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Genome Sequence of the Welan Gum-Producing Strain *Sphingomonas* sp. ATCC 31555

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***Sphingomonas* sp. strain ATCC 31555 can produce an anionic heteropolysaccharide, welan gum, which shows excellent stability and viscosity retention even at high temperatures. Here we present a 4.0-Mb assembly of its genome sequence. We have annotated 10 coding sequences (CDSs) responsible for the welan gum biosynthesis and 55 CDSs related to monosaccharide metabolism.**

Sphingans, a group of exopolysaccharides, are secreted by members of the genus *Sphingomonas*. They include gellan gum produced by *Sphingomonas elodea* ATCC 31461, welan gum produced by *Sphingomonas* sp. strain ATCC 31555, diutan produced by *Sphingomonas* sp. ATCC 53159, and rhamsan produced by *Sphingomonas* sp. ATCC 31961 (2). Welan gum is composed of tetrasaccharide repeating units of D-glucose, L-rhamnose, and D-glucuronic acid with L-rhamnopyranosyl or L-mannosyl as the side chain (5). Unlike gellan gum, welan gum is not gel but produces viscous solutions, showing excellent stability and viscosity retention at temperatures up to 150°C (300°F). Due to its excellent rheological properties, welan gum is used in many applications, such as concrete additives and enhanced oil recovery (6, 10).

Many researchers have focused their efforts on the structure and characteristics of welan gum (6, 9, 10). However, genomic and genetic information involved in the biosynthesis of welan gum has not been well studied. Thus, we announce the genome sequence of *Sphingomonas* sp. ATCC 31555. The genome of *Sphingomonas* sp. ATCC 31555 was sequenced using an Illumina High-Seq 2000 system. The reads were assembled into 62 large contigs ($>$500 bp) using Velvet 1.2.03 (12). The contig N_{50} is approximately 15.6 kb, and the largest contig assembled is approximately 407.1 kb. The draft sequence consists of 4,046,117 bases, with a mean G+C content of 65.9%. Annotation of open reading frames was performed by using the RAST annotation server (1) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (8). A total of 3,768 coding sequences (CDSs) and 50 structural RNAs were predicted.

The genes *pgmG*, *ugpG*, and *ugdG*, involved in the biosynthesis of nucleotide sugar precursors UDP-D-glucose, UDP-D-glucuronic acid, and dTDP-L-rhamnose, were found to be dispersed on the genome of *Sphingomonas* sp. ATCC 31555 like those in *Sphingomonas elodea* ATCC 31461 (4). Four genes (*rmlA*, *rmlC*, *rmlB*, and *rmlD*) responsible for the synthesis of the sugar-nucleotide precursor dTDP-L-rhamnose were also found on the genome of *Sphingomonas* sp. ATCC 31555. The genes designated *welB*, *welK*, and *welL* show high identities with *gelB*, *gelK*, and *gelL*, which encode glycosyl transferases for the tetrasaccharide repeat unit of the backbone of gellan gum (3). The dTDP-L-rhamnose biosynthesis genes *welB*, *welK*, and *welL* are in the same locus in strain *Sphingomonas* sp. ATCC 31555. The organization and sequence of this region are highly similar to those of the *gel* cluster from *Sphingomonas* sp. ATCC 31461, the *sps* cluster from *Sphingomonas* sp. ATCC 31554, and the *dps* cluster from *Sphingomonas* sp. ATCC 53159, required for the synthesis of the sphingans gellan, S-88, and diutan. Moreover, there are 55 CDSs related to monosaccharide metabolism. Several genes (the *crt* cluster) responsible for the biosynthesis of carotenoid were also found. Recently, carotenoid has been reported to play important roles in the synthesis of gellan by *Sphingomonas elodea* ATCC 31461 (11) and in the degradation of heterocycles by *Sphingobium yanoikuyae* XLDN2-5 (7).

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALBQ00000000. The version described in this paper is the first version, ALBQ01000000.

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