

Global surveillance of AMR

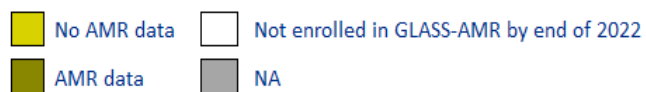
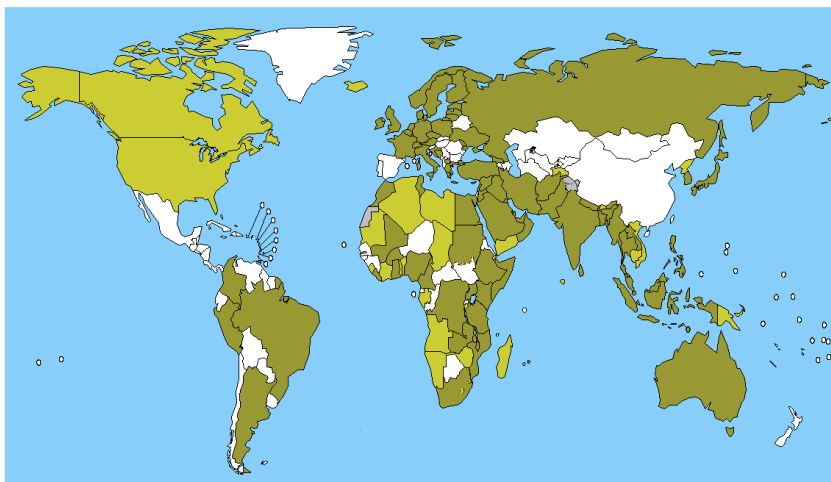
**Complementary methods to
address global data scarcity**

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Global antimicrobial resistance and use surveillance system (GLASS)



116 countries enrolled in GLASS by the end of 2022. 87 reported 2021 AMR data

2023 WHO “GLASS manual for antimicrobial resistance surveillance in common bacteria causing human infection”



Shifting focus from aggregated- to individual-level data



More infectious syndromes, bacterial pathogens, and antibiotic combinations under surveillance



Individual-level molecular AMR data to characterize resistance mechanisms



Detailed population coverage meta-data to facilitate the interpretation of AMR rates



Complementary methods to address the global data scarcity



Enhanced surveillance of fungal infections



GLASS new target pathogens and new specimen types



Target pathogens	Blood	<u>CSF</u>	Urine	Stool	<u>Lower respiratory tract</u>	Urethral, cervical, <u>rectal, pharyngeal</u> swabs
<i>Acinetobacter spp.</i>	●	○			●	
<i>E. coli</i>	●	○	●		○	
<i>K. pneumoniae</i>	●	○	●		●	
<u><i>P. aeruginosa</i></u>	●	○			●	
<i>S. aureus</i>	●	○			●	
<i>S. pneumoniae</i>	●	●			●	
<u><i>N. meningitidis</i></u>	●	●				
<u><i>H. influenzae</i></u>	○	●			●	
<i>Salmonella spp. (non-typhoidal)</i>	●	○		●		
<u><i>S. enterica serovar Typhi</i></u>	●			○		
<u><i>S. enterica serovar Paratyphi A</i></u>	●			○		
<i>Shigella spp.</i>				●		
<i>N. gonorrhoeae</i>						●

13 bacterial pathogens; 9 specimen types; 32 antibiotics across 11 antimicrobial classes (11 “Access”; 18 “Watch”; 3 “Reserve” antibiotics according to WHO AWaRe classification. <https://www.who.int/publications/i/item/9789240076600>)

Limitations of “routine” AMR surveillance data

Undocumented sources of variance limit the interpretation of AMR data at national and global level



