Draft genome sequence of *Bacillus oleronius* DSM 9356 isolated from the termite *Reticulitermes santonensis*

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ABSTRACT

Bacillus oleronius strain DSM 9356 isolated from the termite *Reticulitermes santonensis* was sequenced to gain insights in relation to its closest phylogenetic neighbor *Bacillus sporothermodurans*. The draft genome of strain DSM 9356 contains 5,083,966 bp with an estimated G + C content of 35%, 4899 protein-coding genes, 116 tRNAs and 18 rRNAs. The RAST annotation assigned these genes into 462 subsystems, with the maximum number of genes associated with amino acids and derivatives metabolism (14.84%), followed by carbohydrates (13.89%) and protein metabolism subsystems (9.10%). The draft genome sequence and annotation has been deposited at NCBI under the accession number MTLA00000000.

Specifications

Organism	*Bacillus oleronius*
Strain	DSM 9356
Sequencer	Illumina MiSeq
Data format	Assembled
Experimental factors	Genome sequence of pure microbial culture
Experimental features	Genome sequence followed by assembly and annotation
Consent	N/A
Sample source	île d'Oleron, France

1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/nuccore/MTLA00000000

2. Experimental design, materials and methods

The genus *Bacillus* is a group of Gram-positive, rod-shaped bacteria distributed extensively in the environment. Their ubiquity in nature is because of their ability to produce endospores during adverse conditions. *Bacillus* species includes pathogens of clinical significance, bacterial contaminants in food and as important industrial organisms producing various enzymes. *Bacillus oleronius* is a non-motile endospore-forming bacterium which was originally isolated from the hindgut of the termite *Reticulitermes santonensis* (Feytaud), where it plays a symbiotic role by aiding digestion [1]. It is also found in the human skin parasitic mite *Demodex folliculorum*, and is suspected to be related to the development of rosacea, a chronic inflammatory dermatological condition in humans [2]. A school of thought is that *Demodex* mites are vectors for bacteria including *Staphylococcus albus* and *Microsporon canis* [3], and of interest, *B. oleronius* that cause and exacerbate skin lesions [4].

Despite staining Gram-negative, *B. oleronius* has Gram-positive cell wall components shared amongst all *Bacillus* species [5] and thus closely related to other *Bacillus* sp. that contaminate foods. Although initially isolated from the hindgut of the termite and subsequently from mites, *B. oleronius* has been identified as a potential contaminant of milk and dairy products and has been sporadically identified and isolated from fodder, raw milk and milk processing equipment [6–9]. *B. oleronius* is associated with the *Bacillus firmus-lentus* group [1], with its 16S rRNA sequence 95.6% and 95.5% similar to that of *B. lentus* and *B. firmus* respectively. However, its closest phylogenetic neighbor is the highly heat resistant spore forming *B. sporothermodurans* [10], which may survive ultra-high temperature processing conditions during milk processing. Albeit not as heat resistant as *B. sporothermodurans*, *B. oleronius* spores has been known to survive milk pasteurization, with spores isolated after 30 min heating at 100 °C [6]. In this study, the type strain RT10 (DSM 9356) of *B. oleronius*, procured from the Leibniz Institute in Germany was selected for whole genome sequencing. The principal reason is to enhance understanding of this bacterium in relation to other spore-forming *Bacillus* species of importance to the dairy industry. The dataset has been submitted to NCBI and is reported here.

Overnight fresh culture of *B. oleronius* was inoculated into nutrient agar broth (Oxoid, UK) and incubated at 37 °C for 24 h. Genomic DNA

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Table 1
B. oleronius DSM 9356 genome characteristics and resources.

