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National action plans for antimicrobial resistance and variations in surveillance data platforms

Scott JC Pallett,[a] Esmita Charani,[b] Lois Hawkins,[c] Andrea Mazzella,[d] Vanesa Anton-Vazquez,[c] Rishi Banerjee,[c] Terry J Evans,[c] Benjamin Patterson,[c] Sathyavani Subbarao,[c] Saleh Alqahtani,[e] Marina Basarab,[c] Aodhan S Breathnach,[c] Nabeela Mughal[f] & Luke SP Moore[g]

[a] Centre of Defence Pathology, Royal Centre for Defence Medicine, Queen Elizabeth Hospital Birmingham, Birmingham, B15 2WB, England.

[b] Centre of Excellence in Infectious Diseases Research, University of Liverpool, Liverpool, England.

[c] Infection and Immunity Clinical Academic Group, St George's University Hospitals NHS Foundation Trust, London, England.

[d] Institute for Infection and Immunity, St George's University of London, London, England.

[e] Medicine at Sibley Memorial Hospital, Johns Hopkins University, Baltimore, United States of America.

[f] Clinical Infection Department, Chelsea and Westminster Hospital, London, England.

[g] National Institute for Health Research Health Protection Research Unit in Healthcare Associated Infections and Antimicrobial Resistance, Imperial College London, London, England.

Correspondence to Scott JC Pallett (email: scott.pallett@nhs.net).

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Abstract

Objective To assess how national antimicrobial susceptibility data used to inform national action plans vary across surveillance platforms.

Methods We identified available open-access, supranational, interactive surveillance platforms and cross-checked their data in accordance with the World Health Organization's (WHO's) Data Quality Assurance: module 1. We compared platform usability and completeness of time-matched data on the antimicrobial susceptibilities of four blood isolate species: *Escherichia coli, Klebsiella pneumoniae*, *Staphylococcus aureus* and *Streptococcus pneumoniae* from WHO's Global Antimicrobial Resistance and Use Surveillance System, European Centre for Disease Control's (ECDC's) network and Pfizer's Antimicrobial Testing Leadership and Surveillance database. Using Bland–Altman analysis, paired *t*-tests, and Wilcoxon signed-rank tests, we assessed susceptibility data and number of isolate concordances between platforms.

Findings Of 71 countries actively submitting data to WHO, 28 also submit to Pfizer's database; 19 to ECDC; and 16 to all three platforms. Limits of agreement between WHO's and Pfizer's platforms for organism–country susceptibility data ranged from −26% to 35%. While mean susceptibilities of WHO's and ECDC's platforms did not differ (bias: 0%, 95% confidence interval: −2 to 2), concordance between organism–country susceptibility was low (limits of agreement −18 to 18%). Significant differences exist in isolate numbers reported between WHO–Pfizer (mean

of difference: 674, *P*-value: < 0.001 and WHO–ECDC (mean of difference: 192, *P*-value: 0.04) platforms.

Conclusion The considerable heterogeneity of nationally submitted data to commonly used antimicrobial resistance surveillance platforms compromises their validity, thus undermining local and global antimicrobial resistance strategies. Hence, we need to understand and address surveillance platform variability and its underlying mechanisms.

Introduction

Antimicrobial resistance is a growing threat to global public health.[1] Recognizing the need for coordinated, evidence-based action, the 2015 World Health Assembly endorsed the *Global action plan on antimicrobial resistance*,[2] with Member States agreeing to mandate the development and implementation of national action plans on antimicrobial resistance aligning human, animal and agricultural measures.

Timely, accurate, relevant data are fundamental to informing country measures addressing antimicrobial resistance, hence the second of the five key global action plan implementation objectives is to "strengthen the knowledge and evidence base through surveillance and research."[2] Acknowledging that different countries may be at various starting points, the World Health Organization (WHO) has subsequently helped countries establish antimicrobial resistance surveillance and encouraged them to join their Global Antimicrobial Resistance and Use Surveillance System (known as GLASS).[3] WHO also offers technical support, guidance, laboratory reporting standards and coordinating mechanisms for antimicrobial stewardship to countries needing strengthening of their diagnostic laboratory capacity. An aim of the support is to enable countries to submit clinically linked, nationally gathered data to WHO's surveillance system, to describe both current and emerging resistance, and to monitor antimicrobial resistance and national action plans interventions.[4] Initial assessment of developments of national surveillance capability following the release of the global action plan suggested some improvements, including in access to funding but highlighted ongoing challenges and limited reporting outputs,[5–7] particularly in low- and middle-income countries.[8]

In 2020, researchers were able to identify 71 separate international antimicrobial resistance surveillance platforms, ranging from targeted single disease surveillance, such as for tuberculosis, to supranational regional activity mirroring the aims of WHO's surveillance system. However, very few offered readily available open-access data.[9] These platforms included commercial platforms such as the Pfizer's Antimicrobial Testing Leadership and Surveillance database, which provides user-friendly, open-access and interactive visualization

of available data, and has recently announced a public–private collaboration with Wellcome Trust to address antimicrobial resistance in sub-Saharan Africa.[10]

As the coronavirus disease 2019 (COVID-19) pandemic comes under control, antimicrobial resistance must return to the forefront of the global health agenda. The pandemic has led to deterioration of antimicrobial susceptibility reporting activities[11,12] and many of the national action plans have now expired. Now is an important moment to identify the current issues in global progress so that we can optimize the effectiveness of future actions, thus we need to evaluate the current surveillance platforms. We therefore analysed and compared international open-access antimicrobial resistance surveillance systems, using the WHO Data Quality Assurance framework, dimension 3, that is, external comparison and/or cross-checks with other data sources.[13] This analysis included assessing the consistency of the platforms' data output of key pathogens.

Methods

We conducted a search to identify potential, supranational, open-access, antimicrobial resistance interactive platforms for comparison with WHO's Global Antimicrobial Resistance and Use Surveillance System 2019 data (latest available year of reporting at the time of the search). The search was initially conducted in October 2021 and repeated in July 2022. First, we screened the 71 identified international antimicrobial resistance surveillance platforms in a 2020 review[9] for suitability. We then searched the individual Member States' health ministry (or equivalent) websites for involvement in additional supranational schemes. We screened the individual national action plans that were available in the WHO Library of antimicrobial resistance national action plans[14] for mentions of additional specific platforms. Finally, we conducted a general internet search using the Google search engine and the search words "AMR", "antimicrobial resistance", "national action plan", "NAP" and the specific country of interest.

We used the following inclusion criteria: the platform had to (i) be entirely open access, interactive and web-based for reporting and visualizing antimicrobial resistance data; (ii) have data available to compare to those of 2019; (iii) represent at least supranational reporting of regional data; and (iv) contain data on blood culture isolates. The exclusion criteria were not having open-access data via a readily open-access interactive platform, having no data available on the study period or only partial reporting of data (organism of interest but not suitable antimicrobial).

