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GENOME ANNOUNCEMENT

# Genome Sequence of *Kingella kingae* Septic Arthritis Isolate PYKK081

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***Kingella kingae* is a human oral bacterium that can cause infections of the skeletal system in children. The bacterium is also a cardiovascular pathogen causing infective endocarditis in children and adults. We report herein the draft genome sequence of septic arthritis *K. kingae* strain PYKK081.**

*Kingella kingae* is an oral bacterium causing septic arthritis and osteomyelitis in children and infective endocarditis in children and adults (1, 3–5). Here we report an assembled draft genome sequence of *K. kingae* strain PYKK081 isolated in 1991 from the ankle joint of an 8-month-old boy with septic arthritis.

The 454 shotgun method was used for genome sequencing. First, PYKK081 genomic DNA was fractionated into 300- to 800-bp fragments, and a single-strand DNA library was prepared and sequenced using a GS FLX Titanium instrument. The run yielded 256,078 reads with an average length of 342 bases. The total number of bases read was 87,754,070 (ca. 44-fold coverage). Second, an 8-kb insert size library was prepared and sequenced. The run yielded 245,592 individual reads with an average length of 395 bases. Among them, 170,416 reads were paired reads. The total number of bases read was 97,097,392 (ca. 48-fold coverage).

To decrease the number of gaps, the PYKK081 genome was sequenced using an ABI SOLiD 4 system. PYKK081 genomic DNA was used to prepare a mate-paired sequencing library with insert sizes of about 1 kb. A single experimental run produced a total of 150,000,000 50-base reads (ca. 3,760-fold coverage).

Sequences were assembled using SOLiD *de novo* accessory tools 2.0 (6). The assembled SOLiD contigs were shredded into 1,800-bp size with 900-bp overlapped fake reads. The fake reads from the SOLiD assembly and both single-end and paired-end pyrosequencing reads were assembled using Newbler version 2.4. In the final assembly, 95% of the reads were aligned into 164 unique contigs. The paired-end reads linked the contigs into six final scaffolds. The completed genome of PYKK081 consisted of 2,050,586 bp with an average G+C content of 46.5%.

The PYKK081 draft genome was annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline server at NCBI (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). There were 2,121 predicted protein coding genes. Of these, 1,614 (76%) had functional predictions. Among those, 12 were associated with phages or prophages, 20 with resistance to antibiotics or toxins, 1 with resistance to bacteriocins, and 12 with resistance to invasion or intracellular resistance. Strain PYKK081 had one copy of the LSU rRNA, one copy of the SSU rRNA, and 50 tRNA genes.

To investigate *K. kingae* genome organization, Mummer comparison (http://mummer.sourceforge.net) (2) of PYKK081 with nasal isolate *K. kingae* ATCC 23330 (GenBank no. AFHS01000000) was performed. These two strains were very similar in genomic organization, with an average DNA sequence identity of 97.9%. To study the diversity of *K. kingae* on the family level, the PYKK081 genome was further aligned with related finished or draft genomes downloaded from the HMP-DACC website (http://www.hmpdacc-resources.org): *Kingella oralis* 51147, *Kingella denitrificans* ATCC 33394, *Neisseria meningitidis* FAM18, *Neisseria gonorrhoeae* 1291, and *Moraxella catarrhalis* 035E. No recognizable overall synteny was observed between PYKK081 and any of these strains, suggesting that *K. kingae* represents a distinct taxonomic group in the *Neisseriaceae* family.

**Nucleotide sequence accession numbers.** The *K. kingae* PYKK081 genome sequence was deposited at DDBJ/EMBL/GenBank under the accession number AJGB00000000. The version described in this paper is AJGB01000000.

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