



# Draft Genome Sequence of the Endophyte *Paenibacillus* sp. Strain GM2FR Isolated from *Festuca rubra*

Franziska Wemheuer,<sup>a,b</sup> Bernd Wemheuer,<sup>a</sup> Jacqueline Hollensteiner,<sup>a</sup>  Rolf Daniel,<sup>a</sup>  Anja Poehlein<sup>a</sup>

<sup>a</sup>Genomic and Applied Microbiology & Göttingen Genomics Laboratory, Institute of Microbiology and Genetics, University of Göttingen, Göttingen, Germany

<sup>b</sup>Department of Crop Sciences, Agricultural Entomology, University of Göttingen, Göttingen, Germany

**ABSTRACT** Here, we report the 7.4-Mb draft genome sequence of *Paenibacillus* sp. strain GM2FR, an endophytic bacterium isolated from aerial plant tissues of *Festuca rubra* L. Genome analysis revealed 6,652 coding gene sequences and several gene clusters involved in plant growth promotion, such as that for the siderophore bacillibactin.

Plant-associated bacteria belonging to the genus *Paenibacillus* are able to promote plant growth and health (1, 2). Several *Paenibacillus* spp. are important antagonists of various important plant pathogens and pests (3, 4). The genome sequence of the endophyte strain *Paenibacillus* sp. GM2FR will facilitate further studies on the potential of these bacteria for agricultural applications.

We isolated *Paenibacillus* sp. GM2FR from surface-sterilized aerial tissues of healthy *Festuca rubra* plants. Genomic DNA was extracted using the MasterPure complete DNA purification kit (Epicentre, Madison, WI, USA). The obtained DNA was used to generate Illumina shotgun paired-end sequencing libraries. Sequencing was performed employing a MiSeq system and the MiSeq reagent kit version 3 (600 cycles), as recommended by the manufacturer (Illumina, San Diego, CA, USA). Quality filtering using Trimmomatic version 0.32 (5) resulted in 5,564,116 paired-end reads. The *de novo* genome assembly was performed with the SPAdes genome assembler version 3.8.0 (6). The assembly resulted in 16 contigs (>500 bp) and an average coverage of 154-fold. The assembly was validated and the read coverage determined with QualiMap version 2.1 (7).

The draft genome of strain GM2FR consisted of 7,416,573 bp, with an overall GC content of 49.56%. Gene prediction and annotation were performed using Prokka (Rapid Prokaryotic Genome Annotation) version 1.11 (8). The draft genome harbored 8 rRNA genes, 45 tRNA genes, 2,573 protein-encoding genes with functional predictions, and 4,079 genes coding for hypothetical proteins. Multilocus sequence typing (MLST) based on four housekeeping genes (*gapA*, *groEL*, *gyrA*, and *pgi*) was performed according to Iiyama et al. (9). Strain GM2FR clustered with *Paenibacillus vortex* (10).

An antiSMASH 3.0.5 (11) analysis predicted 51 potential gene clusters involved in secondary metabolite production. These included 48 clusters with no or low ( $\leq 20\%$ ) similarity to known clusters, such as a bacteriocin, terpene, and type III polyketide synthase (T3pks) gene clusters. In addition, a nonribosomal polyketide synthetase (NRPS) cluster was identified with 53% of the genes sharing similarity to a bacillibactin biosynthesis gene cluster. Bacillibactin is a catecholate-type siderophore produced by *Paenibacillus larvae* (12) as well as several *Bacillus* species (13). Siderophores play an important role in competition between microorganisms (13) and can enhance plant growth and health (12–14). Moreover, a gene cluster with 75% of genes exhibiting similarity to an ectoine biosynthetic gene cluster was identified. Ectoines are produced by bacteria as compatible solutes to maintain the stability and correct folding of their proteins under osmotic stress (15). It has been shown that ectoines can enhance the

Received 8 January 2018 Accepted 9 January 2018 Published 8 February 2018

**Citation** Wemheuer F, Wemheuer B, Hollensteiner J, Daniel R, Poehlein A. 2018. Draft genome sequence of the endophyte *Paenibacillus* sp. strain GM2FR isolated from *Festuca rubra*. Genome Announc 6:e00017-18. <https://doi.org/10.1128/genomeA.00017-18>.

**Copyright** © 2018 Wemheuer et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Anja Poehlein, [apoehle3@gwdg.de](mailto:apoehle3@gwdg.de).

nitrogen supply to tobacco leaves by increasing transpiration and by protecting RuBisCO proteins from the deleterious effects of salt (16). In addition, an increased water uptake rate and, subsequently, an increased photosynthesis rate under salt stress were observed in ectoine transgenic tomato plants (17). Thus, *Paenibacillus* sp. GM2FR might be involved in plant growth health in its host plant.

**Accession number(s).** The whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [MKZM00000000](https://doi.org/10.1101/2019.08.28.281111). The version described here is version MKZM01000000.

