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Genome Sequence of *Sphingomonas elodea* ATCC 31461, a Highly Productive Industrial Strain of Gellan Gum

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The commercial gelling agent gellan gum is a heteropolysaccharide produced by *Sphingomonas elodea* ATCC 31461. However, the genes involved in the biosynthesis, regulation, and modification of gellan gum have not been fully characterized. Here we describe the draft genome sequence of stain ATCC 31461 and major findings from its annotation.

Many strains of the genus *Sphingomonas* (11) can produce sphingans with related structures (3, 7). *Sphingomonas elodea* ATCC 31461 (originally designated *Pseudomonas elodea*; also referred to as *Sphingomonas paucimobilis*) was capable of producing a novel gelling polysaccharide designated "gellan gum" (2, 13). Gellan gum has a wide range of applications in food, pharmaceutical, and other industries as a stabilizing, thickening, emulsifying, and gelling agent because of its excellent rheological characteristics (10). Moreover, gellan gum has approval in the United States and European Union for food use (10).

The genes (*pgmG*, *ugpG*, and *ugdG*) coding the enzymes required for the synthesis of the nucleotide sugars (UDP-Glc and UDP-GlcA) from Glc-1-phosphate are dispersed on the *Sphingomonas elodea* ATCC 31461 genome (6, 9, 12). The genes coding for the proteins involved in the synthesis of dTDP-L-Rha, the glycosyltransferases, and the proteins required for gellan polymerization and export are located together in the *gel* cluster (5, 9). However, the mechanistic details of polymerization, chain-length determination, and export of polysaccharides are still poorly understood. Knowledge of the genetics and regulation of polysaccharide synthesis and modification in strain ATCC 31461 may lead to techniques for production of modified polysaccharides to provide polymers with unique rheological properties. Thus, for the first time, we announce the draft genome sequence of strain ATCC 31461.

The genome of strain ATCC 31461 was sequenced using Illumina paired-end technology. The reads were assembled using Velvet software (14). The N50 contig was approximately 32 kb, and the largest contig assembled was approximately 168.4 kb. This assembly generated 127 large (>500-bp) contigs. The draft sequence is 4,124,388 bases in length, with a mean GC content of 67.4%. The genome was annotated using the RAST annotation server (1) and the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (8). A total of 3,813 coding sequences and 49 structural RNAs were predicted. There are 392 subsystems in the genome, as determined by the RAST server (1). Comparison with the genome sequences available at the RAST server suggested that the closest neighbor of strain ATCC 31461 was *Novosphingobium aromaticivorans* (score, 521), followed by *Sphingopyxis alaskensis* RB2256 (score, 503) and *Sphingomonas wittichii* RW1 (score, 475).

Strain ATCC 31461 encodes a diverse array of proteins with predicted roles in sugar metabolism. There are at least 42 enzymes that are related to the metabolism of monosaccharides (such as mannose, D-galactonate, D-gluconate, ketogluconates, D-galacturonate, and D-glucuronate). This capacity may indicate an involvement in heteropolysaccharide biosynthesis. Moreover, we identified a few insertion sequences and transposons elements from the draft genome sequence of *Sphingomonas elodea* ATCC 31461 that are different from those of the carbazole-degrading *Sphingobium yanoikuyae* XLDN2-5 strain (4). Further genomic analysis should provide additional useful information to help elucidate the full mechanism for gellan gum biosynthesis and modification in strain ATCC 31461.

Nucleotide sequence accession numbers. The nucleotide sequence determined in the whole-genome shotgun-sequencing project has been deposited at DDBJ, EMBL, and GenBank under accession no. AGFU00000000. The version described in this paper is the first version (accession no. AGFU01000000).

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