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.

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**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 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
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, 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 results of the assembly contained 587 contig sequences of longer than 500 bp, covers 5,083,966 bp with G + C content of 35.00%, an N50 of 543,331 bp and a longest contig size of 90,648 bp. The total number of genes associated with amino acids and derivatives metabolism (14.84%), followed by carbohydrates (13.89%) and protein metabolism (9.10%) (Fig. 1).

2.1. Nucleotide sequence accession number

The draft genome sequence of \textit{B. oleronius} DSM 9356 has been deposited at NCBI under the BioProject number PRJNA362282, BioSample number SNAV06237156 and Accession number MTLA00000000.

**Table 1**

\begin{tabular}{|c|c|}
\hline
\textbf{S. no} & \textbf{Name} & \textbf{Genome characteristics and resources} \\
\hline
1 & NCBI Bioproject ID & PRJNA362282 \\
2 & NCBI Bio sample 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 & rRNA coding genes & 116 \\
13 & tRNA coding genes & 18 \\
14 & ncRNA coding genes & 5 \\
15 & Pseudogenes & 130 \\
\hline
\end{tabular}

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