SURVEILLANCE REPORT

Antimicrobial resistance in the EU/EEA (EARS-Net)

Annual Epidemiological Report for 2022

Key facts

- In 2022, for the first time, all European Union/European Economic Area (EU/EEA) countries reported data to the European Antimicrobial Resistance Surveillance Network (EARS-Net).
- Compared to 2021, the total number of reported isolates increased from 366 794 to 392 602. The most commonly reported bacterial species in 2022 were *Escherichia coli* (39.2%), followed by *Staphylococcus aureus* (22.1%), *Klebsiella pneumoniae* (12.3%), *Enterococcus faecalis* (8.2%), *Pseudomonas aeruginosa* (6.1%), *Enterococcus faecium* (5.9%), *Streptococcus pneumoniae* (3.7%) and *Acinetobacter* spp. (2.5%). This ranking differed from the ranking in 2021, with *P. aeruginosa* and *S. pneumoniae* one rank higher in 2022.
- On 13 June 2023, the Council of the EU adopted a Recommendation on stepping up EU actions to combat antimicrobial resistance (AMR) in a One Health approach (2023/C 220/01), which recommends targets to be achieved in the EU by 2030. The targets include three AMR targets to reduce the total EU incidence of bloodstream infections with meticillin-resistant *S. aureus* (MRSA), third-generation cephalosporin-resistant *E. coli* and carbapenem-resistant *K. pneumoniae*, by 15%, 10% and 5%, respectively, by 2030 against the baseline year 2019. While the EU incidence of bloodstream infections with both MRSA and third-generation cephalosporin-resistant *E. coli* showed a favourable decreasing trend between 2019 and 2022, the EU incidence of carbapenem-resistant *K. pneumoniae* increased by almost 50%.
- AMR percentages remain high in the EU/EEA and there are specific AMR issues that are a concern, such as the continuous increase in carbapenem-resistant *K. pneumoniae* (10.9% in 2022) and vancomycin-resistant *E. faecium* (17.6% in 2022).
- Of note for 2022 were the decreases in the EU/EEA population-weighted mean AMR percentages for *Acinetobacter* spp. compared to 2021, and a significantly increasing trend for the EU/EEA population-weighted mean percentage of macrolide resistance and penicillin non-wild-type, including combined resistance in *S. pneumoniae* during the period 2018-2022.
- The AMR situation reported by EU/EEA countries varied widely depending on the bacterial species, antimicrobial group and geographical region. In general, the lowest AMR percentages and estimated incidence of bloodstream infections with resistant bacteria were reported by countries in the north of Europe, and the highest by countries in the south and east of Europe.
- For each bacterial species, country-specific information on estimated incidence of bloodstream infections for the EU targets, data availability, and age group, sex and intensive care unit (ICU) patient percentages is available in the country profiles. Results by age group and sex for specific AMR phenotypes are available in European Centre for Disease Prevention and Control (ECDC) Surveillance Atlas of Infectious Diseases (https://atlas.ecdc.europa.eu/).

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Stockholm, November 2023

Methods

The results presented in this report are based on antimicrobial resistance (AMR) data from invasive isolates (retrieved from blood or cerebrospinal fluid samples) reported to the European Antimicrobial Resistance Surveillance Network (EARS-Net) by all (n=30) European Union (EU) and European Economic Area (EEA) countries in 2023 (data referring to 2022). EARS-Net collected data from the United Kingdom (UK), however this stopped as of 2020 when the UK withdrew from the European Union. Data from the UK are excluded from the results in this report. Results for the UK from before 2020, can be found in previous Annual Epidemiological Reports. The latest country-specific data can also be retrieved from the European Centre for Disease Prevention and Control (ECDC) Surveillance Atlas of Infectious Diseases [1].

EARS-Net

EARS-Net is coordinated by ECDC with the aim of collecting, analysing and reporting data on AMR through a network of national surveillance systems across EU/EEA countries and, as defined in the EARS-Net reporting protocol [2], facilitating action to address AMR.

EARS-Net is based on a network of representatives (national focal points for AMR, and operational contact points for epidemiology, microbiology and The European Surveillance System (TESSy)/IT data manager interaction for diseases caused by antimicrobial-resistant microorganisms) from EU/EEA countries that collect routine clinical antimicrobial susceptibility test (AST) data from national AMR surveillance initiatives. Participating institutions are listed in Annex 1. Scientific guidance and support are provided by the EARS-Net Disease Network Coordination Committee, which is composed of experts elected from among the nominated national focal points and operational contact points, complemented by observers from organisations involved in AMR surveillance. EARS-Net activities are coordinated in close collaboration with two other ECDC surveillance networks: the European Surveillance of Antimicrobial Consumption Network (ESAC-Net) and the Healthcare-Associated Infections Surveillance Network (HAI-Net). EARS-Net also collaborates with the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) and with the European Committee on Antimicrobial Susceptibility Testing (EUCAST), which is supported by ECDC and ESCMID. Furthermore, data from EARS-Net are provided to the World Health Organization Regional Office for Europe (WHO/Europe) and available via the WHO/Europe AMR dashboard together with AMR data from the WHO European Region [3]. A summary for the WHO European Region is published jointly with WHO/Europe [4]. ECDC also provides EARS-Net data via WHO/Europe to the WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) [5].

In 2022, all EU Member States and three EEA countries participated in EARS-Net. Since the initiation of the network, there has been a large increase in the number of participating laboratories, which suggests that national AMR surveillance systems in the EU/EEA are being strengthened. The laboratories that participate in the annual EARS-Net external quality assessment (EQA) exercise contribute to improved data quality and an increasing ability of EU/EEA countries to report comparable AMR data [6]. However, not all the laboratories providing EARS-Net data for 2022 choose to participate in the 2022 EARS-Net EQA. The results from the EARS-Net EQA for 2022, including details about the participation rate by country, have been published in a separate report [6].

Antimicrobial susceptibility data

Every year, countries report routine AST results, collected from one or more medical microbiology laboratories, to ECDC. If it is not possible to include data from all the relevant laboratories, countries can report data from sentinel laboratories. Either way, the data reflect the laboratory data that is collected in the surveillance system of each country. The AMR surveillance focuses on invasive isolates of eight key bacterial species (*Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Acinetobacter* species, *Streptococcus pneumoniae*, *Staphylococcus aureus, Enterococcus faecalis* and *Enterococcus faecium*). Other notifiable diseases caused by microorganisms with AMR, such as Campylobacter *spp.*, *Mycobacterium tuberculosis, Neisseria gonorrhoeae*, and *Salmonella spp.*, are also monitored by ECDC but are not included in EARS-Net.

EARS-Net collects AMR data from EU/EEA countries through TESSy in EpiPulse [7], a web-based platform for data submission and storage hosted by ECDC. Previously TESSy was a separate web-based platform, but since 2 July 2023, TESSy has been part of a larger platform called EpiPulse. For detailed information on data collection, refer to the EARS-Net reporting protocol [2].

Only data from invasive (blood and cerebrospinal fluid) isolates are included in EARS-Net. This restriction aims to reduce the impact of different sampling frames which, to some extent, hamper data interpretation. Any bacterial isolate of the species under surveillance found in a sample taken from a normally sterile body fluid may be considered a pathogen. However, including routine, non-invasive isolates may produce incomparable results for surveillance purposes because the processing of such samples is heavily influenced by clinical interpretation, and diagnostic and treatment guidelines, which vary between countries. Historically, EARS-Net accepted data on isolates from both specimen types for *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *Acinetobacter* spp. and

S. pneumoniae, but only isolates from blood for *S. aureus*, *E. faecalis* and *E. faecium*. To harmonise data collection between the Central Asian and European Surveillance of Antimicrobial Resistance (CAESAR) network and EARS-Net, EARS-Net includes data from both specimen types for all bacterial species under surveillance, starting with 2019 data.

Starting with the data collected for 2019, EARS-Net has only accepted data generated using EUCAST clinical breakpoints [8]. Before this, the use of EUCAST breakpoints was encouraged, but results based on other interpretive criteria used by reporting countries were also accepted for analysis.

From 2020 onwards, EUCAST clinical breakpoints for aminoglycosides indicate that in systemic infections caused by *E. coli*, *K. pneumoniae*, *P. aeruginosa* and *Acinetobacter spp.*, aminoglycosides should be used in combination with other active therapies.

It is possible for reporting countries to correct and re-upload historical data. The latest published report therefore supersedes previous reports and reflects the most recent available data. This report is based on data reported to EARS-Net for the period 2018–2022 and retrieved from EpiPulse on 26 August 2023.

Data analysis

Before being analysed, data are de-duplicated to include only the first isolate per patient, year, and bacterial species.

Susceptibility test categories

For the analysis, the qualitative susceptibility categories – 'susceptible, standard dosing regimen' (S), 'susceptible, increased exposure' (I) and 'resistant' (R) – are used, as reported by the laboratory, since quantitative susceptibility information is missing for a large part of the data. An isolate is considered resistant to an antimicrobial agent when tested and interpreted as R in accordance with the clinical breakpoint criteria used by the local laboratory. For *P. aeruginosa*, *E. coli*, *K. pneumoniae*, and *Acinetobacter spp.* and some antimicrobial agent combinations presented in this report, EUCAST breakpoints are available for meningitis versus non-meningitis as of 2021. When possible, EU/EEA countries that generate the susceptibility category at national level are recommended to use non-meningitis breakpoints overall as of 2021 data, but EARS-Net accepts data as it is. As clinical patient data are not collected in EARS-Net, there is no information available regarding which breakpoint was (likely) used to categorise susceptibility. However, it is assumed that a minority of infections reported to EARS-Net stem from meningitis patients, and it is therefore expected that this does not influence the results to a great extent. The term 'penicillin non-wild-type' is used in this report for *S. pneumoniae*, referring to *S. pneumoniae* isolates reported by local laboratories as I or R to penicillin, assuming minimum inhibitory concentrations (MIC) to benzylpenicillin above those of wild-type isolates (> 0.06 mg/L). Before 2019, laboratories not using EUCAST clinical breakpoints may have used different interpretive criteria for the susceptibility categories.

National percentages

AMR/non-wild-type percentages are presented for a single antimicrobial agent and/or group of antimicrobial agents. The bacterial species–antimicrobial agent combinations presented in this report for 2022 are shown in Table 1. When combining results for antimicrobial agents representing an antimicrobial group, the outcome is based on the most resistant result. For example, if the AST result of a bacterial species for imipenem is I and the AST result for meropenem is R, then the AST result for the group carbapenems, which comprises imipenem and meropenem, is set as R. The definition of combined AMR is determined as R to at least one antimicrobial agent in each of the antimicrobial groups (except for *S. pneumoniae*, for which combined AMR is calculated as combined penicillin non-wild-type and R to macrolides). Isolates with missing data for one or more of the required antimicrobial groups are excluded from the analysis of combined AMR. If fewer than 20 isolates are reported for a specific bacterial species–antimicrobial group combination in a country, percentages are not displayed in this report.

Since the analysis of combined resistance excludes isolates with incomplete susceptibility information on the antimicrobial groups included, the analysis can also highlight bacterial species for which the results in EARS-Net may be biased due to selective testing or reporting. For example, if a high proportion of the isolates are missing information on the antimicrobials included for one of the species under EARS-Net surveillance, then this could indicate selective testing.

Population-weighted EU/EEA mean percentage

A population-weighted EU/EEA mean percentage is calculated for each bacterial species–antimicrobial agent combination, based on data reported by EU/EEA countries. Country weightings are used to adjust for imbalances in reporting propensity and population coverage, as in most cases the total number of reported isolates by country does not reflect the population size.

The population-weighted EU/EEA mean percentage is determined by multiplying the AMR percentage for each EU/EEA country with the corresponding national population weight based on the total EU/EEA population, and summing the results. Weights are rescaled if AMR percentages are not available for one or more countries. Annual population data are retrieved from the Eurostat online database [9].

The statistical significance of temporal trends in AMR percentages by country and for the population-weighted EU/EEA (excluding the UK[1]) mean is calculated based on data from the last five years (2018–2022). EU/EEA countries that did not report data for all years within the period under consideration or reported fewer than 20 isolates for the specific bacterial species–antimicrobial agent/group combination in any year within the period are not included in the analysis. The statistical significance of trends is assessed by a chi-square test for trend, and a p-value of < 0.05 is considered significant. An additional sensitivity analysis is performed when assessing the significance of the trends by including only laboratories that continuously reported data for the full five-year period. This minimises bias due to changes in reporting laboratories over time (by expansion of the surveillance network, for instance). In some cases, this restriction results in a considerably lower number of isolates when compared with the analysis that includes all laboratories.

Estimated incidence of bloodstream infections with resistant bacteria

It should be noted that the incidence is an estimate that in turn is based on the estimated national population coverage reported by the countries. The estimated incidence of bloodstream infections with resistant bacteria may therefore need to be interpreted with caution when the national population coverage is estimated as less than 100%. In addition, when the national representativeness is considered by a country to be less than high, further caution in the interpretation may be advisable.

The estimated incidence of bloodstream infections with resistant bacteria is presented for three bacterial species–antimicrobial agent/group combinations: meticillin-resistant *S. aureus*, third-generation cephalosporin-resistant *E. coli*, and carbapenem-resistant *K. pneumoniae*. For each combination, the national incidence is calculated by dividing the number of cases reported as R by the product of the national population, as reported to Eurostat, and multiplying this by the estimated population coverage, as reported to EARS-Net. If the estimated population coverage is missing, the most recently reported coverage for the respective year is used, either the one preceding or following it, whichever comes first. The national results are included in the respective country profile. For the EU the sum of the national cases divided by the national coverage for each country is divided by the total EU population.

The statistical significance of the temporal trend in estimated incidence by country or for the EU is calculated based on data from the last five years (2018–2022). The statistical significance of trends is assessed by negative binomial regression, and a p-value of < 0.05 is considered significant.

The estimated incidence is considered to reflect the incidence of bloodstream infections with the respective resistant bacteria since, in the de-duplicated EARS-Net data, isolates from a blood sample far outweigh those from a cerebrospinal fluid sample. For example, in data for the years 2018–2022 the data each year consisted of less than 1% cerebrospinal fluid samples, and more than 99% blood samples.

Coverage and representativeness of population, hospitals and patients included in EARS-Net

Data sources

Data on coverage, blood culture sets, and representativeness are collected via TESSy/EpiPulse from 2018 onwards [7]. Data for previous years combined TESSy data with data collected through questionnaires distributed to the national focal points for AMR.

[1] Please note that as ECDC collects data from EU/EEA Member States, 2018–2019 data were collected from the UK as the UK was still a Member State of the EU at this time.

Indicators of coverage and representativeness

Population coverage

Population coverage is expressed as the estimated percentage of the population in an entire country under surveillance by the laboratories contributing data to EARS-Net. This value should be considered as an indication of the crude population coverage, since the exact percentage of the population under surveillance is often difficult to assess, due to overlapping hospital catchment areas and patients seeking care in areas where they do not reside. The population coverage is calculated as the mean of the coverage for the following bacterial species: *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *S. aureus*, *E. faecalis* and *E. faecium*. Due to outliers in some countries, *S. pneumoniae* and *Acinetobacter* spp. are not included in the calculation.

Geographical representativeness

Geographical representativeness is a qualitative indicator referring to geographical coverage. The categories for 2022 are listed and described in Table 2. The definition was adjusted as of the data collection done in 2022 [2]. For data reported in 2018–2020, the definition of geographical representativeness can be found in the report 'Antimicrobial resistance surveillance in Europe 2022 – 2020 data' [10].

Hospital representativeness

Hospital representativeness is a qualitative indicator referring to the representativeness of hospitals served by the EARS-Net-participating laboratories, compared to the country distribution of hospital types. The categories are listed and described in Table 2.

Isolate representativeness

Isolate representativeness is a qualitative indicator referring to the representativeness of data reported by EARS-Net laboratories in relation to the microorganisms causing invasive infections in the hospitals included. The categories are listed and described in Table 2. The collection of data related to isolate representativeness was adjusted as of the data collection done in 2022 [2]. For data reported in 2018–2020, isolate representativeness refers to patient and isolate representativeness defined in the report 'Antimicrobial resistance surveillance in Europe 2022 – 2020 data' [10].

Blood culture rate

Blood culture rate refers to the number of blood culture sets taken per 1 000 patient-days in hospitals served by EARS-Net laboratories and sent to these laboratories. The definition of a blood culture set and a patient-day may differ between and within countries and this may influence the estimate. Blood culture rates are calculated as the mean of the blood culture sets divided by the mean total number of patient-days for hospitals served by laboratories that provided the number of blood culture sets taken for the following bacterial species: *E. coli*, *K. pneumoniae*, *P. aeruginosa*, *S. aureus*, *E. faecalis* and *E. faecium*. Due to outliers in some countries, *S. pneumoniae* and *Acinetobacter spp.* are not included in the calculation.

Isolates from intensive care units

The percentage of isolates reported from intensive care units (ICUs) is calculated for each year and each bacterial species. Isolates with missing information on hospital department are excluded from the calculation, and results are only presented if there are ≥20 isolates, 70% of which have data on hospital department.

References

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Table 1. Bacterial species-antimicrobial agent combinations presented in this report for 2022

Bacterial species	Assessed antimicrobial group/agent resistance or specific resistance mechanism	Indicative antimicrobial agent(s)
Escherichia coli	Aminopenicillins	Ampicillin or amoxicillin
	Third-generation cephalosporins	Cefotaxime, ceftriaxone or ceftazidime
	Carbapenems	Imipenem or meropenem
	Fluoroquinolones	Ciprofloxacin, levofloxacin or ofloxacin
	Aminoglycosides	Gentamicin or tobramycin
Klebsiella pneumoniae	Third-generation cephalosporins	Cefotaxime, ceftriaxone or ceftazidime
	Carbapenems	Imipenem or meropenem
	Fluoroquinolones	Ciprofloxacin, levofloxacin or ofloxacin
	Aminoglycosides	Gentamicin or tobramycin
Pseudomonas aeruginosa	Piperacillin-tazobactam	Piperacillin-tazobactam
	Ceftazidime	Ceftazidime
	Carbapenems	Imipenem or meropenem
	Fluoroquinolones	Ciprofloxacin or levofloxacin
	Aminoglycosides	Tobramycin
Acinetobacter species	Carbapenems	Imipenem or meropenem
	Fluoroquinolones	Ciprofloxacin or levofloxacin
	Aminoglycosides	Gentamicin or tobramycin
Staphylococcus aureus	MRSA	Cefoxitin or oxacillin[a]
	Fluoroquinolones	Ciprofloxacin or levofloxacin[b]
	Rifampicin	Rifampicin
Streptococcus pneumoniae	Penicillins	Penicillin or oxacillin[c]
	Third-generation cephalosporins	Cefotaxime or ceftriaxone
	Fluoroquinolones	Levofloxacin or moxifloxacin[d]
	Macrolides	Azithromycin, clarithromycin or erythromycin
Enterococcus faecalis	High-level aminoglycoside resistance	Gentamicin
Enterococcus faecium	Aminopenicillins	Ampicillin or amoxicillin
	High-level aminoglycoside resistance	Gentamicin
	Vancomycin	Vancomycin

MRSA: meticillin-resistant Staphylococcus aureus.

