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Genome announcements

Complete genome sequence of the glidobactin producing strain [*Polyangium*] *brachysporum* DSM 7029

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ABSTRACT

[*Polyangium*] *brachysporum* DSM7029 can produce glidobactin, which is a peptide-based proteasome inhibitor that shows great potential as an anticancer drug. To better understand the glidobactin biosynthesis mechanism and to aid further studies of this strain, we report the annotated complete genome sequence of DSM7029, which is 6,476,147 bp in length.

[*Polyangium*] *brachysporum* DSM 7029 (=K481-B101 = ATCC 53,080) was first isolated from a soil sample in Greece (Oka et al., 1988). This taxonomic name was not validly published at the time of submission of the corresponding sequence entry or entries. Phylogenetic analysis of the 16S ribosomal rRNA gene of strain DSM 7029 indicates that "*Polyangium brachysporum*" was misclassified and should be placed in the *Burkholderiales* (Schellenberg et al., 2007). Strain DSM 7029 can produce a novel type of antifungal and antitumor antibiotic complex, consisting of glidobactins A–C (Oka et al., 1988), which are hybrid nonribosomal peptide synthetase-polyketide synthase (NRPS-PKS) natural products, as proteasome inhibitors (Bian et al., 2014; Imker et al., 2010). Glidobactins are acylated tripeptide derivatives that contain a 12-membered ring structure consisting of two unique non-proteinogenic amino acids, erythro-4-hydroxy-l-lysine and 4(S)-amino-2(E)-pentenoic acid (Schellenberg et al., 2007). A structural difference between glidobactins A–C was found only in their acyl side chain moiety (Numata et al., 1988).

A total of 256,538 reads were generated using a Roche 454 GS FLX Titanium system and they were assembled using the Newbler Program (version 2.7), which resulted in 71 contigs (>500 bp) with an average size of 90,653 bp. The relationship among contigs was displayed using ContigScape (Tang et al., 2013) and confirmed by PCR. Sanger-based sequencing was employed to facilitate gap closing and to amend the low-quality regions (scores <25). The final sequence assembly was conducted using the Phred/Phrap/Consed package. Finally, a consensus circular sequence containing 6476,147 bp, with an estimated error rate of <0.5 per 100,000 bases and providing 20.2-fold coverage, was acquired.

Open reading frames (ORFs) were predicted by Glimmer 3.02 and GeneMark. The CDS annotation was based on the BLASTP results obtained with the KEGG, NR databases and RAST server (Aziz et al., 2008). At last, the annotation was checked by the NCBI Prokaryotic Genomes Annotation Pipeline and manual correction was also implemented. The average GC content of the chromosome is 67.51%. The entire genome contains 5557 coding sequences, with an average length of 1018 bp, 66 tRNA genes, and three complete rRNA operons. Among the coding sequences (CDSs), biological functions could be defined for 3999 (71.96%) of the predicted proteins, while the other 1558 hypothetical proteins (28.04%) are homologous to conserved proteins of unknown function in other organisms or have no match to any known proteins in the databases. Altogether, the CDSs and stable RNA genes represent 87.4% and 0.29% of the genome, respectively. The genome features of DSM 7029 are summarized in Table 1.

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Table 1
Genome features of [*Polyangium*] *brachysporum* DSM 7029.

Features	Genome
Length (bp)	6,476,147
G + C content (%)	67.51
CDSs	5557
Protein coding genes with function prediction	3999
rRNA operons	3
tRNA	66
Gene clusters	14

Glidobactin biosynthesis in DSM 7029 involves eight genes (*glbA-glbH*). *glbF* and *glbC* encode a NRPS and a hybrid NRPS-PKS, respectively, and they are required for the biosynthesis of the tripeptide portion of glidobactins. We found that the glidobactin gene cluster was located in the genome from nucleotides 2696,902 to 2675,407. The potential of DSM 7029 to produce secondary metabolites was analyzed with the secondary metabolites predict tool antiSMASH (Blin et al., 2013). There may be 14 putative gene clusters involved in the biosynthesis of different natural products (Table 1). Among the clusters, three encode NRPSs, two encode hybrid NRPS-PKSs, one encodes a type I PKS, one is involved in the biosynthesis of terpene, two are involved in the biosynthesis of hserlactone, one is involved in lantipeptide production, one is involved in ladderane production, one is involved in butyrolactone production, one is involved in bacteriocin production, and one is involved in the biosynthesis of aryl-polyene. Additionally, several proteins have been shown to contribute to resistance against beta-lactam antibiotics. The genome sequence has a 20.3% DNA–DNA hybridization (DDH) (Auch et al., 2010) value and a 75.13% average nucleotide identity (ANI) (Richter and Rossello-Mora, 2009) value vs. the closest complete genome *Methylibium petroleiphilum* PM1.

Nucleotide sequence accession number

The genome sequence of [*Polyangium*] *brachysporum* DSM 7029 in this project has been deposited in the GenBank/EMBL/DDBJ database under accession number CP011371.

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