Analysis of surveillance data

For comparisons, the WHO Data Quality Assurance framework suggests selecting a core set of four to five tracer indicators to identify any data completeness and quality issues.[13] Thus, to enable direct comparison with other databases, we searched the WHO Global Antimicrobial Resistance and Use Surveillance System for resistance data on four key blood stream infection organisms represented across the platforms: *Escherichia coli, Klebsiella pneumoniae*, *Staphylococcus aureus* and *Streptococcus pneumoniae.* The 2021 *Global Antimicrobial Resistance and Use Surveillance System (GLASS) Report* states that the data collected for each data call (the last was in 2020 for participating countries) are antimicrobial susceptibility rates for the previous calendar year.[15] We extracted the data on the number of isolates submitted for each species, the antimicrobial susceptibility results, age and gender of patients, number of patients tested and the origin of infection for each isolate. We then categorized these according to the system's parameters of (i) no data available; (ii) < 70% data reported; or (iii) 70–100% data reported. We also extracted the reported antimicrobial susceptibilities for the available indicators of resistance. For *E. coli* and *K. pneumoniae*, we selected the third-generation cephalosporin ceftazidime (or when not available, ceftriaxone); for *S. aureus*, oxacillin (or when not available, cefoxitin); and for *S. pneumoniae*, penicillin (or when not available, oxacillin). We selected the alternative antimicrobial when the primary selection was not being reported or less than 30% of isolates having sensitivity results available for primary selection. Six of the authors extracted these data across each identified platform a different author covered each WHO region, and one author cross-checked all the regions.

Comparison of platforms

To compare the strengths and weaknesses of platforms identified, we used pre-defined criteria. These criteria consisted of a broad overview of a combination of WHO Data Quality Assurance framework dimensions (qualitative consideration of data completeness, timeliness and internal consistency)[13] and features specific to platform use, such as data accessibility and extraction, data representation and platform usability. We also pooled and summarized the qualitative comments from the data extractors to identify any strengths and weaknesses in visualization of data between platforms. Finally, we created a minimum recommended data set template as a potential method for increasing antimicrobial resistance reporting, engagement and representation.

Statistical analysis

We conducted the statistical analysis and data visualizations in R version 4. 1.1 (R Foundation, Vienna, Austria), using the tidyverse, gtsummary, sf and rnaturalearth packages.

We summarized the categorical variables as frequencies and percentages and the continuous variables as medians and interquartile ranges (IQRs). We also stratified the countries' key variables by WHO region.

We used Bland–Altman analysis to assess concordances between the proportion of isolate susceptibility that each country reported to WHO's and identified platforms. We matched each organism with each country (hereafter referred to as organism–country combinations). This technique quantifies the concordances between two continuous measurements by calculating the mean difference (bias) and constructing limits of agreement (within which lie 95% of the differences between measurements).[16] We then used paired *t*-tests to assess whether each country reported different mean susceptibility percentages for each organism to the two platforms. The number of isolates that each country reported to different platforms was summarized using medians and the median of the differences. We then compared these using Wilcoxon signed-rank tests to account for the paired data.

Results

Identification of platforms

We did not identify any additional platforms than the 71 previous identified platforms.

In addition to WHO's surveillance system, Pfizer's Antimicrobial Testing Leadership and Surveillance database met the inclusion criteria and had a global scope. The European Centre for Disease Prevention and Control's (ECDC) European Antimicrobial Resistance Surveillance Network was the only regional platform that met the inclusion criteria. Both WHO's and Pfizer's platforms enable the analysis of blood stream infection isolates independently of other specimen types, making direct comparison of the reported susceptibility rates for 2019 across countries possible. The ECDC network combines data on blood stream infections and cerebrospinal fluid. As the ECDC network feeds directly into WHO's system, the aim of the comparison was to assess whether combining reported susceptibility estimates of important blood stream isolates and cerebrospinal fluid together resulted in any significant variance in reported organism susceptibility between the two platforms.

Surveillance platform activity

As of August 2022, a total of 103 of the 194 (53.1%) Member States have enrolled to the WHO's surveillance system. Of these, 100 (97.1%) have signed up to submit antimicrobial resistance surveillance data, and 18 (17.5%) have signed up to submit antimicrobial consumption data (Fig. 1). Of the 100 countries that committed to submit antimicrobial

resistance surveillance data, 67 (67.0%) do so, with a further one country submitting partial data (1.0%). Three countries that have not enrolled also submit data (70/194; 36.1%; Fig. 1). Of the 71 countries actively submitting data to WHO's surveillance system, 28 (39.4%) also submit to Pfizer's platform and 19 (26.8%) submit to ECDC. Sixteen countries (22.5%) submit to all three platforms

Surveillance data quality

Countries reporting on the four pre-set organisms and their associated antimicrobial sensitivity are presented in Table 1 (available at https://www.who.int/publications/journals/bulletin/).

Examining the proportion of organism–country combinations that had 70–100% data reported to the WHO's surveillance system, we found that: 96.8% (271) of combinations had antimicrobial sensitivity data; 88.9% (249) had information on gender; 83.6% (234) had information on age; 35.7% (100) had information on the total numbers of patients tested; and only 21.4% (60) had information on infection origin. The Western Pacific and African Regions provided data more consistently on the numbers of patients tested; the South-East Asia, European, Western Pacific Regions provided data on age, and the Western Pacific Region provided data on infection origin. Across the Regions of the Americas the reliability of the available sensitivity and age data was comparatively low, whereas in the European Region, the reliability of the available infection origin data was notably low (available in the online repository).[17] Across WHO regions, significant variation was noted in the susceptibility data regarding *E. coli*, *K. pneumoniae* and *S. aureus*, but less variation regarding the *S. pneumoniae* data (Table 2).

Comparison of the platform data showed that the data submitted to WHO's surveillance system were more antimicrobial susceptible than average data submitted to Pfizer's platform (bias: 4%, 95% confidence interval, CI: 1 to 7). The concordance between these two platforms' organism-country susceptibilities was extremely low, with 95% limits of agreement ranging from −26% to 35%. This result indicates that for 95% of organism–country combinations, the absolute difference between the susceptibility reported to WHO's surveillance system and that reported to Pfizer's platform was possibly as great as 35% (Fig. 2). We found no evidence that WHO's and ECDC's surveillance platforms had different mean susceptibilities (bias: 0%; 95% CI: −2% to 2%). However, the concordance between the organism–country combinations was low, with 95% limits of agreement from −18% to 18%, even though two outlying data points primarily drove this result (Table 3).

