,130	4.6	4.3	4.5	4.6	4.8	5.4	5.0	5.3	5.4	5.5
Yeasts	265	1.1	1.2	1.2	1.2	1.1	1.4	1.6	1.5	1.6	1.5
Total	**23,419**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**

As seen in Table 56 and Figure 79, aerobic and facultative Gram-positive and Gram-negative bacteria represented 53.1% and 39.0% of all isolates, respectively. The predominance of Gram-positives among all isolates was at the same level as in previous years. The most common Gram-positive species were coagulase negative staphylococci, which constituted 21.2%. This is at the same level as 21.0% recorded in 2024. The difference between aerobic Gram-positives and Gram-negatives was reversed when species of the skin flora (coagulase negative staphylococci, *Micrococcus* spp., *Bacillus* spp., *Corynebacterium* spp. and *Cutibacterium* spp.) were excluded, with 39.0% aerobic Gram-positives and 51.3% aerobic Gram-negatives.

Among aerobic Gram-positives, the prevalence of *S. pneumoniae* steadily declined from 12.1% in 2005 to 4.0% in 2019 (skin contaminants excluded), following the introduction of the conjugate pneumococcal vaccine in the national childhood immunisation programme in June 2006. The prevalence was even lower in the pandemic years 2020-2021 (2.1%) but has now increased again to 4.3%. The occurrence of *Streptococcus pyogenes* decreased from 2023 (n=380) and 2024 (n=339), to 2025 (n=202). Their proportion of invasive isolates is now approximately at the same level as before the pandemic. The rates for other aerobic Gram-positives have remained relatively stable over many years.

E. coli (28.4%) and other *Enterobacterales* (17.6%) accounted for the vast majority of aerobic Gram-negative isolates. The proportion of *E. coli* is relatively stable over time, but further surveillance is needed to confirm this conclusion. *Pseudomonas* spp. remained unchanged at 2.1%, all figures excluding skin flora.

Anaerobic bacteria and yeasts were less prevalent. Anaerobes accounted for 6.8% (8.2% excluding skin flora). Yeasts accounted for 1.1% (1.5% excluding skin flora). The major pathogens among anaerobes were members of *Bacteroides* spp. (2.0%/2.7%) and among yeasts *Candida albicans* (0.6%/0.8%). However, a multitude of other species were also represented.

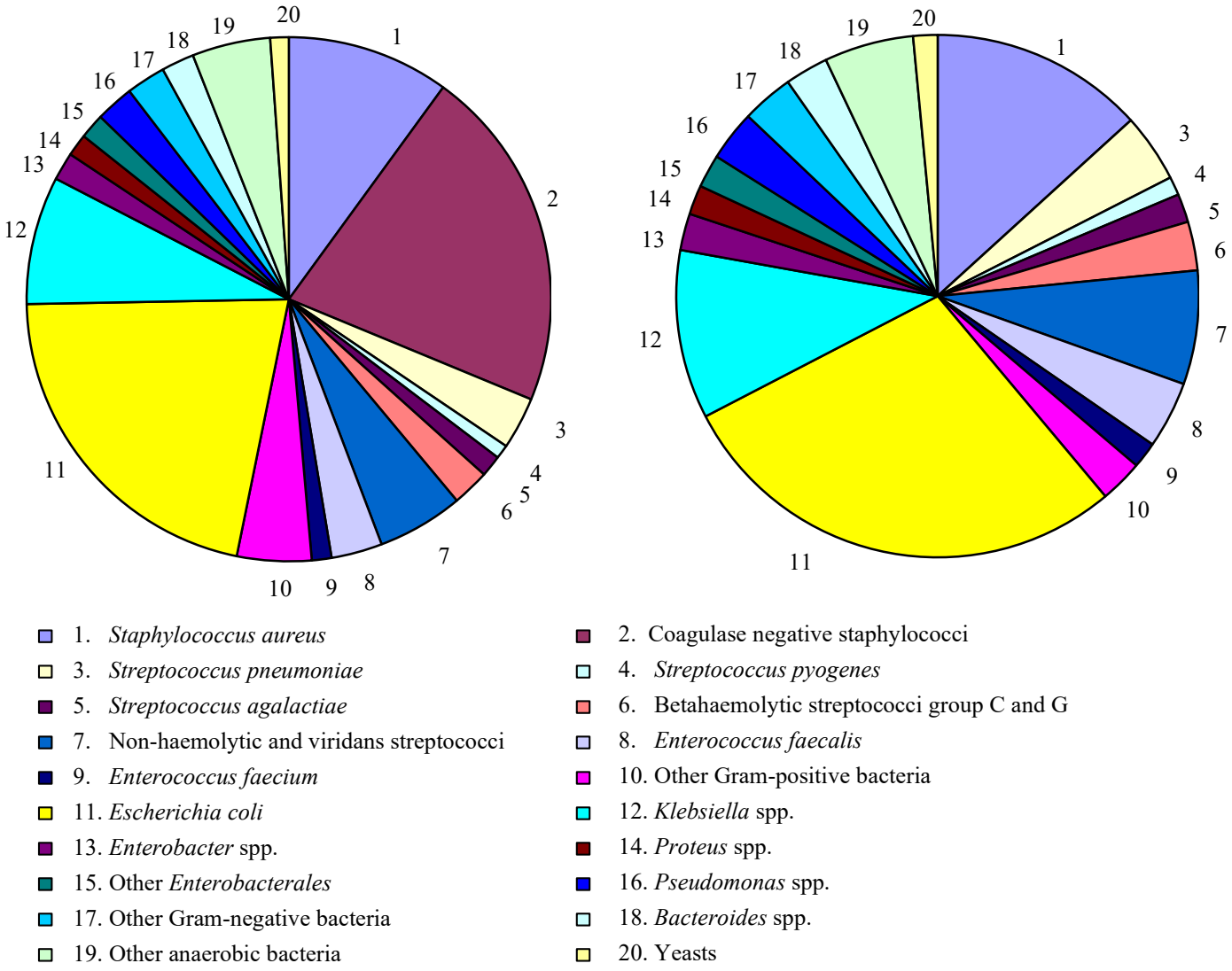

FIGURE 79. Distribution of all blood culture isolates (left, n=23,419) and blood culture isolates excluding common skin contaminants (right, n=17,697) such as coagulase negative staphylococci, *Micrococcus* spp., *Bacillus* spp., *Corynebacterium* spp. and *Cutibacterium* spp. Data for 2025 were retrieved from the information systems of all Norwegian laboratories (n=19).

Two decades of bacteraemia in Norway: Rising incidence and shifting microbial epidemiology, 2005-2024

Bacteraemia – the presence of viable microorganisms in the bloodstream – is a sentinel marker of serious infection and an important driver of antimicrobial use and resistance. NORM has collected aggregate statistics on all positive blood cultures from every Norwegian medical microbiology laboratory for more than two decades, providing a near-complete national picture (see also "Distribution of bacterial species in blood cultures", page 99). A recent study leveraged these data to describe how the incidence and microbial composition of bacteraemia changed between 2005 and 2024, against the backdrop of demographic ageing, hospital activity, immunosuppression and diagnostic intensity [1].

A steady rise in incidence

Across the period, 319,149 blood culture isolates were reported. The annual number more than doubled, from 10,964 in 2005 to 22,679 in 2024, a rise from 238 to 409 isolates per 100,000 population (+72%; Table 57). A negative binomial regression model with a restricted cubic spline for calendar year, an offset for population size and standardisation for the proportion aged 70 years or older showed a near-linear increase, with little difference between crude and age-adjusted estimates. The rise was steeper per hospital bed-day than per capita, consistent with a frailer, more complex inpatient case-mix.

TABLE 57. The absolute number and rate per 100,000 people of blood culture isolates by species in 2005 and 2024 and the percentage change between these years. Counts represent the total number of isolates identified from blood cultures in Norway in each year, with relative change shown as percent difference between 2005 and 2024.

Species	Absolute counts		% change	Rate per 100,000		% change
	2005	2024		2005	2024	
Staphylococcus aureus	1,128	2,312	105.0	24	42	70.1
Coagulase-negative staphylococci	2,230	4,777	114.2	48	86	77.8
Streptococcus pneumoniae	1,027	627	-38.9	22	11	-49.3
Streptococcus pyogenes	239	339	41.8	5	6	17.7
Streptococcus agalactiae	177	294	66.1	4	5	37.9
Streptococcus dysgalactiae	93	465	400.0	2	8	315.0
Viridans and non-haemolytic streptococci	419	1,137	171.4	9	20	125.2
Enterococcus faecalis	444	738	66.2	10	13	38.0
Enterococcus faecium	123	288	134.1	3	5	94.3
Other Gram-positives	335	1,107	230.4	7	20	174.3
Escherichia coli	2,456	4,854	97.6	53	87	64.0
Klebsiella spp.	596	1,769	196.8	13	32	146.3
Enterobacter spp.	171	416	143.3	4	7	101.9
Proteus spp.	206	284	37.9	4	5	14.4
Other *Enterobacterales*	197	612	210.7	4	11	157.8
Pseudomonas spp.	229	354	54.6	5	6	28.3
Acinetobacter spp.	37	92	148.6	1	2	106.4
Other Gram-negatives	199	477	139.7	4	9	98.9
Bacteroides spp.	202	432	113.9	4	8	77.5
Other anaerobic bacteria	238	1,035	334.9	5	19	260.9
Yeasts	218	270	23.9	5	5	2.8
Total	**10,964**	**22,679**	**106.8**	**238**	**409**	**71.7**

Shifts in the microbial landscape

Escherichia coli remained the most frequent pathogen throughout, followed in 2024 by *Staphylococcus aureus* and *Klebsiella* spp.; all increased substantially, with *E. coli* roughly doubling and *Klebsiella* spp. tripling. Coagulase-negative staphylococci, the most common likely contaminant, rose in parallel but held a stable share of all isolates (about 20% in 2005, 21% in 2024). The most striking decline was in *Streptococcus pneumoniae*, which fell by roughly half per capita (22 to 11 per 100,000), most plausibly reflecting childhood pneumococcal conjugate vaccination; this decline occurred mainly early in the period, with later stabilisation and some increase in non-vaccine serotypes. It nonetheless largely explains the apparent shift in the Gram-negative to Gram-positive ratio. Several less common organisms – including *Streptococcus dysgalactiae*, anaerobes and the "other" Gram-positive and Gram-negative categories – showed some of the steepest relative increases, hinting at broadening aetiological diversity and a possible growing contribution of healthcare-associated infection (Figure 80).

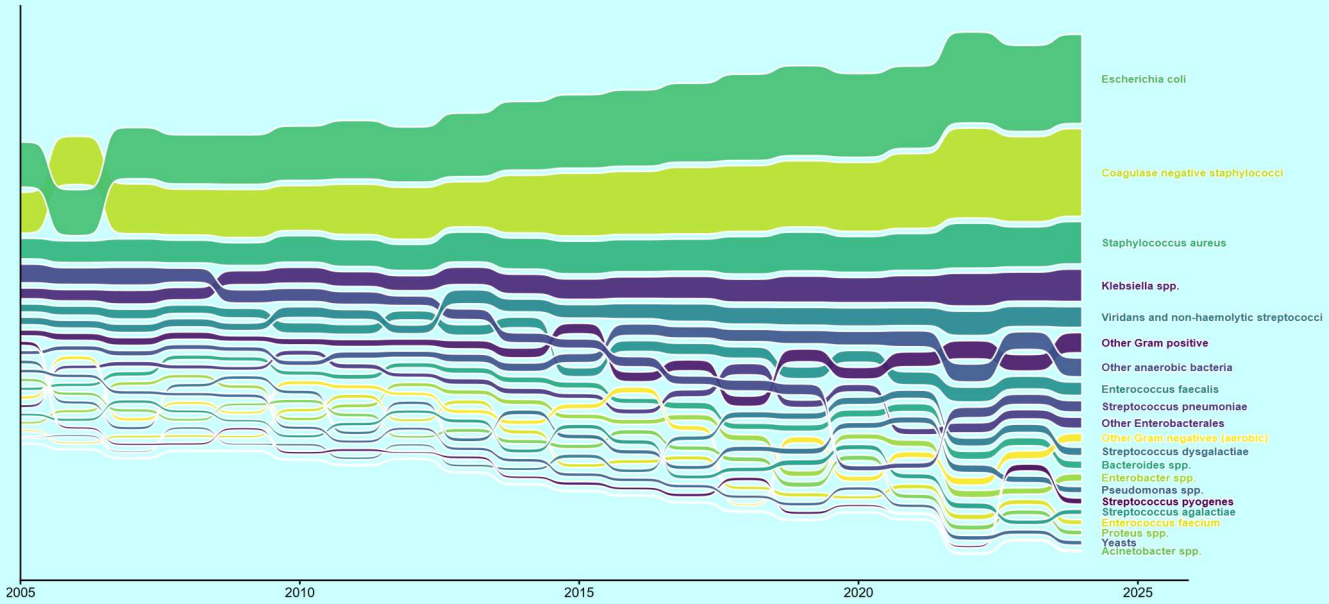

FIGURE 80. The proportional species distribution among bacteraemia cases in Norway from 2005-2024. The figure shows the relative contribution of each species category to the number of bacteraemia cases by year, with category proportions represented as stacked bands and their order representing the rank.

A genuine increase, not simply more testing

The estimated number of blood cultures taken nationally rose by about 80% per capita (roughly 4,100 to 7,300 sets per 100,000) and more than doubled in absolute terms. Crucially, the estimated positivity rate remained essentially stable at around 6% (5.83% in 2005 versus 5.58% in 2024), and the proportion of coagulase-negative staphylococci was unchanged. Together these indicators argue against the rise being an artefact of more indiscriminate sampling or contamination, and instead support a real increase in the underlying burden of bloodstream infections. The increase coincided with marked demographic ageing (the proportion aged ≥70 years grew by 38%), rising immunosuppression (prednisolone users up 53% per capita) and increasing cancer incidence, alongside a fall in hospital bed-days per capita (−37%) suggesting shorter stays and higher patient turnover.

Implications and outlook

A growing pool of Gram-negative bloodstream infections may challenge established empirical treatment regimens and amplify the potential for resistance to spread. The ecological design cannot attribute the rise to specific drivers, nor distinguish community- from hospital-onset infection. Person-level studies linking clinical, microbiological and administrative data, together with improved surveillance that includes denominator data on blood cultures taken, hospital admissions and patient-days, are needed to quantify the relative contributions of ageing, comorbidity and diagnostic practice. The full study, including all data and analysis code, is openly available [1,2].

References

1. Danielsen AS, Johansen A, Sare M, Lim C, Bjørnholt JV, Furberg A-S, et al. Two decades of bacteraemia in Norway: an ecological study of incidence and shifts in microbial epidemiology, 2005–2024. Sci Rep 2025;15:44870. https://doi.org/10.1038/s41598-025-28472-x.
2. Danielsen AS. GitHub: Code and data repository - bacteraemia species 2025. https://github.com/andersskyrud/bacteraemia_species (accessed August 28, 2025)

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Escherichia coli in blood cultures

TABLE 58. *Escherichia coli* blood culture isolates in 2025 (n=2,424). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	63.7	-	36.3
Amoxicillin-clavulanic acid*	≤ 8	> 8	82.5	-	17.5
Piperacillin-tazobactam	≤ 8	> 8	96.7	-	3.3
Cefotaxime**	≤ 1	> 2	93.5	0.5	6.0
Ceftazidime	≤ 1	> 4	93.6	1.5	4.9
Cefepime	≤ 1	> 4	93.7	1.7	4.6
Meropenem**	≤ 2	> 8	100.0	0.0	0.0
Aztreonam	≤ 1	> 4	93.3	2.4	4.3
Gentamicin***	≤ 2	> 2	94.7	-	5.3
Ciprofloxacin**	≤ 0.25	> 0.5	87.8	2.3	9.9
Tigecycline	≤ 0.5	> 0.5	99.8	-	0.2
Trimethoprim-sulfamethoxazole****	≤ 0.5	> 0.5	79.6	-	20.4
ESBL	Negative	Positive	93.6	-	6.4

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. ESBL=Extended-spectrum beta-lactamase. *Breakpoints for intravenous administration. **Breakpoints for indications other than meningitis. ***Breakpoints for infections originating from the urinary tract. ****Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

RESULTS AND COMMENTS

NORM results are interpreted according to NordicAST/ EUCAST clinical breakpoints at the time of analysis and categorised as susceptible with standard exposure (S), susceptible with increased exposure (I), or resistant (R). The vast majority of isolates were fully susceptible (S) to broad-spectrum agents such as cefotaxime (93.5%), ceftazidime (93.6%), gentamicin (94.7%), cefepime (93.7%), piperacillin-tazobactam (96.7%), tigecycline (99.8%), aztreonam (93.3%) and meropenem (100.0%) (Table 58). The breakpoints for trimethoprim-sulfamethoxazole were reduced from R > 4 mg/L to R > 0.5 mg/L and S ≤ 2 mg/L to S ≤ 0.5 mg/L in 2026, but this had no significant impact on resistance rates.

The prevalence of resistance to gentamicin at 5.3% was a small decrease from 5.7% in 2024, and the rate has now been remarkably stable over the last decade (Figure 81). Data were interpreted according to the breakpoints for bacteremia in urinary tract infections, although NordicAST/ EUCAST no longer consider aminoglycosides sufficient for monotherapy in infections originating from other sources. A high proportion of gentamicin resistant isolates (34/128, 26.6%) also produced extended-spectrum beta-lactamase (ESBL) enzymes, but the association was weaker than in 2024 (51/132, 38.6%). The prevalence at individual laboratories varied due to relatively small numbers. When aggregated by region there were minor geographical variations (Middle 3.8%, North 5.1%, West 5.4%, South-East 5.8%).

The prevalence of resistance to ciprofloxacin was 9.9% in 2025 compared to 10.0% in 2023 and 9.9% in 2024. The breakpoint for ciprofloxacin resistance has been changed many times over the years, most recently in 2017 with a reduction from R > 1 mg/L to R > 0.5 mg/L and from S ≤ 0.5 mg/L to S ≤ 0.25 mg/L. The long-term trend for ciprofloxacin resistance cannot be precisely determined due to changes in susceptibility test methodology, but it appears that the increase seen during 2006-2017 has turned to a slowly decreasing trend over the last decade. The temporal association between ciprofloxacin resistance and ciprofloxacin usage is depicted in Figure 82. A similar association between quinolone use and resistance in systemic *E. coli* isolates is also reported internationally. The resistance rates for ampicillin (38.4% in 2024, 36.3% in 2025) and trimethoprim-sulfamethoxazole (21.9% in 2024, 20.4% in 2025) remain essentially unchanged.

Detection of ESBL was based on reduced zone diameters for cefotaxime and/or ceftazidime. All isolates with reduced susceptibility were further characterised by combination disks or MIC gradient tests. A total of 154 isolates (6.4%) were reported as ESBL positive, which is a small decrease from 6.7% in 2024 (Figure 84). The isolates originated from laboratories across the country, and estimates at local level are uncertain due to small numbers. When aggregated at regional level there were geographical differences in the prevalence of ESBL production, but the results should be interpreted with caution; North (2.9%), Middle (4.7%), West (5.2%), and South-East (8.1%). Most of the ESBL isolates were phenotypically resistant to cefotaxime (n=129), ceftazidime (n=104), cefepime (n=100), and aztreonam (n=90), whereas many were susceptible to tigecycline (n=155), piperacillin-tazobactam (n=141), and/or gentamicin (n=120). Ninety isolates were susceptible to amoxicillin-clavulanic acid using breakpoints for non-urinary tract infections, whereas 64 were resistant. The ESBL isolates thus displayed high rates of co-resistance to other antibiotic classes, and 28 (1.2% of all strains) were ESBL positive and concomitantly resistant to both ciprofloxacin and gentamicin. All isolates were clinically susceptible to meropenem. One isolate had a zone diameter below the screening breakpoint, but no carbapenemase genes were detected by molecular analyses.

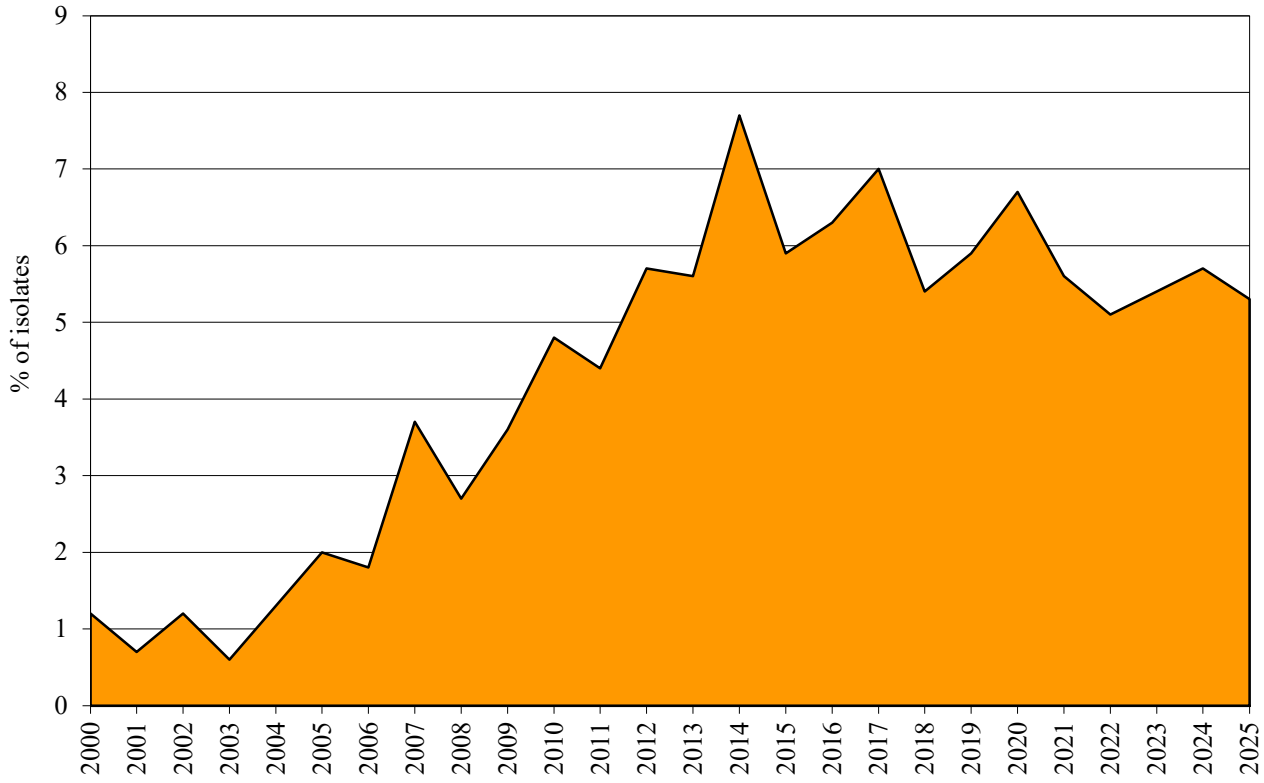

FIGURE 81. Prevalence of resistance to gentamicin in *Escherichia coli* blood culture isolates 2000-2025.

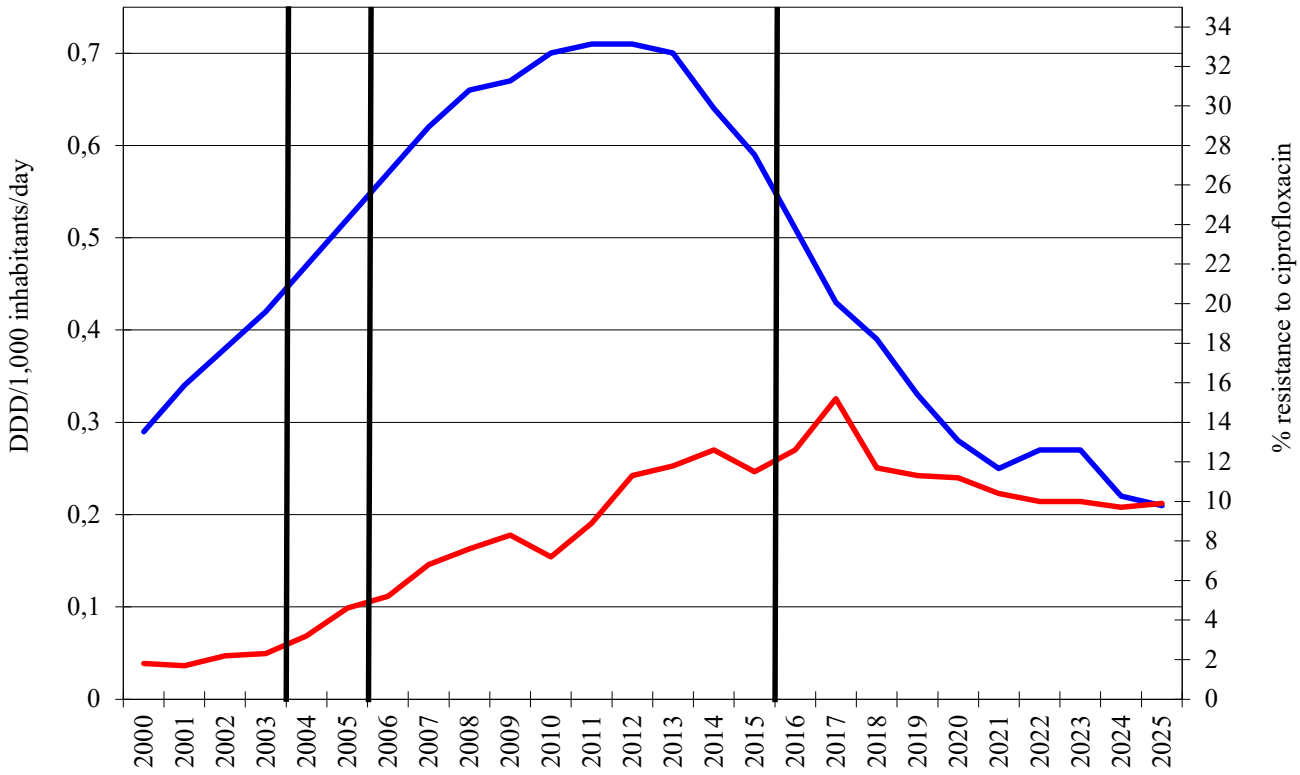

FIGURE 82. Usage of ciprofloxacin (blue) and prevalence of ciprofloxacin resistance in *Escherichia coli* blood culture isolates (red) as defined by MIC > 4 mg/L (2000-2003), MIC > 2 mg/L (2004-2005), MIC > 1 mg/L (2006-2015), and MIC > 0.5 mg/L (2016-2025). The breakpoints cannot be calibrated over the entire time period due to changes in susceptibility test methodology.

Escherichia coli in urine

TABLE 59. *Escherichia coli* urinary tract isolates in 2025 (n=1,210). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 8	> 8	67.3	-	32.7
Mecillinam	≤ 8	> 8	95.5	-	4.5
Amoxicillin-clavulanic acid*	≤ 32	> 32	94.5	-	5.5
Piperacillin-tazobactam	≤ 8	> 8	97.3	-	2.7
Cefalexin	≤ 16	> 16	95.0	-	5.0
Cefotaxime**	≤ 1	> 2	96.0	0.3	3.7
Ceftazidime	≤ 1	> 4	96.3	1.1	2.6
Meropenem**	≤ 2	> 8	100.0	0.0	0.0
Aztreonam	≤ 1	> 4	95.5	1.8	2.7
Gentamicin***	≤ 2	> 2	95.1	-	4.9
Ciprofloxacin**	≤ 0.25	> 0.5	89.8	2.4	7.8
Nitrofurantoin	≤ 64	> 64	99.2	-	0.8
Fosfomycin*	≤ 8	> 8	96.9	-	3.1
Trimethoprim	≤ 2	> 2	78.1	-	21.9
Trimethoprim-sulfamethoxazole****	≤ 0.5	> 0.5	80.1	-	19.9
ESBL	Negative	Positive	96.0	-	4.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. ESBL=Extended-spectrum beta-lactamase. *Breakpoints for oral administration in uncomplicated urinary tract infections. **Breakpoints for indications other than meningitis. ***Breakpoints for infections originating from the urinary tract. ****Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

RESULTS AND COMMENTS

Urinary tract isolates of *E. coli* have been included in the surveillance programme every year since NORM was established in 2000. The prevalence of resistance for 2025 is shown in Table 59 and the rates of resistance for 2000-2025 are shown in Figure 83. The footnotes indicate where EUCAST/NordicAST breakpoints specific for urinary tract infections have been applied. As for blood culture isolates, the breakpoints for trimethoprim-sulfamethoxazole were reduced from R > 4 mg/L to R > 0.5 mg/L and S ≤ 2 mg/L to S ≤ 0.5 mg/L in 2026.

The prevalence of resistance among urinary tract isolates has remained relatively stable over the last 25 years. The prevalence of resistance to ampicillin has gradually increased from approximately 25% to around 35% (32.7% in 2025). Resistance to trimethoprim and trimethoprim-sulfamethoxazole has remained stable around 20% and was determined to be 21.9% and 19.9%, respectively, in 2025. The prevalence of resistance to mecillinam was 4.5% in 2025 compared to 4.8% in 2024. Ciprofloxacin is used as a second-line agent for urinary tract infections in Norway. When adjusting for changes in breakpoint (see legend Figure 82), the prevalence of resistance has remained stable around 8-9% over the last five years. In 2025, 7.8% of the isolates were resistant to ciprofloxacin in addition to 2.4% that were only susceptible to increased exposure through adjustment of dosage or higher concentration at the site of infection. The corresponding rates for blood culture isolates were 9.9% resistance and 2.3% susceptibility to increased exposure. The persistent discrepancy between urinary tract isolates and isolates from bloodstream infections suggests that systemic infections are caused by selected pathogenic lineages with increased virulence and accumulation of mutations in gyrase and/or topoisomerase genes, whereas urinary tract isolates may be more representative of the wild type normal flora. The prevalence of resistance to amoxicillin-clavulanic acid was 5.5% in 2025 compared to 6.7% in 2024, but this phenotype is technically challenging to determine and therefore prone to fluctuations. The breakpoint used (R > 32 mg/L) is only valid for uncomplicated urinary tract infections. Almost all isolates remained fully susceptible to nitrofurantoin (99.2%) and fosfomycin (96.9%).

Forty-eight isolates (4.0%) were reported as ESBL producers. This is at the same level as 3.9% in both 2023 and 2024. As seen in Figure 84, the prevalence of *E. coli* ESBL is still lower in urine than in blood culture isolates (6.4%). ESBL positive strains were isolated in all parts of the country. Thirty-four isolates were retrieved from samples submitted by general practitioners, while the others were found in hospitalised patients (n=4) or patients from outpatient clinics (n=10). The ESBL isolates were all resistant to ampicillin, and the majority were also resistant to cefalexin (46/48), cefotaxime (44/48), ceftazidime (31/48) and aztreonam (31/48). Almost all ESBL isolates were *in vitro* susceptible to mecillinam (45/48). This agent may be a viable treatment option in uncomplicated UTI provided a dosage of 400 mg x 3. Many ESBL isolates were resistant to trimethoprim (30/48), trimethoprim-sulfamethoxazole (27/48) and ciprofloxacin (20/48), but remained susceptible to nitrofurantoin (47/48), fosfomycin (45/48), amoxicillin/clavulanic acid (40/48) and gentamicin (39/48). All isolates were clinically susceptible to meropenem, and no zone diameters below the screening breakpoint for carbapenemase producers were detected.

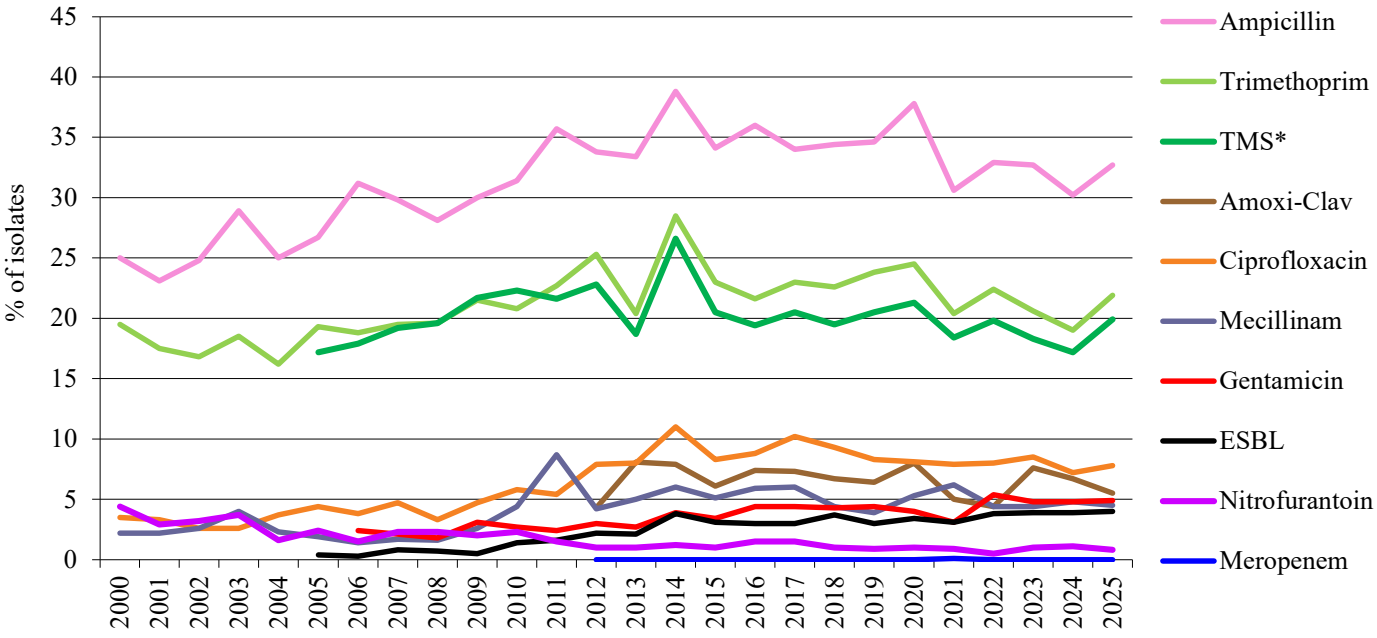

FIGURE 83. Prevalence of resistance to various antimicrobial agents in urinary tract *Escherichia coli* isolates 2000-2025. Isolates are categorised according to the breakpoints at the time of analysis for each year. *TMS=Trimethoprim-sulfamethoxazole.

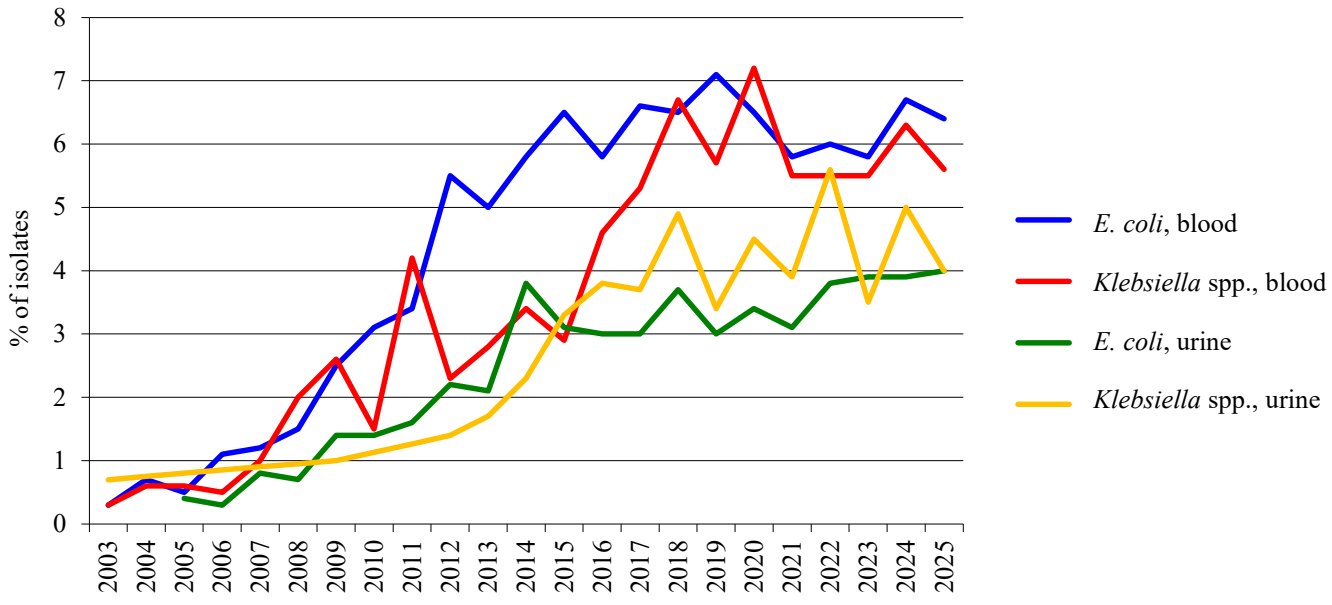

FIGURE 84. Prevalence of ESBL production among *Escherichia coli* and *Klebsiella* spp. isolates from blood and urine 2003-2025.

Methenamine as prophylaxis for recurrent urinary tract infections in older women – a triple-blind, randomised, placebo-controlled, phase IV trial (ImpresU)

A large share of antibiotic prescribing in primary care is driven by urinary tract infections (UTIs)[1]. Older, postmenopausal women are at a higher risk of recurrent episodes (rUTIs)[2], and evidence suggests that repeated exposures to urinary antibiotics select for antimicrobial resistance (AMR) in uropathogens[3]. As the elderly population grows, exploring and implementing effective non-antibiotic preventive UTI treatments for this group are crucial measures to curb the rise of AMR. Despite historically sparse scientific evidence of effect, the urinary antiseptic drug methenamine has been widely used as prophylaxis for rUTIs in Norway for more than 50 years[4]. The drug acidifies the urine to facilitate the formation of formaldehyde from methenamine[5]. Formaldehyde has a broad antimicrobial spectrum acting by cross-linking proteins and causing DNA damage in the bacteria, and the resistance rates to formaldehyde are assumed to be low[6]. Over the past several years, methenamine has gained international attention beyond Scandinavia[7]. Recent evidence from prescription data indicates a preventive effect of methenamine on rUTIs for women ≥40 years and ≥50 years[8,9]. And, in the ALTAR study from 2022, methenamine was found to be non-inferior to low-dose prophylactic antibiotics in women averaging about 50 years of age referred to secondary care[10]. Most regular methenamine users are older women ≥ 75 years treated mainly in primary care[9]. There remains a paucity of controlled trials focusing specifically on these older women. To address this, the current study examined the preventive effect of methenamine on rUTIs in older women in a general practice setting[11].

Methods

Triple-blind, randomised, placebo-controlled phase IV trial with a 6-month treatment period and a 6-month follow-up. Women ≥70 years with rUTIs were recruited from general practice in Norway, Sweden, Poland, and The Netherlands. Recruitment started in December 2019, with follow-up completed at the end of June 2023. Participants were randomly assigned to methenamine hippurate 1g × 2 or placebo 1 tablet × 2 for 6 months. The primary outcome was the number of antibiotic treated UTIs during the treatment period. Secondary outcomes included the number of antibiotic treatments for UTIs during the follow-up period, UTI symptom severity and episode duration. Differences in complications were measured as safety outcomes.

Results

281 women were included in the modified intention to treat analysis with 140 in the methenamine group, and 141 in the placebo group. During the treatment period, the methenamine group had a lower incidence of antibiotic treatments for UTIs than the placebo group, with an incidence rate ratio of 0.75 (95% CI: 0.57-1.0, p 0.049). In the follow-up period, the ratio was reversed: the methenamine group had a higher incidence of antibiotic treatments for UTIs than the placebo group, with an incidence rate ratio of 1.7 (95% CI:1.3-2.3, p<0.001). There were no important differences in UTI symptom severity/duration or complications between the groups.

Conclusion

Methenamine reduces the frequency of rUTIs in older women with a point estimate of a 25% reduction, suggesting advantages over low-dose antibiotic prophylaxis because of its low potential for selection for antimicrobial resistance and mild side effects. The high use of methenamine in Norway may help explain the relatively low use of prophylactic urinary tract antibiotics, and if other countries adopt this practice, the international use of both preventive UTI antibiotics and antibiotics for the treatment of UTIs may be reduced. However, discontinuation after 6-month treatment duration seems to increase the risk of UTI relapses, and physicians should be aware of this risk when initiating or discontinuing treatment. More information on the study can be found in the published research paper[11].

References

1. Haugom LEA, Ruths S, Emberland KE, et al. Consultations and antibiotic treatment for urinary tract infections in Norwegian primary care 2006–2015, a registry-based study. *BMC Fam Pract* 2021;22(1):127. doi: 10.1186/s12875-021-01470-4
2. Medina M, Castillo-Pino E. An introduction to the epidemiology and burden of urinary tract infections. *Ther Adv Urol* 2019;11:1756287219832172. doi: 10.1177/1756287219832172
3. Jensen MLV, Siersma V, Søes LM, et al. Prior Antibiotic Use Increases Risk of Urinary Tract Infections Caused by Resistant Escherichia coli among Elderly in Primary Care: A Case-Control Study. *Antibiotics* 2022; 11(10). doi: 10.3390/antibiotics11101382.
4. NORM/NORM-VET 2024. Usage of Antimicrobial Agents and Occurrence of Antimicrobial. Resistance in Norway. Tromsø / Ås / Oslo 2025. ISSN:1502-2307 (print) / 1890-9965 (electronic).
5. Hamilton-Miller JM, Brumfitt W. Methenamine and its salts as urinary tract antiseptics: variables affecting the antibacterial activity of formaldehyde, mandelic acid, and hippuric acid in vitro. *Investigative urology* 1977;14(4):287–91.
6. Musher Daniel M, Griffith Donald P. Generation of Formaldehyde from Methenamine: Effect of pH and Concentration, and Antibacterial Effect. *Antimicrob Agents Chemother* 1974;6(6):708–11. doi: 10.1128/aac.6.6.708.
7. Lo TS, Hammer KDP, Zegarra M, et al. Methenamine: a forgotten drug for preventing recurrent urinary tract infection in a multidrug resistance era. *Expert review of anti-infective therapy* 2014;12(5):549–54. doi: 10.1586/14787210.2014.904202.
8. Rui L, Lindbaek M, Gjelstad S. Preventive effect of methenamine in women with recurrent urinary tract infections – a case–control study. *Scandinavian Journal of Primary Health Care* 2022;40(3):331–38. doi: 10.1080/02813432.2022.2139363.
9. Heltveit-Olsen SR, Gopinathan U, Blix HS, et al. Effect of methenamine hippurate shortage on antibiotic prescribing for urinary tract infections in Norway—an interrupted time series analysis. *Journal of Antimicrobial Chemotherapy* 2024:dkae078. doi: 10.1093/jac/dkae078.
10. Harding C, Mossop H, Homer T, et al. Alternative to prophylactic antibiotics for the treatment of recurrent urinary tract infections in women: multicentre, open label, randomised, non-inferiority trial. *BMJ* 2022;376:e068229. doi: 10.1136/bmj-2021-0068229.
11. Heltveit-Olsen SR, Arnljots ES, Sundvall PD, et al. Methenamine hippurate as prophylaxis for recurrent urinary tract infections in older women-a triple-blind, randomised, placebo-controlled, phase IV trial (ImpresU). *Clinical microbiology and infection* 2025;31(11):1873–79. doi: 10.1016/j.cmi.2025.07.006

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Klebsiella spp. in blood cultures

TABLE 60. *Klebsiella* spp. blood culture isolates in 2025 (n=1,258), except for amoxicillin-clavulanic acid (n=1,205) where 53 *K. aerogenes* isolates are excluded due to lack of breakpoints. Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Amoxicillin-clavulanic acid*	≤ 8	> 8	87.3	-	12.7
Piperacillin-tazobactam	≤ 8	> 8	89.8	-	10.2
Cefotaxime**	≤ 1	> 2	92.6	1.0	6.4
Ceftazidime	≤ 1	> 4	92.6	1.4	6.0
Cefepime	≤ 1	> 4	91.8	2.4	5.8
Meropenem**	≤ 2	> 8	99.9	0.0	0.1
Aztreonam	≤ 1	> 4	90.6	1.4	8.0
Gentamicin***	≤ 2	> 2	97.3	-	2.7
Ciprofloxacin**	≤ 0.25	> 0.5	89.5	2.9	7.6
Trimethoprim-sulfamethoxazole****	≤ 0.5	> 0.5	86.7	-	13.3
ESBL	Negative	Positive	94.4	-	5.6

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. ESBL=Extended-spectrum beta-lactamase. *Breakpoints for intravenous administration. **Breakpoints for indications other than menigitis. ***Breakpoints for infections originating from the urinary tract. ****Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

TABLE 61. *Klebsiella pneumoniae* blood culture isolates in 2025 (n=899). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Amoxicillin-clavulanic acid*	≤ 8	> 8	88.2	-	11.8
Piperacillin-tazobactam	≤ 8	> 8	91.8	-	8.2
Cefotaxime**	≤ 1	> 2	93.7	0.2	6.1
Ceftazidime	≤ 1	> 4	92.8	1.1	6.1
Cefepime	≤ 1	> 4	92.0	1.8	6.2
Meropenem**	≤ 2	> 8	100.0	0.0	0.0
Aztreonam	≤ 1	> 4	93.1	1.0	5.9
Gentamicin***	≤ 2	> 2	97.1	-	2.9
Ciprofloxacin**	≤ 0.25	> 0.5	86.6	3.7	9.7
Trimethoprim-sulfamethoxazole****	≤ 0.5	> 0.5	84.0	-	16.0
ESBL	Negative	Positive	93.0	-	7.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. ESBL=Extended-spectrum beta-lactamase. *Breakpoints for intravenous administration. **Breakpoints for indications other than menigitis. ***Breakpoints for infections originating from the urinary tract. ****Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

TABLE 62. *Klebsiella oxytoca* blood culture isolates in 2025 (n=283). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Amoxicillin-clavulanic acid*	≤ 8	> 8	84.8	-	15.2
Piperacillin-tazobactam	≤ 8	> 8	87.3	-	12.7
Cefotaxime**	≤ 1	> 2	94.0	2.5	3.5
Ceftazidime	≤ 1	> 4	96.5	1.4	2.1
Cefepime	≤ 1	> 4	92.6	2.5	4.9
Meropenem**	≤ 2	> 8	100.0	0.0	0.0
Aztreonam	≤ 1	> 4	86.9	1.8	11.3
Gentamicin***	≤ 2	> 2	97.2	-	2.8
Ciprofloxacin**	≤ 0.25	> 0.5	97.5	0.7	1.8
Trimethoprim-sulfamethoxazole****	≤ 0.5	> 0.5	92.9	-	7.1
ESBL	Negative	Positive	97.5	-	2.5

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. ESBL=Extended-spectrum beta-lactamase. *Breakpoints for intravenous administration. **Breakpoints for indications other than menigitis. ***Breakpoints for infections originating from the urinary tract. ****Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

TABLE 63. *Klebsiella aerogenes* blood culture isolates in 2025 (n=53). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Piperacillin-tazobactam	≤ 8	> 8	73.6	-	26.4
Cefotaxime*	≤ 1	> 2	67.9	1.9	30.2
Ceftazidime	≤ 1	> 4	67.9	3.8	28.3
Cefepime	≤ 1	> 4	88.7	9.4	1.9
Meropenem*	≤ 2	> 8	98.1	0.0	1.9
Aztreonam	≤ 1	> 4	71.7	3.8	24.5
Gentamicin**	≤ 2	> 2	100.0	-	0.0
Ciprofloxacin*	≤ 0.25	> 0.5	92.4	1.9	5.7
Trimethoprim-sulfamethoxazole***	≤ 0.5	> 0.5	94.3	-	5.7
ESBL	Negative	Positive	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. ESBL=Extended-spectrum beta-lactamase. *Breakpoints for indications other than menigitis. **Breakpoints for infections originating from the urinary tract. ***Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

RESULTS AND COMMENTS

Klebsiella spp. isolates in blood cultures were speciated as follows: 899 (71.5%) *K. pneumoniae* (including *K. pneumoniae, K. quasipneumoniae, K. variicola, K. quasivariicola* and *K. africana*); 283 (22.5%) *K. oxytoca* (including *K. oxytoca, K. michiganensis, K. grimontii, K. pasteurii, K. huaxiensis* and *K. spallanzanii*): 53 (4.2%) *K. aerogens*; and 23 unspeciated *Klebsiella* isolates (1.8%), giving a total of 1,258 *Klebsiella* spp. (Tables 60-63).

