



Draft Genomic Sequence of Multidrug-Resistant *Klebsiella pneumoniae* B8S35, Isolated from Retail Chicken Skin

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ABSTRACT Here, we report the draft genome sequence of *Klebsiella pneumoniae* strain B8S35, isolated from retail chicken skin. It carries genes for resistance to multiple antibiotics, as well as quaternary ammonium compounds used by the food and health care industries.

Klebsiella pneumoniae is involved with gastrointestinal and extraintestinal diseases, including Crohn's disease, sepsis, arthritis, and urinary tract infection (UTI) (1–5). *K. pneumoniae* is a common contaminant in retail meat (6). We report the draft genomic sequence of a *K. pneumoniae* strain isolated from retail chicken skin that is resistant to multiple antimicrobials.

B8S35 was isolated from chicken skin samples using the Food Safety and Inspection Service (FSIS) microbiology laboratory method (7). B8S35 was streaked onto a Trypticase soy agar (TSA) plate and incubated at 37°C for 24 h. DNA was isolated from a single colony scraped from the TSA plate. Genomic DNA was extracted using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany) and quantified with a Qubit 3.0 fluorimeter (Life Technologies, Carlsbad, CA, USA). The genomic DNA library was prepared using the Nextera DNA flex library prep kit (Illumina, San Diego, CA, USA). Libraries were analyzed for concentration, pooled, and denatured for loading onto a flow cell for cluster generation. Denatured libraries were sequenced on an Illumina MiniSeq platform. A total of 8,153,078 sequencing reads using 150-bp paired-end sequencing were obtained.

Read quality was assessed with FastQC version 1.0.0 (Illumina BaseSpace Labs). The genome was assembled *de novo* using SPAdes (version 3.9.0), and 153 contigs (423-fold coverage) were obtained. Default parameters were used for all software unless otherwise specified. The B8S35 genome characteristics were as follows: genome size, 5,787,326 bp; N_{50} , 172,984 bp; GC content, 56.74%; number of coding genes, 5,661; number of pseudogenes, 205; number of RNA genes, 120; number of rRNAs, 19; number of tRNAs, 88; number of noncoding RNAs (ncRNAs), 13; multilocus sequence type (MLST), ST37; and plasmid-MLST, K-A10-like:B-, IncF. These characteristics were determined using the Bacterial Analysis Pipeline (version 1.0.4) and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP; version 4.3). Based on the sequencing data, the strain was identified as *Klebsiella pneumoniae* using the Bacterial Analysis Pipeline.

K. pneumoniae ST37 is of clinical importance (6). The virulence factors of B8S35 include the BrkB superfamily protein, serine protease, type 1 fimbrial protein, capsule assembly protein Wzi, an iron-siderophore ABC transporter substrate-binding protein, and the CbtA toxin. The antimicrobial resistance of B8S35 includes fosfomycin (*fosA*), fluoroquinolones (*oqxA* and *oqxB*), tetracycline (*tetD*), beta-lactam (*bla*_{SHV-11}), phenicol (*catA2*), and quaternary ammonium compound resistance (*sugE*). Decreasing the populations of *K. pneumoniae* in foods could lessen the risk of disease for at-risk populations.

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Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under BioProject number [PRJNA474898](#) and accession number [QKRJ000000000](#). The raw reads are available in the Sequence Read Archive (SRA) under accession number [SRR8187417](#). The versions described in this paper are the first versions.

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