ACCESS

Diagnostics access and affordability



STEWARDSHIP

Diagnostic stewardship



LABORATORY

Microbiology and AST practices



COVERAGE

Testing coverage



REPORTING

AMR cases reported and not reported



EXPOSURES

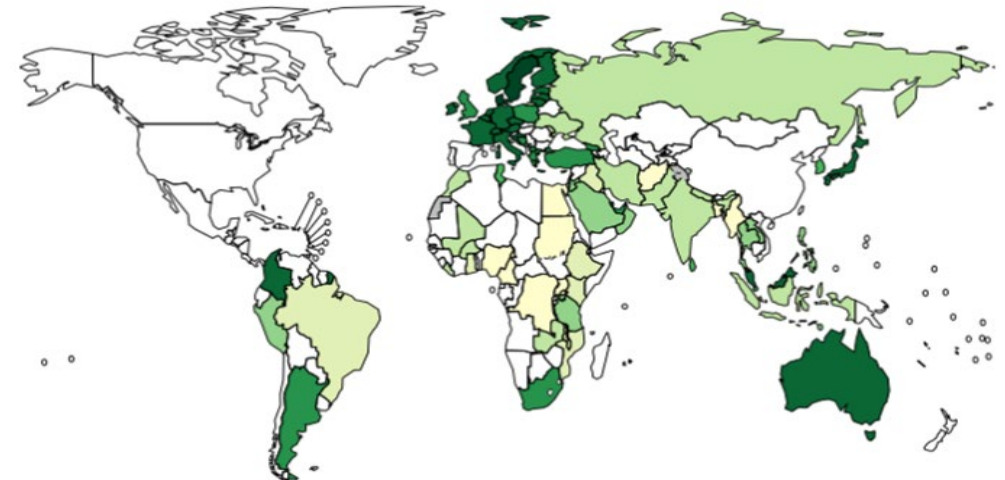
Antibiotic prophylaxis and therapy, invasive devices etc.



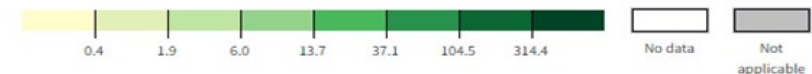
OTHER

Inaccurate classification of infection origin

Data are not comparable: Limited coverage and representativeness and selection bias