The majority of *Klebsiella* spp. isolates were susceptible to aminoglycosides, and the prevalence of gentamicin resistance decreased to 2.7% in 2025 compared to 4.3% in 2023 and 4.5% in 2024. Gentamicin resistance was at the same level in *K. pneumoniae* (2.9%) and *K. oxytoca* (2.8%) but was not detected in *K. aerogenes* (0.0%). Aminoglycoside resistance in common *Enterobacterales* species is a cause for great concern as these antimicrobials are used in the empirical sepsis regimen in Norway.

The breakpoints for ciprofloxacin were reduced from R > 1 mg/L to R > 0.5 mg/L and from S ≤ 0.5 to S ≤ 0.25 in 2017. The prevalence of resistance to ciprofloxacin peaked at 11-12% in 2016-2017 but decreased to 8.9% in 2024 and 7.6% in 2025. Resistance to ciprofloxacin was more common in *K. pneumoniae* (9.7%) than in *K. oxytoca* (1.8%) and *K. aerogenes* (5.7%). As for *E. coli* the breakpoints for trimethoprim-sulfamethoxazole were reduced from R > 4 mg/L to R > 0.5 mg/L and S ≤ 2 mg/L to S ≤ 0.5 mg/L in 2026, but with minimal impact on resistance rates. Overall resistance decreased from 13.8% in 2024 to 13.3% in 2025. The prevalence of resistance was significantly lower in *K. oxytoca* (6.9% in 2024; 7.1% in 2025) and *K. aerogenes* (2.7%; 5.7% in 2025) than in *K. pneumoniae* (16.4% in 2024; 16.0% in 2025).

Comparison of resistance to beta-lactam antibiotics between *Klebsiella* species is complicated by the chromosomal K1 beta-lactamase in *K. oxytoca* and chromosomal AmpC in *K. aerogenes*. Most *Klebsiella* spp. isolates were susceptible (S+I) to cefotaxime (93.6%), ceftazidime (94.0%), cefepime (94.2%) and the beta-lactam/beta-lactamase inhibitor combination piperacillin-tazobactam

(89.8%), see Figure 85. The prevalence of resistance to 3rd generation cephalosporins has remained essentially unchanged 2018-2025. The rate of resistance to piperacillin-tazobactam has not changed over the last three years (10.7% in 2023, 11.2% in 2024 and 10.2% in 2025).

Detection of extended-spectrum beta-lactamases (ESBL) was based on zone diameters of cefotaxime and ceftazidime disks and confirmed by combination disks or MIC gradient tests. The prevalence of phenotypically confirmed ESBL isolates decreased slightly from 2024 (6.3% in *Klebsiella* spp.; 7.4% in *K. pneumoniae*) to 2025 (5.6% in *Klebsiella* spp.; 7.0% in *K. pneumoniae*), see Figure 84. The 70 ESBL isolates originated from 18 different laboratories and were identified as *K. pneumoniae* (n=63, 90%) and *K. oxytoca* (n=7, 10%). ESBL isolates were often resistant to cefotaxime (59/70), ceftazidime (58/70), cefepime (57/70) and aztreonam (56/70), and co-resistance was frequently seen for trimethoprim-sulfamethoxazole (57/70), ciprofloxacin (42/70) and gentamicin (25/70). Some isolates remained susceptible to piperacillin-tazobactam (44/70) and amoxicillin-clavulanic acid (24/70). A single *K. aerogenes* isolate was phenotypically resistant to meropenem, and five additional isolates had meropenem zone diameters below the screening breakpoint. None of these six isolates were verified as carbapenemase producers or contained genes encoding such enzymes. Nineteen ESBL isolates (1.5% of all *Klebiella* isolates) were concomitantly resistant to gentamicin and ciprofloxacin.

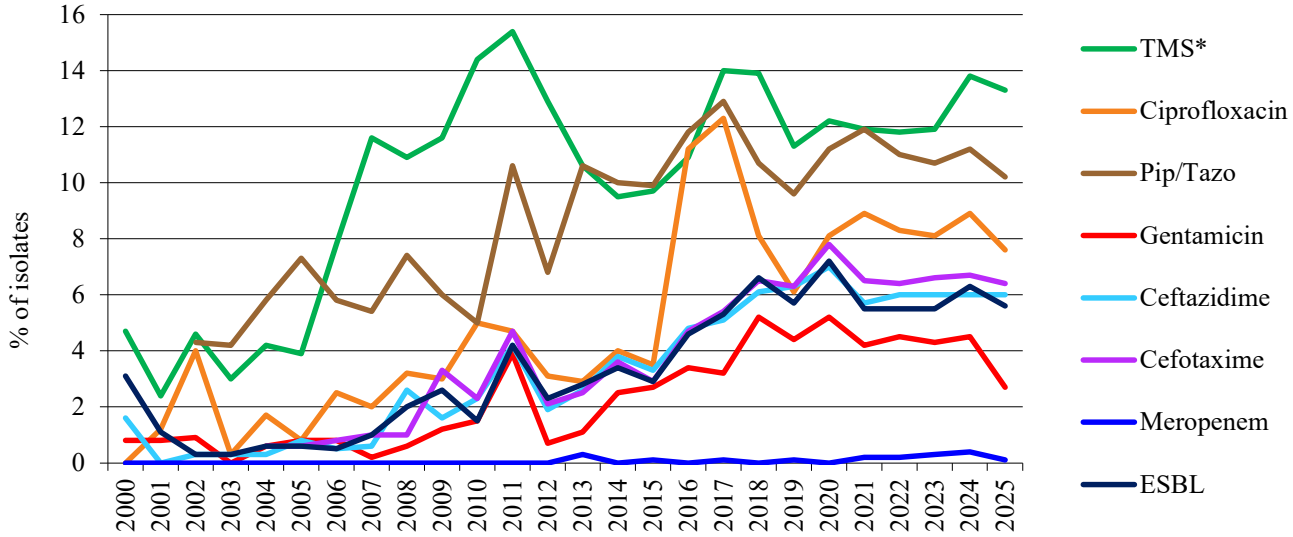

FIGURE 85. Prevalence of resistance to various antimicrobial agents in *Klebsiella* spp. blood culture isolates 2000-2025. Isolates are categorised according to the breakpoints at the time of analysis. *TMS=Trimethoprim-sulfamethoxazole.

Klebsiella spp. in urine

TABLE 64. *Klebsiella* spp. urinary tract isolates in 2025 (n=992), except for amoxicillin-clavulanic acid and cefalexin (n=944) where 48 *K. aerogenes* isolates are excluded due to lack of breakpoints. Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Mecillinam	≤ 8	> 8	94.0	-	6.0
Amoxicillin-clavulanic acid*	≤ 32	> 32	96.0	-	4.0
Piperacillin-tazobactam	≤ 8	> 8	92.5	-	7.5
Cefalexin	≤ 16	> 16	94.2	-	5.8
Cefotaxime**	≤ 1	> 2	95.1	0.5	4.4
Ceftazidime	≤ 1	> 4	94.5	1.3	4.2
Cefepime	≤ 1	> 4	94.2	1.5	4.3
Meropenem**	≤ 2	> 8	100.0	0.0	0.0
Aztreonam	≤ 1	> 4	93.9	1.6	4.5
Gentamicin***	≤ 2	> 2	98.1	-	1.9
Ciprofloxacin**	≤ 0.25	> 0.5	89.2	5.5	5.2
Trimethoprim	≤ 2	> 2	84.3	-	15.7
Trimethoprim-sulfamethoxazole****	≤ 0.5	> 0.5	87.2	-	12.8
ESBL	Negative	Positive	96.0	-	4.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. ESBL=Extended-spectrum beta-lactamase. *Breakpoints for oral administration in uncomplicated urinary tract infections. **Breakpoints for indications other than meningitis. ***Breakpoints for infections originating from the urinary tract. ****Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

TABLE 65. *Klebsiella pneumoniae* urinary tract isolates in 2025 (n=729). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Mecillinam	≤ 8	> 8	93.7	-	6.3
Amoxicillin-clavulanic acid*	≤ 32	> 32	96.6	-	3.4
Piperacillin-tazobactam	≤ 8	> 8	92.3	-	7.7
Cefalexin	≤ 16	> 16	94.4	-	5.6
Cefotaxime**	≤ 1	> 2	95.2	0.3	4.5
Ceftazidime	≤ 1	> 4	94.4	1.5	4.1
Cefepime	≤ 1	> 4	94.2	1.1	4.7
Meropenem**	≤ 2	> 8	100.0	0.0	0.0
Aztreonam	≤ 1	> 4	94.7	1.0	4.3
Gentamicin***	≤ 2	> 2	98.4	-	1.6
Ciprofloxacin**	≤ 0.25	> 0.5	87.1	7.0	5.9
Trimethoprim	≤ 2	> 2	82.3	-	17.7
Trimethoprim-sulfamethoxazole****	≤ 0.5	> 0.5	85.7	-	14.3
ESBL	Negative	Positive	95.6	-	4.4

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. ESBL=Extended-spectrum beta-lactamase. *Breakpoints for oral administration in uncomplicated urinary tract infections. **Breakpoints for indications other than meningitis. ***Breakpoints for infections originating from the urinary tract. ****Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

TABLE 66. *Klebsiella oxytoca* urinary tract isolates in 2025 (n=177). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Mecillinam	≤ 8	> 8	94.9	-	5.1
Amoxicillin-clavulanic acid*	≤ 32	> 32	94.4	-	5.6
Piperacillin-tazobactam	≤ 8	> 8	93.2	-	6.8
Cefalexin	≤ 16	> 16	93.2	-	6.8
Cefotaxime**	≤ 1	> 2	93.2	1.7	5.1
Ceftazidime	≤ 1	> 4	94.4	1.1	4.5
Cefepime	≤ 1	> 4	92.1	3.4	4.5
Meropenem**	≤ 2	> 8	100.0	0.0	0.0
Aztreonam	≤ 1	> 4	89.8	3.4	6.8
Gentamicin***	≤ 2	> 2	96.6	-	3.4
Ciprofloxacin**	≤ 0.25	> 0.5	94.9	1.1	4.0
Trimethoprim	≤ 2	> 2	88.7	-	11.3
Trimethoprim-sulfamethoxazole****	≤ 0.5	> 0.5	90.4	-	9.6
ESBL	Negative	Positive	96.0	-	4.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. ESBL=Extended-spectrum beta-lactamase. *Breakpoints for oral administration in uncomplicated urinary tract infections. **Breakpoints for indications other than meningitis. ***Breakpoints for infections originating from the urinary tract. ****Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

TABLE 67. *Klebsiella aerogenes* urinary tract isolates in 2025 (n=48). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Mecillinam	≤ 8	> 8	95.8	-	4.2
Piperacillin-tazobactam	≤ 8	> 8	95.8	-	4.2
Cefotaxime*	≤ 1	> 2	95.8	0.0	4.2
Ceftazidime	≤ 1	> 4	95.8	0.0	4.2
Cefepime	≤ 1	> 4	97.9	2.1	0.0
Meropenem*	≤ 2	> 8	100.0	0.0	0.0
Aztreonam	≤ 1	> 4	93.8	2.1	4.2
Gentamicin**	≤ 2	> 2	100.0	-	0.0
Ciprofloxacin*	≤ 0.25	> 0.5	95.8	2.1	2.1
Trimethoprim	≤ 4	> 4	97.9	-	2.1
Trimethoprim-sulfamethoxazole***	≤ 2	> 4	97.9	-	2.1
ESBL	Negative	Positive	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. ESBL=Extended-spectrum beta-lactamase. *Breakpoints for indications other than meningitis. **Breakpoints for infections originating from the urinary tract. ***Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

RESULTS AND COMMENTS

Klebsiella spp. urinary tract isolates have previously been included in the NORM surveillance programme in 2001, 2003, 2009 and 2012-2024. Due to methodological changes, it is not possible to directly compare the results from 2001 and 2003 with the ones from later surveys. There are no *Klebsiella* spp. disk diffusion breakpoints for fosfomycin or nitrofurantoin, and *K. aerogenes* is not included in the breakpoints for oral administration of cefalexin and amoxicillin-clavulanic acid. The urinary tract isolates in NORM 2025 were speciated as follows: 729 (73.6%) *K. pneumoniae* (including *K. pneumoniae, K. quasipneumoniae, K. variicola, K. quasivariicola* and *K. africana*); 177 (17.8%) *K. oxytoca* (including *K. oxytoca, K. michiganensis, K. grimontii, K. pasteurii, K. huaxiensis* and *K. spallanzanii*); 48 (4.8%) *K. aerogens*; and 38 isolates (3.8%) not identified to the species level, giving a total of 992 *Klebsiella* spp. isolates (Tables 64-67).

The prevalence of resistance to urinary tract antibiotics was slightly lower in *Klebsiella* spp. than in *E. coli* isolates (Table 59). A majority of isolates remained susceptible to gentamicin at 98.1% compared to 97.4% in 2023 and 96.3% in 2024. Among urinary tract *E. coli*, 95.1% were gentamicin susceptible in 2025. The rate of resistance to ciprofloxacin in *Klebsiella* spp. decreased from 5.9% in 2024 to 5.2% in 2025. The comparable rate for urinary tract *E. coli* was 7.8% in 2025. Susceptibility to trimethoprim (82.7% in 2024; 84.3% in 2025) and trimethoprim-sulfamethoxazole (85.6% in 2024; 87.2% in 2025) was slightly higher than in *E. coli* (78.1% and 80.1%, respectively). The adjustment of breakpoints for trimethoprim from R > 4 mg/L to R > 2 mg/L and S ≤ 4 mg/L to S ≤ 2 mg/L as well as for trimethoprim-sulfamethoxazole from R > 4 mg/L to R > 0.5 mg/L and S ≤ 2 mg/L to S ≤ 0.5 mg/L apparently had no effect on resistance rates for these agents.

All *Klebsiella* isolates are inherently resistant to ampicillin due to the chromosomal SHV beta-lactamase. As for *Klebsiella* spp. blood culture isolates, ESBL detection in urinary tract isolates was based on resistance to cefotaxime and/or ceftazidime and subsequent confirmatory ESBL combination disk or MIC gradient tests. Forty isolates (4.0%) were reported as ESBL producers, of which 32 were *K. pneumoniae*, seven were *K. oxytoca* and one was unspeciated. They were retrieved from 15 different laboratories and originated from hospital inpatients (n=19), outpatient clinics (n=3), general practices (n=16), nursing homes (n=1), and other locations (n=1). The 4.0% ESBL rate (4.4% in *K. pneumoniae*) was a decrease from 2024 (5.0% for *Klebsiella* spp., 5.7% for *K. pneumoniae*) but at the same level as in 2023 (3.5% for *Klebsiella* spp., 3.7% in *K. pneumoniae*). As expected, the 40 ESBL isolates were generally resistant to broad-spectrum beta-lactam antibiotics such as cefalexin (38/40), cefotaxime (37/40), cefepime (36/40), aztreonam (34/40) and ceftazidime (33/40). There was also widespread co-resistance to trimethoprim and trimethoprim-sulfamethoxazole (34/40), amoxicillin-clavulanic acid (23/40) and ciprofloxacin (15/40), whereas many isolates remained susceptible to mecillinam (34/40), gentamicin (28/40) and/or piperacillin-tazobactam (24/40). Eight ESBL isolates (0.8% of all *Klebsiella* isolates) were concomitantly resistant to gentamicin and ciprofloxacin. No isolates were clinically resistant to meropenem, and carbapenemase production was not detected by the screening procedure.

Carbapenemase-producing Gram-negative bacteria in Norway 2025

Infection and colonisation with carbapenemase-producing Gram-negative bacteria (CPO) are notifiable to the Norwegian Surveillance System for Communicable Diseases (MSIS) and confirmed at the Norwegian Centre for Detection of Antimicrobial Resistance (K-res). Here we summarise the 2025 data based on cases and isolates analysed at K-res.

Carbapenemase-producing *Enterobacterales*

In 2025, 284 patients with carbapenemase-producing *Enterobacterales* (CPE) were identified (Figure 86). This represents a small increase of 7% from 265 patients in 2024 and an increase in incidence rate from 4.7 to 5.1 per 100,000 person-years. The proportion of cases with suspected import continued to decline, to 64% in 2025, compared with 69% in 2024 and 77% in 2023. For 12%, there was no suspicion of import in 2025, unchanged from 2024. The proportion with missing information regarding suspected import increased to 24% in 2025, compared with 18% in 2024 and 12% in 2023.

In total, suspected import was associated with 44 different countries plus "abroad", which was reported for 4% of patients. Ukraine accounted for the largest proportion of patients with suspected import, 8% of all cases. This represents a further decrease from 2024 (15%) and 2023 (29%). After Ukraine, the highest proportions of suspected import were from Pakistan (6%), Turkey (5%), and Thailand (5%).

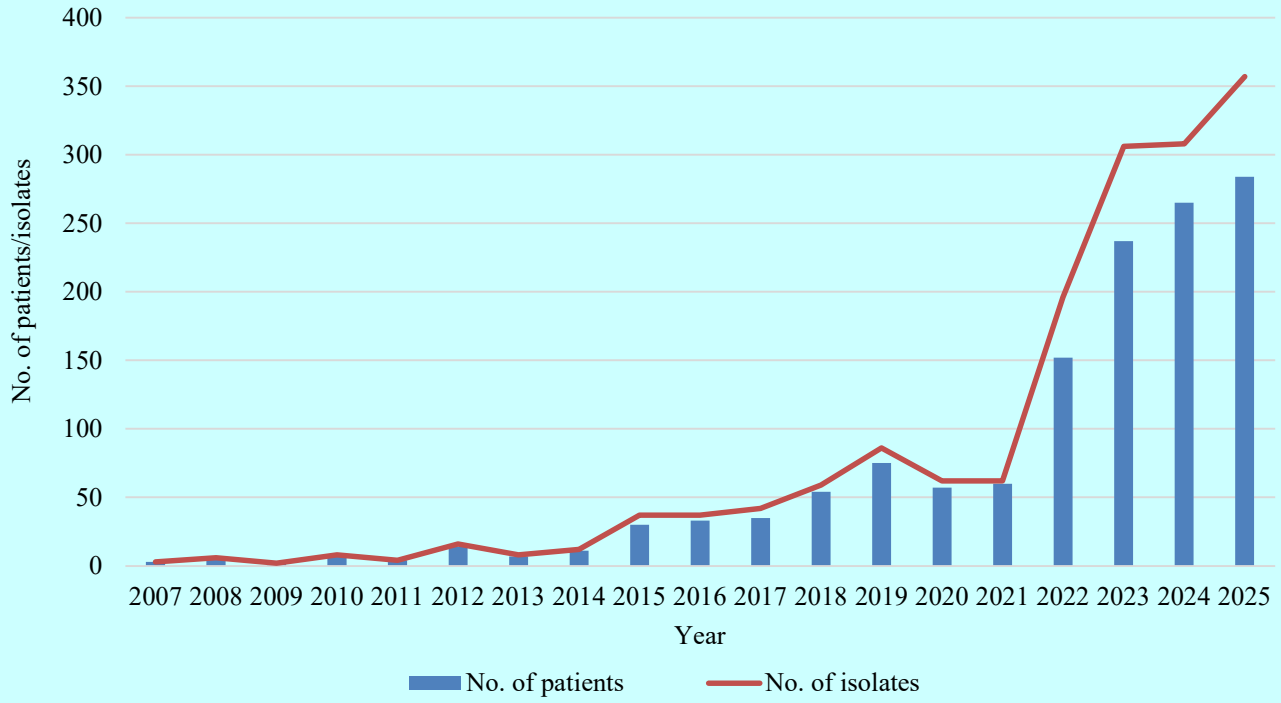

FIGURE 86. Number of patients with CPE and number of CPE isolates in Norway, 2007–2025.

A total of 357 CPE isolates were detected from 284 patients, compared with 308 isolates from 265 patients in 2024 (Figure 86). In 52 patients, 2-5 CPE isolates were detected, representing different species/carbapenemase genes or the same species but different sequence types (STs). In total, 69% of the isolates were reported as screening isolates, which is similar to 2024 (67%). Among clinical isolates, 8.3% were detected in blood cultures and 58% in urine, comparable to 2024 (12% and 41%, respectively).

The CPE population remains dominated by *Escherichia coli* and the *Klebsiella pneumoniae* species complex (Figure 87), but the relative proportions are changing. *E. coli* increased to 61% in 2025, compared with 54% in 2024 and 43% in 2023, while *K. pneumoniae* fell to 27%, compared with 36% in 2024 and 40% in 2023. Other *Enterobacterales* species (n=43) accounted for 12% in 2025, compared with 10% in 2024.

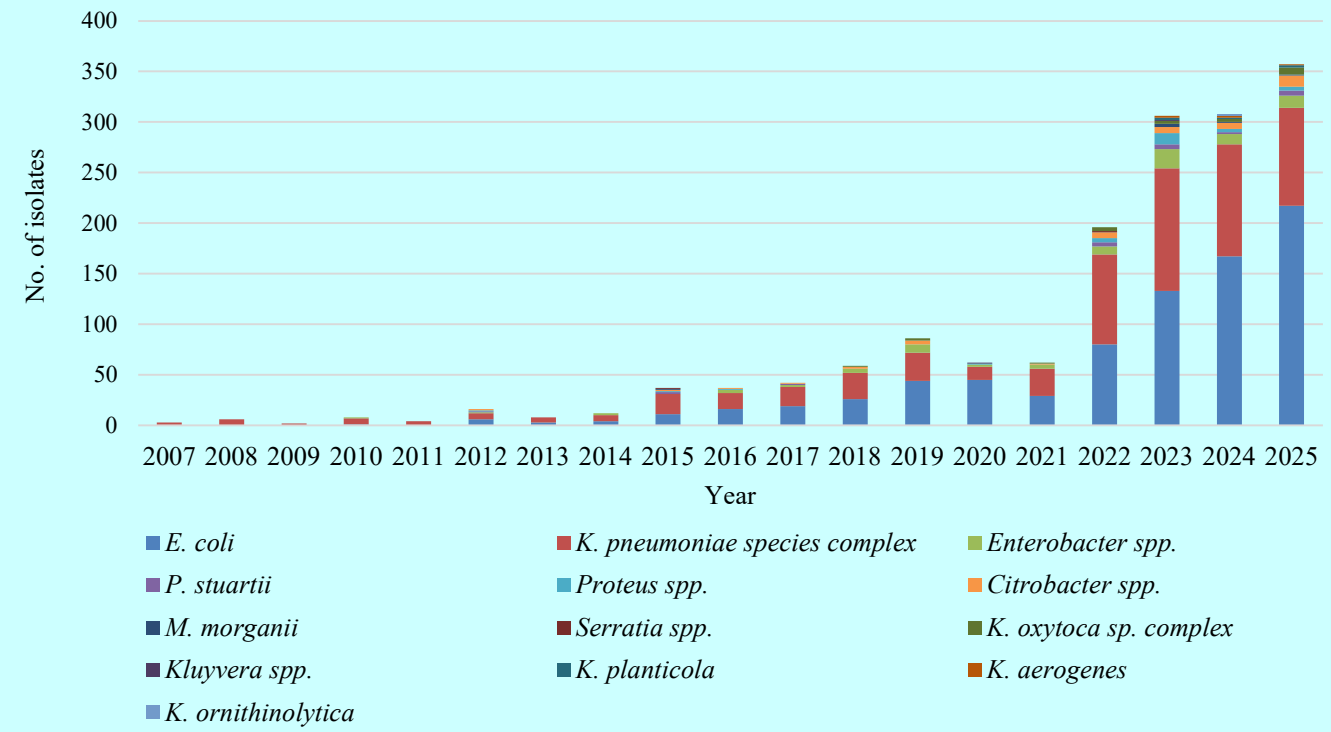

FIGURE 87. Number of CPE isolates distributed by bacterial species in Norway, 2007–2025.

NDM and OXA-48-like enzymes remain the dominant carbapenemases (Figure 88). The trend shows an increase in NDM from 38% in 2023 and 42% in 2024 to 50% in 2025. For OXA-48-like enzymes, the proportion in 2025 was 36%, compared with 41% in 2024 and 37% in 2023. In total, 8% of isolates had both NDM and OXA-48-like enzymes, like 2024 (9%). One *E. coli* and one *Klebsiella quasipneumoniae* subsp. *similipneumoniae* isolate, both from the same patient, had two NDM variants (NDM-1 and NDM-5), and one *K. pneumoniae* isolate had three carbapenemases (NDM-5, OXA-48, and KPC-2). IMI/NMC was not detected in 2025.

NDM-5 was the predominant carbapenemase, alone in 117 isolates and in combination with another carbapenemase in 18 isolates, followed by OXA-244 (53 isolates). The number of isolates with NDM-5 increased markedly from 2024 (80 isolates) to 135 isolates in 2025. Both variants represent distinct challenges. NDM-5 is associated with higher activity against carbapenems than other NDM variants (1), whereas OXA-244 is a variant with relatively low activity against carbapenems and is therefore diagnostically challenging (2).

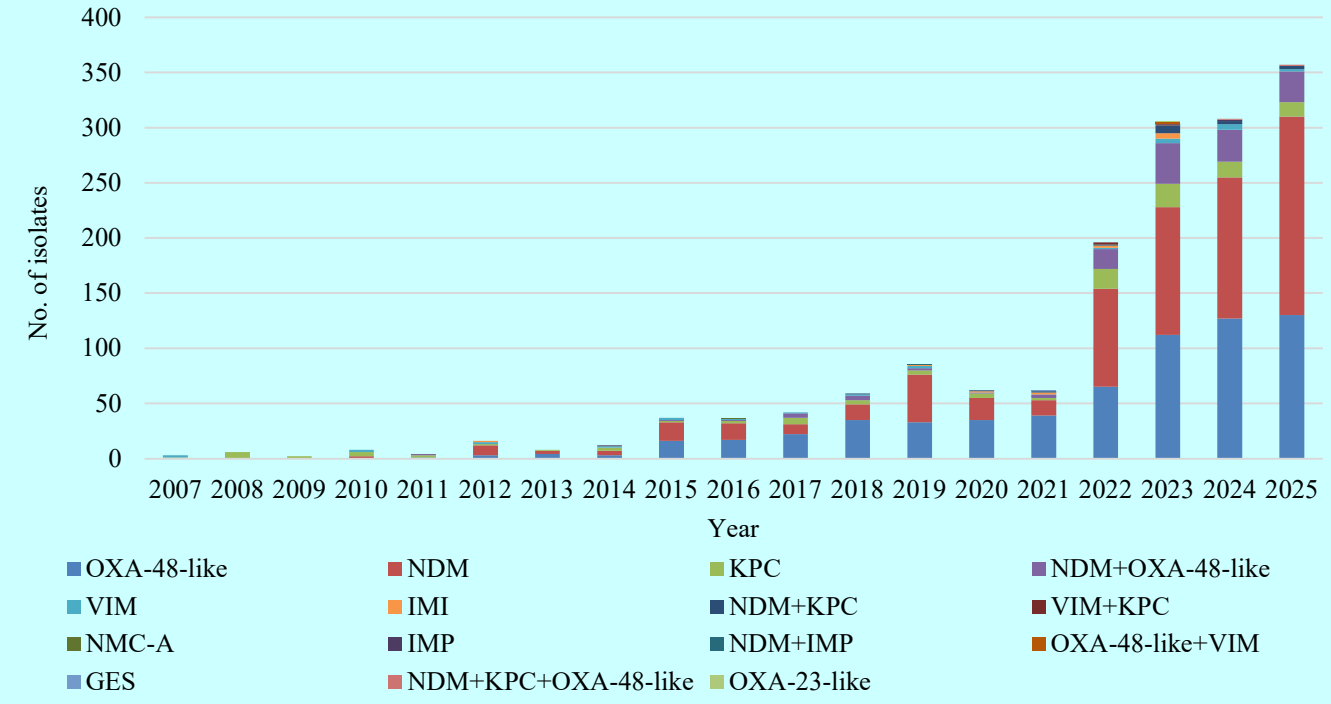

FIGURE 88. Carbapenemase variants among CPE isolates in Norway, 2007-2025.

Among *E. coli*, at least 67 different sequence types (STs) were detected, compared with 49 in 2024 and 40 in 2023 (Figure 89). Three isolates belonged to undescribed STs. Eight STs were detected in ≥10 isolates and accounted for 59% of the population. Seven of these - ST38, ST167, ST410, ST648, ST131, ST405, and ST69 - are known global high-risk clones with increasing prevalence in Europe (3-7). ST10 is generally considered a commensal *E. coli* clone but can acquire resistance traits. Within the clones, a diversity of carbapenemases is observed, but also dominant associations such as ST38 with OXA-244, and ST167, ST648, and ST405 with NDM-5. The increase in ST167 with 23 isolates in 2025 versus 12 in 2024 is concerning, as this clone is associated with reduced susceptibility/resistance to cefiderocol and aztreonam-avibactam (11).

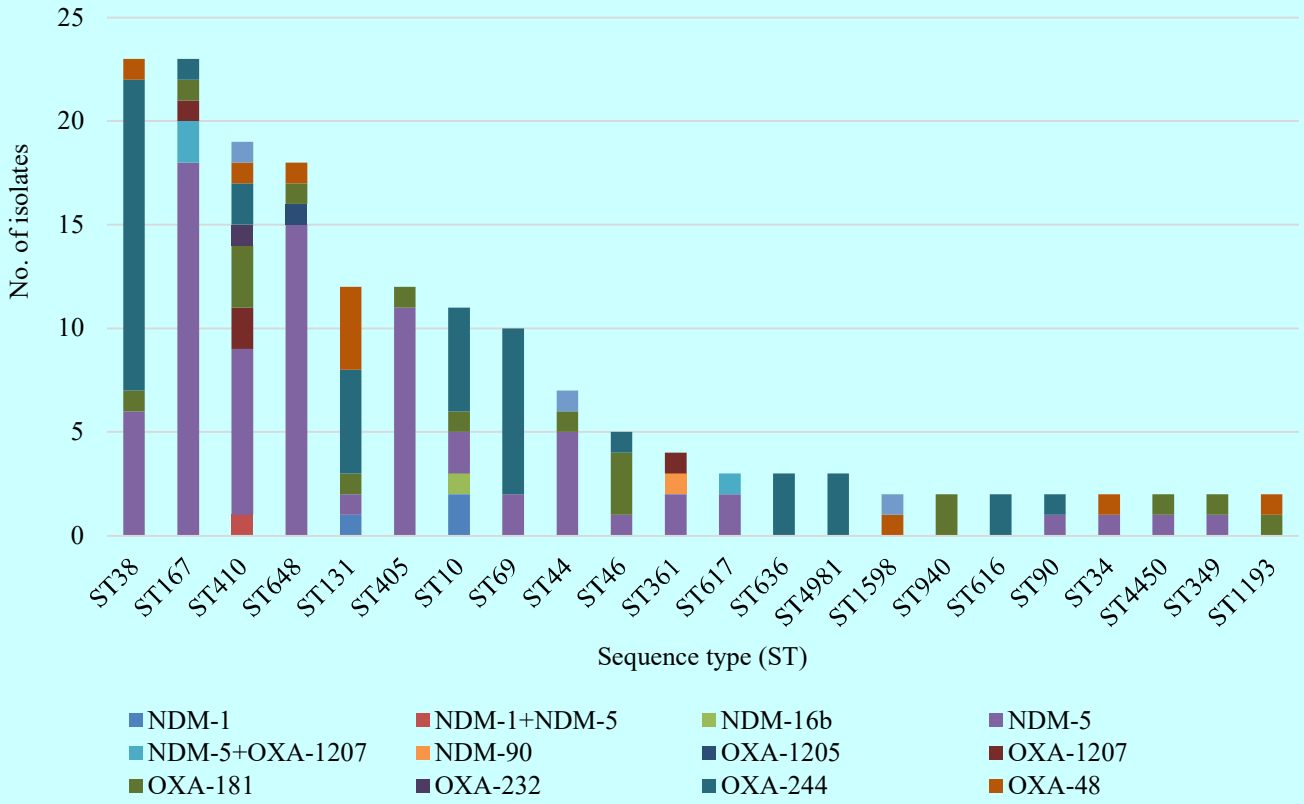

FIGURE 89. Distribution of carbapenemase genes among carbapenemase-producing *E. coli* ST variants with ≥2 isolates in 2025.

Phylogenetic analysis based on core genome multilocus sequence typing (cgMLST) showed 13 clusters consisting of 2-5 related isolates in 2025 (Figure 90, Table 68). Four clusters (clusters 2, 5, 8, and 11) consisted exclusively of isolates associated with import. For these clusters, transmission is assumed to have occurred abroad.

Epidemiological investigations suspected domestic transmission in Norway for two clusters (clusters 7 and 9). Cluster 9 consisted of two *E. coli* ST69-NDM-5 isolates. Cluster 7 comprised five *E. coli* ST405-NDM-5 isolates from three different laboratories, four of which were associated with import. However, detailed genetic and epidemiological analyses supported domestic transmission between two patients, even though both were associated with import.

Cluster 4 consisted of three *E. coli* ST38-NDM-5 urinary tract isolates with zero allelic differences, of which two were from primary health care. The geographical spread of the patients and epidemiological investigations ruled out a healthcare-associated outbreak. The close genetic similarity indicates a common source in the community, but no likely origin was identified.

For the other clusters, epidemiological investigations showed no definite link between the patients, or information on possible links was missing. Transmission cannot be excluded in these cases.

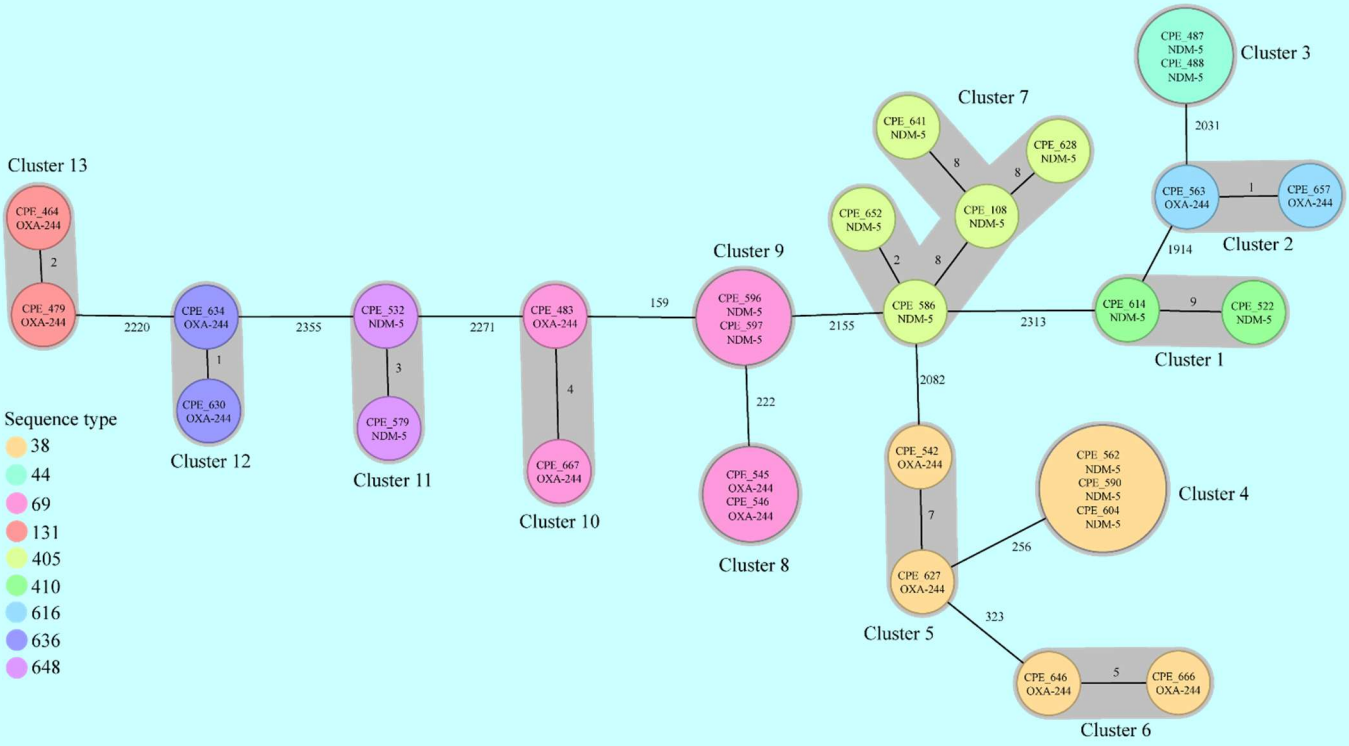

FIGURE 90. Minimum spanning network of related carbapenemase-producing *E. coli* in 2025, based on 2,513 core genome alleles using SeqSphere software and *E. coli* K12 as reference strain. Isolates are coloured by ST. The carbapenemase variant is indicated in the circle. Circle size indicates number of isolates. Number of allelic differences is indicated between isolates. Clusters of isolates with ≤10 allelic differences are highlighted in grey.

TABLE 68. Overview of carbapenemase-producing *E. coli* clusters in 2025.

Cluster no.	ST	Carbapenemase variant	Number of patients	Import
1	ST410	NDM-5	2	Import/no information
2	ST616	OXA-244	2	Import
3	ST44	NDM-5	2	Import/no information
4	ST38	NDM-5	3	No/no information
5	ST38	OXA-244	2	Import
6	ST38	OXA-244	2	No information
7	ST405	NDM-5	5	Import/no information
8	ST69	OXA-244	2	Import
9	ST69	NDM-5	2	No
10	ST69	OXA-244	2	Import/no information
11	ST648	NDM-5	2	Import
12	ST636	OXA-244	2	No
13	ST131	OXA-244	2	No information

Among the 97 *K. pneumoniae* species complex isolates, 95 belonged to *K. pneumoniae*. Two *K. quasipneumoniae* subsp. *similipneumoniae* isolates were detected; one ST334 with both NDM-1 and NDM-5 and one ST1308 with NDM-5. The *K. pneumoniae* isolates covered at least 34 different STs (Figure 91), compared to 27 in 2024. Three isolates were undescribed STs. Like in 2024, ST147 was dominant, accounting for 33%, followed by ST307 (11%). ST147 and ST307, as well as ST101 (6%), ST11 (5%), ST395 (4%), and ST258 (3%), are known global high-risk clones (8-10). ST147 and ST307 were associated with NDM variants, especially NDM-1 and NDM-5, also combined with OXA-48 variants.

ST23 with capsule type 1 (KL1) is a known hypervirulent clone (9). One ST23 isolate with OXA-48 associated with import from Ukraine was detected in 2025, compared with eight ST23 isolates in 2024. The ST23 isolate from 2025 had capsule type KL57. ST23-KL57 represents a different genetic lineage from ST23-KL1, and it is unclear whether ST23-KL57 is associated with a “hypervirulent” clinical phenotype (12-13).

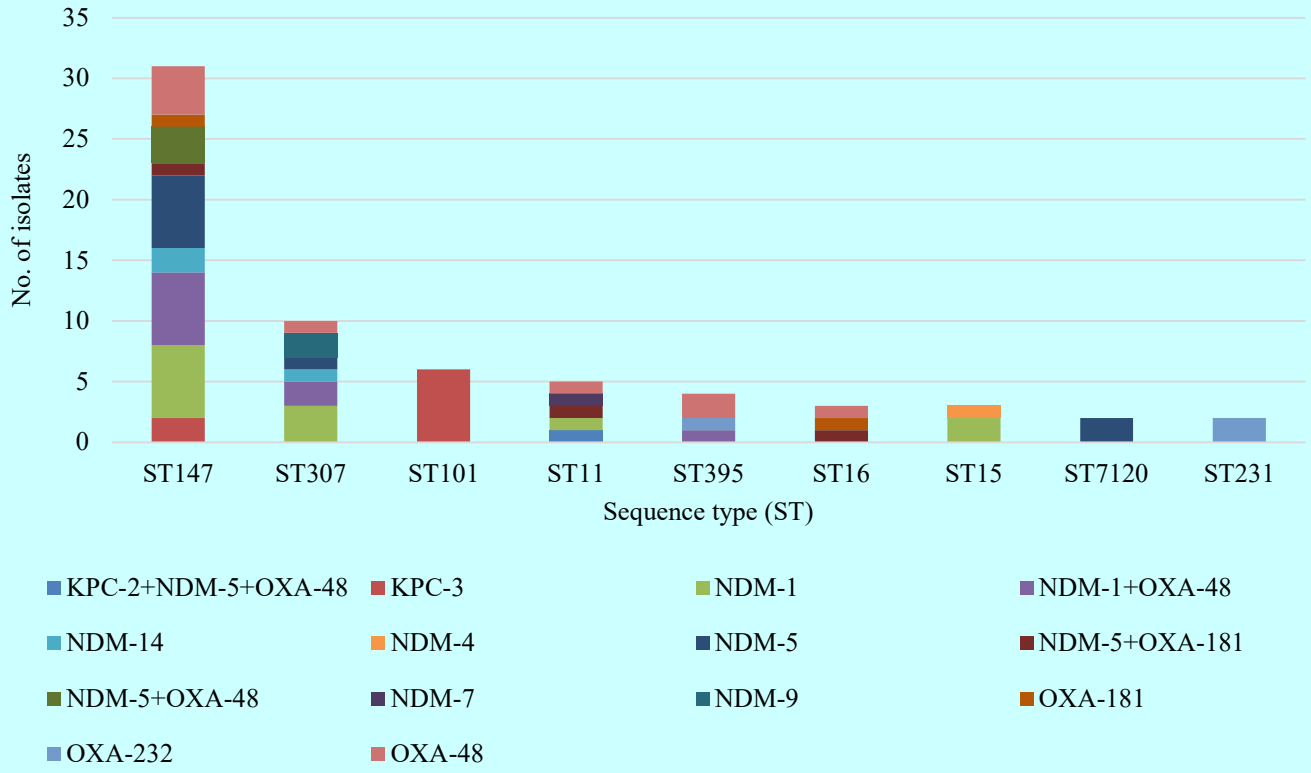

FIGURE 91. Distribution of carbapenemase genes among carbapenemase-producing *K. pneumoniae* ST variants with ≥2 isolates in 2025.

