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Genome Sequence of the Plant-Pathogenic Bacterium *Dickeya dadantii* 3937▽

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***Dickeya dadantii* is a plant-pathogenic enterobacterium responsible for the soft rot disease of many plants of economic importance. We present here the sequence of strain 3937, a strain widely used as a model system for research on the molecular biology and pathogenicity of this group of bacteria.**

Dickeya dadantii, formerly *Erwinia chrysanthemi* (11), is the causative agent of soft rot disease in a wide range of plant species, including many economically important crops (10). Soft rot results from the maceration of plant tissues following degradation of pectin, the major component of primary cell walls (7). *D. dadantii* is a devastating opportunistic pathogen in storage organs and fleshy tissues, particularly when compromised by bruising, excess water, low oxygen levels, or high temperatures. *D. dadantii* is also associated with systemic infections, vascular disorders, foliar necroses, and latent infections in growing plants. We sequenced and annotated the complete genome of *Dickeya dadantii* strain 3937, a strain widely used as a model system for research on the molecular biology and pathogenicity of this group of bacteria. Two whole-genome shotgun libraries were prepared with plasmid pHOS2 with target insert sizes of 2 to 3 kb and 10 to 12 kb. We collected approximately 67,000 dual-end sequences, 67% from small-insert clones and 33% from the larger insert library. Sequences were assembled into contigs using the Celera assembler (9), and this assembly was transferred to SeqMan II (Lasergene) for finishing. Primer walking was employed to close gaps covered by clones available from the shotgun libraries. The remaining gaps were closed by sequencing PCR products generated using primers designed from the ends of assembled and ordered contigs. PCR products spanning each rRNA operon were sequenced separately to resolve sequence differences between copies. We used Glimmer 2.0 (3) for initial prediction of protein coding regions. We added, deleted, and revised endpoints of genes based on comparisons to other genomes, genes, and proteins in the NCBI databases. tRNA sequences were identified using tRNAscan-SE (8) with additional examination to identify specific tRNAs not distinguishable by their anticodons alone. rRNA genes were identified by comparison to other enterobacterial sequences using

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BLASTN. Additional functional RNA genes were identified by sequence similarity to known *Escherichia coli* K-12 RNA genes or entries in the RFAM database (5, 6). The *D. dadantii* gene products were annotated using the RAST automated pipeline (1) and manually augmented by domain experts using ASAP (4). This rich manual annotation is not fully represented in GenBank, but it is publicly available in its entirety through ASAP (https://asap.ahabs.wisc.edu/asap/home.php).

The complete circular chromosome of *D. dadantii* strain 3937 is 4,922,802 bp with 57% GC content. There are no extrachromosomal elements. In ASAP, there are 4,543 predicted or known protein-coding genes, 22 rRNA genes organized into 7 operons, 75 predicted tRNAs, and 20 noncoding RNA genes. Orthologs of the *D. dadantii* proteins in other sequenced enterobacteria were identified as best-matching proteins from pairwise BLASTP searches. Not surprisingly, the highest number of putative orthologs, 2,992, is found in *Pectobacterium atrosepticum*, which is both phylogenetically and phenotypically most similar to *D. dadantii* (2). Interestingly, these account for only 67% of the *P. atrosepticum* and 66% of the *D. dadantii* predicted protein-coding genes, underscoring the differences between these pectinolytic bacteria.

Nucleotide sequence accession number. The sequence has been deposited in GenBank under accession number CP002038.

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