We found strong significant evidence that countries report different numbers of isolates to WHO's surveillance system and Pfizer's platform (*P*-value: < 0.001), and significant evidence that countries report different numbers of isolates to the WHO's and ECDC's platforms (*P*-value: 0.04). Comparison of the number of isolates reported to WHO's and Pfizer's platforms revealed that the median of the differences was 674 isolates (IQR: 175 to 1917 isolates). Comparison of the number of isolates reported to WHO's and ECDC's platforms revealed that the median of differences was 192 isolates (IQR: −273 to 1743 isolates). Table 3 presents a summary of statistics stratified by organism.

Comparison of platforms

Table 4 presents the overall aims of each platform, and their weakness and strengths regarding consistency in presentation and accessibility of data, reporting standards, completeness and quality of data and consistency of data across key demographic indicators.

Proposed data set requirements

As we found that the data representativeness and data quality vary across the platforms and WHO regions, we propose a minimum data set requirement for reporting blood stream infection antimicrobial resistance data in the form of a potential template (Table 5). This template focuses on reporting at least the four blood stream infection organisms analysed here alongside the key antimicrobial susceptibility indicator data and the baseline demographic data.

Discussion

Our findings suggest considerable inconsistencies between the surveillance data in supranational observatory platforms, raising concerns about their reliability for reflecting national or local community needs. In 2021, WHO announced a renewed *Call to action on antimicrobial resistance*, seeking to accelerate the commitments made previously to tackling this global public health concern, using the One Health approach but considering the varied circumstances of individual countries.[19] Having garnered the active support of 113 Member States, an opportunity now exists to identify and address the deficiencies in antimicrobial resistance surveillance data.

Making flexible, open-access antimicrobial resistance surveillance platforms that require minimum entry available to reporting laboratories to facilitate accuracy, rather than striving for unachievable completeness in surveillance data submission, could enable countries lacking the diagnostic or workforce capacity to obtain meaningful surveillance data for national measures and international collaboration.[20] The substantial discrepancies between

surveillance platforms in species susceptibility within countries revealed here reduces the ability to reliably monitor any development in national, regional and global antimicrobial resistance patterns. This variability must be addressed without delay if we are to ensure reliability of private or public platform outputs and to avoid misdirecting antimicrobial stewardship and research on antimicrobial resistance and antimicrobial stewardship at the national and regional levels.[10,21] The wide variation between countries in the amount of species data submitted to each platform highlights sample selection bias. In addition, smaller sample sizes are unlikely to represent any variability in inter-city or regional resistance.[22–24]

To improve the submission of reliable data, we suggest that laboratories should be provided with a minimum required reporting data set template that includes only key pathogens. This approach may be especially useful in invigorating surveillance activity in those countries whose capabilities are still in the early development stage. This template could also stipulate that only the susceptibility of indicator antimicrobials is required (as in the ECDC's network), which would help countries focus on susceptibility testing strategies when funding is scarce but allow for regional variation in the selection of appropriate/available indicator antimicrobial agents. WHO has recently published methodological principles for nationally representative surveys of antimicrobial resistant blood stream infections,[25] which may be further facilitated by a minimal data set approach. While improving diagnostic capability is likely to require substantial financial investment in some situations, this document provides timely guidance for countries with limited surveillance infrastructures to undertake periodic strategic sampling of defined population subsets to address reporting bias issues.[25] This approach could be combined with restricting national data reporting requirements to a minimum and optimizing available funds to ensure adequate diagnostics to support this minimum data set. Subsequently, platforms should be adapted to include information on source data type (periodic survey versus routine national data) and should streamline upload mechanisms for minimum versus expanded data sets. Sharing the lessons learnt with regional partners and considering the adoption of a periodic survey method potentially coordinated by the regional WHO offices will be integral for maximizing efforts and avoiding duplication of work.

Although capacity strengthening is essential for developing surveillance platforms, giving a clinical context to the available data could also be a priority for established platforms.[5] A major benefit of WHO's surveillance system is the option to submit isolate-level clinical information, and although demographic data are often available, information on infection origin (particularly in Europe) and the total number of isolates tested is often lacking. Combining clinical information and antimicrobial resistance data can improve the

scope and applicability of individualized antimicrobial stewardship guidelines.[20] Even accounting for the additional time and resource burden associated with submitting data to WHO's surveillance system in a tertiary hospital in Thailand, for example, the authors consider WHO's system outputs superior in contributing to antimicrobial guideline development.[20] Accurate interpretation of the variation in bacteraemia isolation rates during COVID-19 has been complicated by imprecise denominator estimates, even in countries that are able to provide the most comprehensive data, and this highlights the importance of improving data quality across the board.[26] Multiple platform use is likely to further challenge the already limited workforce capacity, and if opportunities to optimize data quality are not taken, alternative platforms could seek to support the visualization of WHO's system data through enabling submission via a single platform or through providing a specific function, rather than relying on comparatively limited data to address present inconsistencies. At the very least, platforms should provide an opportunity to compare data by individual specimen type, as evidenced by the observed variation in the isolate data in the WHO's and ECDC's platforms, despite reporting via a sophisticated platform using national data.

Although we were able to evaluate comparators, open-access platforms against all the available WHO's system data, we acknowledge that some countries also engage in further closed surveillance networks (such as the Asian Network for Surveillance of Resistant Pathogens), semi-open access networks that look at a limited number of organisms (such as Gram negative surveillance by the Global Study for Monitoring Antimicrobial Resistant Trends) or belong to networks that provide regular reports but have no interactive platform (Central Asian and European Surveillance of Antimicrobial Resistance network). Our results raise concerns about the heterogeneity of the matched country data of some of the most established observatories. We recommend that those seeking to inform policy consider further evaluating the data held within these restricted-access networks. Our findings also reveal data discrepancies during the last full year of reporting before the COVID-19 pandemic, followed by a period of increased antimicrobial use and diverted laboratory capacity. These backdrops are highlighting a need to urgently improve data reliability across platforms to understand the true impact of the COVID-19 pandemic on global antimicrobial resistance. When evaluating the surveillance strategy in their specific regions, policy-makers should bear in mind that in some areas, current reporting capacity is likely to be more limited.

In conclusion, the surveillance data submitted to various supranational antimicrobial resistance monitoring platforms seem to be significantly heterogeneous, which may compromise their validity and undermine national and global strategies. This heterogeneity is particularly concerning for low- and middle-income countries as misinforming of their

decision-makers may affect the perceived need for specific diagnostics or antimicrobial guidelines.

Policy-makers must be made aware of the potential unreliability of the platforms intended for informing strategy or outcomes. Mitigation measures must be taken to reduce surveillance bias through limited reporting and improve the ability to report more representative data in the short-term. These measures are particularly relevant in countries that need to improve their national surveillance platforms. Recent WHO recommendations to consider periodic strategic surveys in such circumstances seek to address this issue and may be further complimented if a minimum required data set is agreed on to streamline reporting and optimize representation in the short-term.