Phylogenetic analysis of carbapenemase-producing *K. pneumoniae* isolates demonstrated eight clusters with 2-6 isolates (Figure 92, Table 69). Four clusters (clusters 1, 2, 6, and 8) consisted exclusively of isolates associated with import (Thailand, Georgia, Ukraine/Poland). The other four clusters (clusters 3, 4, 5, and 7) comprised isolates with both suspected import and isolates where import was not suspected or where import data were not provided. Epidemiological investigations revealed possible transmission in Norway in one of the clusters (cluster 3).

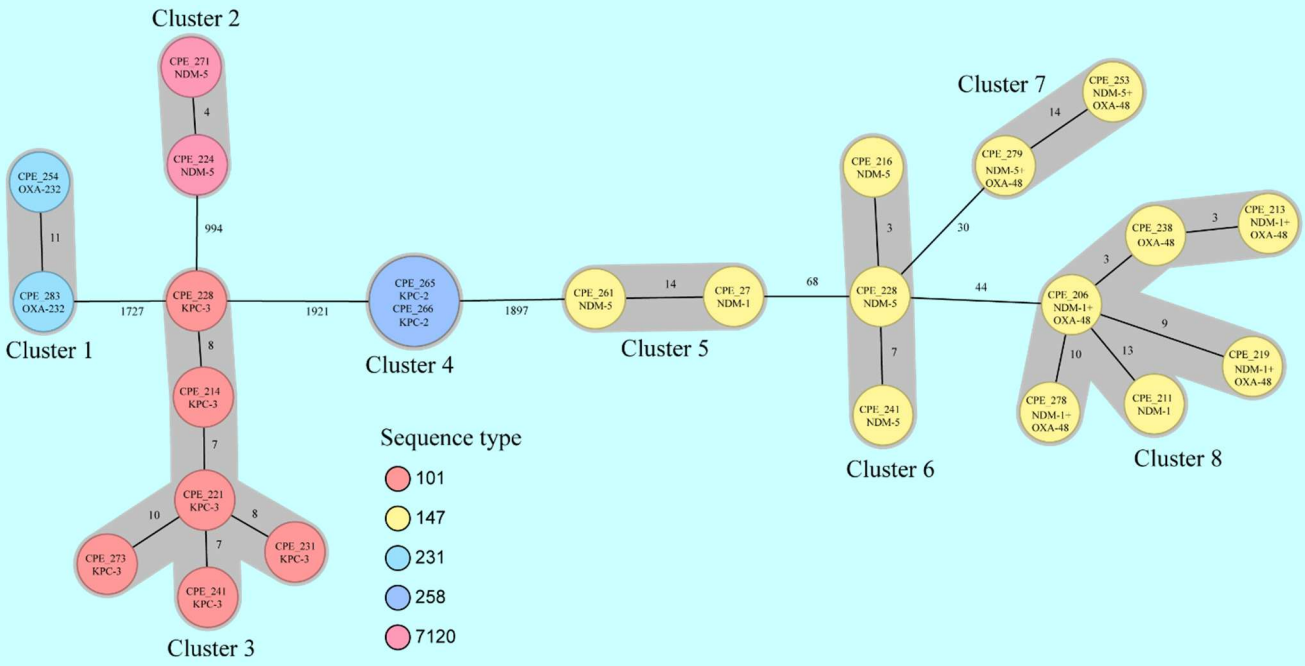

FIGURE 92. Minimum spanning network of related carbapenemase-producing *K. pneumoniae* in 2025, based on 2,358 core genome alleles using SeqSphere software and *K. pneumoniae* NTUH-K2044 as reference strain. Isolates are coloured by ST. The carbapenemase variant is indicated in the circle. Circle size indicates number of isolates. Number of allelic differences is indicated between isolates. Clusters of isolates with ≤15 allelic differences are highlighted in grey.

TABLE 69. Overview of detected carbapenemase-producing *K. pneumoniae* clusters in 2025.

Cluster no.	ST	Carbapenemase variant	Number of patients	Import
1	ST231	OXA-232	2	Import
2	ST7120	NDM-5	2	Import
3	ST101	KPC-3	6	Import/no
4	ST258	KPC-2	2	Import/no
5	ST147	NDM-1/NDM-5	2	Import/no information
6	ST147	NDM-5	3	Import
7	ST147	NDM-5+OXA-48	2	Import/no information
8	ST147	NDM-1+OXA-48/NDM-1/OXA-48	6	Import

Carbapenemase production was detected in 43 isolates from other *Enterobacterales* species (Table 70), compared with 30 in 2024. In total, 51% of isolates were reported as screening isolates, whereas 21% were detected in urine, and two isolates in blood cultures. The isolates were detected in 40 patients, of whom 58% of cases were associated with import, compared with 82% in 2024. In 2025, 20% were not associated with import, and for 23%, information on import was missing. Import was associated with nine different countries plus "abroad" and import from Ukraine accounted for 28% of all cases. In 16 patients (40%), carbapenemase-producing *E. coli* and/or *K. pneumoniae* species complex was also detected. In contrast to previous years, domestic transmission in Norway was detected. Three *E. hormaechei* ST45-NDM-1 isolates were identified in the same laboratory approximately one month apart. The isolates were closely related, with only 1-2 core genome allelic differences. One case was associated with import from Ukraine. The outbreak has continued with new cases in 2026. One *E. hormaechei* ST1344 with NDM-5 associated with import is linked to a larger outbreak (>50 patients) in several European countries with an unknown source (14).

TABLE 70. ST-carbapenemase variant combinations detected in 2025 among *Enterobacterales* species other than *E. coli* and *K. pneumoniae* species complex.

Species	ST-carbapenemase variant combination
C. freundii (n=7)	ST22-NDM-1 (n=1), ST22-NDM-7 (n=1), ST22-OXA-181 (n=1), ST112-NDM-1+KPC-2 (n=1), ST169-NDM-1 (n=1), ST216-NDM-1 (n=1), ST-novel-NDM-1 (n=1)
C. portucalensis (n=1)	ST755-NDM-5 (n=1)
C. braakii (n=1)	ST646-KPC-2 (n=1)
C. cronae (n=1)	ST259-NDM-1 (n=1)
C. youngae (n=1)	ST218-NDM-5 (n=1)
E. hormaechei (n=11)	ST45-NDM-1 (n=3), ST114-NDM-1 (n=1), ST114-NDM-5 (n=1), ST114-OXA-48 (n=1), ST148-NDM-1 (n=1), ST175-NDM-1 (n=1), ST231-NDM-1 (n=1), ST742-OXA-181 (n=1), ST1344-NDM-1 (n=1)
E. cloacae (n=1)	ST1718-NDM-1 (n=1)
K. aerogenes (n=1)	ST93-OXA-181 (n=1)
K. michiganensis (n=5)	ST44-VIM-1 (n=1), ST180-NDM-1 (n=1), ST409-KPC-3 (n=1), ST-novel-OXA-181 (n=1), ST-novel-NDM-1 (n=1)
K. oxytoca (n=2)	ST145-OXA-48 (n=1), ST286-OXA-232 (n=1)
M. morganii (n=1)	ST154-NDM-1 (n=1)
P. mirabilis (n=3)	ST135-NDM-5 (n=1), ST269-NDM-1 (n=1), ST461-NDM-1 (n=1)
P. terrae (n=1)	NDM-1 (n=1)
P. stuartii (n=5)	ST3-NDM-5 (n=3), ST21-NDM-1 (n=1), ST22-NDM-1 (n=1)
K. planticola (n=2)	NDM-1 (n=1), NDM-7 (n=1)

Treatment options for infections with CPE are limited, and susceptibility testing confirms this (Figure 93). New beta-lactam/beta-lactamase inhibitor combinations and cefiderocol have been introduced as therapeutic alternatives, but their activity depends on the inhibitor profiles and the carbapenemases present (15-18). Except for aztreonam-avibactam (5% resistant isolates), the proportion of resistant isolates is high: ceftazidime-avibactam (59%), imipenem-relebactam (42%), meropenem-vaborbactam (24%), and cefiderocol (62%, including area of technical uncertainty, ATU). The high resistance rates reflect that none of the inhibitors have activity against class B carbapenemases (metallo-beta-lactamases) and that Norway has a high proportion of NDM. Aztreonam-avibactam susceptibility testing was performed on 36% of isolates, and the relatively low level of resistance is due to avibactam protecting aztreonam from degradation by beta-lactamases other than NDM, while NDM cannot hydrolyse aztreonam (19). Susceptibility testing of cefiderocol is challenging, and a large proportion of isolates have a zone diameter in the area of technical uncertainty (ATU) (29%), but this has limited impact because the ATU (21-23 mm) is mainly within the resistant range (R <23 mm). The proportion of resistant isolates by carbapenemase variant is presented in Table 71.

As expected, a high proportion of isolates were also resistant to non-beta-lactam antibiotics such as aminoglycosides (30-55%), fluoroquinolones (80%), and trimethoprim-sulfamethoxazole (76%) (Figure 93). Colistin resistance was detected in 5% (excluding expected resistance).

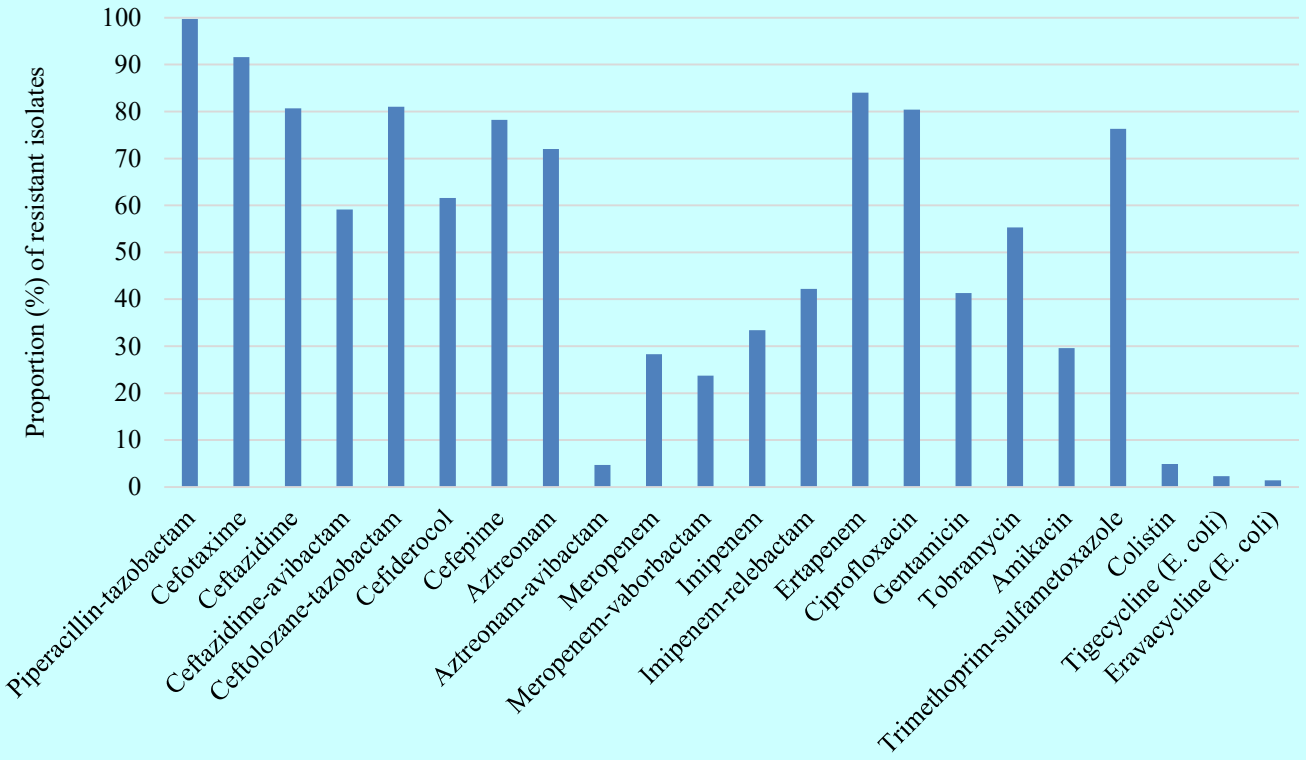

FIGURE 93. Proportion (%) of resistant isolates among CPE isolates in 2025. Categorisation according to the NordicAST breakpoint table v.16. Susceptibility testing was performed using broth dilution, except for cefiderocol (disk diffusion). Aztreonam-avibactam MIC determination was performed on 128 of 357 isolates. Zone diameter/MIC values in the area of technical uncertainty (ATU) for cefiderocol, piperacillin-tazobactam, and ciprofloxacin were interpreted conservatively as resistant. Imipenem and imipenem-relebactam apply to *Enterobacterales* excluding *Morganellaceae*. Colistin applies to *Enterobacterales* excluding *M. morganii*, *P. mirabilis*, and *P. stuartii* (expected R according to EUCAST Expected Resistant Phenotypes v. 1.2). Tigecycline and eravacycline apply only to *E. coli*.

TABLE 71. Proportion (%) of resistant CPE isolates from 2025 for selected beta-lactams and beta-lactam/beta-lactamase inhibitor combinations according to carbapenemase class.

	Proportion of resistant isolates (%)		
Antibiotic	Class A	Class B[1]	Class D
Ceftazidime	100	100	47
Ceftazidime-avibactam	0	99	0
Aztreonam	100	76	62
Aztreonam-avibactam[2]	0	4,3	5,6
Meropenem	77	36	11
Meropenem-vaborbactam	0	34	10
Imipenem[3]	92	46	7,7
Imipenem-relebactam[3]	0	68	6,2
Cefiderocol	39	86	25
Ertapenem	100	96	62
Cefepime	100	99	42
Cefotaxime	100	100	77

[1]Includes isolates with class B carbapenemases in combination with class A and/or class D carbapenemases. [2]Aztreonam-avibactam MIC was determined in 128 of 357 isolates. [3]Imipenem and imipenem-relebactam apply to *Enterobacterales* excluding *Morganellaceae*. [4]Zone diameters in the area of technical uncertainty (ATU) for cefiderocol were interpreted conservatively as resistant.

Carbapenemase-producing *Pseudomonas* spp.

A total of 24 patients with carbapenemase-producing *Pseudomonas* spp. were detected in 2025. This was unchanged from 2024, following a slight decrease from 2023 (Figure 94). The findings were largely linked to importation (83%) from nine countries, with fewer cases imported from Ukraine (40%) than in previous years. In 2024, the proportion of imported cases was similar, with 70% originating from Ukraine. For one patient, importation was not suspected, and for three patients, the importation status remained unclear.

In three patients, two distinct carbapenemase-producing *P. aeruginosa* isolates were identified, bringing the total to 27. Fifteen isolates were reported as screening isolates (faeces, wounds, urine, and other materials), while twelve were obtained from clinical samples (wounds, urine, and other materials). No isolates were recovered from blood.

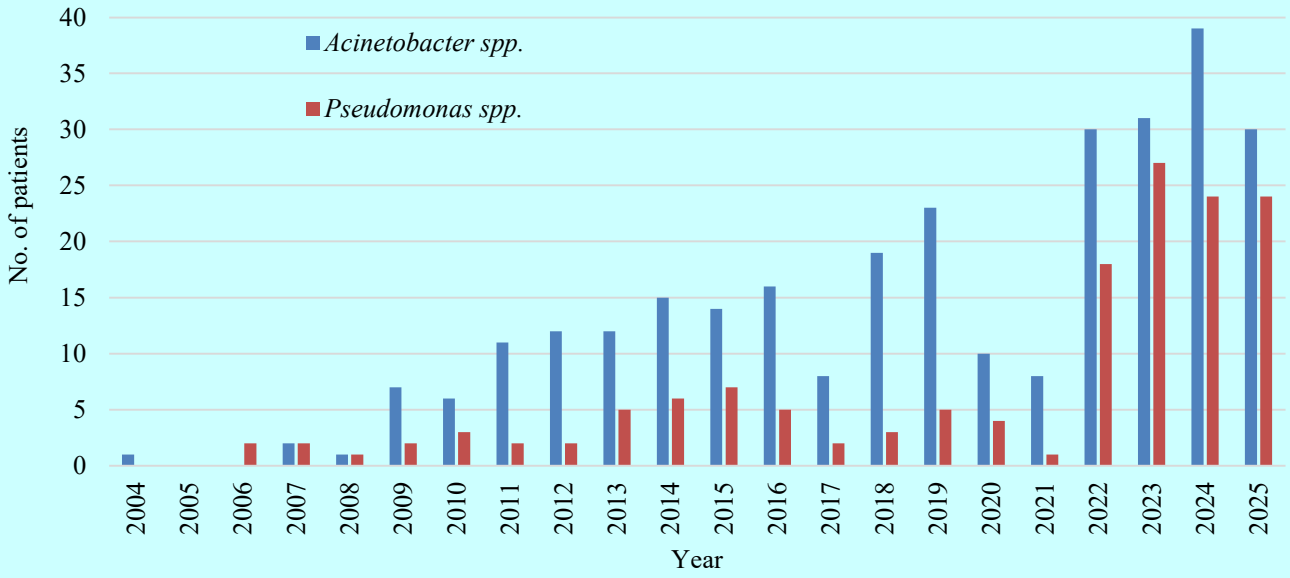

FIGURE 94. Number of persons with detected carbapenemase-producing *Pseudomonas* spp. and *Acinetobacter* spp. in Norway, 2004-2025.

Whole-genome sequencing confirmed that each isolate harboured a single carbapenemase-encoding gene and that all isolates belonged to *P. aeruginosa*. Considerable genetic diversity was observed among the isolates, encompassing 16 STs, including one novel ST, and six carbapenemases (Figure 95). NDM-1 (n=12) was the most prevalent variant, identified across seven sequence types. As previously, the clones associated with Ukraine, ST773-NDM-1 (n=5) and ST1047-IMP-1 (n=4), were most common, with ST773 also including isolates from other countries. In total, seven STs were found among the Ukraine-associated isolates, including the well-known global high-risk clones ST357 and ST654 (20). Additionally, ST2592, a single-allele variant of ST357, was detected. The global high-risk clones, including ST111 (n=1), ST235 (n=1), ST308 (n=1), ST357 (n=1), ST395 (n=1), ST654 (n=3), ST773 (n=5), and ST2592 (n=2), collectively accounted for 60% of the isolates detected in Norway in 2025.

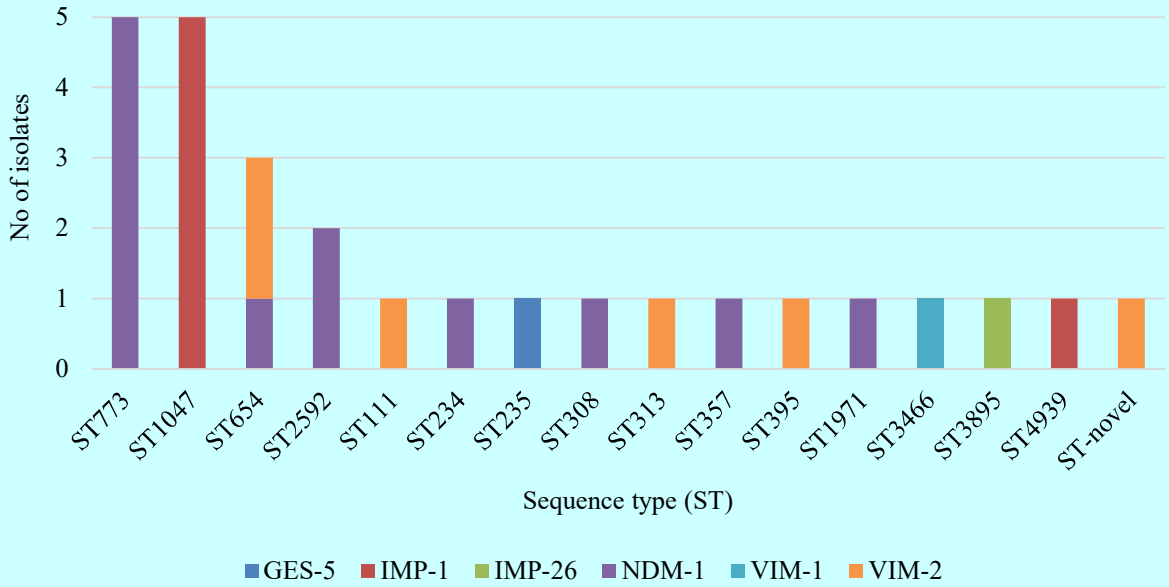

FIGURE 95. Distribution of STs and carbapenemase variants among carbapenemase-producing *Pseudomonas* spp. (n=27) isolated in Norway in 2025.

The genetic relatedness analysis of *P. aeruginosa* (Figure 96) confirmed genetic diversity and identified two clusters: ST2592 (one allelic difference) and ST773 (11 allelic differences). Both clusters were associated with importation from Ukraine. The isolates were collected five and two months apart, respectively, from patients admitted to the same hospital (cluster #1) or to different hospitals (cluster #2). According to epidemiological data, the findings are not considered indicative of domestic transmission within Norway.

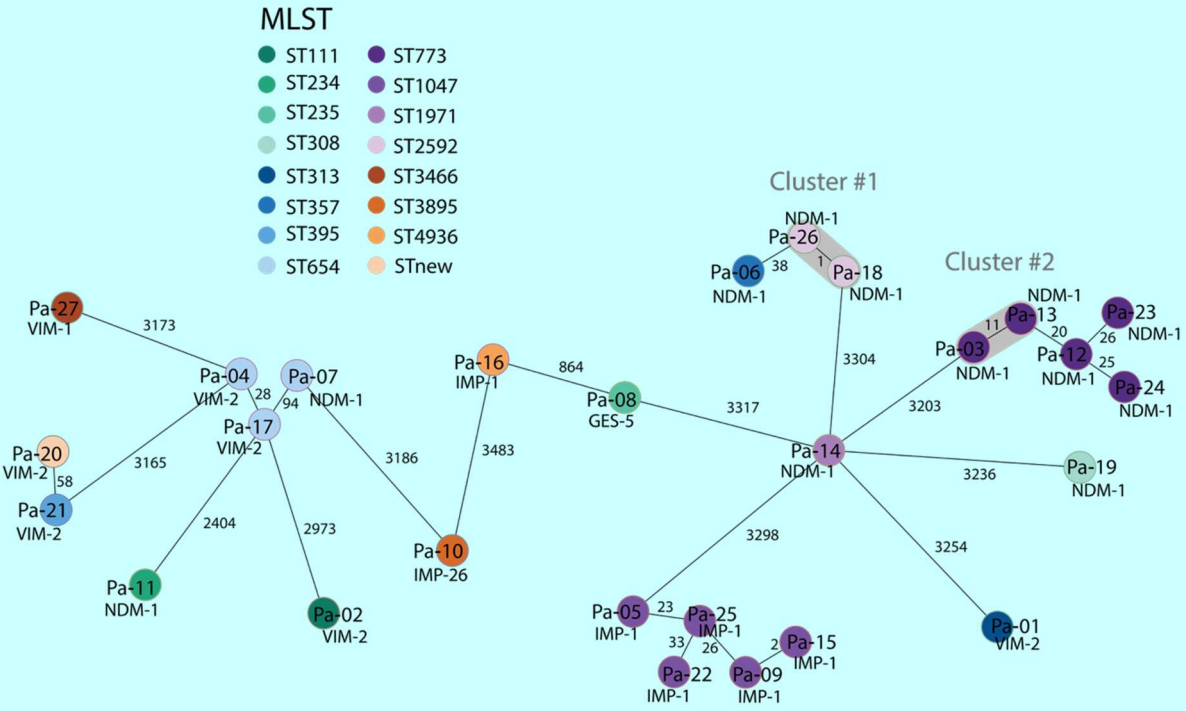

FIGURE 96. Minimum spanning tree of carbapenemase-producing *P. aeruginosa* (n=27) isolated in Norway in 2025. The tree is based on 3,867 core genome alleles (cgMLST) and was generated using SeqSphere+ software with *P. aeruginosa* PAO1 as the reference genome. Each circle represents one isolate, colour-coded by sequence type (MLST), with the carbapenemase variant shown. The number of allelic differences between isolates is indicated. Clusters of closely related isolates (≤12 allele differences) are highlighted in grey.

In addition to being carbapenem resistant, a large proportion of isolates were resistant to most other alternative agents (Table 72). Resistance rates were similar to those observed during 2006-2022 (21), except for cefiderocol, which showed a slightly higher proportion of resistant isolates. All isolates (n=6) categorised as cefiderocol resistant (zone diameter <22 mm) had zone diameters within the ATU range (20-21 mm). No resistance to colistin was observed. Based on standard criteria (22), 14 isolates were classified as XDR (extensively drug-resistant), and the other 13 as MDR (multi-drug resistant).

TABLE 72. Resistance proportions among carbapenemase-producing *P. aeruginosa* (n=27) in 2025[1].

Antibiotic	Resistant isolates (%)
Piperacillin-tazobactam	100
Cefepime	93
Ceftazidime	93
Ceftazidime-avibactam	93
Ceftolozane-tazobactam	100
Aztreonam	41
Meropenem	100
Imipenem	100
Meropenem-vaborbactam	100
Imipenem-relebactam	100
Ciprofloxacin	100
Amikacin	78
Tobramycin	100
Colistin	0
Cefiderocol	22

[1] Categorisation according to the NordicAST breakpoint table v.16. Susceptibility testing was performed using broth dilution, exception for cefiderocol (disk diffusion).

Carbapenemase-producing *Acinetobacter* spp.

In 2025, 30 patients with carbapenemase-producing *Acinetobacter* spp. were detected, compared with 39 patients in 2024 (Figure 94). Twenty-six (87%) of the cases were associated with import, as in 2024 (85%), and from 11 different countries dominated by Thailand (37%). The proportion linked to Ukraine decreased further in 2025 (20%), compared with 2024 (36%) and 2023 (55%). Domestic transmission in Norway was not suspected, but for four patients (13%), information regarding import was missing. In total, 31 carbapenemase-producing *Acinetobacter* spp. isolates were detected in 2025, compared with 43 isolates in 2024. One patient in 2025 had two *Acinetobacter baumannii* isolates with different STs (ST19 and ST78) but the same carbapenemase variant (OXA-72). Ten (32%) of the isolates were reported as clinical isolates, one of which was detected in a blood culture. Twenty-one (68%) of the isolates were reported as screening isolates, of which 14 were from rectal screening. Whole-genome sequencing revealed that 28 (90%) were *A. baumannii* isolates (Table 73) and single isolates of *Acinetobacter pittii*, *Acinetobacter ursingii*, and *Acinetobacter modestus*. As previously, *A. baumannii* ST2 (n=17) was the dominant clone. ST2 and other detected STs (ST164, ST19, ST78, ST1) are known global high-risk clones (23-25). OXA-23 was the dominant carbapenemase variant, detected in 22 (71%) of isolates, including in combination with NDM-1 or NDM-5 in six isolates.

TABLE 73. Species/ST-carbapenemase variant combinations in *Acinetobacter* spp. (n=31) in 2025.

Species	ST	Carbapenemase variant
A. baumannii (n=28)	ST2 (n=17)	OXA-23 (n=11), NDM-5+OXA-23 (n=3), NDM-1+OXA-23 (n=2), NDM-1+OXA-72 (n=1)
	ST164 (n=3)	OXA-23 (n=3)
	ST19 (n=2)	OXA-72 (n=2)
	ST78 (n=1)	OXA-72 (n=1)
	ST1 (n=1)	OXA-23 (n=1)
	ST32 (n=1)	NDM-1 (n=1)
	ST570 (n=1)	NDM-1+OXA-23 (n=1)
	ST821 (n=1)	NDM-1+OXA-420 (n=1)
	ST-ny (n=1)	OXA-23 (n=1)
A. pittii (n=1)	ST93 (n=1)	IMP-14 (n=1)
A. ursingii (n=1)[1]		NDM-1 (n=1)
A. modestus (n=1)[1]		OXA-58 (n=1)

[1]MLST scheme not established.

Genetic relatedness analysis of the *A. baumannii* isolates showed two clusters (≤9 core genome allelic differences). Cluster 1 consisted of three *A. baumannii* isolates with OXA-23. Two isolates belonged to ST2, while one was a single-locus variant of ST2. The isolates were detected at three different laboratories and were all linked to import from Thailand. Cluster 2 consisted of two *A. baumannii* ST2 isolates with OXA-23 detected at two different laboratories, both linked to import from Ukraine. For both clusters, the isolates are considered to have been acquired outside Norway. Domestic transmission in Norway was not suspected in 2025. All isolates were resistant to meropenem and imipenem, and resistance to other antibiotics was widespread (Table 74). Due to a lack of clinical data, there are no clinical breakpoints for cefiderocol, but 15 (48%) of isolates had a zone diameter ≥21 mm, indicating that the isolates usually lack resistance mechanisms and that cefiderocol may be a treatment option. Sulbactam-durlobactam is a new beta-lactam/beta-lactamase inhibitor combination (not yet approved by the EMA) developed specifically for OXA-carbapenemase-producing *A. baumannii* (26). Twenty-nine isolates were tested with sulbactam-durlobactam MIC gradient strips. Based on CLSI breakpoints (S ≤4 mg/L and R ≥16 mg/L), 12 (41%) of the isolates were susceptible to sulbactam-durlobactam - all with only an OXA-carbapenemase. All isolates with NDM (n=10) or IMP (n=1) were resistant to sulbactam-durlobactam. Three isolates with only an OXA-carbapenemase were also resistant. Three isolates, also with only an OXA-carbapenemase, were categorised as I.

TABLE 74. Resistance proportions (%) in carbapenemase-producing *Acinetobacter* spp. (n=31) in 2025[1].

Antibiotic	Resistant isolates (%)
Meropenem	100
Imipenem	100
Ciprofloxacin	90
Amikacin	74
Gentamicin	77
Tobramycin	71
Trimethoprim-sulfamethoxazole	94
Colistin	3

[1]Categorisation according to the NordicAST breakpoint table v.16. Susceptibility testing was performed using broth dilution.

Conclusion

The occurrence of CPO continues to increase gradually in Norway, although the increase has slowed somewhat over the past three years. From 2024 to 2025, the incidence rate increased from 5.9 to 6.0 per 100,000 person-years, compared with 1.3 in 2021. The increase is largely due to more CPE cases, where the incidence rate rose from 4.8 in 2024 to 5.1 in 2025 per 100,000 person-years, compared to 1.1 in 2021.

Although most cases are associated with import (67%), this proportion continues to decline from 72% in 2024 and 80% in 2023. Whole-genome sequencing shows increasing diversity in the genetic backgrounds of isolates and carbapenemase genes, but with dominance of known global high-risk clones associated with substantial potential for further spread. Phylogenetic analyses show clusters of related isolates and a few cases of domestic transmission. The high level of resistance to new agents, including beta-lactam/beta-lactamase inhibitor combinations and cefiderocol, in addition to co-resistance to other antibiotic classes, illustrates the major treatment challenges associated with CPO infections.

References

1. Hornsey M, Phee L, Wareham DW. A novel variant, NDM-5, of the New Delhi metallo-β-lactamase in a multidrug-resistant *Escherichia coli* ST648 isolate recovered from a patient in the United Kingdom. Antimicrob Agents Chemother. 2011 Dec;55(12):5952-4.
2. Hoyos-Mallecot Y, Naas T, Bonnin RA, Patino R, Glaser P, Fortineau N, Dortet L. OXA-244-Producing *Escherichia coli* Isolates, a Challenge for Clinical Microbiology Laboratories. Antimicrob Agents Chemother. 2017 Aug 24;61(9):e00818-17.
3. Linkevicius M, Bonnin RA, Alm E, Svartström O, Apfalter P, Hartl R, et al. Rapid cross-border emergence of NDM-5-producing *Escherichia coli* in the European Union/European Economic Area, 2012 to June 2022. Euro Surveill. 2023;28(19).
4. Kohlenberg A, Svartström O, Apfalter P, Hartl R, Bogaerts P, Huang TD, et al. Emergence of *Escherichia coli* ST131 carrying carbapenemase genes, European Union/European Economic Area, August 2012 to May 2024. Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin. 2024;29(47).
5. European Centre for Disease Control and Prevention. OXA-244-producing *Escherichia coli* in the European Union/European Economic Area and the UK since 2013, first update. ECDC, Stockholm. 2021.
6. Manges AR, Geum HM, Guo A, Edens TJ, Fibke CD, Pitout JDD. Global Extraintestinal Pathogenic Escherichia coli (ExPEC) Lineages. Clin Microbiol Rev. 2019;32(3).
7. Jousset AB, Bouabdallah L, Birer A, Rosinski-Chupin I, Mariet JF, Oueslati S, et al. Population analysis of *Escherichia coli* sequence type 361 and reduced cefiderocol susceptibility, France. Emerg Infect Diseases. 2023;29(9):1877-81.
8. European Centre for Disease Control and Prevention. Carbapenem-resistant *Enterobacterales*, third update. ECDC: Stockholm; 2025. 2025.
9. Wyres KL, Lam MMC, Holt KE. Population genomics of *Klebsiella pneumoniae*. Nat Rev Microbiol. 2020;18(6):344-59.
10. Rodrigues C, Desai S, Passet V, Gajjar D, Brisse S. Genomic evolution of the globally disseminated multidrug-resistant *Klebsiella pneumoniae* clonal group 147. Microb Genom. 2022;8(1).
11. Long H, Zhao F, Feng Y, Zong Z. Global emergence of *Escherichia coli* with PBP3 insertions. J Antimicrob Chemother. 2025 Jan 3;80(1):178-181.
12. Lam MMC, Holt KE, Wyres KL. Comment on: MDR carbapenemase-producing *Klebsiella pneumoniae* of the hypervirulence-associated ST23 clone in Poland, 2009-19. J Antimicrob Chemother. 2023;78(4):1132-4.
13. Nasjonalt senter for påvisning av antibiotikaresistens og Folkehelseinstituttet. Risikovurdering av hypervirulente *Klebsiella pneumoniae* i Norge. 2024. https://www.unn.no/fag-og-forskning/k-res/nyheter/risikovurdering-av-hypervirulente-klebsiella-pneumoniae-i-norge/
14. Roer L, Sandfort M, Haller S, Roth SA, Höfken LM, Javadi S, Balanza N, Friedsam A, Wolf SA, Østergaard C, Wong MTY, Lis-Tønder J, Schoffelen AF, Cormican M, Porsbo LJ, Clarke C, Hasman H, Kerschner H, Hammerum AM, Hart R, Samuelsen Ø, Sare M, Meo M, Lagneaux AS, Perrin M, Müller V, Witteveen S, de Greeff SC, Notermans DW, Svartström O, Alm E, Linkevicius M, Kohlenberg A, Hendrickx APA. Ongoing multi-country outbreak of carbapenem-resistant *Enterobacter hormaechei* ST1344 carrying bla_{NDM-5} in the European Union/European Economic Area, March 2025 to April 2026. Euro Surveill. 2026 Jun;31(25):2600460.
15. Bush K, Bradford PA. Interplay between β-lactamases and new β-lactamase inhibitors. Nat Rev Microbiol. 2019;17(5):295-306.
16. Yahav D, Giske CG, Grāmatniece A, Abodakpi H, Tam VH, Leibovici L. New β-lactam-β-lactamase inhibitor combinations. Clin Microbiol Rev. 2020;34(1).
17. Karakonstantis S, Rousaki M, Vassilopoulou L, Kritsotakis EI. Global prevalence of cefiderocol non-susceptibility in *Enterobacterales*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and *Stenotrophomonas maltophilia*: a systematic review and meta-analysis. Clin Microbiol Infect. 2024;30(2):178-88.
18. NordicAST β-lactam-β-lactamase inhibitor combinations and novel β-lactams targeting Gram-negative bacteria. https://nordicast.org/methods
19. Bush K. Past, present, and future perspectives on aztreonam and avibactam. Expert Rev Anti Infect Ther. 2025:1-14.
20. Oliver A, Rojo-Molinero E, Arca-Suarez J, Beşli Y, Bogaerts P, Cantón R, et al. *Pseudomonas aeruginosa* antimicrobial susceptibility profiles, resistance mechanisms and international clonal lineages: update from ESGARS-ESCMID/ISARPAE Group. Clin Microbiol Infect. 2024;30(4):469-80.
21. Haldorsen BC, Samuelsen Ø, Janice J, Sare M, Molvik M, Sundsfjord A, et al. Import of global high-risk clones is the primary driver of carbapenemase-producing *Pseudomonas aeruginosa* in Norway. J Med Microbiol. 2025;74(1).
22. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, Harbarth S, Hindler JF, Kahlmeter G, Olsson-Liljequist B, Paterson DL, Rice LB, Stelling J, Struelens MJ, Vatopoulos A, Weber JT, Monnet DL. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect. 2012 Mar;18(3):268-81.
23. Castanheira M, Mendes RE, Gales AC. Global epidemiology and mechanisms of resistance of *Acinetobacter baumannii-calcoaceticus* complex. Clin Infect Dis. 2023;76(Suppl 2):S166-S78.
24. Hamidian M, Nigro SJ. Emergence, molecular mechanisms and global spread of carbapenem-resistant *Acinetobacter baumannii*. Microb Genom. 2019;5(10).
25. Liu H, Moran RA, Doughty EL, Hua X, Snaith AE, Zhang L, et al. Longitudinal genomics reveals carbapenem-resistant *Acinetobacter baumannii* population changes with emergence of highly resistant ST164 clone. Nat Commun. 2024;15(1):9483.
26. Papp-Wallace KM, McLeod SM, Miller AA. Durlobactam, a broad-spectrum serine β-lactamase inhibitor, restores sulbactam activity against *Acinetobacter* species. Clin Infect Diseases. 2023;76(Suppl 2):S194-s201.

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Haemophilus influenzae in blood cultures and cerebrospinal fluids

TABLE 75. *Haemophilus influenzae* in blood cultures and cerebrospinal fluids in 2025 (n=132). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin*	≤ 1	> 1	78.8	-	21.2
Amoxicillin-clavulanic acid**	≤ 2	> 2	94.7	-	5.3
Cefuroxime**	≤ 1	> 2	76.5	12.1	11.4
Cefotaxime	≤ 0.125	> 0.125	97.7	-	2.3
Ceftriaxone	≤ 0.125	> 0.125	98.5	-	1.5
Meropenem*	≤ 2	> 2	100.0	-	0.0
Ciprofloxacin	≤ 0.03	> 0.03	98.5	-	1.5
Chloramphenicol	≤ 2	> 2	100.0	-	0.0
Tetracycline	≤ 2	> 2	100.0	-	0.0
Trimethoprim-sulfamethoxazole***	≤ 0.5	> 0.5	81.8	-	18.2
Beta-lactamase	Negative	Positive	81.8	-	18.2

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than meningitis. **Breakpoints for intravenous administration. ***Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

TABLE 76. *Haemophilus influenzae* in blood cultures and cerebrospinal fluids in 2025 (n=132). Distribution (%) of MICs (mg/L).

	≤0.004	0.008	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	≥ 128
Ampicillin*			0.8	0.8	3.0	6.1	28.0	30.3	9.8	12.1	0.8	3.0	3.0	1.5		0.8
Amoxi-clav**			1.5	3.0	3.8	7.6	33.3	31.1	6.1	8.3	4.5	0.8				
Cefuroxime**					0.8	2.3	3.0	18.9	51.5	12.1	4.5	0.8	2.3	2.3		1.5
Cefotaxime	3.0	9.1	30.3	31.1	19.7	4.5		1.5	0.8							
Ceftriaxone			89.4	6.8	1.5	0.8	0.8	0.8								
Meropenem*	0.8	2.3	5.3	10.6	41.7	34.1	5.3									
Ciprofloxacin	17.4	42.4	34.1	4.5				0.8						0.8		
Chloramp.			0.8				3.0	46.1	49.2	0.8						
Tetracycline					2.3	3.8	6.8	74.2	12.9							
TMS***	2.3	3.8	29.5	24.2	13.6	1.5	2.3	4.5	5.3	1.5	2.3	2.3	1.5	5.3		

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than meningitis. **Breakpoints for intravenous administration. ***Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

RESULTS AND COMMENTS

Systemic *H. influenzae* isolates were first included in the NORM surveillance programme in 2013. Resistance data are provided on an annual basis by the Reference Laboratory at the Norwegian Institute of Public Health. The number of isolates in 2025 (n=132) was an increase from 2024 (n=93) but at the same level as in 2022 (n=130) and 2023 (n=121). Eight isolates were retrieved from cerebrospinal fluids, and three of these patients also had a blood culture isolate. Apart from this, all isolates represented unique patients (Tables 75-76). The break-point for resistance to trimethoprim-sulfamethoxazole was reduced from R > 1 mg/L to R > 0.5 mg/L in 2026. All other EUCAST/NordicAST breakpoints remained unchanged.

The rate of ampicillin resistance increased from 16.1% in 2024 to 21.2% in 2025, but this is in line with 21.5% in 2023. Beta-lactamase production was detected in 24/132 isolates (18.2%). This is a increase from 2024 (11.8%), but at the same level as in 2023 (15.7%). Different substrates have been suggested for screening of beta-lactam resistance in *H. influenzae*. The penicillin G 1U disk (PCG1) successfully identified all ampicillin (n=28) and cefuroxime (n=15) resistant isolates. Thirty out of 108 (27.8%) beta-lactamase negative isolates were resistant to PCG1, thus indicating chromosomal alterations in penicillin-binding proteins (PBPs). In addition, four PCG1 resistant and beta-lactamase positive isolates were resistant to amoxicillin-clavulanic acid with the 2-1 µg disk, suggesting concomitant beta-lactamase production and chromosomal resistance. In total, PBP-mediated resistance was detected in 34/132 (25.8%) isolates.

Three isolates were resistant to cefotaxime (MIC 0.5-1 mg/L), and two of them were also resistant to ceftriaxone (MIC 0.25-0.5 mg/L). Two blood isolates were meropenem resistant (MIC 0.5 mg/L) according to meningitis break-points when using MIC gradient methodology, but this was not confirmed by reference microdilution assays. As observed in previous surveys of systemic *H. influenzae* isolates, resistance rates for ciprofloxacin (1.5%), tetracycline (0.0%) and chloramphenicol (0.0%) were very low. The trimethoprim-sulfamethoxazole resistance rate of 18.2% is an increase from 2024 (10.8%) when using new breakpoints for both years.

Mitigating the butterfly effect of antibiotics: local action matters

A causal relationship between antibiotic use and resistance is well established, and optimising their use remains an essential part of strategies to preserve effective antibiotics for the future (1). But what is the optimal use of antibiotics, and which non-optimal use is most costly in terms of lost susceptibility? And at the other end of the scale – does it matter which penicillin we use?

All antibiotics promote resistance, but some are worse than others (1-2). Mechanisms include upregulation of intrinsic mechanisms, increased rates of spontaneous point mutations and horizontal gene transfer, and selection of resistant strains and subpopulations. Within-host selection leads to higher loads of resistant bacteria in the gut and the respiratory tract, thereby increasing the risk of person-to-person transmission and endogenous infection. Selection primarily affects commensals and pathogens other than the intended target (bystander selection) (3), and exposure to one drug may select resistance to other antibiotics (cross-selection) (4).

At the population level, high selective pressure is associated with increased prevalence of resistance in clinical isolates (5-6) and higher frequencies of carriage with multi-drug resistant organisms (7). International travel and migration, especially in the context of war and conflict, contribute to worldwide dissemination of resistant clones, and pathways of development and spread of resistance are not confined to the human sector (2, 6).

The complex, multi-factorial, and multi-dimensional associations between antibiotic use and resistance have important implications. First, exposure of one individual may contribute to resistance to any antibiotic, in any bacterial species, in any host or environment in any part of the world, analogous to the phenomenon in chaos theory known as “the butterfly effect” (8). Second, because the resistance-driving effect depends on an almost infinite number of drug, bug, host, population, and environmental factors, associations may be spurious or masked by confounders or have limited generalisability (2, 9-10). Because context is key, focused investigations using good local data and specific model pathogens may be more useful for informing local antibiotic policies than global analyses, underscoring the value of surveillance (10-11).

