

Complete Genome Sequence of *Paenibacillus polymyxa* SC2, a Strain of Plant Growth-Promoting Rhizobacterium with Broad-Spectrum Antimicrobial Activity[∇]

Mingchao Ma,^{2†} Cuicui Wang,^{1†} Yanqin Ding,^{1†} Li Li,² Delong Shen,² Xin Jiang,² Dawei Guan,² Fengming Cao,² Huijun Chen,² Ruihua Feng,² Xuan Wang,¹ Yifan Ge,² Liangtong Yao,¹ Xiaohui Bing,² Xiaohong Yang,² Jun Li,^{2*} and Binghai Du^{1*}

College of Life Sciences, Shandong Agricultural University/Shandong Key Laboratory of Agricultural Microbiology, 61 Daizong Street, Taian 271018, Shandong, People's Republic of China,¹ and Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing 100081, People's Republic of China²

Received 13 October 2010/Accepted 20 October 2010

***Paenibacillus polymyxa* SC2 is an important plant growth-promoting rhizobacterium (PGPR). Here, we report the complete genome sequence of *P. polymyxa* SC2. Multiple sets of functional genes have been found in the genome. As far as we know, this is the first complete genome sequence of *Paenibacillus polymyxa*.**

Paenibacillus polymyxa (formerly *Bacillus polymyxa*) (2), the type species of *Paenibacillus*, is considered a plant growth-promoting rhizobacterium (PGPR) (12). *P. polymyxa* is widespread in the soil and widely used in agriculture, industry, and environmental remediation because of its multiple functions (10). *P. polymyxa* strain SC2 was isolated from the rhizosphere of pepper in Guizhou, China (15), and has been widely used in biological control of soil-borne plant diseases.

Whole-genome sequencing of SC2 was performed with a combined strategy of Roche/454 sequencing (9) and Solexa paired-end sequencing technology (3). Genomic libraries containing 8-kb inserts were constructed, and 153,770 paired-end reads and 103,401 single-end reads were generated using the GS FLX system, giving 15.3-fold coverage of the genome. A total of 97.42% of the reads were assembled into 25 large scaffolds, including 218 nonredundant contigs, using 454 Newbler (454 Life Sciences, Branford, CT). A total of 34,770,992 reads (3-kb library) were generated to reach a depth of 418-fold coverage with an Illumina Solexa Genome Analyzer IIx and mapped to the scaffolds using the Burrows-Wheeler Alignment (BWA) tool (8). Most of the gaps within the scaffolds were filled by local assembly of 454 and Solexa reads. The remainder and the gaps between scaffolds were filled by sequencing PCR products using an ABI 3730 capillary sequencer. The analysis of the genome was performed as described previously (6, 14).

The complete genome sequence of SC2 is composed of a circular 5,731,816-bp chromosome and a 510,115-bp plasmid,

with mean GC contents of 54.58% and 37.61%, respectively. There are 5,454 coding genes, 14 rRNA operons, and 110 tRNAs in the chromosome, as well as 649 coding genes and 47 tRNAs in the plasmid. There are many essential genes in the plasmid, such as the genes involving the metabolism of purine, pyrimidine, and lipid, as well as ribosomal proteins, translation elongation factors, and different types of DNA methyltransferase, indicating its importance to the strain's life.

In comparison to *Paenibacillus* sp. strain JDR-2, an aggressively xylanolytic strain whose public genome is the most highly related to that of SC2, there are 2,615 shared genes and 2,645 unique genes in the chromosome of SC2. There are many genes involved in antibiotic biosynthesis in the chromosome, such as a fusaricidin-synthetic gene (PPSC2_c0086), a polymyxin-synthetic gene cluster (PPSC2_c4710-c4715), a bacitracin synthetase 1 gene (PPSC2_c2653), an iturin A synthetase gene (PPSC2_c2652), a lantibiotic-synthetic gene cluster (PPSC2_c1561-c1567), a bacillo-rin synthetase B gene (PPSC2_c2638), and a polyketide-synthetic gene cluster (PPSC2_c3386-c3400), according to similarities to the published gene clusters (1, 4, 5, 7, 11, 13).

