



## Draft genome sequence of *Paenibacillus algorifonticola* sp. nov., an antimicrobial-producing strain



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### ABSTRACT

*Paenibacillus algorifonticola* sp. nov. is isolated from a cold spring sample from Xinjiang Uyghur Autonomous Region (China), a novel strain that can produce antimicrobial substance against human pathogenic bacteria and fungi, including *Staphylococcus aureus* and *Candida albicans*. Here we report a 7.60-Mb assembly of its genome sequence and other useful information, including the coding sequences (CDSs) responsible for the biosynthesis of antibacterial factors, anaerobic respiration and several immune-associated reactions. Also, prospective studies on *P. algorifonticola* sp. nov. in the cold spring might offer a potential source for the discovery of bioactive compounds with medical value. The data repository is deposited on the website <http://www.ncbi.nlm.nih.gov/nuccore/LAQO00000000> and the accession number is LAQO00000000.

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### Specifications

|                         |   |
|-------------------------|---|
| Organism/cell/tissue    | <i>Paenibacillus algorifonticola</i> sp. nov.   |
| Strain                  | XJ259 <sup>T</sup>  |
| Sequencer or array type | Illumina Hiseq 2000   |
| Data format             | Raw and processed   |
| Experimental factors    | DNA extracted from a wild-type strain, no treatment                                       |
| Experimental features   | Draft genome sequencing of <i>Paenibacillus algorifonticola</i> , assembly and annotation |
| Consent                 | N/A   |
| Sample source location  | a cold spring sample from Xinjiang Uyghur Autonomous Region (China)                       |

### 1. Direct link to deposited data

<http://www.ncbi.nlm.nih.gov/nuccore/LAQO00000000>

A large-scale metagenomic-based study revealed that the microbes with antibiotic resistance genes are abundant and diverse in nature [1]. However, the widespread misuse or abuse of antibiotics in clinical practice has led to a large number of antibiotic-resistant pathogenic bacteria such as *Staphylococcus aureus* and *Candida albicans*. Recently,

our group has isolated from a cold spring sample from Xinjiang Uyghur Autonomous Region (China) with a novel species of *Paenibacillus algorifonticola* sp. nov., named XJ259<sup>T</sup> (= CGMCC 1.10223<sup>T</sup> = JCM16598<sup>T</sup>), which can produce water-soluble constituents with the significant inhibitory activity against both *S. aureus* and *C. albicans* [2]. Comparisons with 16S rRNA gene sequences as shown in Fig. 1 revealed that the novel strain (1519 nt) had the highest similarity to *Paenibacillus xinjiangensis* B538<sup>T</sup> (96.6%) [3]. However, the phylogenetic distances from recognized species (Fig. 2) indicated that *P. algorifonticola* is not affiliated to any of these recognized species and the proportion of saturated straight-chain fatty acid C<sub>16:0</sub> was relatively high [2]. We can therefore conclude that this strain represents a novel species of the genus *Paenibacillus*. In consequence, investigation of the genetic information and characteristics of *P. algorifonticola* is desired to further investigate its mechanism of metabolic regulation. Knowledge of the genome sequence and bioinformatics will be of great help in this regard.

Here we present the draft genome sequence of strain *P. algorifonticola* XJ259<sup>T</sup> obtained using Illumina Hiseq 2000 system. The reads were assembled with SOAPdenovo [4,5], the version is 2.04, and the sequence was annotated using the RAST annotation server (Fig. 3) [6], and the KEGG metabolic pathway was also constructed (Fig. 4). A library containing 500-bp inserts was constructed. Sequencing was performed based on the paired-end strategy of 478-bp reads to produce 1161 Mb of filtered sequences, representing a 132-fold coverage of the genome. The sequence

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of *P. alborfonticola* is 7,495,641 bases with a G + C content of 48.39%, which was assembled into 115 contigs and 101 scaffolds. It contains 7048 open reading frames (ORFs), 70 tRNA genes, and 4 rRNA genes (Table 1) identified by Glimmer 3.02 [7], Genemark [8], tRNAscan-SE [9], and RNAmmer [10].