The opportunistic pathogen *Haemophilus influenzae*, which has humans as its only host, is the perfect “canary in the coal mine” for this purpose. The organism is the most frequent cause of lower respiratory tract infections in Norway (12) and a major contributor to global morbidity and antibiotic use (13). High colonisation rates, especially in children with respiratory tract infections, makes it a constant target of bystander selection (3). Within-host development of resistance occurs under ongoing treatment, aided by the ability of *H. influenzae* to form a protective biofilm (14). Selection of resistant subpopulations occurs *in vitro* following exposure to several beta-lactams, with the widest selection windows observed for oral cephalosporins (15-16). Accordingly, the rapid emergence of cephalosporin resistant *H. influenzae* in Japan in the 1990s was linked to extensive use of this group.

The *H. influenzae* resistome comprises an array of transferable resistance determinants, many of which belong to the shared supragenome of genus *Haemophilus*. This implies that *H. parainfluenzae* and other commensals act as reservoirs for resistance in *H. influenzae*, dramatically increasing the selective power of antibiotics. Horizontal transfer is mediated by mobile genetic elements, many of which carry multiple resistance genes, and by natural transformation, which may lead to chromosomal alterations through uptake of mutant extracellular DNA followed by homologous recombination.

Accordingly, cefotaxime resistant *H. influenzae* (CRHI) evolves through spontaneous point mutations and transformation, and person-to-person transmission leads to local outbreaks and spread of international clones (17). Phenotypic resistance profiles depend on the number of key substitutions in penicillin-binding protein 3: one substitution confers low-level resistance to aminopenicillins, whereas acquisition of additional substitutions is associated with resistance to third-generation cephalosporins. A recent investigation showed that hospital incidence of CRHI in Norway is significantly associated with the use of oral aminopenicillins and parenteral third-generation cephalosporins (Figure 97A-B) (18). Combining both consumption variables gave the strongest association (Figure 97C), consistent with a modelling study showing that antibiotic use in both sectors contributes to resistance (19).

A highly relevant question in a Scandinavian setting is whether amoxicillin and phenoxymethylpenicillin (PcV) have different impact on resistance, but this was not addressed in the original publication (18). To clarify this, supplementary analyses were performed using PcV consumption based on defined daily doses (DDD). Because consumption rates for PcV and amoxicillin were positively correlated, regional PcV-to-amoxicillin ratios were calculated to assess the impact of consumption patterns. A high ratio was negatively associated with CRHI incidence, but the correlation was not statistically significant (Figure 97D).

However, analysis of age-stratified prescription data (20) revealed a significant negative association between CRHI incidence and the PcV fraction of oral respiratory tract antibiotics, but only in the youngest age group (Figure 97E-F). In support of current treatment guidelines, this indicates that amoxicillin, macrolides, and doxycycline are significantly stronger promoters of CRHI than PcV. Notably, the association was based on CRHI across all ages, suggesting that use of broad-spectrum oral antibiotics in children is a significant driver of the population-wide prevalence of resistance to cefotaxime in *H. influenzae*.

Several hypotheses may explain why the strength of the association varied across age groups. First, colonisation with *H. influenzae* and viral respiratory tract infections are more frequent among children, facilitating bystander selection and transmission of resistant strains to close contacts. Second, resistance is more strongly associated with extensive exposure (many users) than with intensive use (many exposures) (5), and the latter pattern is likely more common in the older age group due to higher frequency of predisposing conditions. The distribution-dependent association between use and resistance

suggests that metrics other than DDD may be more appropriate for quantification and comparison of ecological effects of antibiotics. The failure of the DDD-based analysis to detect a significant association also underscores another well-known limitation of this system, which systematically underrepresents antibiotic exposure in children due to age-dependent lower dosing.

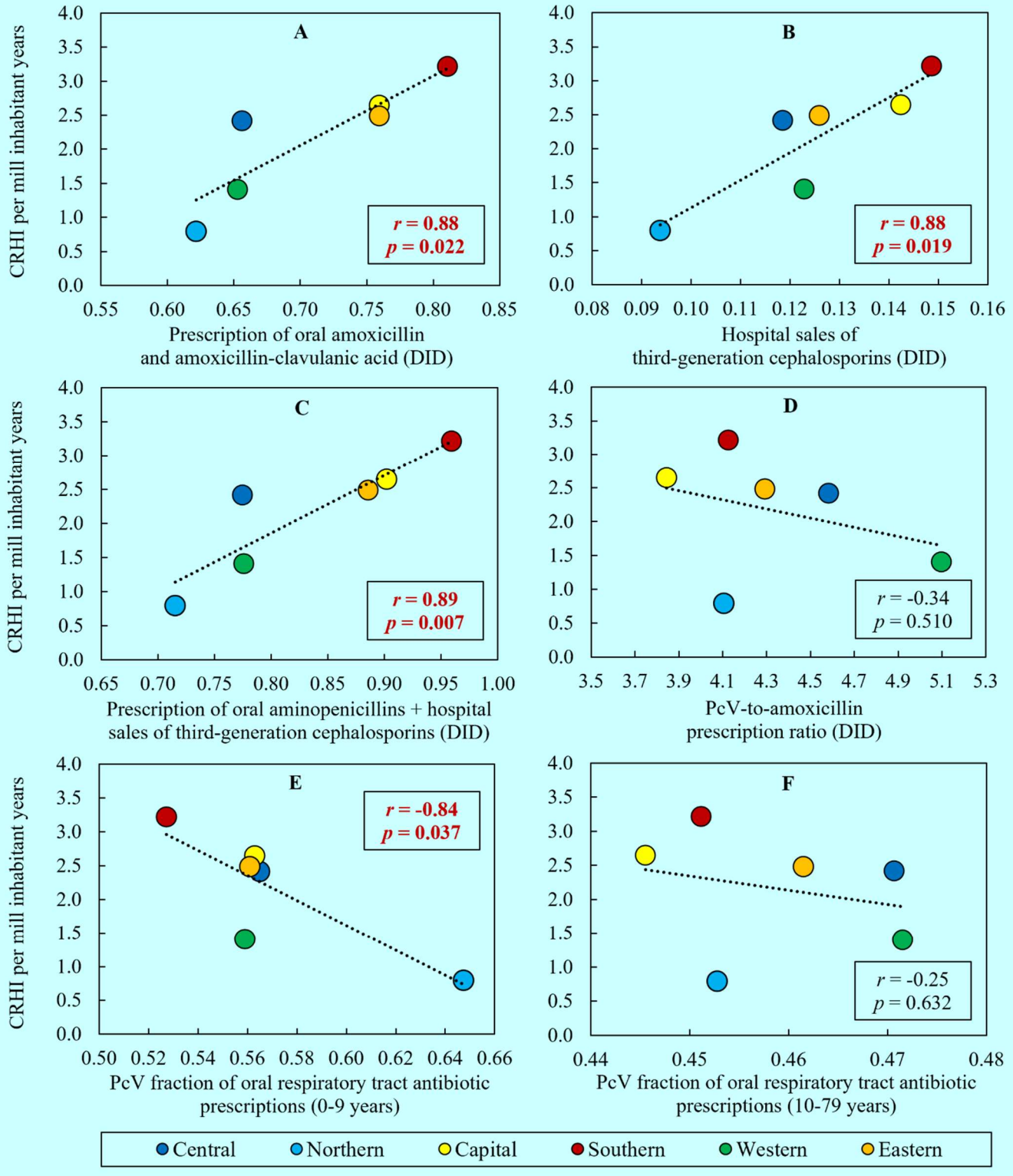

FIGURE 97. Correlations between use of selected beta-lactam antibiotics in six Norwegian regions and hospital incidence of cefotaxime resistant *Haemophilus influenzae* (CRHI). Statistically significant correlations are highlighted. A) Prescription of oral aminopenicillins. B) Hospital sales of third-generation cephalosporins. C) A and B combined. D) PcV-to-amoxicillin prescription ratio. E-F) PcV fraction of oral respiratory tract antibiotic prescriptions (PcV, amoxicillin, macrolides, and doxycycline) by age group. Data from (18) with supplementary analyses based on data from the Norwegian Prescribed Drug Registry (D) and the Norwegian Directorate of Health (20) (E-F). DID, defined daily doses (DDD) per 1,000 inhabitant days.

In conclusion, the Scandinavian narrow-spectrum penicillin-based approach to treatment of respiratory tract infections mitigates beta-lactam resistance in *H. influenzae*. Demonstration of strong correlations between antibiotic use and resistance for multiple drug-bug combinations at the sub-national level (11, 18) confirms that local action matters.

References

1. Moja L, Zanichelli V, Mertz D, et al. WHO's essential medicines and AWaRe: recommendations on first- and second-choice antibiotics for empiric treatment of clinical infections. Clin Microbiol Infect, 2024. doi: 10.1016/j.cmi.2024.02.003.
2. Knudsen CV, Akselsen PE, Fostervold A, et al. Bruk-Spar-Reserve. Tidsskr Nor Legeforen, 2025. doi: 10.4045/tidsskr.25.0062.
3. Tedijanto C, Olesen SW, Grad YH, et al. Estimating the proportion of bystander selection for antibiotic resistance among potentially pathogenic bacterial flora. PNAS, 2018. doi: 10.1073/pnas.1810840115.
4. Sundsfjord A, Simonsen GS, Haldorsen B, et al. Bredspektrede betalaktamaser hos gramnegative stavbakterier. Tidsskr Nor Legeforen, 2008. Dec 4;128(23):2741-5.
5. Olesen SW, Barnett ML, MacFadden D, et al. The distribution of antibiotic use and its association with antibiotic resistance. eLife, 2018. doi: 10.7554/eLife.39435.
6. ECDC/EFSA/EMA. Second joint report on the integrated analysis of the consumption of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from humans and food-producing animals. EFSA, 2017. doi: 10.2903/j.efsa.2017.4872.
7. Sulis G, Sayood S, Katukoori S, et al. Exposure to World Health Organization's AWaRe antibiotics and isolation of multidrug resistant bacteria: a systematic review and meta-analysis. Clin Microbiol Infect, 2022. doi: 10.1016/j.cmi.2022.03.014.
8. Britannica. The butterfly effect. https://www.britannica.com/science/butterfly-effect.
9. Turnidge, Christiansen K. Antibiotic use and resistance—proving the obvious. Lancet, 2005. doi: 10.1016/S0140-6736(05)17920-3.
10. Pöntinen AK, Gladstone RA, Pesonen H, et al. Modulation of multidrug-resistant clone success in *Escherichia coli* populations: a longitudinal, multi-country, genomic and antibiotic usage cohort study. Lancet Microbe, 2024. doi: 10.1016/S2666-5247(23)00292-6.
11. Skaare D, Hannisdal A, Kalager M, et al. Measuring broad-spectrum antibiotic use in hospitals with established versus new indicators. Tidsskr Nor Legeforen, 2023. doi: 10.4045/tidsskr.22.0427.
12. Markussen DL, Lindemann C, Serigstad S, et al. Microbial profiling of community-acquired pneumonia in patients with and without chronic obstructive pulmonary disease: a comprehensive molecular diagnostics study. Pneumonia, 2025. doi: 10.1186/s41479-025-00172-0.
13. Sati H, Carrara E, Savoldi A, et al. The WHO Bacterial Priority Pathogens List 2024: a prioritisation study to guide research, development, and public health strategies against antimicrobial resistance. Lancet Inf Dis, 2025. doi: 10.1016/S1473-3099(25)00118-5.
14. Lindemann PC, Mylvaganam H, Oppegaard O, et al. Case Report: Whole-genome sequencing of serially collected *Haemophilus influenzae* from a patient with common variable immunodeficiency reveals within-host evolution of resistance to trimethoprim-sulfamethoxazole and azithromycin after prolonged treatment with these antibiotics. Front Cell Infect Microbiol, 2022. doi: 10.3389/fcimb.2022.896823.
15. Takahata S, Kato Y, Sanbongi Y, et al. Comparison of the efficacies of oral beta-lactams in selection of *Haemophilus influenzae* transformants with mutated *ftsI* genes. Antimicrob Agents Chemother, 2008. doi: 10.1128/AAC.00936-07.
16. Petersen S, Diricks M, Utpatel C, et al. Evolution of beta-lactam resistance causes fitness reductions and several cases of collateral sensitivities in the human pathogen *Haemophilus influenzae*. Antimicrob Agents Chemother, 2025. doi: 10.1128/aac.00576-25.
17. Skaare D, Anthonisen IL, Zecic N, et al. Genomic profiling of cefotaxime-resistant *Haemophilus influenzae* from Norway and Sweden reveals extensive expansion of virulent multidrug-resistant international clones. Front Microbiol, 2025. doi: 10.3389/fmicb.2025.1601390.
18. Skaare D, Simonsen GS. Incidence of cefotaxime-resistant *Haemophilus influenzae* is linked to regional consumption of oral aminopenicillins and parenteral third-generation cephalosporins in Norway. APMIS, 2026. doi: 10.1111/apm.70201.
19. Knight GM, Costelloe C, Deeny SR, et al. Quantifying where human acquisition of antibiotic resistance occurs: a mathematical modelling study. BMC Med, 2018. doi: 10.1186/s12916-018-1121-8.
20. Helsedirektoratet. Nasjonale kvalitetsindikatorer innen tema antibiotika. https://www.helsedirektoratet.no/statistikk/kvalitetsindikatorer/legemidler.

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Changing strategies for genital chlamydia testing and treatment: Implications for antibiotic consumption and tetracycline resistance

The ‘test-and-treat’ strategy for genital chlamydia is under debate. Widespread testing of asymptomatic individuals has long been advocated on the assumption that early detection reduces prevalence and prevents long-term complications, including pelvic inflammatory disease and infertility. However, the evidence for these benefits is limited,[1] and several European countries are now reconsidering the scope of routine chlamydia screening.

The Dutch experience: a model for change

In November 2019, the Netherlands convened an international expert panel to review the evidence base for asymptomatic chlamydia testing as part of an update to the Dutch National Action Plan on STI, HIV and Sexual Health. The panel concluded that the case for widespread asymptomatic testing was weak and proposed redirecting resources toward symptomatic individuals and the partners of confirmed cases.[1]

In 2025, the Netherlands became the first EU member state to translate this recommendation into policy, restricting *Chlamydia trachomatis* testing at sexual health clinics to symptomatic cases and partner notification. A retrospective observational study modelling the impact of this change estimated that the new strategy would result in approximately half as many diagnoses and antibiotic prescriptions in women and heterosexual men.[2] It should be noted that these are projected rather than observed outcomes, as prospective follow-up data are not yet available.

European epidemiological context

These policy shifts are occurring against a backdrop of declining chlamydia notifications across Europe. The ECDC 2024 Annual Epidemiological Report recorded a crude notification rate of 63.4 cases per 100,000 population across 24 countries with comprehensive surveillance systems, a 10% decrease compared with 2023.[3] A subsequent analysis of surveillance data from six EU/EEA countries, including Norway, has confirmed significant and sustained reductions in notifications in 2024.[4]

The Norwegian situation

Norway reported 22,295 chlamydia cases in 2025, representing a further 4% decrease from 2024 and the lowest annual case count in 20 years.[5] A total of 361,001 tests were performed that year (Table 77). Despite a slight reduction in testing volume, particularly among women and in the primary target group (under 25 years), the overall proportion of positive results remained stable at 6.2%.

TABLE 77. Chlamydia testing and positive results by sex and age group, Norway, 2025. Source: Meldingssystemet for smittsomme sykdommer (MSIS), Norwegian Institute of Public Health.

Sex	Age (years)	Tested	Positive	% positive
Male	0-14	848	16	1.9
	15-19	10,075	1,543	15.3
	20-24	27,577	3,695	13.4
	25-29	22,828	1,889	8.3
	30-39	30,230	1,592	5.3
	40+	27,806	951	3.4
	Total	119,364	9,686	8.1
Female	0-14	1,466	32	2.2
	15-19	36,190	3,617	10.0
	20-24	74,199	5,530	7.5
	25-29	47,654	1,936	4.1
	30-39	49,822	1,075	2.2
	40+	32,306	419	1.3
	Total	241,637	12,609	5.2
All	**Total**	**361,001**	**22,295**	**6.2**

High-volume testing in older age groups is a concern. Among individuals aged 30 years and above, approximately 140,000 tests were performed in 2025 (34% of all tests in women and 49% in men, respectively), yielding 2,543 positive results in women and 1,494 in men. Given that approximately 75% of *C. trachomatis* infections are asymptomatic,[6] a substantial proportion of those tested and treated in this age group are likely to experience minimal or no clinical benefit from treatment.

The antibiotic implications are substantial. The NORM/NORM-VET 2024 report identified tetracyclines (J01A) as the second most-used antibiotic class in Norwegian primary care, accounting for 21% of all defined daily doses (DDDs).[7] Doxycycline (J01AA02) is among the six most frequently prescribed antibiotics in outpatient settings. Data from the Norwegian Prescription Database confirm that dispensing rates of doxycycline are highest in the 20-24-year age group; precisely the cohort with the highest rates of reported chlamydia cases (Legemiddelstatistikk per ATC-kode - FHI Statistikk).

A review of our national 'test-and-treat' strategy for *C. trachomatis* infections is warranted. If a shift toward more targeted testing were to halve the number of chlamydia diagnoses and treatments, as modelled in the Dutch study,[2] this would represent a meaningful reduction in community doxycycline consumption. Reduced selection pressure from tetracycline use may in turn influence resistance development in non-target organisms. Of particular importance is *Neisseria gonorrhoeae*, for which tetracycline resistance is already widespread and known to be strongly associated with population-level consumption.[8]

References

1. Dukers-Muijrers NHTM, Gotz HM, van Bergen JEAM, et al. Where to go to in chlamydia control? From infection control towards infectious disease control. Sex Transm Infect 2021;97:501–506.
2. Werner L, Jongen VW, Bruisten SM, Schim van der Loeff MF, Hoornenborg E, de Vries HJC. et al. Estimated effect of reduced asymptomatic testing on missed *Chlamydia trachomatis* detections among women and heterosexual men in the Netherlands: a retrospective observational study. Lancet Reg Health Eur. 2025 Oct 6;58:101468. doi: 10.1016/j.lanepe.2025.101468. PMID: 41126910; PMCID: PMC12537342.
3. European Centre for Disease Prevention and Control. Chlamydia – Annual Epidemiological Report for 2024. Stockholm: ECDC; 2025.https://www.ecdc.europa.eu/en/publications-data/chlamydia-annual-epidemiological-report-2024
4 Astorga Alsina AM, Gomes Dias J, Adlhoch C, Nerlander L, Olsen AO, Igoe D, Hiltunen-Back E, et al. Decreased chlamydia notifications in six European Union/European Economic Area countries and England, 2024. Euro Surveill. 2026 May;31(21):2500846. doi: 10.2807/1560-7917.ES.2026.31.21.2500846. PMID: 42212419; PMCID: PMC13221617.
5. Folkehelseinstituttet. Blod- og seksuelt overførbare infeksjoner i Norge: årsrapport 2025. Oslo: FHI; 2026.
6. White JA, Dukers-Muijrers NH, Hoebe CJ, Kenyon CR, DC Ross J, Unemo M. 2025 European guideline on the management of Chlamydia trachomatis infections. *International Journal of STD & AIDS*. 2025;36(6):434-449. doi:10.1177/09564624251323678
7. Norwegian Institute of Public Health / Norwegian University of Science and Technology. NORM/NORM-VET 2024: Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway. Tromsø/Oslo; 2025.
8. Campbell P. The Influence of National Antibiotic Consumption on Neisseria Gonorrhoeae Antibiotic Resistance in Norway, 2003-2024. J Infect Dis. 2026 May 15;233(5):e1193-e1202. doi: 10.1093/infdis/jiag076. PMID: 41670362; PMCID: PMC13175608.

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Neisseria meningitidis in blood cultures and cerebrospinal fluids

TABLE 78. *Neisseria meningitidis* in blood cultures and cerebrospinal fluids in 2025 (n=16). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	Susceptible	Resistant	Susceptible	Intermediately susceptible	Resistant
Penicillin G*	≤ 0.25	> 0.25	93.8	-	6.2
Ceftriaxone	≤ 0.125	> 0.125	100.0	-	0.0
Ciprofloxacin	≤ 0.016	> 0.016	100.0	-	0.0
Chloramphenicol	≤ 2	> 2	100.0	-	0.0
Rifampicin	≤ 0.25	> 0.25	100.0	-	0.0
Tetracycline	≤ 2	> 2	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Penicillin G=Benzylpenicillin.

TABLE 79. *Neisseria meningitidis* in blood cultures and cerebrospinal fluids in 2025 (n=16). Distribution (n) of MICs (mg/L).*

	≤0.004	0.008	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	≥ 128
Penicillin G*					8	4	3	1								
Ceftriaxone			16													
Ciprofloxacin	15	1														
Chloramph.							1	2	13							
Rifampicin	1	5	3	4	2		1									
Tetracycline					1	6	5	4								
Azithromycin						1		1	5	7	1	1				

Shaded areas in each row indicate susceptibility with standard exposure (light), susceptibility with increased exposure (medium) and resistance (dark). Non-shaded cells represent MIC values that are not covered by the standard test method. *Penicillin G=Benzylpenicillin.

RESULTS AND COMMENTS

N. meningitidis from blood cultures and cerebrospinal fluids were first included in NORM in 2013. The Reference Laboratory at the Norwegian Institute of Public Health provides data for *N. meningitidis* on an annual basis. The EUCAST/NordicAST breakpoint remained unchanged from the previous year. Results are presented in Tables 78-79.

In 2025, 16 isolates were received from 17 reported cases of systemic infections caused by *N. meningitidis*. No epidemiological links were identified between the invasive meningococcal disease cases. Isolates from 14 patients were recovered from blood cultures. Additionally, isolates from CSF were obtained from two of these patients. The number of isolates represents an increase from the pandemic years 2020-2022 and is now comparable to the levels observed in 2019 (n=16). The isolates belonged to serogroups B (n=5), Y (n=5) and W (n=6). The five serogroup B isolates belonged to four distinct sequence types (STs), with only the two isolates from the same patient being identical. All five serogroup Y isolates were of ST-23. Among the six serogroup W isolates, five were ST-11 and one was ST-9316.

A single serogroup W ST-11 isolate exhibited penicillin G MIC value of 0.5 mg/L and was categorised as resistant. EUCAST/NordicAST has not established breakpoints for azithromycin, but the MIC distribution does not indicate the presence of high-level acquired macrolide resistance (Table 79).

Neisseria gonorrhoeae

TABLE 80. *Neisseria gonorrhoeae* from all specimen types in 2025 (n=1,341). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G*	≤ 0.06	> 1	4.9	69.8	25.3
Ceftriaxone	≤ 0.125	> 0.125	99.9	-	0.1
Cefixime	≤ 0.125	> 0.125	99.5	-	0.5
Ciprofloxacin	≤ 0.03	> 0.06	30.1	0.5	69.4
Tetracycline	≤ 0.5	> 0.5	45.2	-	54.8
Spectinomycin	≤ 64	> 64	100.0	-	0.0
Beta-lactamase	Negative	Positive	69.8	-	31.2

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Penicillin G=Benzylpenicillin.

TABLE 81. *Neisseria gonorrhoeae* from all specimen types in 2025 (n=1,341) Distribution (%) of MICs (mg/L).

	≤0.004	0.008	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	≥ 128
Penicillin G*	0.1	0.1	0.7	0.7	3.1	19.0	30.1	13.9	6.8	12.4	4.5	4.2	1.6	2.5		
Ceftriaxone	32.1	14.4	51.3	1.7	0.3		0.1		0.1							
Cefixime			64.7	20.1	13.7	1.0	0.3	0.1	0.1	0.1						
Ciprofloxacin	28.0	1.5	0.4	0.1	0.5	1.3	0.7	2.5	12.7	28.2	17.4	4.1	1.0	1.5		
Tetracycline					0.9	4.0	13.9	26.3	17.6	1.0	1.5	8.1	19.2	6.8	0.2	0.4
Spectinomycin										0.3	2.2	30.9	38.2	28.3	0.1	
Azithromycin			0.4	1.6	5.8	14.5	17.2	14.7	18.3	21.5	2.8	1.0	1.0	0.3	0.2	0.6

Shaded areas in each row indicate susceptibility with standard exposure (light), susceptibility with increased exposure (medium) and resistance (dark). Non-shaded cells represent MIC values that are not covered by the standard test method. *Penicillin G=Benzylpenicillin.

RESULTS AND COMMENTS

Neisseria gonorrhoeae was surveyed in NORM in 2003 and 2010. Since 2013, yearly surveillance has been performed by the Reference Laboratory at the Norwegian Institute of Public Health in collaboration with Oslo University Hospital. In 2025, a total of 1,341 gonococcal isolates were available for further analyses, a slight decline from 2023 (n=1,500) and 2024 (n=1,471). Of all reported cases to MSIS (including PCR-only positives), 46.9% (1,341/2,860) were culture positive, compared to 50.3% in 2023 and 45.0% in 2024.

The 1,341 gonococcal isolates originated from 1,167 individuals: 897 (77%) men and 270 (23%) women. The corresponding figures for 2024 were 73% men and 27% women. Some patients had isolates collected from different clinical sites at the same point in time. The isolates were recovered from the urethra (n=585), anus/rectum (n=330), cervix uteri/vagina (n= 256), throat (n=146), abscess (n=7), urine (n=6), eye (n=5), blood (n=2), joint fluid (n=2), and unknown (n=2). Whole genome sequencing was applied to characterise 862 of the 1,344 isolates. The most frequent sequence types (STs) were ST-16676 (17%; 9% in 2024), ST-1580 (12%; 16% in 2024 and 28% in 2023), ST-7822 (9%; 7% in 2024) and ST-9362 (7%; 13% in 2024).

The results from susceptibility testing are presented in Tables 80-81. Most isolates were either susceptible only to increased exposure (69.8%) or resistant (25.3%) to penicillin G. The corresponding figures for 2024 were 74.0% and 21.2%, respectively. A total of 418 isolates (31.2%) produced beta-lactamase, which is a further increase from 2023 (13.7%) and 2024 (20.5%). Of the beta-lactamase negative isolates, seven (3.6%) were resistant and 850 (92.1%) were only susceptible to increased exposure to penicillin G. Resistance to ciprofloxacin continues to increase and is now at a very high level (69.4%, compared to 57% in 2024). Most beta-lactamase positive isolates (380/418) were also resistant to ciprofloxacin. Resistance to azithromycin 27% (21% in 2024) and tetracycline 54% (39% in 2024) also increased in 2025 and remain at a high level.

Cefixime resistance (MIC 0.25-2 mg/L) was identified in seven isolates (0.5%) of which two (0.15%) were also resistant to ceftriaxone (MIC 0.25-1 mg/L). The two ceftriaxone resistant isolates belonged to ST-7363 and ST-19270. Both isolates were co-resistant to penicillin, ciprofloxacin, tetracycline and cefixime. ST-19270 was in addition resistant to azithromycin (MIC >256 mg/L), classifying the gonococcal isolate as XDR. These two isolates harbour multiple resistance-associated mutations within the *penA* gene (A311V, A510V, F504L, G545S, I312M, N512Y, T483S, V316T) which have been implicated in mediating resistance to both penicillin and cephalosporins.

In Norway standard gonococcal treatment is ceftriaxone 1g i.m. monotherapy. Ciprofloxacin is not a viable alternative except in cases where susceptibility has been documented. Spectinomycin, to which all isolates were susceptible, is unavailable for human clinical use. Gonococcal antimicrobial resistance surveillance, including culture-based testing, antimicrobial susceptibility testing and genomic surveillance is of even greater importance in the era of increasing resistance, at a global level, to extended-spectrum cephalosporins. A recent rapid risk assessment report from ECDC (2026) flags an upsurge in ceftriaxone resistant MDR/XDR *Neisseria gonorrhoea*, with evidence of domestic transmission in the EU/EEA and the UK.

Staphylococcus aureus in blood cultures

TABLE 82. *Staphylococcus aureus* blood culture isolates in 2025 (n=1,678). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Erythromycin	≤ 1	> 1	92.5	-	7.5
Clindamycin	≤ 0.25	> 0.25	98.9	-	1.1
Fusidic acid	≤ 1	> 1	95.8	-	4.2
Ciprofloxacin	≤ 0.001	> 2	0.0	98.1	1.9
Gentamicin	≤ 2	> 2	99.2	-	0.8
Linezolid	≤ 4	> 4	100.0	-	0.0
Rifampicin	≤ 0.06	> 0.06	98.9	-	1.1
Tetracycline	≤ 1	> 1	96.8	-	3.2
Tigecycline	≤ 0.5	> 0.5	99.8	-	0.2
Trimethoprim-sulfamethoxazole*	≤ 0.5	> 0.5	97.1	-	2.9
Beta-lactamase	Negative	Positive	36.0	-	64.0
Cefoxitin screen	≥ 22	< 22	98.8	-	1.2
MRSA** (*mecA*)	Negative	Positive	98.8	-	1.2

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only. **MRSA=Methicillin resistant *Staphylococcus aureus*.

RESULTS AND COMMENTS

S. aureus blood culture isolates have been included in the NORM surveillance programme since it was initiated in 2000. Data are interpreted according to the most recent EUCAST/NordicAST breakpoint protocol. The breakpoint for resistance to ciprofloxacin was increased from R > 1 mg/L to R > 2 mg/L from 2024 onwards and the breakpoint for resistance to trimethoprim-sulfamethoxazole was reduced from R > 4 mg/L to R > 0.5 mg/L in 2025.

Twenty methicillin resistant *S. aureus* (MRSA) isolates were detected in the NORM surveillance system in 2025, corresponding to a prevalence of 1.2% (Table 82). This is unchanged from 2024 (1.1%). The isolates originated from 11 different hospitals, and clonal relationship among isolates was not detected at the Reference Laboratory for MRSA. Laboratory screening for MRSA in NORM is performed using cefoxitin disks and there was full concordance between cefoxitin and *mecA* PCR results. Some MRSA isolates were concomitantly resistant to erythromycin (8/20), ciprofloxacin (8/20), gentamicin (6/20), tetracycline (4/20), trimethoprim-sulfamethoxazole (4/20), fusidic acid (3/20), clindamycin (3/20) and/or rifampicin (1/20). All MRSA isolates were susceptible to tigecycline and linezolid. The results from susceptibility testing of all Norwegian MRSA isolates are presented in Table 85 on page 136. The NORM findings are slightly lower than the 33/2,366 *S. aureus* blood culture isolates (1.4%) reported from the databases of the participating laboratories. None of the 16 *S. aureus* isolates recovered from cerebrospinal fluids were methicillin resistant, thus bringing the total number of systemic MRSA isolates to 33/2,382 (1.4%). This is a slight decrease from 1.8% in 2023 and 2.2% in 2024.

One hundred twenty-six *S. aureus* isolates (7.5%) were resistant to erythromycin. This is a slight increase from 2023 and 2024 (6.8% both years). The macrolide resistance phenotypes of erythromycin resistant isolates were determined by the double disk diffusion (DDD) test. Seven isolates (5.6%) were constitutively MLS_B resistant, 88 (69.8%) were inducibly MLS_B resistant, and 31 (24.6%) displayed efflux mediated M-type resistance. These figures represent 0.4%, 5.2% and 1.8% of all *S. aureus* isolates from blood cultures, respectively. The distribution of MLS_B resistance phenotypes was essentially the same as in 2024.

The prevalence of resistance to fusidic acid (4.2%) was at the same level as in 2023 (3.7%) and 2024 (3.5%). Ciprofloxacin resistance has apparently stabilised at 1.9% in 2025 (1.7% in 2024), but the decline from 4.9% in 2022 and 3.1% in 2023 may in part be explained by an adjustment of the resistance breakpoint (see above). It should be noted that the wild type population of *S. aureus* is defined as susceptible only to increased exposure to this agent. Resistance to trimethoprim-sulfamethoxazole increased from 0.1% in 2024 to 2.9% in 2025, but this may in part be explained by a reduction of the breakpoint (see above). There were no significant changes for gentamicin, rifampicin or tigecycline, and all isolates were fully susceptible to linezolid. The general test panel for *S. aureus* did not include vancomycin in 2025.

Figure 98 shows the prevalence of resistance to various antimicrobials. A total of 64.0% of the isolates were beta-lactamase positive, which is similar to 62.9% in 2024. Resistance to ciprofloxacin and tetracycline was more common among beta-lactamase positive isolates (2.4% and 4.1%, respectively) than in beta-lactamase negative ones (1.0% and 1.5%, respectively), whereas erythromycin resistance was more common in beta-lactamase negative isolates (8.8%) than in beta-lactamase positive ones (6.8%). There were no significant differences in the prevalence of resistance to other non-beta-lactam antibiotics between beta-lactamase positive and negative isolates.

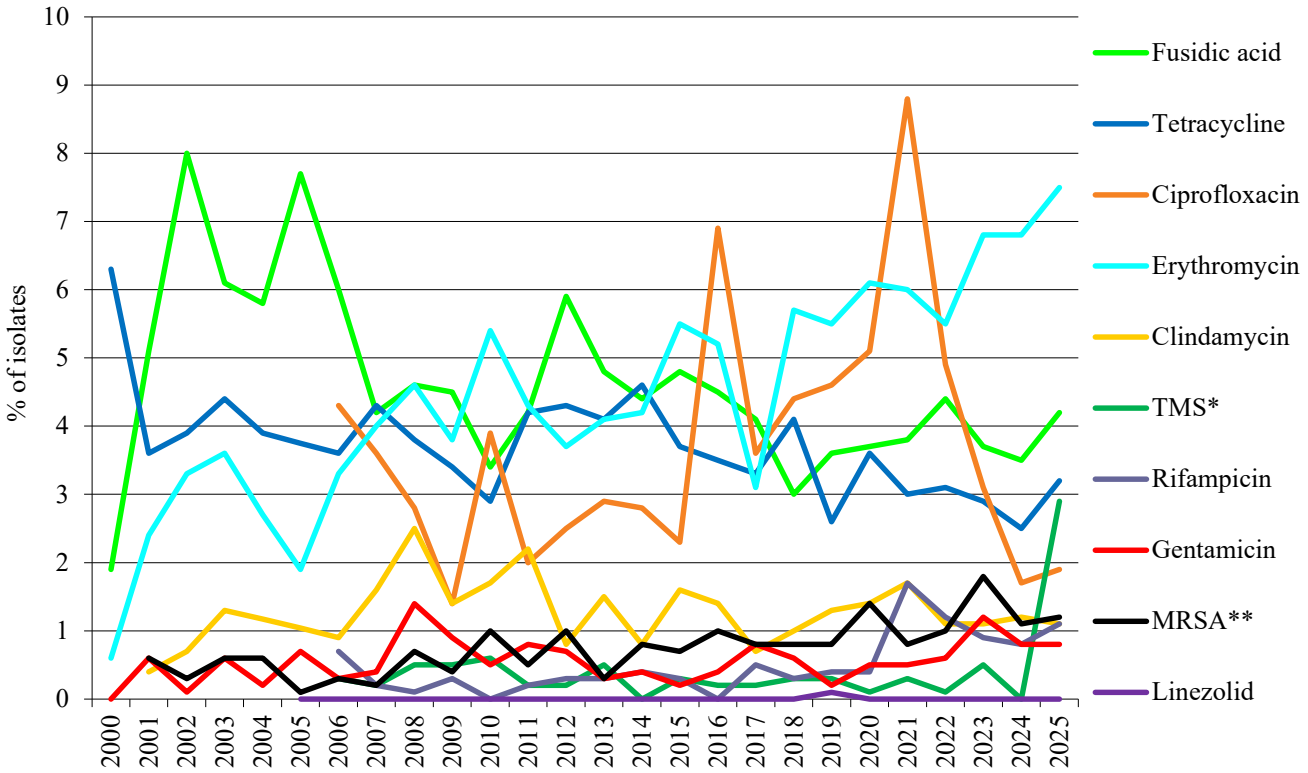

FIGURE 98. Prevalences of antimicrobial resistance among *Staphylococcus aureus* blood culture isolates 2000-2025. Doxycycline was replaced by tetracycline in 2006. Isolates are categorised according to the breakpoints at the time of analysis. *TMS=Trimethoprim-sulfamethoxazole. **MRSA=Methicillin resistant *Staphylococcus aureus*. The breakpoint for resistance to ciprofloxacin was increased from R > 1 mg/L to R > 2 mg/L in 2024 and the breakpoint for resistance to trimethoprim-sulfamethoxazole was reduced from R > 4 mg/L to R > 0.5 mg/L in 2025.

Staphylococcus aureus in wound specimens

TABLE 83. *Staphylococcus aureus* isolates in wound specimens in 2025 (n=804). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Erythromycin	≤ 1	> 1	91.4	-	8.6
Clindamycin	≤ 0.25	> 0.25	99.1	-	0.9
Fusidic acid	≤ 1	> 1	95.1	-	4.9
Ciprofloxacin	≤ 0.001	> 2	0.0	98.1	1.9
Gentamicin	≤ 2	> 2	99.0	-	1.0
Linezolid	≤ 4	> 4	100.0	-	0.0
Rifampicin	≤ 0.06	> 0.06	99.1	-	0.9
Tetracycline	≤ 1	> 1	96.0	-	4.0
Tigecycline	≤ 0.5	> 0.5	100.0	-	0.0
Trimethoprim-sulfamethoxazole*	≤ 0.5	> 0.5	97.4	-	2.6
Beta-lactamase	Negative	Positive	31.6	-	68.4
Cefoxitin screen	≥ 22	< 22	98.0	-	2.0
MRSA** (*mecA*)	Negative	Positive	98.0	-	2.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only. **MRSA=Methicillin resistant *Staphylococcus aureus*.

RESULTS AND COMMENTS

S. aureus from wound specimens were screened for methicillin resistance (MRSA) by the cefoxitin disk method in the same way as blood culture isolates. Sixteen out of 804 isolates (2.0%) were confirmed as MRSA by *mecA* PCR. The prevalence was at the same level as in 2024 (1.9%). MRSA isolates originated from patients visiting general practitioners (n=11), hospital wards (n=4) and an outpatient clinic (n=1) in different parts of the country. Many MRSA isolates (12/16) were co-resistant to erythromycin (7/16), ciprofloxacin (6/16), tetracycline (5/16), fusidic acid (3/16), gentamicin (3/16), rifampicin (2/16) and/or trimethoprim-sulfamethoxazole (2/16) in different combinations. All MRSA isolates were fully susceptible to clindamycin, tigecycline, and linezolid. No isolates were reported with zone diameters below the cefoxitin screening breakpoint without being verified as MRSA by *mecA* PCR. This confirms the high specificity of cefoxitin screening as well as a low prevalence of *mecC* MRSA (see page 136).

The prevalence of resistance to fusidic acid in *S. aureus* wound isolates increased from 4.4% in 2024 to 4.9% in 2025 (Table 83 and Figure 99). The rate of this phenotype has thus stabilised after the previous epidemic which peaked at 25.0% in 2004. The prevalence of resistance to fusidic acid is now at the same level in blood culture isolates (4.2%) as in wound isolates (4.9%). For other antimicrobial agents such as gentamicin, rifampicin and tetracycline there were only minor changes from 2024-2025, and the prevalence of resistance was in general similar for blood culture isolates and isolates from wound specimens. The minor increase in resistance to trimethoprim-sulfamethoxazole from 2024 (0.2%) to 2025 (2.6%) is primarily explained by the change of breakpoint (see above). All isolates were phenotypically susceptible to linezolid and tigecycline.

Sixty-nine isolates (8.6%) were resistant to erythromycin, and this is at the same level as in 2024 (8.3%). All erythromycin resistant isolates were further examined to determine the macrolide resistance phenotype. The majority were either inducibly (55/69; 80% of erythromycin resistant isolates) or constitutively (1/69; 1% of erythromycin resistant isolates) resistant to clindamycin, thus representing the $iMLS_B$ and $cMLS_B$ phenotypes, respectively. A minor proportion of the isolates displayed low-level resistance to erythromycin only (13/69; 19% of erythromycin resistant isolates), which is compatible with efflux mediated M-type resistance. The findings are in accordance with the results from previous years.

A total of 68.4% of isolates were beta-lactamase positive in 2025 compared to 69.0% in 2023 and 72.5% in 2024. Beta-lactamase positive isolates were more often resistant to tetracycline (5.5%) and fusidic acid (6.2%) than beta-lactamase negative isolates (0.8% and 2.0%, respectively), while beta-lactamase negative isolates were more often resistant to erythromycin (10.2% versus 7.8%). There were no significant differences in other non-beta-lactam resistance rates between beta-lactamase negative and positive isolates.

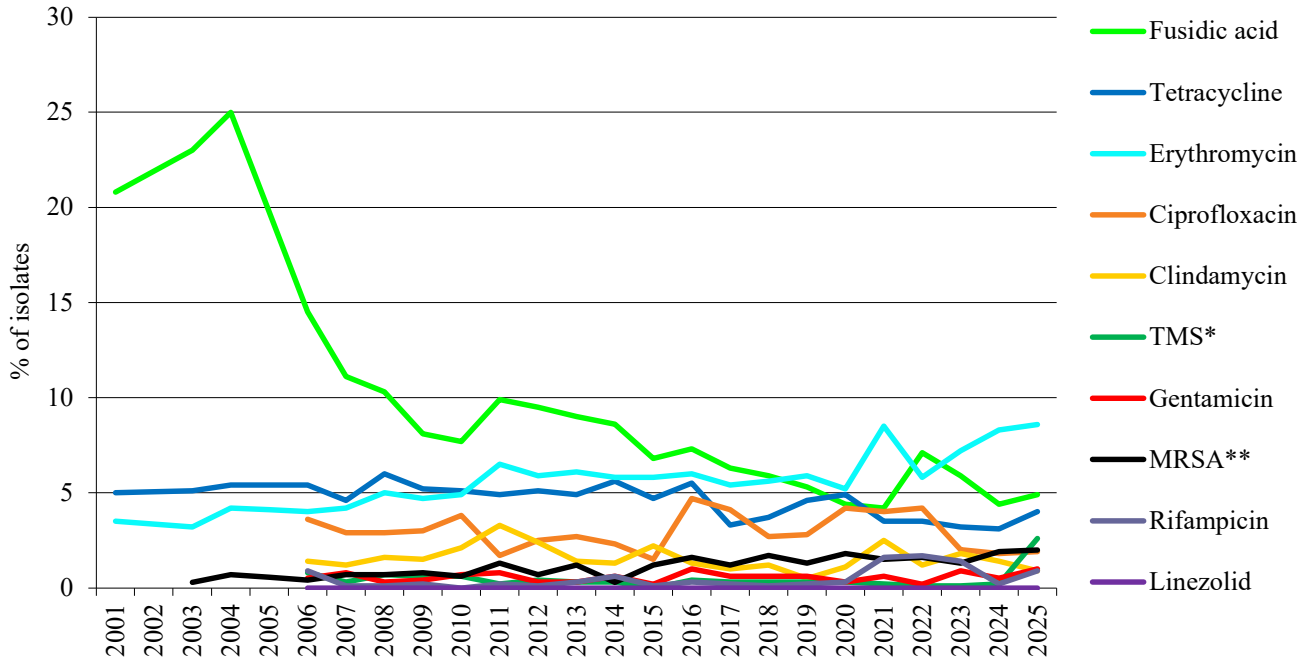

FIGURE 99. Prevalence of antimicrobial resistance among *Staphylococcus aureus* wound isolates 2001-2025. Doxycycline was replaced by tetracycline in 2006. Isolates are categorised according to the breakpoints at the time of analysis. *TMS=Trimethoprim-sulfamethoxazole. **MRSA=Methicillin resistant *Staphylococcus aureus*. The breakpoint for resistance to ciprofloxacin was increased from R > 1 mg/L to R > 2 mg/L in 2024 and the breakpoint for resistance to trimethoprim-sulfamethoxazole was reduced from R > 4 mg/L to R > 0.5 mg/L in 2025.

Methicillin resistant *Staphylococcus aureus* (MRSA) in Norway 2025

The number of persons reported with MRSA to the Norwegian Surveillance System for Communicable Diseases (MSIS) in Norway was 3,153 in 2025, a 7% increase compared to 2024 (2,940 persons). A total of 1,285 (41%) persons were reported with MRSA infection and 1,851 (59%) persons with colonisation. The incidence rate in the form of all MRSA cases per 100,000 person-years was 57, and 23 and 33 for infections and colonisations, respectively (Figure 100).

The incidence of MRSA was relatively stable for a period before the coronavirus pandemic, during which it decreased, probably as a result of strict infection prevention and control measures to curb the spread of Covid-19. In 2025 the incidence rate was higher than it was in the peak year of 2017.