[a] *MRSA is based on AST results for cefoxitin or, if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of* mecA *gene PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA.*

[b] *AST results for norfloxacin are also accepted if neither ciprofloxacin nor levofloxacin results are available.*

[c] *Penicillin results are based on penicillin or, if not available, oxacillin.*

[d] *AST results for norfloxacin are also accepted if neither levofloxacin nor moxifloxacin results are available.*

Table 2. Population and hospitals contributing data: coverage, representativeness and blood culture rate, EU/EEA, 2022 (or latest available data)

Country	Estimated population coverage[a] (%)	Geographical representativeness[b]	Hospital representativeness[c]	Isolate representativeness[d]	Blood culture rate (blood culture sets/ 1 000 patient-days)[e]
Austria	90	High	High	High	ND
Belgium	42[f]	High	Medium	High	115.8[f]
Bulgaria	45	Medium	Medium	Medium	11.3
Croatia	90	High	High	High	34.0
Cyprus	75	High	High	High	84.4
Czechia	80	High	High	High	21.7
Denmark	100	High	High	High	261.2
Estonia	100	High	High	High	39.9
Finland	87	High	High	High	188.6
France	55	High	High	High	58.5
Germany	36	High	Medium	High	ND
Greece	68	High	High	High	ND
Hungary	90	High	High	High	18.4
Iceland	100	High	High	High	69.8
Ireland	93	High	High	High	55.8
Italy	61	High	High	High	60.1
Latvia	90	High	Medium	Medium	16.8
Liechtenstein	40	Medium	Medium	Medium	2.7
Lithuania	100	High	High	High	7.9
Luxembourg	99	High	High	High	43.9
Malta	95	High	High	High	34.9
Netherlands	74	High	High	High	ND
Norway	94	High	High	High	97.3
Poland	18	Medium	Medium	High	51.2
Portugal	97	High	High	High	363.7
Romania	6	ND	Medium	ND	32.5
Slovakia	56	High	High	High	29.5
Slovenia	99	High	High	High	56.4
Spain	30	Medium	High	High	705.3
Sweden	89	High	High	High	ND

ND: no data available.

[a] *As estimated by the national focal points for AMR and/or operational contact points for AMR. Estimated national population coverage: mean population coverage (%) of laboratories reporting* Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, Enterococcus faecalis *and* Enterococcus faecium *to EARS-Net. Due to outliers in some countries,* Streptococcus pneumoniae *and* Acinetobacter *spp. are not included in the calculation.*

[b] *Geographical representativeness. High: all main geographical regions of the country are covered. Medium: most geographical regions of the country are covered. Low: only a few geographical areas of the country are covered.*

[c] *Hospital representativeness. High: the hospital selection is representative of the acute care hospital distribution in the country. Medium: the hospital selection is partly representative of the acute care hospital distribution in the country. Low: the hospital selection is poorly representative of the acute care hospital distribution in the country.*

[d] *Isolate representativeness. High: the isolate selection is representative of microorganisms causing invasive infections in the hospitals included. Medium: the isolate selection is partly representative of microorganisms causing invasive infections in the hospitals included. Low: the isolate selection is poorly representative of microorganisms causing invasive infections in the hospitals included.*

[e] *Blood culture rate (blood culture sets/1 000 patient-days): refers to the mean of the blood culture sets divided by the mean total of patient-days of hospitals served by laboratories that provided the number of blood culture sets performed, as reported for the following bacterial species:* Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Staphylococcus aureus, Enterococcus faecalis *and* Enterococcus faecium*, and multiplied by 1 000. The definition of a blood culture set and a patient-day might differ between countries and influence the estimate.*

[f] *Not including the country's* S. pneumoniae *network.*

Overview of EU/EEA country participation in EARS-Net

In 2023, all EU Member States and EEA countries reported data for 2022 to EARS-Net. Twenty (66.7%) of these 30 countries reported that their participating laboratories had a population coverage of over two-thirds of the national population, including 14 countries that reported having a national population coverage of 90.0% or more. However, seven countries reported data for less than half of their population (Table 2).

Twenty-two (73.3%) of the 30 participating countries indicated that their reported data had a high national representativeness, in terms of three metrics: the geographical areas covered, the acute care hospitals included, and the microorganisms that caused invasive infections in those hospitals. A further three countries reported that the representativeness was 'high' for two of the three metrics, and one country reported that no data were available for two of the three metrics (Table 2).

In hospitals served by the laboratories that reported data to EARS-Net in 2022, the blood culture rate was reported by 25 countries. In the 18 countries that reported a high national representativeness for all three representativeness metrics and provided a blood culture rate, the national average blood culture rate was 3.7 times higher than in the five countries reporting medium, low or no data on national representativeness for at least two of the metrics (84.8 versus 22.9 blood culture sets per 1 000 patient-days, respectively). The reported blood culture rates were highest in Belgium, Denmark, Finland, Portugal and Spain (>100 sets per 1 000 patient-days), and lowest in Bulgaria, Hungary, Latvia, Liechtenstein and Lithuania (<20 sets per 1 000 patient-days) (Table 2).

All but one country reported isolate data for all eight bacterial species under surveillance by EARS-Net (*E. coli*, *K. pneumoniae*, *P. aeruginosa*, *Acinetobacter* spp., *S. pneumoniae*, *S. aureus*, *E. faecalis* and *E. faecium*), while one country (Liechtenstein) reported isolate data for only *E. coli*, *S. pneumoniae* and *S. aureus*.

The number of laboratories participating in EARS-Net has increased since 2018, indicating that national AMR surveillance systems are being strengthened in the EU/EEA. In 2022, 1 845 laboratories reported data, 942 of which were in France. Based on the laboratory identifiers provided by the countries, there were 692 laboratories identifiable as having reported data for each year during the period 2018–2022.

Epidemiology of bacterial species under surveillance in EARS-Net in the EU/EEA

Compared to 2021, the total number of reported isolates increased from 366 794 to 392 602, and among continuously reporting laboratories from 237 630 to 246 944 isolates. The most commonly reported bacterial species from all reporting laboratories in 2022 were *E. coli* (39.2%), followed by *S. aureus* (22.1%), *K. pneumoniae* (12.3%), *E. faecalis* (8.2%), *P. aeruginosa* (6.1%), *E. faecium* (5.9%), *S. pneumoniae* (3.7%) and *Acinetobacter spp.* (2.5%). This ranking differed from the ranking in 2021, with *P. aeruginosa* and *S. pneumoniae* one rank higher in 2022.

Both 2020 and 2021 coincided with extreme COVID-19 pandemic-associated pressures on healthcare. Therefore, it is informative to also compare 2022 data with data from 2019. In addition, even though the representativeness of EARS-Net data is high, restricting analysis to laboratories known to have reported data continuously throughout 2018–2022 ('restricted' dataset) is a way of confirming trends. To analyse changes in the reported number of isolates over time, we excluded two countries from the 'restricted' dataset: France due to changes in the national surveillance system, and Greece for *S. pneumoniae* as this country only started reporting *S. pneumoniae* as of 2022 data. Within this 'restricted' group of laboratories and comparing 2019 to 2022, the largest increases in the number of reported isolates were for *Acinetobacter* spp. (+35.2%; 3 528 and 4 770, respectively), *E. faecium* (+33.2%; 10 584 and 14 097, respectively), *E. faecalis* (+18.5%; 16 096 and 19 075, respectively), *P. aeruginosa* (+12.5%; 12 711 and 14 299, respectively), and *K. pneumoniae* (+11.8%; 26 836 and 29 996, respectively), followed by *S. aureus* (+9.0%; 49 064 and 53 467, respectively). There was a decrease in the number of reported *E. coli* (-1.6%; 101 415 and 99 743, respectively) and *S. pneumoniae* isolates (-12.4%; 12 379 and 10 842, respectively). However, more recently, from 2021 to 2022, a different pattern has emerged: *S. pneumoniae* has increased (+71.2%; 6 333 and 10 842, respectively), and *Acinetobacter* spp. decreased (-29.0%; 6 714 and 4 770, respectively). The remaining pathogens saw changes of ≤6% (*E. faecium and E. faecalis* decreasing; *P. aeruginosa, E. coli, S. aureus, K. pneumoniae* increasing). This more recent pattern indicates that some of the most pronounced changes in the number of isolates reported between 2019 and 2022 are possibly on their way to being reversed.

The AMR situation reported by EU/EEA countries to EARS-Net for 2022 varied widely, depending on the bacterial species, antimicrobial group and geographical region, as demonstrated by both varying AMR percentages and estimated incidences of bloodstream infections with resistant bacteria (Table 3a, Figures 1–10 and country profiles). Overall, for the EU/EEA (excluding the UK), most of the bacterial species–antimicrobial combinations in this report showed either a significantly decreasing trend or no significant trend in the population-weighted mean AMR percentage during 2018−2022. The exceptions were carbapenem resistance in *K. pneumoniae*, piperacillin-tazobactam resistance in *P. aeruginosa*, penicillin non-wild-type and macrolide resistance (a combination of these two types of resistance) in *S. pneumoniae*, and vancomycin resistance in *E. faecium*, for which there was a significant increase during the period 2018−2022 (Table 3a).

In 2022, more than half of the *E. coli* isolates reported to EARS-Net, and almost a third of the *K. pneumoniae* isolates, were resistant to at least one antimicrobial group under surveillance, and combined resistance to several antimicrobial groups was a frequent occurrence. With one notable exception (i.e. carbapenem resistance in *K. pneumoniae*), both *E. coli* and *K. pneumoniae* saw either decreasing trends in the EU/EEA (excluding the UK) population-weighted mean AMR percentages, or no trend. For third-generation cephalosporin-resistant *E. coli*, a decreasing trend in the estimated incidence of bloodstream infections was also noted from 2018 to 2022 for the EU with a 16.8% decrease in 2022 against the baseline year 2019 (Table 3b). Among antimicrobial groups monitored for both species, EU/EEA population-weighted mean AMR percentages were generally higher in *K. pneumoniae* than in *E. coli*.

Carbapenem resistance remained rare in *E. coli*, but almost one third of EU/EEA countries reported carbapenem resistance percentages above 10% in *K. pneumoniae*. Notably, the largest increase (+2.4%) in population-weighted mean AMR percentage under EARS-Net surveillance during 2018−2022 occurred in carbapenem-resistant *K. pneumoniae,* resulting in a significantly increasing trend. In addition, there was a significantly increasing trend in the estimated incidence of bloodstream infections with carbapenem-resistant *K. pneumoniae,* with a 49.7% increase in 2022 against the baseline year 2019 (Table 3b). Carbapenem resistance was also common in *P. aeruginosa* and *Acinetobacter* spp., with a higher EU/EEA population-weighted mean percentage than in *K. pneumoniae*. For most gram-negative bacteria under surveillance, increases in the EU/EEA (excluding the UK) population-weighted mean AMR percentages between 2018 and 2022 were moderate, although AMR remained at high levels, as previously reported. It is also interesting to note that for 2022 the EU/EEA population-weighted mean AMR percentages in *Acinetobacter* spp. showed decreases for all antimicrobial groups under surveillance against 2021.

For *S. aureus*, a significantly decreasing trend in the EU/EEA (excluding the UK) population-weighted mean percentage of meticillin-resistant *S. aureus* (MRSA) isolates, and in the estimated EU incidence of bloodstream infections with MRSA was reported during the period 2018−2022 (Table 3a and Table 3b). Moreover in 2022, there was a 12.2% decrease in the estimated incidence compared to the baseline year 2019. Nevertheless, MRSA remains an important pathogen in the EU/EEA, with levels still high in several countries and combined resistance to another antimicrobial group quite common.

In addition to the increase in the number of reported isolates in 2022 compared to 2021, the last five years have seen a significantly increasing trend for the EU/EEA (excluding the UK) population-weighted mean percentage of macrolide resistance and penicillin non-wild-type, including combined resistance in *S. pneumoniae* (Table 3a).

One development of particular concern was that the significantly increasing trend in the EU/EEA (excluding the UK) population-weighted mean percentage of vancomycin-resistant isolates of *E. faecium* rose further, from 16.2% in 2018 to 17.6% in 2022.

The reported AMR percentages and estimated incidences of bloodstream infections with resistant bacteria varied widely among EU/EEA countries, often with a north-to-south and west-to-east gradient. In general, the lowest AMR percentages were reported by countries in the north of Europe and the highest by countries in the south and east of Europe.

For each bacterial species, country-specific information on the estimated incidence of bloodstream infections (EU recommended targets), data availability and age group, sex and ICU patient percentages is available in the country profiles. Results by age group and sex for specific AMR phenotypes are available in ECDC's Surveillance Atlas of Infectious Diseases [1].

Discussion

In 2022, for the first time, all EU/EEA countries reported data to EARS-Net. Representativeness, as reported by the countries, was high for over 70% of countries. This indicates that, although all EU/EEA countries are included in EARS-Net, there is still work to be done in some countries to improve surveillance representativeness.

Overall, the EU/EEA population-weighted mean AMR percentages for the bacterial species-antimicrobial group combinations under surveillance continued to be high in the EU/EEA in 2022.

Specifically, 2022 saw the largest increase in carbapenem-resistant *K. pneumoniae* in the EU/EEA (excluding the UK) population-weighted mean percentage AMR from 2018 against all other bacterial species antimicrobial group combinations. An increasing trend in the percentage of carbapenem-resistant *K. pneumoniae* and a significantly increasing trend in the estimated incidence of bloodstream infections at EU level for the same period were also of considerable concern. Similarly, the increase in the number of *E. faecium* isolates reported since 2019, with a significantly increasing trend in the EU/EEA population-weighted mean vancomycin resistance percentage since 2018, indicates that AMR remains a serious challenge in the EU/EEA.

Another development of concern in 2022 was the fact that the number of *S. pneumoniae* invasive infections reported showed signs of returning to a level similar to that in 2019, following a decline in 2020–2021 when more COVID-19 non-pharmaceutical interventions were in place in the EU/EEA [2]. In addition, there was an increasing trend in EU/EEA population-weighted mean combined penicillin non-wild-type and macrolide resistance.

As in previous years, overall there was a wide variability in the AMR percentages across EU/EEA countries in 2022, highlighting the opportunities for significant AMR reduction through interventions to improve infection prevention and control (IPC) and antimicrobial stewardship practices.

There were also indications of potential improvements. The previously-noted deterioration in the *Acinetobacter* spp. situation [3,4] showed signs of improving, with decreasing numbers of reported isolates and EU/EEA population-weighted mean resistance percentages in 2022 compared to 2021. This suggests a continued requirement for *Acinetobacter* spp.-specific control interventions in affected hospitals [5], while indicating that interventions may have had some effect. In addition, *E. coli* showed either no trend or decreasing trends in the EU/EEA population-weighted mean resistance percentages, further supported by a decreasing trend in the estimated incidence of third-generation cephalosporin-resistant *E. coli* bloodstream infections at EU level. *S. aureus* also saw a declining trend in the EU/EEA population-weighted mean percentage of MRSA, as well as in the estimated EU incidence of MRSA bloodstream infections from 2018 to 2022. However, despite these encouraging developments, AMR percentages remain high in the EU/EEA. ECDC estimated that in the EU/EEA in 2020 alone, the number of infections with antibiotic-resistant bacteria that are under EARS-Net surveillance was more than 800 000, resulting in over 35 000 deaths [6].

On 13 June 2023, the Council of the EU adopted a Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health approach (2023/C 220/01), which recommends targets to be achieved by the EU by 2030 [7]. These include three AMR targets to reduce the total incidence of bloodstream infections with MRSA, third-generation cephalosporin-resistant *E. coli* and carbapenem-resistant *K. pneumoniae*, by 15%, 10% and 5%, respectively, by 2030 against the baseline year 2019. The data for 2022 have shown favourable decreasing trends in the estimated incidence of bloodstream infections at EU level for the EU targets on MRSA and third-generation cephalosporin-resistant *E. coli*.

For the third EU indicator – the total incidence of bloodstream infections with carbapenem-resistant *K. pneumoniae* – there was an almost 50% increasing trend during the period 2019–2022, which means that, instead of progressing towards its 5% reduction target by 2030, the situation in the EU has worsened since 2019. This increase indicates the need to rapidly strengthen prevention and control actions, in the EU and in Member States, as highlighted in the Council Recommendation [7]. The widely varying estimated incidences of bloodstream infections with resistant bacteria and AMR percentages among countries suggest that there are further opportunities for reduction (see country profiles). For carbapenem-resistant *K. pneumoniae* and other carbapenem-resistant Enterobacterales (CRE) specifically, the options for action are highlighted in the 2019 update of ECDC's rapid risk assessment on CRE, including timely and appropriate diagnosis, high standards of IPC and antimicrobial stewardship [8].

The data for the years 2020 and 2021 coincided with the first years of the COVID-19 pandemic. Changes to human behaviour in 2020–2021 to control the pandemic, and then again in 2022 as the number of non-pharmaceutical interventions were reduced, may have modified the risk of infection by pathogens with AMR. However, unlike antimicrobial consumption in the EU/EEA [9], for AMR under EARS-Net surveillance there was no uniform pattern across the surveillance data. Some of the bacterial species, such as *Acinetobacter* spp. and *S. pneumoniae,* showed indications of having been affected by the COVID-19 pandemic and the actions taken during this time. However, these two bacterial species followed different patterns (increases and decreases, respectively, during 2020–2021, and a reversal of the changes in 2022). These changes point towards the importance of IPC in healthcare settings, as well as non-pharmaceutical interventions in the community.

