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Complete genome sequence of *Luteibacter rhizovicinus* strain LJ96T, isolated from the rhizosphere of barley (*Hordeum vulgare* L.) in Denmark

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ABSTRACT

We present the complete genome sequence of *Luteibacter rhizovicinus* type strain LJ96T, a yellow-pigmented gammaproteobacterium isolated from the rhizosphere of barley (*Hordeum vulgare*) Johansen et al. (2005) , a species with numerous potential applications. The genome sequence was deposited to NCBI GenBank with the accession number CP017480.

Specifications	
Organism	*Luteibacter rhizovicinus*
Strain	LJ96T
Sequencer or array type	PacBio RS II
Data format	Analyzed
Experimental factors	Bacterial type strain
Experimental features	Whole genome analysis and gene annotation of LJ96T
Sample source location	Rhizosphere soil of spring barley (*H. vulgare*) in an organic field at Højbakkegaard, Taastrup, Denmark.

1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/nuccore/1109359792/

2. Experimental design, material and methods

The genus *Luteibacter* belongs to the family *Xanthomonadaceae* in the class *Gammaproteobacteria* [1]. Since it was first isolated from rhizosphere of barley [1], *Luteibacter* sp. has typically been associated with soil or rhizosphere [2–5]. *Luteibacter* sp. has shown the ability to degrade PCB [3], produce lipases [5], metabolize cephalomannine [4], chelate ferric ions and solubilize monocalcium phosphate *in vitro*, as well as to promote plant growth [6]. Genomic DNA from *L. rhizovicinus* type strain LJ96T [1] was extracted using Genomic-tip 500/G kit (Qiagen GmbH, Hilden, Germany). A library was created using PacBio (Pacific Biosciences, California, USA) 20 kb library preparation protocol and whole genome sequencing was performed using PacBio RS II. The library was sequenced using *P6-C4* chemistry with 360 min movie time on one single-molecule real-time (SMRT) cell. The reads were assembled using HGAP v3 (Pacific Biosciences, SMRT Analysis Software v2.3.0). The Minimus2 software of the Amos package was used to circularize the contig, which was confirmed by a dot plot to contain the same sequence at the beginning and end of the contig. RS_Resequencing.1 software (SMRT Analysis version v2.3.0) was used to map reads back to the assembled and circularized sequence in order to correct the sequence after circularization. The sequencing service was provided by the Norwegian Sequencing Centre (www.sequencing.uio.no), a national technology platform hosted by the University of Oslo and supported by the "Functional Genomics" and "Infrastructure" programs of the Research Council of Norway and the Southeastern Regional Health Authorities.

2.1. Data description

The genome of *L. rhizovicinus* type strain LJ96T was annotated using the NCBI Prokaryotic Genome Annotation Pipeline [7], GeneMarkS + v 3.3 and the Rapid Annotation System Technology (RAST) server [8]. Fig. 1 presents an overview of the count of each subsystem feature and the subsystem coverage. The genome had a GC content of 64.7%, consisted of 4,765,486 bp and contained 4247 coding sequences, 6 rRNA genes, 51 tRNAs, and 4 noncoding RNA genes.

2.2. Nucleotide accession number

This whole genome project has been deposited at NCBI GenBank under the accession number CP017480.

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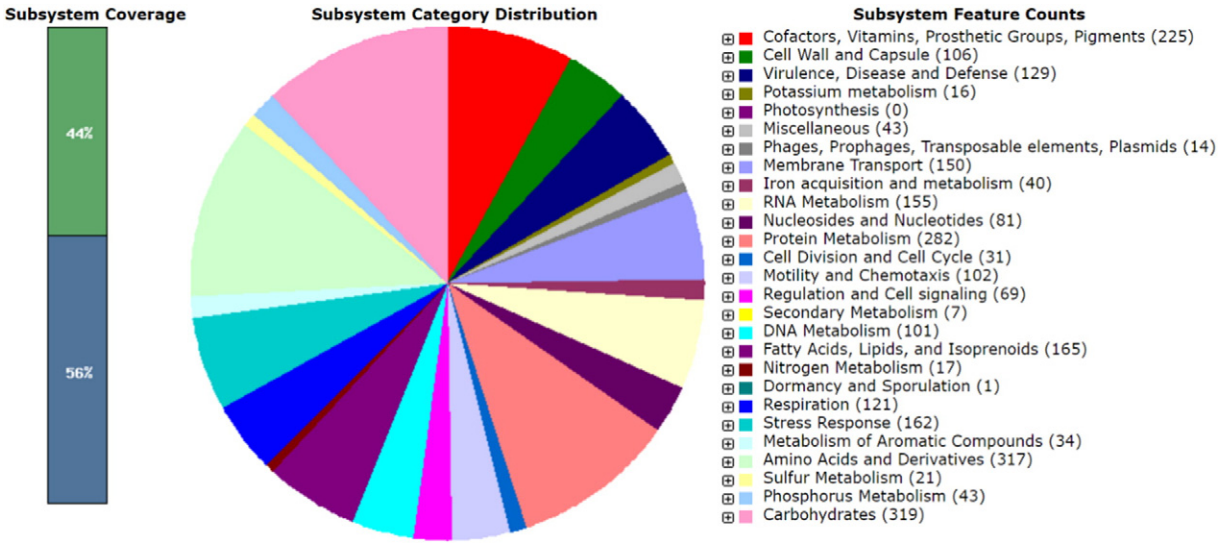

Fig. 1. Subsystem category distribution of major protein coding genes of *Luteibacter rhizovicinus* type strain LJ96T as annotated by the RAST annotation server. The bar chart shows the subsystem coverage in percentage (blue bar corresponds to percentage of proteins included). The pie chart shows percentage distribution of the 27 most abundant subsystem categories.

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