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

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ARTICLE INFO

Article history: Received 1 June 2015 Received in revised form 11 June 2015 Accepted 16 June 2015 Available online 2 July 2015

Keywords: Paenibacillus algorifonticola Cold spring Antimicrobial factors Genome analysis

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 bio-synthesis 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/LAQ000000000 and the accession number is LAQ000000000.

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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 $X[259^{T}] = CGMCC$

 $1.10223^{T} = [CM16598^{T})$, which can produce water-soluble constit-

uents 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 xiniiangensis B538^T (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_{16:0} 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 informa-

tion 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

XJ259^T obtained using Illumina Hiseq 2000 system. The reads were as-

sembled 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

Here we present the draft genome sequence of strain P. algorifonticola

Specifications

Organism/cell/tissue Paenibacillus algorifonticola sp. nov. Strain XI259¹ Illumina Hiseq 2000 Sequencer or array type Data format Raw and processed DNA extracted from a wild-type strain, no treatment Experimental factors Experimental Draft genome sequencing of Paenibacillus algorifonticola, assembly and annotation features Consent N/A a cold spring sample from Xinjiang Uyghur Autonomous Sample source location Region (China)

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/nuccore/LAQ00000000

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,

http://dx.doi.org/10.1016/j.gdata.2015.06.023

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regard.







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of *P. algorifonticola* 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. algorifonticola*, we identified 6 neutrophil extracellular traps (NETs)-associated proteins, including the calcium ion binding protein and cytoplasmic

calprotecin 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. algorifonticola* can also utilize other complex immune responses that lead to production of soluble effectors, including 14 antimicrobial peptides (AMPs), or to

4P. : TTAGAGTTTGATCCCCTGCTCAG GACGAACGCTGGCGGCGTGCCTAATA 5P. : -TAGAGTTTGATCCTG-GCTCAG GACGAACGCTGGCGGCGTGCCTAATA 6P. :AGAGTTTGATCCTG-GCTCAG GACGAACGCTGGCGGCGTGCCTAATA 3P. :CCTG-GCTCAG GACGAACGCTGGCGGCGTGCCTAATA P. :CCTG-GCTCAG GACGAACGCTGGCGGCGTGCCTAATA 2P. :		50 48 47 37 27 6
4P. : ATGCAAGTCGAGCGGAC TTGATGCAGTGCTTGCACTCCTGATACTTAGC 5P. : ATGCAAGTCGAGCGGAC TTGAACAGGTGCTTGCACCTCTGATACTTAGC 6P. : ATGCAAGTCGAGCGGAC TTGAACAGGTGCTTGCACTCTGATGCTTAGC 3P. : ATGCAAGTCGAGCGGAC TTGATGCAGTGCTTGCACTCTGAAGCGAGCGGAC P. : ATGCAAGTCGAGCGGAC TTGATGCAGTGCTTGCACTCTGAAGCTTAGC 2P. : ATGCAAGTCGAGCGGAC TTGATGCAGTGCTTGCACTCCGATACTTAGC 2P. : ATGCAAGTCGAGCGGAC TTGATGCAGTGCATGCACTCCGATACTTAGC	6 : 6 : 6 :	100 98 97 87 77 56
4P. : GCGGACGGGTGAGTAACACGTGGGTAACCTGCCCATAAGACTGGGATAA5P. : GCGGACGGGTGAGTAACACGTGGGTAACCTGCCTTTAAGACTGGGATAA6P. : GCGGACGGGTGAGTAACACGTAGGTAACCTGCCCTAAGACTGGGATAA3P. : GCGGACGGGTGAGTAACACGTAGGTAACCTGCCCTTAAGACTGGGATAAP. : GCGGACGGGTGAGTAACACGTAGGTAACCTGCCCCTAAGACTGGGATAA2P. : GCGGACGGGTGAGTAACACGTAGGTAACCTGCCCCTAAGACTGGGATAA	0 : : 0 : : : 0 :	150 148 147 137 127 106
4P. : ATTCGGAAACGAATGCTAATACCGGATACGCAATTTGGTCGCATGGCCG 5P. : ATTCGGAAACGAATGCTAATACCGGATACGCGATACGGTCGCATGACTG 6P. : ATTCGGAAACGAATGCTAATACCGGATACACAACTTGGTCGCATGATCG 3P. : ATTCGGAAACGAATGCTAATACCGGATACACAACTTGGTCGCATGATCG P. : ATTCGGAAACGAATGCTAATACCGGATACACAACTTGGTCGCATGATCG 2P. : ATTCGGAAACGAATGCTAATACCGGATACACAACTTGGTCGCATGATCG	- : G : G :	199 197 197 187 177 156
4P. : ARTIGGGAAAGCGGAGCAATCTCCCACTTATCGATGGACCTGCGGTGC5P. : AATCGGGAAAGATGGACCAATCTATCACTTAGAGATGGACCCGCGCGCG	A : A : A : A :	249 247 247 237 227 206
4P. : TTAGCTAGTTGGTGGGGTAACGGCTCACCAAGGCGACGATGCATAGCCG5P. : TTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCTAGCCG6P. : TTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCTAGCCG3P. : TTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCTAGCCGP. : TTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCCTAGCCG2P. : TTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCCTAGCCG	A: A: A: A:	299 297 297 287 277 256
4P. :CCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCC5P. :CCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCC6P. :CCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCC3P. :CCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCP. :CCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCC2P. :CCTGAGAGGGTGATCGGCCACACTGCGACTGAGACACGGCCCAGACTCC		349 347 347 337 327 306

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 algorifonticola).

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