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Competing interests:

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Table 1. **Reported species susceptibility to open-access antimicrobial resistance surveillance platforms, by country, 2019**

WHO Region, country, organism	WHO's surveillance system[a]			Pfizer's surveillance database[b]			ECDC's surveillance network[c]		
	Antibiotic	No. of isolates	Susceptibility, %	Antibiotic	No. of isolates	Susceptibility, %	Antibiotic	No. of isolates	Susceptibility, %
African Region									
South Africa									
E. coli	Ceftazidime	4 306	70.2	Ceftazidime	39	87.2	NR	NR	NR
K. pneumoniae	Ceftazidime	653	26.9	Ceftazidime	47	51.1	NR	NR	NR
S. aureus	Oxacillin	744	78.6	Oxacillin	46	89.1	NR	NR	NR
S. pneumoniae	Penicillin	6 315	72.2	Penicillin	9	77.8	NR	NR	NR
Region of the Americas									
Argentina									
E. coli	Ceftazidime	154	81.8	Ceftazidime	27	63.0	NR	NR	NR
K. pneumoniae	Ceftazidime	2 017	44.3	Ceftazidime	26	30.8	NR	NR	NR
S. aureus	Oxacillin	296	58.0	Oxacillin	47	57.5	NR	NR	NR
S. pneumoniae	Penicillin	1 732	75.4	Penicillin	2	100.0	NR	NR	NR
Brazil									
E. coli	Ceftazidime	214	88.2	Ceftazidime	39	76.9	NR	NR	NR
K. pneumoniae	Ceftazidime	166	39.8	Ceftazidime	53	35.9	NR	NR	NR
S. aureus	Oxacillin	6	79.4	Oxacillin	78	57.7	NR	NR	NR
S. pneumoniae	ND	6	ND	Penicillin	16	68.8	NR	NR	NR
South-East Asian Region									
India									
E. coli	Ceftazidime	ND	28.6	Ceftazidime	69	31.9	NR	NR	NR
K. pneumoniae	Ceftazidime	ND	40.0	Ceftazidime	57	29.8	NR	NR	NR
S. aureus	Cefoxitin	ND	44.2	Oxacillin	64	56.6	NR	NR	NR
S. pneumoniae	ND	ND	ND	Penicillin	17	29.4	NR	NR	NR
Thailand							NR	NR	NR
E. coli	Ceftazidime	1 121	71.7	Ceftazidime	47	72.3	NR	NR	NR
K. pneumoniae	Ceftazidime	2 453	61.2	Ceftazidime	39	53.9	NR	NR	NR
S. aureus	Cefoxitin	702	87.6	Oxacillin	37	73.0	NR	NR	NR
S. pneumoniae	Penicillin	180	61.4	Penicillin	2	0	NR	NR	NR
European Region									
Austria									
E. coli	Ceftazidime	2 382	90.4	NR	NR	NR	Cephalosporin[d]	61 06	90.3

K. pneumoniae	Ceftazidime	478	87.3	NR	NR	NR	Cephalosporin[d]	1 326	88.5
S. aureus	Oxacillin	478	94.7	NR	NR	NR	Meticillin	3 323	94.4
S. pneumoniae	Penicillin	1 305	93.5	NR	NR	NR	Penicillin	458	93.2
Croatia									
E. coli	Ceftazidime	143	84.1	Ceftazidime	63	84.1	Cephalosporin[d]	1 085	83.0
K. pneumoniae	Ceftazidime	1 111	48.1	Ceftazidime	52	40.4	Cephalosporin[d]	317	45.4
S. aureus	Cefoxitin	153	75.1	Oxacillin	90	78.9	Meticillin	358	75.1
S. pneumoniae	Penicillin	358	72.8	Penicillin	14	92.7	Penicillin	154	79.9
Cyprus									
E. coli	Ceftazidime	60	83.5	NR	NR	NR	Cephalosporin[d]	92	79.3
K. pneumoniae	Ceftazidime	8	54.6	NR	NR	NR	Cephalosporin[d]	60	50.0
S. aureus	Oxacillin	32	0	NR	NR	NR	Meticillin	58	63.8
S. pneumoniae	ND	92	ND	NR	NR	NR	Penicillin	2	0
Czechia									
E. coli	Ceftazidime	95	84.0	Ceftazidime	33	84.9	Cephalosporin[d]	3 557	82.7
K. pneumoniae	Ceftazidime	387	84.1	Ceftazidime	24	54.2	Cephalosporin[d]	1 563	47.9
S. aureus	Oxacillin	387	88.0	Oxacillin	38	89.5	Meticillin	2 108	87.4
S. pneumoniae	Penicillin	1 563	94.9	Penicillin	9	77.8	Penicillin	387	95.1
Finland									
E. coli	Ceftazidime	1 494	92.3	NR	NR	NR	Cephalosporin[d]	5 413	91.3
K. pneumoniae	Ceftazidime	628	92.4	NR	NR	NR	Cephalosporin[d]	868	91.8
S. aureus	Oxacillin	957	97.7	NR	NR	NR	Meticillin	53	97.9
S. pneumoniae	Penicillin	6 225	88.1	NR	NR	NR	Penicillin	594	88.0
France									
E. coli	Ceftazidime	1 264	91.3	Ceftazidime	110	94.6	Cephalosporin[d]	13 019	90.2
K. pneumoniae	Ceftazidime	13 097	69.1	Ceftazidime	82	72.0	Cephalosporin[d]	3 075	68.1
S. aureus	Oxacillin	1 264	88.4	Oxacillin	140	88.6	Meticillin	6 467	88.4
S. pneumoniae	Penicillin	472	74.7	Penicillin	71	77.5	Penicillin	1 264	74.7
Germany									
E. coli	Ceftazidime	1 981	88.2	Ceftazidime	27	96.3	Cephalosporin[d]	23 413	87.9
K. pneumoniae	Ceftazidime	10 939	86.7	Ceftazidime	25	76.0	Cephalosporin[d]	4 719	86.5
S. aureus	Oxacillin	23 387	93.2	Oxacillin	27	88.9	Meticillin	11 950	93.3
S. pneumoniae	Penicillin	154	94.3	Penicillin	20	95.0	Penicillin	1 962	94.3
Greece									
E. coli	Ceftazidime	1 946	83.8	Ceftazidime	15	100.0	Cephalosporin[d]	190	80.0
K. pneumoniae	Ceftazidime	1 588	35.4	Ceftazidime	26	11.5	Cephalosporin[d]	310	32.6

