



Public Consultation

Consultation name: The role of whole genome sequencing in antimicrobial susceptibility prediction of bacteria

Closing Date: 09 January 2026

Please send comments to the EUCAST Scientific Secretary at Mandy.Wootton@wales.nhs.uk

Comment from (name, contact details)	Comments	EUCAST Responses
Robin Howe robin.howe@wales.nhs.uk on behalf of the BSAC AST committee.	BSAC would suggest the following changes to the manuscript: <ol style="list-style-type: none"> 1. Bullet points to simplify the message of what needs to be done to enable this technology to be used in a clinical setting. 2. We acknowledge that this manuscript is predominantly focussed on predictability of susceptibility but suggest including a clearer breakdown for where utility is acceptable, i.e where can <u>resistance</u> be reliably predicted. Bullet points listing where it has utility and where it does not would be useful. 	Thank you for your comments, we appreciate them. We have attempted to address them in Text box summary and Table 6.
Emily Dickens, Leonid Chindelevitch and Romain Derelle e.dickens@imperial.ac.uk l.chindelevitch@imperial.ac.uk r.derelle@imperial.ac.uk Imperial College London	We would like to highlight our recently released 'Comprehensive Assessment of Bacterial-Based AMR prediction from GENotypes' (CABBAGE) database for inclusion into this document. CABBAGE is the largest database of its kind, comprising over 170,000 bacterial isolates and 1.7 million genotype-phenotype entries, freely available via EBI's Antimicrobial Resistance Portal (https://www.ebi.ac.uk/amr). The document states that there is 'a lack of standardization and	Thank you for your comments, we appreciate them. We agree this is a useful initiative, and therefore the CABBAGE database has been commented and cited in the databases section.



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	<p>aggregation of genotype-phenotype data'. This is a key challenge that we addressed in the development of CABBAGE through the standardisation, curation, and de-duplication of data sourced both from existing databases and publications, resulting in a single, unified database. We agree that contextual metadata is important for the interpretation of WGS data (section 'The importance of metadata'), which is addressed in CABBAGE through the inclusion of extensive metadata, such as the isolation source, country, collection year, and antibiotic susceptibility testing method. CABBAGE therefore represents a valuable resource for the advancement of genotype-phenotype predictions of antimicrobial resistance, as well as facilitating the exploration of spatiotemporal AMR trends. Referencing CABBAGE would provide additional context on the current availability of genotype-phenotype data and the progress that has been made in unifying such data.</p>	
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