



# Complete Genome Sequence of *Bacillus vallismortis* NBIF-001, a Novel Strain from Shangri-La, China, That Has High Activity against *Fusarium oxysporum*

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**ABSTRACT** *Bacillus vallismortis* NBIF-001, a Gram-positive bacterium, was isolated from soil in Shangri-La, China. Here, we provide the complete genome sequence of this bacterium, which has a 3,929,787-bp-long genome, including 4,030 protein-coding genes and 195 RNA genes. This strain possesses a number of genes encoding virulence factors of pathogens.

*Bacillus vallismortis* is a bacterial species in the genus *Bacillus* with a high affinity for *B. subtilis* (1). In its growth process, *B. vallismortis* can produce numerous antimicrobial bioactive metabolites, such as thermostable alkalophilic cellulase and bacillomycin D (2, 3). These antibiotic compounds may provide alternative resources for the biocontrol of plant diseases (4, 5). Strain NBIF-001 belongs to the species *B. vallismortis*. The type strain of the species produces many bioactive metabolites showing specific activity against *Fusarium oxysporum* f. sp. *niveum*, which causes watermelon wilt disease, the most destructive disease to melon crops worldwide (6, 7).

Strain NBIF-001 was isolated from soil in Shangri-La, China, in October 2010. Its 16S rRNA sequence has 99.0% similarity to that of *B. vallismortis*. The genome sequencing of *B. vallismortis* NBIF-001 was performed with a strategy involving the Pacific Biosciences (PacBio) RS II sequencing platform and Solexa paired-end sequencing technology. Two libraries containing 10-kb and 400-bp inserts were constructed. Sequencing with an Illumina Solexa Ix genome analyzer (Wuhan Yanxing Biotechnology Co., Ltd., Wuhan, China) was performed using a paired-end strategy of 500-bp reads to produce 571 Mb and 622 Mb of filtered sequences, representing 192-fold coverage. Reads were then *de novo* assembled using the Hierarchical Genome Assembly Process (HGAP) version 3.0 to generate one contig without gaps (8).

The assembled NBIF-001 genome revealed a single circular chromosome with a size of 3,929,787 bp and an overall G+C content of 46.5%. A total of 4,030 protein-coding genes were predicted in the genome, and 86 tRNAs, 27 rRNAs, and 82 other noncoding RNAs were found in the chromosome. Genome annotation was performed with the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP), and the NCBI nonredundant (NR), KEGG (9), and Clusters of Orthologous Groups (COG) (10) databases were employed for BLASTp identification (11). Of the 4,030 genes, 3,285 were classified into 21 functional categories based on COGs of proteins (12). The genome contained 11 virulence genes relative to the resistance of pathogens, *clpC*, *clpE*, *galE*, *lplA1*, *acpXL*, *bsIA*, *yuaB*, *clpP*, *cps4I*, *capC*, and *ureB*. Moreover, there are 64 antibiotic resistance genes, including 39 genes on the antibiotic resistance, 22 genes on the antibiotic target, and 3 genes on the antibiotic biosynthesis; 11 gene clusters were found to direct the synthesis of inhibition of plant pathogen factors, including surfactin, butirosin,

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terpene, lantipeptide, macrolactin, bacillaene, fengycin, iturin, difficidin, bacillibactin, and bacilysin.

**Accession number(s).** The complete genome sequence of *B. vallismortis* NBIF-001 has been deposited in GenBank under the accession number [CP020893](https://doi.org/10.1111/1574-6968.12305). The strain is available from the China Center for Type Culture Collection (CCTCC) in Wuhan under the accession number CCTCC M 2015087.

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## REFERENCES

1. Wang LT, Lee FL, Tai CJ, Yokota A, Kuo HP. 2007. Reclassification of *Bacillus axarquiensis* Ruiz-García et al. 2005 and *Bacillus malacitensis* Ruiz-García et al. 2005 as later heterotypic synonyms of *Bacillus Mojaven-sis* Roberts et al. 1994. *Int J Syst Evol Microbiol* 57:1663–1667. <https://doi.org/10.1099/ijs.0.64808-0>.
2. Gaur R, Tiwari S. 2015. Isolation, production, purification and characterization of an organic-solvent-thermostable alkalophilic cellulase from *Bacillus vallismortis* RG-07. *BMC Biotechnol* 15:19. <https://doi.org/10.1186/s12896-015-0129-9>.
3. Zhao Z, Wang Q, Wang K, Brian K, Liu C, Gu Y. 2010. Study of the antifungal activity of *Bacillus vallismortis* ZZ185 *in vitro* and identification of its antifungal components. *Bioresour Technol* 101:292–297. <https://doi.org/10.1016/j.biortech.2009.07.071>.
4. Park KS, Paul D, Kim JS, Park JW. 2009. L-Alanine augments rhizobacteria-induced systemic resistance in cucumber. *Folia Microbiol* 54:322–326. <https://doi.org/10.1007/s12223-009-0041-6>.
5. Kaur PK, Joshi N, Singh IP, Saini HS. 2017. Identification of cyclic lipopeptides produced by *Bacillus vallismortis* R2 and their antifungal activity against *Alternaria alternata*. *J Appl Microbiol* 122:139–152. <https://doi.org/10.1111/jam.13303>.
6. Zhao B, Yan J, Zhang S, Liu X, Gao Z. 2014. Phylogeny and pathogenicity of *Fusarium* spp. isolated from greenhouse melon soil in Liaoning Province. *Saudi J Biol Sci* 21:374–379. <https://doi.org/10.1016/j.sjbs.2013.10.004>.
7. Peng J, Zhan Y, Zeng F, Long H, Pei Y, Guo J. 2013. Development of a real-time fluorescence loop-mediated isothermal amplification assay for rapid and quantitative detection of *Fusarium oxysporum* f. sp. *niveum* in soil. *FEMS Microbiol Lett* 349:127–134. <https://doi.org/10.1111/1574-6968.12305>.
8. Chin CS, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Non-hybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat Methods* 10:563–569. <https://doi.org/10.1038/nmeth.2474>.
9. Kanehisa M, Araki M, Goto S, Hattori M, Hirakawa M, Itoh M, Katayama T, Kawashima S, Okuda S, Tokimatsu T, Yamanishi Y. 2008. KEGG for linking genomes to life and the environment. *Nucleic Acids Res* 36:D480–D484. <https://doi.org/10.1093/nar/gkm882>.
10. Tatusov RL, Galperin MY, Natale DA, Koonin EV. 2000. The COG database: a tool for genome-scale analysis of protein functions and evolution. *Nucleic Acids Res* 28:33–36. <https://doi.org/10.1093/nar/28.1.33>.
11. Tatusova TA, Madden TL. 1999. BLAST 2 SEQUENCES, a new tool for comparing protein and nucleotide sequences. *FEMS Microbiol Lett* 174:247–250. <https://doi.org/10.1111/j.1574-6968.1999.tb13575.x>.
12. Tatusov RL, Fedorova ND, Jackson JD, Jacobs AR, Kiryutin B, Koonin EV, Krylov DM, Mazumder R, Mekhedov SL, Nikolskaya AN, Rao BS, Smirnov S, Sverdlov AV, Vasudevan S, Wolf YI, Yin JJ, Natale DA. 2003. The COG database: an updated version includes eukaryotes. *BMC Bioinformatics* 4:41. <https://doi.org/10.1186/1471-2105-4-41>.