S. aureus	Oxacillin	1 059	56.6	Oxacillin	26	76.9	Meticillin	170	37.6
S. pneumoniae	ND	1221	ND	Penicillin	9	88.9	Penicillin	0	0
Ireland									
E. coli	Ceftazidime	885	85.9	Ceftazidime	8	87.5	Cephalosporin[d]	3 231	86.1
K. pneumoniae	Ceftazidime	348	81.8	Ceftazidime	13	46.2	Cephalosporin[d]	527	80.6
S. aureus	Oxacillin	64	87.2	Oxacillin	13	92.3	Meticillin	1 146	87.4
S. pneumoniae	Penicillin	3 229	85.6	Penicillin	4	100.0	Penicillin	348	85.6
Italy									
E. coli	Ceftazidime	8 356	70.3	Ceftazidime	74	75.7	Cephalosporin[d]	18 409	68.2
K. pneumoniae	Ceftazidime	1 639	42.3	Ceftazidime	73	30.1	Cephalosporin[d]	7 699	40.8
S. aureus	Oxacillin	1 166	64.8	Oxacillin	119	63.9	Meticillin	9 681	65.7
S. pneumoniae	Penicillin	18 404	88.1	Penicillin	38	81.6	Penicillin	1 017	88.1
Latvia									
E. coli	Ceftazidime	640	81.6	Ceftazidime	9	66.7	Cephalosporin[d]	442	79.9
K. pneumoniae	Ceftazidime	604	62.9	Ceftazidime	9	77.8	Cephalosporin[d]	198	63.1
S. aureus	Cefoxitin	112	92.0	Oxacillin	14	100.0	Meticillin	421	92.6
S. pneumoniae	Penicillin	112	88.0	Penicillin	10	90.0	Penicillin	79	89.9
Lithuania									
E. coli	Ceftazidime	439	86.9	Ceftazidime	27	77.8	Cephalosporin[d]	1 132	84.5
K. pneumoniae	Ceftazidime	120	45.0	Ceftazidime	22	50.0	Cephalosporin[d]	440	43.2
S. aureus	Cefoxitin	107	90.7	Oxacillin	52	88.5	Meticillin	656	90.7
S. pneumoniae	Penicillin	120	89.2	Penicillin	13	84.6	Penicillin	120	89.2
Luxembourg									
E. coli	Ceftazidime	38	88.0	NR	NR	NR	Cephalosporin[d]	1 132	84.5
K. pneumoniae	Ceftazidime	209	73.8	NR	NR	NR	Cephalosporin[d]	103	73.8
S. aureus	Oxacillin	38	93.8	NR	NR	NR	Meticillin	209	93.8
S. pneumoniae	Penicillin	10	79.0	NR	NR	NR	Penicillin	38	78.9
Malta									
E. coli	Ceftazidime	9	81.3	NR	NR	NR	Cephalosporin[d]	332	82.2
K. pneumoniae	Ceftazidime	358	57.7	NR	NR	NR	Cephalosporin[d]	129	58.9
S. aureus	Oxacillin	16	76.6	NR	NR	NR	Meticillin	75	76.0
S. pneumoniae	Penicillin	77	63.0	NR	NR	NR	Penicillin	27	66.7
Netherlands (Kingdom of the)									
E. coli	Ceftazidime	7 300	92.6	Ceftazidime	18	100.0	Cephalosporin[d]	7 300	92.0
K. pneumoniae	Ceftazidime	1 434	90.2	Ceftazidime	8	87.5	Cephalosporin[d]	1 434	89.5
S. aureus	Oxacillin	1 256	98.4	Oxacillin	18	100.0	Meticillin	3 221	98.4

S. pneumoniae	Penicillin	2 627	96.1	Penicillin	25	100.0	Penicillin	1 360	96.0
Norway									
E. coli	Ceftazidime	1 106	93.9	NR	NR	NR	Cephalosporin[d]	4 075	93.2
K. pneumoniae	Ceftazidime	62	91.3	NR	NR	NR	Cephalosporin[d]	832	91.0
S. aureus	Oxacillin	504	99.0	NR	NR	NR	Meticillin	1 644	98.9
S. pneumoniae	Penicillin	23	93.7	NR	NR	NR	Penicillin	504	93.7
Poland									
E. coli	Ceftazidime	65	83.1	Ceftazidime	20	95.0	Cephalosporin[d]	2 803	82.2
K. pneumoniae	Ceftazidime	1 161	41.5	Ceftazidime	25	24.0	Cephalosporin[d]	1 166	40.8
S. aureus	Cefoxitin	254	85.1	Oxacillin	43	86.1	Meticillin	1 841	85.1
S. pneumoniae	Penicillin	319	85.3	Penicillin	21	76.2	Penicillin	310	84.5
Russian Federation									
E. coli	Ceftazidime	216	53.3	Ceftazidime	41	24.4	NR	NR	NR
K. pneumoniae	Ceftazidime	5	20.5	Ceftazidime	60	23.3	NR	NR	NR
S. aureus	Cefoxitin	23	76.7	Oxacillin	95	74.7	NR	NR	NR
S. pneumoniae	Penicillin	418	93.3	Penicillin	7	85.7	NR	NR	NR
Sweden									
E. coli	Ceftazidime	1 069	92.3	Ceftazidime	ND	ND	Cephalosporin[d]	9 419	91.9
K. pneumoniae	Ceftazidime	5 948	91.1	Ceftazidime	13	92.3	Cephalosporin[d]	1 795	90.6
S. aureus	Cefoxitin	9 421	98.2	Oxacillin	ND	ND	Meticillin	5 948	98.8
S. pneumoniae	Penicillin	253	93.5	Penicillin	2	50.0	Penicillin	1 070	93.5
Switzerland									
E. coli	Ceftazidime	63	89.7	Ceftazidime	24	83.3	NR	NR	NR
K. pneumoniae	Ceftazidime	75	91.3	Ceftazidime	11	81.8	NR	NR	NR
S. aureus	Cefoxitin	6 048	96.5	Oxacillin	10	90.0	NR	NR	NR
S. pneumoniae	Penicillin	726	94.8	Penicillin	9	88.9	NR	NR	NR
United Kingdom									
E. coli	Ceftazidime	1 932	87.5	Ceftazidime	56	94.6	Cephalosporin[d]	26 593	87.4
K. pneumoniae	Ceftazidime	705	85.3	Ceftazidime	36	77.8	Cephalosporin[d]	4 867	85.4
S. aureus	Cefoxitin	3 556	89.6	Oxacillin	40	92.5	Meticillin	9 114	94.0
S. pneumoniae	Penicillin	5 085	94.7	Penicillin	16	93.8	Penicillin	3 667	94.5
Eastern Mediterranean Region									
Jordan									
E. coli	Ceftriaxone	183	33.6	Ceftriaxone	ND	ND	NR	NR	NR
K. pneumoniae	Ceftriaxone	195	26.0	Ceftriaxone	ND	ND	NR	NR	NR
S. aureus	Oxacillin	137	27.6	Oxacillin	ND	ND	NR	NR	NR

