Genome Sequence of the Curdlan-Producing Agrobacterium sp. Strain ATCC 31749

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Received 14 May 2011/Accepted 6 June 2011

Agrobacterium sp. ATCC 31749 is an industrial strain for the commercial production of curdlan, an important exopolysaccharide with food and medical applications. Here we report the genome sequence of the curdlan-producing strain ATCC 31749. Genome sequencing is the first step toward the understanding of regulation of curdlan biosynthesis.

Agrobacterium sp. ATCC 31749 is an alphaproteobacterium of the Rhizobiaceae family (6). But unlike other species of the rhizobium family, ATCC 31749 is not plant associated. This agrobacterium is unique in its ability to synthesize, upon nitrogen exhaustion, a linear β-1,3-glucan exopolysaccharide (EPS) known as curdlan. Curdlan has been commercialized for applications in the food, construction, and pharmaceutical industries, and numerous other applications, such as antitumor and anticancer treatments, are being pursued (3, 5, 14). While extensive studies have led to optimized conditions for curdlan synthesis (8–12), very little is known about the genome, including the curdlan biosynthesis operon (crdASG) (16), and as with many other microbial EPSs, its regulation is largely unexplored.

Agrobacterium sp. ATCC 31749 was sequenced using the Genome Sequencer FLX system from 454 Life Sciences. A total of 92,994,272 bp were sequenced in 399,219 reads, with an average read length of 233 bp. Using the GS de novo assembler, the reads were assembled into 95 contigs of 500 bp or longer, yielding an approximate genome size of 5.5 Mbp with 48% GC content. The contigs were arranged in random order with stop and start codons inserted in each reading frame between the contigs to generate a pseudochromosome. From this pseudochromosome, 5,585 genes were predicted using the GeneMarkS (1) and Glimmer v3.02 (2) software programs. Annotation with BLAST identified 3,466 predicted genes with GGDEF/EAL domains, known to regulate the production of many bacterial polysaccharides (7, 18). The genome contains genes associated with the production of acidocalcisomes, organelles that contain large quantities of polyphosphate (polyP) (4).

The genome sequence of Agrobacterium sp. ATCC 31749 provides the basis for subsequent experimentation to decipher the regulation mechanisms. Synthesis of EPSs is common among many bacterial species, some of which are involved in biofilms and have important medical implications (17). While chemically diverse, their syntheses share common environmental triggers, suggesting that EPS regulatory elements may be more universal than their chemical structures suggest. Continued study of curdlan synthesis, aided by the genome sequence, may uncover these common mechanisms.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. AECL00000000. The version described here is the first version, AECL01000000.

This work was funded by the National Science Foundation (BES 0455193) and the American Cancer Society. A. M. Ruffing acknowledges support from an NSF Graduate Research Fellowship.

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†Published ahead of print on 17 June 2011.