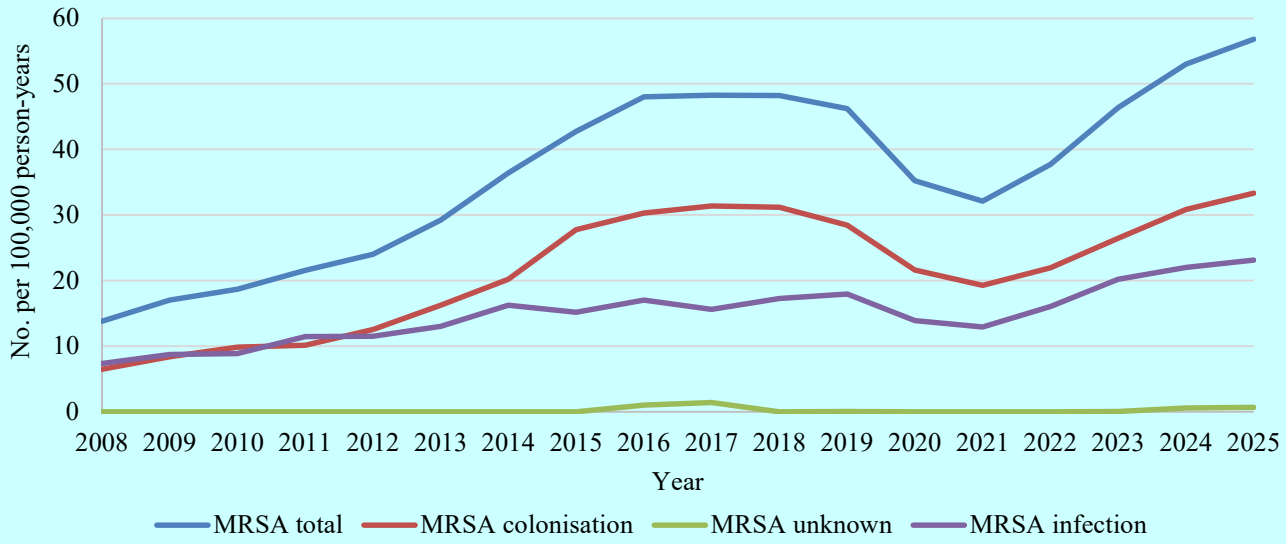

FIGURE 100. Number of persons notified with MRSA per 100,000 person-years in Norway 2008-2025, in total, and by infection and colonisation.

In 2025, 597 (19%) persons were reported to have acquired MRSA abroad, and 622 (20%) persons to have acquired MRSA in Norway (Figure 101). Of note, however, is that information regarding a possible place of infection is lacking in 61% of all cases.

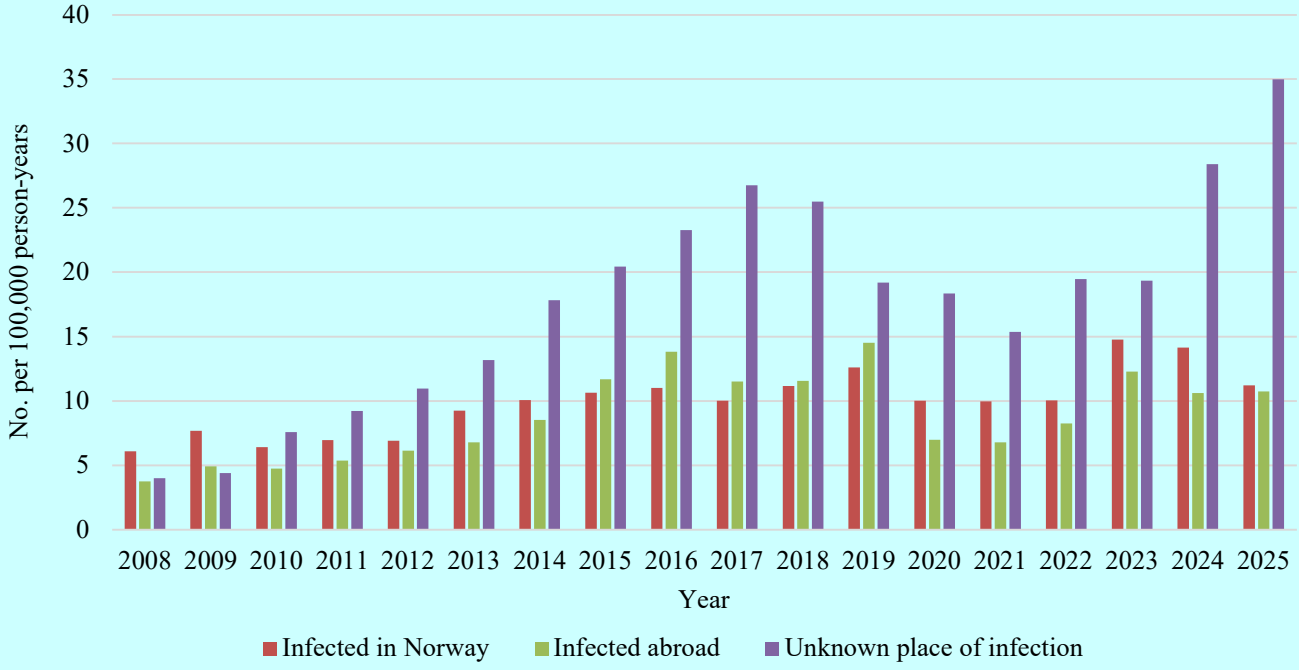

FIGURE 101. Number of persons notified with MRSA per 100,000 person-years in Norway 2008-2025, by assumed place of infection.

Further information on the epidemiology of MRSA in Norway can be found at https://www.fhi.no/sm/antibiotikaresistens/forekomst-av-antibiotikaresistente-bakterier-og-sopp/om-bakterier-og-sopp/meticillinresistente-gule-stafylokokker-mrsa/.

The Norwegian Reference Laboratory for Methicillin Resistant *Staphylococcus aureus* (MRSA) at St. Olavs hospital, Trondheim University Hospital, received 3,645 MRSA isolates from 3,232 persons in 2025, including both MRSA carriage and infections (Figure 102). There has been a continued increase in MRSA cases in the last years compared with the lower numbers observed in 2020 and 2021 during the Covid-19 pandemic. The reasons for this trend remain unclear, partly due to limited epidemiological data available for the MRSA isolates.

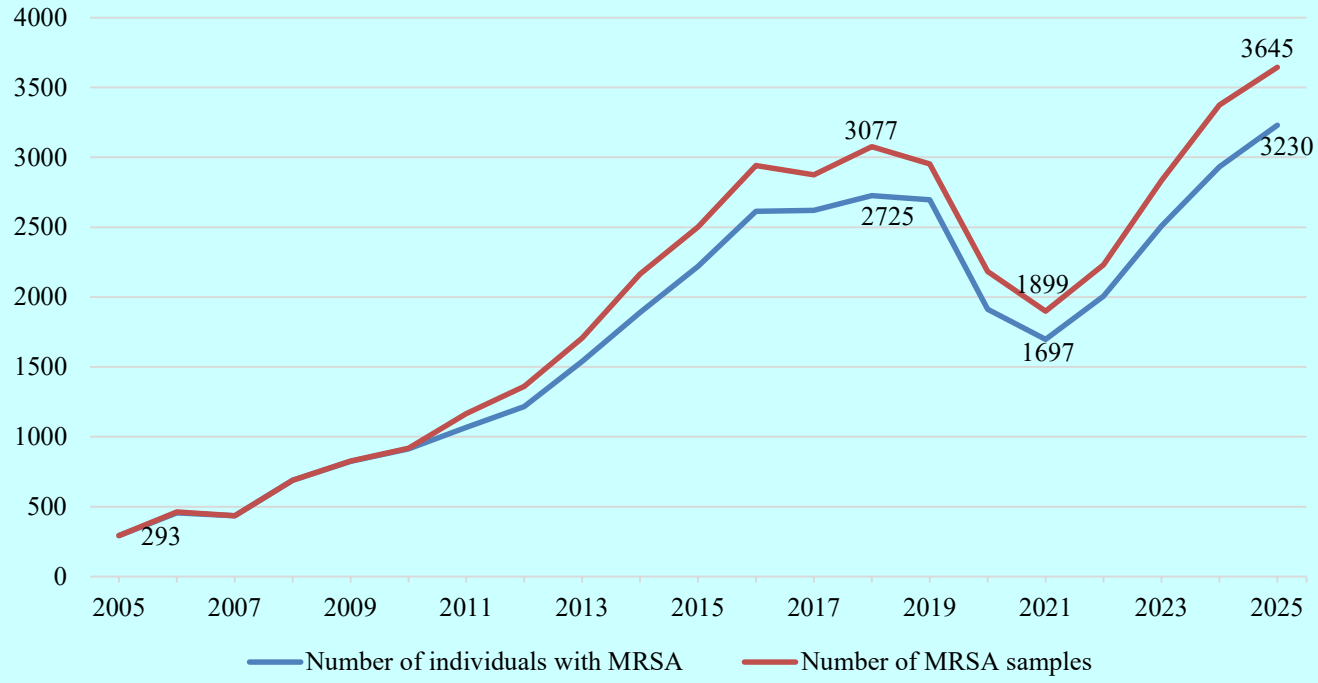

FIGURE 102. Number of MRSA samples and affected individuals 2005-2025.

Staphylococcal protein A (*spa*)-typing was the main genotyping method applied to all isolates, while whole-genome sequencing was performed on selected isolates. In 2025, a total of 497 different *spa*-types were identified. Of these, the majority (n=397; 79.9%) were reported less than five times. This high proportion of rarely observed *spa*-types reflects the considerable genotypic diversity of MRSA in Norway, consistent with findings from other Nordic countries.

Table 84 shows the 10 most common MRSA *spa*-types identified in Norway in 2025, along with their associated clonal complexes (CC). *spa*-type t304 has been the most common *spa*-type since 2021 and is still increasing. *spa*-types t355 and t008 are also showing a rising trend, while most of the other *spa*-types on the top 10-list seem to have stabilised for now.

TABLE 84. The ten most common MRSA *spa*-types in Norway in 2025.

spa-type	CC	No. of isolates	% of isolates
t304	CC6	398	10.8
t355	CC152	249	6.8
t127	CC1	204	5.6
t008	CC8	197	5.4
t002	CC5	150	4.1
t223	CC22	150	4.1
t3841	CC672	127	3.5
t034	CC398	96	2.6
t688	CC5	88	2.4
t1476	CC8	82	2.2

Beyond the top ten most prevalent types, spa-type t272 is of particular interest. This genotype is associated with a well-known fusidic acid resistant European MRSA clone that has caused outbreaks of impetigo and has been identified in Norway since 2022. Most Norwegian cases were seen in children with impetigo, and some of the cases were part of outbreaks. All except one of the Norwegian isolates were resistant to fusidic acid, often in combination with gentamicin resistance (see Figure 103).

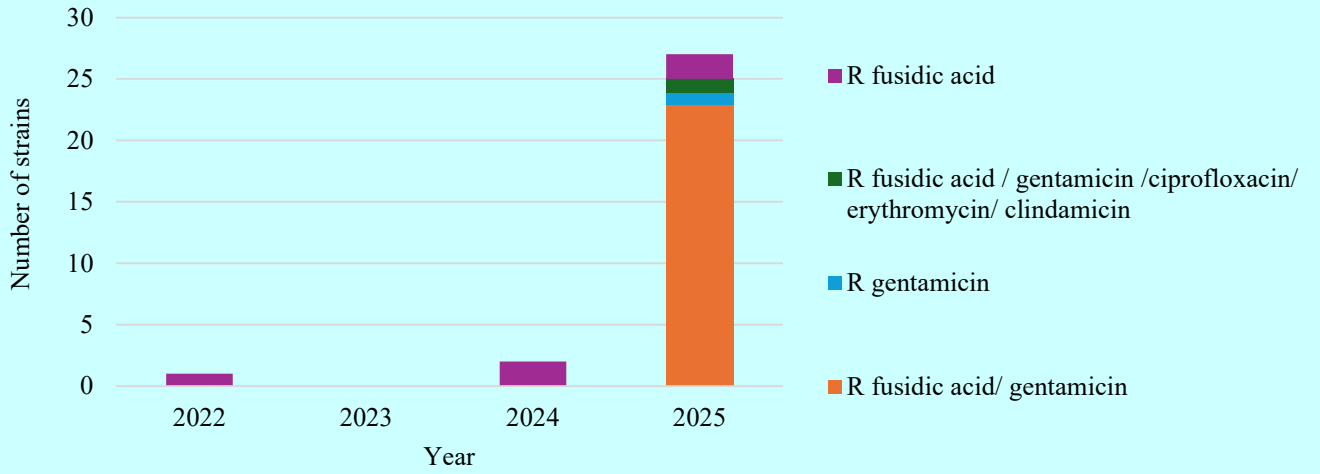

FIGURE 103. Annual distribution and antimicrobial resistance profiles of MRSA t272/CC121 strains.

Livestock-associated MRSA (LA-MRSA), in this report defined as PVL-negative MRSA of CC398, still had a low incidence with 23 human isolates identified in 2025. PVL-positive MRSA CC398 is however increasing, with 97 human isolates in 2025, versus 67 human isolates in 2024 and 46 in 2023. This PVL-positive genotype is often associated with travel to or immigration from Asian countries rather than contact with livestock animals. Two isolates were *mecC*-positive in 2025.

The laboratory received 42 *mecA*-positive *Staphylococcus argenteus* (MRSArg) (41 in 2024) and 60 *mecA*-positive *Staphylococcus lugdunensis* (54 in 2024). The increase in *mecA*-positive *S. lugdunensis* may reflect a true rise in incidence, although increased diagnostic testing or awareness could also have contributed.

Antimicrobial susceptibility testing was performed with the EUCAST disc diffusion method by the referring laboratories and the results in Table 85 were interpreted according to the 2026 NordicAST breakpoints.

TABLE 85. Antibiotic susceptibility results from all human MRSA and MRSArg collected in 2025. Susceptibility was interpreted according to Breakpoint Tables v.16.0 (January 2026). Breakpoints are given as minimum inhibitory concentrations (mg/L).

	Breakpoints (mg/L)		Proportion of isolates (%)			Isolates (n)
	S	R	S	I	R	
Erytromycin	≤ 1	> 1	62.5	-	37.5	3,684
Clindamycin*	≤ 0.25	> 0.25	79.1	-	20.9	3,684
Fusidic acid	≤ 1	> 1	79.9	-	20.1	3,686
TMS**	≤ 0.5	> 0.5	79.7	-	20.3	3,686
Tetracycline	≤ 1	> 1	70.7	-	29.3	3,682
Gentamicin	≤ 2	> 2	82.7	-	17.3	3,684
Ciprofloxacin	≤ 0.001	> 2	-	72.0	28.0	3,533
Mupirocin	≤ 1	> 1	97.5	-	2.5	3,643
Rifamipicin	≤ 0.06	> 0.06	98.6	-	1.4	3,682
Linezolid	≤ 4	> 4	100.00	-	0.0	3,685
Vancomycin	≤ 2	> 2	100.0	-	-	3,673

TMS=Trimethoprim-sulfamethoxazole. *Total clindamycin resistance including inducible resistant MRSA cases (14.2%). **Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only. S=Susceptible with standard exposure. I=Susceptible with increased exposure. R=Resistant.

The highest proportion of co-resistance was found for erythromycin (37.5%), followed by tetracycline (29.3%) and ciprofloxacin (28.0%). In recent years, resistance to erythromycin, tetracycline and ciprofloxacin has increased, but this trend now appears to have levelled off or stabilised (Figure 104).

Intermediate levels of resistance were seen with clindamycin (20.9%), trimethoprim-sulfamethoxazole (20.3%), fusidic acid (20.1%) and gentamicin (17.3%). The considerable increase in trimethoprim-sulfamethoxazole resistance from 2.3% in 2024

to 20.3% in 2025 was mainly caused by a significant change in the breakpoints from January 2026. The resistance rate to fusidic acid continued to rise modestly, and the emergence of *spa*-type t272 may have contributed to this trend.

An increase in resistance to mupirocin (2.5%) was observed, rising from 0.2% in 2024; however, this increase is attributable to the elimination of the intermediate susceptibility category rather than a true shift in resistance pattern. Resistance to rifampicin remained infrequent, at 1.4%. In 2025, one linezolid resistant MRSA isolate was detected, identified from a carriage sample. As this represented less than 0.1% of all isolates, it is not apparent in Table 85. No isolates showed reduced susceptibility to vancomycin. Ceftaroline was excluded from the table due to insufficient data.

In general, changes in susceptibility rates may partly reflect shifts in the epidemiological distribution of dominant *spa*-types as well as changes in breakpoints. However, methodological factors are also relevant, especially for ciprofloxacin and clindamycin. For ciprofloxacin, many isolates had inhibition zone diameters close to the breakpoint, which may have resulted in inter-laboratory variation in interpretation. For clindamycin, observed fluctuations over time may not only represent true changes in resistance, but could also be influenced by differences in interpretation or incomplete reporting of inducible resistance.

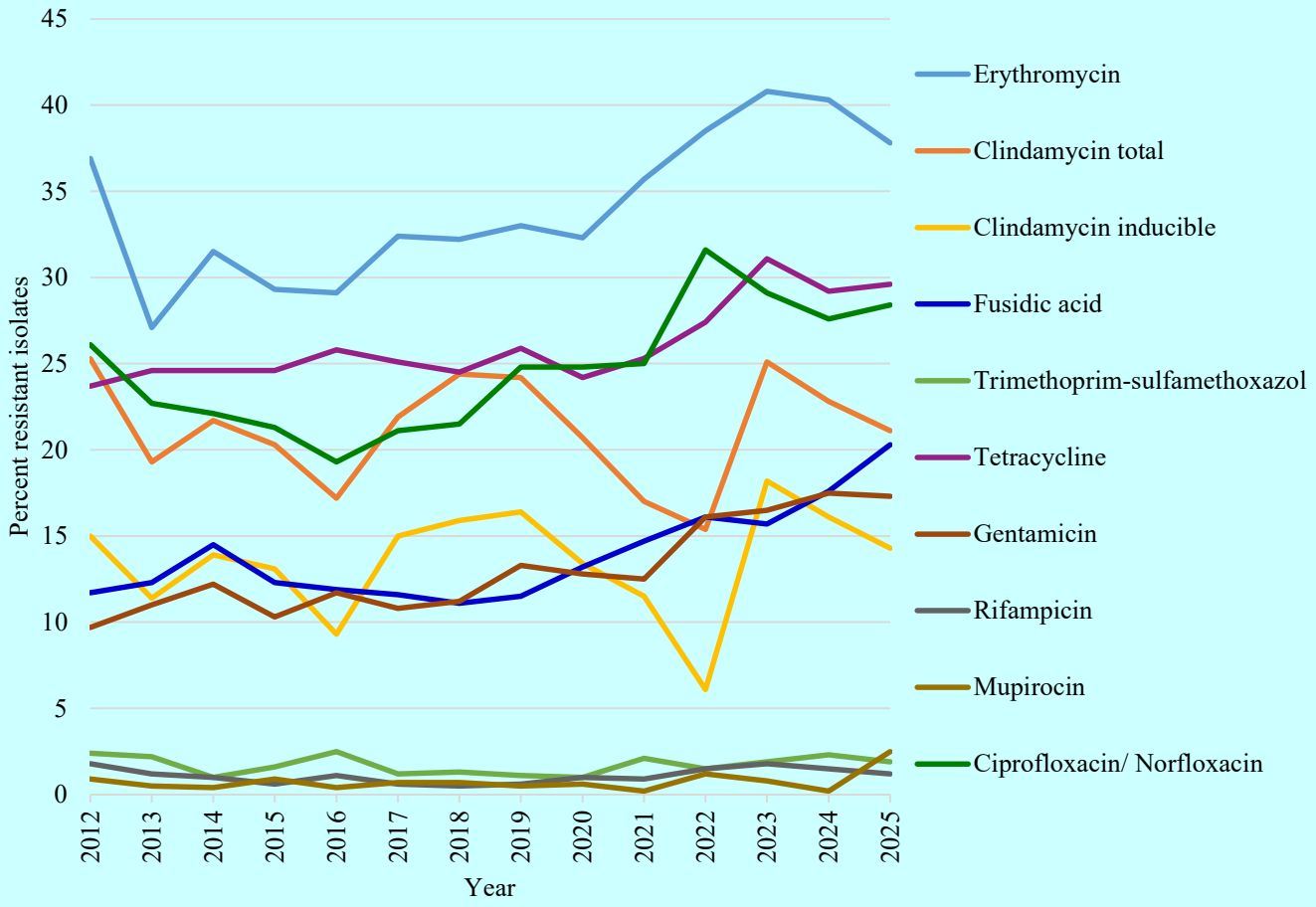

FIGURE 104. Annual prevalence of antimicrobial resistance among MRSA and MRSArg isolates 2012-2025. Isolates were classified as susceptible or resistant according to the EUCAST breakpoints applicable at the time of testing. Results for cefoxitin are not included.

Figure 105 shows the most frequent resistance patterns among MRSA isolates tested in 2025. Resistance to cefoxitin alone was by far the most common profile for Norwegian MRSA isolates (29.7%). This was followed by combined resistance to cefoxitin, erythromycin and tetracycline (7.1%), and to cefoxitin, erythromycin, tetracycline and clindamycin (6.2%).

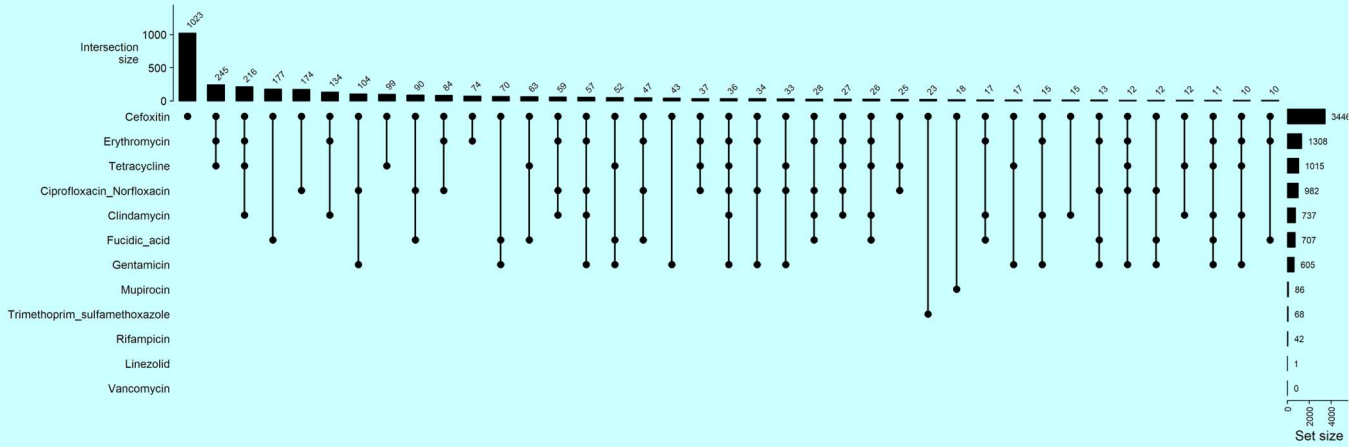

FIGURE 105. The most common combinations of antimicrobial resistance in Norwegian MRSA isolates in 2025. Clindamycin resistance is given as total resistance including inducible resistant isolates.

Conclusion
The increase in MRSA incidence after the pandemic remains unexplained. Resistance to cefoxitin alone was the most common resistance profile. Observed changes in resistance patterns were largely driven by breakpoint revisions and shifts in the prevalence of the most common genotypes.

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Outbreaks of resistant microbes in Norway 2025

In Norway, it is mandatory to report outbreaks of infectious diseases to the Norwegian Institute of Public Health (NIPH). According to the Norwegian Surveillance System for Communicable Diseases (MSIS) regulation (1), the following outbreaks must be reported: 1) outbreaks of diseases that are notifiable to MSIS, 2) suspected food- and waterborne outbreaks, 3) outbreaks of particularly severe diseases (e.g. those with high mortality, complication rates, or serious clinical manifestations), 4) particularly extensive outbreaks, and 5) outbreaks in health care institutions.

The aims of outbreak reporting include alerting and sharing information with relevant authorities and asking for assistance if needed. Reported local outbreaks can be seen in connection and reveal larger national outbreaks. The reporting contributes to an overview of the epidemiological situation at both local and national levels. Additionally, the data is a basis for infection control recommendations, outbreak management strategies, and national and international reporting.

Outbreaks are reported by municipal medical officers, hospitals, and food safety authorities through a web-based system called Vesuv. Data collected in Vesuv include information on the time and place of the outbreak, number of cases, main symptoms, suspected or confirmed pathogen, transmission route, and more. No individual patient data is registered in Vesuv. Although mandatory, some underreporting is suspected. This may be because outbreaks are not detected or because detected outbreaks are not reported. Because outbreaks should be reported as soon as they are suspected, some data in Vesuv – such as the number of cases – may be incomplete or not updated as the situation evolves.

Definition of an outbreak
An outbreak can be defined as two or more cases of the same infectious disease where a common source is suspected, or a number of cases that exceeds the expected level within a given area and time (2).

Reported outbreaks in 2025
The following data are obtained from Vesuv and the annual report of infectious disease outbreaks (3). In 2025, a total of 311 outbreaks were reported to Vesuv. Of those, 86% were reported from health care institutions. Of the 266 nosocomial outbreaks, 24 were caused by antimicrobial resistant microbes, with a total of 105 cases. Four community outbreaks of antimicrobial resistant microbes were reported in 2025; three caused by methicillin resistant *Staphylococcus aureus* (MRSA) with a total of 18 cases, and one by carbapenemase-producing *E. coli* with three cases. Table 86 shows the outbreaks of resistant microbes in health care institutions 2021-2025. Table 87 shows the outbreaks in 2025 by type of health care institution.

TABLE 86. Outbreaks of antimicrobial resistant microbes in healthcare institutions, Vesuv 2021-2025.

Pathogen	2025		2021	2022	2023	2024
	Outbreaks (n)	Cases (n)	Outbreaks (n)			
Methicillin resistant *Staphylococcus aureus* (MRSA)	12	75	3	2	5	12
Carbapenemase-producing organisms (CPO)	7	15	0	2	8	12
ESBL-producing organisms (microbe unknown)	2	7	0	0	0	0
Vancomycin resistant enterococci (VRE)	2	5	0	1	5	10
Klebsiella spp. (ESBL-producing)	1	3	0	1	1	1
Linezolid resistant enterococci (LRE)	0	0	1	1	2	2
E. coli (ESBL-producing)	0	0	0	0	2	2
Total	24	105	4	7	23	39

TABLE 87. Outbreaks of antimicrobial resistant microbes by type of healthcare institution, Vesuv 2025.

Pathogen	Long-term care facility	Hospital
Methicillin resistant *Staphylococcus aureus* (MRSA)	5	7
Vancomycin resistant enterococci (VRE)	0	2
Carbapenemase-producing organisms (CPO)	0	7
ESBL-producing organisms (microbe unknown)	2	0
Klebsiella spp. (ESBL-producing)	1	0
Total	8	16

CPO outbreaks

There were 2-3 cases in each of the seven carbapenamase-producing organisms (CPO) outbreaks. All seven were outbreaks of carbapenemase-producing *Enterobacterales*; three were caused by *Klebsiella pneumoniae*, three by *E. coli*, and one by *Enterobacter hormaechei*. The rise in CPO outbreaks in recent years is partly due to an increase in hospital-reported cases, but also driven by a routine implemented in 2023, whereby NIPH is notified by The Norwegian Centre for Detection of Antimicrobial Resistance about genetically linked CPO clusters. NIPH has subsequently reported these outbreaks in Vesuv. In 2025 this routine was further developed, and now NIPH systematically reviews these clusters in collaboration with infection control personnel in the relevant hospitals to identify whether transmission has occured within a health care institution. This can explain the decline in reported outbreaks in 2025 compared to 2023 and 2024.

VRE outbreaks

Of the two vancomycin resistant enterococci (VRE) outbreaks, one was caused by *E. faecium* with three cases, and one by *E. faecalis* with two cases.

MRSA outbreaks

Outbreaks of methicillin resistant *Staphylococcus aureus* (MRSA) are affecting both hospitals and long-term care facilities, and the number of reported outbreaks remains higher than in previous years, with the same number of outbreaks as in 2024.

Other microbes

No linezolid resistant enterococci (LRE) outbreaks were notified in 2025. No outbreak of *Candida auris* has ever been reported in Norway.

References

1. The Norwegian Surveillance System for Communicable Diseases (MSIS) regulation (in Norwegian). https://lovdata.no/dokument/SF/forskrift/2003-06-20-740
2. Manual of Infectious Diseases (in Norwegian), Folkehelseinstituttet. https://www.fhi.no/sm/smittevernveilederen/temakapitler/06.-utbrudd-av-smittsomme-sykdommer?term=
3. Annual report. Outbreaks of infectious diseases in Norway 2025 (in Norwegian). https://www.fhi.no/contentassets/cf699f6ab9f743ceb42ef2173253c42d/arsrapport-for-vesuv-2025.pdf

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Enterococcus spp. in blood cultures

TABLE 88. *Enterococcus* spp. blood culture isolates in 2025 (n=779), except for piperacillin-tazobactam and imipenem (n=551) where 228 enterococcal isolates not identified as *E. faecalis* are excluded due to lack of breakpoints, and vancomycin (n=746) where 33 isolates not identified as *E. faecalis* or *E. faecium* are excluded due to lack of breakpoints. Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 4	> 4	79.8	-	20.2
Piperacillin-tazobactam	≤ 0.001	> 16	0.0	99.6	0.4
Imipenem	≤ 0.001	> 4	0.0	99.5	0.5
Gentamicin HLR*	≤ 128	> 128	85.4	-	14.6
Linezolid	≤ 4	> 4	99.7	-	0.3
Tigecycline	≤ 0.5	> 0.5	98.5	-	1.5
Vancomycin	≤ 4	> 4	100.0	-	0.0
Vancomycin (*vanA* or *vanB*)	Negative	Positive	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *HLR=High Level Resistance.

TABLE 89. *Enterococcus faecalis* blood culture isolates in 2025 (n=551). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 4	> 4	100.0	-	0.0
Piperacillin-tazobactam	≤ 0.001	> 16	0.0	99.6	0.4
Imipenem	≤ 0.001	> 4	0.0	99.5	0.5
Gentamicin HLR*	≤ 128	> 128	95.1	-	4.9
Linezolid	≤ 4	> 4	100.0	-	0.0
Tigecycline	≤ 0.5	> 0.5	97.8	-	2.2
Vancomycin	≤ 4	> 4	100.0	-	0.0
Vancomycin (*vanA* or *vanB*)	Negative	Positive	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *HLR=High Level Resistance.

TABLE 90. *Enterococcus faecium* blood culture isolates in 2025 (n=195). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 4	> 4	22.1	-	77.9
Gentamicin HLR*	≤ 128	> 128	56.9	-	43.1
Linezolid	≤ 4	> 4	99.0	-	1.0
Tigecycline	≤ 0.5	> 0.5	100.0	-	0.0
Vancomycin	≤ 4	> 4	100.0	-	0.0
Vancomycin (*vanA* or *vanB*)	Negative	Positive	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *HLR=High Level Resistance.

RESULTS AND COMMENTS

As in previous years, enterococci were analysed both as a genus and separately for *E. faecalis* and *E. faecium*. The results for each species are microbiologically more valid as resistance rates differ significantly between *E. faecalis* and *E. faecium*. However, overall rates of resistance are of interest when formulating empirical treatment strategies because they include the probability of systemic infections with each enterococcal species. The overall results for enterococci are presented in Table 88. Surveillance in NORM 2025 included 551 (70.8%) *E. faecalis* isolates (68.4% in 2024), 195 (25.0%) *E. faecium* isolates (26.7% in 2024), and 33 (4.2%) isolates unspeciated or belonging to other species (4.9% in 2024). The ratio of *E. faecalis* to *E. faecium* isolates has declined in many countries but has remained stable in Norway around 2.5 over the last years (2.8 in 2025). The EUCAST/NordicAST breakpoints for piperacillin-tazobactam and imipenem are only valid for *E.*

faecalis, whereas vancomycin breakpoints are only valid for *E. faecalis* and *E. faecium*.

E. faecalis was universally susceptible to ampicillin (Table 89). The results for piperacillin-tazobactam and imipenem closely mirrored those of ampicillin, but wild type *E. faecalis* is only susceptible to increased exposure to these agents. The prevalence of resistance to ampicillin in *E. faecium* was 77.9% in 2025 compared to 77.0% in 2024 (Table 90). The prevalence of high-level gentamicin resistance (HLGR) in *E. faecalis* was 4.9% in 2025, which is a slight decrease from 6.4% in 2023 and 6.2% in 2024 (Figure 106). The prevalence of HLGR in *E. faecium* remained unchanged at 43.1% in 2025 compared to 43.4% in 2024. Practically all HLGR *E. faecium* isolates (83/84) were also resistant to ampicillin. Conversely, 83/152 (54.6%) ampicillin resistant *E. faecium* isolates displayed HLGR. High-level gentamicin resistance in enterococci is of great concern as it abolishes the bactericidal synergy between aminoglycosides and beta-lactams often used for treatment of severe enterococcal infections.

Transferrable vancomycin resistance has not yet become endemically established in clinical enterococcal isolates in Norway, but recent outbreaks have occurred in different parts of the country. No *E. faecalis* or *E. faecium* blood culture isolates were reported as vancomycin resistant in NORM in 2025, but nine isolates of other enterococcal species (five *E. casseliflavus* and four *E. gallinarum*) displayed phenotypical vancomycin resistance compatible with their chromosomally encoded *vanC* genotype. Two *E. faecium* isolates (1.0%) were phenotypically resistant to linezolid and harboured G2576T mutations. Twelve *E. faecalis* isolates (2.2%) were tigecycline resistant.

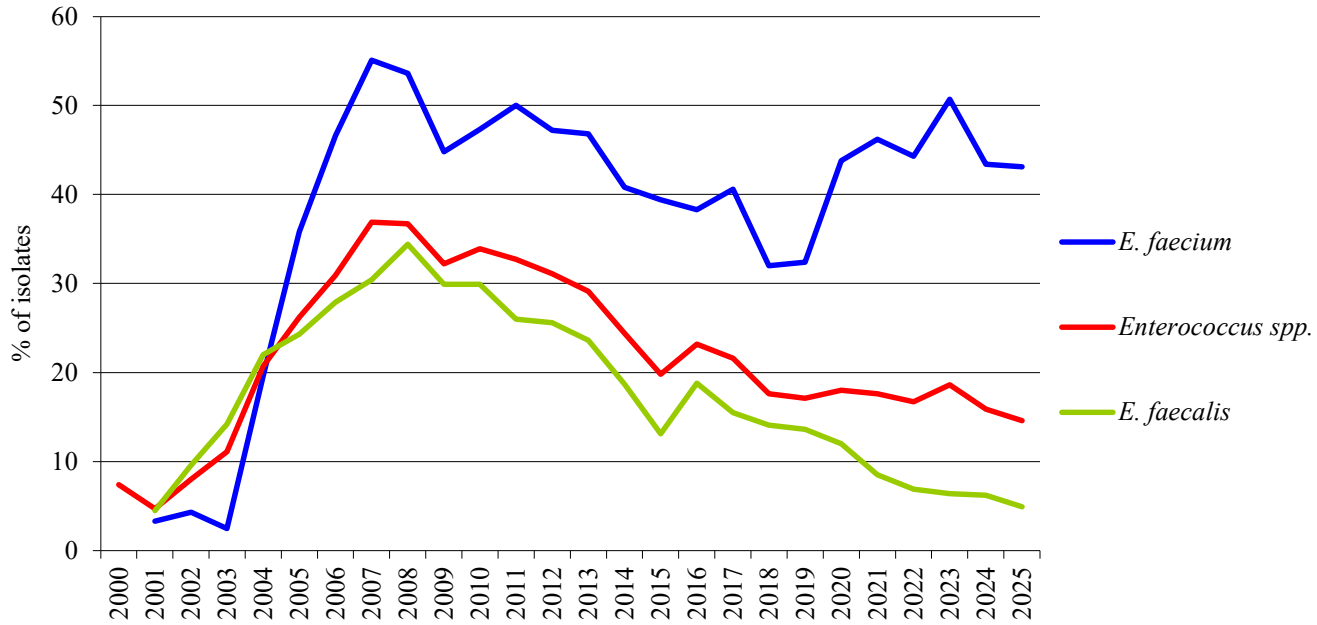

FIGURE 106. Prevalence of high-level resistance to gentamicin in blood culture isolates of *Enterococcus faecalis*, *E. faecium* and all enterococci combined during 2000-2025. The breakpoint was decreased from R ≥ 1,024 mg/L to R > 128 mg/L in 2004.

Enterococcus spp. in urine

TABLE 91. *Enterococcus* spp. urinary tract isolates in 2025 (n=915), except for piperacillin-tazobactam and nitrofurantoin (n=819) where 96 enterococcal isolates not identified as *E. faecalis* are excluded due to lack of breakpoints, and for vancomycin, trimethoprim and trimethoprim-sulfamethoxazole (n=883) where 32 isolates not identified as *E. faecalis* or *E. faecium* are excluded due to lack of breakpoints. Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 4	> 4	93.4	-	6.6
Piperacillin-tazobactam	≤ 0.001	> 16	0.0	99.5	0.5
Gentamicin HLR*	≤ 128	> 128	90.6	-	9.4
Ciprofloxacin**	≤ 4	> 4	89.7	-	10.3
Linezolid	≤ 4	> 4	99.7	-	0.3
Tigecycline	≤ 0.5	> 0.5	99.0	-	1.0
Nitrofurantoin	≤ 64	> 64	99.4	-	0.6
Trimethoprim**/***	≤ 1	> 1	83.3	-	16.7
Trimethoprim-sulfamethoxazole***	≤ 1	> 1	88.6	-	11.4
Vancomycin	≤ 4	> 4	100.0	-	0.0
Vancomycin (*vanA* or *vanB*)	Negative	Positive	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *HLR=High Level Resistance. **Breakpoints for uncomplicated urinary tract infections. ***Cut-off for detection of acquired resistance mechanisms.

TABLE 92. *Enterococcus faecalis* urinary tract isolates in 2025 (n=819). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 4	> 4	100.0	-	0.0
Piperacillin-tazobactam	≤ 0.001	> 16	0.0	99.5	0.5
Gentamicin HLR*	≤ 128	> 128	93.7	-	6.3
Ciprofloxacin**	≤ 4	> 4	96.1	-	3.9
Linezolid	≤ 4	> 4	99.6	-	0.4
Tigecycline	≤ 0.5	> 0.5	98.9	-	1.1
Nitrofurantoin	≤ 64	> 64	99.4	-	0.6
Trimethoprim**/***	≤ 1	> 1	86.7	-	13.3
Trimethoprim-sulfamethoxazole***	≤ 1	> 1	92.2	-	7.8
Vancomycin	≤ 4	> 4	100.0	-	0.0
Vancomycin (*vanA* or *vanB*)	Negative	Positive	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *HLR=High Level Resistance. **Breakpoints for uncomplicated urinary tract infections. ***Cut-off for detection of acquired resistance mechanisms.

TABLE 93. *Enterococcus faecium* urinary tract isolates in 2025 (n=64). Sampling, laboratory methods, and data handling are described in Appendix 5. Distributions of zone diameters are available at www.antibiotikaresistens.no.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Ampicillin	≤ 4	> 4	7.8	-	92.2
Gentamicin HLR*	≤ 128	> 128	53.1	-	46.9
Ciprofloxacin**	≤ 4	> 4	6.2	-	93.8
Linezolid	≤ 4	> 4	100.0	-	0.0
Tigecycline	≤ 0.5	> 0.5	100.0	-	0.0
Trimethoprim**/***	≤ 1	> 1	42.2	-	57.8
Trimethoprim-sulfamethoxazole***	≤ 1	> 1	45.3	-	54.7
Vancomycin	≤ 4	> 4	100.0	-	0.0
Vancomycin (*vanA* or *vanB*)	Negative	Positive	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *HLR=High Level Resistance. **Breakpoints for uncomplicated urinary tract infections. ***Cut-off for detection of acquired resistance mechanisms.

RESULTS AND COMMENTS

Enterococcal urinary tract isolates have previously been surveyed in NORM in 2001, 2010, 2015 and 2018. The results from 2001 were not stratified by species, and the breakpoints have changed considerably over the years. Comparisons over time are therefore of limited value. Since 2018, the breakpoint for resistance to ampicillin has been reduced from R > 8 mg/L to R > 4 mg/L, thus eliminating the I category. Tigecycline has been added to the panel, and both trimethoprim and trimethoprim-sulfamethoxazole have gained cut-off values corresponding to the presence of acquired resistance mechanisms > 1 mg/L.

The proportion of *E. faecalis* isolates was significantly higher among urinary tract isolates (89.5%) than in blood cultures (70.8%), but lower than in the 2018 urine samples (94.5%). The proportion of *E. faecium* was correspondingly lower in urine (7.0% in urine versus 25.0% in blood cultures), and there were relatively few enterococcal isolates from urine that were either unspeciated or belonged to species other than *E. faecalis* and *E. faecium* (3.5%).

E. faecalis isolates from urine were uniformly susceptible to ampicillin, and almost all isolates were also susceptible to increased exposure (I) of piperacillin-tazobactam (99.5%), corresponding to the wild type. The prevalence of high-level gentamicin resistance (HLGR) among *E. faecalis* isolates from urine (6.3%) was at the same level as in blood cultures (4.9%), but significantly lower than in 2018 urinary tract isolates (14.0%).

The rate of ampicillin resistance among *E. faecium* urine isolates (92.2%) was even higher than in blood culture isolates (77.9%), and it has increased since 2018 (80.8%). The prevalence of *E. faecium* high-level gentamicin resistance has apparently increased from 2018 (9.6%) to 2025 (46.9%), but the number of isolates is limited. Similarly, the prevalence of resistance to ciprofloxacin is much higher in *E. faecium* (72.5% in 2018; 93.8% in 2025) than in *E. faecalis* (8.4% in 2018; 3.9% in 2025). Ciprofloxacin breakpoints are only valid for uncomplicated urinary tract infections.

The clinical benefit of trimethoprim and trimethoprim-sulfamethoxazole in the treatment of enterococcal urinary tract infections is uncertain. According to the ecological cut-off value (ECOFF) issued by EUCAST, 13.3% of *E. faecalis* and 57.8% of *E. faecium* isolates displayed zone diameters > 1 mg/L. The corresponding rates for trimethoprim-sulfamethoxazole were 7.8% for *E. faecalis* and 54.7% for *E. faecium.* Almost all *E. faecalis* isolates (99.4%) were susceptible to nitrofurantoin, but this agent is not suitable for treatment of *E. faecium* infections. Practically all isolates remained phenotypically susceptible to tigecycline (99.0%) and linezolid (99.7%), although three *E. faecalis* isolates were linezolid resistant and contained *optrA* determinants (two *optrA*-15 and one *optrA*-7). All isolates were susceptible to vancomycin and thus, no cases of transferable vancomycin resistance were detected.

Vancomycin resistant enterococci and linezolid resistant enterococci in Norway 2025

Vancomycin resistant enterococci

Vancomycin resistance in enterococci is caused by gene clusters that contribute to altering the peptide side chain termini that are important for cross-linking in the cell wall, thereby preventing vancomycin from binding to them (1). To date, 10 different gene clusters are known in enterococci (*vanA*, *vanB*, *vanC*, *vanD*, *vanE*, *vanG*, *vanL*, *vanM*, *vanN* and *vanP*), of which *vanC* is intrinsic to *Enterococcus casseliflavus* and *Enterococcus gallinarum*. The other gene clusters are considered acquired and most frequently detected in *Enterococcus faecalis* and *Enterococcus faecium* associated with mobile genetic elements such as plasmids and integrative conjugative elements (2).

In Europe, a concerning increase in vancomycin resistant *E. faecium* in invasive isolates was observed from 2016 to 2020 (3). In Norway, the incidence of VRE (including linezolid resistant VRE (LVRE)) has fluctuated since 2010 due to intermittent outbreaks. Between 2021 and 2025 the incidence has ranged from 0.6 to 4.4 per 100,000 person-years, peaking in 2024 and declining to 1.8 in 2025. In 2025, 101 individuals with VRE (including LVRE) were registered in the Norwegian Surveillance System for Communicable Diseases (MSIS), a decrease of 139 (58%) cases compared with 2024. Five 2025 isolates were LVRE (Figure 107), of which three were also resistant to ampicillin and high levels of gentamicin. The Norwegian Centre for Detection of Antimicrobial Resistance (K-res) performed whole-genome sequencing (WGS) of 102/106 VRE (96%) isolates from 2025. This therefore does not provide a complete national overview.

