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Complete genome sequence of the biofilm-forming *Microbacterium* sp. strain BH-3-3-3, isolated from conventional field-grown lettuce (*Lactuca sativa*) in Norway

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ABSTRACT

The genus *Microbacterium* contains bacteria that are ubiquitously distributed in various environments and includes plant-associated bacteria that are able to colonize tissue of agricultural crop plants. Here, we report the 3,508,491 bp complete genome sequence of *Microbacterium* sp. strain BH-3-3-3, isolated from conventionally grown lettuce (*Lactuca sativa*) from a field in Vestfold, Norway. The nucleotide sequence of this genome was deposited into NCBI GenBank under the accession CP017674.

Specifications	
Organism/cell line/tissue	*Microbacterium* sp.
Strain	BH-3-3-3
Sequencer or array type	PacBio RS II
Data format	Analyzed
Experimental factors	Bacterial strain
Experimental features	Whole genome analysis and gene annotation of BH-3-3-3
Sample source location	Lettuce (*Lactuca sativa*) from a conventional field in Vestfold, Norway

1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/nuccore/CP017674.

2. Experimental design, materials and methods

The Gram-positive genus *Microbacterium* belongs to the family Microbacteriaceae, within the phylum Actinobacteria. *Microbacterium* spp. have been isolated from diverse environments including agricultural crop plants [1–4]. An orange-pigmented *Microbacterium* sp. strain (BH-3-3-3) was isolated from the leaf surface of lettuce (*Lactuca sativa*) originating from a conventional field in Vestfold, Norway [5]. Genomic DNA was extracted using Genomic-tip 500/G kit (Qiagen GmbH, Hilden, Germany), a library was created using PacBio (Pacific Biosciences, California, USA) 20 kb library preparation protocol and whole genome sequencing was performed using PacBio RS II. The library was sequenced using P6-C4 chemistry with 360 min movie time on one single-molecule real-time (SMRT) cell. The reads were assembled using HGAP v3 (Pacific Biosciences, SMRT Analysis Software v2.3.0). The minimus2 software of the Amos package was used to circularize the contig, which was confirmed by a dot plot to contain the same sequence at the beginning and end of the contig. RS_Resequencing.1 software (SMRT Analysis version v2.3.0) was used to map reads back to the assembled and circularized sequence in order to correct the sequence after circularization. The sequencing service was provided by the Norwegian Sequencing Centre (www.sequencing.uio.no), a national technology platform hosted by the University of Oslo and supported by the "Functional Genomics" and "Infrastructure" programs of the Research Council of Norway and the Southeastern Regional Health Authorities.

3. Data description

The genome of *Microbacterium* sp. BH 3-3-3 was annotated using NCBI Prokaryotic Genome Annotation Pipeline [6], GeneMarkS + v 3.3 and the Rapid Annotation System Technology (RAST) server [7]. Fig. 1 presents an overview of the count of each subsystem feature and the subsystem coverage. The circular chromosome has a GC content of 70.5%, consisted of 3,508,491 bp and contained 3113 coding sequences (CDSs), 9 rRNA genes, 45 tRNAs, and 3 noncoding RNA (ncRNA) genes.

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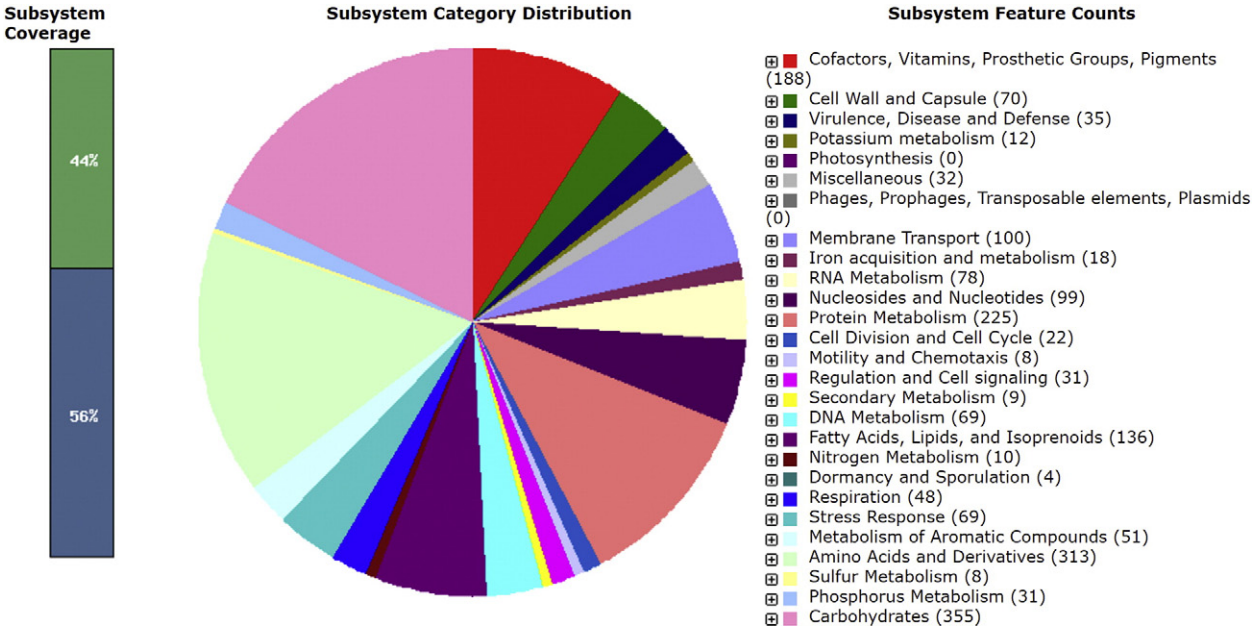

Fig. 1. Subsystem category distribution of major protein coding genes of *Microbacterium* sp. strain BH 3-3-3 as annotated by the RAST annotation server. The bar chart shows the subsystem coverage in percentage (blue bar corresponds to percentage of proteins included). The pie chart shows percentage distribution of the 25 most abundant subsystem categories.

4. Nucleotide accession number

This whole genome project has been deposited at NCBI GenBank under the accession number CP017674.

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