

Comparative genomics and antibiotic-resistance determinants profile of clinical *Pseudomonas aeruginosa* isolates from Kenya

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INTRODUCTION: *Pseudomonas aeruginosa* is an opportunistic pathogen classified by the World Health Organization as a priority antibiotic-resistant pathogen due to the rapid increase worldwide in the prevalence of infections by multidrug resistant (MDR) strains leading to poor clinical outcomes. Ongoing surveillance activities at USAMRD-A,K have identified clinical *P. aeruginosa* isolates from several hospitals across Kenya. This study will use these isolates to understand the population and genomic structure of clinical *P. aeruginosa* and the genomic traits associated with antibiotic resistance in Kenyan isolates.

METHODOLOGY: 158 whole-genome sequences generated on Illumina and Nanopore platforms of MDR *P. aeruginosa* Kenyan clinical isolates, and publicly available *Pseudomonas* genomes will be analyzed. The quality of the sequence reads will be assessed using FastQC and MultiQC tools for short reads and NanoQC tool of Nanopack for long reads. The adapters will be trimmed for short and long reads using trimmomatic and porechop tools respectively. Denovo assembly using Unicycler tool will be followed by genome annotation using Prokka and Patric. Multilocus sequence typing (MLST) based on the PubMLST *P. aeruginosa* scheme will be done using ABRicate tool and pan-genome analysis using Roary pipeline. Phylogenetic analysis using the parsnp pipeline and multiple sequence alignment using mafft tool will constitute the comparative genomic analysis. Antimicrobial resistance (AMR) determinants will be profiled on the ABRicate tool which utilizes the Resfinder, CARD, ARG-ANNOT, MEGARES and, NCBI AMRFinderPlus databases.

EXPECTED OUTCOMES: This study will define the genomic characteristics, strain types, and resistance determinants of clinical *P. aeruginosa* isolates from Kenya, allowing for tracking of hospital and community-based resistance patterns, mapping the geographical distribution and tracking the spread of known and novel genetic determinants of resistance of *P. aeruginosa* in Kenya.