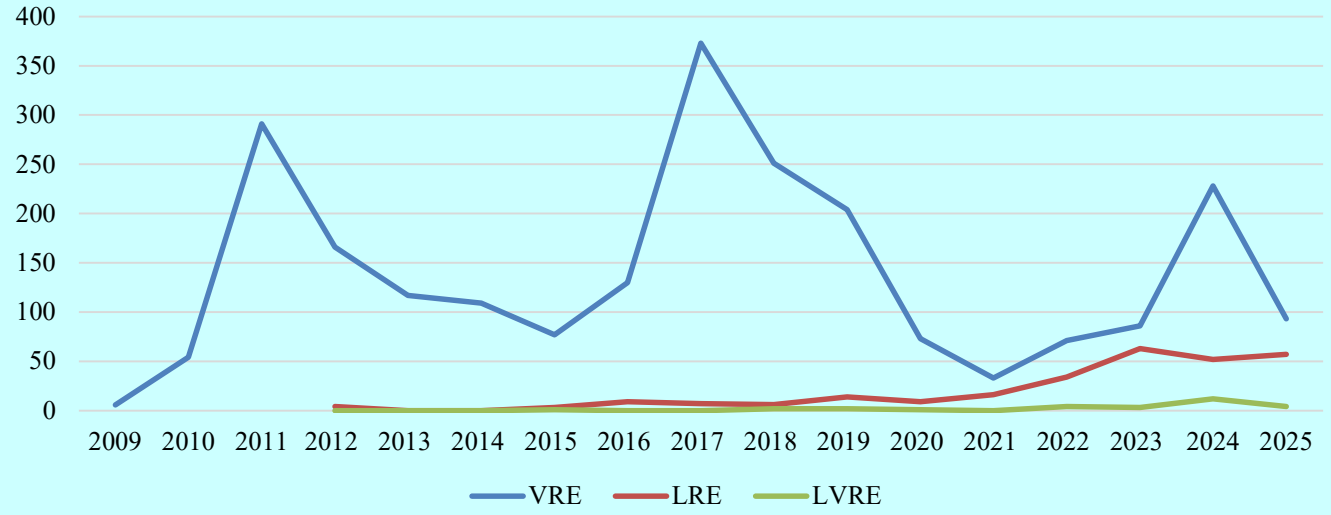

FIGURE 107. Number of persons with vancomycin resistant (VRE), linezolid resistant (LRE), and both vancomycin and linezolid resistant (LVRE) enterococci in Norway, 2009-2025. VRE data from MSIS and LRE+LVRE data from K-res.

WGS revealed a dominance of *E. faecium* with *vanA* (n=80) and *vanB* (n=12), but also *vanA* (n=3) and *vanB* (n=2) *E. faecalis*, as well as *vanA Enterococcus avium* (n=3), *vanA Enterococcus raffinosus* (n=1), and *E. gallinarum* (n=1) carrying both *vanA* and intrinsic *vanC* (Figure 108). Globally, VRE is also dominated by *E. faecium*, and *vanA* is more common than *vanB* (2).

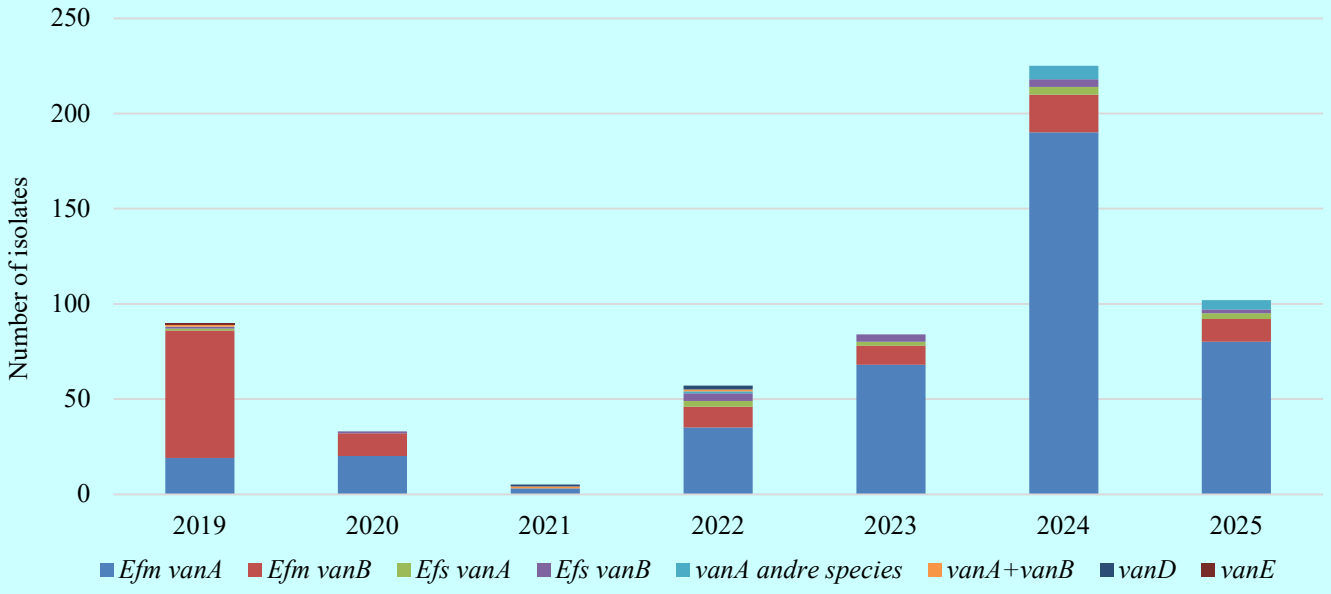

FIGURE 108. Distribution of species and genotype in Norwegian VRE isolates for which K-res has whole-genome sequencing data from 2019-2025. Also includes LVRE. *Efm* = *E. faecium*, *Efs* = *E. faecalis*.

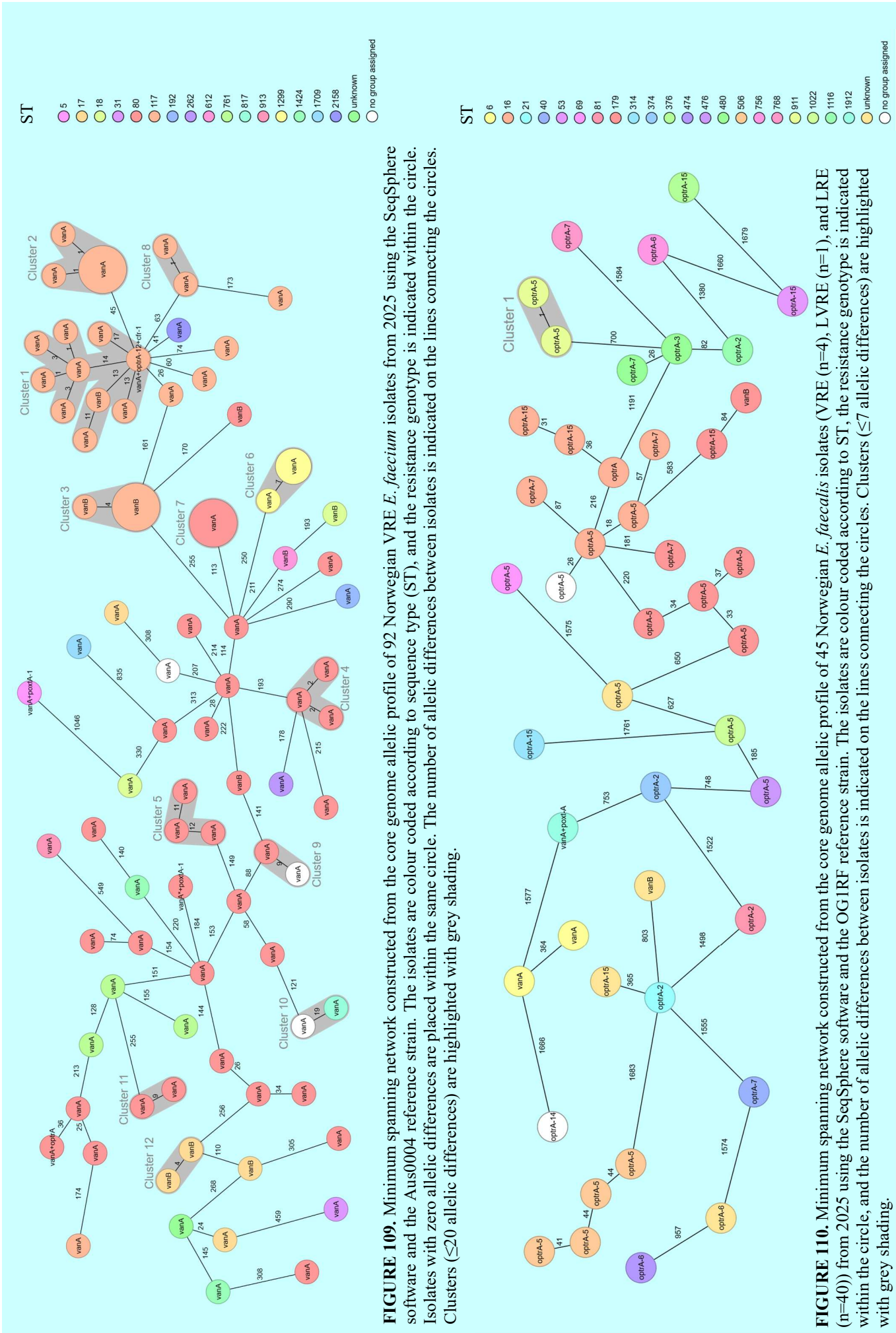

FIGURE 109. Minimum spanning network constructed from the core genome allelic profile of 92 Norwegian VRE *E. faecium* isolates from 2025 using the SeqSphere software and the Aus0004 reference strain. The isolates are colour coded according to sequence type (ST), and the resistance genotype is indicated within the circle. Isolates with zero allelic differences are placed within the same circle. The number of allelic differences between isolates is indicated on the lines connecting the circles. Clusters (≤20 allelic differences) are highlighted with grey shading.

FIGURE 110. Minimum spanning network constructed from the core genome allelic profile of 45 Norwegian *E. faecalis* isolates (VRE (n=4), LVRE (n=1), and LRE (n=40)) from 2025 using the SeqSphere software and the OG1RF reference strain. The isolates are colour coded according to ST, the resistance genotype is indicated within the circle, and the number of allelic differences between isolates is indicated on the lines connecting the circles. Clusters (≤7 allelic differences) are highlighted with grey shading.

We identified 16 different sequence types (STs) of *E. faecium* in 2025, as well as three isolates with unknown sequence type (Figure 109). The majority (n=86/92; 93%) of the *E. faecium* isolates belonged to known hospital adapted clones (ST17, ST18, ST31, ST80, ST117, ST192, ST262, ST612, ST761, ST817, ST1299, ST1424, ST2158, and ST2860) that are found in many countries. For *E. faecalis*, three different sequence types as well as one unknown sequence type were recorded in 2025 (Figure 110). Two of five *E. faecalis* VRE isolates were ST6, which is often associated with clinical isolates and hospitals (4).

Twelve clusters containing two to nine isolates of ST17, ST80, ST117, ST817 and ST1299 *E. faecium* were identified (Figure 109). No clusters of VRE *E. faecalis* were observed (Figure 110). Six *E. faecium* clusters contained isolates with a possible epidemiological link (*vanA* ST117 cluster 1 (n=9), *vanA* ST117 cluster 2 (n=7), *vanA* ST80 cluster 4 (n=3), *vanA* ST1299 cluster 6 (n=3), *vanA* ST80 cluster 7 (n=3), and *vanA* ST80 cluster 11 (n=2) in Figure 109) and were therefore considered domestic outbreaks. All these outbreaks included isolates from the South-Eastern health region, and one of the outbreaks (cluster 1) has been ongoing since 2023. The remaining six *E. faecium* clusters contained two to four isolates not closely linked in time and/or place and/or associated with import, thus not considered domestic outbreaks.

Known hospital-adapted clones of *E. faecium* can typically survive in the hospital environment for extended periods, and patient mobility between hospitals can also make it difficult to determine which isolates belong to a specific outbreak. Studies from the Public Health Laboratory in Melbourne, Australia (5) support the use of a three-month window in genomic outbreak analyses of *E. faecium*, an approach applied at K-res. A total of 87 (85%) VRE 2025 isolates were screening isolates. Of these, only 28 (27%) were related to outbreaks and domestic transmission, while 57 (56%) of the VRE isolates were associated with known import.

Conclusion

A total of 101 individuals with VRE (including linezolid resistant VRE) were reported to MSIS in 2025 - a 58% decrease compared with 2024 and a decline in annual incidence from 4.4 to 1.8 per 100,000 person-years. K-res generated WGS data for 102 of 106 VRE isolates from 2025. The majority were *E. faecium* with *vanA*, followed by *E. faecium* with *vanB* of which (93%) belonged to global hospital-adapted clones. Most cases (85%) originated from screening samples. Six domestic outbreaks involving two to nine *E. faecium vanA* isolates (ST117, ST80 and ST1299) were recorded in the South-Eastern health region. One of the outbreaks has been ongoing since 2023 (ST117). Of the WGS-analysed VRE cases, 27% were linked to domestic transmission and 56% to known import, while the remaining lacked a confirmed epidemiological source.

Linezolid resistant enterococci

Linezolid binds to the ribosome and inhibits bacterial protein synthesis. Mutational based changes in ribosomal RNA and ribosomal proteins can prevent linezolid from binding. Another resistance mechanism is caused by genes (*optrA* and *poxtA/poxtA-Ef*) that encode proteins protecting the ribosome from linezolid binding. Both *optrA* and *poxtA* may be located on mobile genetic elements (6-8). Mutational based resistance most often occurs following linezolid treatment. The most common chromosomal mutation causing linezolid resistance is G2576T, affecting the 23S rRNA domain V. Most species have more than one copy of the 23S rRNA gene in their genome, and the level of resistance correlates with the number of copies carrying the mutation (9).

A global increase in LRE cases has been observed in recent years. However, the proportion remains low; 2.2% in *E. faecalis* and 1.1% in *E. faecium* (10). In Norway, an increase in LRE (including LVRE) has also been observed recently, peaking in 2023 (Figure 111) corresponding to an incidence of 1.2 per 100,000 person-years. In 2025, K-res received isolates from 61 individuals with LRE (including LVRE) in Norway, equivalent to an annual incidence of 1.1 per 100,000 person-years. This is three fewer (a 5% decrease) compared with 2024 (Figure 111). One individual had two different LRE isolates. Most 2025 LRE (n=46/62; 74%) originated from infections, which probably reflects that routine screening is not established. The majority of the infection isolates (n=41/62; 66%) belonged to *E. faecalis*.

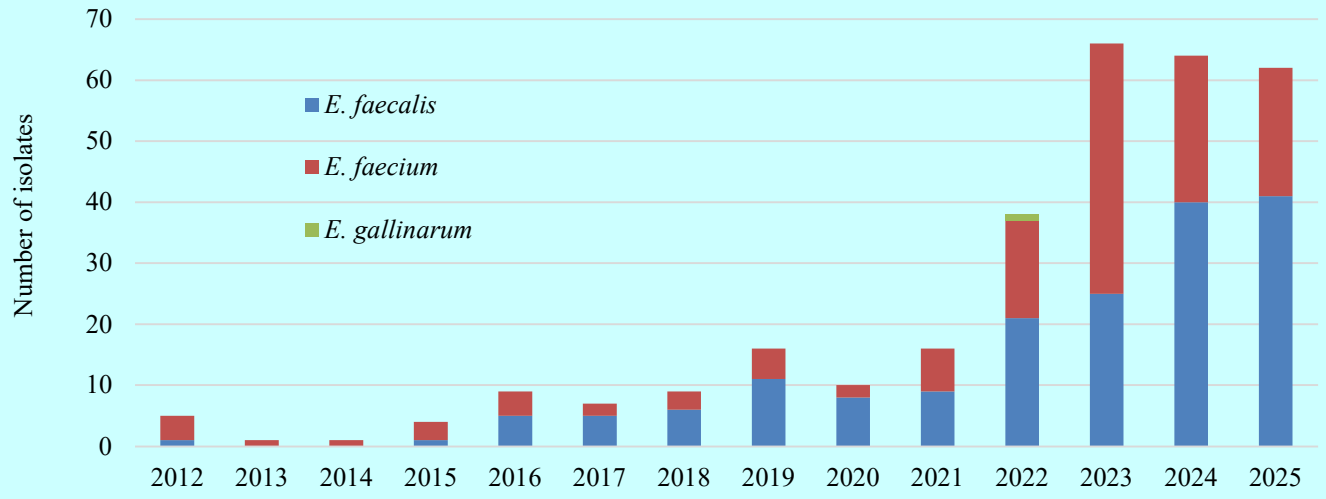

FIGURE 111. Number of linezolid resistant *E. faecium*, *E. faecalis*, and *E. gallinarum* in Norway, 2012-2025. The overview also includes LRE that are vancomycin resistant.

Mutational based chromosomal resistance, mainly the G2576T mutation in 23S rDNA, has traditionally been the dominant resistance mechanism against linezolid. It is known to arise following prolonged exposure to linezolid (11). In 2025, 21 linezolid resistant *E. faecium* isolates were detected, of which 13 had a mutational based resistance mechanism, six carried *optrA*, and two carried *poxtA*. Among the *E. faecalis* isolates (n=41), 40 carried *optrA* and one isolate carried *poxtA-Ef* (Table 94).

The clinical LRE isolates from 2025 (n=46) comprised 33 *optrA*-positive *E. faecalis*, 11 *E. faecium* with mutational based resistance, and two *optrA*-positive *E. faecium*. Carriage isolates (n=16) consisted of *E. faecalis* with *optrA* (n=7) or *poxtA-Ef* (n=1), and *E. faecium* with *optrA* (n=4), *poxtA* (n=2), or mutational based resistance (n=2). Twelve isolates were associated with known import, while epidemiological source information was unavailable for 40 isolates.

Most *E. faecium* isolates (n=18) belonged to known hospital associated sequence types (ST17, ST80, ST117, and ST1353). The *E. faecalis* isolates (n=41) belonged to 22 different STs, while three isolates had unknown STs. ST16, ST179, ST480, ST506, and ST911 were detected in two or more isolates (Table 94).

TABLE 94. Species, resistance mechanism, and sequence type among LRE isolates in Norway, 2025.

Species	Resistance mechanism	ST
E. faecalis (n=41)	*optrA* (n=40)	ST16 (n=7); ST179 (n=6); ST506 (n=4); ST480 (n=2); ST911 (n=2); ST21 (n=1); ST40 (n=1); ST53 (n=1); ST69 (n=1); ST81 (n=1); ST314 (n=1); ST374 (n=1); ST376 (n=1); ST474 (n=1); ST476 (n=1); ST756 (n=1); ST768 (n=1); ST1022 (n=1); ST1116 (n=1); ST2047(n=1); ST2050(n=1); unknown ST (n=3)
	poxtA-Ef (n=1)	ST1912 (n=1)
E. faecium (n=21)	23S rRNA G2576U mutation (n=13)	ST17 (n=10); ST80 (n=3)
	optrA (n=6)	ST80 (n=2); ST117 (n=1); ST1353 (n=1); unknown ST (n=2)
	poxtA (n=2)	ST5 (n=1); ST80 (n=1)

In 2025, three LRE outbreaks were identified. WGS showed two clustered ST911 *optrA*-positive *E. faecalis* isolates from the Central health region, for which an epidemiological link was also identified (Cluster 1 in Figure 110). The phylogenetic analyses also revealed two clusters of *E. faecium* carrying the G2576T mutation (ST17 n=11 cluster 1 and ST80 n=2 cluster 2) (Figure 112) from the South-Eastern health region, where epidemiological links were also identified. Two of the outbreaks have been ongoing since 2022 (*E. faecium* ST17) and 2024 (*E. faecium* ST80).

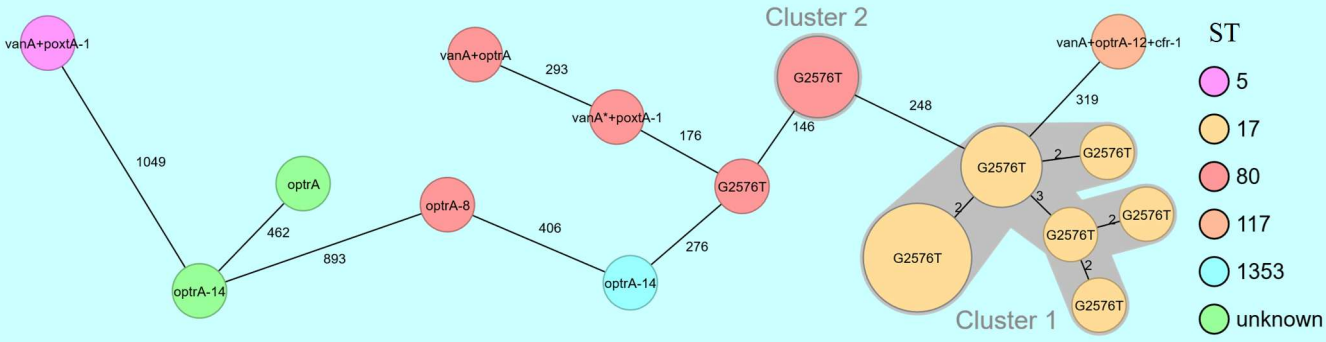

FIGURE 112. Minimum spanning network constructed from the core genome allelic profile of 21 Norwegian LRE *E. faecium* isolates from 2025 using the *SeqSphere* software and the Aus0004 reference strain. The isolates are colour coded according to ST, and the resistance genotype is indicated within the circle. Isolates with zero allelic differences are placed within the same circle. The number of allelic differences between isolates is indicated on the lines connecting the circles. Clusters with ≤20 allelic differences are highlighted with grey shading.

Conclusion

In 2025, K-res received LRE isolates from 61 persons (including vancomycin resistant LRE) in Norway, corresponding to an incidence of 1.1 per 100,000 person-years. This represents a 5% decrease from 2024. Most 2025 LRE isolates originated from infections (n=46/62; 74%). The majority of LRE isolates were *E. faecalis* carrying *optrA* (n=40), followed by *E. faecium* with mutational based resistance (n=13). Phylogenetic analyses and epidemiological data show that there were three LRE clusters in 2025. Two *E. faecium* clusters represented domestic outbreaks in the South-Eastern health region, while the *E. faecalis* cluster represented a domestic outbreak in the Central health region. The two *E. faecium* outbreaks have been ongoing since 2022 (ST17) and 2024 (ST80).

References

1. Courvalin P. Vancomycin resistance in gram-positive cocci. Clin Infect Dis. 2006;42 Suppl 1:S25-34.
2. Hegstad K, Samuelsen Ø, Hegstad J, Sundsfjord A, Molecular methods for detection of antibacterial resistance genes: rationale and applications. In: Amsterdam D, editor. Antibiotics in laboratory medicine. 6th ed: Wolters Kluver; 2015; p. 408-49.
3. European Centre for Disease Control and Prevention and World Health Organization Regional Office for Europe. Antimicrobial resistance surveillance in Europe - 2020 data. Stockholm: ECDC. 2022.
4. Pöntinen AK, Top J, Arredondo-Alonso S, Tonkin-Hill G, Freitas AR, Novais C, *et al*. Apparent nosocomial adaptation of *Enterococcus faecalis* predates the modern hospital era. Nat Commun. 2021;12(1):1523.
5. Gorrie CL, Da Silva AG, Ingle DJ, Higgs C, Seemann T, Stinear TP, *et al*. Key parameters for genomics-based real-time detection and tracking of multidrug-resistant bacteria: a systematic analysis. Lancet Microbe. 2021;2(11):e575-e83.
6. Bender JK, Cattoir V, Hegstad K, Sadowy E, Coque TM, Westh H, *et al*. Update on prevalence and mechanisms of resistance to linezolid, tigecycline and daptomycin in enterococci in Europe: Towards a common nomenclature. Drug Resist Updates. 2018;40:25-39.
7. Sadowy E. Linezolid resistance genes and genetic elements enhancing their dissemination in enterococci and streptococci. Plasmid. 2018;99:89-98.
8. Brenciani A, Fioriti S, Morroni G, Cucco L, Morelli A, Pezzotti G, *et al*. Detection in Italy of a porcine *Enterococcus faecium* isolate carrying the novel phenicol-oxazolidinone-tetracycline resistance gene *poxtA*. J Antimicrob Chemother. 2019;74(3):817-8.
9. Marshall SH, Donskey CJ, Hutton-Thomas R, Salata RA, Rice LB. Gene dosage and linezolid resistance in *Enterococcus faecium* and *Enterococcus faecalis*. Antimicrob Agents Chemother. 2002;46(10):3334-6.
10. Dadashi M, Sharifian P, Bostanshirin N, Hajikhani B, Bostanghadiri N, Khosravi-Dehaghi N, *et al*. The global prevalence of daptomycin, tigecycline, and linezolid-resistant *Enterococcus faecium* strains from human clinical samples: A systematic review and meta-analysis. Front Med. 2021;8:720647.
11. Pai MP, Rodvold KA, Schreckenberger PC, Gonzales RD, Petrolatti JM, Quinn JP. Risk factors associated with the development of infection with linezolid- and vancomycin-resistant *Enterococcus faecium*. Clin Infect Dis. 2002;35(10):1269-72.

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Streptococcus pneumoniae in blood cultures and cerebrospinal fluids

TABLE 95. *Streptococcus pneumoniae* in blood cultures and cerebrospinal fluids in 2025 (n=783). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G*	≤ 0.06	> 1	92.2	7.0	0.8
Cefotaxime*	≤ 0.5	> 2	99.1	0.9	0.0
Ceftriaxone*	≤ 0.5	> 2	99.0	1.0	0.0
Erythromycin	≤ 0.25	> 0.25	94.5	-	5.5
Clindamycin	≤ 0.5	> 0.5	96.2	-	3.8
Tetracycline	≤ 1	> 1	93.6	-	6.4
Trimethoprim-sulfamethoxazole**	≤ 1	> 1	90.2	-	9.8

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than endocarditis and meningitis. **Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

TABLE 96. *Streptococcus pneumoniae* in blood cultures and cerebrospinal fluids in 2025 (n=783). Distribution (%) of MICs (mg/L).

	≤0.008	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	≥ 128
Penicillin G*	5.6	33.8	49.9	2.8	0.6	3.8	2.2	0.4	0.3	0.5					
Cefotaxime*	2.2	46.2	41.9	3.7	3.1	1.3	0.8	0.5	0.4						
Ceftriaxone*	0.1	8.9	78.8	4.5	4.1	1.3	1.3	0.5	0.5						
Erythromycin			17.8	73.8	2.9		0.1		0.3	0.3	0.8	0.6	0.1		3.3
Clindamycin			3.6	61.9	30.7				0.1			0.2	0.3	0.3	3.1
Tetracycline				0.4	17.5	67.3	8.3	0.1	0.3	0.5	0.4	0.8	2.5	2.0	
TMS**				0.3	29.2	53.8	3.8	3.1	1.9	3.2	4.0	0.8			
Chloramph.								0.6	37.8	60.5	0.5	0.5			
Norfloxacin								0.1	0.8	10.0	57.5	27.6	4.1		

Shaded areas in each row indicate susceptibility with standard exposure (light), susceptibility with increased exposure (medium) and resistance (dark). Non-shaded cells represent MIC values that are not covered by the standard test method and antibiotics without defined breakpoints. *Breakpoints for indications other than endocarditis and meningitis. **Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

RESULTS AND COMMENTS

All systemic *S. pneumoniae* isolates in Norway are submitted to the National Reference Laboratory for Pneumococci at the Norwegian Institute of Public Health. The EUCAST/NordicAST penicillin G resistance breakpoint for infections other than endocarditis and meningitis was reduced from R > 2 mg/L to R > 1 mg/L in 2025, and all comparisons with previous results have been adjusted accordingly. Similarly, the breakpoint for resistance to trimethoprim-sulfamethoxazole was reduced from R > 2 mg/L to R > 1 mg/L in 2026, and previous results are categorised using the new breakpoint. Breakpoints for chloramphenicol are no longer applicable, and norfloxacin screening for quinolone resistance is only validated using disk diffusion. For both agents, MIC distributions are presented without categorisation. The oxacillin screening disk was not used in the NORM 2025 protocol. The number of pneumococcal isolates was significantly reduced during the pandemic years 2020-2021 but has now returned to pre-pandemic levels.

The results are summarised in Tables 95-96 and Figures 113-114. Twenty-one strains were isolated from cerebrospinal fluids and 16/21 were concomitantly retrieved from blood cultures. Both blood culture isolates and isolates from cerebrospinal fluids were included from patients with positive cultures from both specimen types. The results for penicillin G, cefotaxime and ceftriaxone were interpreted according to the general breakpoints for pneumococci. The isolates from cerebrospinal fluids were in addition categorised according to the breakpoints for endocarditis and meningitis (penicillin G R > 0.06 mg/L, cefotaxime and ceftriaxone both R > 0.5 mg/L).

A total of 7.0% (55/783) of *S. pneumoniae* isolates were only susceptible to increased penicillin G exposure (MIC 0.125-1 mg/L), and six isolates (0.8%) were classified as resistant (MIC > 1 mg/L). The rates of susceptibility only to increased penicillin G exposure (I) have fluctuated over the years, and this may in part be due to technical issues. The 7.0% prevalence recorded in 2025 is an increase from 5.6% in 2024 but at the same level as 7.4% in 2023. One cerebrospinal fluid isolate was resistant to penicillin G (MIC 1 mg/L) as well as cefotaxime and ceftriaxone (both 1 mg/L) according to meningitis breakpoints. Six additional cerebrospinal isolates were resistant to penicillin G (MIC 0.25-0.5 mg/L) but remained susceptible to cephalosporins. Six penicillin resistant blood culture isolates (MIC 2-4 mg/L) were only susceptible to increased cefotaxime and ceftriaxone exposure (MIC 1-2 mg/L), but none of them were classified as cephalosporin resistant. Forty-eight blood culture isolates were susceptible only to increased penicillin G exposure (0.125-1 mg/L), and one of them was also susceptible only to increased ceftriaxone exposure (MIC 1 mg/L).

The prevalence of erythromycin resistance decreased from 6.0% in 2024 to 5.5% in 2025 (Figure 113). Most of these isolates (30/43) were resistant to both erythromycin and clindamycin, which is compatible with a constitutive MLS_B phenotype. The remaining 13 isolates displayed low-level resistance to erythromycin and were susceptible to clindamycin, as seen in efflux-mediated M-type resistance. Double disk diffusion tests were not performed. The distribution of MLS_B phenotypes was not significantly altered from previous years. The results may suggest a continuing predominance of *erm*-encoded macrolide resistance as opposed to the *mef*-dominated peak 2002-2009 (Figure 114).

Resistance rates for trimethoprim-sulfamethoxazole are relatively stable around 10% (9.8% in 2025) according to the new breakpoint of R > 1 mg/L. The prevalence of tetracycline resistance remained essentially unchanged at 6.4% compared to 7.3% in 2024 (Figure 113). The vast majority of isolates (> 99%) apparently belonged to the wild type distribution for chloramphenicol, but clinical breakpoints for this antibiotic are no longer available. The low prevalence of high-level norfloxacin resistance (Table 96) may reflect the limited use of levofloxacin and moxifloxacin for respiratory tract infections in Norway.

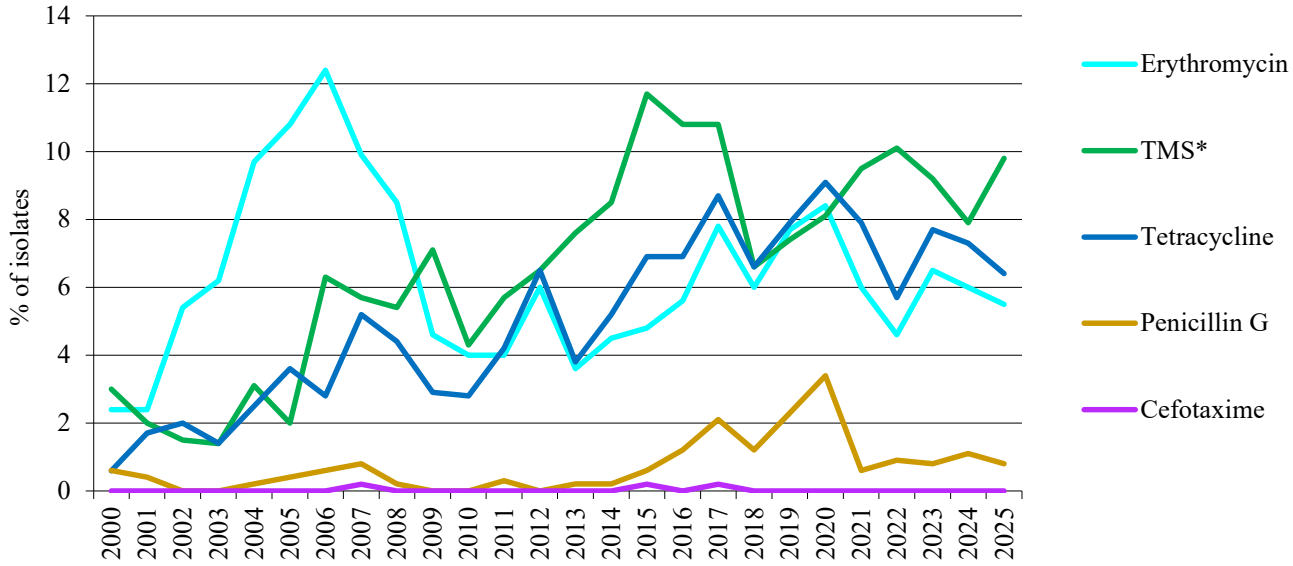

FIGURE 113. Prevalence (%) of resistance to antimicrobial agents in *Streptococcus pneumoniae* blood culture and cerebrospinal fluid isolates during 2000-2025. Doxycycline was substituted by tetracycline in 2005. *TMS=Trimethoprim-sulfamethoxazole.

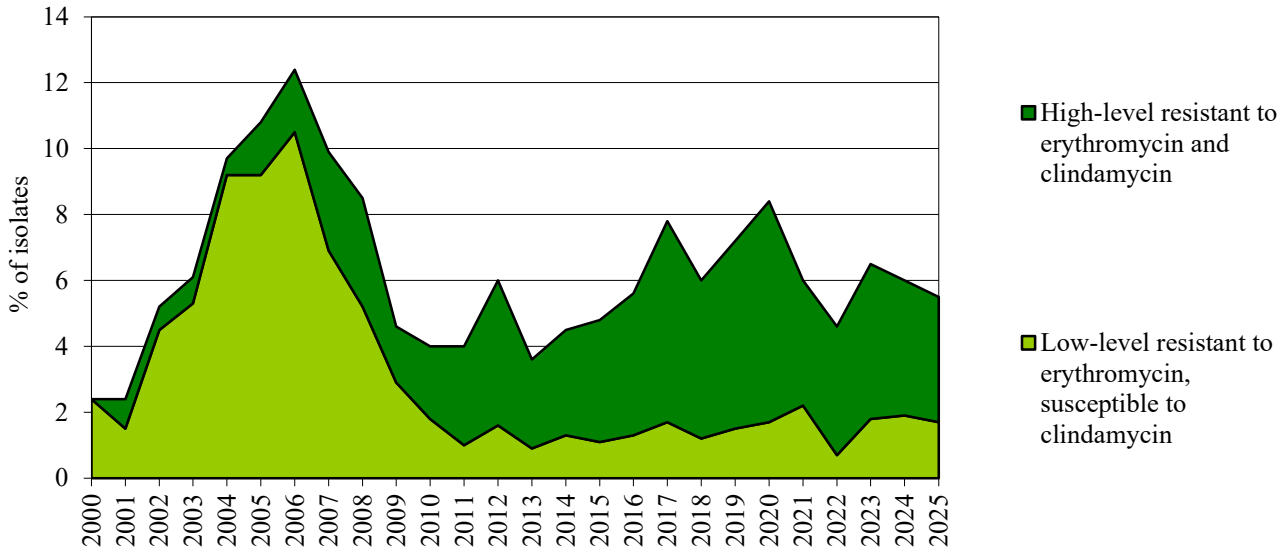

FIGURE 114. Prevalence of resistance (%) to erythromycin and clindamycin in *Streptococcus pneumoniae* blood culture isolates during 2000-2025.

Streptococcus pneumoniae in respiratory tract specimens

TABLE 97. *Streptococcus pneumoniae* in respiratory tract specimens in 2025 (n=256). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G*	≤ 0.06	> 1	84.3	14.1	1.6
Erythromycin	≤ 0.25	> 0.25	88.3	-	11.7
Clindamycin	≤ 0.5	> 0.5	94.9	-	5.1
Tetracycline	≤ 1	> 1	88.3	-	11.7
Trimethoprim-sulfamethoxazole**	≤ 1	> 1	87.9	-	12.1
Linezolid	≤ 2	> 2	99.6	-	0.4
Rifampicin	≤ 0.125	> 0.125	99.6	-	0.4
Norfloxacin screen	≥ 10 mm	< 10 mm	98.4	-	1.6

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than endocarditis and meningitis. **Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

RESULTS AND COMMENTS

S. pneumoniae isolates from respiratory tract specimens were last surveyed in NORM in 2023. The EUCAST/ NordicAST breakpoint for resistance to trimethoprim-sulfamethoxazole was reduced from R > 2 mg/L to R > 1 mg/L in 2026, and all previous results have been adjusted accordingly. Also, the analyses in 2025 were shifted from MIC gradient strips to disk diffusion, and results are therefore interpreted according to EUCAST recommend-dations for this method. The rates of resistance to various antimicrobials are shown in Table 97 and Figure 115.

Oxacillin screening identified 40/256 isolates (15.6%) as either resistant (R) or susceptible to increased exposure (I) for penicillin G. By use of the penicillin G screening disk, 36/256 isolates (14.1%) were classified as I and 4/256 (1.6%) as R. In 2023 15% of isolates were classified as I and none as R for penicillin G. The penicillin G screening disk is more sensitive for detecting penicillin resistance, which could explain the slight increase in resistant isolates. In addition, the EUCAST/NordicAST penicillin G resistance breakpoint for infections other than endocarditis and meningitis was reduced from R > 2 mg/L to R > 1 mg/L in 2024/2025. Furthermore, a zone diameter for oxacillin < 9 mm suggested broader resistance to penicillins and cefalosporins in 11 isolates (4.3%), but MIC determination was not performed. The remaining 29 isolates with oxacillin zone diameters 9-19 mm should be interpreted as susceptible to ampicillin/amoxicillin and 3rd generation cefalosporins. Isolates with reduced susceptibility to penicillin G were often cross-resistant to erythromycin (18/40), trimethoprim-sulfamethoxazole (18/40), tetra-cycline (18/40) and/or clindamycin (8/40).

The prevalence of resistance to erythromycin was 11.7% in 2025 compared to 9.8% in 2020 and 10.0% in 2023. Macrolide resistance was higher in respiratory tract isolates than in isolates from blood cultures and sterile sites (5.5%). The MLS_B phenotype of erythromycin resistant isolates was determined by double disk diffusion. Two isolates displayed constitutive MLS_B resistance to erythromycin and clindamycin, whereas three isolate were inducibly resistant to clindamycin. Low-level M-type resistance was detected in 25 isolates (83% of erythromycin resistant isolates, 9.8% of all isolates). Tetracycline resistance increased from 8.3% in 2023 to 11.7% in 2025, whereas trimethoprim-sulfamethoxazole resistance decreased from 16.6% in 2023 to 12.1% in 2025. Only 1.6% of the isolates had zone diameters below the norfloxacin screening breakpoint for fluoroquinolone resistance. A single isolate had reduced susceptibility to linezolid, but no relevant determinants were detected by whole-genome sequencing.

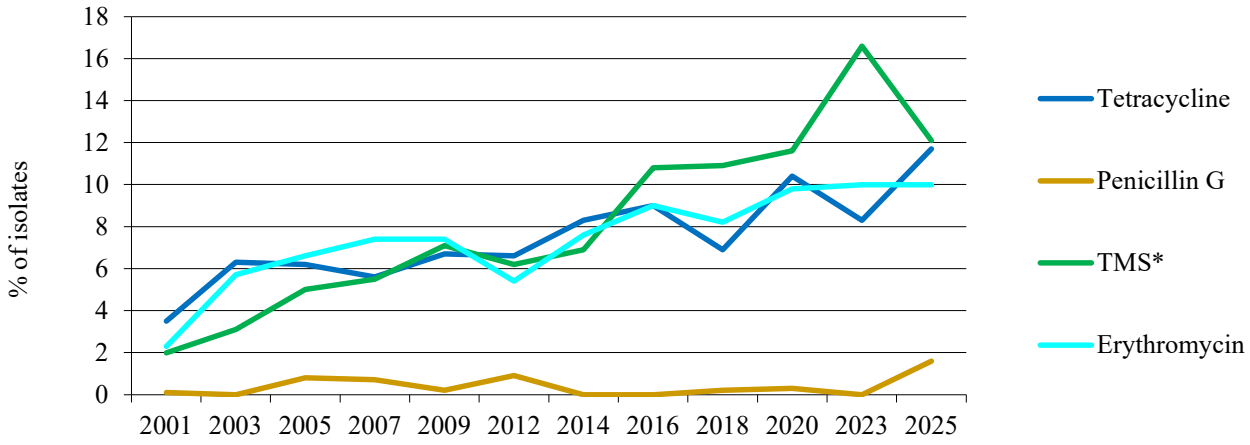

FIGURE 115. Prevalence of antimicrobial resistance in *Streptococcus pneumoniae* from respiratory tract samples 2001-2025. Isolates are categorised according to the breakpoints at the time of analysis. Doxycycline was replaced by tetracycline in 2005. *TMS=Trimethoprim-sulfamethoxazole. Please note that the x-axis is not to scale.

Streptococcus pyogenes in blood cultures

TABLE 98. *Streptococcus pyogenes* in blood cultures in 2025 (n=198). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G	≤ 0.03	> 0.03	100.0	-	0.0
Erythromycin	≤ 0.25	> 0.25	93.9	-	6.1
Clindamycin	≤ 0.5	> 0.5	98.0	-	2.0
Tetracycline	≤ 1	> 1	74.2	-	25.8
Trimethoprim-sulfamethoxazole*	≤ 0.5	> 0.5	99.5	-	0.5

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

TABLE 99. *Streptococcus pyogenes* in blood cultures in 2025 (n=198). Distribution (%) of MICs (mg/L) and zone diameters for oxacillin (mm).

	≤0.004	0.008	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	≥ 128
Penicillin G	1.5	51.0	47.5													
Erythromycin				5.6	42.4	43.4	2.5			2.0	0.5	0.5				3.0
Clindamycin			1.0	20.7	49.0	24.7	1.0	1.5		0.5						1.5
Tetracycline					8.1	54.5	11.1	0.5			1.0	2.5	7.6	11.1	3.0	0.5
TMS*			5.6	30.3	43.4	16.2	2.5	1.5		0.5						

Shaded areas in each row indicate susceptibility with standard exposure (light), susceptibility with increased exposure (medium) and resistance (dark). Non-shaded cells represent MIC values that are not covered by the standard test method. *TMS=Trimethoprim-sulfamethoxazole. Breakpoints for the trimethoprim-sulfamethoxazole combination are given for the trimethoprim component only.

RESULTS AND COMMENTS

The Reference Laboratory at the Norwegian Institute of Public Health provides resistance data for systemic *S. pyogenes* (beta-haemolytic group A streptococci - GAS) isolates on an annual basis. The number of isolates was reduced during the pandemic years 2020-2022, but a sharp increase was seen in 2023 (n=382) and 2024 (n=354) before decreasing again in 2025 (n=198). The results were categorised according to the most recent EUCAST/ NordicAST clinical breakpoint protocol. The breakpoints for trimethoprim-sulfamethoxazole were changed from S ≤ 0.5 mg/L to S ≤ 1 mg/L and from R > 2 mg/L to R > 1 mg/L in 2026.

As expected, all isolates were fully susceptible to penicillin G (Tables 98-99). The rate of resistance to erythromycin remained stable at 6.1% in 2025 compared to 6.5% in 2023 and 6.8% in 2024. The prevalence of clindamycin resistance decreased from 4.5% in 2024 to 2.0% in 2025, but this is at the same level as 2.3% in 2023. Four of the twelve erythromycin resistant isolates were constitutively resistant to clindamycin ($cMLS_B$), and the remaining eight displayed inducible resistance ($iMLS_B$). The *mef*-encoded phenotype of low-level resistance to erythromycin without induction of clindamycin resistance was not detected.

The prevalence of tetracycline resistance increased from 14.4% in 2024 to 25.8% in 2025. The changing rate of tetracycline resistance is linked to shifts in the distribution of *S. pyogenes* clones (particularly emm type 104.0 and 63.3) in the population. The prevalence of resistance to trimethoprim-sulfamethoxazole has been stable at very low levels (0.3% in 2022; 2.0% in 2024), and only a single isolate (0.5%) with this phenotype was detected in 2025.

Streptococcus agalactiae in blood cultures and cerebrospinal fluids

TABLE 100. *Streptococcus agalactiae* isolates in blood cultures and cerebrospinal fluids in 2025 (n=318). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G	≤ 0.125	> 0.125	100.0	-	0.0
Erythromycin	≤ 0.25	> 0.25	73.9	-	26.1
Clindamycin	≤ 0.5	> 0.5	82.7	-	17.3
Tetracycline	≤ 1	> 1	23.6	-	76.4
Linezolid	≤ 2	> 2	100.0	-	0.0
Vancomycin	≤ 2	> 2	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant.

