European foulbrood is a worldwide disease affecting the honey bee brood. Here, we report the draft genome sequence of *Fructobacillus* sp. EFB-N1, which was isolated from an infected honey bee larva derived from a Swiss European foulbrood outbreak. The genome consists of 68 contigs and harbors 1,629 predicted protein-encoding genes.

*Fructobacillus* sp. EFB-N1 was isolated from a honey bee larva infected with European foulbrood (EFB). The nonmotile isolate grows aerobically on de Man/Rogosa/Sharpe (MRS) agar (1) at 32°C. The 16S rRNA gene sequence comparison showed a 99.7% DNA sequence identity to *Fructobacillus* tropaeoli F214-1, which is a fructophilic lactic acid bacterium isolated from a flower (2). Comparison of *recA* gene sequences is used as a marker for classification of *Fructobacillus* species (3, 4). The *recA* gene sequence of strain EFB-N1 revealed 91% DNA sequence similarity to the corresponding gene of *F. tropaeoli*.

Chromosomal DNA of *Fructobacillus* sp. EFB-N1 was isolated with the MasterPure complete DNA purification kit as recommended by the manufacturer (Epicentre, Madison, WI, USA). The extracted DNA was used to generate Illumina shotgun libraries, which were subsequently sequenced on the Genome Analyzer IIx as recommended by the manufacturer (Illumina, San Diego, CA, USA). Trimming and removal of low-quality reads with Trim Galore version 0.4.0 (http://www.RNA detection were verified with Prodigal version 2.6.2 (6) and Barnnap version 0.6 (http://www.vichbioinformatics.com/software.barrnap.shtml), respectively. Annotation was performed with Prokka version 1.11 (7). The draft genome harbored one rRNA cluster, 46 tRNA genes, 1,210 predicted protein-coding genes with function assignment, and 419 putative genes coding for hypothetical proteins.

Genes coding for a putative bacterial conjugation machinery were located on contig FEFB_c000008. In addition, potential genes encoding proteins involved in adhesion and biofilm formation that showed high amino acid sequence similarity to corresponding predicted proteins encoded by the genomes of other Frutobacilli were identified. Noteworthy, the genome of *Fructobacillus* sp. EFB-N1 lacks a complete glycolysis system and pentose phosphate pathway, as putative genes encoding phosphofructokinase, fructose-bisphosphate aldolase, transketolase, and transaldolase were missing. Additionally, strain EFB-N1 completely lacked genes coding for citrate cycle enzymes. A putative lactate dehydrogenase-encoding gene as part of a homolactic fermentation pathway is present. In addition, the presence of a putative sucrose-encoding gene indicated the ability to convert sucrose to fructose and glucose.

### Nucleotide sequence accession numbers.
This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LDUY0000000. The version described in this paper is the first version, LDUY0100000.

### REFERENCES

