



Data Article

Draft genome sequence data of *Microbacterium* sp. strain Be9 isolated from uranium-mill tailings porewaters



Pablo Martínez-Rodríguez^{1,*}, Iván Sánchez-Castro¹,
Michael Descostes², Mohamed L. Merroun¹

¹ Department of Microbiology, University of Granada, Campus Fuentenuueva s/n, 18071 Granada, Spain

² R&D Department, Orano Mining, Chatillon, 92330, France

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ABSTRACT

Microbacterium are Gram-positive, nonspore-forming, rod-shaped bacteria inhabiting a wide range of environments including soil, water, dairy products, other living organisms, etc. *Microbacterium* sp. strain Be9, isolated from mill tailings porewaters in France, shows a remarkable behavior in presence of uranium under distinct conditions, which is the main reason for the interest in sequencing its genome. In this work, we describe the draft genome sequence of Be9, comprising 4,046,806 bp, with a G+C content of 68.10% and containing 3,947 protein-coding sequences. The preliminary genome annotation analysis identified some genes encoding for resistance to antibiotics and toxic compounds like heavy metals. This draft genome has been deposited at DDBJ/ENA/GenBank under the accession PRJNA590666.

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* Corresponding author(s):

E-mail address: pmartinez@ugr.es (P. Martínez-Rodríguez).

Specifications Table

Subject	Biology
Specific subject area	Bacterial Genomics, Applied Microbiology and Biotechnology
Type of data	Table
How data were acquired	Figure Genome sequencing: Illumina Novaseq platform and CLC Genomics Workbench 12.0. Bioinformatics approaches: Rapid Annotation using Subsystems Technology (RAST), RNAMmer v1.2 and tRNAscan-SE v. 2.0.
Data format	Raw and Analyzed
Parameters for data collection	Genomic DNA was extracted from a pure culture of Be9 isolate. Raw high-quality reads were generated through next-generation sequencing and a list of contigs was generated through <i>de novo</i> assembly.
Description of data collection	Genomic DNA extracted from <i>Microbacterium</i> sp. Be9 strain, following draft genome assembly and annotation.
Data source location	Region: Bellezane, Limousin Country: France Latitude and longitude (and GPS coordinates) for collected samples: 46°5'49.09"N, 1°23'28.51"E
Data accessibility	Genome assembly and raw FASTQ reads data are available in Mendeley Data repository. Draft genome has been also deposited at DDBJ/ENA/GenBank with BioProject number: PRJNA590666 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA590666), BioSample number: SAMN13336457 under the accession WNW00000000 (https://www.ncbi.nlm.nih.gov/nucleotide/WWN00000000). The version described in this paper is version WNW01000000.
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Value of the Data

- Draft genome sequence provides molecular information of *Microbacterium* sp. Be9 strain about its behavior with toxic ions as heavy metals.
- Data of Be9 strain will be useful to further study its taxonomical affiliation.
- Draft genome of *Microbacterium* sp. Be9 strain will provide further information of protein-coding sequences involved in uranium tolerance and to elucidate the active and/or passive mechanisms involved in U uptake and biomineralization.

1. Data Description

Microbacterium spp. are Gram-positive, nonspore-forming and rod-shaped. Strains of the genus are distributed widely, such as in soil, water, dairy products or other living organisms [1–3]. *Microbacterium* sp. Be9 strain was isolated from porewaters sampled in mill tailings, located near Bessines-sur-Gartempe (Limousin, France). By a 16S rRNA gene sequence analysis (unpublished data), we classified Be9 within the genus *Microbacterium*. In previous studies, isolate Be9 was evaluated and displayed high tolerance values for different metals/metalloids as U, Pb, Se or Zn [4], indicating that this strain may have a potential ability in bioremediation of heavy metals. Based on this fact and other previous experiments (unpublished data), we selected *Microbacterium* sp. Be9 for genome sequencing to identify genes potentially involved in its uranium removal ability (Table 1). The draft genome was comprised by 14 contigs, with 4,046,806 bp in length and N50 value of 1,332,702. The G+C content of the sequence was 68.10%. Main assembly statistics of the draft genome are shown in Table 2. Three copies of rRNA genes were predicted in the genome by using the RNAMmer V1.2 [5] while 50 copies of tRNA were anticipated by tRNAscan-SE v. 2.0 [6].

Table 1Project features and general information of *Microbacterium* sp. Be9 strain according to MIGS recommendations [9].

Property	Term	Evidence code ^a
Geographic location	Limousin/France	TAS
Latitude	46°5'49.09" N	TAS
Longitude	1°23'28.51" E	TAS
Depth	25 m	TAS
Time of sample collection	March 2012	TAS
Habitat	Groundwater	TAS
Number of replicons	-	-
Extrachromosomal elements	-	-
Reference for biomaterial	dx.doi.org/10.1016/j.jenvrad.2016.03.016	TAS
Source material identifiers	Still not deposited	-
Pathogenicity	Unknown	-
Biotic relationship	Free-living	TAS
Specific host	Environmental	TAS
Trophic level	Heterotroph	TAS
Oxygen requirement	Aerobic	TAS
Isolation and growth conditions	Isolated in R2A medium at 28°C	TAS
Nucleic acid preparation	Genomic DNA extraction [8]	IDA
Sequencing method	150bp paired-end sequencing reads	IDA
Assembly	<i>De novo</i> assembly, based on <i>de Bruijn</i> graphs [7]	IDA
Finishing quality	Draft sequence	IDA
Sequencing platforms	Illumina Novaseq	IDA
Fold coverage	462x	IDA

^a Evidence codes - IDA: inferred from direct assay; TAS: traceable author statement (i.e., a direct report exists in the literature). These evidence codes are from the Gene Ontology project [10].

