Data Article

Complete genome sequence data of *Bacillus pumilus* GLB197, an effective antagonist of grape downy mildew

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**A R T I C L E   I N F O**

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**A B S T R A C T**

*Bacillus pumilus* GLB197 isolated from grape leaves exhibited strong inhibitory activity against grape downy mildew. The whole genome of the strain was sequenced to gain new insights into its molecular mechanism underlying the biocontrol on phytopathogens. The complete genome contains one chromosome (3,733,835 bp) and one plasmid (7061 bp). Several gene clusters related to biosynthesis of antimicrobial compounds were predicted. The genome provides insights into the possible biocontrol mechanisms and further application of this specific bacterium.

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### Specification table

| Subject area               | Biology                                                                 |
|---------------------------|-------------------------------------------------------------------------|
| More specific subject area| Microbiology and Genomics                                               |
| Type of data              | Complete genome sequence data of *Bacillus pumilus* GLB197              |
| How data was acquired     | Genome sequencing using PacBio RS II and Illumina HiSeq at Tianjin Biochip Co., Ltd, China |
| Data format               | Raw and analyzed data                                                   |
| Parameters for data       | DNA was extracted from *B. pumilus* GLB197                              |
| Description of data       | Whole genome sequencing, assembly, and annotation.                      |
| Data source location      | *B. pumilus* GLB197 was isolated from the grape leaves, China.         |
| Data accessibility        | The genome sequence of *B. pumilus* GLB197 has been deposited in DDBJ/ENA/GenBank under the accession number CP018574 ([https://www.ncbi.nlm.nih.gov/nuccore/CP018574](https://www.ncbi.nlm.nih.gov/nuccore/CP018574)) and CP018575 ([https://www.ncbi.nlm.nih.gov/nuccore/CP018575](https://www.ncbi.nlm.nih.gov/nuccore/CP018575)).

### Value of the data

- The genome data of *B. pumilus* GLB197 may be helpful in understanding biological traits related to biocontrol against plant pathogens.
- The genome sequence of *B. pumilus* GLB197 provides fundamental knowledge of this organism and insight for biotechnological application in agriculture.
- The genome data of *B. pumilus* GLB197 will provide valuable information to perform comparative genomics analysis.

### 1. Data Description

To decrease the pesticide residue and environmental pollution in agricultural production, more and more bacteria are being applied as biological agents to suppress plant pathogens and promote plant growth [1–3]. Many antagonistic bacteria play fundamental roles in the sustainability natural ecosystem, and some of them can be used as inoculants to benefit plant growth and health [4,5]. In recent years, *B. pumilus* has been used as a biocontrol agent for protecting crops against fungal disease. For example, *B. pumilus* INR7 is an endophytic bacterium that has been commercialized as a biocontrol product against soil-borne and foliar pathogens [6]. *B. pumilus* GM3FR isolated from aerial plant tissues are used as biocontrol agents against phytopathogens [7].

Recently, we isolated strain GLB197 from grape leaves. This strain exhibits strong inhibitory effect on the growth of *Plasmopara viticola*, a fungal pathogen causing grape downy mildew. The strain is assigned to *B. pumilus* based on 16S rRNA and *gyrB* sequence analyses [8]. The potential mechanisms of action of *B. pumilus* GLB197, such as inhibition of the growth of plant pathogens, should be explored further. To gain knowledge on the genetic equipment of this bacterium and provide insight into the mechanism by which it plays its biocontrol roles, we sequenced and annotated the complete genome sequence of the strain. The complete genome sequence of *B. pumilus* GLB197 is composed of two replicons, a circular chromosome of 3,733,835 bp with a mean G + C content of 41.56%. Strain GLB197 harbors a plasmid of 7061 bp with G + C content of 35.14%, which is lower than that in the chromosomes. The chromosome contains 3,770 putative coding sequences, 80 tRNAs, 24 rRNAs, and 1 tmRNA. Six gene clusters were predicted to be responsible for the antimicrobial activity of *B. pumilus* GLB197. The GLB197 genome contains one gene clusters of nonribosomal peptide synthetase, such as lichenysin, for antibiotic production. The lichenysin cluster may be responsible for the inhibition of grape downy mildew and needs
to be further studied. The complete genome data will be helpful to understand the molecular mechanisms of biocontrol of *B. pumilus* GLB197 and are beneficial for development of microbial fertilizers or biocontrol agents to improve crop production.