S. pneumoniae	Ceftriaxone	97	90.0	Penicillin	ND	ND	NR	NR	NR
Qatar									
E. coli	Ceftazidime	ND	62.2	Ceftazidime	18	22.2	NR	NR	NR
K. pneumoniae	Ceftazidime	ND	71.7	Ceftazidime	11	54.6	NR	NR	NR
S. aureus	Oxacillin	ND	66.2	Oxacillin	29	51.7	NR	NR	NR
S. pneumoniae	Penicillin	ND	79.0	Penicillin	17	64.7	NR	NR	NR
Saudi Arabia									
E. coli	Ceftazidime	591	42.1	Ceftazidime	6	50.0	NR	NR	NR
K. pneumoniae	Ceftazidime	42	27.8	Ceftazidime	8	37.5	NR	NR	NR
S. aureus	Cefoxitin	60	51.1	Oxacillin	6	50.0	NR	NR	NR
S. pneumoniae	Oxacillin	307	57.9	Penicillin	1	0	NR	NR	NR
Western Pacific Region									
Australia									
E. coli	Ceftazidime	3 157	87.0	Ceftazidime	24	79.2	NR	NR	NR
K. pneumoniae	Ceftazidime	4 914	90.1	Ceftazidime	18	94.4	NR	NR	NR
S. aureus	Cefoxitin	1 143	81.5	Oxacillin	17	100.0	NR	NR	NR
S. pneumoniae	ND	110	ND	Penicillin	32	96.9	NR	NR	NR
Japan									
E. coli	Ceftazidime	26 176	86.3	Ceftazidime	21	61.9	NR	NR	NR
K. pneumoniae	Ceftazidime	78 923	95.5	Ceftazidime	14	92.9	NR	NR	NR
S. aureus	Oxacillin	608	63.6	Oxacillin	34	64.7	NR	NR	NR
S. pneumoniae	Penicillin	3 241	98.7	Penicillin	4	100.0	NR	NR	NR
Malaysia									
E. coli	Ceftazidime	699	75.7	Ceftazidime	20	60.0	NR	NR	NR
K. pneumoniae	Ceftazidime	8 875	66.3	Ceftazidime	22	54.6	NR	NR	NR
S. aureus	Oxacillin	2 001	81.7	Oxacillin	28	57.1	NR	NR	NR
S. pneumoniae	Penicillin	1 079	86.3	Penicillin	11	100.0	NR	NR	NR
Philippines									
E. coli	Ceftazidime	256	66.2	Ceftazidime	20	60.0	NR	NR	NR
K. pneumoniae	Ceftazidime	1 583	46.2	Ceftazidime	12	58.3	NR	NR	NR
S. aureus	Oxacillin	166	49.1	Oxacillin	37	56.8	NR	NR	NR
S. pneumoniae	Penicillin	1 420	86.2	Penicillin	6	83.3	NR	NR	NR
Republic of Korea									
E. coli	Ceftazidime	683	79.9	Ceftazidime	54	63.0	NR	NR	NR
K. pneumoniae	Ceftazidime	716	80.7	Ceftazidime	6	66.7	NR	NR	NR
S. aureus	Cefoxitin	225	51.4	Oxacillin	27	51.9	NR	NR	NR

S. pneumoniae	Penicillin	47	58.3	Penicillin	3	66.7	NR	NR	NR

ECDC: European Centre for Disease Prevention and Control; NR: not reported; WHO: World Health Organization.

[a] Full name: Global Antimicrobial Resistance and Use Surveillance System.

[b] Full name: Antimicrobial Testing Leadership and Surveillance.

[c] Full name: European Antimicrobial Resistance Surveillance Network.

[d] 3rd generation cephalosporin.

Note: Cephalosporin antibiotic is 3

Table 2. **Reported organism susceptibility data in WHO Global Antimicrobial Resistance and Use Surveillance System across WHO regions, 2019**

Organism	WHO region, median % (IQR)					
	African (8 countries)	Americas (4 countries)	Eastern Mediterranean (18 countries)	European (24 countries)	South-East Asian (8 countries)	Western Pacific (9 countries)
Escherichia coli	60 (55 to 72)	85 (83 to 87)	46 (34 to 54)	85 (82 to 90)	42 (28 to 47)	76 (66 to 83)
Klebsiella pneumoniae	22 (8 to 34)	42 (41 to 43)	30 (26 to 46)	66 (42 to 87)	35 (23 to 42)	77 (67 to 85)
Staphylococcus aureus	84 (78 to 96)	69 (63 to 74)	51 (33 to 62)	89 (77 to 94)	57 (48 to 70)	76 (61 to 83)
Streptococcus pneumoniae	72 (63 to 72)	75 (75 to 75)	84 (62 to 92)	88 (79 to 94)	80 (71 to 85)	86 (69 to 86)

IQR: interquartile range; WHO: World Health Organization.

Note: Median susceptibilities are presented as a percentage of susceptible isolates for each WHO region for *E. coli* and *K. pneumoniae* and third-generation cephalosporins, *S. aureus* and oxacillin, and *S. pneumoniae* and penicillin. Countries are reported in Table 1.

Table 3. **Comparison of median of differences in antimicrobial susceptibility and number of isolates reported to supernational open access surveillance databases, 2019**

Comparison, organism	Susceptibility %			No. of isolates		
	Median		Median of differences (IQR)*	Median		Median of differences (IQR)*
	WHO[a]	Comparator platform		WHO[a]	Comparator platform	
WHO[a] vs Pfizer[b] (28 countries)						
Escherichia coli	83.8	77.4	−0.3 (−6.7 to 14.0)	699	27	655.0 (175.0 to 1936.8)
Klebsiella pneumoniae	61.2	54.2	7.3 (−3.7 to 12.0)	705	24	1136.0 (363.0 to 2414.0)
Staphylococcus aureus	79.4	77.9	−0.7 (−4.8 to 2.2)	478	37	461.5 (89.2 to 1124.5)
Streptococcus pneumoniae	88.0	84.6	0.9 (−4.8 to 8.3)	472	10	411.0 (178.0 to 1730.0)
WHO[a] vs ECDC[c] (19 countries)						
Escherichia coli	86.9	86.1	1.0 (0.3 to 1.5)	1069	3557	−2738.0 (−6134.5 to −388.5)
Klebsiella pneumoniae	69.0	68.1	0.6 (0.1 to 1.4)	628	868	−5.0 (−545.0 to 600.0)
Staphylococcus aureus	89.6	90.7	0 (−0.4 to 0)	478	1644	−549.0 (−1843.0 to −42.5)
Streptococcus pneumoniae	88.1	88.1	0 (−0.1 to 0.1)	358	387	90.0 (−14.0 to 1244.0)

ECDC: European Centre for Disease Prevention and Control; IQR: interquartile range; WHO: World Health Organization.

[a] Full name: Global Antimicrobial Resistance and Use Surveillance System.

[b] Full name: Antimicrobial Testing Leadership and Surveillance.

