Genomics Data 13 (2017) 38–40

Contents lists available at ScienceDirect

Genomics Data

journal homepage: www.elsevier.com/locate/gdata

Data in Brief

# Draft genome sequence of *Bradyrhizobium paxllaeri* LMTR 21$^T$ isolated from Lima bean (*Phaseolus lunatus*) in Peru

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## ABSTRACT

*Bradyrhizobium paxllaeri* is a prevalent species in root nodules of the Lima bean (*Phaseolus lunatus*) in Peru. LMTR 21$^T$ is the type strain of the species and was isolated from a root nodule collected in an agricultural field in the Peruvian central coast. Its 8.29 Mbp genome encoded 7635 CDS, 71 tRNAs and 3 rRNAs genes. All genes required to stablish a nitrogen-fixing symbiosis with its host were present. The draft genome sequence and annotation have been deposited at GenBank under the accession number MAXB00000000.

| Specifications | |
|---|---|
| Organism/cell line/ tissue | *Bradyrhizobium paxllaeri* LMTR 21$^T$ |
| Sex | – |
| Sequencer or array type | HiSeq (Illumina) |
| Data format | Analyzed |
| Experimental factors | Wild type strain |
| Experimental features | Genome sequence and annotation |
| Consent | – |
| Sample source location | San Camilo, Ica, Peru (14°04′31.5″S 75°42′41.5″W) |

## 1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/nuccore/MAXB00000000

## 2. Introduction

Lima bean (*Phaseolus lunatus*) forms nitrogen-fixing symbioses with Alphaproteobacteria such as *Bradyrhizobium paxllaeri*, *Bradyrhizobium icense*, *Bradyrhizobium yuanmingense* and with other non-classified bradyrhizobial isolates [1,2]. Among them, *B. paxllaeri* is found associated with Lima bean in all areas of the central coast of Peru where this legume is grown [3,2]. The basis for this wide spread distribution of the species is presently unknown. Here we present the genome sequence and functional annotation of LMTR 21$^T$, the type strain of *B. paxllaeri* [4].

## 3. Experimental design, materials and methods

### 3.1. Strain culture and DNA isolation

*B. paxllaeri* LMTR 21$^T$ was grown in arabinose gluconate liquid medium [5] for 7 days at 28 °C. Cells from 1 ml culture were pelletized by centrifugation and genomic DNA was obtained with the DNA Isolation Kit for Cells and Tissues (Roche) according to the manufacturer's instructions. Quality and quantity of DNA was evaluated by spectrophotometry and gel electrophoresis.

### 3.2. Next generation sequencing and assembly

Two 500 bp-insert libraries were constructed using the Illumina TruSeq DNA nano kit following manufactures' instructions. Each library was run independently on an Illumina HiSeq machine to generate 90 bp

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http://dx.doi.org/10.1016/j.gdata.2017.06.008
Received 26 May 2017; Received in revised form 18 June 2017; Accepted 23 June 2017
Available online 30 June 2017

paired-end reads. Raw sequences were quality-trimmed with Trimmomatic [6] using the options SLIDINGWINDOW:4:15 and MINLEN:50 prior to assembly with SPAdes [7]. Completeness of the assembly was assessed with the BUSCO software [8].

### 3.3. Bioinformatics

Gene prediction and annotation was performed by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) [9] and the Rapid Annotations using Subsystems Technology server (RAST) [10] using default parameters.

## 4. Data description

### 4.1. Genomic features

The assembled sequence reached 100 × coverage and was distributed into 147 contigs with N50 size of 169,170 bp. Genome size and G + C content were estimated at 8.29 Mbp and 62.5%, respectively. All the genome was recovered in the assembly as completeness reached a score of 100%. The genome encoded 7635 CDS, 71 tRNAs and 3 rRNAs genes. Proteins with unknown functions (i.e. hypothetical proteins) represented 36% of the proteome. No plasmid replication proteins were found.

### 4.2. Overall functional annotation

Forty percent of the total CDS genes were assigned to RAST functional categories (Fig. 1). Genes devoted to metabolism (including catabolism) and transport of carbohydrates and amino acids were the most abundant in the LMTR 21$^T$ genome, probably reflecting a versatile life style as a soil, root and nodule inhabitant.

### 4.3. Symbiosis genes

The presence of *nodS*, *nodU* and *nolO* genes showed that this strain can produce nodulation factors decorated with methyl and two carbamoyl groups on the non-reducing end, while genes *nodZ*, *noeI* and *nolL* indicated that fucose with attached methyl and acetyl groups can be present on the reducing end [11]. An uptake hydrogenase gene cluster was found in the vicinity of nodulation genes indicating the ability for hydrogen recycling during symbiosis [12]. A copy of *nifV*, coding for homocitrate synthase, may suggest that LMTR21$^T$ is also able to perform free-living nitrogen fixation [13]. Strain LMTR 21$^T$ possessed all 15 *nif* genes which have been described to be required for biological nitrogen fixation in rhizobia [14] (Table 1).