Nucleotide sequence accession numbers. The *Paenibacillus polymyxa* SC2 chromosome and plasmid sequences have been deposited in GenBank under accession numbers CP002213 and CP002214.

We thank Tianjin Biochip Corporation for assistance with sequencing and analysis. We thank all teachers for their contributions to the accomplishment of this task.

This work was supported by a National 863 Program of China grant (number 2010AA10A203), the Basic Scientific and Business Fund and Central Public Research Project (grant number 2010-34), and the Special Fund for the Establishment of Modern Agricultural R&D Systems (grant number ncyctx-004), Ministry of Finance and Ministry of Agriculture, China.

REFERENCES

1. Altana, K., A. Guder, C. Cramer, and G. Bierbaum. 2000. Biosynthesis of the lantibiotic mersacidin: organization of a type B lantibiotic gene cluster. *Appl. Environ. Microbiol.* **66**:2565–2571.
2. Ash, C., F. G. Priest, and M. D. Collins. 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.

* Corresponding author. Mailing address for Binghai Du: College of Life Sciences, Shandong Agricultural University, 61 Daizong Street, Taian 271018, Shandong, People's Republic of China. Phone: 86-538-8242908. Fax: 86-538-8242908. E-mail: bhdu@sdau.edu.cn. Mailing address for Jun Li: Institute of Agricultural Resources and Regional Planning, Chinese Academy of Agricultural Sciences, Beijing 100081, People's Republic of China. Phone: 86-10-82106208. Fax: 86-10-82108702. E-mail: jli@caas.ac.cn.

† Mingchao Ma, Cuicui Wang, and Yanqin Ding contributed equally to this work.

[∇] Published ahead of print on 29 October 2010.

