

Q&A

GLASS technical note on whole genome sequencing (WGS) for AMR surveillance

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1. What is Whole Genome Sequencing?

Whole Genome Sequencing (WGS) is a molecular biology tool used to obtain the complete DNA sequence of an organism, there are some advantages of this new technology, for example, provides better understanding of the mechanisms of resistance and the relatedness of strains for investigating the emergence and spread of AMR, offers a vast amount of information and the highest resolution for molecular subtyping of pathogens.

2. What use is this technical note providing for use of WGS for AMR surveillance?

This document 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. Address the benefits, limitations and practical challenges in various settings globally.

3. What does WGS add to our current phenotypic and molecular methods for AMR surveillance?

WGS offers a vast amount of information and the highest resolution for identifying and characterizing pathogens. With epidemiological and clinical information, WGS can therefore enhance surveillance capacity to better inform strategies to tackle AMR.

4. Can WGS-based genetic AMR surveillance replace phenotypic antimicrobial susceptibility testing?

WGS is not a substitute for phenotypic methods for detecting AMR for public health or for guiding the clinical treatment of most bacterial infections. WGS data can be used to verify the identity of AMR mechanisms in isolates with relevant phenotypic AMR or with discordant phenotypic AMR. It cannot, however, be used to quantify the level of phenotypic AMR, so that it is unsuitable for routine or predictive AST and therefore cannot replace phenotypic methods. It can, however, complement phenotypic methods by adding information on molecular determinants and mechanisms of AMR and genetic factors that facilitate their transmission in microbial populations.

5. What are the current limitations and the considerations for countries to implement WGS in support of the AMR surveillance system?

The use of WGS in surveillance of AMR in fast-growing bacteria has several limitations for public health, including substantial initial and recurrent investment and incomplete understanding of the molecular mechanisms underlying resistance to some antimicrobial classes. As only known resistance mechanisms can be detected, WGS cannot currently replace phenotypic surveillance of AMR in fastgrowing bacteria. Additional challenges that must be met before WGS can be included in surveillance of AMR in fast-growing bacteria include local capacity-building, laboratory infrastructure and techniques, standardization of bioinformatics methods, storage technology in settings with little or no prior experience in the use of molecular methods and agreement on QA protocols and on protocols for data-sharing and use.