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Complete genome of *Planococcus rifietoensis* M8^T, a halotolerant and potentially plant growth promoting bacterium

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Highlights

- *Planococcus rifietoensis* M8^T (=DSM 15069^T =ATCC BAA-790^T) is a halotolerant bacterium with potential plant growth promoting properties
- Various key genes coding for these properties were identified
- This is the first complete genome sequence of *Planococcus rifietoensis*

Abstract

Planococcus rifietoensis M8^T (=DSM 15069^T =ATCC BAA-790^T) is a halotolerant bacterium with potential plant growth promoting properties isolated from an algal mat collected from a sulfurous spring in Campania (Italy). This paper presents the first complete genome of *P. rifietoensis* M8^T. Genes coding for various potentially plant growth promoting properties were identified within its genome.

Keyword: nitrogen fixing, potassium homeostasis, biotechnology, biofertilizer

High salinity in agricultural soils is of global concern, affecting productivity of crops (Mayak et al., 2004). The plant growth promoting (PGP) properties of halotolerant bacteria are highly sought after biotechnological traits for facilitating plant growth in saline soils (Yildirim & Taylor, 2005; Barassi et al., 2006). *Planococcus rifietoensis* is a moderately halotolerant (Romano et al., 2003) bacterium capable of promoting wheat growth by converting ammonia to nitrogen, thereby enabling fertilization of soil under high salinity stress, as well as metabolizing potassium to reduce ion imbalance of plant cells (Rajput et al., 2013). Here, we present the first complete genome of *Planococcus rifietoensis* M8^T, identifying finding of its various key genes for PGP properties.

Genomic DNA of *P. rifietoensis* M8^T was isolated from an overnight cell suspension culture using the MasterPure™ Gram positive DNA purification kit (Epicentre Technologies). The genomic DNA was then constructed into a 20-kb SMRTbell template library. Pacific Biosciences (PacBio) RSII sequencing platform was used to perform whole genome sequencing using C4 chemistry in two single molecule real time (SMRT) cells (Ee et al., 2015). A total of 41,347 reads with a mean read length of 12,808 bp were generated. The reads were *de novo* assembled using hierarchical genome assembly process (HGAP) algorithm version 2 into a circular contig with an average genome coverage of 124-fold (Goh et al., 2015).

Genome annotation was performed using NCBI Prokaryotic Genome Annotation Pipeline (PGAP) version 2.10 and Rapid Annotation using Subsystem Technology (RAST) version 2.0 (Aziz et al., 2008, Overbeek et al., 2014, Brettin et al., 2015). The genome of *P. rifietoensis* M8^T consists of a 3,527,718 bp circular chromosome with a G+C content of 48.4%. A total of 3,514 protein coding genes were predicted along with 6 rRNA and 49 tRNA genes (Table 1).

Functional annotation of the genome revealed genes coding for assimilation of ammonia via both the GDH pathway using NAD-specific glutamate dehydrogenase (NCBI locus tag: AUC31_04065 & AUC31_0581; EC 1.4.1.2 & EC 1.4.1.4) the and glutamine synthetase (GS)-glutamate synthase (GOGAT) pathway using glutamine synthetase (NCBI locus tag: AUC31_00390, EC 6.3.1.2), glutamate synthase (NCBI locus tag: AUC31_12670, AUC31_12675, AUC31_03115; EC 1.4.1.13), serine hydroxymethyltransferase (NCBI locus tag: AUC31_14095, EC 2.1.2.1), glycine dehydrogenase (NCBI locus tag: AUC31_02400, AUC31_02405; EC 1.4.4.2), serine-glyoxylate aminotransferase (EC 2.6.1.45), potassium homeostasis gene (NCBI locus tag: AUC31_11595, AUC31_11650, AUC31_11655, AUC31_16700, AUC31_05695, AUC31_0775, EC: 2.7.3) and phosphate metabolism and transporter gene (NCBI locus tag: AUC31_02645, AUC31_02760, AUC31_02525, EC: 2.7.13.3, TC: 3.A.1.7.1). Furthermore, genes coding for various chemical compounds metabolism processes were found, including genes for degradation of gentisate, glycerol, mannitol, inositol, glycerate, formaldehyde, ribulose and carotenoids, isoprenoids, and isopropanoids. This finding may indicate the application of this strain in bioremediation (Urbieta et al.,

2015). Further study of the full PGP capacity of this strain is required in order to further confirm its potential for biotechnological application.

Nucleotide sequence accession number

The complete chromosome sequence has been deposited in GenBank under the accession number CP013659.

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Table 1. Genome features of *P. rifietoensis* M8^T.

Attributes	Value
Genome size (bp)	3,527,718
GC content (%)	48.4
Total number of genes	4,141
Protein coding genes	3,901
Contigs	1
rRNA genes	27
tRNA genes	63