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Draft Genome Sequence of *Brevundimonas* sp. Strain SH203, Producing Cellouronate (β-1,4-Linked Polyglucuronate) Lyase

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ABSTRACT In this study, we report the draft genome sequence of *Brevundimonas* sp. strain SH203, which was previously isolated from natural soil and has the ability to degrade β-1,4-polygluculonate (cellouronate). This genomic information may provide new insight into the mechanisms by which cellouronate is degraded.

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A bacterial strain with the ability to degrade cellouronate and isolated from natural soil was identified as *Brevundimonas* sp. strain SH203 by comparing its 16S rRNA gene sequence with that in the GenBank database (1). *Brevundimonas* sp. SH203 was reported to degrade β-1,4-polygluculonate (cellouronate), which is artificially prepared from regenerated cellulose by TEMPO (2,2,6,6-tetramethylpiperidine-1-oxyl radical)-mediated oxidation. We have purified two types of cellouronate lyases from the strain, CUL-I and CUL-II, which catalyze the depolymerization of cellouronate by cleaving glycoside bonds through β-elimination (1–4).

Brevundimonas sp. SH203 was cultivated in 10 ml of LB broth at 30°C for 2 days, and genomic DNA extracted using the DNeasy blood and tissue kit, followed by RNase A digestion. The sheared genomic DNA, resulting in fragments with an average size of 550 bp, and a paired-end DNA library were constructed using the TruSeq DNA PCR-free library preparation kit, according to the manufacturer's instructions. The DNA library then sequenced on a MiSeq instrument at the Center for Bioscience Research and Education, Utsunomiya University, Japan. The raw sequencing data (2 × 301 bp in length) were trimmed to remove low-quality ends (<15) and adapters, using Trimmomatic (version 0.36) (5). To remove contaminant sequences or sequence errors, reads with low coverage (<5×) were removed using khmer (version 2.0) (6), resulting in 1,084,068 high-quality reads (542,034 pairs) totaling 266 Mb (~84-fold coverage). The high-quality reads were further assembled using SPAdes version 3.9.0 (7), with the "careful" option selected, and contigs of less than 200 bp were eliminated. The draft genome of *Brevundimonas* sp. SH203 assembled into 16 contigs, with a total length of 3,145,540 bp (N_{50}, 497,772 bp) and 67.6% G+C content.

The resultant draft genome sequence was annotated using Prokka version 1.11 (8). Furthermore, tRNA genes and rRNA sequences were predicted using tRNAscan-SE version 1.3.1 (9) and RNAmer version 1.2 (10), respectively. The annotated genome contains 2,961 protein-coding sequences, 47 tRNA genes, and 3 rRNA sequences. Functional annotation of the predicted proteins was conducted using Clusters of Orthologous Groups (COG) (11) and Pfam (12). Among 2,961 proteins, 2,496 (84.2%) and 2,469 (83.3%) proteins were annotated by COG and Pfam, respectively. From the results of Pfam analysis, one alginate-lyase (PF05426) and three β-eliminating lyase (PF01212) domain-containing sequences were detected which might be involved in

cellouronate degradation. This genomic information may provide new insight into the mechanisms by which cellouronate is degraded.

Accession number(s). The draft genome sequence of *Brevundimonas* sp. strain SH203 been deposited to the DDBJ/EMBL/GenBank database under the accession no. BDMM00000000.

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