RESULTS AND COMMENTS

All systemic isolates of *Streptococcus agalactiae* (beta-haemolytic group B streptococci) in Norway are referred to the National Reference Laboratory at St. Olavs Hospital, Trondheim University Hospital, where confirmatory identification and susceptibility testing is performed. Since 2014, the Reference Laboratory has provided resistance data for invasive *S. agalactiae* isolates to NORM on a yearly basis. EUCAST/NordicAST breakpoints used in this report have remained unchanged since 2024. The test methodology was in 2025 switched from MIC gradient tests to EUCAST disk diffusion, except for vancomycin.

A total of 318 isolates were retrieved from invasive infections in 2025 compared to 279 in 2024. Thirty-three isolates (10.4%) originated from neonates and small children < 1 year of age. Almost all isolates (316/318; 99.4%) were recovered from blood cultures, but there were also two isolates from cerebrospinal fluids. No patients had isolates from both specimen types, and the 318 included isolates thus represented unique infection episodes.

As seen in Table 100 there were no isolates with reduced susceptibility to penicillin G or vancomycin. A total of 83 isolates (26.1%) were resistant to erythromycin compared to 24.0% in 2024. All isolates were analysed by double disk diffusion for MLS_B resistance phenotype. Constitutive MLS_B resistance was found in 53/83 isolates (63.8%), while inducible MLS_B resistance was detected in 18/83 isolates (21.7%). The remaining 12/83 isolates (14.5%) had results in accordance with the efflux-mediated M phenotype encoded by *mef* genes. Three erythromycin susceptible isolates were concomitantly resistant to clindamycin. The results were not confirmed by alternative testing but may be due to mutations in ribosomal proteins.

The prevalence of tetracycline resistance (76.4%) was at the same level as in 2024 (71.3%) with most isolates displaying markedly reduced zone diamaters. The clinical efficacy of trimethoprim-sulfamethoxazole against *S. agalactiae* is uncertain and may depend on the concentration of folic acid at the site of infection. EUCAST/NordicAST has issued MIC breakpoints for the detection of acquired resistance, but no such breakpoints are available for disk diffusion.

Viridans group streptococci in blood cultures

TABLE 101. Viridans group streptococci in blood cultures in 2025 (n=685), except for tedizolid (n=206) where 479 streptococcal isolates not identified as *S. anginosus* are excluded due to lack of breakpoints. Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G*	≤ 0.25	> 1	87.7	9.1	3.2
Ampicillin*	≤ 0.5	> 2	89.5	7.0	3.5
Cefuroxime	≤ 0.5	> 0.5	95.8	-	4.2
Cefotaxime	≤ 0.5	> 0.5	94.9	-	5.1
Cefepime	≤ 0.5	> 0.5	96.1	-	3.9
Clindamycin	≤ 0.5	> 0.5	94.7	-	5.3
Tedizolid	≤ 0.5	> 0.5	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than endocarditis.

TABLE 102. *Streptococcus mitis* blood cultures in 2025 (n=235). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G*	≤ 0.25	> 1	81.3	14.0	4.7
Ampicillin*	≤ 0.5	> 2	83.8	11.9	4.3
Cefuroxime	≤ 0.5	> 0.5	92.8	-	7.2
Cefotaxime	≤ 0.5	> 0.5	93.2	-	6.8
Cefepime	≤ 0.5	> 0.5	95.3	-	4.7
Clindamycin	≤ 0.5	> 0.5	92.3	-	7.7

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than endocarditis.

TABLE 103. *Streptococcus anginosus* blood cultures in 2025 (n=206). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G*	≤ 0.25	> 1	98.5	0.5	1.0
Ampicillin*	≤ 0.5	> 2	97.5	1.5	1.0
Cefuroxime	≤ 0.5	> 0.5	98.5	-	1.5
Cefotaxime	≤ 0.5	> 0.5	97.6	-	2.4
Cefepime	≤ 0.5	> 0.5	96.6	-	3.4
Clindamycin	≤ 0.5	> 0.5	97.1	-	2.9
Tedizolide	≤ 0.5	> 0.5	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than endocarditis.

TABLE 104. *Streptococcus sanguinis* blood cultures in 2025 (n=69). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G*	≤ 0.25	> 1	91.3	5.8	2.9
Ampicillin*	≤ 0.5	> 2	89.9	5.8	4.3
Cefuroxime	≤ 0.5	> 0.5	97.1	-	2.9
Cefotaxime	≤ 0.5	> 0.5	98.6	-	1.4
Cefepime	≤ 0.5	> 0.5	98.6	-	1.4
Clindamycin	≤ 0.5	> 0.5	97.1	-	2.9

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than endocarditis.

TABLE 105. *Streptococcus salivarius* blood cultures in 2025 (n=66). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G*	≤ 0.25	> 1	69.7	24.2	6.1
Ampicillin*	≤ 0.5	> 2	77.2	16.7	6.1
Cefuroxime	≤ 0.5	> 0.5	92.4	-	7.6
Cefotaxime	≤ 0.5	> 0.5	89.4	-	10.6
Cefepime	≤ 0.5	> 0.5	93.9	-	6.1
Clindamycin	≤ 0.5	> 0.5	95.5	-	4.5

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than endocarditis.

TABLE 106. *Streptococcus bovis* blood cultures in 2025 (n=28). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G*	≤ 0.25	> 1	92.9	7.1	0.0
Ampicillin*	≤ 0.5	> 2	89.3	3.6	7.1
Cefuroxime	≤ 0.5	> 0.5	96.4	-	3.6
Cefotaxime	≤ 0.5	> 0.5	92.9	-	7.1
Cefepime	≤ 0.5	> 0.5	89.3	-	10.7
Clindamycin	≤ 0.5	> 0.5	89.3	-	10.7

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than endocarditis.

TABLE 107. *Streptococcus mutans* blood cultures in 2025 (n=24). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Penicillin G*	≤ 0.25	> 1	100.0	0.0	0.0
Ampicillin*	≤ 0.5	> 2	100.0	0.0	0.0
Cefuroxime	≤ 0.5	> 0.5	100.0	-	0.0
Cefotaxime	≤ 0.5	> 0.5	100.0	-	0.0
Cefepime	≤ 0.5	> 0.5	100.0	-	0.0
Clindamycin	≤ 0.5	> 0.5	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant. *Breakpoints for indications other than endocarditis.

RESULTS AND COMMENTS

Viridans group streptococci have never been surveyed in NORM before 2025, and these organisms are rarely included in antimicrobial resistance surveillance programmes. The 685 isolates were grouped as *S. mitis* (n=235) including *S. australis*, *S. cristatus*, *S. infantis*, *S. massiliensis*, *S. mitis*, *S. oligofermentans*, *S. oralis*, *S. peroris*, *S. pseudopneumoniae* and *S. sinensis*; *S. anginosus* (n=206) including *S. anginosus*, *S. constellatus* and *S. intermedius*; *S. sanguinis* (n=69) including *S. sanguinis*, *S. parasanguinis* and *S. gordonii*; *S. salivarius* (n=66) including *S. salivarius*, *S. vestibularis* and *S. thermophilus*; *S. bovis* (n=28) including *S. equinus, S. gallolyticus* (*S. bovis*), *S. infantarius, S. lutetiensis* and *S. pasteurianus*;; and *S. mutans* (n=24) including *S. mutans* and *S. sobrinus*. All other species were recorded as *Streptococcus* species (n=57). Susceptibility testing was performed using disk diffusion and the newly published breakpoints from EUCAST/NordicAST.

Most isolates were susceptible to penicillin G and ampicillin with standard (87.7% and 89.5%, respectively) or increased (9.1% and 7.0%, respectively) exposure using breakpoints for infections other than endocarditis. This implies that 3.2% of isolates were penicillin G resistant and 3.5% ampicillin resistant. In cases of endocarditis, 12.3% should be categorised as resistant to penicillin G and 10.5% to ampicillin. Among isolates positive by the penicillin G screening breakpoint, 21/84 were resistant to cefuroxime (3.1% of all isolates), 23/84 to cefotaxime (3.4% of all isolates) and 15/84 to cefepime (2.2% of all isolates). Beta-lactam resistance was common in *S. salivarius* (30.3%) and *S. mitis* (16.2%) but very rare in *S. anginosus* (2.5%) and *S. mutans* (0.0%). Clindamycin resistance rates varied among species (0.0-10.7%), but formal MLS testing was not performed. Among oxazolidinones, disk diffusion breakpoints only apply to *S. anginosus* and tedizolid. All isolates were fully susceptible.

Resistance to empiric antibiotic combinations used to treat bloodstream infections – favourable rates, increasing burden

The resistance rates to empiric antibiotic combinations among major bloodstream infection (BSI) pathogens (Table 108) have remained largely unchanged since 2024 (1). Thus, beta-lactam/gentamicin combinations continue to provide *in vitro* coverage at least comparable to cefotaxime and piperacillin-tazobactam for the major BSI pathogens.

However, stable resistance rates do not necessarily imply a stable burden of antimicrobial resistance. The incidence of BSI in Norway has been steadily increasing over many years. A recent analysis of two decades of NORM blood culture data showed that the absolute number of blood culture isolates doubled in the period 2005-2024. Many major pathogens increased 2-3-fold, including high-volume pathogens like *Escherichia coli, Klebsiella* spp. and *Staphylococcus aureus* (2).

This rising incidence means that stable resistance rates nevertheless translate into increasing numbers of patients affected by antimicrobial resistance. For example, an ESBL rate in BSI *E. coli* of 6.1% in 2015 corresponded to an estimated 244 patients, while a similar rate of 6.4% in 2025 corresponded to 322 patients. The favourable and largely stable resistance rates must therefore be read in the context of increasing BSI incidence: if this trend continues, unchanged resistance rates will still mean a growing absolute burden of antimicrobial resistant BSI in Norway.

TABLE 108. Resistance (%) to broad-spectrum antibiotics and antibiotic combinations in key bloodstream infection pathogens.

Antibiotic drug combinations[1]		Proportion of invasive isolates resistant (%)									
		E. coli (n=2,424)	*Klebsiella* spp. (n=1,258)	ESBL *Enterobacterales** (n=224)	*H. influenzae* (n=132)	*Enterococcus* spp. (n=779)	*Streptococcus pneumoniae* (n=783)	*Streptococcus pyogenes* (n=198)	*Streptococcus agalactiae* (n=318)	*Staphylococcus aureus* (n=1,678)	MRSA** (n=3,684)
PEN	GEN	5.3	2.7	26.3	40.9[2]	-	0.8	0.0	0.0	0.6	17.3
PEN	CIP	9.9	7.6	56.7	0.8[2]	-	0.8	0.0	0.0	1.6	28.0
CLI	GEN	5.3	2.7	26.3	100.0	100.0	3.8	2.0	17.3	0.2	4.6
AMP	GEN	4.8	2.7	26.3	21.2	20.2	X	0.0[3]	0.0[3]	0.6	17.3
PTZ	GEN	0.6	1.5	10.7	5.3[3]	20.2	X	0.0[3]	0.0[3]	0.4[3]	17.3
CTX		6.0	6.4	83.9	2.3	100.0	0.0	0.0[3]	0.0[3]	1.2[3]	100.0
PTZ		3.3	10.2	17.9	5.3[3]	20.2	X	0.0[3]	0.0[3]	1.2[3]	100.0
MER		0.0	0.1	0.0	0.0	100.0	X	0.0[3]	0.0[3]	1.2[3]	100.0

[1]Antibiotic abbreviations: PEN=penicillin G, GEN=gentamicin, CIP=ciprofloxacin, CLI=clindamycin, AMP=ampicillin, PTZ=piperacillin-tazobactam, CTX=cefotaxime, MER=meropenem. [2]Inferred from benzylpenicillin 1 unit (PCG1). [3]Inferred according to current breakpoint tables (3). X: No data available. -: No breakpoint/susceptibility testing not recommended. **Escherichia coli* and *Klebsiella* spp. **Includes MRSA from all specimen types.

References

1. NORM/NORM-VET 2024. Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway.
2. Danielsen AS, Johansen A, Sare M, Lim C, Bjørnholt JV, Furberg A-S, Simonsen GS. Two decades of bacteraemia in Norway: an ecological study of incidence and shifts in microbial epidemiology, 2005–2024. Sci Rep. 2025;15:44870.
3. The European Committee on Antimicrobial Susceptibility Testing. Breakpoint tables for interpretation of MICs and zone diameters. Version 16.1, 2026. https://www.eucast.org.

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Mycobacterium tuberculosis

In 2025 (2024 in parenthesis), 155 (180) persons were reported with tuberculosis disease (TB) to MSIS. Of these, 21 (12) were born in Norway. In addition to these 155 persons in 2025, three came to Norway under TB treatment. 127 (155) cases were confirmed with *M. tuberculosis* complex (MTBC) by culture, and ten (13) cases were confirmed by genotypic test only (culture negative). Among the culture positive cases, all were identified as *M. tuberculosis*. Since 2021, six cases of *M. africanum* or *M. orygis*, and one case of *M. bovis* have been identified among the culture positive cases. Resistance results reported to MSIS are shown in Table 109. Results from testing isolates or direct in samples are included. There were six (15) multi-drug resistant (MDR-)TB cases (resistant to both rifampicin and isoniazid), and none (2) cases with mono-resistance to rifampicin (RR-TB). All the RR/MDR-TB cases in 2024 and 2025 were culture positive. Of the MDR-TB cases two (6) had resistance to fluoroquinolones, so-called pre-XDR (extensively drug resistant) TB, and two had received chemotherapy in the past (including one case of pre-XDR).

In addition to the MDR-TB cases, 12 (13) TB cases had strains resistant to isoniazid (sensitive to rifampicin), five (6) of them only with low-level resistance.

TABLE 109. Antimicrobial resistance for MTBC reported to MSIS (not *M. bovis* BCG) in 2025 from isolates or direct samples. Figures from 2024 in parentheses.

Origin of birth	No. of cases	Resistance to antimicrobial agents				
		Isoniazid 131 (157)	Rifampicin 134 (162)	Ethambutol 145 (146)	Pyrazinamide 124 (140)	MDR-TB 131 (157)
Norway	21 (11)	1 (1)	1 (1)	1 (0)	2 (1)	1 (0)
Europe excluding Norway	25 (52)	5 (17)	4 (12)	4 (9)	4 (7)	4 (12)
Asia	66 (76)	8 (4)	1 (0)	1 (0)	0 (4)	1 (0)
Africa	39 (39)	4 (6)	0 (4)	0 (0)	0 (1)	0 (3)
America	4 (2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Total	155 (180)	18 (28)	6 (17)	6 (9)	6 (13)	6 (15)
Proportion resistant isolates (%)		13.7 (17.8)	4.5 (10.5)	3.1 (6.1)	4.8 (9.3)	4.6 (9.6)

MDR-TB: Multi-drug resistant tuberculosis, resistant to at least rifampicin and isoniazid.

Candida spp. in blood cultures

TABLE 110. Antimicrobial susceptibility of *Candida albicans* blood culture isolates in 2025 (n=144). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Amphotericin B	≤ 1	> 1	100.0	-	0.0
Fluconazole	≤ 2	> 4	100.0	0.0	0.0
Voriconazole	≤ 0.06	> 0.25	100.0	0.0	0.0
Anidulafungin	≤ 0.016	> 0.016	100.0	-	0.0
Micafungin	≤ 0.03	> 0.03	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant.

TABLE 111. *Candida albicans* blood culture isolates in 2025 (n=144). Distribution (%) of MICs (mg/L).

	≤0.004	0.008	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	128	≥ 256
Ampho. B				2.1	13.9	63.9	20.1										
Fluconazole						10.4	58.3	29.9	1.4								
Voriconazole	5.6	58.3	34.0	2.1													
Anidulafungin	45.9	36.1	18.1														
Micafungin	1.4	34.0	54.2	10.3													
Caspofungin		0.7	1.4	17.4	36.1	33.3	11.1										

Shaded areas in each row indicate susceptibility with standard exposure (light), susceptibility with increased exposure (medium) and resistance (dark). Non-shaded rows indicate that breakpoints have not been defined.

TABLE 112. Antimicrobial susceptibility of *Candida glabrata* blood culture isolates in 2025 (n=36). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Amphotericin B	≤ 1	> 1	100.0	-	0.0
Fluconazole	≤ 0.001	> 16	0.0	100.0	0.0
Anidulafungin	≤ 0.06	> 0.06	100.0	-	0.0
Micafungin	≤ 0.06	> 0.06	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant.

TABLE 113. *Candida glabrata* blood culture isolates in 2025 (n=36). Distribution (%) of MICs (mg/L).

	≤0.004	0.008	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	128	≥256
Ampho. B			2.8		5.6	22.2	44.4	22.2	2.8								
Fluconazole									2.8	16.7	33.3	41.7	5.6				
Voriconazole					19.4	36.1	33.3	8.3		2.8							
Anidulafungin	2.8		58.3	27.8	11.1												
Micafungin		8.3	80.6	11.1													
Caspofungin						41.7	55.6	2.8									

Shaded areas in each row indicate susceptibility with standard exposure (light), susceptibility with increased exposure (medium) and resistance (dark). Non-shaded rows indicate that breakpoints have not been defined.

TABLE 114. Antimicrobial susceptibility of *Candida parapsilosis* blood culture isolates in 2025 (n=22). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Amphotericin B	≤ 1	> 1	100.0	-	0.0
Fluconazole	≤ 2	> 4	86.4	4.5	9.1
Voriconazole	≤ 0.125	> 0.25	91.0	4.5	4.5
Anidulafungin	≤ 4	> 4	100.0	-	0.0
Micafungin	≤ 4	> 4	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant.

TABLE 115. *Candida parapsilosis* blood culture isolates in 2025 (n=22). Distribution (%) of MICs (mg/l).

	≤0.004	0.008	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	128	≥ 256
Ampho. B				4.5	9.1	4.5	40.9	40.9									
Fluconazole						9.1	13.6	36.4	27.3		4.5	9.1					
Voriconazole		9.1	13.6	22.7	31.8	13.6	4.5	4.5									
Anidulafungin						4.5		4.5	13.6	54.5	22.7						
Micafungin						4.0		20.0	56.0	20.0							
Caspofungin								63.6	31.8	4.5							

Shaded areas in each row indicate susceptibility with standard exposure (light), susceptibility with increased exposure (medium) and resistance (dark). Non-shaded rows indicate that breakpoints have not been defined.

TABLE 116. Antimicrobial susceptibility of *Candida dubliniensis* blood culture isolates in 2025 (n=15). Sampling, laboratory methods, and data handling are described in Appendix 5.

	Breakpoints (mg/L)		Proportion of isolates (%)		
	S	R	S	I	R
Amphotericin B	≤ 1	> 1	100.0	-	0.0
Fluconazole	≤ 2	> 4	100.0	0.0	0.0
Voriconazole	≤ 0.06	> 0.25	100.0	0.0	0.0
Anidulafungin	≤ 0.03	> 0.03	100.0	-	0.0
Micafungin	≤ 0.06	> 0.06	100.0	-	0.0

S=Susceptible with standard exposure, I=Susceptible with increased exposure, R=Resistant.

TABLE 117. *Candida dubliniensis* blood culture isolates in 2025 (n=15). Distribution (%) of MICs (mg/L).

	≤0.004	0.008	0.016	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	64	128	≥256
Ampho. B		6.7	13.3	13.3	33.3	26.7	6.7										
Fluconazole						33.3	46.7	20.0									
Voriconazole		53.3	40.0	6.7													
Anidulafungin	13.3	46.7	40.0														
Micafungin		26.7	40.0	33.3													
Caspofungin			13.3	6.7	20.0	53.3	6.7										

Shaded areas in each row indicate susceptibility with standard exposure (light), susceptibility with increased exposure (medium) and resistance (dark). Non-shaded rows indicate that breakpoints have not been defined.

RESULTS AND COMMENTS

The National Reference Laboratory of Medical Mycology at Oslo University Hospital performs confirmatory identification and susceptibility testing of all fungal isolates from invasive fungal infections in Norway and is responsible for the NORM surveillance.

All unique yeast isolates from blood culture from Norwegian patients taken in 2025 are registered. Identical isolates from the same episode, defined as cultures less than four weeks apart without changes in the susceptibility pattern, are counted as one.

The proposed nomenclature of fungi with renaming of many previous *Candida* spp. into new species challenges the definition of candidemia. In this report, species nomenclature follows the traditional *Candida* classification, as the recently proposed taxonomic revisions have not yet been adopted by EUCAST and remain a source of ongoing debate. The new proposed names are shown in brackets.

In 2025 there were 248 unique yeast isolates from 216 patients of whom 241 were unique *Candida* spp. from 212 patients compared to 238 *Candida* spp. in 223 different patients in 2024.

Fungemia with traditionally defined non-*Candida* species is still very rare, 2.8 % (n=7) of all fungemias in 2025: one fungemia with *Cryptococcus neoformans*, five with *Saccharomyces cerevisiae,* and one *Rhodotorula mucilaginosa* were registrered. *Rhodotorula mucilaginosa* is regarded resistant to azoles and echinocandins, whereas *Saccharomyces cerevisiae* shows reduced sensitivity to the same agents. Both species are low-virulent and are normally regarded sensitive to amphotericin B. Eleven of the fungemias were mixed infections with more than one yeast, of whom four with the combination of *C. albicans* and *C. glabrata* (*Nakaseomyces glabratus*). There were six recurrent infections with the same species more than four weeks apart: *C. albicans* (n=2), *C. parapsilosis* (n=2) and one *C. glabrata* (*Nakaseomyces glabratus*) and *C. kefyr* (*Kluyveromyces marxianus*), respectively. There were also 12 reinfections with *another* species of which five infections were initial *C. albicans* infections followed by an infection with a species with reduced sensitivity to fluconazole: two *C. krusei* (*Pichia kudriavzevii*), two *C. glabrata* (*Nakaseomyces glabratus*), and one by a double infection with *C. lipolytica* (*Yarrowia lipolytica*) and *Rhodutorola mucilaginosa.*

Of the 241 unique candidemia isolates from 212 patients, the species distribution of the two most frequent species, *Candida albicans* (n=144, 59.8%) and *C. glabrata* (*Nakaseomyces glabratus*) (n=36, 14.9*%)* is similar compared to 2024 (56.3% and 15.5%, respectively). Other species were less frequently represented: 22 *C. parapsilosis* (9.1%), 15 *C. dubliniensis* (6.2%), and only four *C. tropicalis* isolates in 2025, a marked decrease from 24 in 2024. *C. krusei* (*Pichia kudriavzevii*) (n=8) is the most frequent among "other *Candida* species" (n=20) not shown in the tables. *Candida auris* (*Candidozyma auris*) was not detected in blood cultures in Norway in 2025.

All isolates were susceptibility tested to amphotericin B, fluconazole, voriconazole, caspofungin, anidulafungin and micafungin. All but voriconazole are tested by E-test according to the manufacturer's instructions (AB bioMérieux), while voriconazole is tested according to MTS™ (Liofilchem). MIC values were categorised according to the EUCAST clinical breakpoints version 12.1, valid from 2026-04-10. Unexpected susceptibility patterns were confirmed by EUCAST standardised broth microdilution method at Statens Serum Institut in Copenhagen. The results of the most common species are presented in Tables 110-117.

In 2025, all isolates of *C. albicans, C. dubliniensis* and *C. tropicalis* (data not shown in the tables), were susceptible to all antifungal agents, and all *C. glabrata (Nakaseomyces glabratus)* isolates belonged to the wild type without acquired azole resistance and were susceptible to other agents.

Two azole resistant isolates of *C. parapsilosis* and one isolate with reduced sensitivity to fluconazole was identified in 2025, all from one patient on long-term treatment. Of the other 20 *Candida* isolates not shown in the tables, there were eight naturally fluconazole resistant *C. krusei* (*Pichia kudriavzevii*), compared to two *C. krusei* (*Pichia kudriavzevii*) last year. There were also one *C. pelliculosa* (*Wickerhamomyces anomalus*) and three *C. guillermondii* (*Meyerozyma guilliermondii*) both regarded as species with reduced sensitivity to fluconazole as well. *C. lusitaniae* (*Clavispora lusitaniae*) (n=3) is regarded amphotericin B resistant. Three of four *C. kefyr* (*Kluyveromyces marxianus*) isolates displayed echinocandin resistance, all originating from a single patient on long-term antifungal therapy. This is noteworthy given that *C. kefyr* (*Kluyveromyces marxianus*) typically demonstrates low MICs across all major antifungal classes, making most agents suitable for treatment.

In conclusion, the number of blood culture positive yeast infections and the species distribution remain stable, and acquired antifungal resistance continues to be uncommon in Norway. The proportion of *C. glabrata* (*Nakaseomyces glabratus*) and other isolates with reduced fluconazole susceptibility remains low. The Norwegian treatment guidelines for candidemia with echinocandins as first-line treatment due to fungicidal effect, and de-escalation to fluconazole in stable patients infected with susceptible *Candida* spp. remain appropriate.

Appendix 1:
Material and methods for sales and use of antibacterial agents in animals

General information

In Norway, all medicinal products containing antibacterial agents are prescription-only medicines – this includes both veterinary medicinal products (VMPs) and human medicinal products (HMPs). The latter can be prescribed to animals according to the so-called cascade (Regulation (EU) 2019/6, Article 112-114) – i.e. if there is no VMP authorised for the condition, a HMP is allowed to be used. For food-producing species, it is required that a maximum residue level (MRL) has been established for the active substance in question, or that it has been demonstrated that an MRL is not necessary, as specified in the annex to Commission Regulation (EU) No 37/2010. Veterinarians in Norway are not allowed to dispense VMPs or HMPs, except for treatments until a pharmacy can provide the products. In such cases the medicinal products must be sold at cost price.

Both VMPs and HMPs must be dispensed through pharmacies that are supplied by wholesalers. Medicated feed (manufactured from premix VMPs) is supplied to the end user by feed mills and is currently only used for farmed fish; this is due to the small size of livestock herds in Norway and the low use of group/flock treatments. Group treatment of livestock (terrestrial animals) with antibacterial agents is administered through drinking water or as top-dressing on the feed.

Data sources

Sales data – terrestrial animals

Wholesalers and feed mills in Norway are mandated to provide sales statistics for all veterinary medicinal products, including when supplied as medicated feed, to the Norwegian Institute of Public Health (NIPH), according to "Forskrift om grossistvirksomhet med legemidler" (in Norwegian). Data on sales of each product presentation (name, form, strength and pack size) for terrestrial animals of the included VMPs (see Table) were obtained from the NIPH.

Use data – farmed fish and terrestrial animals

The Norwegian Food Safety Authority established the Veterinary Prescription Register (VetReg) for farmed fish 1st January 2011 and for terrestrial animals 1st January 2012. The veterinarians are mandated to report any administration and dispensings of VMPs and HMPs to VetReg for all food-producing animals and horses while it is voluntary for all other animal species such as companion animals. Pharmacies and feed mills must report all dispensings, i.e. for all terrestrial animals and farmed fish, to veterinarians or animal owners, including medicines prescribed for companion animals and HMPs. Reporting is regulated in "Forskrift om melding av opplysninger om utleverte og brukte legemidler til dyr" (in Norwegian).

For farmed fish the reporting of use (kg active substance) of antibacterials, calculated from prescription data reported to VetReg, was shown to be in the same magnitude as the sales of the same VMPs reported by NIPH for the years 2013-2018 (1) and this is also the case for the years 2019-2025 (unpublished data). For the period 2013-2025, VetReg data are used for reporting of use of antibacterials for farmed fish.

For terrestrial food-producing animals the annual reporting of use (kg active substance) calculated from prescription data reported to VetReg was lower by form and antibacterial substance when compared to the sales data from NIPH for the corresponding year (2, 3). This is thought to be partly due to underreporting by pharmacies and veterinarians, but also due to medicinal wastage, that use for companion animals by veterinarians are not covered by the data and several data-quality issues. However, these data are reported to and presented by European Medicines Agency (EMA) for cattle, pigs, chicken and turkey as required by Regulation (EU) 2019/6, Article 57. The same data are presented in the current report in a text box on use of antibacterial agents per species and data quality.

The use of VMPs and HMPs for cattle, pigs, chickens and turkeys was estimated by use of the following data reported to VetReg:

- Delivery to animal owners from pharmacies of antibacterial VMPs and HMPs for use in these species plus
- Veterinarians' use/delivery of antibacterial VMPs or HMPs for these species.

Note that the textbox figures only include data for the VMPs included in Union Product Database (UDP, EU's database on all currently marketed VMPs in EU/EEA). The use of HMPs for companion animals was estimated by use of the following data reported to VetReg:

- Delivery to animal owners from pharmacies of antibacterial HMPs for use in companion animals

Antibacterials included in the data set

The Anatomical Therapeutic Chemical classification system for veterinary medicinal products (ATCvet) classification system was used to identify the VMPs to be included in the data. Sales and use of VMPs belonging to the ATCvet codes shown in the table below were requested from NIPH and included from VetReg data, for terrestrial animals. For farmed fish, data of use of products belonging to these codes were included from VetReg. This is identical to the inclusion criteria by the European Surveillance of Veterinary Antimicrobial Consumption (ESVAC) (4). This also follows the inclusion criteria for sales data mandatory to report to the EMA from the reporting year 2023 and onwards according to Annex 1 of Commission Delegated Regulation (EU) 2021/578, except for an addition of three ATCvet codes: QA07AX03, QA07AX04 and QJ54. There were, however, no sales or use of VMPs belonging to any of these three ATCvet codes in 2023-2025. For the estimation of prescription of HMP antibacterials belonging to the ATC codes found in Annex 3 of Commission Delegated Regulation (EU) 2021/578 are included (extracted from VetReg data).

ATCvet codes/Antibacterial veterinary medicinal products included in the data.

Categories	ATCvet codes
Intestinal use	QA07AA; QA07AB
Intrauterine use	QG01AA; QG01AE; QG01BA; QG01BE; QG51AA; QG51AG
Systemic use	QJ01
Intramammary use	QJ51
Antiparasitic agents[1]	QP51AG

[1] Only sulfonamides

Antibacterial veterinary medicinal products belonging to the ATCvet categories shown in the table and sold on special exemption from market authorisation are included in the data. Dermatological preparations (QD) and preparations for sensory organs (QS) are not included in the data which is in accordance with the ESVAC protocol (4) and Annex 1 and 3 of (EU) 2021/578.

Data source animal population data. Denominator.
In the current report, biomass, to serve as a denominator, was calculated according to the ESVAC protocol (4). This method was chosen to be able to include historical data. It must be emphasised that the calculated biomass is purely a surrogate for the animal population at risk.

The biomass for each terrestrial animal category was calculated by multiplying numbers of livestock animals (cows, sows, sheep and horses) and slaughtered animals (cattle, pigs, sheep, goats, poultry and rabbits) by a theoretical weight at the most likely time for treatment (4). The biomass is calculated for each species, weight class and/or production type, as follows:

- Number of animals slaughtered × standardised weight
- Number of livestock × standardised weight

The total biomass is calculated by summarising the above data. For farmed fish, biomass slaughtered fish was used. Animal population data, including the sources for these data, for 2025 are presented in Table 2 in the chapter Population statistics of the current report.

Analysis of the overall sales and use data
The sales and use data for each antibacterial VMP and HMP presentation were calculated to express weight of active substance. To comply with the ESVAC protocol (4), sales of derivatives – e.g. procaine benzylpenicillin and penethamate hydriodide – has been calculated to the corresponding values for the active ingredient, here benzylpenicillin by use of standardised conversion factors (4). For VMPs where the strength is given in international units (IU), the weight of active substance has been calculated by use of ESVAC conversion factors for IUs (4). For data from 2023 and onwards the conversion factors used in the ESUAvet report has been applied for sales data (5). ESVAC kept its own database with metadata on the VMPs (e.g. on strength and active substance) and so did the Norwegian Veterinary Institute for the analysis of sales data till 2022. ESUAvet uses UPD to obtain this information and UPD is the main source of metadata for sales and use data from 2023 in the current report. UPD's HMP counterpart is not fully functional yet and the textbox figures (Figures 10 and 11) does therefore not cover HMPs. For the estimations of use of VMPs not included in UPD and HMPs, metadata were obtained from the Norwegian prescription and dispensing support database called FEST. The results are presented as numbers or percentages in the figure captions.

Stratification of sales data
The sales data of antibacterial VMPs for terrestrial animals have been split into sales for food-producing animals (including horses) and companion animals. Up to 2022, sales of antibacterial VMPs for companion animals refers to sales of tablets, injectables, oral solution and oral paste that were approved solely for companion animals; in addition, dihydrostreptomycin tablets of pack size 10 pieces have been included in the data on sales for companion animals (no sales after 2004). The other antibacterial VMPs are assumed sold for use only in food-producing animals (including horses). From the reporting year 2023 and onwards, the same stratification is done according to which species the VMPs are approved for: food-producing species if they are approved for any food-producing species, companion animals if not. This is in accordance with the ESUAvet methodology (6). There is some use in companion animals of VMPs marketed for food-producing animals. The sales are therefore slightly underestimated for companion animals and slightly overestimated for food-producing animals.

Sales data of VMPs for food-producing animals have been further stratified into VMPs for treatment of individual food-producing animals – i.e. bolus, oral paste, injectables, intramammary preparations, intrauterine preparations and tablets – and for group treatment – i.e. oral solution, including oral powder intended for solution, and oral powder.

Because cattle, pigs, sheep, and poultry accounted for more than 99% of the meat production in 2025 in Norway (https://www.ssb.no/slakt) these species as well as goats were included in a separate analysis of sales data. The sales data for 2013-2025 have been refined to obtain estimates on sales for the food-producing terrestrial species, excluding horses. Data on prescriptions per animal species obtained from VetReg have been used as supportive information for this refinement of the sales data. VetReg data show that for the years 2016-2023 and in 2025, more than 95% of the number of prescriptions of antibacterial oral paste VMPs was for horses. For 2024 this figure was 88%. Oral paste (numerator) and biomass for horses (denominator) have therefore been excluded from the analysis of data for the estimation of sales of antibacterial VMPs for cattle, pigs, sheep, goats and poultry, as shown in Figure 4.

Analysis of use data
The use data were cleansed to correct for erroneous reporting as described in Udhwani et al. (2025) and Löfling and Helgesen (2025) (2,3). Coverage was calculated separately for 1) chicken and turkeys and 2) cattle and pigs. All use of VMPs (for all animals) where more than 85% of the use was reported for poultry was calculated as percent of sales of the same VMPs and presented as coverage for chicken and turkeys. Coverage of all other VMPs used for cattle and pigs was calculated as percent of sales of the same products and presented as coverage for use for all animals as cattle and pigs.

References

1. Grave K, Helgesen KO, 2018. Antibacterials for farmed fish – prescribing, usage and diagnoses 2013–2017 (In Norwegian: Antibakterielle midler til oppdrettsfisk – rekvirering, forbruk og diagnose 2013 - 2017). Norwegian Veterinary Institute report.
2. Udhwani T, Grave K, Hopp P, Helgesen KO, 2025. Quality assessment of antibiotic use data in the Norwegian veterinary prescription register for 2023. BMC Vet Res 21: 510. doi: 10.1186/s12917-025-04903-9
3. Löfling LL, Helgesen KO, 2025. Quality Evaluation of the Norwegian Veterinary Prescription Registry (VetReg) – comparing anibiotc data for 2023 and 2024. Norwegian Veterinary Institute report
4. European Surveillance of Veterinary Antimicrobial Consumption (ESVAC). European Surveillance of Veterinary Antimicrobial Consumption (ESVAC) Sales Data and Animal Population Data Reporting Protocol (version 4). https://www.ema.europa.eu/en/documents/other/european-surveillance-veterinary-antimicrobial-consumption-esvac-web-based-sales-and-and-animal-population-data-collection-protocol_en.pdf.
5. EMA, 2025. European Sales and Use of Antimicrobials for veterinary medicine (ESUAvet). Annual surveillance report for 2024. EMA/CVMP/ESUAVET/376993/2025. https://www.ema.europa.eu/en/documents/report/european-sales-use-antimicrobials-veterinary-medicine-annual-surveillance-report-2024_en.pdf.
6. EMA, 2024. Antimicrobial Sales and Use (ASU) technical implementation protocol EMA/27838/2024. https://www.ema.europa.eu/en/documents/other/antimicrobial-sales-and-use-asu-technical-implementation-protocol_en.pdf

Appendix 2
Collection and analysis of data on usage of antimicrobial agents in humans

Data sources
In Norway, antimicrobials are prescription-only medicines and only allowed sold through pharmacies. These data are collected from three databases: the Norwegian Drug Wholesales Statistics Database, the Hospital Pharmacies Drug Statistics Database and the Norwegian Prescribed Drug Registry (NorPD). The Norwegian Institute of Public Health collects data on drug use from wholesalers. The wholesales database covers total sales of antimicrobials to humans and animals in Norway and is based on sales of medicaments from drug wholesalers to pharmacies and health institutions in Norway. The figures presented should be regarded as maximum figures based on the assumption that all medicines sold are consumed. The actual drug consumption will probably be somewhat lower. Data are available since the beginning of the nineteen-seventies.

Data on antibacterial use in hospitals are retrieved from *Sykehusapotekenes legemiddelstatistikk* (the Hospital Pharmacies Drug Statistics Database) which is a cooperation of the four regional pharmaceutical health trusts operating the hospital pharmacies in Norway. *Sykehusapotekenes legemiddelstatistikk* collects sales data from each pharmacy delivering drugs to hospitals. Data are collected as sales from the pharmacy to hospital wards. Data have been available since 2006. National Centre for the Use of Antibiotics in Hospitals (*Nasjonal kompetanse-tjeneste for antibiotikabruk i spesialisthelsetjenesten*) has analysed the data according to activity (bed days).

Population statistics per 1st January are collected from Statistics Norway. Information on bed-days and admissions are collected from the Norwegian Patient Register. The definition of bed-days is: "*the number of whole days an admitted patient disposes a bed*". An admission is defined as: "*admission of patient where the medical interventions usually are complex and require hospitalisation for one or more days*" (1).

Data from nursing home setting have until today not been available. However, total sales data from the Norwegian Drug Wholesales Statistics Database include the nursing home setting and volume of use can be estimated. By legislation, nursing homes may purchase medicines directly from the wholesalers, but another option is to purchase from the local pharmacy. The shares of the two ways of purchasing antibiotics may vary from one year to another, but in recent years the share purchased from wholesalers has increased. Sales from wholesalers can be measured through the Norwegian Drug Wholesales Statistics Database while sales through the local pharmacies will be captured in the NorPD. Some municipalities announce tenders to obtain the most optimal agreement for drug deliveries to their nursing homes. The wholesaler winning the tender will keep the business agreement until the next tender. This change of delivering wholesalers makes it difficult to follow antibiotic sales over years. Moreover, it is difficult to get exact sales, which hampers the ability to provide aggregated national statistics for Norwegian nursing homes. This year we have included the estimated consumption of antibiotic use in nursing homes. The sales data from the nursing homes purchasing medications from Norwegian drug wholesalers is captured. In 2025, the sales to approximately 55% of all Norwegian nursing homes are included in the Norwegian drug wholesales statistics database. Total national use in nursing homes is an estimate as it is recalculated and adjusted from these data.

Data on the use in ambulatory care are retrieved from NorPD, a nation-wide prescription database situated at the Norwegian Institute of Public Health. This database includes all prescriptions being prescribed to out-patients in Norway. For analyses on prescriptions and DDDs, all prescriptions and DDDs to outpatients are included. For the results on annual prevalence (number of individuals per population group being prescribed antibiotics within a year) only prescriptions to individuals with national ID numbers are included. The data give us the exact population prevalence of antibacterial use in the total population in ambulatory care. More information is available at www.fhi.no. Data are available from 2004.

Drug Classification
The data are categorised according to the ATC classification system (2). Defined Daily Doses (DDDs) are employed as units of measurement. The ATC/DDD index of 2026 is used for all years.

Unit of measurement
The ATC/DDD system is recommended by the WHO to serve as a tool for drug utilisation research in order to improve quality of drug use. One component of this is the presentation and comparison of drug consumption statistics at international and other levels. The use of defined daily dose (DDD) as a unit of measurement, simplifies and improves the evaluation of drug consumption over time, nationally and internationally. The DDD is a theoretical unit of measurement and does not necessarily reflect the recommended or Prescribed Daily Dose.

The basic **definition** of the unit is:
The DDD is the assumed average maintenance dose per day for a drug used for its main indication in adults.

The DDDs for antibacterials are as a main rule based on the use in infections of moderate severity. Some antibacterials are only used in severe infections and their DDDs are assigned accordingly. The DDDs assigned are based on daily treatment.

Inclusion criteria
The antibacterials for human use included in this report belong to ATC group J01 *antibacterials for systemic use*. Oral vancomycin (A07AA09), fidaxomycin (A07AA12) and oral and rectal metronidazole (P01AB01) are also included in some figures. In addition to J01, antimycotics for systemic use (J02), rifaximin (A07AA11), rifampicin (J04AB02), and mupirocin (D06AX09/ R01AX06) are included in the report. Antibacterials used for dermatological preparations (ATC group D) and preparations intended for sensory organs (ATC group S) are not included in the material.

References
1. Definitions Norwegian Patient Register https://www.fhi.no/he/npr/Ord-og-uttrykk-Norsk-pasientregister/
2. WHO Collaborating Centre for Drug Statistics Methodology. ATC index with DDDs 2026. WHO Collaborating Centre, Oslo

Appendix 3:
Sampling, microbiological methods and data processing in NORM-VET

Sampling strategy
Clinical isolates of *Actinobacillus pleuropneumoniae* and *Escherichia coli* from pigs, and *Staphylococcus felis* and *E. coli* from cats were retrieved through submissions to the Norwegian Veterinary Institute. The *A. pleuropneumoniae* isolates (n=70) were from pigs with respiratory infections and collected in 2021-2025, while the *E. coli* isolates (n=71) were from pigs with the diagnosis enteritis or oedema disease (serotypes K88, O138, O149, O141, O139, O45) and collected in the years 2021-2025. The isolates from cats were all collected in the years 2018-2025. The *E. coli* (n=29) isolates were mainly from urinary tract infections, while the *S. felis* isolates were from both local skin/ear infections (n=15) and other infections (n=19).

Faecal and oral/nasal/perineum swab samples from a total of 291 cats were collected by practicing veterinarians throughout the year. The sampled cats were between a few months and 19 years of age and from all over the country. Two cats had been abroad/imported the last 12 months, from the United States of America and Poland, respectively. A total of 170 cats had outdoor access. Clinical symptoms from ear or skin was reported from 20 cats and two of these had been treated with antimicrobials in the last 12 months. Clinical symptoms from intestinal tract was reported from 15 cats of which none had received antimicrobials last six months. Overall, 26 cats were reported to have received antimicrobial treatment. The indicator *E. coli* were retrieved from faecal swab samples. The same samples were also used for selective isolation of *E. coli* resistant to extended-spectrum cephalosporins (ESC) and carbapenem resistant *Enterobacterales* (CRE). The oral/nasal/perineum swabs were used for retrieving *S. felis* and for selective isolation of methicillin resistant *S. pseudintermedius* (MRSP) and/or *S. aureus* (MRSA).

Caecal samples from cattle and fattening pigs were collected at slaughter throughout the year by the Norwegian Food Safety Authority (NFSA), following the specifications set by the European Food Safety Authority (EFSA; EFSA Journal 2019;17(6):5709) with one exception; EFSA specifications require caecal samples from cattle under one year, and this is not required in NORM-VET. One individual caecal sample was included per herd, in total 308 and 299 samples from cattle and pigs, respectively, except from 11 pig and two cattle herds where samples were collected twice.

All food samples were collected by the NFSA. Beef and pork samples, 320 and 317, respectively, were collected at retail in all regions of Norway following the specifications set by EFSA (EFSA Journal 2019;17(6):5709). Samples were collected without taking place of origin into account. In addition, samples of berries (i.e. blueberries (n=324), strawberries (n=304) and raspberries (n=317)) were collected at retail.

All the caecal and food samples were used for selective isolation of *E. coli* resistant to ESC and CRE. The samples of berries were also used for retrieving indicator bacteria *E. coli*, and for selective screening of MRSA. The included indicator bacteria *E. coli*, *Enterococcus faecalis* and *Enterococcus faecium* were also retrieved from the caecal samples. In addition, the caecal samples were used for isolation of *Campylobacter coli* and *Campylobacter jejuni* (see Appendix 4).

Indicator isolates of *E. coli*
Sample material, i.e. faecal content from cats and caecal content from cattle and fattening pigs, were plated directly onto MacConkey agar (Difco) and incubated at 44±0.5°C for 20±2h. Also, a loopful (10 µL) of the overnight BPW-ISO broth from berries were plated and incubated as described above. Typical colonies were subcultured on blood agar and incubated at 37±1°C for 20±2h. Colonies were identified as *E. coli* by typical colony appearance and a positive indole reaction, or by using Matrix Assisted Laser Desorption/Ionization – Time of Flight Mass Spectrometry (MALDI-TOF MS; Bruker Daltonics GmbH).

