Pantoea ananatis is an emerging phytopathogen that infects a broad spectrum of plant hosts. Here, we present the genomes of two South African isolates, P. ananatis PA4, which causes center rot of onion, and BD442, isolated from brown stalk rot of maize.

The genomes of P. ananatis BD442 and PA4 were sequenced using the Illumina HiSeq 2500 platform (2×151-bp shotgun sequencing). This yielded 62,901,136 (BD442) and 70,825,216 (PA4) paired-end reads representing an estimated coverage of 652× (BD442) and 744× (PA4), respectively. The genomes were assembled de novo using the Velvet short-read assembler plugin (7) of the Geneious Server (Biomatters, Ltd., Auckland, New Zealand) with approximately 16,000,000 reads per strain. Further gap closure was done by scaffolding the genomes against the complete P. ananatis clinical strain LMG5342 (8) and Eucalyptus strain LMG20103 (9) using Mauve version 2.3.1 (10).

The P. ananatis BD442 genome was assembled into seventeen contigs, with a total size of 4.80 Mb, a mean G+C content of 53.59%, and an average contig length of ~436 kb, while that of PA4 was assembled into seventeen contigs, with a genome size of 5.16 Mb, a mean G+C content of 53.56%, and an average contig length of ~303 kb. Both assemblies incorporate complete circular plasmids, pPANA1BD442 (~353 kb; G+C%=51.13%) and pPANA1PA4 (~313 kb; G+C%=52.17%), that belong to the Large Pantoea plasmid-1 group, which plays a major role in the evolutionary diversification of Pantoea spp. (11). The genomes were annotated using the Rapid Annotations using Subsystems Technology (RAST) server (12). The genomes code for 4,673 (BD442) and 5,111 (PA4) proteins, respectively. Of these, 3,749 proteins are conserved between the two strains, while variability can largely be ascribed to prophage integration (13). We previously described three type VI secretion system (T6SS) loci in P. ananatis that play a role in animal and plant pathogenesis (14). All three loci (T6SS-1, -2, and -3) are present in P. ananatis PA4, whereas T6SS-3 is missing in BD442 (13, 14). These genomes will provide new insights into the pathogenic lifestyle of Pantoea ananatis and how it is able to cause disease symptoms on such a broad range of host plants.

Nucleotide sequence accession numbers. These whole-genome shotgun projects have been deposited in DDBJ/ENA/GenBank under the accession no. JMJK00000000 (P. ananatis PA4) and JMJL00000000 (P. ananatis BD442). The versions described in this paper are the first versions, JMJK01000000 (PA4) and JML01000000 (BD442).

ACKNOWLEDGMENTS

This study was supported by the University of Pretoria, the National Research Foundation (NRF), the Forestry and Agricultural Biotechnology Institute (FABI), the Tree Protection Cooperative Programme (TPCP), the NRF/Department of Science and Technology Centre of Excellence in tree Health Biotechnology (CTHBB), and the THRIP support program of the Department of Trade and Industry, South Africa.

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