

Draft Genome Sequence of *Paenibacillus polymyxa* EBL06, a Plant Growth-Promoting Bacterium Isolated from Wheat Phyllosphere

Shengxian Liang,^a Decai Jin,^b Xinxin Wang,^c Haiyan Fan,^a Zhihui Bai^b

College of Bioscience and Biotechnology, Shenyang Agricultural University, Shenyang, China^a; Research Center for Eco-Environmental Sciences, Key Laboratory of Environmental Biotechnology, Chinese Academy of Sciences, Beijing, China^b; China Offshore Environmental Service Co. Ltd., Tianjin, China^c

***Paenibacillus polymyxa* strain EBL06 is a plant growth-promoting bacterium with high antifungal activity. The estimated genome of this strain is 5.68 Mb in size and harbors 4,792 coding sequences (CDSs).**

Received 23 March 2015 Accepted 25 March 2015 Published 7 May 2015

Citation Liang S, Jin D, Wang X, Fan H, Bai Z. 2015. Draft genome sequence of *Paenibacillus polymyxa* EBL06, a plant growth-promoting bacterium isolated from wheat phyllosphere. *Genome Announc* 3(3):e00414-15. doi:10.1128/genomeA.00414-15.

Copyright © 2015 Liang et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/3.0/).

Address correspondence to Haiyan Fan, hyfan74@163.com, or Zhihui Bai, zhbai@rcees.ac.cn.

Paenibacillus polymyxa (formally *Bacillus polymyxa*) is a Gram-positive, endospore-forming bacterium belonging to a diverse group of plant growth-promoting bacteria (PGPB). Our previous study showed that *P. polymyxa* strain EBL06, isolated from wheat phyllosphere, had a high level of antagonistic fungus activity (1) and could stimulate tea plant growth and improve the quality of *Brassica rapa* L. *chinensis* (2, 3).

Here, we report the draft genome sequence of *P. polymyxa* EBL06. Genome DNA was extracted and sequenced using the Illumina HiSeq 2000 platform. Shotgun sequencing produced 17,775,760 paired-end reads with approximately 264-fold coverage. Filtered reads were assembled filled by SOAPdenovo 2.04 (4). This assembly generated 102 contigs, with an N_{50} length of 627,482 bp and an average length of 55,594 bp, which were assembled into 45 scaffolds, with an N_{50} length of 1,481,754 bp and an average length of 126,218 bp. Genome annotation was performed by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/).

The draft genome is 5.68 Mb, with a G+C% content of 45.59%. A total of 4,792 coding sequences (CDSs), 105 pseudogenes, 41 tRNA genes, 1 noncoding RNA (ncRNA), and 9 rRNAs were identified.

Average nucleotide identity (ANI) analysis (5) revealed that *P. polymyxa* EBL06 is phylogenetically related to *P. polymyxa* SC2 (94.5%) (6), *P. polymyxa* M1 (94.5%) (7), *P. polymyxa* E681 (89.4%) (8), *P. polymyxa* SQR-21 (98.6%) (9), *P. polymyxa* CR1 (89.6%) (10), and *P. polymyxa* Sb3-1 (94.7%) (11).

Nucleotide sequence accession number. The whole-genome shotgun project of *P. polymyxa* EBL06 has been deposited at DDBI/EMBL/GenBank under the accession no. JYCW00000000. The version described in this paper is the first version.

ACKNOWLEDGMENTS

This study was supported by the Key Project of Chinese Academy of Sciences (KZZD-EW-09-3 and XDB15010404) and the Hi-Tech Research and Development Program (863) of China (2013AA06A205).

REFERENCES

- Gu L, Bai Z, Jin B, Zhang J, Li W, Zhuang G, Zhang H. 2010. Production of a newly isolated *Paenibacillus polymyxa* biocontrol agent using mono-

- sodium glutamate wastewater and potato wastewater. *J Environ Sci China* 22:1407–1412. [http://dx.doi.org/10.1016/S1001-0742\(09\)60267-9](http://dx.doi.org/10.1016/S1001-0742(09)60267-9).
- Xu S, Bai Z, Jin B, Xiao R, Zhuang G. 2014. Bioconversion of wastewater from sweet potato starch production to *Paenibacillus polymyxa* biofertilizer for tea plants. *Sci Rep* 4:4131. <http://dx.doi.org/10.1038/srep04131>.
- Su Y, Bai Z, Lv X, Zhang L, Peng X. 2011. Effect of *Paenibacillus polymyxa* on nitrate content in rape. *Chin Agric Sci Bull* 27:144–148. (In Chinese.)
- Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung DW, Yiu SM, Peng S, Xiaoqian Z, Liu G, Liao X, Li Y, Yang H, Wang J, Lam TW, Wang J. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. *Gigascience* 1:18. <http://dx.doi.org/10.1186/2047-217X-1-18>.
- Richter M, Rosselló-Móra R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. *Proc Natl Acad Sci U S A* 106:19126–19131. <http://dx.doi.org/10.1073/pnas.0906412106>.
- Ma M, Wang C, Ding Y, Li L, Shen D, Jiang X, Guan D, Cao F, Chen H, Feng R, Wang X, Ge Y, Yao L, Bing X, Yang X, Li J, Du B. 2011. Complete genome sequence of *Paenibacillus polymyxa* SC2, a strain of plant growth-promoting rhizobacterium with broad-spectrum antimicrobial activity. *J Bacteriol* 193:311–312. <http://dx.doi.org/10.1128/JB.01234-10>.
- Niu B, Rueckert C, Blom J, Wang Q, Borriss R. 2011. The genome of the plant growth-promoting rhizobacterium *Paenibacillus polymyxa* M-1 contains nine sites dedicated to nonribosomal synthesis of lipopeptides and polyketides. *J Bacteriol* 193:5862–5863. <http://dx.doi.org/10.1128/JB.05806-11>.
- Kim JF, Jeong H, Park SY, Kim SB, Park YK, Choi SK, Ryu CM, Hur CG, Ghim SY, Oh TK, Kim JJ, Park CS, Park SH. 2010. Genome sequence of the polymyxin-producing plant-probiotic rhizobacterium *Paenibacillus polymyxa* E681. *J Bacteriol* 192:6103–6104. <http://dx.doi.org/10.1128/JB.00983-10>.
- Li S, Yang D, Qiu M, Shao J, Guo R, Shen B, Yin X, Zhang R, Zhang N, Shen Q. 2014. Complete genome sequence of *Paenibacillus polymyxa* SQR-21, a plant growth-promoting rhizobacterium with antifungal activity and rhizosphere colonization ability. *Genome Announc* 2(2):e00281-14. <http://dx.doi.org/10.1128/genomeA.00281-14>.
- Eastman AW, Weselowski B, Nathoo N, Yuan ZC. 2014. Complete genome sequence of *Paenibacillus polymyxa* CR1, a plant growth-promoting bacterium isolated from the corn rhizosphere exhibiting potential for biocontrol, biomass degradation, and biofuel production. *Genome Announc* 2(1):e01218-13. <http://dx.doi.org/10.1128/genomeA.01218-13>.
- Rybakova D, Wetzlinger U, Müller H, Berg G. 2015. Complete genome sequence of *Paenibacillus polymyxa* strain SB3-1, a soilborne bacterium with antagonistic activity toward plant pathogens. *Genome Announc* 3(2):e00052-15. <http://dx.doi.org/10.1128/genomeA.00052-15>.