

3rd High Level Technical Consultation and Meeting on Surveillance of Antimicrobial Resistance and Use for Concerted Actions







Q&A

Draft GLASS-AMR Manual 2.0

What are the major differences between version 1.0 and 2.0 of the GLASS manual?

Who should read the GLASS-AMR manual?

What are the core components of a national AMR surveillance system?

What types of AMR surveillance data are collected by GLASS?

Does a country need to collect data on all pathogens selected by GLASS?

Where and how is the collected data presented?

What is the difference between isolate-based and sample-based data?

We cannot estimate the number of negative cultures, or number of other pathogens (not included in GLASS) per specimen type, can we still submit data?

Can any hospital function as a surveillance site for GLASS?

Can we submit data on non-priority specimens and bug/drug combinations if we collect them?



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1. What are the major differences between version 1.0 and 2.0 of the GLASS manual?

GLASS was designed to be implemented in five-year cycles followed by revision and further development. The GLASS manual for early implementation (1.0) has been updated and revised, taking into consideration lessons learned and best practices identified during the first five years of the GLASS early implementation, as well as suggestions and proposals for further development made by participating countries, WHO regional and country offices, and international partners.

The GLASS-AMR methodology has not been dramatically changed in the version 2.0, but several modifications and additions have been made, including the following:

- New specimen types added: cerebrospinal fluid and respiratory samples for common bacteria and rectal and pharyngeal swabs for the surveillance of AMR in gonococci;
- Five new pathogens added: *Pseudomonas aeruginosa*, *Neisseria meningitidis*, *Haemophilus influenzae*, *Salmonella enterica* serovar Typhi, and *Salmonella enterica* serovar Paratyphi A;
- Several new antimicrobials included to describe the resistance of newly added target pathogens and to include both first- and second-line antimicrobials according to the WHO <u>AWaRe</u> antibiotic categorization;
- A GLASS approach to assessing and improving the validity and representativeness of surveillance data has been introduced;
- An option for submission of anonymized individual-level data has been included, providing additional opportunities for AMR surveillance data validation and analysis;
- An option for submission of data generated by molecular AMR diagnostics has been included to complement phenotypic AMR diagnostics data and improve understanding of the underlying mechanisms responsible for resistance.

2. Who should read the GLASS-AMR manual?

The manual is written for national GLASS focal points, national public health professionals and national health authorities responsible for AMR surveillance in humans, and those contributing to national surveillance data collection. National professionals from other sectors supporting surveillance of AMR in the context of the "One Health" approach may benefit from reading the manual too.

3. What are the core components of a national AMR surveillance system?

The core components include a national coordinating centre (NCC), a national reference laboratory (NRL), and surveillance sites.

- The NCC establishes and oversees the national AMR surveillance programme, gathers national AMR data and ensures that the system is functional.
- The NRL promotes and facilitates good laboratory practice in the country and promotes the harmonization of methods and standards used in the national AMR surveillance system.



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• The surveillance sites are the foundation of the surveillance system. Surveillance sites for AMR in humans are usually primary, secondary or tertiary care hospitals, or outpatient clinics capable of collecting the required patient information, together with performing appropriate microbiological testing, epidemiological analysis and timely reporting.

4. What types of AMR surveillance data are collected by GLASS?

GLASS requires AMR data to be collected through a surveillance system which gathers results from susceptibility testing for human bacterial pathogens isolated from clinical specimens sent routinely to laboratories for diagnostic purposes. Together with patients' microbiological results (species identification and AST), countries are also invited to report demographic and epidemiological variables, either in aggregated or individual-level format.

5. Does a country need to collect data on all pathogens selected by GLASS?

GLASS encourages countries to include all pathogens included in the GLASS-AMR manual in their national AMR surveillance targets. At the same time, it is understood that countries may still need to build capacities needed to include some GLASS pathogens, and others may not be considered a national priority. That is why reporting data on all pathogens is desirable but not an obligation.

It should be noted also that priorities for local and national surveillance may include other organisms and antimicrobial agents which should be addressed properly in the national systems, even though they are not yet requested to be reported in GLASS.

6. Where and how is the collected data presented?

GLASS publishes yearly reports summarizing information on the status of development of national AMR surveillance systems and AMR rates. They also include summaries of global AMR surveillance in DR-TB, HIV-DR, and malaria, and describe AMR surveillance activities in all WHO Regions and ongoing development of GLASS. In addition to the printable reports, the country data are visualized on the WHO Global Health Observatory website.

7. What is the difference between isolate-based and sample-based data?

- Isolate-based data include information on the patient population with laboratory confirmed infections caused by the target pathogens. They provide information on the proportion of patients with positive samples whose infections are caused by target pathogens resistant to specific antimicrobials.
- Sample-based data include information on the whole patient population with suspected infection from whom the clinical specimens have been collected. This population comprises patients with



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confirmed infection caused by the target pathogens, as well as patients with no microbial growth in collected specimens and those with positive samples with the growth of any other organisms, including other pathogens and commensal organisms. The sample-based approach allows to calculate the frequency of infections caused by antimicrobial drug-resistant pathogens in the patient population under surveillance.

8. We cannot estimate the number of negative cultures, or number of other pathogens (not included in GLASS) per specimen type, can we still submit data?

Yes, the data will be accepted. But, although both isolate-based and sample-based data can be reported, GLASS encourages countries to collect and report sample-based data. In settings where patients with suspected infections are systematically tested, the sample-based approach provides a proxy for all patients with the infection under surveillance. For example, using the tested population as the denominator allows an estimation of frequency of reported infectious syndromes associated with a resistant pathogen, which can be stratified to identify prevalence of AMR by demographic or epidemiological categories, for example by age, gender, hospital or community infection onset.

9. Can any hospital function as a surveillance site for GLASS?

Surveillance sites can be primary, secondary or tertiary care hospitals, or outpatient clinics with access to appropriate data management systems, staff with clinical expertise, epidemiologists, and quality-assured bacteriology laboratory support to provide basic clinical, epidemiological and microbiological data. Countries are expected to select surveillance sites in a way that ensures balanced geographical, demographic and socio-economic sample characteristics of the surveillance network.

10. Can we submit data on non-priority specimens and bug/drug combinations if we collect them?

GLASS focuses on some of the most important pathogens for surveillance at the global level, and the GLASS IT platform (a web-based platform for global data sharing on AMR) will only accept data from the specimen types and pathogens included in the GLASS-AMR manual. However, the list of pathogens selected for GLASS is growing. 4 new specimen types and 5 new pathogens have been already added in the new GLASS-AMR manual, and *Candida* spp. is planned to be added after the early implementation of the surveillance protocol for this pathogen.