

Draft Genome Sequence of Entomopathogenic *Serratia liquefaciens* Strain FK01

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In the present study, we determined the draft genome sequence of the entomopathogenic bacterium *Serratia liquefaciens* FK01, which is highly virulent to the silkworm. The draft genome is ~5.28 Mb in size, and the G+C content is 55.8%.

Received 29 May 2014 Accepted 6 June 2014 Published 26 June 2014

Citation Taira E, Iiyama K, Mon H, Mori K, Akasaka T, Tashiro K, Yasunaga-Aoki C, Lee JM, Kusakabe T. 2014. Draft genome sequence of entomopathogenic *Serratia liquefaciens* strain FK01. *Genome Announc.* 2(3):e00609-14. doi:10.1128/genomeA.00609-14.

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Serratia liquefaciens Kuo1-1, which was originally isolated from the ant lion, is highly virulent to the silkworm, *Bombyx mori*, and the American cockroach, *Periplaneta americana* (1). A spontaneous nalidixic acid-resistant mutant, FK01, was isolated from Kuo1-1 for genetic experiments; this mutant retained virulence against the silkworm (2).

In the present study, a paired-end (fragment size, 400 bp) library of *S. liquefaciens* FK01 was generated. Sequencing was performed using MiSeq sequencing technology with MiSeq Reagent Kits v. 2 (300-cycle kit; Illumina, San Diego, CA, USA). A total of 908,930 reads covering ~136 Mb were yielded after filtering with Trimmomatic v. 0.32 (3). Assembly was performed using Velvet v. 1.2.03 in the DDBJ Read Annotation Pipeline using the following parameters: k-mer, 83; expected coverage, 26; coverage cutoff, 5 (4, 5), resulting in 28 scaffolds. The scaffolds consisted of 49 contigs of 5,279,587 bp. The genome is 5,280,113 bp in length (GC content, 55.8%), with a mean coverage of 25.8-fold. The longest scaffold was 3,043,604 bp, and the N_{50} and N_{90} sizes of the scaffolds were 3,043,604 bp and 296,035 bp, respectively.

Sequences were annotated using the Microbial Genome Annotation Pipeline (MiGAP) (see <http://www.migap.org/>) (6). A total of 4,884 protein-coding sequences, 5 rRNAs, and 80 tRNAs were identified in the *S. liquefaciens* FK01 draft genome.

Further analysis of the genome and comparative analyses with related bacteria will contribute to our understanding of the pathogenicity of *S. liquefaciens* in insects.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank un-

der the accession number [BAZB00000000](https://www.ncbi.nlm.nih.gov/nuclink/BAZB00000000). The version described in this paper is the first version, BAZB01000000.

ACKNOWLEDGMENTS

This work was supported by the Japan Society for the Promotion of Science (JSPS) KAKENHI (grant number 23580075). The cost of publication was supported in part by a Research Grant for Young Investigators from the Faculty of Agriculture, Kyushu University.

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