S. no	Name	Genome characteristics and resources
1	NCBI Bioproject ID	PRJNA362282
2	NCBI Biosample ID	SAMN06237156
3	NCBI genome accession number	MTLA00000000
4	Sequence type	Illumina MiSeq
5	Total number of reads	2,305,932
6	Read length	300
7	Overall coverage	>100×
8	Estimated genome size	5,083,966 bp
9	G + C content (%)	35.00
10	Genes (total)	5168
11	Protein coding genes	4899
12	tRNA coding genes	116
13	rRNA coding genes	18
14	ncRNA coding genes	5
15	Pseudogenes	130

was extracted using the ZR Bacterial DNA Miniprep kit (Zymo Research, USA). DNA extract was quantified using the Qubit instrument and dsDNA BR Assay kit (Life Technologies, USA). Multiplexed paired-end libraries were prepared using Nextera XT DNA Sample Preparation kit (Illumina, USA). Genome sequencing was carried out on an Illumina MiSeq system (Illumina, San Diego, USA). The paired-end reads were checked for quality, trimmed and de novo assembled using the Qiagen CLC Genomics Workbench version 9 (Qiagen, Netherlands). All resultant contigs were then submitted to GenBank, where gene annotation was implemented using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) [11]. The annotation was further uploaded to Rapid Annotation using Subsystem Technology (RAST) for subsystems-based annotation [12–14].

The assembly contains 587 contig sequences of longer than 500 bp, covers 5,083,966 bp with G + C content of 35.00%, an N_{50} of 543,331 bp and a longest contig size of 90,648 bp. The total number of 5168 genes predicted by PGAP includes 4899 protein coding genes, 130 pseudo genes, and 139 RNA genes (Table 1). The RAST annotation assigned these genes into 462 subsystems, with maximum number of genes associated with amino acids and derivatives metabolism (14.84%), followed by carbohydrates (13.89%) and protein metabolism subsystems (9.10%) (Fig. 1).

2.1. Nucleotide sequence accession number

The draft genome sequence of B. oleronius DSM 9356 has been deposited at NCBI under the BioProject number PRJNA362282, BioSample number SAMN06237156 and Accession number MTLA00000000.

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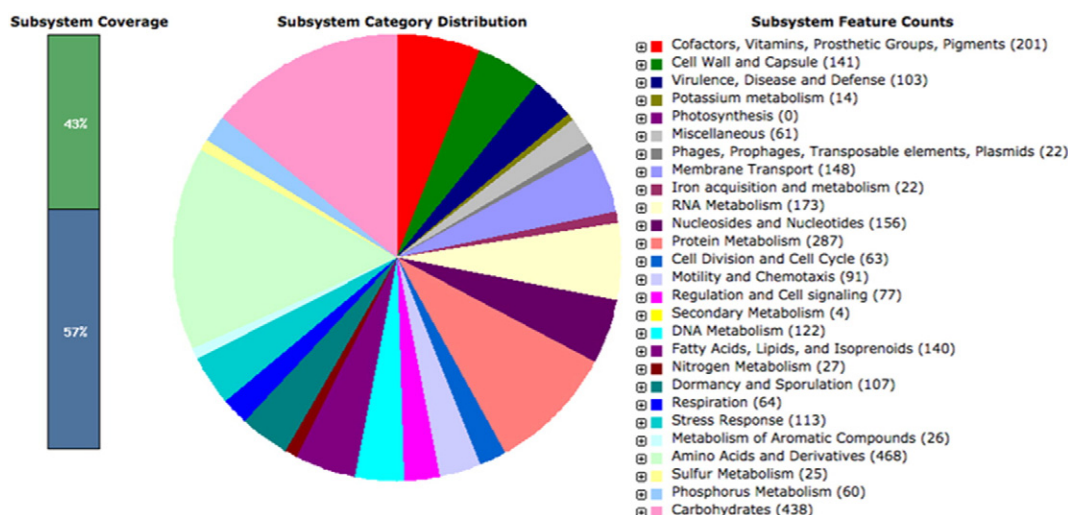

Fig. 1. Distribution and counts of genes in COG categories for genome of Bacillus oleronius strain DSM 9356.

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