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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Klebsiella pneumoniae* subsp. *pneumoniae* HS11286, a Multidrug-Resistant Strain Isolated from Human Sputum

Pinglei Liu,[a] Peng Li,[a] Xiaofei Jiang,[b] Dexi Bi,[a] Yingzhou Xie,[a] Cui Tai,[a] Zixin Deng,[a] Kumar Rajakumar,[c] and Hong-Yu Ou[a]

State Key Laboratory of Microbial Metabolism, Shanghai Jiaotong University, Shanghai, China[a]; Department of Laboratory Medicine, Huashan Hospital, Shanghai Medical College, Fudan University, Shanghai, China[b]; and Department of Infection, Immunity and Inflammation, University of Leicester, Leicester, United Kingdom[c]

***Klebsiella pneumoniae* is an important pathogen commonly associated with opportunistic infections. Here we report the genome sequence of a strain, HS11286, isolated from human sputum in 2011 in Shanghai, China. It contains one chromosome (5.3 Mb), three multidrug resistance plasmids (~110 kb), including a carbapenemase producer, and three small plasmids (~3 kb).**

Klebsiella pneumoniae is an important bacterial pathogen in humans that is commonly associated with opportunistic and hospital-associated infections. Increasing levels of multiple-antibiotic resistance associated with this species pose a major emerging clinical problem (7). The multidrug-resistant *K. pneumoniae* strain HS11286 was isolated from a sputum specimen in 2011 at Huashan Hospital, Shanghai, China.

The whole genome of *K. pneumoniae* HS11286 was sequenced by a Roche 454 GS-FLX sequencer, resulting in 286,971 reads (~21-fold coverage). A total of 283 contigs (500 to 282,476 bp) were then generated using the Newbler assembler, with the base quality score above 40. Gaps were closed by sequencing PCR products. The assembled genome sequence was annotated on a high-performance server (NF8560M2; Inspur) containing the programs Glimmer 3.0 for identification of protein-coding genes (2), tRNAscan-SE for tRNA genes (8), and RNAmmer for rRNA genes (6). The replication origins were predicted by Ori-Finder (4).

K. pneumoniae HS11286 consists of seven circular replicons, including one chromosome and six plasmids. The chromosome (5,332,752 bp, 57.5% G+C content) codes for 5,316 putative proteins and carries 87 tRNAs, 1 tmRNA, and 8 copies of 16S-23S-5S rRNAs. A total of 422 HS11286 strain-specific genes were identified from *in silico* "subtractive hybridizations" of the HS11286 chromosome against four other completely sequenced *K. pneumoniae* chromosomes (MGH 78578, NTUH-K2044, Kp342, and KCTC2242) by using mGenomeSubtractor with a BLASTN-derived *H* value of <0.42 (9). Interestingly, seven prophage regions were detected, of which three regions were intact. In addition, the HS11286 chromosome contains two novel integrative and conjugative elements, an *asn* tRNA gene-associated ICE*Kpn*HS11286-1 (62 kb, 52.5% G+C content) and a *phe* tRNA gene-associated ICE*Kpn*HS11286-2 (56 kb, 50.2% G+C content) (1).

Six plasmids occur naturally in the HS11286 strain: pKPHS1 (122,799 bp, 49.5% G+C content), pKPHS2 (111,195 bp, 53.3% G+C content), pKPHS3 (105,974 bp, 52.5% G+C content), pKPHS4 (3,751 bp, 52.2% G+C content), pKPHS5 (3,353 bp, 42.8% G+C content), and pKPHS6 (1,308 bp, 47.9% G+C content). pKPHS1 codes for a CTX-M-14 extended-spectrum beta-lactamase. pKPHS2 carries the bla_{TEM-1} gene and the carbapenemase gene bla_{KPC-2} and has a similar backbone with the recently reported *K. pneumoniae* plasmid pKP048 (5). pKPHS3 possesses 13 important resistance determinants, such as *tetG*, *cat*, *sul1*, *dfra12*, *aac(3)-Ia*, and *aph*, and is most similar to a *Yersinia pestis* plasmid, pIP1202 (3). Remarkably, the conjugation transfer genes such as *tra* in pKPHS2 and pKPHS3 may lead to the spread of multidrug resistance among different genera. The three small plasmids pKPHS4, pKPHS5, and pKPHS6 code for the unknown proteins. To our knowledge, the 1-kb pKPHS6 is the smallest *K. pneumoniae* plasmid ever identified.

Comparative analyses of the clinical and environmental *K. pneumoniae* strains have revealed that this species possesses an extremely plastic genome (10). Mining the completely sequenced *K. pneumoniae* genomes will be helpful to reveal the key roles of mobile genetic elements in the adaptive evolution and spread of antibiotic resistance.

Nucleotide sequence accession numbers. The GenBank accession number for the *K. pneumoniae* HS11286 chromosome is CP003200, and those for the six plasmids (pKPHS1 to pKPHS6) are CP003223 to CP003228.

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Address correspondence to Hong-Yu Ou, hyou@sjtu.edu.cn.

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