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Complete and Assembled Genome Sequence of *Bifidobacterium kashiwanohense* PV20-2, Isolated from the Feces of an Anemic Kenyan Infant

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The complete genome sequence of *Bifidobacterium kashiwanohense* strain PV20-2, an infant feces isolate, was determined using single-molecule real-time sequencing (SMRT). Hierarchical genome assembly resulted in a completely assembled genome of 2,370,978 bp. The *B. kashiwanohense* PV20-2 genome is the first completely sequenced and assembled genome of the species.

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Bifidobacteria represent an important commensal group of bacteria, being among the first microbial colonizers of the infant gut (1). *Bifidobacterium kashiwanohense* was originally isolated from feces of a healthy Japanese infant and is closely related to *Bifidobacterium pseudocatenulatum* and *Bifidobacterium catenulatum*, species commonly encountered in the infantile gut (2). *B. kashiwanohense* strain PV20-2 was isolated from the feces of an anemic Kenyan infant obtained during an iron intervention study (3). *B. kashiwanohense* PV20-2 was functionally characterized and selected for its high siderophore activity and high iron internalization activity (4). Genomic DNA was prepared using a lysozyme/mutanolysine-based cell lysis and subsequent purification using the Wizard genomic DNA purification kit (Promega, Madison, WI, USA) (5). The genome was sequenced using 3 single-molecule real-time sequencing (SMRT) cells on a PacBio RS II (Pacific Biosciences, Menlo Park, CA, USA) at the Functional Genomics Center Zurich (Zurich, Switzerland). A total of 119,341 reads with a mean length of 4,390 bp were assembled into a single contig using the hierarchical genome-assembly process (6). The genome was automatically annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline and manually curated using annotations obtained through the Rapid Annotation using Subsystems Technology (RAST) platform (7). The genome of *B. kashiwanohense* PV20-2 consists of a single 2,370,978-bp circular molecule and comprises 58 tRNA genes and 5 rRNA operons. The G+C content of the genome is 56.1%, and a total of 1,875 protein coding sequences (CDS) were predicted.

B. kashiwanohense PV20-2 is the first completely sequenced and assembled genome of the species. The genome will contribute to the understanding of genus' evolution and adaptation to infantile gut.

Nucleotide sequence accession number. The genome sequence of *B. kashiwanohense* PV20-2 was deposited at the GenBank under the accession no. CP007456.

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