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GENOME SEQUENCES

Draft Genome Sequence of *Enterobacter* sp. Strain OLF, a Colonizer of Olive Flies

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ABSTRACT *Enterobacter* sp. strain OLF colonizes laboratory-reared and wild individuals of the olive fruit fly *Bactrocera oleae*. The 5.07-kbp genome sequence of *Enterobacter* sp. strain OLF encodes metabolic pathways that allow the bacterium to partially supplement the diet of the olive fly when its dominant endosymbiont, *Erwinia dacicola*, is absent.

Enterobacter sp. strain OLF was sequenced due to its prevalence in laboratory-reared and, occasionally, wild olive fly populations (1). It is the only culturable isolate obtained from olive fly abdomen homogenate (2). We are interested in its potential as a probiotic replacement or supplement for olive flies in mass rearing activities aimed at pest control that are lacking *Erwinia dacicola*, the dominant beneficial endosymbiont (3).

Enterobacter sp. strain OLF was originally isolated from the abdomen of a wild male olive fly from the western United States (2). Only round, smooth, white colonies of *Enterobacter* sp. strain OLF were found on LB plates after 24 h at 27°C. *Enterobacter* sp. strain OLF can grow between 27 and 37°C (2). Based on a Bayesian analysis (2) of sequences concatenated from the 16S rRNA (~1,400 bp), *ompA* (~900 bp), and *recA* (~870 bp), it was determined to be in the family *Gammaproteobacteria* and, more specifically, the genus *Enterobacter*.

To isolate DNA for genome sequencing, a single colony of *Enterobacter* sp. strain OLF was grown overnight in LB broth with aeration at 37°C. Approximately 8 μg of DNA was purified using the Gram-negative protocol in the DNeasy kit (Qiagen, Valencia, CA), which was used by the Arizona Genomics Institute at the University of Arizona to construct 75-bp paired-end Illumina libraries. Libraries were tagged and multiplexed for sequencing on one lane of an Illumina Genome Analyzer II. The sequencing run generated 28,937,299 paired-end reads. Except where otherwise specified, default parameters were used for all software. Sequences were assembled into contigs using *de novo* assembly in ABySS-pe (version 1.2.5) with 4 different k-mer sizes (40, 45, 50, and 55) with a cutoff of 300 bp. The k50 assembly was selected based on closest similarity to *Enterobacter cloacae* subsp. *cloacae* ATCC 13047, the closest sequenced relative, and yielded 67 contigs with an N_{50} value of 180,401 bp, GC content of 55.1%, a >300× sequencing depth, and a maximum contig size of 362 kbp. The *Enterobacter* sp. strain OLF genome was annotated using the IGS Annotation Engine (4) with Glimmer version 3.02 (5), yielding 4,760 coding sequences, of which 89.1% encoded proteins. The genome encodes the ability to supplement amino acids and vitamins missing from the olive fruit on which the larvae feed, supporting further testing of *Enterobacter* sp. strain OLF as a probiotic.

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Data availability. The reads, assembly, and annotation can be accessed through BioProject number PRJNA288712 and BioSample number SAMN03836970. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number LJAN00000000. The version described in this paper is the first version, LJAN01000000.

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