

Complete Genome Sequence of *Klebsiella pneumoniae* YH43

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We report here the complete genome sequence of *Klebsiella pneumoniae* strain YH43, isolated from sweet potato. The genome consists of a single circular chromosome of 5,520,319 bp in length. It carries 8 copies of rRNA operons, 86 tRNA genes, 5,154 protein-coding genes, and the *nif* gene cluster for nitrogen fixation.

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The genus *Klebsiella* belongs to the family *Enterobacteriaceae*. Bacteria belonging to the genus *Klebsiella* are nonmotile, rod-shaped, Gram negative, and produce polysaccharide capsule. This genus consists of 7 species, including *Klebsiella pneumoniae*. *K. pneumoniae* is a free-living bacterium, which can be found in soil, water, and a wide range of plants and animals, including humans. While *K. pneumoniae* is the medically most important species in this genus, the organism is also known as a nitrogen-fixing bacterium in agriculture (1–6). Recently, we isolated a *K. pneumoniae* strain (YH43) from sweet potato (*Ipomoea batatas*) with nitrogen-fixing ability. To gain the genetic basis for analyzing the characteristics of this bacterium, we have first determined its complete genome sequence.

The genome sequence of strain YH43 was determined using the 454 GS FLX Titanium system (Roche). A total of 524,416 single-end reads (218 Mb) and 142,440 8-kb paired-end reads (46 Mb) were assembled with the GS Assembler software version 2.6 into a single scaffold containing 58 gaps. The gaps were closed by *in silico* analysis using the GenoFinisher software (7) (http://www.ige.tohoku.ac.jp/joho/gf_e/), and gap-spanning PCR products were sequenced using an ABI3130xl DNA sequencer (Applied Biosystems). To correct sequence errors, a paired-end library of the YH43 genome was constructed using the TruSeq DNA sample prep kit (Illumina) and sequenced by the Illumina MiSeq platform (2 × 150 bp). By mapping the obtained 2,085,021 reads (626 Mb) to the initial genome sequence using BWA (8) and SAMtools (9), a total of 38 insertions/deletions were corrected. The gene identification and annotation were conducted using the Microbial Genome Annotation Pipeline (MiGAP) (<http://www.migap.org/>).

The complete sequence of the YH43 genome consists of a single circular chromosome of 5,520,319 bp in length. No plasmid was identified. The chromosome contains 8 copies of the rRNA operons, 86 tRNA genes, and 5,154 protein-coding genes. It is known that one-third of *Klebsiella* isolates have nitrogen-fixing ability (10), which one of the model systems for studying nitrogen fixation (5). The *nif* gene cluster consisted of 20 genes that were identified on the YH43 chromosome. The number and orientation of

genes were consistent with a previous report on strain *K. pneumoniae* 342 (11), which was isolated from the stems of *Zea mays* L. cv. CIMMYT 342 (12), suggesting a well-conserved genetic organization of the *nif* gene cluster among *K. pneumoniae* strains.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at DDBJ under the accession no. AP014950.

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