The magnitude of the impact of the Russian war of aggression against Ukraine on the data reported to EARS-Net is unclear. In 2022, there were reports from EU/EEA countries of the detection of multi-drug resistant organisms in patients having recently been hospitalised in Ukraine [10, 11]. On 8 March 2022, ECDC published a report entitled 'Operational public health considerations for the prevention and control of infectious diseases in the context of Russia's aggression towards Ukraine' [12]. The report presents considerations for hospitalised patients in the EU/EEA, including recommendations that patients transferred from hospitals in Ukraine, or with a history of hospitalisation in Ukraine during the last 12 months, should be isolated pre-emptively and screened for carriage of multidrug-resistant organisms.

The results in this report provide an overview of the AMR situation in the EU/EEA. However, when interpreting the EARS-Net data, it is important to be mindful of the structure of this surveillance system, including the large variation in national blood culture rates, and the changes in the national surveillance systems and in EARS-Net over time. It is also worth noting that there has not been a systematic assessment of the characteristics and AMR data of the EU/EEA laboratories that do not report to EARS-Net. Nevertheless, EARS-Net surveillance data do reflect the overall AMR situation in the EU/EEA.

The European Health Union has been created to better protect the health of EU citizens [13]. This includes strengthened mandates for ECDC and the European Medicines Agency (EMA), the creation of the European Health Emergency preparedness and Response Authority (HERA) and a new Regulation on serious cross-border threats to health that was adopted by the Council on 24 October 2022 [14]. Moreover, a large budget is available under the EU4Health programme (EUR 5.3 billion for the period 2021–2027), which is one of the main instruments for the European Health Union, dedicated to wider policy areas and including action on AMR. In line with this, the recently adopted 'Council of the EU Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health approach' includes not only AMR and antimicrobial consumption targets, but also encourages Member States to improve surveillance where needed, and develop National Action Plans (NAPs) against AMR including implementation and regular updates. In addition, the Recommendation highlights the need for Member States to provide the necessary resources to implement the NAPs, with the European Commission providing support for this where required.

Public health implications

Public health action to tackle AMR in the EU/EEA remains insufficient, despite the increased awareness of AMR as a threat to public health and the availability of evidence-based guidance for IPC, antimicrobial stewardship, and adequate microbiological capacity. AMR will be an increasing concern unless governments respond more robustly to the threat. More specifically, the fear is that more infections with bacteria resistant to antibiotics will be harder to treat, leading to an increase in suffering and deaths. Estimates based on data from EARS-Net show that in 2020, more than 800 000 infections in the EU/EEA were due to bacteria resistant to antibiotics, and that more than 35 000 people died as a direct consequence of these infections [6].

Data from 2022 not only indicate the necessity for IPC in healthcare settings, even during trying circumstances such as a pandemic, but also the potential effects of non-pharmaceutical interventions. Data from 2022 also show that AMR levels remain high in the EU/EEA and that there are specific AMR issues of concern, such as the continuing increase in carbapenem-resistant *K. pneumoniae* and vancomycin-resistant *E. faecium*.

Further investment in public health interventions is urgently needed to tackle AMR. This would have a significant positive impact on population health and future healthcare expenditure in the EU/EEA. These interventions could include infection prevention and control measures, such as promotion of better hand hygiene in healthcare to prevent transmission; antibiotic stewardship programmes, such as rapid testing of patients to discriminate viral from bacterial infections, and the promotion of prudent antibiotic usage, to prevent bacteria developing AMR; and mass media campaigns, to raise public awareness of AMR. In 2019, the Organisation for Economic Co-operation and Development (OECD) estimated that a mixed intervention package including enhanced hygiene, antibiotic stewardship programmes, mass media campaigns, and the use of rapid diagnostic tests would have the potential to prevent approximately 27 000 deaths each year in the EU/EEA. In addition to saving lives, such a package could pay for itself within just one year and save around EUR 1.4 billion per year in the EU/EEA [15].

Table 3a. Total number of invasive isolates tested (n) and percentages isolates with AMR phenotype (%) in the EU/EEA (excluding the UK), by bacterial species and antimicrobial group/agent, population-weighted EU/EEA mean and trend (excluding the UK)[a], 2018–2022

Bacterial species	Antimicrobial group/agent resistance	2018		2019		2020		2021		2022		2022 EU/EEA country range[b]	Trend 2018–2022[c]
		n	%	n	%	n	%	n	%	n	%		
Escherichia coli	Aminopenicillin (amoxicillin/ampicillin) resistance	104 198	57.0	102 375	56.6	107 371	54.6	108 836	53.1	116 543	53.4	32.5–68.6	↓*
	Third-generation cephalosporin (cefotaxime/ceftriaxone/ceftazidime) resistance	124 043	15.7	131 325	15.6	139 057	14.9	143 286	13.8	152 633	14.3	5.8–40.2	↓*
	Carbapenem (imipenem/meropenem) resistance	120 215	0.1	127 262	0.3	135 624	0.2	137 632	0.2	147 793	0.2	0.0–1.5	-
	Fluoroquinolone (ciprofloxacin/levofloxacin/ofloxacin) resistance	123 358	26.4	132 015	24.7	139 372	23.8	143 359	21.9	151 842	22.0	9.9–46.4	↓*
	Aminoglycoside (gentamicin/netilmicin/tobramycin) resistance[d]	122 147	11.2	130 984	10.8	136 101	10.9	139 541	9.6	147 616	9.7	4.4–24.3	↓*
	Combined resistance to third-generation cephalosporins, fluoroquinolones, and aminoglycosides[d]	120 450	6.4	129 083	6.1	134 115	5.7	137 863	5.1	144 919	5.1	1.5–14.2	↓*
Klebsiella pneumoniae	Third-generation cephalosporin (cefotaxime/ceftriaxone/ceftazidime) resistance	33 239	34.4	36 190	34.1	39 848	33.9	43 317	34.3	47 855	32.7	3.1–78.5	↓
	Carbapenem (imipenem/meropenem) resistance	32 548	8.5	35 439	9.0	39 279	10.0	42 063	11.6	46 847	10.9	0.0–72.0	↑*
	Fluoroquinolone (ciprofloxacin/levofloxacin/ofloxacin) resistance	33 154	34.3	36 315	34.0	40 066	33.9	43 192	33.6	47 579	32.0	5.7–78.7	↓*
	Aminoglycoside (gentamicin/netilmicin/tobramycin) resistance[d]	32 830	24.7	36 078	24.5	38 977	23.7	42 237	23.7	46 660	22.5	0.0–67.9	↓*
	Combined resistance to third-generation cephalosporins, fluoroquinolones, and aminoglycosides[d]	32 381	21.6	35 622	21.5	38 331	21.0	41 646	21.2	45 815	20.0	0.0–66.2	↓
Pseudomonas aeruginosa	Piperacillin-tazobactam resistance	16 018	18.5	16 894	18.6	19 799	18.8	21 455	18.7	23 039	19.3	3.8–50.5	↑*
	Ceftazidime resistance	16 327	15.5	17 328	15.7	20 122	15.5	21 786	15.7	23 480	16.2	2.1–56.6	-
	Carbapenem (imipenem/meropenem) resistance	16 473	18.8	17 496	18.1	20 517	17.9	22 303	18.1	23 873	18.6	2.4–53.9	-
	Fluoroquinolone (ciprofloxacin/levofloxacin) resistance	16 460	21.2	17 635	20.5	20 425	19.6	22 165	18.7	23 665	18.6	2.8–49.2	↓*
	Aminoglycoside (gentamicin/netilmicin/tobramycin) resistance[e]	16 393	12.9	17 552	12.6	12 880	9.4	14 573	8.9	18 153	8.9	0.0–42.2	NA
	Combined resistance to ≥3 antimicrobial groups (among piperacillin-tazobactam, ceftazidime, carbapenems, fluoroquinolones and aminoglycosides)[e]	15 514	14.1	16 289	13.5	12 041	13.6	13 720	12.6	17 177	13.4	0.0–47.7	NA
Acinetobacter species	Carbapenem (imipenem/meropenem) resistance	5 798	36.4	5 209	36.9	7 507	37.9	10 732	39.9	9 397	36.3	1.0–98.6	-
	Fluoroquinolone (ciprofloxacin/levofloxacin) resistance	5 754	41.1	5 181	40.9	7 372	41.7	10 626	43.0	9 339	38.8	0.0–98.6	-
	Aminoglycoside (gentamicin/netilmicin/tobramycin) resistance[d]	5 711	35.2	5 170	36.9	7 275	37.0	10 399	39.6	9 169	34.1	0.0–96.2	-
	Combined resistance to carbapenems, fluoroquinolones and aminoglycosides[d]	5 607	32.4	4 998	33.6	7 111	34.0	10 172	36.8	8 835	31.8	0.0–96.2	-
Staphylococcus aureus	MRSA[f]	63 837	17.8	65 604	17.2	72 976	16.7	78 665	15.8	84 397	15.2	1.1–50.8	↓*

Bacterial species	Antimicrobial group/agent resistance	2018		2019		2020		2021		2022		2022 EU/EEA country range[b]	Trend 2018–2022[c]
		n	%	n	%	n	%	n	%	n	%		
Streptococcus pneumoniae	Penicillin non-wild-type[g]	14 498	14.0	14 568	13.2	8 076	15.5	8 479	16.2	13 230	16.3	2.8–46.7	↑*
	Macrolide (azithromycin/clarithromycin/erythromycin) resistance	14 753	16.6	15 069	15.9	8 407	16.8	8 773	18.3	13 947	17.9	3.4–36.1	↑*
	Combined penicillin non-wild-type and resistance to macrolides[g]	14 016	8.6	14 102	8.0	7 782	8.9	8 155	9.8	12 694	9.7	0.8–33.3	↑*
Enterococcus faecalis	High-level gentamicin resistance	15 343	27.1	13 577	25.3	14 316	29.0	16 324	28.9	17 146	25.3	6.7–100.0	-
Enterococcus faecium	Vancomycin resistance	13 346	16.2	14 095	17.7	18 349	16.8	22 328	17.2	22 709	17.6	0.0–67.7	↑*

NA: not applicable.

[a] The population-weighted EU/EEA mean and trend, including UK data between 2018 and 2019, can be found in previous Annual Epidemiological Reports.

[b] Lowest and highest national AMR percentage among reporting EU/EEA countries (n=30).

*[c] ↑ and ↓ indicate statistically significant increasing and decreasing trends, respectively, in the overall data; * indicates confirmation by a significant trend in the data that only includes laboratories reporting continuously for all five years; – indicates no statistically significant trend. NA: not applicable indicates that a significant change in data sources occurred during the period.*

[d] The aminoglycoside group includes only gentamicin and tobramycin from 2020 onwards.

[e] The aminoglycoside group includes only tobramycin from 2020 onwards.

[f] MRSA is based on AST results for cefoxitin or, if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of mecA *gene PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA.*

[g] Penicillin results are based on penicillin or, if unavailable, oxacillin. For S. pneumoniae*, the term penicillin non-wild-type is used in this report, referring to* S. pneumoniae *isolates reported by local laboratories as susceptible, increased exposure or resistant (R) to penicillin, assuming MIC to benzylpenicillin above those of wild-type isolates (> 0.06 mg/L). The qualitative susceptibility categories (S/I/R) as reported by the laboratory are used, since quantitative susceptibility information is missing for a large part of the data. Laboratories not using EUCAST clinical breakpoints in 2018 may have used different interpretive criteria for the susceptibility categories.*

Table 3b. Estimated total incidence of bloodstream infections with MRSA, third-generation cephalosporin-resistant *Escherichia coli*, and carbapenem-resistant *Klebsiella pneumoniae* (number per 100 000 population) and trend, 2018–2022, as well as the percentage change 2019–2022, by bacterial species and antimicrobial group/agent, EU[a] (excluding the UK)

Bacterial species	Antimicrobial group/agent resistance	Estimated incidence[b] of isolates from bloodstream infections with resistance phenotype (number per 100 000 population)						
		2018	2019 (baseline year)	2020	2021	2022	Trend 2018–2022[c]	Change 2019–2022 (%)[d]
Staphylococcus aureus	MRSA[e]	5.80	**5.63**	5.41	4.76	4.94	↓	**-12.2**
Escherichia coli	Third-generation cephalosporin (cefotaxime/ceftriaxone/ceftazidime) resistance	10.10	**10.42**	8.69	7.54	8.67	↓	**-16.8**
Klebsiella pneumoniae	Carbapenem (imipenem/meropenem) resistance	1.87	**2.18**	3.18	3.70	3.26	↑	**+49.7**

[a] For each individual EU Member State, a similar table is available as part of the country profiles.
[b] Incidence was estimated using the EARS-Net data reported to EpiPulse. Each de-duplicated isolate from a blood sample (>99% data) or cerebrospinal fluid sample (<1% data) was considered a proxy for a bloodstream infection.
[c] ↑ and ↓ indicate statistically significant increasing and decreasing trends, respectively.
[d] The 'Council Recommendation on stepping up EU actions to combat antimicrobial resistance in a One Health approach', (2023/C 220/01), includes 2030 EU targets, with 2019 as the baseline year: https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=OJ:JOC_2023_220_R_0001
[e] MRSA is based on AST results for cefoxitin or, if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of mecA *gene PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA.*

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Bacterial species-specific results

Escherichia coli

Epidemiology

For 2022, 30 EU/EEA countries reported 153 874 isolates of *E. coli*. Among the laboratories that continuously reported data during 2018–2022 (excluding France due to changes in the surveillance system), when comparing 2019 to 2022, there was a decrease in the number of reported *E. coli* isolates (-1.6%; 101 415 and 99 743, respectively). However, more recently, from 2021 (n=95 631) to 2022, the number or reported *E. coli* isolates increased by +4.3%.

Of all reported isolates, 152 633 (99.2%) had AST results for third-generation cephalosporins, 151 842 (98.7%) for fluoroquinolones, 147 793 (96.0%) for carbapenems, 147 616 (95.9%) for aminoglycosides, and 116 543 (75.7%) for aminopenicillins (Table 3a).

At EU/EEA level, more than half (53.2%) of the *E. coli* isolates reported to EARS-Net for 2022 were resistant to at least one of the antimicrobial groups under surveillance (aminopenicillins, fluoroquinolones, third-generation cephalosporins, aminoglycosides and carbapenems) (Table 4). In 2022, the highest EU/EEA population-weighted mean resistance percentage was reported for aminopenicillins (53.4%), followed by fluoroquinolones (22.0%), third-generation cephalosporins (14.3%), and aminoglycosides (9.7%). Resistance to carbapenems remained rare (0.2%) (Table 3a).

Between 2018 and 2022, there was no significant trend in the EU/EEA population-weighted mean percentage for carbapenem resistance, while the EU/EEA trends for aminopenicillin resistance, third-generation cephalosporin resistance, fluoroquinolone resistance, and aminoglycoside resistance decreased significantly during the same period. When restricting the analysis to include only laboratories that continuously reported data for all five years, all trends remained significant (Table 3a). However, compared to the period 2018−2021, annual increases in EU/EEA-level resistance percentages were seen in 2022 for third-generation cephalosporins (+0.5%), aminopenicillins (+0.3%), fluoroquinolones (+0.1%), and aminoglycosides (+0.1%) (Table 3a).

During the period 2018-2022, the estimated incidence of bloodstream infections with third-generation cephalosporin-resistant *E. coli* decreased and showed a significantly decreasing trend in the EU (Table 3b). Moreover, in 2022 there was a 16.8% decrease in the estimated incidence against the baseline year 2019.

Resistance to multiple antimicrobial groups was common. Among the resistant phenotypes, resistance to aminopenicillins, both as single resistance and in combination with other antimicrobial groups, was the most common at EU/EEA level (Table 4). In 2022, the percentage of combined resistance, measured as resistance to third-generation cephalosporins, fluoroquinolones and aminoglycosides, was 5.1% (EU/EEA population-weighted mean) and this showed a statistically significant decreasing trend during the period 2018–2022. When the analysis was restricted to include only laboratories that continuously reported data for all five years (Table 3a), the decreasing trend remained.

With the exception of carbapenem resistance, which remained low in all countries, large inter-country variations were noted for all the antimicrobial groups under surveillance (Table 3a), with generally higher AMR percentages reported from southern and eastern Europe than from northern Europe (Figures 1–3).

Table 4. ***Escherichia coli.*** **Total number of invasive isolates tested (n = 105 282)[a] and AMR percentage (%) per phenotype, EU/EEA, 2022**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**49 223**	**46.8**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**34 241**	**32.5**
Aminopenicillins	31 227	29.7
Fluoroquinolones	2 612	2.5
Other antimicrobial groups	402	0.4
Resistance to two antimicrobial groups		
Total (any two-group combinations)	**10 519**	**10.0**
Aminopenicillins + fluoroquinolones	5 925	5.6
Aminopenicillins + third-generation cephalosporins	2 731	2.6
Aminopenicillins + aminoglycosides	1 739	1.7
Other antimicrobial group combinations	124	0.1
Resistance to three antimicrobial groups		
Total (any three-group combinations)	**7 223**	**6.9**
Aminopenicillins + third-generation cephalosporins + fluoroquinolones	4 995	4.7
Aminopenicillins + fluoroquinolones + aminoglycosides	1 625	1.5
Other antimicrobial group combinations	603	0.6
Resistance to four antimicrobial groups		
Total (any four-group combinations)	**4 028**	**3.8**
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides	3 980	3.8
Other antimicrobial group combinations	48	<0.1
Resistance to five antimicrobial groups		
Aminopenicillins + third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	**48**	**<0.1**

[a] Only isolates with complete susceptibility information for aminopenicillins (amoxicillin or ampicillin), third-generation cephalosporins (cefotaxime, ceftriaxone or ceftazidime), carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin, levofloxacin or ofloxacin) and aminoglycosides (gentamicin or tobramycin) were included in the analysis. This represented 68% (105 282/153 874) of all reported E. coli *isolates.*
[b] Only AMR combinations >1% of the total are specified.
[c] Not adjusted for population differences in the reporting countries.
[d] Aminopenicillins (amoxicillin or ampicillin), third-generation cephalosporins (cefotaxime, ceftriaxone or ceftazidime), carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin, levofloxacin or ofloxacin) and aminoglycosides (gentamicin or tobramycin).