## ACKNOWLEDGMENTS

We thank the Ministry of Science and Culture of Lower Saxony and the “Niedersächsisches Vorab” (part of the cluster of excellence “Functional Biodiversity Research”) for funding and Melanie Heinemann for technical support.

The funder had no role in the study design, data collection, and interpretation, or the decision to submit the work for publication.

## REFERENCES

- McSpadden Gardener BB. 2004. Ecology of *Bacillus* and *Paenibacillus* spp. in agricultural systems. *Phytopathology* 94:1252–1258. <https://doi.org/10.1094/PHYTO.2004.94.11.1252>.
- Grady EN, MacDonald J, Liu L, Richman A, Yuan ZC. 2016. Current knowledge and perspectives of *Paenibacillus*: a review. *Microb Cell Fact* 15:203. <https://doi.org/10.1186/s12934-016-0603-7>.
- Son SH, Khan Z, Kim SG, Kim YH. 2009. Plant growth-promoting rhizobacteria, *Paenibacillus polymyxa* and *Paenibacillus lentimorbus* suppress disease complex caused by root-knot nematode and fusarium wilt fungus. *J Appl Microbiol* 107:524–532. <https://doi.org/10.1111/j.1365-2672.2009.04238.x>.
- 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. <https://doi.org/10.1111/1574-6968.12089>.
- Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- García-Alcalde F, Okonechnikov K, Carbonell J, Cruz LM, Götz S, Tarazona S, Dopazo J, Meyer TF, Conesa A. 2012. Qualimap: evaluating next-generation sequencing alignment data. *Bioinformatics* 28:2678–2679. <https://doi.org/10.1093/bioinformatics/bts503>.
- Seemann T. 2014. Prokka: Rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>.
- Iiyama K, Nishi O, Mon H, Lee JM, Kusakabe T, Asano S-I, Yasunaga-Aoki C, Shimizu S. 2013. Phylogenetic analysis of *Paenibacillus popilliae* and its related taxa based on housekeeping genes. *J Insect Biotechnol Sericol* 82:1–11. [https://doi.org/10.11416/jibs.82.1\\_001](https://doi.org/10.11416/jibs.82.1_001).
- Sirota-Madi A, Olender T, Helman Y, Ingham C, Brainis I, Roth D, Hagi E, Brodsky L, Leshkowitz D, Galatenko V, Nikolaev V, Mugasimangalam RC, Bransburg-Zabary S, Gutnick DL, Lancet D, Ben-Jacob E. 2010. Genome sequence of the pattern forming *Paenibacillus vortex* bacterium reveals potential for thriving in complex environments. *BMC Genomics* 11:710. <https://doi.org/10.1186/1471-2164-11-710>.
- Weber T, Blin K, Duddela S, Krug D, Kim HU, Brucoleri R, Lee SY, Fischbach MA, Müller R, Wohlleben W, Breitling R, Takano E, Medema MH. 2015. antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Res* 43:W237–W243. <https://doi.org/10.1093/nar/gkv437>.
- Hertlein G, Müller S, Garcia-Gonzalez E, Poppinga L, Süßmuth RD, Genersch E. 2014. Production of the catechol type siderophore bacillibactin by the honey bee pathogen *Paenibacillus larvae*. *PLoS One* 9:e108272. <https://doi.org/10.1371/journal.pone.0108272>.
- Khan A, Doshi HV, Thakur MC. 2016. *Bacillus* spp.: a prolific siderophore producer, p 309–323. In Islam MT, Rahman MM, Pandey P, Jha CK, Aeron A (ed), *Bacilli and agrobiotechnology*. Springer International, Cham, Switzerland.
- Yaqoob A, Shahid AA, Samiullah TR, Rao AQ, Khan MAU, Tahir S, Mirza SA, Husnain T. 2016. Risk assessment of *Bt* crops on the non-target plant-associated insects and soil organisms. *J Sci Food Agric* 96:2613–2619. <https://doi.org/10.1002/jsfa.7661>.
- Graf R, Anzali S, Buenger J, Pfluecker F, Driller H. 2008. The multifunctional role of ectoine as a natural cell protectant. *Clin Dermatol* 26:326–333. <https://doi.org/10.1016/j.clindermatol.2008.01.002>.
- Moghaieb REA, Tanaka N, Saneoka H, Murooka Y, Ono H, Morikawa H, Nakamura A, Nguyen NT, Suwa R, Fujita K. 2006. Characterization of salt tolerance in ectoine-transformed tobacco plants (*Nicotiana tabacum*): photosynthesis, osmotic adjustment, and nitrogen partitioning. *Plant Cell Environ* 29:173–182. <https://doi.org/10.1111/j.1365-3040.2005.01410.x>.
- Moghaieb REA, Nakamura A, Saneoka H, Fujita K. 2011. Evaluation of salt tolerance in ectoine-transgenic tomato plants (*Lycopersicon esculentum*) in terms of photosynthesis, osmotic adjustment, and carbon partitioning. *GM Crops* 2:58–65.