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GENOME ANNOUNCEMENT

Complete Genome Sequence of Clinical Isolate *Pantoea ananatis* LMG 5342

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The enterobacterium *Pantoea ananatis* is an ecologically versatile species. It has been found in the environment, as plant epiphyte and endophyte, as an emerging phytopathogen, and as a presumptive, opportunistic human pathogen. Here, we report the complete genome sequence of *P. ananatis* LMG 5342, isolated from a human wound.

Members of the genus *Pantoea* are Gram-negative, motile rods belonging to the family *Enterobacteriaceae* and display ecological versatility, as they are commonly recovered from water, soil, insects, and plants (11, 14). *Pantoea ananatis* is associated primarily with plants, as epiphyte or endophyte, and as an emerging phytopathogen infecting a wide range of important crop and forest plants (e.g., maize, onion, rice, pineapple, *Eucalyptus*) (4). *P. ananatis* has also been reported as an occasional clinical isolate and a presumptive opportunistic human pathogen, associated with septicemia following penetrating trauma with plant material, nosocomial infections due to exposure to contaminated hospital materials, and secondary complications of preexisting illnesses (5, 11, 12). *Enterobacter agglomerans* LMG 5342 (ATCC 29920; CDC6070-69) was isolated from a human wound in Georgia (3, 7) and has been taxonomically reassigned to *P. ananatis* (9, 11). Here, we describe the complete genome sequence of *P. ananatis* LMG 5342, the first clinical isolate of this species and genus to be sequenced.

Whole-genome pyrosequencing using a single run on the Roche 454 GS-Junior sequencer (454 Life Sciences) yielded 165,189 high-quality reads with an average read length of 430 bp (total of 72,654,851 bases), providing 15-times genome coverage. *De novo* assembly using Newbler assembler version 2.5 (454 Life Sciences) yielded 68 contigs which were further assembled using the Lasergene package, version 8.1 (DNAstar, Madison, WI), and by scaffolding against the reference genome of the *Eucalyptus* phytopathogen *P. ananatis* LMG 20103 (6). PCR amplification and Sanger sequencing were performed to close all gaps. Protein coding sequences (CDS) were predicted (8) using Glimmer (13) and Critica (1). The GenDB annotation pipeline (10) was used for automated function assignment, followed by manual optimization.

The genome of *P. ananatis* LMG 5342 consists of a 4,604-kb chromosome with a G+C content of 53.4% and a 303-kb circular plasmid with 51.5% G+C. Primers based on the LMG 5342 plasmid were utilized for gap closure of the homologous plasmid in the *Eucalyptus* pathogen *P. ananatis* LMG 20103, which was previously misassembled into the chromosome (6). A total of 4,675 CDS, seven ribosomal DNA operons, and 77 tRNAs are encoded on the LMG 5342 genome. Comparative genomic analysis using EDGAR (2) indicated that the genome of the clinical strain is highly conserved both in synteny and gene content with that of LMG 20103 (6), with 3,843 (82.2%) orthologous CDS and 833 (17.8%) singletons. Some of these singletons may potentially be linked to human pathogenesis. Detailed genome comparisons and functional analyses will be performed to characterize these factors. The genome sequence of *P. ananatis* LMG 5342 thus represents an extensive resource to broaden our understanding of *P. ananatis* plant and human associations.

Nucleotide sequence accession numbers. The *P. ananatis* LMG 5342 chromosome and plasmid sequences are deposited in EMBL under accession numbers HE617160 (chromosome) and HE617161 (pPANA10 plasmid).

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