Data in brief

Draft genome sequence of **Mycobacterium tuberculosis** strain B9741 of Beijing B0/W lineage from HIV positive patient from Siberia

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**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_LVJJ00000000.

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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...
predicted using the PGAAP.

tered regularly interspaced short palindromic repeats (CRISPR) were

tRNAs. A total of 250 pseudogenes, 3 noncoding RNAs (ncRNAs), 1 clus-

tered 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 associ-

ated 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 se-

quenced DNA with B0/W DNA sequences and revealed the presence of

three polymorphisms at virulence genes. We carried out a deeper anal-

ysis of these genes involved in virulence. In the gene mce3F, which es-

sential for survival of Mtbs in macrophages and invasion to the host

cells, we found substitution - D410A [8], in irrB gene, which encode the part of IrrAB iron importer - A175T [9,10]. This protein play an es-

sential 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

peristence. 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

This Whole Genome Shotgun (WGS) project has been deposited at

GenBank under the accession LVJJ01000000 (Mycobacterium tuber-

culosis strain B9741).

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 clus-
tered 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

oxaA gene showed that this strain belongs to B0/W subtype [5]. We com-
pared 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.

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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