**Table 1**
Nitrogen fixation (*nif*) genes encoded in the *B. paxllaeri* LMTR 21$^T$ genome.

| Gene | Function |
|---|---|
| *nifA* | Regulation |
| *nifH*, *nifD*, *nifK* | Nitrogenase structural gene |
| *nifZ* | Nitrogenase maturation |
| *nifB*, *nifE*, *nifN*, *nifX*, *nifQ*, *nifS*, *nifU*, *nifV* | FeMo-co biosynthesis |
| *nifT*, *nifW* | Unknown |

### 4.4. Traits involved in host colonization

A search for functions which may be involved in root or nodule colonization revealed genes for pilus assembly; adhesins; chemotaxis and motility; type III and IV secretion; siderophore production, exopolysaccharide and biotin biosynthesis; and quorum sensing.

## Nucleotide sequence accession numbers

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession MAXB00000000. The version described in this paper is version MAXB01000000.

## Conflict of interest

The authors declare no conflicts of interest in this study.

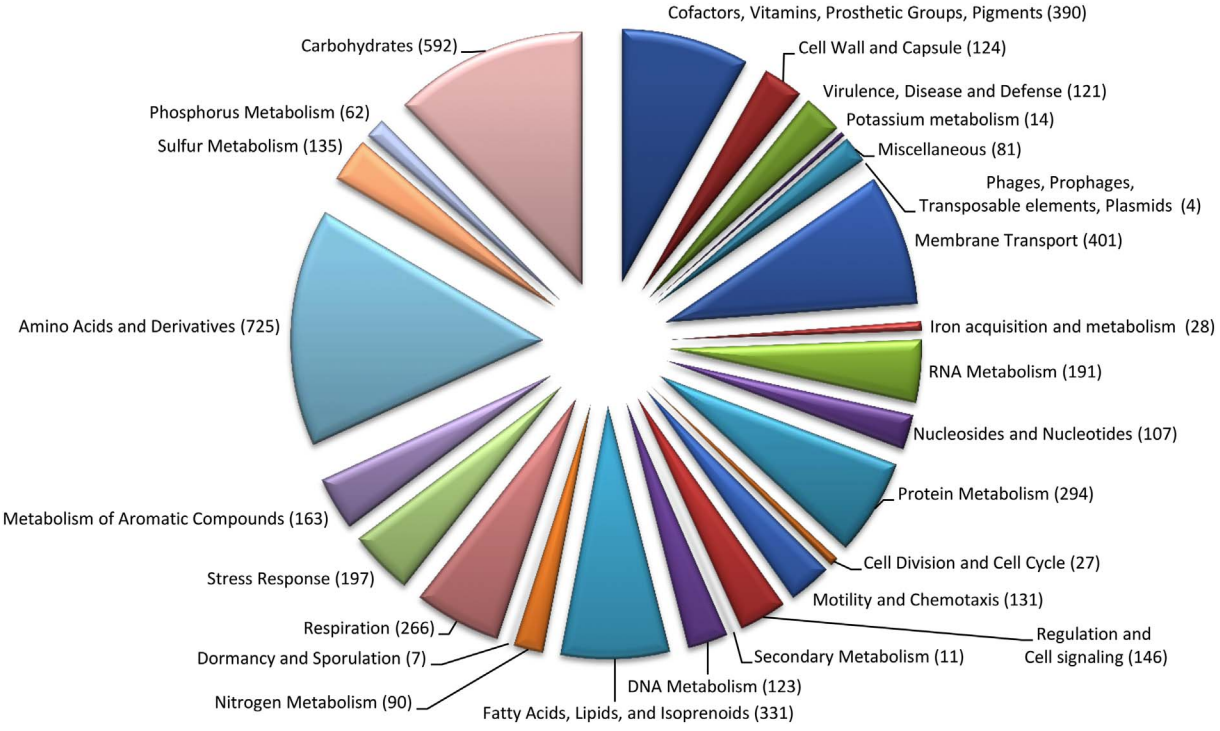


**Fig. 1.** CDS gene counts among RAST functional categories.

## Acknowledgements

This work was funded in whole or part by PNICP project 449-PNICP-BRI-2014. CC was funded by an “Isidro Parga Pondal” research fellowship from Xunta de Galicia (Spain). The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

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