GLASS 2020 consultation 2021 meeting

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

Government Offices of Sweden
Ministry of Health and Social Affairs

Ministry of Health and Welfare
Republic of Korea

World Health Organization

Structured feedback on

Whole genome sequencing for surveillance of antimicrobial resistance

Context

Molecular methods are becoming common and important tools to support AMR surveillance, particularly as support for National Reference Laboratories[1] to better characterise emerging AMR. The methods currently in use include targeted DNA sequence tests[2] and whole genome sequencing (WGS).

The WHO GLASS document ***Whole genome sequencing for surveillance of antimicrobial resistance***[3] addresses the applications of WGS for AMR surveillance, including the benefits and limitations of current WGS technologies. Local, subnational, national and international case studies are included as examples of use of WGS in AMR surveillance. Information is also provided on the requirements for setting up and upgrading laboratories to ensure capacity for WGS and for introducing WGS into AMR surveillance systems. This technical note is intended to assist countries that are considering to increase their capacity for use of WGS for AMR detection and surveillance.

Questionnaire

This questionnaire is intended to obtain feedback from countries on the WHO technical note ***Whole genome sequencing for surveillance of antimicrobial resistance*** and also on the application of molecular methods to support AMR surveillance in your country.

Please discuss this questionnaire with colleagues in charge of microbiological support for AMR surveillance in your country to ensure the responses reflect the views and experiences of national AMR surveillance. Please provide one consolidated response for your country to reflect your country's views.

The responses should be submitted through the online version of this questionnaire found on the GLASS 2020 platform.

Thank you for your support to the development of GLASS!

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[1] WHO, 2020. GLASS Guidance for National Reference Laboratories. https://www.who.int/glass/resources/publications/

[2] WHO, 2019. Molecular methods for antimicrobial resistance (AMR) diagnostics to enhance the Global Antimicrobial Resistance Surveillance System at https://www.who.int/glass/resources/publications/molecular-methods-for-amr-diagnostics/en/

[3] WHO, 2020. Whole genome sequencing for AMR surveillance at https://www.who.int/glass/resources/publications/

1: Does the document *Whole genome sequencing for surveillance of antimicrobial resistance* provide clear guidance on the application of whole genome sequencing (WGS) as a tool for AMR surveillance?

Yes ☐
No ☐
Don't know ☐

If your response is ‘No’: What is missing in the document *Whole genome sequencing for surveillance of antimicrobial resistance* in order to provide clear guidance?

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2: Does the document *Whole genome sequencing for surveillance of antimicrobial resistance* present useful and practical examples for implementing WGS in support of AMR surveillance?

Yes ☐
No ☐
Don't know ☐

If your response is ‘No’: What is missing in the document *Whole genome sequencing for surveillance of antimicrobial resistance* in terms of presenting useful examples for implementation?

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3: Do you find the document *Whole genome sequencing for surveillance of antimicrobial resistance* useful for assisting with enhancing the national AMR surveillance system in your country?

Yes ☐
No ☐
Don't know ☐

If your response is ‘No’: What is missing in the document *Whole genome sequencing for surveillance of antimicrobial resistance* for you to find it useful for assisting with enhancing your national AMR surveillance system?

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4: Is the AMR national surveillance system in your country applying any type of molecular methods targeting specific resistance genes in support to phenotypic methods?

Yes ☐
No ☐
Don't know ☐

If your response is 'Yes':

For each pathogen and associated antimicrobial class/resistance mechanism in the list below, indicate the molecular test used in your country where applicable.

Pathogen:

***Enterobacteriaceae (Escherichia coli, Klebsiella pneumoniae, Salmonella* spp., *Shigella* spp.), *Acinetobacter* spp.**

Add molecular test used in your country, where applicable.

Antimicrobial class	Molecular test
Extended-spectrum Betalactamases	
Carbapenemases	
Colistin resistance	

Pathogen:

Staphylocuccus aureus

Add molecular test used in your country, where applicable.

Antimicrobial class	Molecular test
mec a	

Pathogen:

Streptococcus pneumoniae

Add molecular test used in your country, where applicable.

Antimicrobial class	Molecular test
Penicillin	
Extended-spectrum Cephalosporins	

Pathogen:

Neisseria gonorrhoeoe

Add molecular test used in your country, where applicable.

Antimicrobial class	Molecular test
Extended-spectrum Cephalosporins	
Fluororquinolones	
Macrolides	

5: Is the AMR national surveillance system in your country applying WGS in support of AMR surveillance?

Yes ☐
No ☐
Don't know ☐

If your response is ‘Yes’: What has been required to implement WGS in support of AMR surveillance?

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If your response is ‘No’: Is the application of WGS within your national AMR surveillance system being considered?

Yes ☐
No ☐
Don't know ☐

What support would you need from WHO to facilitate the application of WGS within your national AMR surveillance system?

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6: Identification of high-risk clones is based on phylogenetic analyses, and identification of new high-risk lineages is based on the genetics of the local or regional pathogen population. Databases are therefore required to compare sequences. Standardised databases are available for the storage of genomic and AMR data, but due consideration must be given to the type of database to be used (open, public or closed access, see section 4.2.3 in the document Whole genome sequencing for surveillance of antimicrobial resistance). GLASS envisages the inclusion of sequencing data in the future. Please indicate which type of database you would advise GLASS to use:

Open-access database: data for which the providers do not retain rights. ☐

Public-access database: a tool or database that may be used for free but only by those people who require access (e.g. public health officials and epidemiologists). Data providers seek information and control of the downloading and use of sequence data, most notably acknowledgement for collaboration if used in publications and/or public communications based on analyses of sequences they have provided, and assurances that products, such as diagnostics, therapeutics and preventive agents, developed with sequence data are accessible to the countries in which the disease burden is greatest and from which the sequences originated. Access may be approved upon registration. ☐

Closed-access database: a database that may be accessed only by individuals who have been granted access. The sequence data providers require that only non-publicly accessible databases be used, and members of a network may collaborate and share information, but sequences are not accessible to the general public. There is no open registration. ☐

Don't know ☐

7. Please share any additional comments you have on the document *Whole genome sequencing for surveillance of antimicrobial resistance*.

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