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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 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.

Specifications	
Organism/cell line/tissue	*Mycobacterium tuberculosis 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 M. tuberculosis, 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_LVJJ00000000.1

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 BO\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

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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

- 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.

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References

[1] N. Reiling, S. Homolka, K. Walter, J. Brandenburg, L. Niwinski, M. Ernst, C. Herzmann, C. Lange, R. Diel, S. Ehlers, S. Niemann, Clade-specific virulence patterns of *Mycobacterium tuberculosis* complex strains in human primary macrophages and aerogenically infected mice. MBio. 4 (2013), http://dx.doi.org/10.1128/mBio.00250-13.

[2] A.A. Prozorov, I.A. Fedorova, O.B. Bekker, V.N. Danilenko, The virulence factors of *Mycobacterium tuberculosis*: Genetic control, new conceptions. Russ. J. Genet. 50 (2014) 775–797, http://dx.doi.org/10.1134/S1022795414080055.

[3] I. Mokrousov, O. Narvskaya, A. Vyazovaya, T. Otten, W.W. Jiao, L.L. Gomes, P.N. Suffys, A.D. Shen, B. Vishnevsky, Russian "successful" clone B0/W148 of *Mycobacterium tuberculosis* Beijing genotype: A multiplex PCR assay for rapid detection and global screening. J. Clin. Microbiol. 50 (2012) 3757–3759, http://dx.doi.org/10.1128/JCM.02001-12.

[4] Y.P., B.I. Vishnevskiy, O.A. Manicheva, Mycobacterium tuberculosis. Russ. J. Infect. Immun. 4 (2004) 37–41 (doi:AJT724 [pii]\n10.1111/j.1600-6135.2004.00724.x).

[5] S. Homolka, M. Projahn, S. Feuerriegel, T. Ubben, R. Diel, U. Nubel, S. Niemann, High resolution discrimination of clinical *Mycobacterium tuberculosis* complex strains based on single nucleotide polymorphisms. PLoS One 7 (2012), e39855, http://dx.doi.org/10.1371/journal.pone.0039855\rPONE-D-12-02200 [pii].

[6] M.V. Zaychikova, N.V. Zakharevich, M.O. Sagaidak, N.A. Bogolubova, T.G. Smirnova, S.N. Andreevskaya, E.E. Larionova, M.G. Alekseeva, L.N. Chernousova, V.N. Danilenko, *Mycobacterium tuberculosis* Type II toxin-antitoxin systems: genetic polymorphisms and functional properties and the possibility of their Use for genotyping. PLoS One 10 (2015), e0143682, http://dx.doi.org/10.1371/journal.pone.0143682.

[7] M. Zaychikova, N. Mikheecheva, V.N. Danilenko, Genetic Determinants of *M. tuberculosis* Pathogenicity. 2016.

[8] S. Ahmad, S. El-Shazly, A.S. Mustafa, R. Al-Attiyah, Mammalian cell-entry proteins encoded by the mce3 operon of *Mycobacterium tuberculosis* are expressed during natural infection in humans. Scand. J. Immunol. 60 (2004) 382–391, http://dx.doi.org/10.1111/j.0300-9475.2004.01490.x.

[9] A. Farhana, S. Kumar, S.S. Rathore, P.C. Ghosh, N.Z. Ehtesham, A.K. Tyagi, S.E. Hasnain, Mechanistic insights into a novel exporter-importer system of *Mycobacterium tuberculosis* unravel its role in trafficking of iron. PLoS One 3 (2008), http://dx.doi.org/10.1371/journal.pone.0002087.

[10] G.M. Rodriguez, I. Smith, Identification of an ABC transporter required for iron acquisition and virulence in *Mycobacterium tuberculosis*. J. Bacteriol. 188 (2006) 424–430, http://dx.doi.org/10.1128/JB.188.2.424-430.2006.

[11] V.L. Arcus, P.B. Rainey, S.J. Turner, The PIN-domain toxin-antitoxin array in mycobacteria. Trends Microbiol. 13 (2005) 360–365, http://dx.doi.org/10.1016/j.tim.2005.06.008.

[12] A. Sala, P. Bordes, P. Genevaux, Multiple toxin-antitoxin systems in *Mycobacterium tuberculosis*. Toxins (Basel) 6 (2014) 1002–1020, http://dx.doi.org/10.3390/toxins6031002.