2. Experimental Design, Materials, and Methods

A high-quality genomic DNA was extracted, randomly fragmented, and then sequenced using the Illumina HiSeq and Pacific Biosciences (PacBio) platforms. A total of 1,397 M of sequence was generated from a 300-bp paired-end library, giving 349.25-fold coverage of the genome. Meanwhile, 604 M of sequences were obtained from a PacBio 10-kb library. Adaptor sequence removal, trimming, error correction, and assembly were performed using HGAP software [9]. Annotation was performed using rapid prokaryotic genome annotation software Prokka [10]. Putative proteins were searched against the COG, Gene Ontology, NCBI non-redundant protein database, and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases. In addition, the secondary metabolite gene cluster was identified using the antiSMASH program [11].

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Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships which have, or could be perceived to have, influenced the work reported in this article.

Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.dib.2020.105423.

References

[1] Y.S. Kim, K. Balaraju, Y. Jeon, Biological Control of Apple Anthracnose by Paenibacillus polymyxa APEC128, an Antagonistic Rhizobacterium, PLANT PATHOLOGY JOURNAL 32 (3) (2016) 251–259 https://doi.org/10.5423/PPJ.OA.01.2016.0015.

[2] B. Wang, et al., Bacillus amylolyiquefaciens Strain W19 can Promote Growth and Yield and Suppress Fusarium Wilt in Banana Under Greenhouse and Field Conditions, PEDOSPHERE 26 (5) (2016) 733–744 https://doi.org/10.1016/S1002-0160(15)60083-2.

[3] S. Fousia, E.J. Paplomatas, S.E. Tjamos, Bacillus subtilis QST 713 Confers Protection to Tomato Plants Against Pseudomonas syringae pv tomato and Induces Plant Defence-related Genes, JOURNAL OF PHYTOPATHOLOGY 164 (4) (2016) 264–270. https://doi.org/10.1111/jph.12455.

[4] C. Pliego, et al., Screening for candidate bacterial biocontrol agents against soilborne fungal plant pathogens, PLANT and SOIL 340 (1-2S) (2011) 505–520 https://link.springer.com/article/10.1007%2Fs11104-010-0615-8.

[5] R.L. Berendsen, et al., Effects of fluorescent Pseudomonas spp. isolated from mushroom cultures on Lecanicillium fungicola, BIOLOGICAL CONTROL 63 (2) (2012) 210–221 https://doi.org/10.1016/j.biocontrol.2012.07.012.

[6] H. Jeong, et al., Genome Sequence of the Plant Endophyte Bacillus pumilus INR7, Triggering Induced Systemic Resistance in Field Crops, Genome announcements 2 (5) (2014) https://mra.asm.org/content/2/5/e01093-14.

[7] J. Hollenstein, et al., Draft Genome Sequence of Bacillus pumilus Strain GM3FR, an Endophyte Isolated from Aerial Plant Tissues of Festuca rubra L, Genome announcements 5 (13) (2017) https://mra.asm.org/content/5/13/e00085-17.

[8] X. Zhang, et al., Screening and characterization of endophytic Bacillus for biocontrol of grapevine downy mildew, Crop Protection 96 (2017) 173–179 http://dx.doi.org/10.1016/j.cropro.2017.02.018.

[9] C. Chin, et al., Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data, NATURE METHODS 10 (6) (2013) 563–568 https://www.nature.com/articles/nmeth.2474.
[10] T. Seemann, Prokka: rapid prokaryotic genome annotation, BIOINFORMATICS 30 (14) (2014) 2068–2069 https://doi.org/10.1093/bioinformatics/btu153.

[11] M.H. Medema, et al., antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences, NUCLEIC ACIDS RESEARCH 392 (2011) W339–W346 https://doi.org/10.1093/nar/gkr466.