3. Bentley, D. R., S. Balasubramanian, H. P. Swerdlow, G. P. Smith, J. Milton, C. G. Brown, K. P. Hall, D. J. Evers, C. L. Barnes, H. R. Bignell, J. M. Boutell, J. Bryant, R. J. Carter, R. Keira Cheetham, A. J. Cox, D. J. Ellis, M. R. Flatbush, N. A. Gormley, S. J. Humphray, L. J. Irving, M. S. Karbelashvili, S. M. Kirk, H. Li, X. Liu, K. S. Maisinger, L. J. Murray, B. Obradovic, T. Ost, M. L. Parkinson, M. R. Pratt, I. M. Rasolonjatovo, M. T. Reed, R. Rigatti, C. Rodighiero, M. T. Ross, A. Sabot, S. V. Sankar, A. Scally, G. P. Schroth, M. E. Smith, V. P. Smith, A. Spiridou, P. E. Torrance, S. S. Tzonev, E. H. Vermaas, K. Walter, X. Wu, L. Zhang, M. D. Alam, C. Anastasi, I. C. Aniebo, D. M. Bailey, I. R. Bancarz, S. Banerjee, S. G. Barbour, P. A. Baybayan, V. A. Benoit, K. F. Benson, C. Bevis, P. J. Black, A. Boodhun, J. S. Brennan, J. A. Bridgham, R. C. Brown, A. A. Brown, D. H. Buermann, A. A. Bundu, J. C. Burrows, N. P. Carter, N. Castillo, E. C. M. Chiara, S. Chang, R. Neil Cooley, N. R. Crake, O. O. Dada, K. D. Diakoumakos, B. Dominguez-Fernandez, D. J. Earnshaw, U. C. Egbujor, D. W. Elmore, S. S. Etchin, M. R. Ewan, M. Fedurco, L. J. Fraser, K. V. Fuentes Fajardo, W. Scott Furey, D. George, K. J. Gietzen, C. P. Goddard, G. S. Golda, P. A. Granieri, D. E. Green, D. L. Gustafson, N. F. Hansen, K. Harnish, C. D. Haudenschild, N. I. Heyer, M. M. Hims, J. T. Ho, A. M. Horgan, *et al.* 2008. Accurate whole human genome sequencing using reversible terminator chemistry. *Nature* **456**:53–59.
4. Choi, S. K., S. Y. Park, R. Kim, C. H. Lee, J. F. Kim, and S. H. Park. 2008. Identification and functional analysis of the fusaricidin biosynthetic gene of *Paenibacillus polymyxa* E681. *Biochem. Biophys. Res. Commun.* **365**:89–95.
5. Choi, S. K., S. Y. Park, R. Kim, S. B. Kim, C. H. Lee, J. F. Kim, and S. H. Park. 2009. Identification of a polymyxin synthetase gene cluster of *Paenibacillus polymyxa* and heterologous expression of the gene in *Bacillus subtilis*. *J. Bacteriol.* **191**:3350–3358.
6. Ferenci, T., Z. Zhou, T. Betteridge, Y. Ren, Y. Liu, L. Feng, P. R. Reeves, and L. Wang. 2009. Genomic sequencing reveals regulatory mutations and recombinational events in the widely used MC4100 lineage of *Escherichia coli* K-12. *J. Bacteriol.* **191**:4025–4029.
7. Konz, D., A. Klens, K. Schorgendorfer, and M. A. Marahiel. 1997. The bacitracin biosynthesis operon of *Bacillus licheniformis* ATCC 10716: molecular characterization of three multi-modular peptide synthetases. *Chem. Biol.* **4**:927–937.
8. Li, H., and R. Durbin. 2010. Fast and accurate long-read alignment with Burrows-Wheeler transform. *Bioinformatics* **26**:589–595.
9. Margulies, M., M. Egholm, W. E. Altman, S. Attiya, J. S. Bader, L. A. Bemben, J. Berka, M. S. Braverman, Y. J. Chen, Z. Chen, S. B. Dewell, L. Du, J. M. Fierro, X. V. Gomes, B. C. Godwin, W. He, S. Helgesen, C. H. Ho, G. P. Irzyk, S. C. Jando, M. L. Alenquer, T. P. Jarvie, K. B. Jirage, J. B. Kim, J. R. Knight, J. R. Lanza, J. H. Leamon, S. M. Lefkowitz, M. Lei, J. Li, K. L. Lohman, H. Lu, V. B. Makhijani, K. E. McDade, M. P. McKenna, E. W. Myers, E. Nickerson, J. R. Nobile, R. Plant, B. P. Puc, M. T. Ronan, G. T. Roth, G. J. Sarkis, J. F. Simons, J. W. Simpson, M. Srinivasan, K. R. Tartaro, A. Tomasz, K. A. Vogt, G. A. Volkmer, S. H. Wang, Y. Wang, M. P. Weiner, P. Yu, R. F. Begley, and J. M. Rothberg. 2005. Genome sequencing in microfabricated high-density picolitre reactors. *Nature* **437**:376–380.
10. Sadhana, L., and S. Tabacchioni. 2009. Ecology and biotechnological potential of *Paenibacillus polymyxa*: a minireview. *Indian J. Microbiol.* **49**:2–10.
11. Straight, P. D., M. A. Fischbach, C. T. Walsh, D. Z. Rudner, and R. Kolter. 2007. A singular enzymatic mega-complex from *Bacillus subtilis*. *Proc. Natl. Acad. Sci. U. S. A.* **104**:305–310.
12. Timmusk, S., B. Nicander, U. Granhall, and E. Tillberg. 1999. Cytokinin production by *Paenibacillus polymyxa*. *Soil Biol. Biochem.* **31**:1847–1852.
13. Tsuge, K., T. Akiyama, and M. Shoda. 2001. Cloning, sequencing, and characterization of the iturin A operon. *J. Bacteriol.* **183**:6265–6273.
14. Zhou, Z., X. Li, B. Liu, L. Beutin, J. Xu, Y. Ren, L. Feng, R. Lan, P. R. Reeves, and L. Wang. 2010. Derivation of *Escherichia coli* O157:H7 from its O55:H7 precursor. *PLoS One* **5**:e8700.
15. Zhu, H., B. H. Du, and Y. Q. Ding. 2008. Screening and study on biological characteristics of antagonistic bacteria against *Fusarium solani*. *J. Biotechnol. Bull.* **1**:156–159. (In Chinese.)