Table 2Main *de novo* assembly statistics of Be9 draft genome

Feature	Value
Contig count	14
Total contigs length (bp)	4,046,806
Total number of aligned bases (Mbp)	1,871
N50 (bp)	1,332,702
N75 (bp)	370,482
Maximum contig length (bp)	1,434,936
Average contig length (bp)	289,057
G+C content	68.10%
rRNA genes	3
tRNA genes	50

A total of 3947 protein-coding sequences were predicted using Rapid Annotation Subsystem Technology (RAST) [11], where 1002 coding sequences (26%) were annotated as seed subsystem features and 2945 coding sequences (74%) as outside of the seed subsystem. Most of the annotated genes (Fig. 1) determined the synthesis of amino acids and derivatives (306), carbohydrates (206), protein metabolism (171) and cofactors, vitamins, prosthetic groups and pigments (148). As well, the strain Be9 possesses a substantial number of genes responsible for resistance to antibiotics and toxic compounds (36), membrane transport (78) and stress response (26). In the genome of *Microbacterium* sp. Be9 was uncovered the presence of *amt* gene, whose expression was regulated in response to ammonium availability to ensure an adequate supply of nitrogen during in-situ uranium bioremediation [12]. Cobalt-zinc-cadmium resistance protein coding region (*CzcD*) was found in the draft genome of Be9 as well as in other *Microbacterium* species exposed to high metal concentrations, suggesting a relevant role implicated in its tolerance [13]. In addition, the Be9 genome annotation suggested the presence of ABC-type Fe³⁺ siderophore transport proteins related to iron metabolism whose levels were increased under uranium stress as it was reported earlier [14]. Numerous genes involved in the interaction with

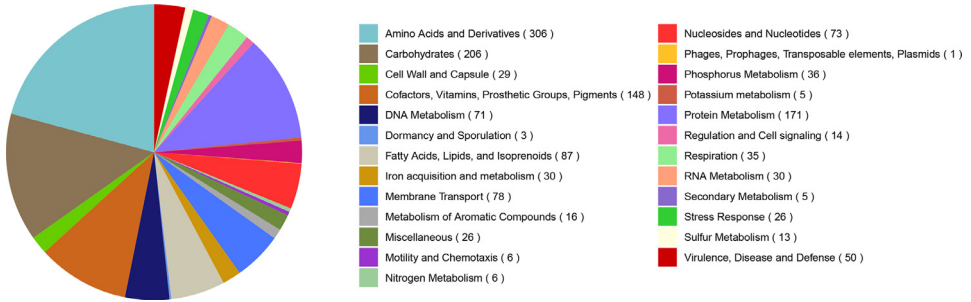


Fig. 1. An overview of the subsystem categories assigned to the genome of *Microbacterium* sp. Be9 strain. Genome sequence was annotated using Rapid Annotation System Technology (RAST) server.

metals/metalloids like copper (*CopC* and *CopD*), selenate and selenite (*DedA*), zinc (*Ypff*) and arsenic (*ArsR*, *ArsB*, *ArsC* and *ACR3*) were also detected.

2. Experimental Design, Materials, and Methods

2.1. Isolation of *Microbacterium* sp. Be9 strain

Microbacterium sp. Be9 strain was isolated from uranium-containing porewaters of mill tailings, located near Bessines-sur-Gartempe (Limousin, France). These porewaters were collected from a monitoring well at 25 m depth, using an inertial water-pump (WaTerra Pumps Ltd.) and sterilized high-density polyethylene (HDPE) tubing and storing HDPE containers. At the time of sampling, pH and Eh of porewater were 6.25 and 161 mV/SHE respectively. The strain was isolated in R2A oligotrophic medium (low-nutrient medium) [15] and incubated at 28°C for 3 days.

2.2. DNA isolation and sequencing

Biomass of Be9 strain was grown in LB solid medium for 24h at 28°C, and genomic DNA extraction was performed as described by Martín-Platero [8]. One μL of gDNA sample was used to test the integrity and purity by 1.5% agarose gel electrophoresis. Afterwards, the sample was quantified using the Qubit 3.0 Fluorometer (Life Technology) and used for library construction using the TruSeq DNA Whole genome library preparation kit (Illumina, USA). The generated DNA fragments (DNA libraries) were sequenced using the Illumina Novaseq platform, using 150bp paired-end sequencing reads. Low-quality reads were trimmed by CLC Genomics Workbench 12.0 to generate 14,144,710 reads with mean read length of 150bp.

2.3. Genome assembly and annotation

Quality-filtered reads were *de novo* assembled using an algorithm based on de Bruijn graphs performed by CLC Genomics Workbench 12.0 and resultant genome assemblies were evaluated with QCAST 5.0.2 [16]. The final 4,046,806-bp-long genome assembly was functionally annotated through Rapid Annotation System Technology (RAST) server using the default RASTtk parameter [11]. Additionally, assembled sequence was uploaded to RNAmmer v1.2 [5] and tRNAscan-SE v. 2.0 [6] to predict the rRNA and tRNA genes respectively.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships which have, or could be perceived to have, influenced the work reported in this article.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi: [10.1016/j.dib.2020.105732](https://doi.org/10.1016/j.dib.2020.105732).

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