Genome Sequence of Growth-Improving *Paenibacillus mucilaginosus* Strain KNP414

Jing-Jiang Lu, Jian-Feng Wang, Xiu-Fang Hu

College of Life Science, Zhejiang Sci-Tech University, Xiasha, Hangzhou, People’s Republic of China

*Paenibacillus mucilaginosus* is a critical growth-improving silicate bacterium. Here, we report the complete genome sequence of *P. mucilaginosus* strain KNP414. This information will provide us with the opportunity to understand its molecular mechanisms and develop more effective utilization of the strain.

Received 24 September 2013 Accepted 27 September 2013 Published 24 October 2013

Citation Lu J-J, Wang J-F, Hu X-F. 2013. Genome sequence of growth-improving *Paenibacillus mucilaginosus* strain KNP414. Genome Announc. 1(5):e00881-13. doi:10.1128/genomeA.00881-13.

Copyright © 2013 Lu et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Xiu-Fang Hu, huxiuf@zstu.edu.cn.

**P. mucilaginosus** is a silicate bacterium (1) that is Gram positive, facultatively anaerobic, and spore forming (2) and is widely distributed in the soil, rhizosphere, and other locations (3). *P. mucilaginosus* strain KNP414 forms a large number of capsular polysaccharides when cultured in nitrogen-free medium and produces organic acid (4). It is able to degrade insoluble soil minerals (4), release nutritional ions (5), and fix nitrogen (6). Because of its many functions, *P. mucilaginosus* KNP414 is widely used in agriculture as a biofertilizer. Here, we report the complete genome sequence of *P. mucilaginosus* KNP414. To date, only two genome sequences, those of *P. mucilaginosus* strains K02 (GenBank accession no. NC_017672) and 3016 (accession no. NC_016935), have been completed for *P. mucilaginosus*.

The genomic DNA was isolated from cells of *P. mucilaginosus* KNP414 after culturing in Aleksandrov medium with 0.2% (NH₄)₂SO₄ using a DNA isolation kit (catalog no. 17900, bacterial genomic DNA isolation kit; Norgen, Canada). We constructed three genome libraries (400 bp, 2 to ~3 kb, and 4 to ~9 kb) and sequenced using the Illumina Solexa genome analyzer II platform. In total, 15,510,396 reads were obtained with 126-fold sequencing depth, and the accuracy rate of the sequences was 99.82%. Illumina reads were assembled using Velvet (7), ABySS (8) and SOAPdenovo (9), and the scaffolds were contrasted using SOAPdenovo. The genome was finished by amplifying across gaps using information of the super genome library (4 to ~9 kb) and PCR.

The *P. mucilaginosus* KNP414 genome consists of a circular chromosome (8,663,821 bp) with a 58.38% G+C content, which is similar to the other two sequenced *P. mucilaginosus* strains (K02 and 3016), and their genomic G+C contents are a little higher than those of most *Paenibacillus* strains (45 to 54%) in accordance with a previous report (10). The replication origin was predicted at position 8663004 using Ori-Finder (11) (http://ubic.tju.edu.cn/Ori-Finder/), and the potential coding sequences (CDSs) were predicted using GeneMark and Glimmer. The KNP414 genome encodes 7,811 potential proteins, with 85% coding density. Among these genes, 4,608 (58.99%) are assigned to encode known proteins, whereas 3,203 (41.01%) are identified to encode hypothetical proteins, which do not have BLASTp matches to any protein entries in the NR or UniProt database with an E value cutoff of e⁻10. In addition, the genome contains 13 rRNA operons, 107 tRNAs, and 6 potential small RNAs (sRNAs) based on the conserved sequence features in the intergenic regions identified using RfamScan (12); all of these values are lower than those for the other two *P. mucilaginosus* strains.

The genome of *P. mucilaginosus* KNP414 harbors eight genes related to nitrogen assimilation, and a comparison analysis shows that most of these genes are specifically distributed in the genome. These genes make KNP414 able to fix nitrogen and grow in a nitrogen-free environment. However, the mechanisms for this are unknown. Further analysis of the KNP414 genome will advance our understanding of the molecular mechanisms and develop more effective utilization of the strain.

**Nucleotide sequence accession number.** The sequence of *P. mucilaginosus* KNP414 has been deposited at GenBank under the accession no. CP002869.

**ACKNOWLEDGMENT**

This work was supported by the National Natural Science Foundation of China (2006AA10Z428).

**REFERENCES**

1. Aleksandrov V, Blagodyr R, Ilev I. 1967. Liberation of phosphoric acid from apatite by silicate bacteria. Mikrobiol. Zh. (Kiev) 29:111–114.

2. Ash C, Priest FG, Collins MD. 1993. Molecular identification of rRNA group 3 bacilli (Ash, Farrow, Wallbanks and Collins) using a PCR probe test. Proposal for the creation of a new genus *Paenibacillus*. Antonie Van Leeuwenhoek 64:253–260.

3. Lal S, Tabacchioni S. 2009. Ecology and biotechnological potential of *Paenibacillus polymyxa*: a minireview. Indian J. Microbiol. 49:2–10.

4. Hu X, Chen J, Guo J. 2006. Two phosphate- and potassium-solubilizing bacteria isolated from Tianmu Mountain, Zhejiang, China. World J. Microbiol. Biotechnol. 22:983–990.

5. Basak B, Biswas D. 2009. Influence of potassium solubilizing microorganism (*Bacillus mucilaginosus*) and waste mica on potassium uptake dynamics by Sudan grass (*Sorghum vulgare* Pers.) grown under two Alfisols. Plant Soil 317:235–255.

6. Aichouak W, Normand P, Heulin T. 1999. Comparative phylogeny of *rrs* and *nifH* genes in the *Bacillaceae*. Int. J. Syst. Bacteriol. 49(Pt 3):961–967.

7. Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res. 18:821–829.
8. Simpson JT, Wong K, Jackman SD, Schein JE, Jones SJ, Birol I. 2009. 
ABySS: a parallel assembler for short read sequence data. Genome Res. 
19:1117–1123.
9. Li R, Zhu H, Ruan J, Qian W, Fang X, Shi Z, Li Y, Li S, Shan G, 
Kristiansen K, Li S, Yang H, Wang J, Wang J. 2010. De novo assembly of 
human genomes with massively parallel short read sequencing. Genome 
Res. 20:265–272.
10. Hu XF, Li SX, Wu JG, Wang JF, Fang QL, Chen JS. 2010. Transfer of 
Bacillus mucilaginosus and Bacillus edaphicus to the genus 
Paenibacillus as 
Paenibacillus mucilaginosus comb. nov. and Paenibacillus edaphicus comb. 
ov. Int. J. Syst. Evol. Microbiol. 60:8–14.
11. Gao F, Zhang CT. 2008. Ori-finder: a web-based system for finding oriCs 
in unannotated bacterial genomes. BMC Bioinformatics 9:79. doi:10.1186/ 
1471-2105-9-79.
12. Gardner PP, Daub J, Tate JG, Nawrocki EP, Kolbe DL, Lindgreen S, 
Wilkinson AC, Finn RD, Griffiths-Jones S, Eddy SR, Bateman A. 2009. 
Rfam: updates to the RNA families database. Nucleic Acids Res. 37: 
D136–D140. doi:10.1093/nar/gkn766.