Figure 1. ***Escherichia coli.*** **Percentage of invasive isolates resistant to fluoroquinolones (ciprofloxacin/levofloxacin/ofloxacin), by country, EU/EEA, 2022**

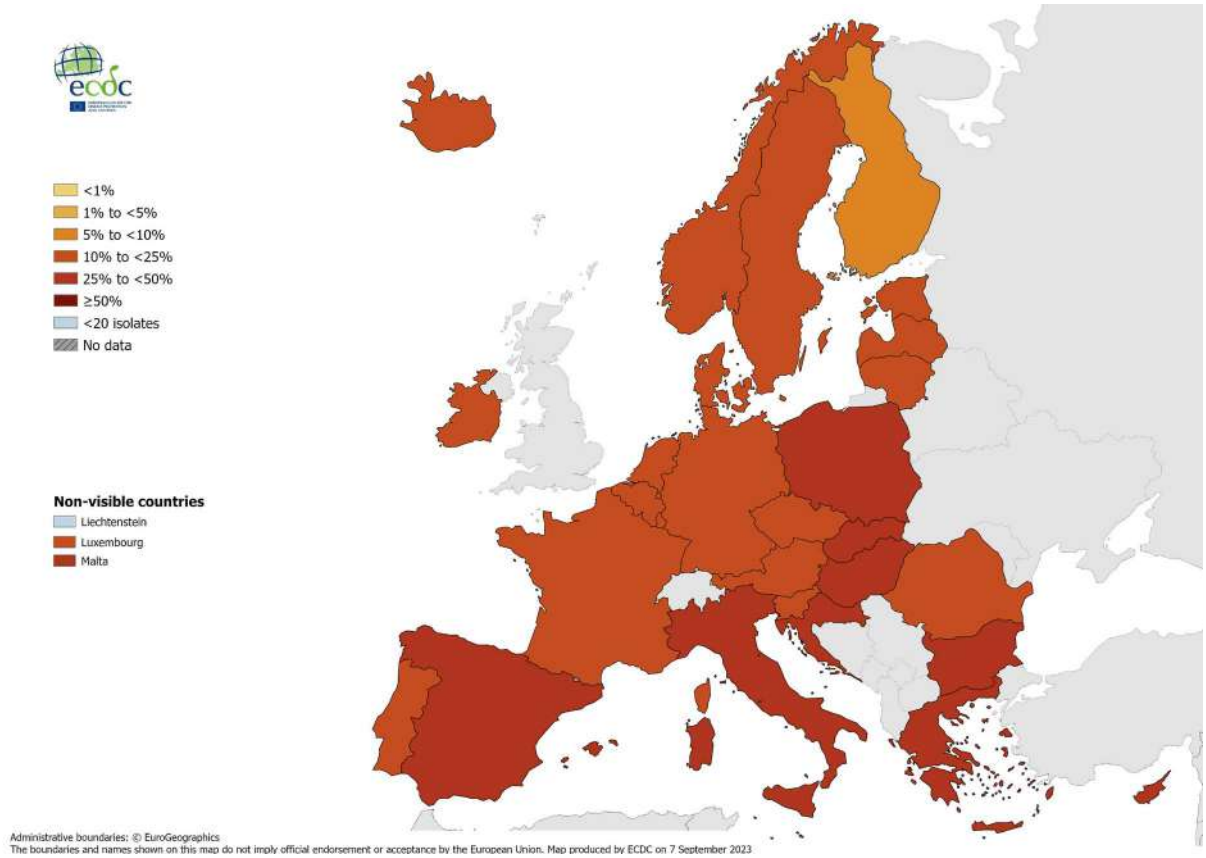


Figure 2. ***Escherichia coli*****. Percentage of invasive isolates resistant to third-generation cephalosporins (cefotaxime/ceftriaxone/ceftazidime), by country, EU/EEA, 2022**

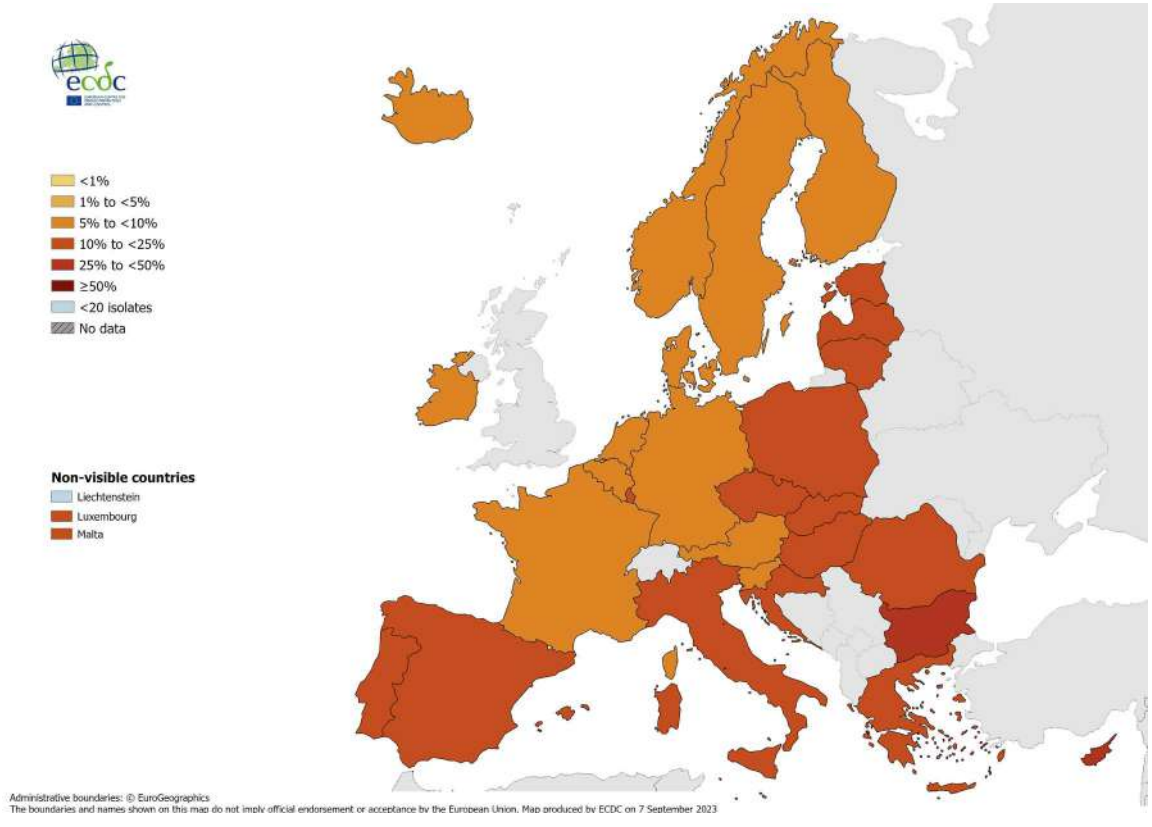
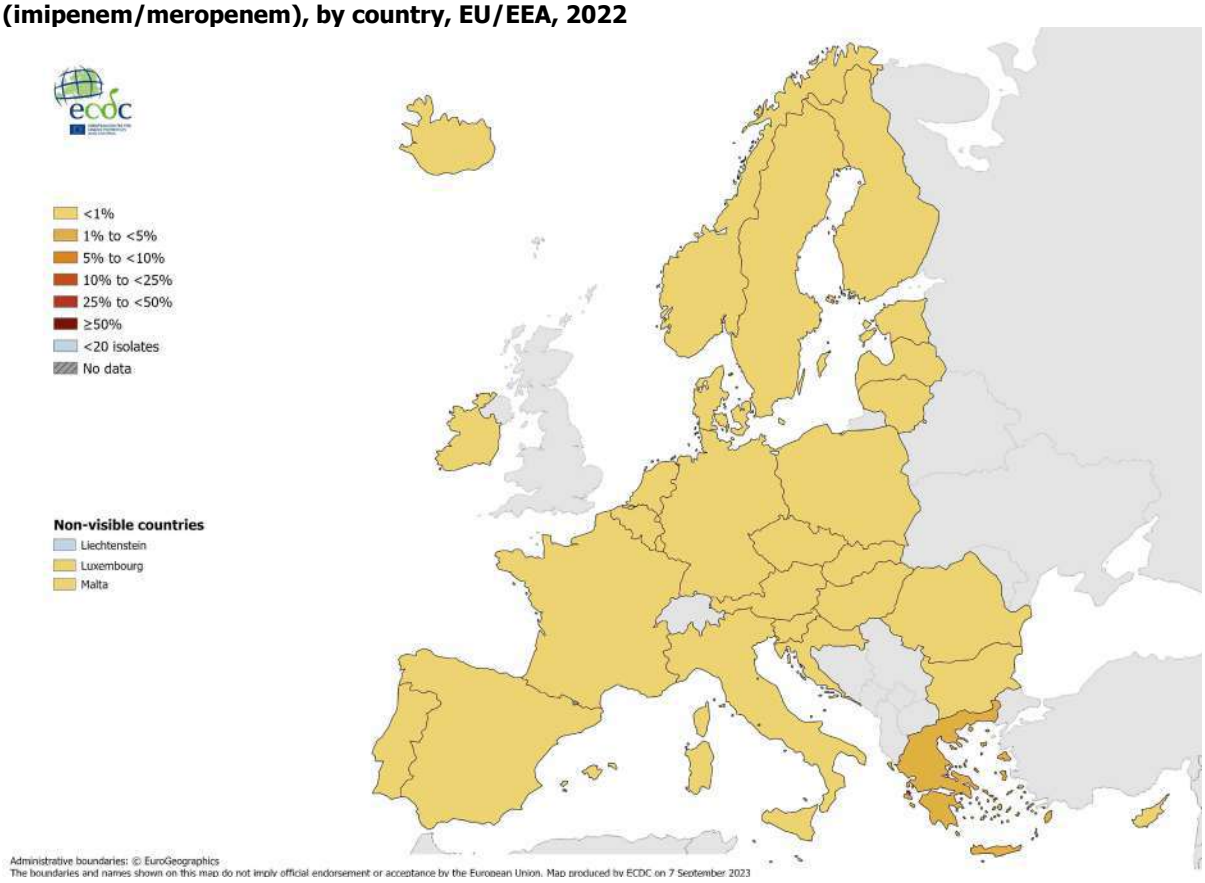


Figure 3. *Escherichia coli*. Percentage of invasive isolates resistant to carbapenems (imipenem/meropenem), by country, EU/EEA, 2022



Discussion

E. coli is a major cause of bloodstream infection in Europe, and prompt access to effective antimicrobial treatment is essential to reduce the health-related and economic burden caused by *E. coli* infection. In ECDC's study of the EU/EEA health burden of AMR for the period 2016–2020, the largest burden of disease was caused by infections with third-generation cephalosporin-resistant *E. coli*, both in terms of the number of cases and the number of attributable deaths [1]. As antimicrobial-resistant *E. coli* infections commonly occur in the community, interventions to reduce the burden of infection should not be restricted to hospital settings, but should also target primary and community care.

With a decrease of 16.8% against the baseline year 2019, the estimated EU incidence of bloodstream infections with third-generation cephalosporin-resistant *E. coli* for 2022 indicates that the EU has been progressing towards the agreed target of a 10% reduction in incidence by 2030 [2].

Time-series analyses of EU/EEA population-weighted means for third-generation cephalosporin resistance and fluoroquinolone resistance in *E. coli* reported to EARS-Net for the years 2002–2018 have shown that, although AMR percentages increased substantially during the period, the increase was most prominent until around 2012, before becoming less pronounced [3]. A significantly declining EU/EEA trend was noted for both antimicrobial groups for the five-year period presented in this report (2018–2022). This was further underpinned by the 2022 EARS-Net EQA results, indicating that the under-reporting of decreased susceptibility towards fluroquinolones noted in the 2021 EARS-Net EQA is no longer present, and that in the 2022 EARS-Net EQA there was over-reporting of resistance to ceftazidime [4]. Nevertheless, percentages of AMR reported for 2022 remain high, underlining the need for further efforts to improve antimicrobial stewardship and IPC.

Use of broad-spectrum antimicrobials is a known risk factor for the colonisation and spread of antimicrobial-resistant Enterobacterales, including *E. coli*. Associations between national AMR percentages in *E. coli* and national antimicrobial consumption rates have been reported [5]. Although the latest data from ESAC-Net show a considerable decrease in antimicrobial consumption in 2020 and 2021 compared to previous years and an increase for 2022 [6], such a pattern is not clearly reflected for the EU/EEA population-weighted mean AMR percentages for *E. coli* and *K. pneumoniae*.

Given that high levels of AMR have been reported in *E. coli* isolates from food-producing animals in Europe, including a low occurrence of isolates with carbapenemase production [7], ensuring cross-sectoral collaboration between the human, veterinary and food-production sectors is essential in a 'One-Health' approach, which addresses AMR in both humans and food-producing animals. ECDC is working closely with the European Food Safety Authority (EFSA) and the EMA to better understand the interrelationships between antimicrobial use and AMR in humans and animals across Europe. In 2021, the three agencies produced the third joint inter-agency report on integrated analysis of antimicrobial agent consumption and occurrence of AMR in bacteria from humans and food-producing animals [5].

Carbapenem-resistant isolates remained rare among the invasive *E. coli* isolates included in EARS-Net. However, an increase in serious infections caused by carbapenem-resistant *E. coli* would have severe consequences on the burden of AMR in the EU/EEA. Carbapenem-resistant Enterobacterales (CRE) infections are associated with high mortality, primarily due to delays in the administration of effective treatment and the limited availability of treatment options. The 2019 update of ECDC's rapid risk assessment on CRE highlights the need for high standards in IPC, combined with adequate microbiological capacity to detect and prevent further spread [8].

Carbapenem resistance is most often mediated by a range of carbapenemases and there are carbapenemase-producing isolates that test susceptible to meropenem and/or imipenem, based on clinical breakpoints. One example is OXA-244-producing *E. coli* which, in routine clinical microbiology laboratories may only be classified as extended-spectrum beta-lactamase-producing rather than carbapenemase-producing *E. coli*, unless specifically tested for OXA-48-like carbapenemases. An ECDC risk assessment on OXA-244-producing *E. coli* [9] indicated a pan-European problem, with a high risk of OXA-244-producing *E. coli* spreading further in the EU/EEA, given the rapid and simultaneous increase in multiple countries between 2016 and 2019. In addition, a recent study based on *E. coli* data from the EU/EEA in 2012−2020 collected by ECDC with a focus on another carbapenemase, New Delhi metallo-β-lactamase (NDM)-5, concluded that *E. coli* carrying the related gene $bla_{\text{NDM-5}}$ are spreading rapidly and could contribute to further carbapenem resistance in the coming years [10]. There is a risk that spread of carbapenemase-producing *E. coli* in the community may further contribute to the loss of carbapenems as options for treatment of multidrug-resistant *E. coli* infections. This highlights the need to further investigate the sources and routes of transmission for carbapenemase-producing *E. coli*.

To address the need and to complement the phenotypic-based surveillance data available from EARS-Net, the periodic carbapenem- and/or colistin-resistant Enterobacterales (CCRE) surveys are now incorporated into a network – the European Antimicrobial Resistance Genes Surveillance Network (EURGen-Net) [11]. The latest survey results will provide information on the prevalence and distribution of carbapenemases and contribute to a better understanding of the epidemiology of CRE in Europe and risk factors associated with CRE infection and colonisation. ECDC is also able, to a limited extent, to provide Member States with access to whole-genome sequencing services, primarily for investigating potential multi-country outbreaks. By way of example, these services were provided for a combined clonal and plasmid-mediated outbreak of carbapenemase-producing Enterobacterales (CPE) in Lithuania during the period 2019−2020 [12].

Klebsiella pneumoniae

Epidemiology

For 2022, 29 EU/EEA countries reported 48 261 isolates of *K. pneumoniae*. Among the laboratories that continuously reported data during 2018–2022 (excluding France due to changes in the surveillance system), when comparing 2019 to 2022, there was an increase in the number of reported *K. pneumoniae* isolates (+11.8%; 26 836 and 29 996, respectively). This includes a 6.0% increase in the number of reported *K. pneumoniae* isolates between 2021 and 2022.

Of all reported isolates, 47 855 (99.2%) had AST results for third-generation cephalosporins, 47 579 (98.6%) for fluoroquinolones, 46 847 (97.1%) for carbapenems, and 46 660 (96.7%) for aminoglycosides (Table 3a).

At EU/EEA level, more than a third (39.2%) of the *K. pneumoniae* isolates reported to EARS-Net for 2022 were resistant to at least one of the antimicrobial groups under surveillance (fluoroquinolones, third-generation cephalosporins, aminoglycosides, and carbapenems) (Table 5). In 2022, the highest EU/EEA population-weighted mean resistance percentage was reported for third-generation cephalosporins (32.7%), followed by fluoroquinolones (32.0%), aminoglycosides (22.5%) and carbapenems (10.9%) (Table 3a).

Between 2018 and 2022, there was a significantly increasing trend in the EU/EEA population-weighted mean percentage for carbapenem resistance, and the largest increase (+2.4%) in population-weighted mean AMR percentage under EARS-Net surveillance during 2018−2022 occurred in carbapenem-resistant *K. pneumoniae*. At the same time, the EU/EEA trend for third-generation cephalosporins, fluoroquinolones and aminoglycoside resistance decreased significantly. When the trend analysis was restricted to include only laboratories that continuously reported data, the EU/EEA trends for carbapenems, fluoroquinolones and aminoglycosides remained significant (Table 3a).

It is interesting to note that the annual change in resistance percentage at EU/EEA level decreased for all of the antimicrobial groups, including carbapenems, between 2021 and 2022. During the same period, the annual decrease for third-generation cephalosporins, fluoroquinolones and aminoglycosides was larger than during the period 2018−2021 (Table 3a).

During the period 2018-2022, the estimated EU incidence of bloodstream infections with carbapenem-resistant *K. pneumoniae* increased from 1.87 to 3.26 cases per 100 000 population, indicating a significantly increasing trend (Table 3b). Moreover in 2022, there was a 49.7% increase in the estimated incidence compared to the baseline year 2019.

