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GENOME SEQUENCES

First Whole-Genome Sequence of a Highly Resistant *Klebsiella pneumoniae* Sequence Type 14 Strain Isolated from Sudan

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ABSTRACT *Klebsiella pneumoniae* is an opportunistic pathogen that accounts for a significant proportion of hospital-acquired infections and is a leading cause of nosocomial outbreaks. Here, we describe the genomic sequence of a highly resistant *K. pneumoniae* sequence type 14 (ST14) strain isolated from Sudan.

Klebsiella pneumoniae is a Gram-negative bacterium well known as an opportunistic pathogen that causes pneumonia, septicemia, and urinary tract infection (1). Nosocomial outbreaks of multidrug-resistant *Klebsiella* spp. are often caused by extended-spectrum β-lactamase (ESBL) producers. The emergence of ESBL-producing strains among clinical *Klebsiella* isolates has been progressively increasing over the years with very limited therapeutic options (2). Here, we report the draft genome sequence of a highly resistant ESBL *K. pneumoniae* strain (NUBRI-K) isolated from Sudan.

A sample of sputum was collected from a 44-year-old female who was admitted to the Omdurman Teaching Hospital in Khartoum, Sudan, with a pneumonia infection. The specimen was directly inoculated onto MacConkey agar and, afterward, incubated overnight under aerobic conditions at 37°C. The colony was identified using Gram staining and biochemical tests that included oxidase, catalase, kligler's iron agar (KIA), sulfide indole motility, citrate agar, and urea tests. The analytical profile index was used to confirm the species (3). Disk diffusion testing was carried out on the isolate according to the Clinical and Laboratory Standards Institute (CLSI; M100 2007) guidelines (4). The genomic DNA was extracted using a QIAamp DNA minikit (Qiagen, Germany). Paired-end libraries were prepared using the Nextera DNA flex library prep kit, followed by 2 × 300-bp sequencing on the MiSeq platform (Illumina, Inc., USA). The resultant paired-end reads were quality trimmed using Sickle version 1.33 (with the parameters -q 20 and -l 75) (5) and *de novo* assembled using SPAdes version 3.11 (with the parameters careful and cutoff auto) (6). The contiguous sequences were then submitted to the NCBI Prokaryotic Genome Annotation Pipeline (7). The multilocus sequence types (MLST) (8), resistance genes, and plasmids were predicted using ResFinder (9) and PlasmidFinder (10) through the GoSeqIt tools Web platform (9). Virulence factors were determined using the VirulenceFinder database (11). Default settings were used in all software unless otherwise noted.

A total of 1,493,916 paired-end reads were obtained from the whole-genome sequence of strain NUBRI-K. Quality-controlled reads (1,486,286 reads, average length of 198.6 bp) with a Phred score of >20 were assembled *de novo* with a minimum contig cutoff of 200 bp to 137 contigs (smallest contig, 223 bp; largest contig, 490,613 bp; N_{50}, 267,178 bp; and 52× genome coverage). The genome total length was 5,880,496 bp, with a G+C content of 56.6%. In total, the NUBRI-K genome contains 5,988 genes, including 5,895 protein-coding genes and 93 RNA genes. The MLST was defined as sequence type 14 (ST14). A total of 24 acquired antibiotic resistance genes were found

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in NUBRI-K, including aminoglycoside resistance genes [*aac(3)-Iia*, *aac(6′)-Ib-cr*, *aph(3″)-Ib*, *aph(3′)-Ia*, *aph(6)-Id*, and *armA*], β-lactam resistance genes ($bla_{CTX-M-15}$, bla_{OXA-1}, bla_{SHV-28}, and bla_{TEM-1B}), fluoroquinolone resistance genes [*aac (6′)-Ib-cr*, *oqxA*, *oqxB*, and *qnrB1*], a fosfomycin resistance gene (*fosA*), macrolide resistance genes *mdf*(A), *mph*(A), *mph*(E), and *msr*(E), a phenicol resistance gene (*catB3*), sulphonamide resistance genes (*sul1* and *sul2*), and trimethoprim resistance genes (*dfrA14* and *dfrA5*) which showed between 99.77% and 100% identity to query sequences in the ResFinder database. The NUBRI-K genome harbored a total of six plasmids [Col440I, ColpVC, IncFIB(K), IncFIB(Mar), IncFII, and IncHI1B] which showed between 89.47% and 99.54% identity to query sequences in the PlasmidFinder database. Col440I and ColpVC are circular plasmids. In the NUBRI-K genome, 131 virulence determinants were identified, namely, 19 adherence and biofilm-formation genes, 1 antiphagocytosis gene, 2 efflux pump genes, 34 iron acquisition genes, 6 nutritional factor genes, 4 regulation genes, 46 secretion system genes, 1 serum resistance gene, and 18 toxin genes.

Data availability. The draft whole-genome project for NUBRI-K has been deposited at DDBJ/EMBL/GenBank under accession number SOYT00000000. Raw sequence reads have been deposited at DDBJ/EMBL/GenBank under BioProject accession number PRJNA526408.

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