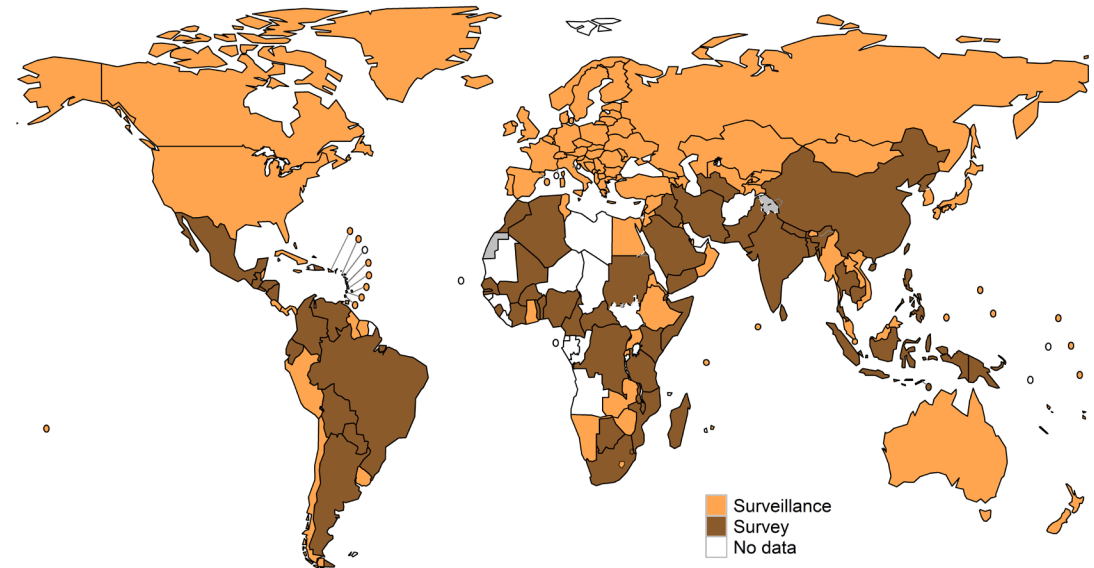
BSIs with AST per million population



Two-pronged model for global surveillance of AMR

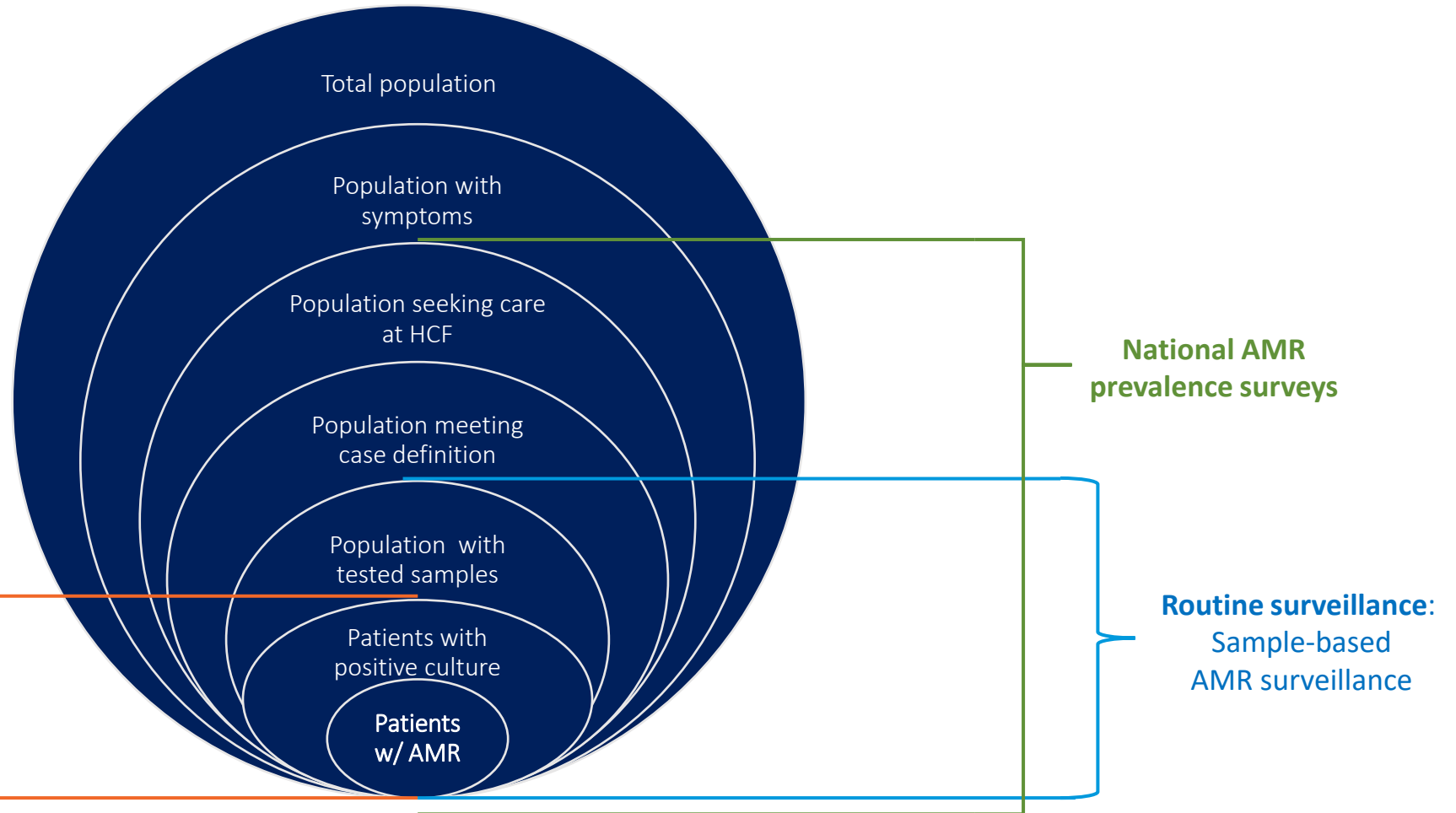
- “Successfully implemented since the 1990s by WHO global programmes monitoring and tackling drug resistance in malaria, tuberculosis and HIV
- Combines data collection based on routine clinical sampling of patients, **and complementary strategies such as periodic surveys** to improve quality, completeness and representativeness of data
- Surveys have greatly contributed to evidence-based policy development and advocacy, and diagnostic and treatment capacity

Example: source of data for rifampicin resistance among new tuberculosis cases, 1995-2020

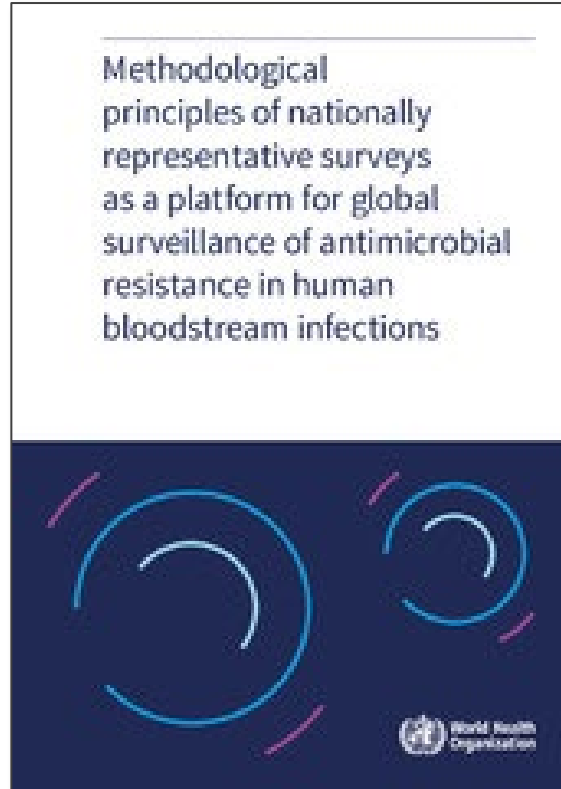


<https://www.who.int/publications/i/item/9789240013131>

Surveys to help forecast needs and cost-effectiveness of microbiology diagnostic services



