

## GENOME AND RESISTOME OF DRUG-RESISTANT *ENTEROBACTER* SPECIES ISOLATED FROM LIVESTOCK WASTE USING NANOPORE SEQUENCING

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Antibiotic resistance (ABR) is a major global health issue. *Enterobacter* species are common nosocomial pathogens that acquire multiple drug resistance (MDR) in addition to the intrinsic  $\beta$  lactam resistance. The study determined the whole genome and the antibiotic resistome of selected bacterial isolates from livestock farms in the Kandy District using Oxford Nanopore sequencing. Collected cow dung samples were screened for the presence of  $\beta$ -lactam resistant bacteria using a 96-well plate-based assay. The DNA from the selected antibiotic-resistant bacteria (ARB) was extracted using QIAamp DNA mini kit. The whole genome was sequenced using Oxford Nanopore® MinION Rapid Barcoding Sequencing (SQK-RBK004). Generated FastQ files from MinKNOW software were analyzed using EPI2ME with WIMP. In the Galaxy platform, generated genomes were assembled using Flye, visualized using Bandage image, evaluated using QUAST, and assessed MDR using ABRicate in the CARD database. Plasmids were detected using PlasFlow/Staramr tools and annotated using Prokka. According to the WIMP analysis (threshold = 750,000 score), one strain of ARB was identified as *Enterobacter cloacae* (strain 1) with 100% read count, while three isolates were identified as *Enterobacter hormaechei*. All genomes generated circularized chromosomes ranging from 4.8–4.9 Mb, while circularized plasmids were present in strains 2, 3, and 4 ranging from 53 - 225 kb. A list of MDR of *E. cloacae* carried carbapenem, cephalosporin, cephamycin, fluoroquinolone, glycylicycline, monobactam, penam, penem, phenicol, rifamycin, tetracycline, and triclosan resistance genes of ramA (efflux pump) and blaCHM-1 genes. Three *E. hormaechei* isolates contained 13 different ABR genes, which were common to all three isolates. The Oxford Nanopore sequencing coupled with Galaxy bioinformatics tools were successfully used to determine the whole genomes, taxonomy, and the genomic and plasmid resistomes in *Enterobacter* spp.

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