Complete Genome Sequence of *Bacillus amyloliquefaciens* Strain Co1-6, a Plant Growth-Promoting Rhizobacterium of *Calendula officinalis*

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The genome sequence of *Bacillus amyloliquefaciens* strain Co1-6, a plant growth-promoting rhizobacterium (PGPR) with broad-spectrum antagonistic activity against plant-pathogenic fungi, bacteria, and nematodes, consists of a single 3.9-Mb circular chromosome. The genome reveals genes putatively responsible for its promising biocontrol and PGP properties.

The closest relative of Co1-6 based on the full-length 16S rRNA gene sequence is *B. amyloliquefaciens* subsp. *plantarum* FZB42 (NCBI reference sequence no. NR_075005, 99% sequence similarity). FZB42 is a well-known PGPR serving as the basis of a commercially available product (RhizoVital 42; ABiTEP GmbH, Berlin, Germany) with the ability to stimulate plant growth and suppress plant pathogens (6). Digital DNA-DNA hybridization (DDH) using GGDC 2.0 (7–9) against the genome sequence of FZB42 (accession no. NC_009725) estimated a DDH of 80.30% ± 2.77%, indicating that they have 90.8% probability of being the same species but only 48.3% probability of being the same subspecies.

Annotation was conducted on the RAST Web server using RAST gene calling based on FIGfam version Release70 (10, 11), and additional annotation was completed on the BASys Web server using Glimmer gene prediction (12, 13). The genome annotation contained 3,913 predicted protein-coding genes, 86 tRNA and 19 rRNA loci, and 457 predicted SEED subsystem features.

The genome encodes synthases for mycosubtilin, plipastatin, and surfactin antibiotics, which most probably contribute to the promising abilities of Co1-6 for pathogen suppression. Co1-6 revealed six additional polyketide synthases, some at up to seven copies, and a dimodular nonribosomal peptide synthase. We further identified genes most probably involved in the direct promotion of plant growth, such as biosynthesis gene clusters for rhizobactin siderophores, spermidine, and auxin.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited in the European Nucleotide Archive under the accession no. CVPQA00000000. The version described in this paper is the first version, CVPQA01000000.

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REFERENCES

1. Köberl M, Müller H, Ramadan EM, Berg G. 2011. Desert farming benefits from microbial potential in arid soils and promotes diversity and plant health. PLoS One 6:e24452. http://dx.doi.org/10.1371/journal.pone.0024452.

2. Luske B, van der Kamp J. 2009. Carbon sequestration potential of reclaimed desert soils in Egypt. Louis Bolk Instituut & Soil and More International, Brussels, Belgium. http://orgprints.org/16438/1/2192.pdf.

3. Köberl M, Ramadan EM, Adam M, Cardinale M, Hallmann J, Heuer H, Smalla K, Berg G. 2013. Bacillus and Streptomyces were selected as broad-spectrum antagonists against soilborne pathogens from arid areas in Egypt. FEMS Microbiol Lett 342:168–178. http://dx.doi.org/10.1111/1574-6968.12089.

4. Adam M, Heuer H, Hallmann J. 2014. Bacterial antagonists of fungal pathogens also control root-knot nematodes by induced systemic resistance of tomato plants. PLoS One 9:e90402. http://dx.doi.org/10.1371/journal.pone.0090402.

5. Schmidt R, Köberl M, Mostafa A, Ramadan EM, Monschein M, Jensen KB, Bauer R, Berg G. 2014. Effects of bacterial inoculants on the indigenous microbiome and secondary metabolites of chamomile plants. Front Microbiol 5:64. http://dx.doi.org/10.3389/fmicb.2014.00064.

6. Chen XH, Koundoutsi A, Scholz R, Eisenreich A, Schneider K, Heinemeyer I, Morgenstern B, Voss B, Hess WR, Reva O, Junge H, Voigt B, Jungblut PR, Vater J, Süßmuth R, Liesegang H, Strittmatter A, Gottschalk G, Borris R. 2007. Comparative analysis of the complete genome sequence of the plant growth-promoting bacterium Bacillus amyloliquifaciens FZB42. Nat Biotechnol 25:1007–1014. http://dx.doi.org/10.1038/nbt1325.

7. Auch AF, von Jan M, Klenk HP, Göker M. 2010. Digital DNA-DNA hybridization for microbial species delineation by means of genome-to-genome sequence comparison. Stand Genomic Sci 2:117–134. http://dx.doi.org/10.4056/sigs.531120.

8. Auch AF, Klenk HP, Göker M. 2010. Standard operating procedure for calculating genome-to-genome distances based on high-scoring segment pairs. Stand Genomic Sci 2:142–148. http://dx.doi.org/10.4056/sigs.541628.

9. Meier-Kolthoff JP, Auch AF, Klenk HP, Göker M. 2013. Genome sequence-based species delimitation with confidence intervals and improved distance functions. BMC Bioinformatics 14:60. http://dx.doi.org/10.1186/1471-2105-14-60.

10. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil I, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. BMC Genomics 9:75. http://dx.doi.org/10.1186/1471-2164-9-75.

11. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Diz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Res 42:D206–D214. http://dx.doi.org/10.1093/nar/gkt1226.

12. Van Domselaar GH, Stothard P, Shrivastava S, Cruz JA, Guo A, Dong X, Lu P, Szafron D, Greiner R, Wishart DS. 2005. BAGsys: a Web server for automated bacterial genome annotation. Nucleic Acids Res 33:W455–W459. http://dx.doi.org/10.1093/nar/gki593.

13. Delcher AL, Harmon D, Kasif S, White O, Salzberg SL. 1999. Improved microbial gene identification with Glimmer. Nucleic Acids Res 27:4636–4641. http://dx.doi.org/10.1093/nar/27.23.4636.