Routine surveillance:
Isolate-based
AMR surveillance



<https://www.who.int/publications/i/item/9789240067004>

Nationally representative AMR prevalence surveys

- Cross-sectional (< 12 months survey)
- Acute care health facilities with inpatient services, selected using probability sampling methods independent of the availability of microbiology diagnostic services (access to be granted)
- Inclusion of consecutive patients with suspected BSIs (meeting case definition)
- Quality-assured microbiology diagnostics for pathogen identification and AST
- Collation of demographics and clinical information

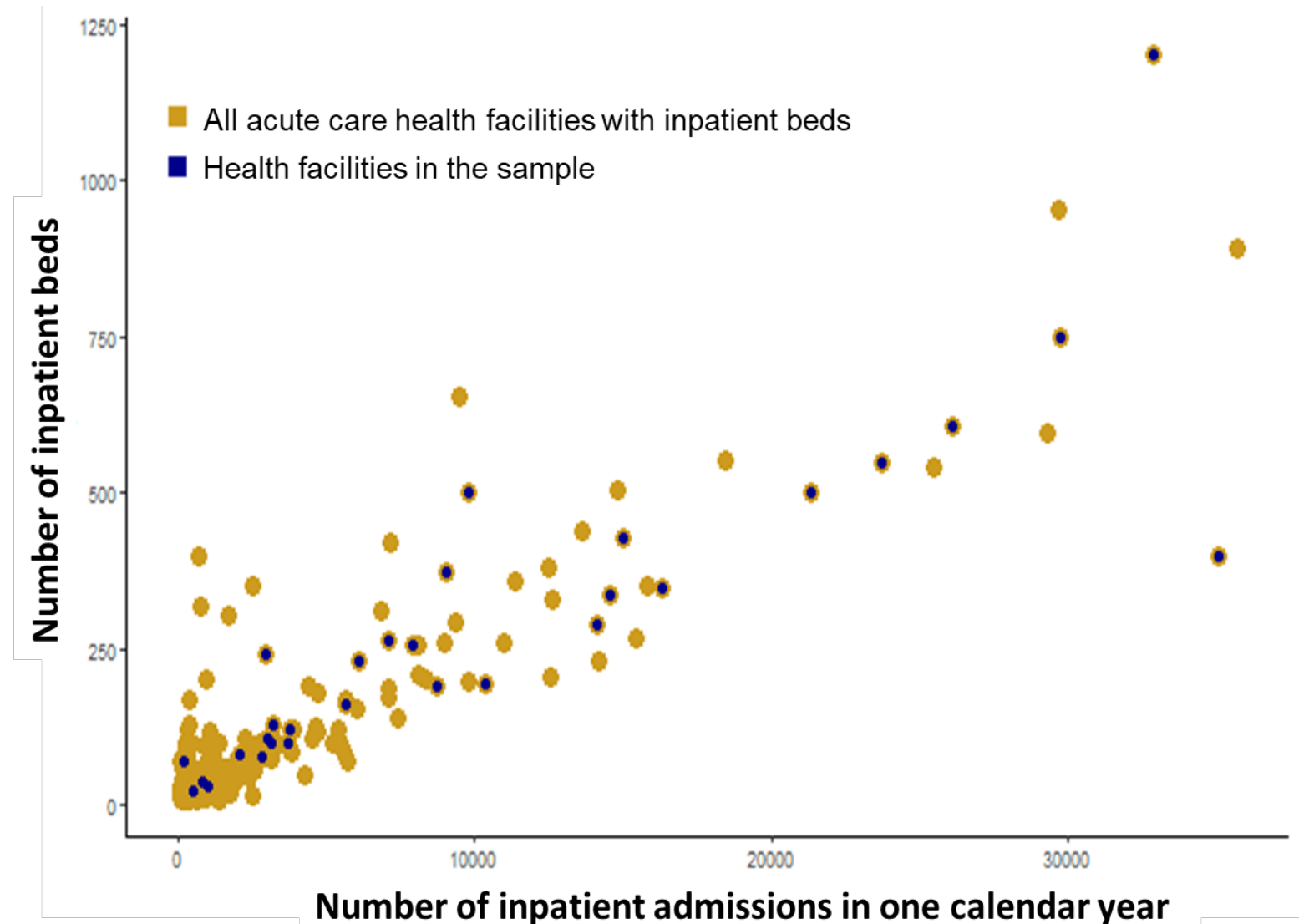
Survey design

- Survey powered to estimate resistance with the desired precision in the most common bacterial pathogen

$$n = \frac{N * Z_{\alpha}^2 * p * q}{d^2 * (N - 1) + Z_{\alpha}^2 * p * q}$$

- Data for less common pathogens is collected opportunistically until the sample for the target bacterial species is reached