Single resistance was less commonly reported than resistance to two, three or four antimicrobial groups, with the most common AMR phenotype being combined resistance to third-generation cephalosporins, fluoroquinolones and aminoglycosides (Table 5). The EU/EEA population-weighted mean for combined resistance to fluoroquinolones, third-generation cephalosporins and aminoglycosides was 20.0% in 2022 and showed a statistically significant decreasing trend during the period 2018−2022 (Table 3a). However, when the analysis was restricted to laboratories that continuously reported data, this trend disappeared.

Large inter-country variations were noted for all antimicrobial groups under surveillance (Table 3a), with generally higher AMR percentages reported from southern and eastern Europe than from northern Europe (Figures 4 and 5). Nine countries reported carbapenem resistance percentages above 10.0% for *K. pneumoniae* [13]. The countries reporting the highest percentages of carbapenem resistance in *K. pneumoniae* were also among those reporting the highest AMR percentages for the other antimicrobial groups.

Table 5. ***Klebsiella pneumoniae.*** **Total number of invasive isolates tested (n = 44 610)[a] and AMR percentage (%) per phenotype, EU/EEA, 2022**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups [d]	**27 103**	**60.8**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**3 590**	**8.0**
Third-generation cephalosporins	1 774	4.0
Fluoroquinolones	1 620	3.6
Other antimicrobial groups	196	0.4
Resistance to two antimicrobial groups		
Total (any two-group combinations)	**3 846**	**8.6**
Third-generation cephalosporins + fluoroquinolones	2 748	6.2
Third-generation cephalosporins + aminoglycosides	520	1.2
Other antimicrobial group combinations	578	1.3
Resistance to three antimicrobial groups		
Total (any three-group combinations)	**6 100**	**13.7**
Third-generation cephalosporins + fluoroquinolones + aminoglycosides	4 855	10.9
Third-generation cephalosporins + fluoroquinolones + carbapenems	1 188	2.7
Other antimicrobial group combinations	57	0.1
Resistance to four antimicrobial groups		
Third-generation cephalosporins + fluoroquinolones + aminoglycosides + carbapenems	**3 971**	**8.9**

[a] Only isolates with complete susceptibility information for third-generation cephalosporins (cefotaxime, ceftriaxone or ceftazidime), carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin, levofloxacin or ofloxacin) and aminoglycosides (gentamicin or tobramycin) were included in the analysis. This represented 92% (44 610/48 261) of all reported K. pneumoniae *isolates.*
[b] Only AMR combinations >1% of the total are specified.
[c] Not adjusted for population differences in the reporting countries.
[d] Third-generation cephalosporins (cefotaxime, ceftriaxone or ceftazidime), carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin, levofloxacin or ofloxacin) and aminoglycosides (gentamicin or tobramycin).

Figure 4. ***Klebsiella pneumoniae*****. Percentage of invasive isolates resistant to third-generation cephalosporins (cefotaxime/ceftriaxone/ceftazidime), by country, EU/EEA, 2022**

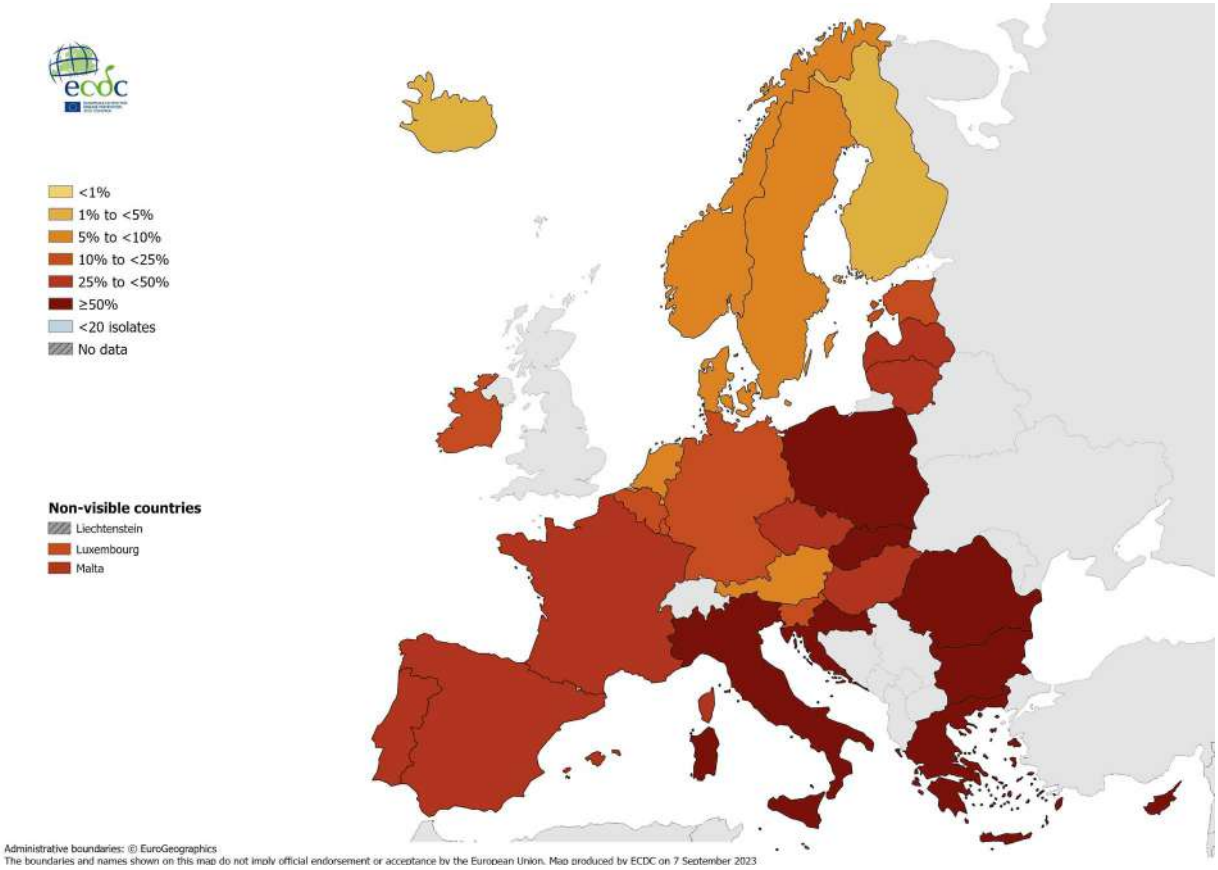
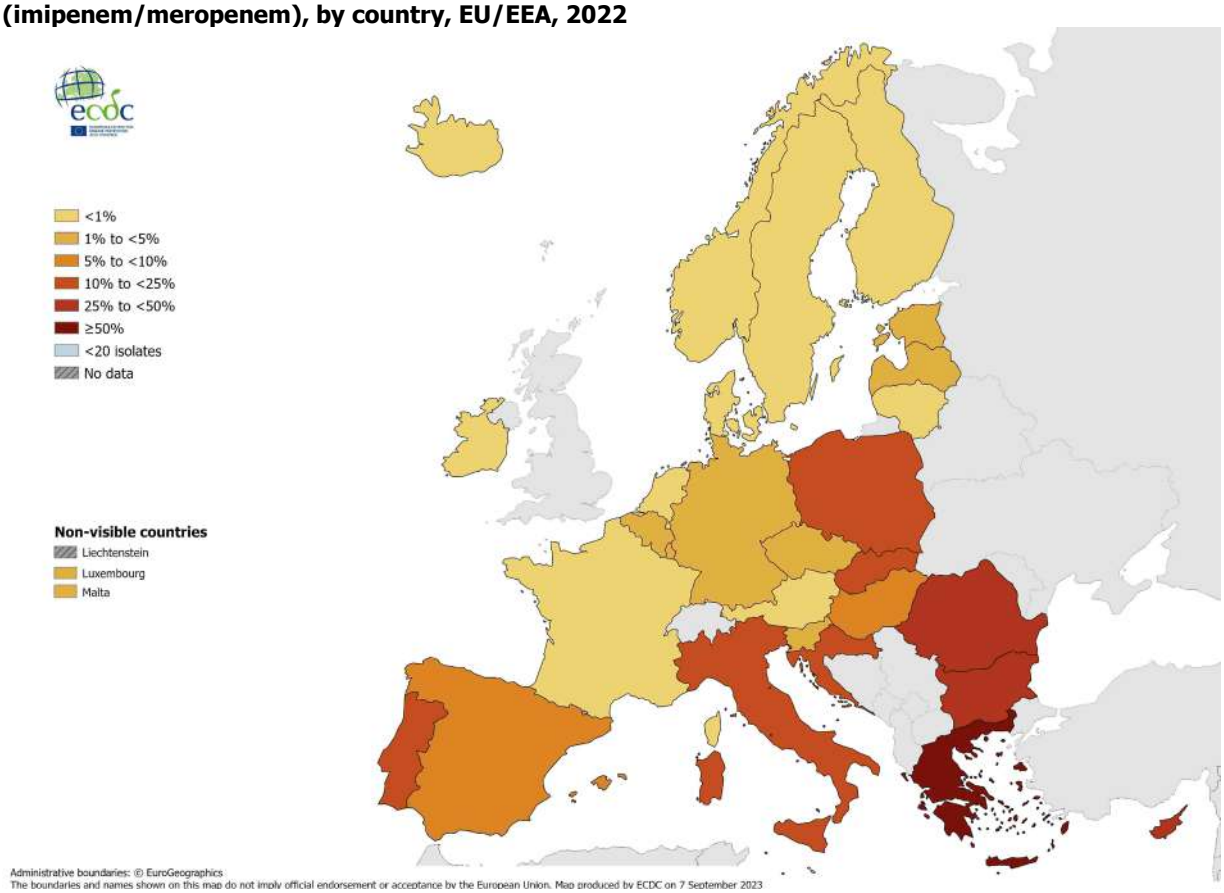


Figure 5. ***Klebsiella pneumoniae*****. Percentage of invasive isolates resistant to carbapenems (imipenem/meropenem), by country, EU/EEA, 2022**



Discussion

The AMR situation with *K. pneumoniae* in the EU/EEA remains problematic. ECDC's study of the EU/EEA health burden of AMR for the period 2016–2020 showed that the largest burden of disease was caused by infections with third-generation cephalosporin-resistant *E. coli*, followed by MRSA and third-generation cephalosporin-resistant *K. pneumoniae*. Infections with these three antibiotic-resistant bacteria resulted in the largest health impact, generating 58.2% of the total burden, as measured in disability-adjusted life years (DALYs) [1].

Moreover, the estimated EU incidence of bloodstream infections with carbapenem-resistant *K. pneumoniae* for 2022, which increased by just under 50% against 2019, is an indication that overall the EU is not progressing towards the agreed target of a 5% reduction in incidence by 2030, compared to baseline year 2019 [2].

In addition, although the 2021 EARS-Net EQA indicated that decreased carbapenem susceptibility in *K. pneumoniae* was probably over-reported in 2021 [14], there was nevertheless a significantly increasing trend in the EU/EEA population-weighted mean percentages for carbapenem resistance during the period 2018 to 2022. Carbapenem resistance was almost always combined with resistance to several other key antimicrobial groups, leading to a severely limited range of treatment options for serious infections caused by this type of bacteria. ECDC's studies of the AMR health burden found that even though the level of carbapenem-resistant *K. pneumoniae* was relatively low, the impact of AMR on the EU/EEA health burden is heavy because of the high level of attributable mortality caused by these infections [1,15]. In 2020, the number of deaths attributable to carbapenem-resistant *K. pneumoniae* in 2020 was estimated to be 4 076 [1]. This underlines the need for continuous close monitoring and greater efforts to respond efficiently to this public health threat.

The highest percentages of carbapenem resistance were observed in southern and eastern Europe, similar to the distribution of CPE reflected in a survey conducted by EURGen-Net [16]. Results from EURGen-Net also show that in several EU/EEA countries the situation deteriorated between 2010 and 2018 with regard to the spread of CPE [16]. Numerous reports on outbreaks with varying potential for or recorded cross-border spread of CRE demonstrate the transmission potential in the healthcare systems of EU/EEA countries [17–19]. Outbreaks and clusters in EU/EEA countries also highlight the importance of detecting CRE early in settings with low incidence, due to high transmissibility [17–21].

CRE can be resistant to carbapenems as a result of a variety of mechanisms, but most frequently through production of carbapenemase enzymes. It is not possible to assess the overall presence and spread of CPE from the data available through EARS-Net, as some carbapenemases do not confer a fully carbapenem-resistant phenotype. One example is the OXA-48-like carbapenemase enzymes, which present a particular problem for laboratory detection because of their weak capacity to hydrolyse carbapenems [17].

Recent outbreaks of carbapenemase (NDM-1 and OXA-48)-producing and colistin-resistant *K. pneumoniae* have highlighted the concomitant increase in virulence, transmissibility and AMR among certain *K. pneumoniae* strains. These strains pose a considerably higher risk to human health than the *K. pneumoniae* strains that previously circulated. A 2021 rapid risk assessment by ECDC raised the issue of emerging hypervirulent *K. pneumoniae* ST23 carrying carbapenemase genes [22]. The limited information available so far indicates that very few cases and clusters have been reported in the EU/EEA. Nevertheless, early detection of such strains, and close cooperation between clinicians and public health services is crucial to prevent them spreading among the patient population in the EU/EEA.

There is a need for increased capacity in the EU/EEA to support outbreak investigations and surveillance with real-time whole genome sequencing in order to identify high-risk clones and implement enhanced control measures to avoid further spread [20-21]. One initiative to address this need is the CCRE surveys (part of EURGen-Net) that will provide updated and more detailed information on the distribution of carbapenemase-producing *K. pneumoniae* in Europe [11].

As highlighted in the 2019 update of ECDC's rapid risk assessment on CRE, options for action include timely and appropriate diagnosis, high standards of IPC and antimicrobial stewardship [8]. Many EU/EEA countries have developed and implemented recommendations and guidance documents on multidrug-resistant Enterobacterales and/or CRE [23], indicating a trend towards nationally coordinated responses to this public health threat. To support countries, ECDC published a guidance document on how to prevent the entry and spread of CRE into healthcare settings in 2017. The guidance outlines evidence-based best practices for the prevention of CRE, including measures for intervention that can be adopted or adapted to local needs, depending on the availability of financial and structural resources [24].

It should be noted that the data reported on *K. pneumoniae* may have been affected by changes over time in the identification and nomenclature of *K. pneumoniae*. Species previously but no longer identified as *K. pneumoniae* are less often found to be resistant. As a result, the reported percentage of resistant *K. pneumoniae* in the EU/EEA may have increased over time. The size of the impact, in terms of changes in identification and nomenclature, is unknown.

Resistance to newly released antimicrobials has turned out to be a challenge for the optimal treatment of infections with CRE that are resistant to these new antimicrobials [25]. This highlights the need to also monitor for resistance to new antimicrobials. In addition, WHO sees a critical need for research and development of new antibiotics targeting ESBL-producing and carbapenem-resistant Enterobacterales, including *K. pneumoniae* and *E. coli* [26].

Pseudomonas aeruginosa

Epidemiology

For 2022, 29 EU/EEA countries reported 24 136 isolates of *P. aeruginosa*. Among the laboratories that continuously reported data during 2018–2022 (excluding France due to changes in the surveillance system), when comparing 2019 to 2022, there was an increase in the number of reported *P. aeruginosa* (+12.5%; 12 711 and 14 299, respectively). This includes an increase from 2021 to 2022, when the number or reported *P. aeruginosa* isolates increased by +4.0%.

Of all reported isolates, 23 873 (98.9%) had AST results for carbapenems, 23 665 (98.0%) for fluoroquinolones, 23 480 (97.3%) for ceftazidime, 23 039 (95.5%) for piperacillin-tazobactam and 18 153 (75.2%) for aminoglycosides (Table 3a).

In the EU/EEA, 32.4% of the *P. aeruginosa* isolates reported to EARS-Net for 2022 were resistant to at least one of the antimicrobial groups under surveillance (piperacillin-tazobactam, fluoroquinolones, ceftazidime, aminoglycosides and carbapenems) (Table 6). The highest EU/EEA population-weighted mean resistance percentage in 2022 was reported for piperacillin-tazobactam (19.3%), followed by fluoroquinolones (18.6%) and carbapenems (18.6%), and ceftazidime (16.2%) and aminoglycosides (8.9%) (Table 3a).

Between 2018 and 2022, EU/EEA population-weighted mean resistance percentage trends decreased significantly for fluoroquinolones and increased for piperacillin-tazobactam. When the analysis was restricted to include only laboratories that continuously reported data for all five years, the trends remained statistically significant (Table 3a). For *P. aeruginosa* and aminoglycosides there was a considerable change in the analysis as of 2020 which could affect the results when compared with the period 2018−2019, and the trend for this bacterial species antimicrobial group combination is therefore not calculated (Table 3a).

It is interesting to note that the annual change in EU/EEA population-weighted mean resistance percentage indicated an increase for all of the antimicrobial groups/agents from 2021 to 2022, except for fluoroquinolones and aminoglycosides. For the former antimicrobial groups/agents the annual increase was larger than in the previous years of the period 2018−2021 (Table 3a).

Resistance to two or more antimicrobial groups was common: found in 19.7% of all tested isolates (Table 6). Between 2018 and 2022, the EU/EEA population-weighted mean percentage of combined resistance, defined as resistance to at least three of the antimicrobial groups under surveillance, was not calculated due to the considerable change in the analysis as of 2020 that could affect the results when compared with the period 2018−2019 (Table 3a). Large inter-country variations were noted for all antimicrobial groups (Table 3a), with reported AMR percentages generally higher from southern and eastern Europe than northern Europe (Figure 6) [13].