Indicator isolates of *E. faecalis* and *E. faecium*
Sample material, i.e. caecal content from cattle and fattening pigs were plated directly onto Slanetz and Bartley agar (Oxoid) and incubated at 44±0.5°C for 24-48h. Typical colonies were subcultured on blood agar incubated at 37±1°C for 20±2h. Colonies were identified as *E. faecalis* or *E. faecium* using MALDI-TOF MS.

Indicator isolates of *Staphylococcus felis*
Sample material, i.e. nasal/perineum swabs from cats were enriched in 5 mL Mueller Hinton broth with 6.5% NaCl and incubated at 37±1°C for 18-24 h. Aliquots from the overnight broth were plated onto mannitol-salt agar (MAST, Oxoid) and incubated at 37±1°C for 20±2h. Typical colonies were subcultured on blood agar incubated at 37±1°C for 20±2h. Colonies were identified as *S. felis* using MALDI-TOF MS.

Enrichment of samples before selective isolation
All samples were enriched prior to plating onto selective media. A total of 1±0.1 g caecal sample material was homogenised with 9 mL of BPW-ISO. Faecal swab samples from cats were inoculated in 5 mL of BPW-ISO. A total of 25±0.5 g sample material of beef, pork and berries were homogenised with 225 mL of BPW-ISO. Samples were incubated at 37±1°C for 20±2h according to the protocol from the EURL-AR (https://www.eurl-ar.eu/protocols.aspx). After incubation, 10 µL aliqouts of the enrichment broth was plated onto selective media as described in the sections below.

***E. coli* resistant to extended-spectrum cephalosporins (ESC)**
Aliquots from the overnight BPW-ISO broth from the faecal, caecal, meat and berry samples were plated onto MacConkey agar containing 1 mg/L cefotaxime and MacConkey agar containing 2 mg/L ceftazidime. Agar plates were incubated at 44±0.5°C for 18-24h. Presumptive ESC-resistant *E. coli* were subcultured on MacConkey agar containing 1 mg/L cefotaxime and blood agar and confirmed as *E. coli* using MALDI-TOF MS before further phenotypical testing.

Carbapenem resistant *Enterobacterales* (CRE)
Aliquots from the overnight BPW-ISO broth from the caecal, faecal, meat and berry samples were plated onto CHROMID® CARBA and CHROMID® OXA-48 agar (bioMérieux, Marcy l'Etoile, France). Agar plates were incubated at 35±2°C for 18-24h. Presumptive CRE were subcultured on CHROMID® selective and blood agar, and species confirmed using MALDI-TOF MS before further phenotypical testing.

Methicillin resistant *Staphylococcus aureus* (MRSA) and/or *Staphylococcus pseudintermedius* (MRSP)
Sample material, i.e. nasal/perineum swabs from cats and 25 g of berries were enriched in 5 and 225 mL, respectively, Mueller Hinton broth with 6.5% NaCl and incubated at 37±1°C for 18-24 h. A loopful of the overnight broth (10 µL) was plated onto Brilliance™ MRSA2 agar plate (Oxoid) and incubated at 37±1°C for 24±2 hours. Suspected colonies were subjected to species identification using MALDI-TOF MS before further phenotypical testing.

Genotyping
For genotyping of presumptive antimicrobial resistant isolates, whole-genome sequencing (WGS) was performed on an Illumina® MiSeq or Illumina® NextSeq (Illumina, San Diego, California, USA). Paired end reads were subjected for analysis for both aquired genes and chromosomal point mutations using the ResPointFinder3 pipeline (equals ResFinder_EFSA2023, http://genepi.food.dtu.dk/resfinder) which the NVI has implemented on the IRIDA platform (www.irida.ca).

Susceptibility testing
Isolates were tested for antimicrobial susceptibility using a broth microdilution method. Minimum inhibitory concentration (MIC) values were obtained using panels from Sensititre® (TREK Diagnostic LTD, Thermo Scientific™, Waltham, Massachusetts, USA) with different panels depending on the bacteria to be tested as recommended by Decision 2020/1729/EU. Epidemiological cut-off values (ECOFF) recommended by the European Committee on Antimicrobial Susceptibility Testing (EUCAST, accessed 06.02.2026) with some exceptions as explained further in Appendix 7, were used as interpretation of bacteria as susceptible or resistant. See Appendix 6 for definitions of cut-off values. The table below gives an overview of which panel was used for which clinical isolates. The NVI has decided to use the same panels for clinical isolates as used in the Swedish Veterinary Antimicrobial Resistance Monitoring (Svarm) (Swedres-Svarm).

Staphylococcus felis isolates from cats were also investigated for penicillinase (beta-lactamase) production using the clover leaf test and for methicillin resistance using oxacillin disk.

Overview of which Sensititre® TREK panel was used for which clinical isolate:

Clinical isolate tested	Panel
A. pleuropneumoniae	CLIN AnRoPa
E. coli	CLIN GN
S. felis local infection	CLIN local strep/staph
S. felis other infections	CLIN strep/staph

Quality assurance systems
The following susceptible bacteria were included as quality control on a regular basis: *E. coli* ATCC 25922, *E. faecalis* ATCC 29212, *S. aureus* ATCC 29213 and *Haemophilus influenzae* ATCC 49766. In addition to the regular susceptible bacteria, the following bacteria received from EURL-AR were included: *Acinetobacter baumannii* 2012-70-100-69 (EUVSEC3 and EUVSEC2 panel), and *E. faecium* 2012-70-76-8 and *E. faecalis* 2012-70-103-3 (EUVENC panel). The results were approved according to reference values given by EUCAST or EURL-AR when available. Additional control strains were included when necessary. The laboratories at the NVI are accredited according to the requirements of NS-EN ISO/IEC 17025 and participate in quality assurance programmes for veterinary pathogens (Veterinary Laboratories Agency Quality Assurance Unit. Loughborough. UK) and for resistance monitoring (EURL for Antimicrobial Resistance in Denmark).

Data processing
Susceptibility data were recorded and stored in the sample registration system at the NVI as discrete values (MIC). Data management was performed in R version 4.5.1 Copyright (C) 2023 (The R Foundation for Statistical Computing Platform). All changes and differences yielding a p-value <0.05 were considered as statistically significant. The 95% confidence intervals were calculated using the exact binomial test.

Appendix 4:
Sampling, microbiological methods and data processing of zoonotic and non-zoonotic enteropathogenic bacteria in NORM and NORM-VET

NORM-VET – enteropathogenic bacteria
Sampling strategy – animals and food

***Salmonella* spp.**
Isolates of *Salmonella* spp. were retrieved from the Norwegian *Salmonella* control programme for live animals. Additional isolates were obtained from submissions to the National Reference Laboratory for Salmonella, and from clinical submissions or necropsies at the Norwegian Veterinary Institute (NVI). One isolate of each serovar per incident was included for susceptibility testing.

Campylobacter jejuni* and *Campylobacter coli
Samples of caecal content from cattle and fattening pigs decribed in Appendix 3, were used for isolation of *Campylobacter jejuni* and *Campylobacter coli,* respectively. Sample material, i.e. caecal content from one fattening pig and one cattle per herd as described in Appendix 3, were plated directly onto mCCDA agar and Bützler agar and incubated under microaerophilic conditions at 41.5±0.5°C for 48h. Typical colonies were subcultured on blood agar and confirmed as *C. jejuni* or *C. coli* using Matrix Assisted Laser Desorption/Ionization – Time of Flight Mass Spectrometry (MALDI-TOF MS; Bruker Daltonics GmbH).

Susceptibility testing – animal isolates
Isolates were antimicrobial susceptibility tested and MIC values were obtained using panels from Sensititre® (TREK Diagnostic LTD) with different panels depending on the bacteria to be tested as recommended by Decision 2020/1729/EU, see table below. For animal isolates, epidemiological cut-off (ECOFF) values recommended by the European Committee on Antimicrobial Susceptibility Testing (EUCAST, accessed 06.02.2026) were used, with some exceptions as explained further in Appendix 7.

Overview of Sensititre® TREK panels used:

Bacteria tested	Sensititre® TREK panel
Salmonella spp.	EUVSEC3
Campylobacter jejuni/coli	EUCAMP3

Quality assurance systems NORM-VET
The following susceptible bacteria were included as quality controls on a regular basis: *E. coli* ATCC 25922 and *C. jejuni* ATCC 33560. In addition to the regular susceptible bacteria, the following bacteria received from EURL-AR were included: *C. coli* 2012-70-443-2 (EUCAMP3 panel) and *Acinetobacter baumannii* 2012-70-100-69 (EUVSEC3). The NVI and the Reference Laboratory for Enteropathogenic Bacteria/NIPH have a quality assurance system according to the requirements of NS-EN ISO/IEC 17025. The participating laboratories at the NVI are accredited according to the requirements of NS-EN ISO/IEC 17025 and participate in external quality assurance programmes for veterinary pathogens (Veterinary Laboratories Agency Quality Assurance Unit Loughborough, United Kingdom) and for resistance monitoring (EURL for Antimicrobial Resistance, Denmark).

Data processing – animal isolates
Susceptibility data were recorded and stored in the sample registration system at NVI as discrete values (MIC). Data management and analyses were performed in R version 4.5.1 Copyright (C) 2023 (The R Foundation for Statistical Computing Platform). All changes and differences yielding a p-value <0.05 were considered as statistically significant. The 95% confidence intervals were calculated using the exact binomial test.

Susceptibility testing – human isolates
Salmonella spp., *Yersinia* spp. and *Shigella* spp. isolates from humans were susceptibility tested at the NRL for Enteropathogenic Bacteria at the NIPH by agar disk diffusion tests according to the EUCAST standardised method for AMR testing of non-fastidious bacteria. *Campylobacter* isolates from humans were tested for antimicrobial susceptibility using MIC Test Strips.

For human isolates EUCAST clinical breakpoints for *Enterobacteriaceae*, v.16.0 (2026) were used if defined. In absence of clinical breakpoints, ECOFFs or national zone distributions were used (e.g. tetracycline). Pefloxacin was used to infer ciprofloxacin resistance in *Salmonella* and *Shigella*.

Isolates with reduced susceptibility to cefotaxime or ceftazidime were tested for the presence of $ESBL_A$ by a double disk approximation test, and for the presence of $ESBL_M$ by an AmpC detection test. Isolates with reduced susceptibility to meropenem were forwarded to the Norwegian National Advisory Unit on Detection of Antimicrobial Resistance (K-Res) for further analyses.

Genotyping – human isolates
All *Enterobacterales* isolates received at NRL from primary diagnostic laboratories in Norway were screened for antimicrobial resistance determinants using NCBI AMRFinderPlus (v.4.0.15) following whole-genome sequencing (paired end, Illumina) and *de novo* assembly (SKESA 2.4.0) in Ridom SeqSphere+ (v.11.1.0).

Quality assurance systems – human isolates
The NRL for Enteropathogenic Bacteria at the NIPH is accredited according to the requirements of NS-EN ISO/IEC 17025. *E. coli* ATCC 25922 was used as quality control strain for AMR testing of non-fastidious *Enterobacteriaceae.* The NRL participated in the external quality assessment programme of ECDC for *Salmonella* spp. and *Campylobacter* for antimicrobial susceptibility testing.

Data processing – human isolates
The NRL at the NIPH stores susceptibility data of human isolates as either millimeter zone diameters or MIC values. The results were further analysed by WHONET 5.6 with the aid of the BacLink programme, both developed by Dr. John Stelling.

Appendix 5: Sampling, microbiological methods and data processing in NORM

General considerations and sampling

NORM is based on a combination of periodic sampling and testing in primary diagnostic laboratories, and annual results from national reference laboratories for specific microoganisms. Isolates are included from defined clinical conditions such as respiratory tract infections, wound infections, urinary tract infections, and sepsis. Surveillance schemes 2000-2025 are presented in the table below, for enteric infections see Appendix 4. In 2025, all 21 diagnostic laboratories in Norway participated in the surveillance system in addition to eleven reference laboratories. All diagnostic laboratories followed the same sampling strategy and used identical criteria for the inclusion of microbial strains. Only one isolate per patient and infectious episode was included unless otherwise stated. All microbes were identified using conventional methods as described in the ASM Manual of Clinical Microbiology. The surveillance period started in the beginning of January, and consecutive isolates were included for defined time periods for each surveillance category. The surveillance categories and sampling periods in 2025 were as follows: *E. coli* from blood cultures (6 months); *Klebsiella* spp., *Enterococcus* spp., *Staphylococcus aureus* and viridans streptococci from blood cultures (9 months); *Candida* spp. from blood cultures (12 months); *Streptococcus pneumoniae*, *Streptococcus pyogenes, Streptococcus agalactiae, Haemophilus influenzae* and *Neisseria meningitidis* from blood cultures and cerebrospinal fluids (12 months); *S. aureus* from wound specimens (1 week); *S. pneumoniae* from respiratory tract specimens (3 weeks); *E. coli* (3 days), *Klebsiella* spp. and *Enterococcus* spp. (3 weeks) from urinary tract infections; and *Mycobacterium tuberculosis* and *Neisseria gonorrhoeae* from all specimen types (12 months). *S. pneumoniae*, *S. pyogenes*, *N. meningitidis* and *H. influenzae* from blood cultures and cerebrospinal fluids were analysed at the the Norwegian Institute of Public Health (NIPH) in Oslo. *N. gonorrhoeae* was analysed at NIPH and Oslo University Hospital (OUS)/Ullevål. *Candida* spp. isolates were analysed at OUS/Rikshospitalet. MRSA and *S. agalactiae* isolates were analysed at St. Olav University Hospital in Trondheim. *M. tuberculosis* isolates were analysed at NIPH, OUS/Ullevål and Rikshospitalet.

Susceptibility testing

E. coli, *Klebsiella* spp., *Enterococcus* spp., *S. aureus*, viridans streptococci, *S. agalactiae* and *S. pneumoniae* (respiratory tract) were examined according to the EUCAST disk diffusion method using antibiotic disks and Mueller Hinton (MH) II or MH-F agar from either Oxoid or Beckton Dickinson. Suitable antibiotics were selected for each bacterial species, and the results were interpreted according to the most recent breakpoints from NordicAST, which are harmonised with EUCAST. Beta-lactamase production in *S. aureus, H. influenzae* and *N. gonorrhoeae* was examined by nitrocefin disks, acidometric agar plates (3.6 mg/L penicillin G and phenol red) or clover leaf test. *Enterococcus* strains were screened for glycopeptide resistance using vancomycin 6 mg/L BHI agar. *H. influenzae*, *S. pyogenes*, *N. meningitidis* and *N. gonorrhoeae* were susceptibility tested using MIC gradient tests (bioMerieux or Liofilchem) on MH-F agar or GC agar with 1% haemoglobin and Isovitalex (*N. gonorrhoeae*), whereas *S. pneumoniae* (blood and cerebrospinal fluids) isolates were examined using Sensititre microdilution plates from Thermo Fisher Scientific. Susceptibility testing of *Candida* spp. isolates was performed by MIC gradient tests using RPMI agar containing 2% glucose and MOPS. Resistance values were recorded as inhibition zone sizes or MIC values in order to monitor trends in the occurrence of resistance. *M. tuberculosis* isolates were tested using the BACTEC MGIT 960 systems. All three test laboratories for *M. tuberculosis* participate in the WHO external DST quality control programme. They were also tested for mutations in the *rpoB* gene to detect rifampicin resistance.

Confirmation of resistance phenotypes

E. coli and *Klebsiella* spp. with reduced susceptibility to 3rd generation cephalosporins were examined for ESBL production using ESBL combination MIC gradient tests (Liofilchem), disks (BD) or tablets (Rosco) according to the instructions of the manufacturer. *S. aureus* isolates with reduced susceptibility to cefoxitin were examined by *mecA* PCR for confirmation of methicillin resistance (MRSA). *Enterococcus faealis* and *E. faecium* isolates displaying growth on the vancomycin screening agar were examined by *van* PCRs. The MLS phenotype of erythromycin resistant *S. aureus, S. pyogenes, S. agalactiae* and *S. pneumoniae* (respiratory tract) isolates were analysed using the double disk diffusion (DDD) synergy assay with erythromycin and clindamycin disks.

Molecular typing and characterisation of isolates

The NORM report includes specific molecular analyses of carbapenemase-producing Gram-negatives, vancomycin resistant enterococci (VRE) and linezolid resistant enterococci (LRE). These microbes are notifiable to the Norwegian Surveillance System for Communicable Diseases (MSIS) and characterised by the Norwegian Centre for Detection of Antimicrobial Resistance (K-res). The analyses include whole-genome sequencing of the isolates followed by analysis for resistance genes/mutations and molecular typing. Presence of resistance genes/ mutations was analysed using AMR-FinderPlus combined with the Bacterial Antimicrobial Resistance Reference Gene Database (1) plus LRE-Finder specifically for linezolid resistance markers (2). Molecular typing of the isolates was performed at two hierarchal levels using species-specific multilocus sequence typing (MLST) schemes, standard MLST and core genome MLST (cgMLST). Standard MLST includes comparison of the sequence of seven defined species-specific house-keeping genes (alleles) where each allele is assigned an arbitrary number. The standard MLST scheme enables definition of a specific sequence type (ST) (see e.g. https://pubmlst.org/). In contrast, cgMLST includes a defined set of ~1,400-3,800 alleles depending on the species allowing for analysis at a higher resolution (see e.g. references 3 and 4). For each cgMLST scheme a defined reference genome is applied and the analysis includes an allele-by-allele comparison with defined thresholds for cluster analysis (https://www.cgmlst.org/ncs). A comparison table is used for distance calcu-

lation and enables creation of a minimum spanning tree (MST) (5). In the MST, isolates are visualised as circles and lines are created between the closest related isolates. This creates a network of the population. The length of the line is not proportional to the evolutionary distance. However, the number of allele differences between samples are indicated in the MST. Using species-specific defined cut-offs of allele differences for cluster determination, clusters of closely related isolates can be determined and visualised.

References

1. Feldgarden M, Brover V, Gonzalez-Escalona N, et al. AMRFinderPlus and the Reference Gene Catalog facilitate examination of the genomic links among antimicrobial resistance, stress response, and virulence. *Scientific reports* 2021; **11**(1): 12728.
2. Hasman H, Clausen P, Kaya H, et al. LRE-Finder, a Web tool for detection of the 23S rRNA mutations and the optrA, cfr, cfr(B) and poxtA genes encoding linezolid resistance in enterococci from whole-genome sequences. *Journal of antimicrobial chemotherapy* 2019; **74**(6): 1473-6.
3. Zhou Z, Alikhan NF, Mohamed K, Fan Y, Agama Study G, Achtman M. The EnteroBase user's guide, with case studies on Salmonella transmissions, Yersinia pestis phylogeny, and Escherichia core genomic diversity. *Genome Res* 2020; **30**(1): 138-52.
4. Neumann B, Prior K, Bender JK, et al. A Core Genome Multilocus Sequence Typing Scheme for Enterococcus faecalis. *Journal of clinical microbiology* 2019; **57**(3).
5. Francisco AP, Bugalho M, Ramirez M, Carrico JA. Global optimal eBURST analysis of multilocus typing data using a graphic matroid approach. *BMC bioinformatics* 2009; **10**: 152.

Quality control

The following strains were used for quality control: *E. coli* ATCC 25922, *K. pneumoniae* ATCC 700603 (ESBL positive), *E. faecalis* ATCC 29212, *E. faecalis* ATCC 51299 (*vanB* positive), *S. pneumoniae* ATCC 49619, *S. pneumoniae* TIGR4, *S. aureus* ATCC 29213, *S. aureus* ATCC 25923, *S. aureus* ATCC 43300 (heterogeneous MRSA), *S. aureus* CCUG 35600 (homogeneous MRSA), *H. influenzae* ATCC 49766, *N. gonorrhoeae* CCUG 26213/ ATCC 49266, *N. gonorrhoeae* WHO L, *C. albicans* ATCC 90028, *C. krusei* ATCC 6258 and *C. parapsillosis* ATCC 22019.

Data processing

The specially designed web-based eNORM computer programme was used for registration and storage of patient data, sample data and resistance data. The results were further analysed by WHONET 5.6 with the aid of the BacLink programme, both developed by Dr. John Stelling. The distribution of microbial species in blood culture was based on extraction of routine data from the laboratory information systems of the participants. Additional isolates of the same species from the same patient recovered within one month after the initial finding were considered duplicates and omitted from the survey. No attempts were made to evaluate the clinical significance of each finding.

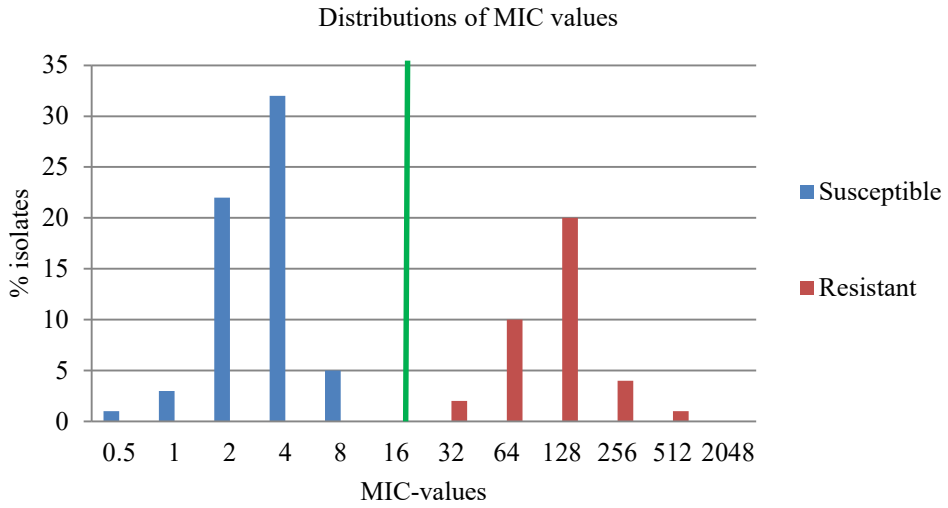
	Microbe	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025
Respiratory tract	*S. pneumoniae*	50	50		50		50		3 w		3 u			3 w		3 w		3 w		3 w		3 w			3 w		3 w
	H. influenzae	50	50			25			3 w				3 w			3 w			3 w					3 w			
	S. pyogenes			50		25		25		2 w					3 w						3 w					3 w	
	GCS/GGS																									3 w	
	M. catarrhalis				50					4 w																	
Urine	*E. coli*	50	50	50	50	50	50	50	1 w	2 d	2 d	2 d	2 w	2 d	2 d	3 d	3 d	3 d	3 d	3 d	3 d	1 w	3 d	3 d	3 d	3 d	3 d
	Klebsiella spp.	50	50		50						3 u			3 w	3 w	3 w	3 w	3 w	3 w	3 w	3 w	3 w	3 w	3 w	3 w	3 w	3 w
	Enterococcus spp.	50	50									2 w					3 w			3 w							3 w
	Enterobacter spp.						50											3 w						3 w			
	Citrobacter spp.																							3 w			
	Serratia spp.																							3 w			
	Proteus spp.							25											3 w								
	P. aeruginosa																				3 w						
Wounds	*S. aureus*		50		50	50		50	2 w	2 w	2 u	1 w	1 w	1 w	1 w	1 w	1 w	1 w	1 w	1 w	1 w	1 w	1 w	1 w	1 w	1 w	1 w
	S. lugdunensis			50		25		25		4 w					3 w						3 w				3 m		
	S. pyogenes			50		25		25		4 w					3 w						3 w					3 w	
	GCS/GGS																			4 w						3 w	
Blood	*E. coli*	50	50	50	50	50	50	50	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m	6 m
	Klebsiella spp.	25	25	25	25	25	25	25	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m
	Enterobacter spp.							12 m	12 m	9 m								9 m						9 m			
	Citrobacter spp.																							9 m			
	Serratia spp.																							9 m			
	Proteus spp.																		9 m								
	P. aeruginosa			12 m	12 m				12 m			12 m					9 m				9 m				12 m		
	Acinetobacter spp.								12 m	12 m															12 m		
	*H. influenzae**														12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m
	*N. menigitidis**														12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m
	S. aureus	50	50	50	50	50	50	50	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m
	S. lugdunensis																								12 m		
	Enterococcus spp.	20	20	20	20	20	20	20	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m	9 m
	*S. pneumoniae**	50	50	50	50	50	50	50	9 m	9 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m
	S. pyogenes (GAS)*						12 m	12 m							12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m
	S. agalactiae (GBS)*							50		12 m			12 m			12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m
	GCS/GGS																			12 m						9 m	
	Obligate anaerober			12 m	12 m	12 m				12 m	12 m	12 m				12 m						12 m					
	Candida spp.							12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m
	Viridans streptococci																										9 m
All locations	*N. gonorrhoeae*											12 m			12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m
	M. tuberculosis	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m	12 m

Surveillance at reference laboratories in red. d=days; w=weeks; m=months. *Also included isolates from cerebrospinal fluids.

Appendix 6:
Definitions and classification of resistances used in this report

General guidelines for the reader of this report

The results presented in the NORM and NORM-VET programmes are not directly comparable. This is because the sampling and also the classification of resistance differ between the programmes. Clinical breakpoints are used for the classification within NORM, while epidemiological cut-off values (ECOFF) are used for the classification of resistance within NORM-VET.



Epidemiological cut-off values

Based on the distribution of the MIC values, or the inhibition zone diameter distribution, each bacterial population could (in an ideal case) be divided into two sub-populations by a biphasic curve as shown in the example above. The curve to the left (blue) shows the susceptible or wild type distribution, whereas the curve to the right (red) shows the resistant or non-wild type distribution. In NORM-VET we have chosen to define the non-wild type distribution as resistant. The green line indicates a possible ECOFF value applicable to the distributions in the example. ECOFF may be used to detect emerging resistance in the bacterial populations.

However, for several bacterial populations and corresponding tested antimicrobial substances these distributions may be overlapping. A part of the population within the overlapping area may carry resistance mechanisms and others not. In the area with the non-wild type distribution, new resistance mechanisms are responsible for the resistance either alone or in addition to the resistance mechanisms present at lower MIC values. In order to establish MIC values for each specific bacterial population and antimicrobial agent, large amounts of data are collected and assessed. In the NORM-VET part of this report, we have mainly used the ECOFF values recommended by EUCAST.

Clinical breakpoints

Clinical breakpoints are defined to indicate if treatment of a specific pathogen is likely to succeed or not. Other factors like dosage and formulations also affect the clinical result. The MIC values are ideally obtained for the pathogen *in vitro*, and this is compared with the pre-determined clinical breakpoint to determine whether the organism is likely to respond *in vivo*.

Term used to describe antimicrobial resistance levels

In this report the levels of resistance (i.e. the percentage of resistant isolates among the tested isolates) in the NORM-VET programme have been classified according to the levels presented in the EFSA and ECDC Summary Report from 2023 and 2024, as follows:

Rare:	< 0.1%
Very Low:	0.1% to 1%
Low:	> 1% to 10%
Moderate:	> 10% to 20%
High:	> 20% to 50%
Very high:	> 50% to 70%
Extremely high:	> 70%

Appendix 7: Cut-off values NORM-VET

Epidemiological cut-off (ECOFF) values recommended by the European Committee on Antimicrobial Susceptibility Testing (EUCAST, accessed 06.02.2026) were used. For additional antimicrobial agents not defined in the EUCAST recommendations, EFSA recommended cut-off values were used.

In the NORM-VET figures; the penicillins are grouped together in the class Beta-lactams/penicillins; trimethoprim and sulfonamides are grouped together in the class Sulfonamides and trimethoprim; macrolides, lincosamides and streptogramins are grouped together in the class Macrolides/lincosamides/streptogramins and the streptomycins are grouped together with other aminoglycosides in the class Aminoglycosides.

Overview of the antimicrobial classes and agents tested for with corresponding epidemiological cut-off values (mg/L) used in NORM-VET 2025:

Antimicrobial class	Antimicrobial agents	*Escherichia coli* (indicators)	*Salmonella enterica*	*Campylobacter coli* / *C. jejuni*	*Enterococcus faecalis* / *E. faecium*	*Staphylococcus felis* (indicators)	*Escherichia coli* (clinical isolates)	*Actinobacillus pleuropneumoniae*	*Staphylococcus felis* (general infections/local ear infections)*
Tetracyclines	Doxycycline							>2	
	Tetracycline	>8	>8	>2 / >1	>4	>1	>8	>2	>1
	Tigecycline	>0.5	ND		>0.25				
Amphenicols	Chloramphenicol	>16	>16	>16	>32	>16			>16
	Florfenicol							>1	>8
Penicillins with extended-spectrum	Ampicillin	>8	>4		>4		>8	>0.5	
	Temocillin	(>16)							
Beta-lactamase sensitive penicillins	Benzylpenicillin					>0.125		>1	>0.125
	Oxacillin								>2
Combinations of penicillins, incl. beta-lactamase inhibitors	Amoxicillin/clavulanate						>8	>1	
1st generation cephalosporins	Cefalexin						>32		ND
2nd generation cephalosporins	Cefoxitin	(>16)				>4			>4
3rd generation cephalosporins	Cefotaxime	>0.25	>0.5				>0.25		
	Ceftazidime	>1	>2						
Combinations of 3rd generation cephalosporins and clavulanic acid	Cefotaxime/clavulanate	(>0.25)							
	Ceftazidime/clavulanate	(>1)							
4th generation cephalosporins	Cefepime	(>0.125)							
Carbapenems	Meropenem	>0.06	ND				>0.06		
	Ertapenem	(>0.03)		ND/>0.125					
	Imipenem	(ND)							
Trimethoprim and derivatives	Trimethoprim	>2	>2			>2			
Sulfonamides	Sulfamethoxazole	>64	ND			ND			
Combinations of sulfonamides and trimethoprim, incl. derivates	Sulfamethoxazole and trimethoprim						>0.5	>0.06	>0.25
Macrolides	Erythromycin			>8 / >4	>4	>1			>1
Lincosamides	Clindamycin					>0.25			>0.25
Streptogramins	Quinupristin and dalfopristin				>32 / >2	>1			
Streptomycins	Streptomycin					>16			

Antimicrobial class	Antimicrobial agents	*Escherichia coli* (indicators)	*Salmonella enterica*	*Campylobacter coli* / *C. jejuni*	*Enterococcus faecalis* / *E. faecium*	*Staphylococcus felis* (indicators)	*Escherichia coli* (clinical isolates)	*Actinobacillus pleuropneumoniae*	*Staphylococcus felis* (general infections/local ear infections)*
Other aminoglycosides	Tobramycin								>2
	Gentamicin	>2	>2	>2	>64 / >32	>2	>2		>2
	Amikacin	>8	>4						
	Kanamycin					>8			
	Neomycin						>8		>1
Fluoroquinolones	Ciprofloxacin	>0.064	>0.064	>0.5	>4 / >8	>2			
	Enrofloxacin						>0.125	>0.125	ND
Other quinolones	Nalidixic acid	>8	>8						
Glycopeptid antibacterials	Vancomycin				>4	>2			
	Teicoplanin				>2				
Polymyxins	Colistin	>2	ND				>2		
	Polymyxin B								
Steroid antibacterial	Fusidic acid					>0.5			>0.5
Nitrofuran derivates	Nitrofurantoin						>64		>32
Pleuromutilins	Tiamulin					>2			
Other antibacterials	Linezolid				>4	>4			
	Daptomycin				>4 / >8				
	Rifampicin					>0.03			
	Mupirocin					>0.1			

ND = not defined, ( ) = only ESBL/AmpC suspected isolates tested as described in Commission Implementing Decision of 17. Nov 2020 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria (2020/1729/EU), data not shown in the report tables. *ECOFFs for *Staphylococcus aureus* used.

Appendix 8: Breakpoints NORM

NORM data are categorised according to the breakpoints of the Nordic Committee on Antimicrobial Susceptibility Testing (NordicAST) which are harmonised with EUCAST breakpoints. NordicAST breakpoints are available at www.nordicast.org.

Zoonotic and non-zoonotic enteropathogenic bacteria are also categorised based on EUCAST epidemiological cut-off values (ECOFF) as specified below.

Antimicrobials	MIC (mg/L) S	MIC (mg/L) R	*Escherichia coli*	*Klebsiella* spp.	*Haemophilus influenzae*	*Neisseria meningitidis*	*Neisseria gonorrhoeae*	*Salmonella* spp.	*Shigella* spp.	*Yersinia enterocolitica*	*Campylobacter jejuni*	*Campylobacter coli*	*Staphylococcus aureus*	*Enterococcus* spp.	*Streptococcus pneumoniae*	*Streptococcus pyogenes*	*Streptococcus agalactiae*	Viridans streptococci	*Candida albicans*	*Candida glabrata*	*Candida parapsilosis*	*Candida dubliniensis*
Amphotericin B	≤ 1	> 1																	■	■	■	■
Ampicillin	≤ 0.5	> 2																■				
	≤ 1	> 1			■																	
	≤ 4	> 4						■[1]						■								
	≤ 8	> 8	■					■	■[2]	■[2]												
Amoxi-Clav*	≤ 2	> 2			■																	
	≤ 8	> 8	■	■[4]																		
	≤ 32	> 32	■	■[4]																		
Anidulafungin	≤ 0.016	> 0.016																	■			
	≤ 0.03	> 0.03																				■
	≤ 0.06	> 0.06																		■		
	≤ 4	> 4																			■	
Aztreonam	≤ 1	> 4	■	■																		
Cefalexin	≤ 16	> 16	■	■[4]																		
Cefepim	≤ 0.5	> 0.5																■				
	≤ 1	> 4	■	■																		
Cefixime	≤ 0.125	> 0.125					■															
Cefotaxime	≤ 0.125	> 0.125			■																	
	≤ 0.25	> 0.25								■[1]												
	≤ 0.5	> 0.5						■[1]										■				
	≤ 0.5	> 2													■							
	≤ 1	> 2	■	■				■	■[2]	■												
Cefoxitin	≥ 22 mm	< 22 mm											■									
Ceftazidime	≤ 1	> 4	■	■				■	■[2]	■[2]												
	≤ 2	> 2						■[1]														
Ceftriaxone	≤ 0.125	> 0.125			■	■	■															
	≤ 0.5	> 2													■							
Cefuroxime	≤ 0.5	> 0.5																■				
	≤ 1	> 2			■																	
Chloramphenicol	≤ 2	> 2			■	■																
	≤ 8	> 8						■[2]	■[2]	■[2]												

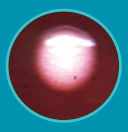
Antimicrobials	MIC (ml/L) S	MIC (ml/L) R	*Escherichia coli*	*Klebsiella* spp.	*Haemophilus influenzae*	*Neisseria meningitidis*	*Neisseria gonorrhoeae*	*Salmonella* spp.	*Shigella* spp.	*Yersinia enterocolitica*	*Campylobacter jejuni*	*Campylobacter coli*	*Staphylococcus aureus*	*Enterococcus* spp.	*Streptococcus pneumoniae*	*Streptococcus pyogenes*	*Streptococcus agalactiae*	Viridans streptococci	*Candida albicans*	*Candida glabrata*	*Candida parapsilosis*	*Candida dubliniensis*
Ciprofloxacin	≤ 0.001	> 0.5									■[2]	■[2]										
	≤ 0.001	> 2											■									
	≤ 0.016	> 0.016				■																
	≤ 0.03	> 0.03			■																	
	≤ 0.03	> 0.06					■															
	≤ 0.06	> 0.06						■[2]	■[2]													
	≤ 0.125	> 0.125								■[1]												
	≤ 0.25	> 0.5	■	■						■												
	≤ 4	> 4												■								
Clindamycin	≤ 0.25	> 0.25											■									
	≤ 0.5	> 0.5													■	■	■	■				
Erythromycin	≤ 0.25	> 0.25													■	■	■					
	≤ 1	> 1											■									
	≤ 4	> 4									■[2]											
	≤ 8	> 8										■[2]										
Fluconazole	≤ 0.001	> 16																		■		
	≤ 2	> 4																	■		■	■
Fosfomycin	≤ 8	> 8	■																			
Fusidic acid	≤ 1	> 1											■									
Gentamicin	≤ 2	> 2	■	■							■[1]	■[1]	■									
	≤ 128	> 128												■								
Imipenem	≤ 0.001	> 4												■[5]								
Linezolid	≤ 2	> 2													■		■					
	≤ 4	> 4											■	■								
Mecillinam	≤ 8	> 8	■	■																		
Meropenem	≤ 2	> 2			■																	
	≤ 2	> 8	■	■				■[2]	■[2]	■[2]												
Micafungin	≤ 0.016	> 0.016																				
	≤ 0.03	> 0.03																	■	■		
	≤ 0.06	> 0.06																				■
	≤ 4	> 4																			■	
Mupirocin	≤ 1	> 1											■									
Nitrofurantoin	≤ 64	> 64	■											■								
Norfloxacin	≥ 10 mm	< 10 mm													■							
Pefloxacin	≥ 23 mm	< 23 mm						■[1]														
	≥ 24 mm	< 24 mm						■	■[2]													

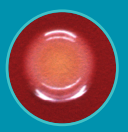
Antimicrobials	MIC (mg/L) S	MIC (mg/L) R	*Escherichia coli*	*Klebsiella* spp.	*Haemophilus influenzae*	*Neisseria meningitidis*	*Neisseria gonorrhoeae*	*Salmonella* spp.	*Shigella* spp.	*Yersinia enterocolitica*	*Campylobacter jejuni*	*Campylobacter coli*	*Staphylococcus aureus*	*Enterococcus* spp.	*Streptococcus pneumoniae*	*Streptococcus pyogenes*	*Streptococcus agalactiae*	Viridans streptococci	*Candida albicans*	*Candida glabrata*	*Candida parapsilosis*	*Candida dubliniensis*
Penicillin G	≤ 0.03	> 0.03														■						
	≤ 0.06	> 1					■								■							
	≤ 0.125	> 0.125															■					
	≤ 0.25	> 0.25				■																
	≤ 0.25	> 1																■				
Pip-Tazo**	≤ 0.001	> 16												■[5]								
	≤ 8	> 8	■	■																		
Rifampicin	≤ 0.06	> 0.06											■									
	≤ 0.125	> 0.125													■							
	≤ 0.25	> 0.25				■																
Spectinomycin	≤ 64	> 64					■															
Tedizolid	≤ 0.5	> 0.5																■[7]				
Tetracycline	≤ 0.5	> 0.5					■															
	≤ 1	> 1											■		■	■	■					
	≤ 2	> 2			■	■					■[2]	■[2]										
	≤ 4	> 4								■[1]												
	≤ 8	> 8						■[1]														
	≥ 17 mm	< 17 mm						■[3]	■[3]	■[3]												
Tigecycline	≤ 0.5	> 0.5	■										■	■								
Trimethoprim	≤ 1	> 1												■								
	≤ 2	> 2	■	■																		
TMS***	≤ 0.5	> 0.5	■	■	■								■			■						
	≤ 1	> 1												■	■							
Vancomycin	≤ 2	> 2											■				■					
	≤ 4	> 4												■[6]								
Voriconazole	≤ 0.06	> 0.25																	■			■
	≤ 0.125	> 0.25																			■	

*Amoxi-Clav=Amoxicillin-clavulanic acid. **Pip-Tazo=Piperacillin-Tazobactam. ***TMS Trimethoprim-sulfamethoxazole. Breakpoints for the combination are given for the trimethoprim component only. [1]Epidemiological cut-off value (ECOFF) based on wild type distribution by EUCAST applied to separate between wild type and non-wild type populations. [2]EUCAST clinical breakpoints or screening cut-off values applied to separate between wild type and non-wild type populations. [3]There are no clinical breakpoints for tetracycline for *Salmonella*, *Shigella* and *Yersinia*. A clinical breakpoint of R < 17 mm based on national data was applied for all three species, and also as screening breakpoint for *Shigella*. [4]*Klebsiella* spp. breakpoints for amoxicillin-clavulanic acid and cefalexin do not apply to *K. aerogenes*. [5]*Enterococcus* spp. breakpoints for imipenem and piperacillin-tazobactam do not apply to species other than *E. faecalis*. [6]*Enterococcus* spp. breakpoints for vancomycin do not apply to species other than *E. faecalis* and *E. faecium*. [7]Viridans streptococci breakpoints for tedizolid do not apply to species other than *S. anginosus*.

Appendix 9:
References used in NORM-VET

- Day MJ, Rodríguez I, van Essen-Zandbergen A, Dierikx C, Kadlec K, Schink AK, Wu G, Chattaway MA, DoNascimento V, Wain J, Helmuth R, Guerra B, Schwarz S, Threlfall J, Woodward MJ, Coldham N, Mevius D, Woodford N. Diversity of STs, plasmids and ESBL genes among *Escherichia coli* from humans, animals and food in Germany, the Netherlands and the UK. J Antimicrob Chemother. 2016 May;71(5):1178-82. https://doi.org/10.1093/jac/dkl095
- Dorado-García A, Smid JH, van Pelt W, Bonten MJM, Fluit AC, van den Bunt G, Wagenaar JA, Hordijk J, Dierikx CM, Veldman KT, de Koeijer A, Dohmen W, Schmitt H, Liakopoulos A, Pacholewicz E, Lam TJGM, Velthuis AG, Heuvelink A, Gonggrijp MA, van Duijkeren E, van Hoek AHAM, de Roda Husman AM, Blaak H, Havelaar AH, Mevius DJ, Heederik DJJ. Molecular relatedness of ESBL/AmpC-producing *Escherichia coli* from humans, animals, food and the environment: a pooled analysis. J Antimicrob Chemother. 2018 Feb 1;73(2):339-347. doi: 10.1093/jac/dkx397. PMID: 29165596.
- European Food Safety Authority (EFSA) and European Centre for Disesase Prevention and Control (ECDC). (2026) The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2023-2024. EFSA Journal 24:e9887. https://doi.org/10.2903/j.efsa.2026.9887
- EURL-AR Laboratory protocol. Isolation of ESBL-, AmpC- and carbapenemase-producing *E. coli* from caecal samples. December 2024. Version 9. https://www.eurl-ar.eu/protocols.aspx
- EURL-AR Laboratory protocol. Isolation of ESBL-, AmpC- and carbapenemase-producing *E. coli* in fresh meat. December 2024. Version 9. https://www.eurl-ar.eu/protocols.aspx
- European Commission 2013. Commission implementing decision of 12 November 2013 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria (2013/652/EU).
- European Commission 2020. Commission implemeting decision (EU) 2020/1729 of 17 November 2020 on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria and repealing Implementing Decision 2013/652/EU.
- NORM/NORM-VET 2004. Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway. Tromsø / Oslo 2005. ISSN: 1502-2307 (print) / 1890-9965 (electronic).
- NORM/NORM-VET 2011. Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway. Tromsø / Oslo 2012. ISSN: 1502-2307 (print) / 1890-9965 (electronic).
- NORM/NORM-VET 2015. Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway. Tromsø / Oslo 2016. ISSN: 1502-2307 (print) / 1890-9965 (electronic).
- NORM/NORM-VET 2017. Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway. Tromsø / Oslo 2018. ISSN: 1502-2307 (print) / 1890-9965 (electronic).
- NORM/NORM-VET 2019. Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway. Tromsø / Oslo 2020. ISSN: 1502-2307 (print) / 1890-9965 (electronic).
- NORM/NORM-VET 2020. Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway. Tromsø / Oslo 2021. ISSN: 1502-2307 (print) / 1890-9965 (electronic).
- NORM/NORM-VET 2021. Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway. Tromsø / Oslo 2022. ISSN: 1502-2307 (print) / 1890-9965 (electronic).
- NORM/NORM-VET 2022. Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway. Tromsø / Oslo 2023. ISSN: 1502-2307 (print) / 1890-9965 (electronic).
- NORM/NORM-VET 2023. Usage of Antimicrobial Agents and Occurrence of Antimicrobial Resistance in Norway. Tromsø / Oslo 2024 ISSN: 1502-2307 (print) / 1890-9965 (electronic).
- Sunde M og Urdahl AM (2025). Første funn av karbapenemase-produserende Enterobacterales hos hund i Norge. Norsk veterinærtidsskrift nr. 9 2025 / 137. https://nvt.vetnett.no/journal/2025/9/m-485/Aktuelle_sykdomsutbrudd_og_diagnoser
- Swedres-Svarm 2024. Sales of antibiotics and occurrence of antibiotic resistance in Sweden. Solna/Uppsala, ISSN2001-7901.
- van der Zwaluw K, de Haan A, Pluister GN, Bootsma HJ, de Neeling AJ, et al. (2015) The Carbapenem Inactivation Method (CIM), a Simple and Low-Cost Alternative for the Carba NP Test to Assess Phenotypic Carbapenemase Activity in Gram-Negative Rods. PLOS ONE 10(3): e0123690. https://doi.org/10.1371/journal.pone.0123690
- World Health Organization. (2019). Critically important antimicrobials for human medicine, 6th rev. World Health Organization. https://iris.who.int/handle/10665/312266. License: CC BY-NC-SA 3.0 IGO





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