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Draft genome of the strain RCAM1026 *Rhizobium leguminosarum* bv. *viciae*

Alexey Afonin*, Anton Sulima, Aleksandr Zhernakov, Vladimir Zhukov

All-Russia Research Institute for Agricultural Microbiology (ARRIAM), Russia

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ABSTRACT

Rhizobium leguminosarum bv. *viciae* RCAM1026 is a strain first isolated in 1964 from nodules of "Ramensky 77" cultivar of garden pea (*Pisum sativum* L.) now routinely used as a model strain in inoculation experiments on pea. Assembly with SPAdes yielded 133 contigs longer then 200 bp (N50 = 202,321, GC% = 60.84). Resulting annotated genome is 7,248,686 bp encoding 6792 genes.

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Specifications	
Organism/cell line/tissue	*Rhizobium leguminosarum* bv. *viciae* RCAM1026
Sex	N.A.
Sequencer or array type	Illumina HiSeq 2000
Data format	Processed
Experimental factors	Nodule bacteria
Experimental features	Whole genome sequence assembly and annotation
Consent	Level of consent allowed for reuse if applicable
Sample source location	Kostanay Region of Kazakhstan

1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/nuccore/MPZP01000000.

2. Introduction

Genus *Rhizobium* consists of aerobic, gram-negative bacteria capable of forming nitrogen-fixing symbiosis with plants of the Fabaceae family. *Rhizobium leguminosarum* species is subdivided into biovars that include strains isolated from the nodules of corresponding host plants (bv. *viciae* — from *Vicia* spp., *Pisum sativum* L., *Lens* spp., *Lathyrus* spp.; bv. *trifolii* — from *Trifolium* spp.; bv. *phaseoli* — from *Phaseolus vulgaris* L.) [1]. The *Rhizobium leguminosarum* bv. *viciae* strain RCAM1026 (deposited in Russian Collection of Agricultural Microorganisms (RCAM), ARRIAM, Saint-Petersburg, Russia) was originally isolated from nodules of "Ramensky 77" cultivar of pea in Kostanay Region of Kazakhstan. RCAM1026 can effectively nodulate garden pea and therefore is routinely used as a model active strain in inoculation experiments on pea of different genetic backgrounds [2,3].

3. Strain isolation

The strain was originally isolated from "Ramensky 77" cultivar of garden pea in the Kostanay Region of Kazakhstan [2] and later deposited in the **Russian Collection of Agricultural Microorganisms**(RCAM, http://:arriam.ru/kollekciya-kul-tur1/) belonging to the **All-Russia Research Institute for Agricultural Microbiology, Saint-Petersburg, Russia**.

4. DNA isolation and sequencing

Prior to sequencing a strain culture was cultivated for 3 days at 28 °C in a liquid medium (tryptone — 5 g/l, yeast extract — 3 g/l, $CaCl_2$ — 0.5 g/l, pH 7.0). 50 ml of the culture were pelleted by centrifugation and suspended in 50 µl of deionized water. DNA isolation was carried out with the GBD kit from Biosilica, Novosibirsk, Russia. Libraries were created and barcoded with the New England Biolabs NEBNext®Ultra™DNA Library Prep Kit for Illumina®, then additionally barcoded with NEBNext®Multiplex Oligos for Illumina®(Dual Index Primers Set 1). Genome was sequenced on an Illumina HiSeq 2000 platform with TruSeq PE Cluster Kit v3 and TruSeq SBS Kit v3 by Genotek Ltd, Moscow, Russia.

* Corresponding author.
E-mail address: AAfonin@ARRIAM.ru (A. Afonin).

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5. Genome assembly and annotation

De novo assembly was performed with SPAdes genome assembler (v3.9.0) set to default parameters [4]. Contigs shorter than 200 bp were deleted yielding a full genome sequence of 7,239,605 bp consisting of 133 contigs with G/C content of 60.84%. ORF prediction and automatic annotation was carried out with NCBI PGAAP pipeline. Complete genome contained 6792 genes, 48 tRNAs, 3 rRNAs and 4 ncRNA.

6. Phylogenetic analysis

The analysis was performed using the *in silico* DNA-DNA hybridization method [5]. The closest related strain appears to be *Rhizobium leguminosarum* bv. *viciae* strain GB30 with similarity of 95% (NCBI reference sequence NZ_ATTP00000000.1).

7. Nucleotide sequence accession numbers

This draft genome for *Rhizobium leguminosarum* bv. *viciae* RCAM1026 project has been deposited at GenBank under the accession MPZP00000000. The 133 contigs were deposited under accession numbers MPZP000000001-MPZP00000133.

8. Conflict of interest

The authors declare that there is no conflict of interests with respect to the work published in this paper.

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