Whole-Genome Sequence of *Hafnia alvei* HUMV-5920, a Human Isolate


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A complete isolate of *Hafnia alvei* (strain HUMV-5920) was obtained from a urine sample from an adult patient. We report here its complete genome assembly using PacBio single-molecule real-time (SMRT) sequencing, which resulted in a chromosome with 4.5 Mb and a circular contig of 87 kb. About 4,146 protein-coding genes are predicted from this assembly.

1. *Hafnia alvei* is a Gram-negative facultatively anaerobic bacillus that belongs to the family *Enterobacteriaceae*. In humans, it has generally been considered an opportunistic bacterium, causing infections associated with underlying illnesses or predisposing conditions, as in immunocompromised patients (1). Although some virulence traits have been studied in *H. alvei*, little is known about the factors that contribute to their pathogenesis within a host, including adherence, cytotoxicity, biofilm formation, and quorum sensing (2–4). Moreover, recent investigations have focused on associations between the genus *Hafnia* and emerging antimicrobial resistance patterns (5, 6).

The strain used in this study (HUMV-5920) was isolated from the urine sample of a woman at the Hospital Universitario Marqués de Valdecilla in Santander, Spain. The strain was routinely cultured in Luria-Bertani (LB) agar or broth at 37°C and frozen at -80°C with 20% glycerol. This strain produces quorum-sensing signals and forms biofilms. The total genomic sample of *H. alvei* strain HUMV-5920 was extracted and purified using the GeneJET genomic DNA isolation kit (Thermo Scientific). The genomic DNA was submitted to Macrogen (South Korea) for PacBio single-molecule real-time (SMRT) sequencing. A single library was prepared for *H. alvei* HUMV-5920 and run on one SMRT cell. With a genome size of approximately 4.6 Mb, PacBio SMRT sequencing provided approximately 100% coverage of the whole *H. alvei* HUMV-5920 genome. SMRT sequencing initially resulted in 141,257 raw reads, with a mean subread length of 7,457 bp, totaling 1,053,404,563 nucleotides. The generated reads resulted in 141,257 raw reads, with a mean subread length of 7,457 bp, totaling 1,053,404,563 nucleotides. The generated reads resulted in 141,257 raw reads, with a mean subread length of 7,457 bp, totaling 1,053,404,563 nucleotides. The generated reads resulted in 141,257 raw reads, with a mean subread length of 7,457 bp, totaling 1,053,404,563 nucleotides. The generated reads resulted in 141,257 raw reads, with a mean subread length of 7,457 bp, totaling 1,053,404,563 nucleotides.