Table 6. ***Pseudomonas aeruginosa.*** **Total number of invasive isolates tested (n = 17 180)[a] and AMR percentage (%) per phenotype, EU/EEA, 2022**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**11 622**	**67.6**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**2 170**	**12.6**
Carbapenems	859	5.0
Fluoroquinolones	804	4.7
Piperacillin-tazobactam	344	2.0
Other antimicrobial groups	163	0.9
Resistance to two antimicrobial groups		
Total (any two group combinations)	**1 473**	**8.6**
Piperacillin-tazobactam + ceftazidime	746	4.3
Fluoroquinolones + carbapenems	295	1.7
Other antimicrobial group combinations	432	2.5
Resistance to three antimicrobial groups		
Total (any three group combinations)	**723**	**4.2**
Piperacillin-tazobactam + ceftazidime + carbapenems	272	1.6
Piperacillin-tazobactam + ceftazidime + fluoroquinolones	193	1.1
Other antimicrobial group combinations	258	1.5
Resistance to four antimicrobial groups		
Total (any four group combinations)	**480**	**2.8**
Piperacillin-tazobactam + fluoroquinolones + ceftazidime + carbapenems	283	1.6
Other antimicrobial group combinations	197	1.1
Resistance to five antimicrobial groups		
Piperacillin-tazobactam + fluoroquinolones + ceftazidime + aminoglycosides + carbapenems	**712**	**4.1**

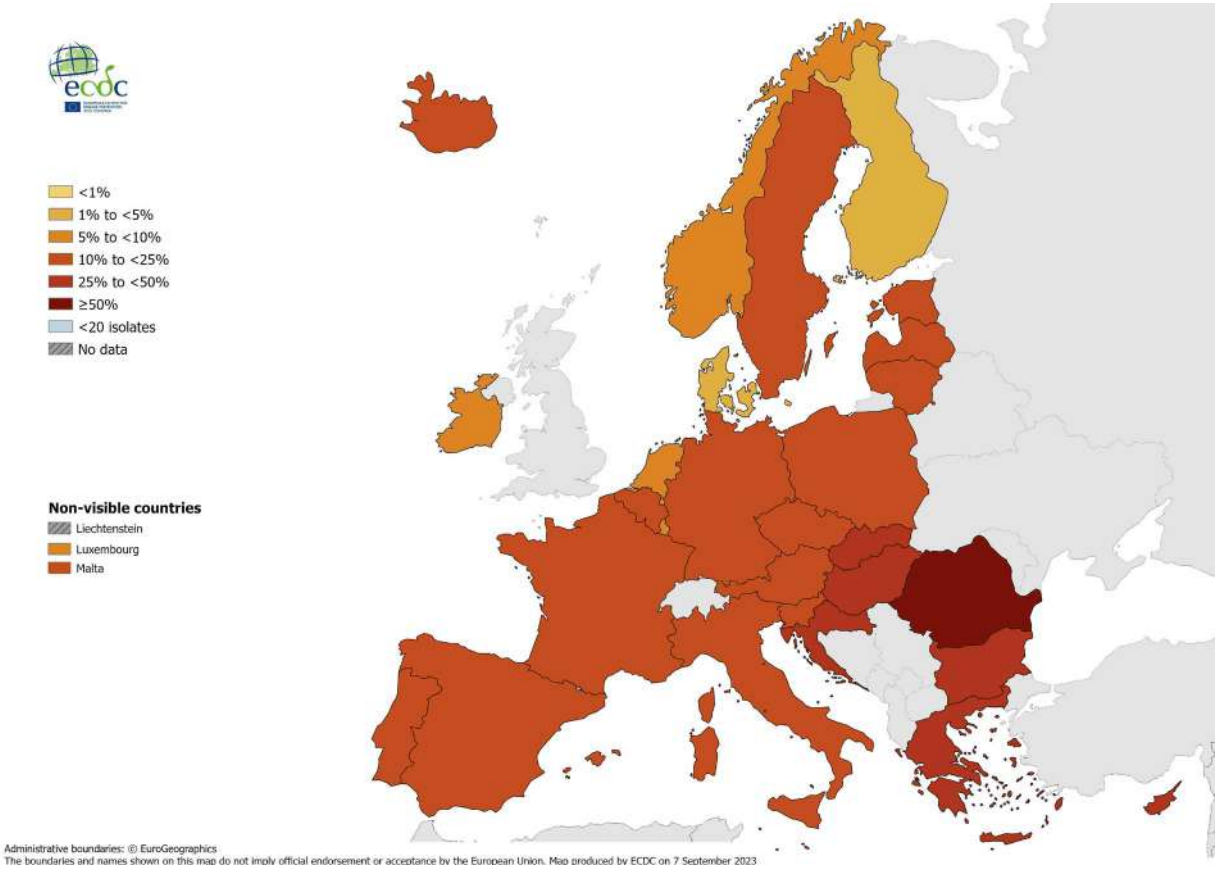
[a] *Only isolates with complete susceptibility information for piperacillin-tazobactam, ceftazidime, carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin or levofloxacin) and aminoglycosides (tobramycin) were included in the analysis. This represented 71% (17 180/24 136) of all reported* P. aeruginosa *isolates.*

[b] *Only AMR combinations >1% of the total are specified.*

[c] *Not adjusted for population differences in the reporting countries.*

[d] *Piperacillin-tazobactam, ceftazidime, carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin or levofloxacin) and aminoglycosides (tobramycin).*

Figure 6. ***Pseudomonas aeruginosa.*** **Percentage of invasive isolates with resistance to carbapenems (imipenem/meropenem), by country, EU/EEA, 2022**



Discussion

EARS-Net data showed that at EU/EEA level, trends in resistance both decreased significantly for *P. aeruginosa* (fluoroquinolones) and increased (piperacillin-tazobactam) during the period 2018 to 2022. The decreasing trend noted for fluoroquinolone resistance was further supported by the fact that the 2022 EARS-Net EQA showed an over-reporting of resistance towards levofloxacin in EARS-Net [4]. Nevertheless, high AMR percentages were observed in many countries, especially in the eastern and southern parts of Europe, and carbapenem resistance was common. As *P. aeruginosa* is intrinsically resistant to many antimicrobial agents, additional acquired resistance is further complicating the treatment of *P. aeruginosa* infections.

The public health implications of AMR in *P. aeruginosa* should not be ignored, as *P. aeruginosa* remains one of the major causes of healthcare-associated infection in Europe [27-28]. In addition, an ECDC report based on EARS-Net data estimated that in 2020 there were 67 638 infections with carbapenem-resistant *P. aeruginosa,* and 3 210 deaths attributable to the same bacterial species antimicrobial group combination [1].

An analysis based on 2016 EARS-Net data highlighted that countries reporting high percentages of *P. aeruginosa* and *Acinetobacter* spp. bloodstream infections among all reported bloodstream infections were also those where the percentage of isolates with acquired AMR in gram-negative bacteria was generally highest [29]. This finding is probably attributable to shared risk factors, such as a high consumption of broad-spectrum antimicrobials and varying IPC practices in healthcare [30]. Addressing these factors and implementing high standards of IPC in healthcare within these countries would probably have a positive impact, both on the burden of infections caused by bacteria with high levels of intrinsic AMR, such as *P. aeruginosa* and *Acinetobacter* spp., and on bacteria with acquired AMR.

At the global level, WHO has listed carbapenem-resistant *P. aeruginosa* as a pathogen of critical priority that requires research and the development of new antibiotics [26].

Acinetobacter species

Epidemiology

For 2022, 29 EU/EEA countries reported 9 661 isolates of *Acinetobacter* spp., with six EU/EEA countries each reporting fewer than 30 isolates, including Liechtenstein which did not report any isolates.

Compared to the number of reported isolates for 2019 (n=5 375) there has been an increase of almost 80%, but compared to 2021 (n=10 885) the number has decreased by more than 10%. Among the laboratories that continuously reported data during 2018–2022 (excluding France due to changes in the surveillance system), when comparing 2019 to 2022, there was an increase in the number of reported *Acinetobacter* spp. isolates (+35.2%; 3 528 and 4 770, respectively). However, more recently, from 2021 to 2022, the number of reported *Acinetobacter* spp. isolates decreased by almost a third (-29.0%; 6 714 and 4 770, respectively).

Of all reported isolates reported for 2022, 9 397 (97.3%) had AST results for carbapenems, 9 339 (96.7%) for fluoroquinolones, and 9 169 (94.9%) for aminoglycosides (Table 3a).

More than two thirds (67.8%) of the *Acinetobacter* spp. isolates reported by EU/EEA countries to EARS-Net for 2022 were resistant to at least one of the antimicrobial groups under surveillance (fluoroquinolones, aminoglycosides and carbapenems) (Table 7). The highest EU/EEA population-weighted mean AMR percentage in 2022 was reported for fluoroquinolones (38.8%), followed by carbapenems (36.3%) and aminoglycosides (34.1%) (Table 3a).

Between 2018 and 2022, no significant trend was detected for the antimicrobial groups under surveillance in the EU/EEA (Table 3a). Among laboratories that continuously reported, the increasing trends in resistance percentages previously noted for 2017−2021 [31] continued for 2018–2022.

In 2022, relatively large annual decreases in the EU/EEA population-weighted mean resistance percentage were seen for aminoglycosides (-5.5%), fluoroquinolones (-4.2%) and carbapenems (-3.6%) compared with the period 2018−2021 (Table 3a). Similar decreases in resistance percentages were also seen among the laboratories that continuously reported for 2018−2022 (aminoglycosides (-6.0%), fluoroquinolones (-3.7%) and carbapenems (-3.1%)).

Resistance to one or two antimicrobial groups was considerably less common than combined resistance to all three groups under surveillance (Table 7). Between 2018 and 2022, the EU/EEA population-weighted mean percentage for combined resistance to carbapenems, fluoroquinolones and aminoglycosides increased (from 32.4% to 36.8% between 2018 and 2021) and then decreased in 2022 to 31.8%. However, when the analysis was restricted to include only laboratories continuously reporting data for all five years, the combined resistance increased from 32.1% to 38.1% and there was a statistically significant increasing trend.

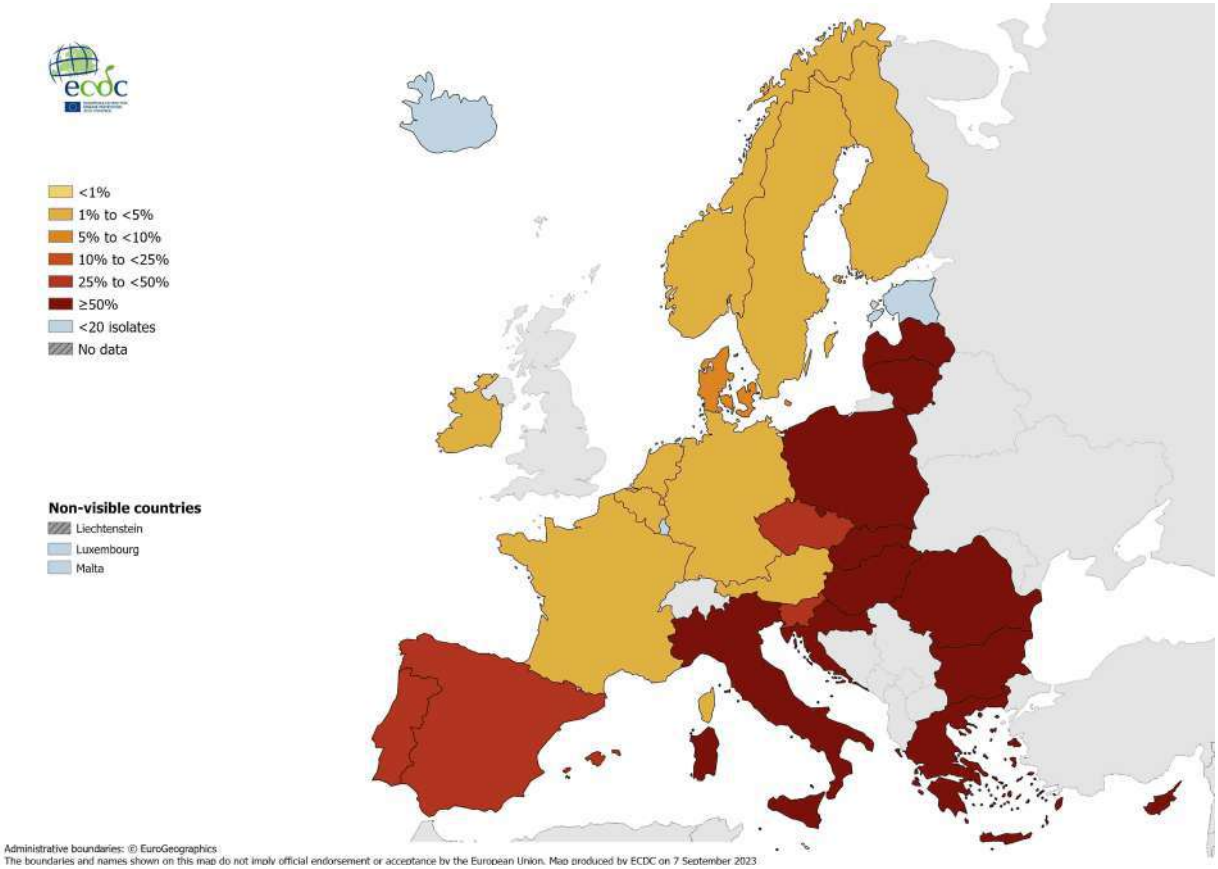
Large inter-country variations were noted for all antimicrobial groups (Table 3a), with higher AMR percentages generally reported from southern and eastern Europe than northern Europe (see country profiles and Figure 7).

Table 7. ***Acinetobacter*** **species. Total number of invasive isolates tested (n = 8 865)[a] and AMR percentage (%) per phenotype, EU/EEA, 2022**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**2 853**	**32.2**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**227**	**2.6**
Fluoroquinolones	129	1.5
Other antimicrobial groups	98	1.1
Resistance to two antimicrobial groups		
Total (any two-group combinations)	**547**	**6.2**
Fluoroquinolones + carbapenems	460	5.2
Other antimicrobial group combinations	87	1.0
Resistance to three antimicrobial groups		
Fluoroquinolones + aminoglycosides + carbapenems	**5 238**	**59.1**

[a] Only isolates with complete susceptibility information for carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin or levofloxacin) and aminoglycosides (gentamicin or tobramycin) were included in the analysis. This represented 92% (8 865/9 661) of all reported Acinetobacter *spp. isolates.*
[b] Only AMR combinations >1% of the total are specified.
[c] Not adjusted for population differences in the reporting countries.
[d] Carbapenems (imipenem or meropenem), fluoroquinolones (ciprofloxacin or levofloxacin) and aminoglycosides (gentamicin or tobramycin).

Figure 7. ***Acinetobacter*** **species. Percentage of invasive isolates with resistance to carbapenems (imipenem/meropenem), by country, EU/EEA, 2022**



Discussion

Of all the bacterial species under surveillance by EARS-Net, *Acinetobacter spp*. was the least commonly reported during the period 2018–2022, with the exception of 2021. In that year, the number of reported *Acinetobacter spp*. isolates increased, while the number of reported *S. pneumoniae* decreased so that their ranking interchanged. A publication based on 2017–2021 EARS-Net data from laboratories that continuously reported during these five years showed an increase in reported isolates in 2020–2021. A major part of these isolates consisted of carbapenem-resistant infections in ICU patients, in the countries with carbapenem resistance percentages in *Acinetobacter spp*. exceeding 50% in 2018–2019 [32]. This development implied that the situation with *Acinetobacter spp*. in the EU/EEA had deteriorated and indicated the need for reinforced *Acinetobacter spp*. preparedness, and IPC in EU/EEA healthcare facilities. This need for action was further emphasised by ECDC's estimate that in 2020 3 656 deaths were attributable to carbapenem-resistant *Acinetobacter* spp. [1].

Acinetobacter spp., and multidrug-resistant strains in particular, are notoriously difficult to eradicate from the hospital environment once established, surviving on dry surfaces, readily contaminating healthcare providers' hands, and being spread by asymptomatic carriers [33]. However, the data reported to EARS-Net indicates, that at the EU/EEA level, based both on data from all laboratories and restricted to those that reported continuously for the last five years, the previous deterioration in the *Acinetobacter* spp. situation may possibly be improving. However, it should be noted that *Acinetobacter* spp. continue to display high EU/EEA population-weighted mean AMR percentages for the antimicrobial groups under EARS-Net surveillance. In addition, the 2022 EARS-Net EQA indicated that EARS-Net resistance to aminoglycosides is under-reported, and this result should therefore be interpreted with some caution [4].

The inter-country range in AMR percentages remains the widest range for all pathogens included in EARS-Net. In 2022, the percentage of isolates resistant to at least one of the antimicrobial groups under surveillance (fluoroquinolones, aminoglycosides or carbapenems) ranged between 0.0% and 98.6%, depending on the reporting country. In general, the highest AMR percentages were reported from southern and eastern Europe. The high levels of AMR in these countries are of great concern since the most frequently reported AMR phenotype was combined resistance to all three antimicrobial groups under surveillance, severely limiting options for patient treatment. It should be pointed out that *Acinetobacter* spp. are intrinsically resistant to many antimicrobial agents, and hence additional acquired AMR is further complicating treatment of *Acinetobacter* spp. infections.

ECDC's risk assessment on carbapenem-resistant *Acinetobacter baumannii* in healthcare settings highlights the need for increased efforts to face this significant threat to patients and healthcare systems in all EU/EEA countries. The document outlines options for reducing risks through clinical management; prevention of transmission in hospitals and other healthcare settings; prevention of cross-border transmission and improvement in the preparedness of EU/EEA countries. Options for response presented in the risk assessment include timely laboratory reporting, screening and pre-emptive isolation of high-risk patients, good IPC, rigorous environmental cleaning and disinfection, and antimicrobial stewardship programmes [34].

WHO has listed carbapenem-resistant *A. baumannii* as a pathogen of critical priority in its global priority list of antibiotic-resistant bacteria requiring research and the development of new antibiotics [26].

Staphylococcus aureus

Epidemiology

For 2022, 30 EU/EEA countries reported 86 752 isolates of *S. aureus*. Among the laboratories that continuously reported data during 2018–2022 (excluding France due to changes in the surveillance system), when comparing 2019 to 2022, there was an increase in the number of reported *S. aureus* isolates (+9.0%; 49 064 and 53 467, respectively). This includes an increase from 2021 to 2022, when the number of reported *S. aureus* isolates increased by +4.4%.

Of all reported isolates, 84 397 (97.3%) had AST results or molecular confirmation test results available to determine MRSA (Table 3a).

A little less than one fifth (17.9%) of the *S. aureus* isolates reported by EU/EEA countries to EARS-Net for 2022 were resistant to at least one of the antimicrobial groups under surveillance (meticillin/MRSA, fluoroquinolones and rifampicin) (Table 8).