[c] Full name: European Antimicrobial Resistance Surveillance Network.

Note: The raw data used to calculate the medians are available in Table 1. The values pertaining to WHO's system may vary between the two comparisons because the same countries do not report to both Pfizer's and ECDC's platforms.

Table 4. **Comparison of key usability features of open-access, international antimicrobial resistance surveillance platforms**

Dimensions, perceived strength or weakness	WHO's Global Antimicrobial Resistance and Use Surveillance System	Antimicrobial Testing Leadership and Surveillance database	European Antimicrobial Resistance Surveillance Platform
Broad aims	Global surveillance system using national-level routine surveillance data to estimate antimicrobial resistance burden and identify emerging resistance across sectors by using the One Health approach	Provides a privately funded service to assess emerging bacterial and fungal resistance through a user-friendly website and mobile application interface. Data are drawn from regions participating in three surveillance programmes[a]	Large, publicly funded continental surveillance platform that aims to collect comparable, representative, temporospatial data to identify timely antimicrobial resistance trends across Europe, inform policy and optimize national surveillance programmes
Consistency in presentation and accessibility			
Strength	Qualitative summary pages for each country provide detailed overview (i.e. no. of reporting rounds per year, no. of reporting stations) of available data	Representation of changes in antimicrobial resistance over time can be easily visualized using embedded interactive heat maps. Data extraction in multiple formats	Easy to use interface requiring minimal learning. Data visualization provided in multiple tabular and graphical formats on one interactive page to provide regional overview. Data presented using clearly defined antimicrobial resistance indicators for clinically important mechanisms
Weakness	Data retrieved for individual countries are displayed separately with limited visualization of trends or differences across more than one country; the platform is embedded within a webpage meaning it can be more difficult to visualize complete data on one page	A period of learning time for end-users wishing to optimize data extraction across different formats was felt to be required when compared to other platforms	Limited ability to visualize all collated data for individual countries
Antimicrobial susceptibility reporting standards			
Strength	Antimicrobial susceptibility data provided according to Clinical and Laboratory Standards Institute and/or European Committee on Antimicrobial Susceptibility Testing interpretation rules, with confirmation of reporting standards used by each country in periodic reports	Users can switch between Clinical and Laboratory Standards Institute and European Committee on Antimicrobial Susceptibility Testing susceptibility cut-offs to allow greater flexibility in comparing country susceptibility results	Unified European Committee on Antimicrobial Susceptibility Testing reporting from 2019 onwards

Weakness	Potential for misinterpreting susceptibility data when comparing countries that report to both Clinical and Laboratory Standards Institute and European Committee on Antimicrobial Susceptibility Testing standards	None identified	Mixed Clinical and Laboratory Standards Institute and European Committee on Antimicrobial Susceptibility Testing reporting before 2019
Completeness of antimicrobial susceptibility data			
Strength	A detailed periodic report providing an overview of changes in data is provided. Option to search by a range of sample types, including blood, genital, urine and stool	Data reports can be prepared for detailed and discrete combinations of pathogens, specific antimicrobial susceptibilities, time periods and countries	Provides a detailed periodic report with an overview of changes in data. Data are presented using clearly defined antimicrobial resistance indicators antimicrobial agents for clinically important mechanisms i.e. third-generation cephalosporins as a screening indicator for possible extended spectrum β lactamases
Weakness	Infection origin and overall no. of patients tested variably presented qualitatively only or qualitatively and quantitatively. Difficult for users to interpret antimicrobial resistance results for different origins (community vs hospital) of infection, despite intent that such data are included in the surveillance reports[15]	Data on infection source are unavailable. Available antimicrobial susceptibility reporting can limit analysis of changes in indicator agents	Data on infection source are unavailable. Data presentation is restricted to pooled invasive cerebrospinal and blood isolates only
Quality of antimicrobial susceptibility data			
Strength	Indication of available susceptibility data for each antibiotic is provided with a cut-off of less or greater than 30%. If data set contains < 10 patients, no susceptibility value is provided	Data can be analysed for highly specific situations including pathogen–antimicrobial susceptibility combinations by age, source and location	Cut-offs are applied for minimum required pathogen-antimicrobial combination reporting to reduce misleading data representation
Weakness	Limited ability to view data across specific time periods	Susceptibility data may be presented for very small sample sets, risking misinterpretation of available data. Data volume for any given year is substantially less than the two other platforms, limiting interpretation. Data collection strategy through specific studies limits representation of data to national susceptibility rates	Data presented are not disaggregated by community or hospital source
Consistency of data across key demographic indicators			
Strength	Provides of antimicrobial resistance-stratified	Data search functions by hospital division (i.e. surgical, medical,	Option to assess demographic data

	frequency data (per 100 000 tested patients) for age and gender with CIs for a set of pathogen–antimicrobial combinations. Presents qualitative demographics, infection source and no. of patients tested for isolates. CIs provided for antimicrobial sensitivity testing data	intensive care as well as non-hospital health care environments such as nursing homes). Data search function by source of infection	quality as discrete percentages (tabular) and via a graphical heat map with an upper range > 90% cut-off
Weakness	Demographics, no. of patients tested and infection origin data are limited by qualitative presentation, with a low upper-band cut-off of > 70% data availability. Limited ability to apply demographic data to susceptibility data	No gender data available. Available data limited to health-care environments	Limited ability to apply demographic data to pathogen–antimicrobial combinations

CI: confidence interval; WHO: World Health Organization.

[a] Surveillance programmes that inform Pfizer's platform include Tigecycline evaluation Surveillance Trial, Assessing Worldwide Antimicrobial Resistance Evaluation and International Network for Optimal Resistance Monitoring.[18]

