GENOME ANNOUNCEMENTS

Genome Sequence of *Agrobacterium tumefaciens* Strain F2, a Biofloculant-Producing Bacterium

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***Agrobacterium tumefaciens* F2 is an efficient biofloculant-producing bacterium. But the genes related to the metabolic pathway of biofloculant biosynthesis in strain F2 are unknown. We present the draft genome of *A. tumefaciens* F2. It could provide further insight into the biosynthetic mechanism of polysaccharide-like biofloculant in strain F2.**

Agrobacterium tumefaciens (former name, *Rhizobium radiobacter*) F2 is a Gram-negative, rod-shaped bacterium isolated from soil and is an alphaproteobacterium in the family *Rhizobiaceae*. Strain F2 can produce biofloculants (microbial flocculants) during its growth (2). Biofloculants produced by strain F2 are polysaccharides and are able to flocculate a variety of wastewaters. Until now, the biosynthetic pathway and related genes for producing biofloculants in *A. tumefaciens* F2 have not been determined. In order to improve the biofloculant yield using metabolic engineering methods, we sequenced the complete genome of *A. tumefaciens* strain F2.

The genome sequence of *Agrobacterium tumefaciens* F2 was determined by using Roche 454 GS FLX Titanium technology. Raw sequence reads (298,265) were assembled into 63 contigs with 22.5× sequence coverage by using Newbler software (version 2.3). Based on gene order conservation between *Agrobacterium tumefaciens* strains F2 and C58 (AE007869.2) (1, 3), these contigs were assigned into different chromosomes, and the order of the contigs was actually determined by a series of PCR products. The gaps were filled by multiplex PCR followed by sequencing using an ABI 3730 sequencer. Finally, we determined that the genome of F2 has a circular chromosome with two contigs, a linear chromosome with four contigs, and two complete plasmids. The genome annotation and analysis were done by the same method as that described previously (4).

A circular chromosome of 2,982,075 bp with an average GC content of 59.41%, a linear chromosome of 1,976,596 bp with a

GC content of 60.02%, one plasmid of 105,065 bp with a GC content of 56.71%, and another plasmid of 401,969 bp with 59.52% GC content were also characterized. There are 4,793 coding genes, 31 tRNA genes, and 4 rRNA operons in the F2 chromosome and 528 coding genes in 2 plasmids.

Interestingly, we found that the genes related to polysaccharide production were present in the genome of strain F2, which is on the circular chromosome (Agau_C100061, Agau_C100168, Agau_C100484, Agau_C100505, Agau_C101145, Agau_C101708, Agau_C101710, Agau_C200960, and Agau_C201628) and linear chromosome (Agau_L100089, Agau_L100091, Agau_L100898, Agau_L100919, Agau_L300100, Agau_L300463, Agau_L300464, and Agau_L300466). Meanwhile, the biofloculant produced by strain F2 was identified as a polysaccharide-like substance, which was composed of α-galactopyranose, β-mannopyranose, and α-glucopyranose with a mass ratio of 1:3:5. As described in previous reports, *A. tumefaciens* strain C58 could produce the succinoglycan exopolysaccharide, but the genes encoding the polysaccharide production protein were located only on the linear chromosome (1, 3). These results indicated that strain F2 contained a novel metabolic pathway for polysaccharide biosynthesis.

Nucleotide sequence accession number. The whole-genome shotgun project for *Agrobacterium tumefaciens* strain F2 has been deposited at DDBJ/EMBL/GenBank under the accession number AFSD00000000.

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