Using WGS to identify antibiotic resistance genes and predict antimicrobial resistance phenotypes in MDR Acinetobacter baumannii in Tanzania

Reliable phenotypic antimicrobial susceptibility testing can be a challenge in clinical settings in low- and middle-income countries. WGS is a promising approach to enhance current capabilities. To study diversity and resistance determinants and to predict and compare resistance patterns from WGS data of Acinetobacter baumannii with phenotypic results from classical microbiological testing at a tertiary care hospital in Tanzania. MLST using Pasteur/Oxford schemes yielded eight different STs from each scheme. Of the eight, two STs were identified to be global clones 1 (n=4) and 2 (n=1) as per the Pasteur scheme. Resistance testing using classical microbiology determined between 50% and 92.9% resistance across all drugs. Percentage agreement between phenotypic and genotypic prediction of resistance ranged between 57.1% and 100%, with coefficient of agreement (κ) between 0.05 and 1. Seven isolates harboured mutations at significant loci (S81L in gyrA and S84L in parC). A number of novel plasmids were detected, including pKCRI-309C-1 (219000 bp) carrying 10 resistance genes, pKCRI-43-1 (34935bp) carrying two resistance genes and pKCRI-49-1 (11681bp) and pKCRI-28-1 (29606bp), each carrying three resistance genes. New ampC alleles detected included ampC-69, ampC-70 and ampC-71. Global clone 1 and 2 isolates were found to harbour ISAba1 directly upstream of the ampC gene. Finally, SNP-based phylogenetic analysis of the A. baumannii isolates revealed closely related isolates in three clusters. The validity of the use of WGS in the prediction of phenotypic resistance can be appreciated, but at this stage is not sufficient for it to replace conventional antimicrobial susceptibility testing in our setting.

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