The EU/EEA population-weighted mean MRSA percentage was 15.2% in 2022. This denotes a significantly decreasing trend for the period 2018−2022, from 17.8% to 15.2%, a trend that remained statistically significant when the analysis was restricted to include only laboratories that continuously reported data for all five years (Table 3a).

During the period 2018−2022, the estimated EU incidence of bloodstream infections with MRSA decreased, from 5.80 to 4.94 cases per 100 000 population, and showed a significantly decreasing trend (Table 3b). Moreover in 2022, there was a 12.2% decrease compared against the baseline year 2019 (Table 3b).

With MRSA, combined resistance to another antimicrobial group was quite common. The most common AMR combination was MRSA and resistance to fluoroquinolones (Table 8).

Large inter-country variations were noted for MRSA (Table 3a), with higher AMR percentages generally reported from southern and eastern Europe than northern Europe (Figure 8).

Table 8. ***Staphylococcus aureus.*** **Total number of invasive isolates tested (n = 60 484)[a] and AMR percentage (%) per phenotype, EU/EEA, 2022**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**49 631**	**82.1**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**5 369**	**8.9**
Fluoroquinolones	2 988	4.9
Meticillin/MRSA	2 010	3.3
Other antimicrobial groups	371	0.6
Resistance to two antimicrobial groups		
Total (any two-group combinations)	**5 125**	**8.5**
Meticillin/MRSA + fluoroquinolones	4 962	8.2
Other resistance combinations	163	0.3
Resistance to three antimicrobial groups		
Meticillin/MRSA + fluoroquinolones + rifampicin	**359**	**0.6**

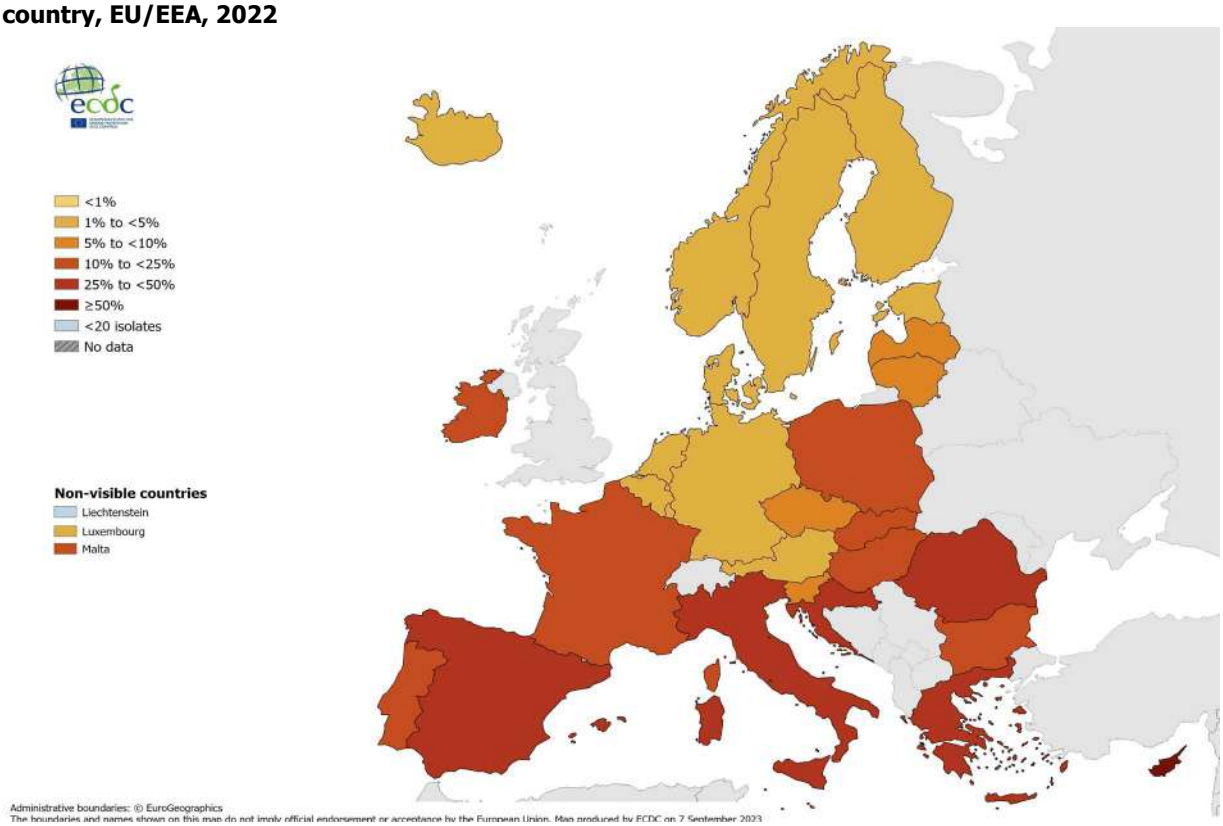
[a] *Only isolates with complete susceptibility information for MRSA, fluoroquinolones and rifampicin were included in the analysis. This represented 70% (60 484/86 752) of all reported* S. aureus *isolates. MRSA is based on AST results for cefoxitin, or if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of* mecA *gene by PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA. For fluoroquinolones (ciprofloxacin or levofloxacin) AST results for norfloxacin are also accepted if neither ciprofloxacin nor levofloxacin results are available.*

[b] *Only AMR combinations >1% of the total are specified.*

[c] *Not adjusted for population differences in the reporting countries.*

[d] *MRSA, fluoroquinolones and rifampicin. MRSA is based on AST results for cefoxitin, or if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of* mecA *gene by PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA. For fluoroquinolones (ciprofloxacin or levofloxacin) AST results for norfloxacin are also accepted if neither ciprofloxacin nor levofloxacin results are available.*

Figure 8. ***Staphylococcus aureus.*** **Percentage of invasive isolates resistant to meticillin (MRSA),[a] by country, EU/EEA, 2022**



[a] *For EARS-Net, MRSA is based on AST results for cefoxitin or, if unavailable, oxacillin. AST results reported for cloxacillin, dicloxacillin, flucloxacillin or meticillin are accepted as a marker for oxacillin resistance if oxacillin is not reported. If no phenotypic results are available, data from molecular confirmation tests (detection of* mecA *gene PCR or a positive PBP2A-agglutination test) are accepted as a marker for MRSA.*

Discussion

In 2022, the MRSA percentage trend was relatively stable or declining in most EU/EEA countries, and a decreasing EU/EEA population-weighted mean MRSA percentage was noted. Several countries have developed and implemented national recommendations and guidance documents on preventing the spread of MRSA, focusing on improved IPC and prudent antimicrobial use [23].

Despite this positive development, MRSA remains an important pathogen in Europe, with combined resistance to another antimicrobial group quite common and high MRSA percentages in several countries. *S. aureus* is one of the most common causes of bloodstream infections, exhibiting a high burden in terms of morbidity and mortality [1,15]. In ECDC's study of the EU/EEA health burden of AMR for the period 2016–2020, the second largest burden of disease was caused by infections with MRSA [1]. Although the EU/EEA population-weighted MRSA percentage, as reported by EARS-Net, has been decreasing for many years, ECDC's study of the health burden of AMR reported an increase in estimated incidence of MRSA infections between 2007 and 2015. Further analysis of the age-group-specific incidence found that this mainly related to infants and those aged 55 years or above [15]. A separate study based on EARS-Net data for the period 2005–2018 highlighted that the decrease in the percentage of MRSA among *S. aureus* bloodstream infections was mainly due to the increasing number of meticillin-susceptible *S. aureus* bloodstream infections. The seemingly conflicting results highlighted the need to improve surveillance of AMR by reporting not only AMR percentages, but also the incidence of infections with antimicrobial-resistant bacteria such as MRSA [35]. The estimation of the incidence of bloodstream infections with MRSA was added to the 2023 annual epidemiological report for EARS-Net and showed that the estimated incidence of bloodstream infections with MRSA for the EU overall decreased from 2018 to 2022, and in particular by 12.2% compared to 2019. As a result, the EARS-Net data currently indicate that the EU is progressing towards the agreed target of a 15% reduction in the incidence by 2030, compared to the baseline year 2019 [2].

Comprehensive MRSA strategies targeting all healthcare sectors are essential for slowing down the spread of MRSA in Europe. At present, monitoring of MRSA in animals and food is voluntary and only performed in few countries. Nevertheless, this monitoring detected MRSA, mainly livestock-associated MRSA (LA-MRSA), in food and food-producing animals in 2019–2020 [7]. LA-MRSA has gained attention as it poses a zoonotic risk, particularly for those working in close contact with livestock. Although data collected through EARS-Net do not allow the identification of LA-MRSA isolates, an ECDC survey documented increasing numbers of detections and geographical dispersion of LA-MRSA in humans in the EU/EEA during the period 2007–2013 and highlighted the veterinary and public health significance of LA-MRSA as a 'One-Health' issue [36].

Streptococcus pneumoniae

Epidemiology

For 2022, 30 EU/EEA countries reported 14 568 isolates of *S. pneumoniae*. This is a clear increase compared to 2021 (n=9 166) but still lower than for 2018–2019 (n=15 292–15 608). In several of the countries the reported number of isolates is higher for 2022 than 2019 (see 'Country summaries - antimicrobial resistance in the EU/EEA 2022' available on the web page for this report).

Among the laboratories that continuously reported data during the period 2018–2022 (excluding France due to changes in the surveillance system, and Greece due to missing data for 2018–2021), when comparing 2019 to 2022, there was a decrease in the number of reported *S. pneumoniae* isolates (-12.4%; 12 379 and 10 842, respectively). However, more recently, from 2021 to 2022, the number or reported *S. pneumoniae* isolates increased by +71.2% from n=6 333 to n=10 842.

For all reported isolates, the increase compared to the previous two years was also reflected in the number of reported isolates with AMR phenotype in the EU/EEA (Table 3a). Of the isolates reported, 13 947 (95.7%) had AST results for macrolides and 13 230 (90.8%) had AST results for penicillins (Table 3a).

For this report, the term penicillin non-wild-type refers to *S. pneumoniae* isolates reported by local laboratories as susceptible, increased exposure (I) or resistant (R) to penicillin, assuming an MIC for benzylpenicillin above that for the wild-type isolates (> 0.06 mg/L). The analysis was based on the qualitative susceptibility categories S/I/R, since quantitative susceptibility information was missing for a large part of the reported data.

More than one fifth (20.9%) of the *S. pneumoniae* isolates reported by EU/EEA countries to EARS-Net for 2022 were resistant to at least one of the antimicrobial groups under surveillance (penicillins, third-generation cephalosporins, fluoroquinolones and macrolides) (Table 9). In 2022, the EU/EEA population-weighted mean percentage was 16.3% for penicillin non-wild-type and 17.9% for macrolide resistance (Table 3a).

Between 2018 and 2022, the trend in the EU/EEA population-weighted mean percentage of penicillin non-wild-type resistance and macrolide resistance increased significantly, with percentages increasing from 14.0% to 16.3% and from 16.6% to 17.9%, respectively (Table 3a). These trends remained significant when the analysis was restricted to include only laboratories that continuously reported data for all five years.

The EU/EEA population-weighted mean percentage for combined penicillin non-wild-type and resistance to macrolides was 9.7% in 2022, with a significantly increasing trend during the period 2018–2022 (Table 3a). Moreover, the trend remained when the analysis was restricted to include only laboratories that continuously reported data for all five years. Resistance to antimicrobial groups other than penicillin and macrolides was less common (Table 9).

Large inter-country variations were noted for all antimicrobial groups (Table 3a, Figure 9), with higher macrolide and penicillin non-wild-type resistance percentages generally reported from southern and eastern Europe than northern Europe.

Table 9. ***Streptococcus pneumoniae.*** **Total number of invasive isolates tested (n = 9 076)[a] and percentage non-wild-type/ AMR (%) per phenotype, EU/EEA, 2022**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**7 180**	**79.1**
Single non-wild-type/resistance (to indicated antimicrobial groups)		
Total (any single resistance)	**1 192**	**13.1**
Macrolides	596	6.6
Penicillin non-wild-type[e]	496	5.5
Fluoroquinolones	99	1.1
Other antimicrobial groups	1	<0.1
Non-wild-type/resistance to two antimicrobial groups		
Total (any two-group combinations)	**668**	**7.4**
Penicillin non-wild-type + macrolides	622	6.9
Other antimicrobial group combinations	46	0.5
Non-wild-type/resistance to three antimicrobial groups		
Total (any three-group combinations)	**33**	**0.4**
Other antimicrobial group combinations	33	0.4
Non-wild-type/resistance to four antimicrobial groups		
Penicillin non-wild-type + third-generation cephalosporins + fluoroquinolones + macrolides	**3**	**<0.1**

[a] *Only isolates with complete susceptibility information for penicillins (based on penicillin or, if unavailable, oxacillin), third-generation cephalosporins (cefotaxime or ceftriaxone) and fluoroquinolones (levofloxacin or moxifloxacin - AST results for norfloxacin are also accepted if neither levofloxacin nor moxifloxacin results are available) and macrolides (azithromycin, clarithromycin or erythromycin) were included in the analysis. This represented 62% (9 076/14 568) of all reported* S. pneumoniae *isolates.*

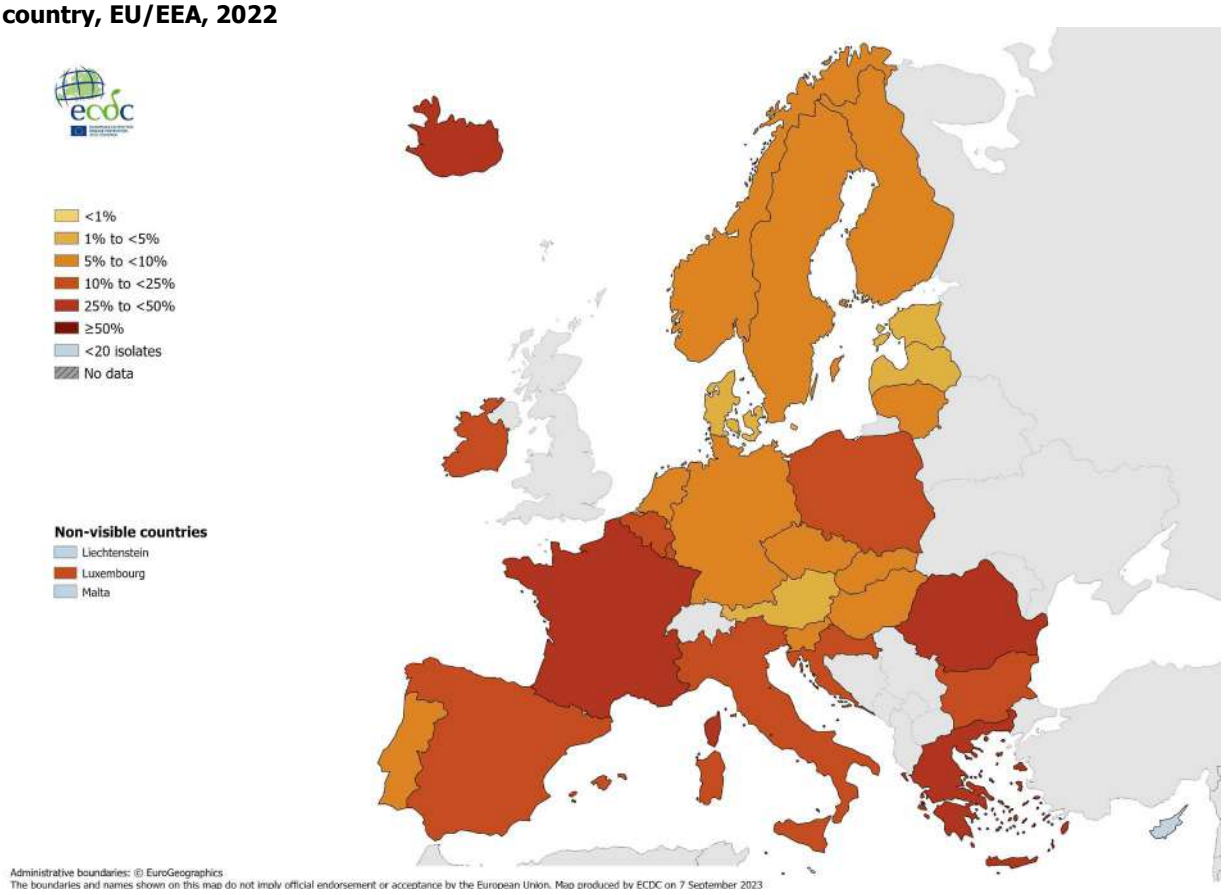
[b] *Only AMR combinations >1% of the total are specified.*

[c] *Not adjusted for population differences in the reporting countries.*

[d] *Penicillins (based on penicillin or, if unavailable, oxacillin), third-generation cephalosporins (cefotaxime or ceftriaxone) and fluoroquinolones (levofloxacin or moxifloxacin - AST results for norfloxacin are also accepted if neither levofloxacin nor moxifloxacin results are available) and macrolides (azithromycin, clarithromycin or erythromycin) were included in the analysis.*

[e] *For* S. pneumoniae*, the term penicillin non-wild-type is used in this report, referring to* S. pneumoniae *isolates reported by local laboratories as 'susceptible, increased exposure' (I) or resistant (R) to penicillin, assuming MIC for benzylpenicillin above that for wild-type isolates (>0.06 mg/L). The qualitative susceptibility categories (S/I/R) as reported by the laboratory are used, since quantitative susceptibility information is missing for a large part of the data.*

Figure 9. ***Streptococcus pneumoniae*****. Percentage of penicillin[a] non-wild type[b] invasive isolates, by country, EU/EEA, 2022**



[a] *Penicillin results are based on penicillin or, if unavailable, oxacillin.*

[b] *For* S. pneumoniae*, the term penicillin non-wild-type is used in this report, referring to* S. pneumoniae *isolates reported by local laboratories as susceptible, increased exposure (I) or resistant (R) to penicillin, assuming MIC for benzylpenicillin above that for wild-type isolates (> 0.06 mg/L). The qualitative susceptibility categories (S/I/R) as reported by the laboratory are used, since quantitative susceptibility information is missing for a large part of the data.*

Discussion

Non-pharmaceutical interventions introduced to reduce severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission, and the lifting of these non-pharmaceutical interventions [37], could potentially have resulted in decreased circulation of pathogens in the community followed by an increase. This could explain the decrease in the number of *S. pneumoniae isolates* reported by EU/EEA countries for 2020 and 2021 compared to 2018–2019, and the subsequent increase in 2022.

