The Enterobacteriaceae bacterium strain FGI 57 was isolated from a fungus garden of the leaf-cutter ant Atta colombica. Analysis of its single 4.76-Mbp chromosome will shed light on community dynamics and plant biomass degradation in ant fungus gardens.

The genome of Enterobacteriaceae bacterium strain FGI 57 was generated at the U.S. Department of Energy (DOE) Joint Genome Institute (JGI) using a combination of Illumina (6) and 454 (7) technologies. For this genome we constructed and sequenced an Illumina GAii shotgun library (46,058,996 reads) totaling 4,605.9 Mb together with both a 454 Titanium standard library (110,558 reads) and a paired-end 454 library (269,554 reads, average insert size of 7 kb) totaling 110.8 Mb. Assemblies were generated using a combination of Newbler, version 2.3-PreRelease-6/30/2009; Velvet, version 1.0.13 (8); and parallel Phrap version SPS-4.24 (High Performance Software, LLC). Consed was used in the finishing process (9–11). Illumina data were used to correct potential base errors and increase consensus quality using the software Polisher developed at JGI (A. Lapidus, unpublished). Possible misassemblies were corrected using gapResolution (Cliff Han, unpublished) or Dupfinisher (12) or by sequencing cloned bridging PCR fragments. Gaps between contigs were closed by editing in Consed, and by PCR and bubble PCR (J.-F. Cheng, unpublished data) primer walks. A total of 38 additional reactions were necessary to close gaps and to raise the quality of the finished sequence. All general aspects of library construction and sequencing performed at the JGI can be found at http://www.jgi.doe.gov/.

The complete genome of the Enterobacteriaceae bacterium strain FGI 57 comprises a single circular chromosome of 4.76 Mb with an average of 228.5-fold coverage and a G+C content of 54.0%. Annotation of the finished chromosome was performed using the Integrated Microbial Genomes-Expert Review (IMG-ER) pipeline (13). A total of 9 copies of 16S rRNA, 86 tRNAs, and 4,548 protein-coding genes were identified in this way. This bacterium was originally classified in the genus Cronobacter, but Basic Local Alignment Search Tool (BLAST)-based comparison (14) of its 16S rRNA genes with those of other Enterobacteriaceae indicate that Raoulettia planticola, Kluvyera georgiana, and Citrobacter freundii all have high nucleic acid identity (all 98%). Phylogenetic analysis of the 16S rRNA genes using FastTree (15) failed to resolve the placement of this bacterium, suggesting that strain FGI 57 may represent a novel group within the Enterobacteriaceae. The availability of the complete genome of this bacterium will facilitate future investigations of the symbiotic microbial community residing in leaf-cutter ant fungus gardens.

**Nucleotide sequence accession number.** The complete genome sequence of Enterobacteriaceae bacterium strain FGI 57 has been deposited at DDBJ/EMBL/GenBank under the accession number CP003938.

**ACKNOWLEDGMENTS**

The work conducted by the U.S. Department of Energy Joint Genome Institute is supported by the Office of Science of the U.S. Department of Energy under contract no. DE-AC02-05CH11231; this work was also supported by the National Science Foundation (grants DEB-0747002, MCB-0702025, and MCB-0731822 to C.R.C.) and the DOE, Great
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