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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Klebsiella pneumoniae* 1084, a Hypermucoviscosity-Negative K1 Clinical Strain

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We report the complete genome sequence of *Klebsiella pneumoniae* 1084, a hypermucoviscosity-negative K1 clinical strain. Sequencing and annotation revealed a 5,386,705-bp circular chromosome (57.4% G+C content), which contains 4,962 protein-coding genes, 80 tRNA genes, and 25 rRNA genes.

The hypermucoviscosity (HV) phenotype, also known as a capsule-associated mucopolysaccharide web, was considered a characteristic associated with pyogenic *Klebsiella pneumoniae* infections (2). The increasing incidence of *K. pneumoniae* strains negative for the HV phenotype suggests that HV-negative strains have emerged as etiologic as HV-positive strains in causing pyogenic infections. We selected two K1 strains, 1112 and 1084, which have relatively high genetic similarity among our clinical isolates, to assess how essential the HV phenotype is for *K. pneumoniae* pathogenesis. Not surprisingly, in naïve mice, the HV-positive strain 1112 demonstrated greater virulence than the HV-negative strain 1084 in either a pneumonia or liver abscess infection model. However, 1084 was as potent as 1112 in inducing liver abscesses and exhibited an ability superior to that of 1112 in causing bacteremia and mortality in diabetic mice. The advantageous tissue-invasive ability of 1084 indicates that the HV phenotype *per se* is not a determinant for *K. pneumoniae* virulence in a diabetic host (4). The naturally selected strain 1084, therefore, serves as an ideal model for identifying virulence factors, rather than reliance on the HV phenotype that contributes significantly to the pathogenesis of *K. pneumoniae*.

Complete genome sequencing was performed on *K. pneumoniae* 1084, which was isolated from a diabetic patient with a bacteremic liver abscess at a referral medical center in central Taiwan between 2002 and 2004 (4). The strain was confirmed as *K. pneumoniae* using the API 20E system and was classified K1 by PCR detection of the K-serotype-specific *wzx* locus. The strain is not an extended-spectrum β-lactamase (ESBL) producer, exhibits an oral 50% lethal dose (LD_{50}) of 9×10^6 CFU for naïve BALB/c mice, and is resistant to killing by normal human sera.

Genomic sequencing was performed by sequencing the shotgun library prepared from the genomic DNA of *K. pneumoniae* 1084 on two 454 GS Junior (Roche) runs. In addition, paired-end libraries 8 kb apart on the genomic DNA were prepared and sequenced also using 454 GS Junior. The sequencing reads were assembled using Newbler (Roche). Gap filling between the contigs was accomplished by adding Sanger reads with the aid of Consed (3). Ambiguities of homopolymers and repetitive sequences were manually inspected and corrected, with the aid of additional Sanger sequence reads. Sequence annotation was performed using RAST Server (1) followed by manual inspection.

The completed *K. pneumoniae* 1084 genome is composed of a circular chromosome of 5,386,705 bp (57.4% G+C content). Annotation of the chromosome revealed 4,962 protein-coding genes, 80 tRNA genes, and 25 rRNA genes. Comparative genomic analysis will provide further understanding of the virulence factors encoded in the *K. pneumoniae* genome and will also contribute to knowledge of the genomic evolution of the *Klebsiella* genus.

Nucleotide sequence accession number. The genome sequence of *K. pneumoniae* 1084 has been deposited in NCBI GenBank under accession number CP003785.

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