Although the number of reported *S. pneumoniae* isolates was overall lower in 2022 than in 2019, an increase against 2021 was noted in the data, irrespective of whether all reporting laboratories or only the continuously reporting laboratories were included. There were also increasing trends in the population-weighted EU/EEA mean percentages for penicillin non-wild-type and macrolide resistance between 2018 and 2022. However, there were large inter-country variations.

When considering the increasing trend in penicillin non-wild-type, it should be noted that the 2022 EARS-Net EQA indicated that reduced susceptibility to benzylpenicillin is under-reported in EARS-Net [4]. However, differences in the clinical breakpoints used historically to determine penicillin susceptibility in *S. pneumoniae* (based on the guidelines used and the sites of infection) could introduce bias when comparing national data reported to EARS-Net before 2021. (Since 2019, there has been a restriction to EUCAST clinical breakpoints which should lessen this particular aspect in the future). Limited information on the guidelines and breakpoints used for interpretation and incomplete quantitative susceptibility data hamper assessment of inter-country differences to some extent and may also influence the assessment of changes over time.

However, results from ESAC-Net did indicate that, compared to 2019, the 2022 community macrolide consumption increased significantly [6]. The noted increase in reported *S. pneumoniae* isolates and macrolide resistance among the isolates could potentially be associated with this increase in macrolide consumption.

In parallel with EARS-Net, surveillance of invasive pneumococcal disease in the EU/EEA is covered by another surveillance network - the European Invasive Bacterial Disease Surveillance Network (EU-IBD), also coordinated

by ECDC. This network collects additional data on invasive pneumococcal disease cases throughout the EU/EEA – for example data on outcome [38]. Data from this surveillance show that the percentage of resistance to penicillin was 2% and to erythromycin 18%, based on the reporting of antimicrobial susceptibility data by 10 countries in 2018 [38]. It is, however, difficult to compare data from the two surveillance systems due to differences – for example the number of reporting countries.

Most EU/EEA countries have implemented routine immunisation for children with multivalent pneumococcal conjugated vaccines (PCVs). In some countries, high-risk adult groups, such as elderly people and immunocompromised individuals, are also targeted with the polysaccharide vaccine or with PCVs [39]. Changes in immunisation and serotype coverage of the PCVs available will probably have an impact on the epidemiology of *S. pneumoniae* in the EU/EEA, both in terms of changes in the age-specific incidence and potential serotype replacement. It is also conceivable that the COVID-19 pandemic and related public health interventions and changes in antibiotic consumption [40] may further affect *S. pneumoniae* epidemiology in the EU/EEA.

Enterococcus faecalis

Epidemiology

For 2022, 29 EU/EEA countries reported 32 360 isolates of *E. faecalis* – 17 146 (53.0%) with AST results for high-level gentamicin (Table 3a).

Over the last four years, the number of reported isolates of *E. faecalis* at EU/EEA level (excluding the UK) from laboratories that continuously reported between 2018 and 2022 (excluding France due to changes in the surveillance system) has increased by +18.5% from 16 096 isolates in 2019 to 19 075 in 2022. At the same time, the number of reported isolates with AMR phenotype in the EU/EEA increased from 13 577 in 2019 to 17 146 in 2022. More recently however, between 2021 and 2022, the number or reported *E. faecalis* isolates among continuously reporting laboratories decreased by -4.2%.

In 2022, the EU/EEA population-weighted mean percentage of high-level gentamicin resistance in *E. faecalis* was 25.3%. This represents a small decrease since 2018, when the percentage was 27.1%, and a larger decrease compared to 2021, when the percentage was 28.9% (Table 3a). No significant trend was noted for high-level gentamicin resistance during the period 2018–2022.

Large inter-country variations were noted for high-level gentamicin resistance in *E. faecalis* (Table 3a), with generally higher AMR percentages reported from southern and eastern Europe than from northern Europe (see 'Country summaries - antimicrobial resistance in the EU/EEA 2022' available on the web page for this report). More information is provided in ECDC's Surveillance Atlas of Infectious Diseases [13].

Discussion

While the number of isolates has increased over the last four years, no trend in high-level gentamicin resistance level in *E. faecalis* was noted by EARS-Net at EU/EEA level. This indicates that high levels of antimicrobial-resistant enterococci remain a major IPC challenge and an important cause of healthcare-associated infections in Europe. In addition to the fact that infections caused by resistant strains are difficult to treat, enterococci are also easily disseminated in healthcare settings.

Enterococcus faecium

Epidemiology

For 2022, 29 EU/EEA countries reported 22 970 isolates of *E. faecium* – 22 709 (98.9%) with AST results for vancomycin (Table 3a).

Over the last four years the number of reported isolates of *E. faecium* at EU/EEA level from laboratories that continuously reported between 2018 and 2022 (excluding France due to changes in the surveillance system) has increased by +33.2% from 10 584 in 2019 to 14 097 in 2022. However, compared to 2021 (n=14 790) there was a decrease (-4.7%) in the number of reported isolates in the same 'restricted' dataset. During the time period 2019–2022, the number of reported isolates with AMR phenotype in the EU/EEA increased from 14 095 in 2019 to 22 709 in 2022.

More than nine-tenths (92.5%) of the *E. faecium* isolates reported by all EU/EEA countries to EARS-Net for 2022 were resistant to at least one of the antimicrobial groups under surveillance (aminopenicillins, gentamicin (high-level resistance) and vancomycin) (Table 10).

AMR to two or more antimicrobial groups was common - seen in 57.1% of all tested isolates (Table 10).

The EU/EEA population-weighted mean percentage of vancomycin resistance in *E. faecium* was 17.6% in 2022, representing a significant increase since 2018 when the percentage was 16.2%. The trend remained significant when the analysis was restricted to include only laboratories that continuously reported data for all five years.

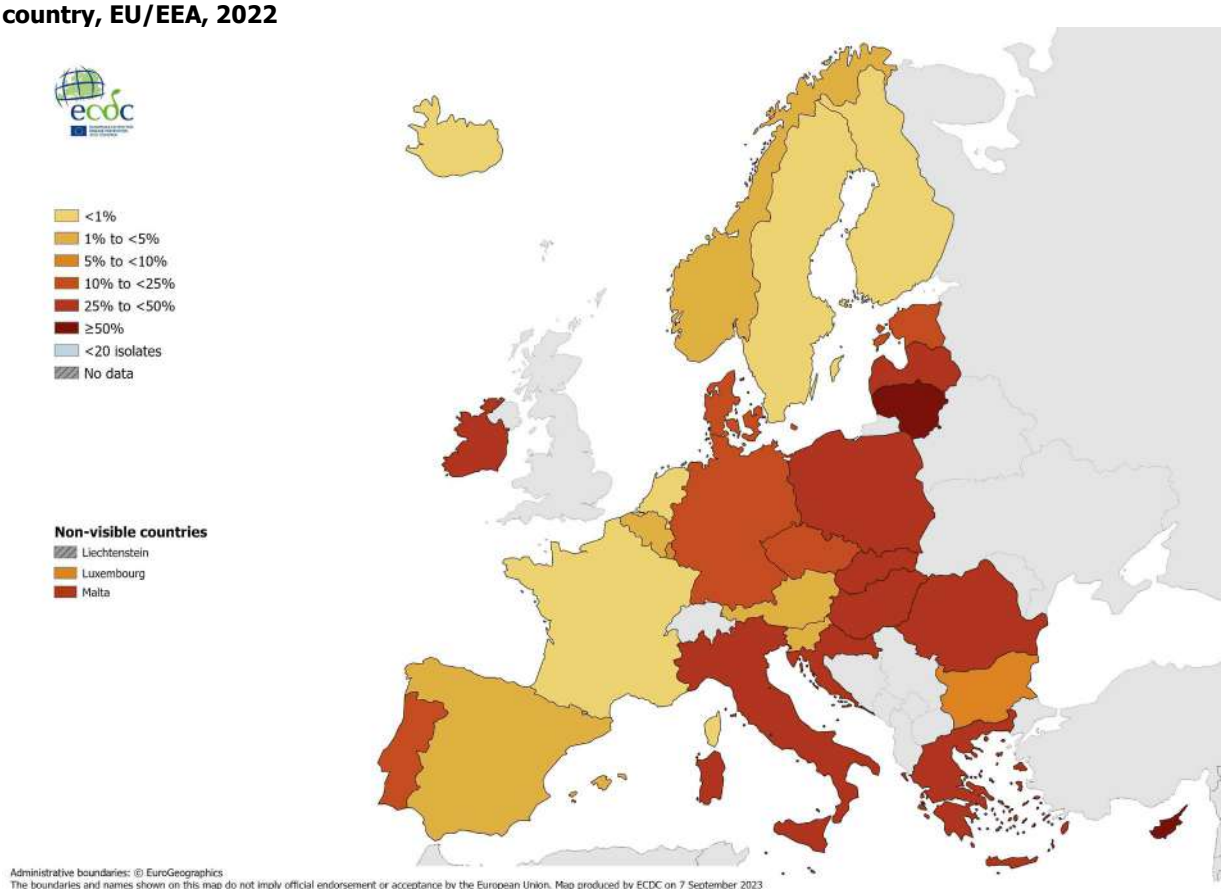
National percentages ranged from 0.0% to 67.7% (Table 3a), 10 of the 29 EU/EEA countries reported vancomycin resistance percentages below 5.0% and Liechtenstein did not report any isolates (Figure 10). High vancomycin-resistant *E. faecium* levels were reported from countries in central, southern, and eastern Europe, as well as Ireland.

Table 10. ***Enterococcus faecium.*** **Total number of invasive isolates tested (n = 12 423)[a] and AMR percentage (%) per phenotype, EU/EEA, 2022**

AMR pattern[b]	Number of isolates	Percentage of total[c]
Susceptible to all included antimicrobial groups[d]	**929**	**7.5**
Single resistance (to indicated antimicrobial group)		
Total (any single resistance)	**4 397**	**35.4**
Aminopenicillins	4 328	34.8
Other antimicrobial groups	69	0.6
Resistance to two antimicrobial groups		
Total (any two-group combinations)	**5 629**	**45.3**
Aminopenicillins + gentamicin (high level resistance)	4 341	34.9
Aminopenicillins + vancomycin	1 278	10.3
Other resistance combinations	10	0.1
Resistance to three antimicrobial groups		
Aminopenicillins + gentamicin (high level resistance) + vancomycin	1 468	11.8

[a] *Only isolates with complete susceptibility information for aminopenicillins (ampicillin or amoxicillin), gentamicin (high-level resistance) and vancomycin were included in the analysis. This represented 54% (12 423/22 970) of all reported* E. faecium *isolates.*
[b] *Only AMR combinations >1% of the total are specified.*
[c] *Not adjusted for population differences in the reporting countries.*
[d] *Aminopenicillins (ampicillin or amoxicillin), gentamicin (high-level resistance) and vancomycin.*

Figure 10. *Enterococcus faecium*. Percentage of invasive isolates resistant to vancomycin, by country, EU/EEA, 2022



Discussion

The rapid and continuous increase in not only the number of reported isolates of *E. faecium,* but also the percentage of vancomycin resistance in *E. faecium* in the EU/EEA is a cause for concern.

A previous ECDC study of the AMR health burden estimated that the median number of infections and deaths attributable to vancomycin-resistant enterococci almost doubled between 2007 and 2015 [15]. A more recent ECDC study estimated that these infections increased from 47 124 in 2016 to 117 866 in 2020, with a concomitant increase in the number of attributable deaths from 1 335 to 3 414 [1]. The rise in both the number of reported isolates and the EU/EEA population-weighted mean vancomycin resistance percentage for *E. faecium* in 2022 contributes to a further increase in the health burden of vancomycin-resistant enterococci infections.

In addition, the significantly increasing trend, observed at EU/EEA level and in some individual countries, highlights the urgent need for close monitoring to better understand the epidemiology, clonal diversity and risk factors associated with vancomycin-resistant *E. faecium* infection. Contrary to many other bacterial species–antimicrobial group combinations under surveillance by EARS-Net, the geographical pattern for vancomycin-resistant *E. faecium* was slightly different, indicating high AMR levels reported from countries in central, southern and eastern Europe, as well as Ireland.

In addition to the fact that infections caused by resistant strains are difficult to treat, enterococci are also easily disseminated in healthcare settings. A recently published report confirmed that *Enterococcus* spp. continued to be a frequently observed healthcare-associated infection in European acute care hospitals in 2016−2017 and the same study reported high levels of vancomycin resistance in healthcare-associated infections with *E. faecium* [28]. The results in this report support that high levels of antimicrobial-resistant enterococci remain a major infection control challenge in Europe.

Enterococci have intrinsic resistance to several antimicrobial classes, and any additional acquired AMR severely limits the number of treatment options. WHO has listed vancomycin-resistant *E. faecium* as a pathogen of high priority in its global priority list of antibiotic-resistant bacteria, emphasising the paucity of available and effective treatment options [26].

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Annex 1. Participating institutions

Country	Participating institutions	Web link
Austria	Federal Ministry of Social Affairs, Health, Care and Consumer Protection	www.sozialministerium.at
	Medical University Vienna	www.meduniwien.ac.at
	Ordensklinikum Linz, Elisabethinen	www.ordensklinikum.at
Belgium	Sciensano	www.sciensano.be
Bulgaria	National Center of Infectious and Parasitic Diseases	https://ncipd.org/index.php?option=com_content&view=featured&Itemid=730&lang=en
Croatia	Reference Center for Antimicrobial Resistance Surveillance	https://bfm.hr/referentni-centar-za-pracenje-rezistencije-bakterija-na-antibotike/
	Ministry of Health Zagreb University Hospital for Infectious Diseases (Dr Fran Mihaljević)	https://bfm.hr/
Cyprus	Microbiology Department, Nicosia General Hospital	https://shso.org.cy/clinic/mikroviologiko/
Czechia	National Institute of Public Health	www.szu.cz
	National Reference Laboratory for Antibiotics	https://szu.cz/odborna-centra-a-pracoviste/centrum-epidemiologie-a-mikrobiologie/oddeleni-bakterialni-rezistence-na-antibiotika-a-sbirka-kultur/nrl-pro-antibiotika
Denmark	Statens Serum Institut	https://www.ssi.dk/
	Danish Study Group for Antimicrobial Resistance Surveillance (DANRES)	www.danmap.org
Estonia	Estonian Health Board	https://www.terviseamet.ee/et
	East-Tallinn Central Hospital	https://itk.ee/
	Tartu University Hospital	https://www.kliinikum.ee/partnerile/uhendlabor/
Finland	Finnish Institute for Health and Welfare, Department of Health Security	www.thl.fi
	Finnish Study Group for Antimicrobial Resistance (FiRe)	www.finres.fi
	Finnish Hospital Infection Program (SIRO)	https://thl.fi/en/web/infectious-diseases-and-vaccinations/diseases-and-disease-control/healthcare-associated-infections
France	Santé Publique France	www.santepubliquefrance.fr
	Since 2020:	
	Surveillance and Prevention of Antimicrobial RESistance in hospital settings (SPARES)	https://www.preventioninfection.fr/
	National Reference Centre for Pneumococci	www.cnr-pneumo.com
	Up to 2019:	
	French National Observatory for the Epidemiology of Bacterial Resistance to Antimicrobials (ONERBA) through three participating networks:	www.onerba.org
	Azay-Résistance	
	Île-de-France	
	Réussir	
Germany	Robert Koch Institute	www.rki.de
Greece	National Public Health Organization, Central Public Health Laboratory	https://eody.gov.gr/en/
	University of West Attica, Department of Public Health Policy, School of Public Health	https://php.uniwa.gr/en/homepage/
Hungary	National Public Health Center	www.oek.hu
Iceland	National University Hospital of Iceland	https://www.landspitali.is
	Centre for Health Security and Infectious Disease Control	https://www.landlaeknir.is
	Akureyri hospital	www.sak.is
Ireland	Health Protection Surveillance Centre	www.hpsc.ie

Country	Participating institutions	Web link
Italy	National Institute of Health	www.iss.it
Latvia	Disease Prevention and Control Center of Latvia	www.spkc.gov.lv
Liechtenstein	Liechtensteinisches Landesspital	https://www.landesspital.li/
	Laboratory Dr Risch[a]	https://www.risch.ch/de
Lithuania	National Public Health Surveillance Laboratory	www.nvspl.lt
	Institute of Hygiene	www.hi.lt
Luxembourg	National Health Laboratory	https://lns.lu/
	Microbiology Laboratory, Centre Hospitalier de Luxembourg	https://www.chl.lu/fr/service/laboratoire-de-bacteriologie-microbiologie
Malta	Malta Mater Dei Hospital, Msida	https://healthservices.gov.mt/en/MDH/Pages/Home.aspx
Netherlands	National Institute for Public Health and the Environment	www.rivm.nl
Norway	University Hospital of North Norway	
	Norwegian Institute of Public Health	
	St Olav University Hospital, Trondheim	
Poland	National Medicines Institute, Department of Epidemiology and Clinical Microbiology	https://www.nil.gov.pl
	National Reference Centre for Susceptibility Testing	https://korld.nil.gov.pl
Portugal	National Institute of Health Doutor Ricardo Jorge	https://www.insa.min-saude.pt/
	Directorate-General of Health	https://www.dgs.pt/
Romania	National Institute of Public Health	www.insp.gov.ro
Slovakia	National Reference Centre for Antimicrobial Resistance	
	Public Health Authority of the Slovak Republic	https://www.uvzsr.sk
	Regional Public Health Authority Banska Bystrica	
Slovenia	National Institute of Public Health	www.nijz.si
	Medical Faculty, University of Ljubljana	https://imi.si/
	National Laboratory of Health, Environment and Food	https://www.nlzoh.si/
Spain	Health Institute Carlos III	www.isciii.es
	National Centre for Microbiology	
Sweden	The Public Health Agency of Sweden	www.folkhalsomyndigheten.se

[a] *Liechtenstein uses Laboratory Dr Risch as a participating institution at national level.*