**Table 2.** Advantages and disadvantages of genotypic vs phenotypic surveillance of antimicrobial resistance

|  |  |  |  |
| --- | --- | --- | --- |
| **Phenotypic/susceptibility testing methods¤** | | **Genotypic methods\*** | |
| **Advantages** | **Disadvantages** | **Advantages** | **Disadvantages** |
| Easy access globally (?) | Select for indicator bacterial organisms and largely ignore non-pathogenic bacterial species | Yield data about any resistance gene or mutation present | Insufficient knowledge about all genetic variation may complicate accurate prediction of resistance[50](#_ENREF_50) |
| Low costs | Rely on bacterial growth, i.e. time-consuming | Can be performed directly on clinical specimens not relying on bacterial growth, i.e. faster turnaround times | Quality controls essential to assess whether WGS data have reached a suitable standard, while there are currently no international standards for QC thresholds to use for assessing quality[50](#_ENREF_50) |
| Guidelines available to apply and teach interpretation of results (capacity building) | Screening of a limited number of (known) resistance genes | Meta-transcriptomic analysis can determine the expression of resistance genes at the moment of sampling | Need for a standardized comprehensive databases containing the relevant DNA or protein sequence targets known to be associated with AMR[32](#_ENREF_32), [50](#_ENREF_50) |
|  | Limit possible conclusions about co-transmission of resistance genes and relatedness of identified isolates to reconstruct transmission networks |  | Appropriate bioinformatic methodologies needed to accurately extract relevant information from WMGS data based on target databases[32](#_ENREF_32) |
|  | Limited opportunities to compare genotype with phenotype |  | High costs (mainly related to the complex bioinformatics infrastructure) |

Footnotes:

¤Phenotypic methods: agar and broth microdilution (the latter being the reference standard) or disc diffusion, followed by interpretation according to agreed guidelines.

\*Genotypic methods: metagenomics; PCR assays are not included as they provide valid information on AMR determinants known to be associated with the identified pathogen, but they are not suitable for detecting completely new genes families, novel genes, or new point mutations.

Abbreviations: AMR, antimicrobial resistance; QC, quality control; WGS, whole-genome sequencing