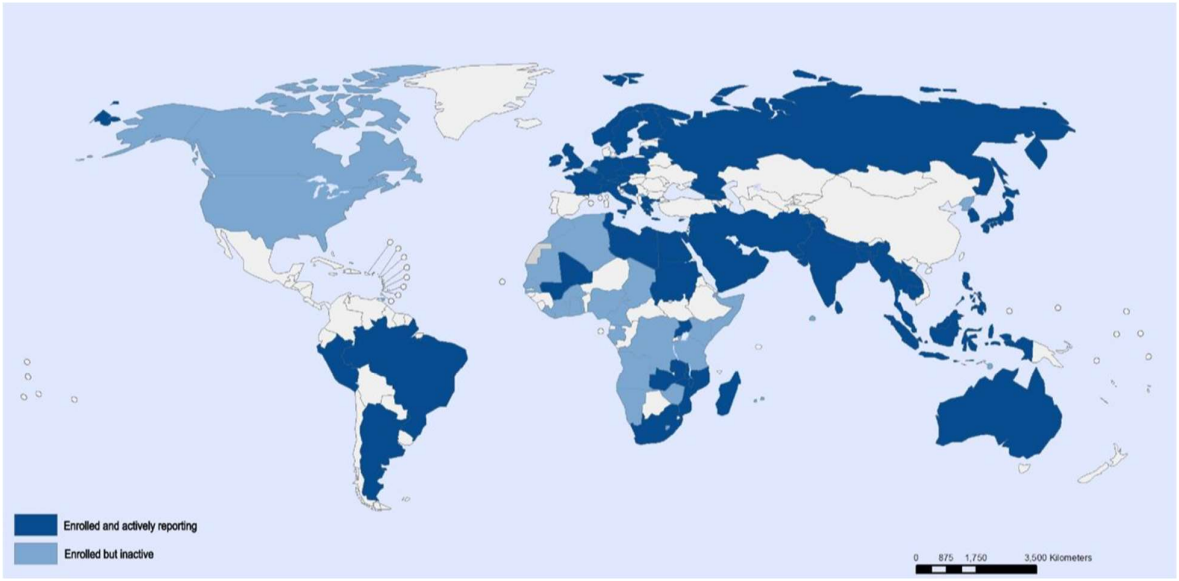
Note: Perceived strengths and weaknesses of evaluated antimicrobial resistance surveillance platforms have been considered according to use for data extraction, broadly considering topics that reflect relatable elements of the WHO Data Quality Assurance Framework and general usability.

Table 5. **Proposed minimum and optimal data requirement for antimicrobial resistance surveillance reporting for international systems/platforms**

Data category	Proposed minimum data requirement– to ensure accuracy and consistency	Proposed optimum data set once effective surveillance platform established
Time interval	Annual	Annual
Pathogen-antimicrobial combinations	*Escherichia coli* and *Klebsiella pneumoniae* - third-generation cephalosporin (cefotaxime or cefpodoxime or ceftriaxone and ceftazidime) - carbapenem (imipenem and/or meropenem) - a quinolone (ciprofloxacin, levofloxacin and/or ofloxacin) - aminoglycoside (gentamicin or amikacin) *Staphylococcus aureus* - Methicillin resistant *Staphylococcus aureus* indicator (oxacillin or cefoxitin) *Streptococcus pneumoniae* - Penicillin (Penicillin G or benzylpenicillin)	*Candida* species - Fluconazole *Enterococcus faecalis* and *faecium* - *Vancomycin* or *teicolplanin* *Pseudomonas aeruginosa* - Beta-lactam (ceftazidime and/or piperacillin-tazobactam and/or meropenem) *Acinetobacter baumannii* - Meropenem
Source of blood stream infection	Provide confirmation on whether source was identified (reported as yes or no).	Consider option for discrete data matching pathogen results with source of infection (i.e. urinary, biliary, soft tissue skin infection).
Origin of infection	Provide data on hospital or community origin of infection	Consider option of splitting community data to include long-term care facilities. Disaggregate hospital data by specialty, e.g. infections arising from medical wards, surgical wards, rehabilitation wards and intensive care units
Demographics of interest	Gender and age (grouped)	Discrete age by year. Standard ethnicity metric to capture variation in different populations across and within countries

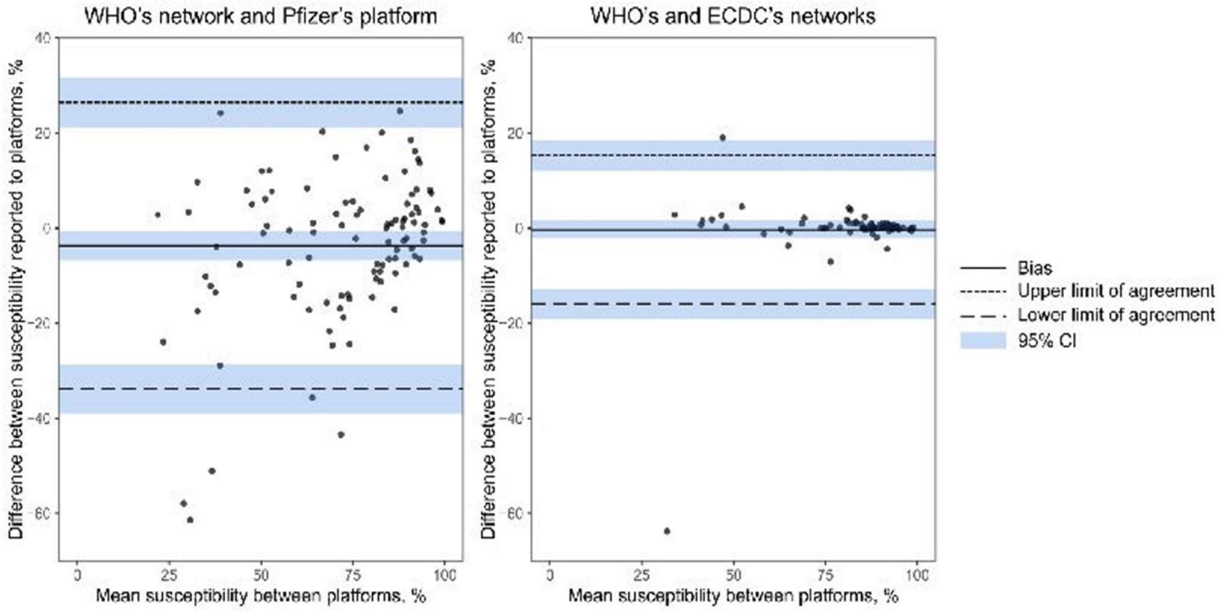
Notes: A suggested approach to a minimum data set requirement for countries developing national surveillance capability, with antimicrobial indicators to provide both flexibility and comparability across countries. Minimum data set requirements could complement a periodic national survey approach and assist harmonization across platforms. A desirable data set is also postulated for countries with established platforms to further optimize surveillance.

Fig. 1. **Reporting activity to Global Antimicrobial Resistance and Use Surveillance System, August 2022**



Note: We obtained evidence that 71 countries submitted surveillance data during the Global Antimicrobial Resistance and Use Surveillance System's 2020 data call. Countries that are enrolled in the system but have no data for the 2020 data call are also highlighted on the map.

Fig. 2. **Bland–Altman plots demonstrating variation in organism–country susceptibility results between supranational open access antimicrobial resistance platforms, 2019**



CI: confidence interval; ECDC: European Centre for Disease Prevention and Control; WHO: World Health Organization.

Note: Included databases are WHO's Global Antimicrobial Resistance and Use Surveillance System, Pfizer's Antimicrobial Testing Leadership and Surveillance and ECDC's European Antimicrobial Resistance Surveillance Network. The y-axes show the differences between the susceptibilities of each organism–country combination result (i.e. the difference between the *E. coli* susceptibility to third-generation cephalosporins for Japan reported to WHO's system and those reported to Pfizer's platform).