According to the genomic analysis of the strain *P. alborfonticola*, we identified 6 neutrophil extracellular traps (NETs)-associated proteins, including the calcium ion binding protein and cytoplasmic

calprotectin protein complex (e.g., Mrp8/14-complex or S100A8/A9) with potent antimicrobial properties [11]. We also identified 6 ORFs relate to the immune-associated reactions, including the nucleotide-binding oligomerization domain(NOD)-like receptor signaling pathway, antigen processing and immune-responsive domain IPR011614. The strain *P. alborfonticola* can also utilize other complex immune responses that lead to production of soluble effectors, including 14 antimicrobial peptides (AMPs), or to

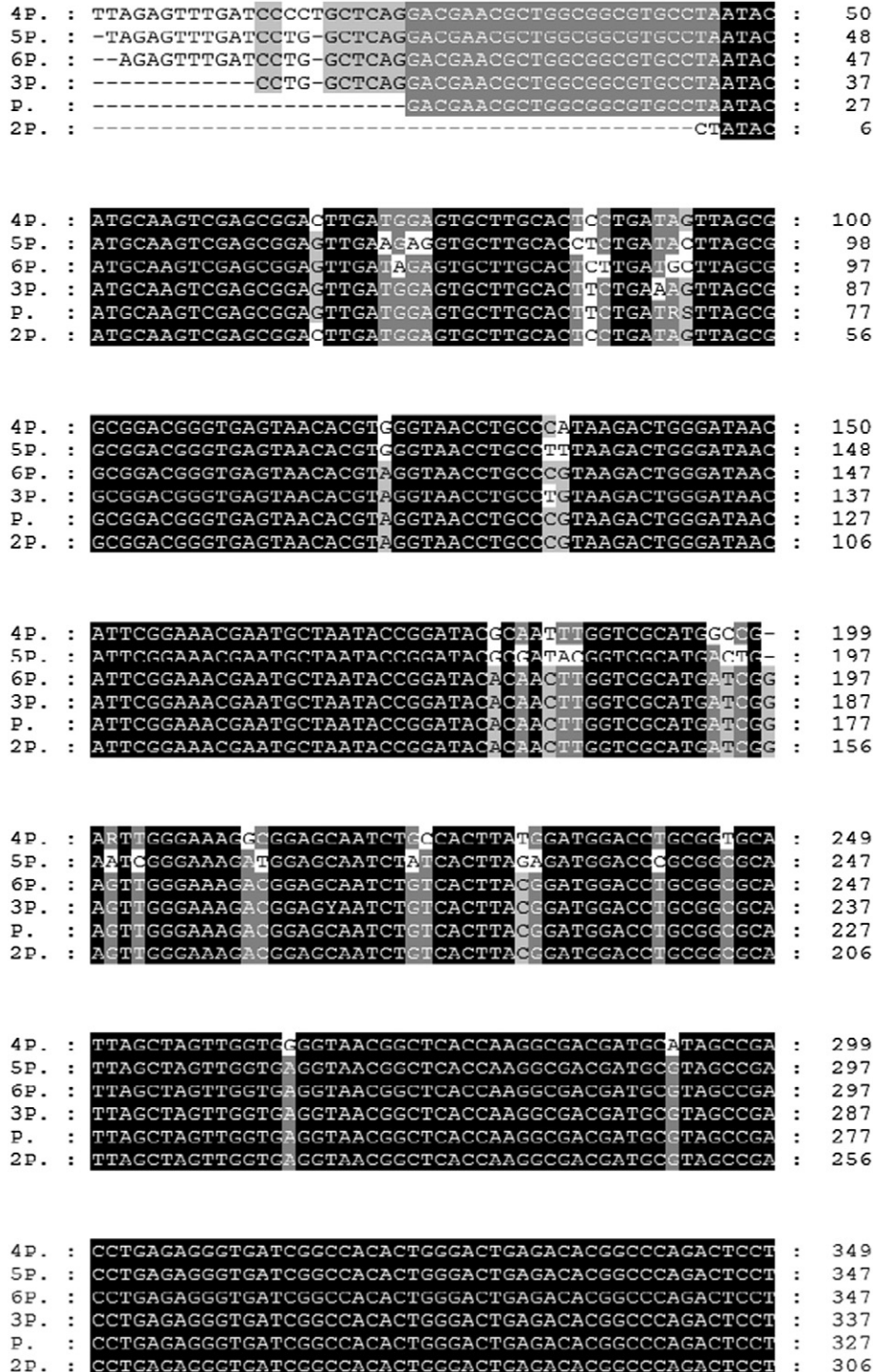


Fig. 1. Multiple sequences alignment of *Paenibacillus* (P: *Paenibacillus telluris*; 2P: *Paenibacillus* sp. LNUB461; 3P: *Paenibacillus telluris* strain JS01-08; 4P: *Paenibacillus xinjiangensis* strain B538; 5P: *Paenibacillus castaneae* strain Ch-32; 6P: *Paenibacillus alborfonticola*).

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