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Data in brief

Draft genome sequence of *Mycobacterium tuberculosis* strain B9741 of Beijing B0/W lineage from HIV positive patient from SiberiaK.V. Shur^a, M.V. Zaychikova^a, N.E. Mikheecheva^a, K.M. Klimina^a, O.B. Bekker^a, S.N. Zhdanova^b, O.B. Ogarkov^b, V.N. Danilenko^{a,*}^a Laboratory of Bacterial Genetics, Vavilov Institute of General Genetics (VIGG RAS), Gubkina str. 3, 119991 Moscow, Russia^b Scientific Centre for Family Health and Human Reproduction Problems (SCFHHRP), Irkutsk, Russia

ARTICLE INFO

Article history:

Received 11 July 2016

Received in revised form 22 July 2016

Accepted 2 August 2016

Available online 3 August 2016

Keywords:

Mycobacterium tuberculosis

Virulence

Beijing lineage

HIV

draft genome sequencing

ABSTRACT

We report a draft genome sequence of *Mycobacterium tuberculosis* strain B9741 belonging to Beijing B0/W lineage isolated from a HIV patient from Siberia, Russia. This clinical isolate showed MDR phenotype and resistance to isoniazid, rifampin, streptomycin and pyrazinamide. We analyzed SNPs associated with virulence and resistance. The draft genome sequence and annotation have been deposited at GenBank under the accession NZ_LVJJ000000000.

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Specifications

| | |
|---------------------------|--|
| Organism/cell line/tissue | <i>Mycobacterium tuberculosis</i> B9741 |
| Sex | – |
| Sequencer or array type | 454 GS Junior, Roche |
| Data format | analyzed |
| Experimental factors | Genomic DNA isolated from sputum of 33 years old HIV + female patient |
| Experimental features | Whole genome sequence of <i>M. tuberculosis</i> , assembly and annotation, SNPs search |
| Consent | Citation |
| Sample source location | Scientific Centre for Family Health and Human Reproduction Problems (SCFHHRP), Irkutsk, Russia |

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/nuccore/NZ_LVJJ000000000.1

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2. Experimental design, materials and methods

2.1. Introduction

The Beijing genotype is commonly present in Russian population and in Eurasia as a whole. This lineage, especially B0/W subline is characterized by high-level virulence [1–4].

For our analysis, we chose the *Mycobacterium tuberculosis* strain B9741, isolated from a 33-years-old HIV-positive female patient from Irkutsk Oblast, Russia, with firstly diagnosed fibrocavernous tuberculosis, provided by the SCFHHRP, Irkutsk, Russia. This strain was resistant to isoniazid (INH), rifampin (RIF), streptomycin (SM) and pyrazinamide (PZA). The genomic DNA from *Mycobacterium tuberculosis* strain B9741 was purified by “PREP-NA” kit (“DNA-technology”, Russia).

2.2. Sequencing and data description

Genome sequencing was carried out on Roche 454 GS Junior instrument (Roche, Switzerland), in the Laboratory of Bacterial Genetics, VIGG RAS (Moscow, Russia). A total of 139,538 reads were generated. All reads were assembled to an initial draft genome: 4,322,170 bp (total length) nucleotides at 13-fold coverage using the GS *de novo* Assembler (version 3.0; Roche) (Table 1). The resulting draft genome sequence consists of 195 contigs. The automatic functional annotation results were

Table 1

Assembly statistics.

| | |
|---------------------------|---------|
| Number of aligned reads | 137,543 |
| Number of assembled reads | 134,468 |
| Number of contigs | 227 |
| Number of large contigs | 166 |
| Average contig size | 25,986 |
| N50 Contig size | 65,873 |
| Peak Depth | 13.0 |
| Estimated genome size | 4.8 MB |

obtained using NCBI Prokaryotic Genome Annotation Pipeline (PGAAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>).

The B9741 genome contains 4193 genes (total), 4 rRNAs, and 46 tRNAs. A total of 250 pseudogenes, 3 noncoding RNAs (ncRNAs), 1 clustered regularly interspaced short palindromic repeats (CRISPR) were predicted using the PGAAP.

According to housekeeping gene and toxin-antitoxin analysis [5,6], we classified this strain to belong to B0/W Beijing lineage. Analysis of *oxcA* gene showed that this strain belongs to B0/W subline [5]. We compared our output sequence with DNA sequence of the high-virulent *M. tuberculosis* W-148 strain which belongs to B0/W cluster of Beijing group [3]. In this announcement, we focused on genes, which determine virulence and drug resistance.

2.3. Results and discussion

We developed the catalog of 342 genes determinate virulence [1,2,4]. For this analysis, we have developed the program for identifying the SNPs [7]. In addition, we analyzed SNPs in genes, which are associated with drug resistance to INH, RIF, SM, and PZA. We found SNPs in INH resistance gene *katG*, RIF – *rpoB*, in SM – *rpsL*, *gidB* in PZA resistance gene *pncA* and *rpsA*.

For virulence genes analysis we provide the comparison of sequenced DNA with B0/W DNA sequences and revealed the presence of three polymorphisms at virulence genes. We carried out a deeper analysis of these genes involved in virulence. In the gene *mce3F*, which essential for survival of *Mtbs* in macrophages and invasion to the host cells, we have found substitution - D410A [8], in *irtB* gene, which encode the part of IrtAB iron importer - A175T [9,10]. This protein play an essential role for iron homeostasis in stress conditions. And in *vapC46* - A38G [11,12]. *VapC46* is a toxin of toxin-antitoxin pair *VapBC46*. These genes play a key role in survival in macrophages and transition to persistence. Thus, identified genes will be used for understanding of *M. tuberculosis* adaptation to patients with low immune level, including HIV + patients.

2.4. Nucleotide sequence accession number

- o This Whole Genome Shotgun (WGS) project has been deposited at GenBank under the accession LVJJ01000000 (*Mycobacterium tuberculosis* strain B9741).

Conflict of interest

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

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Acknowledgements

We thank Natalia Zakharevich for her assistance and fruitful discussion.

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