Probability proportional to size sampling of patient-clusters in healthcare facilities with inpatient beds



Rwanda survey design and logistics

	SAMPLE SIZE
BCIs due to the most common bloodstream pathogen	716
Total BCIs if expected percentage of bloodstream infections attributable to the most common pathogen = 30%	2,387
Patients with indication for blood culture if expected percentage of BCIs = 10% of the individuals sampled	23,867

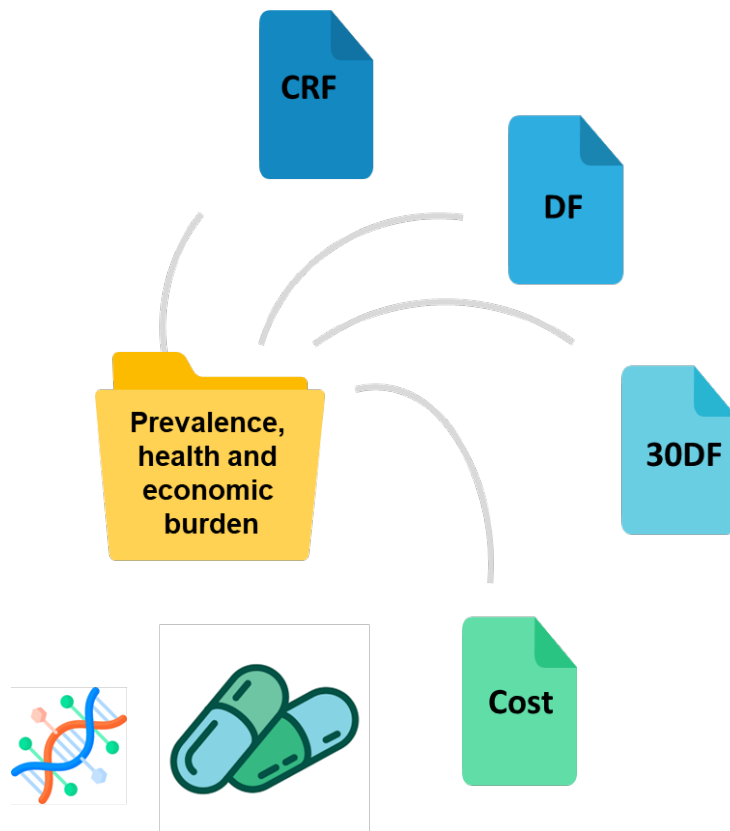


Design: 85 clusters of 281 patients with indication for blood culture in 35 out 102 acute healthcare facilities with inpatient services (45 in the private sector). Referral of positive blood cultures to four laboratories covering all areas (< 3.5 hours commute). **BCI:** Bacteriologically confirmed bloodstream infection.

HOSTED BY

Surveys of prevalence, health and economic burden of AMR

Granular information allows consideration of health and economic burden metrics



<u>Infected cohort (DR, DS)</u>	<u>Uninfected cohort</u>
<u>Case report form</u>	"
<u>Discharge form</u>	"
<u>30 days follow-up form</u>	"
<u>Cost of hospital episode</u>	"
n = 2,400 /country	n = 2,400 / country

E.g.

- **Mortality associated and attributable to AMR**
- Excess length of stay
- Disability-adjusted life years (DALYs)
- Years of life lost
- Cost per disability-adjusted life year (DALY)



Conclusions

- “Two-pronged” model in new phase of GLASS to remedy paucity of data.
- Surveys to help scale up comprehensive nationally representative studies addressing evidence gaps on antimicrobial use, health and economic burden of AMR, and the molecular basis of AMR.
- Combined, the data can inform on the health and economic advantages of interventions to reduce AMR.
- Planning and implementation of pilot AMR prevalence surveys began in 2022 and is ongoing.

High scientific and quality standards ensure that survey data are comparable within and between countries and over time, and can be used to strengthen and inform national policies

Tools for active case finding and management of blood cultures

