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<th>Draft genome sequence of Klebsiella pneumoniae strain KP-1</th>
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<td>Author(s)</td>
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Klebsiella pneumoniae is ubiquitous in the environment and is a member of a three-species biofilm model. We compared the genome sequence of an environmental isolate, K. pneumoniae strain KP-1, to those of two clinical strains (NTUH-K2044 and MGH 78578). KP-1 possesses strain-specific prophage sequences that distinguish it from the clinical strains.

**Draft Genome Sequence of Klebsiella pneumoniae Strain KP-1**

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K. pneumoniae is ubiquitous in the environment, where it is involved in nitrogen fixation (1). It also causes bovine mastitis (2) and nosocomial infections in humans (3). It coexists with *Pseudomonas aeruginosa* and *Pseudomonas protegens* in metalworking fluids and the gut of the silk moth *Bombyx mori* (4, 5). A reproducible, mixed-species biofilm model comprising *K. pneumoniae* KP-1, *P. aeruginosa* PAO1, and *P. protegens* Pf-5 was thus developed to study bacterial interspecies interactions and their effects on biofilm development and fitness (6). While the complete genome sequences of PAO1 and Pf-5 were available to facilitate ”omics” studies such as transcriptomics, KP-1 is a newly isolated environmental isolate, and its genome has not been sequenced previously.

The strain was shotgun sequenced on a 454 GS-FLX sequencing platform (Roche, Basel, Switzerland) and an Illumina MiSeq benchtop sequencer (Illumina, CA, USA). The reads from both platforms were trimmed, and de novo assembly was performed using Newbler v2.6 (Roche). With 1,673,246 and 1,840,620 reads from the 454 GS-FLX and MiSeq sequencing platforms, respectively, 24 contigs with a total length of 5,131,085 bp and an average GC content of 57.6% were assembled. The open reading frames (ORFs) were predicted using Glimmer v3.02 (7). The complete genome sequences of PAO1 and Pf-5 were deposited previously.


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**REFERENCES**