

Whole-Genome Sequence of *Rummeliibacillus stabekisii* Strain PP9 Isolated from Antarctic Soil

Fábio Faria da Mota,^a Renata Estebanez Vollú,^b Diogo Jurelevicius,^b Lucy Seldin^b

Laboratório de Biologia Computacional e Sistemas, Instituto Oswaldo Cruz, Fundação Oswaldo Cruz (IOC/Fiocruz), Rio de Janeiro, Brazil^a; Instituto de Microbiologia Paulo de Góes, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil^b

The whole genome of *Rummeliibacillus stabekisii* PP9, isolated from a soil sample from Antarctica, consists of a circular chromosome of 3,412,092 bp and a circular plasmid of 8,647 bp, with 3,244 protein-coding genes, 12 copies of the 16S-23S-5S rRNA operon, 101 tRNA genes, and 6 noncoding RNAs (ncRNAs).

Received 4 April 2016 Accepted 12 April 2016 Published 26 May 2016

Citation da Mota FF, Vollú RE, Jurelevicius D, Seldin L. 2016. Whole-genome sequence of *Rummeliibacillus stabekisii* strain PP9 isolated from Antarctic soil. *Genome Announc* 4(3):e00416-16. doi:10.1128/genomeA.00416-16.

Copyright © 2016 da Mota 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 Lucy Seldin, lseldin@micro.ufrj.br.

Rummeliibacillus stabekisii is constituted of strains of aerobic, Gram-positive, rod-shaped, round-spore-forming bacteria. Strains first described to belong to this species were isolated from different geographical locations (the type strain was isolated from the Payload Hazardous Servicing Facility at the Kennedy Space Center, FL), and their 16S rRNA gene sequence similarities demonstrated that they were most closely affiliated with *Bacillus pycnus* NRRL NRS-1691^T (98%), *Kurthia* sp. (96%), and *Viridibacillus* sp. (94 to 96%) (1). *R. stabekisii* was proposed as the type species of the genus *Rummeliibacillus* (1).

Strain PP9 was isolated from a soil sample collected from Punta Plaza located in King George Island, which is part of the South Shetlands archipelago in Maritime Antarctica, and identified as *R. stabekisii* (2). No genome sequences were available for any of the recognized species of the genus *Rummeliibacillus*. To gain a better understanding of this poorly studied species, the whole-genome sequence of *R. stabekisii* PP9 was determined.

The genome of *R. stabekisii* PP9 was sequenced in Seoul, South Korea, by DNA Link, Inc., using the PacBio RSII platform and two single-molecule real-time (SMRT) cells of P6-C4 chemistry with a 20-kb size-selected library; 450,876 raw reads resulted in 237,668 quality-filtered trimmed reads yielding 3,295 Mb, with a mean genome-wide coverage of about 969×. The filtered reads were assembled using HGAP version 2.3 (3). Annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline version 3.1 to predict protein-coding genes, structural RNAs, small noncoding RNAs, and tRNAs (4).

The genome of *R. stabekisii* PP9 consists of a circular chromosome of 3,412,092 bp and a circular plasmid of 8,647 bp, with a G+C content of 37.6%. The genome includes 3,244 protein-coding genes, 101 tRNA genes, 6 noncoding RNAs (ncRNAs), and 12 copies of the 16S-23S-5S rRNA operon. From the assigned protein-coding genes, only 1,939 have a putative function, while the remaining 1,305 genes (about 40%) were annotated as hypothetical proteins.

Genes related to sporulation and flagellar assembly were found in the PP9 genome. Round spores and motility observed by light

microscopy and in soft agar stabbing, respectively, confirmed that their products are expressed and functional.

The average nucleotide identity (ANI) was calculated based on MUMmer (5) between the PP9 chromosome and six other complete chromosomes of strains belonging to the *Planococcaceae* family. *Kurthia* (accession no. CP013217.1) was the genus most closely related to *R. stabekisii* PP9 (accession no. CP014806.1), with 85.64% ANI, followed by *Solibacillus* (84.85%; accession no. NC_018065.1), *Jeotgalibacillus* (84.5%; accession no. CP009416.1), *Planococcus* (83.84%; accession no. CP013661.2), *Sporosarcina* (82.64%; accession no. CP014616.1), and *Planomicrobium* (82.45%; accession no. NZ_CCSX0100001.1). The resulting averages reflect a high degree of evolutionary distance between *R. stabekisii* and other members of its family.

Nucleotide sequence accession numbers. The genome sequences have been deposited at GenBank under the accession numbers CP014806 (chromosome) and CP014807 (plasmid). Strain PP9 is deposited in The Culture Collection of *Bacillus* and Related Genera (CCGB), under the accession no. CCGB1722.

FUNDING INFORMATION

This work, including the efforts of Lucy Seldin, was funded by MCTI | Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq). This work, including the efforts of Renata Estebanez Vollú and Lucy Seldin, was funded by Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES). This work, including the efforts of Diogo Jurelevicius and Lucy Seldin, was funded by Fundação Carlos Chagas Filho de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ). This work, including the efforts of Diogo Jurelevicius and Lucy Seldin, was funded by Petrobras.

REFERENCES

1. Vaishampayan P, Miyashita M, Ohnishi A, Satomi M, Rooney A, La Duc MT, Venkateswaran K. 2009. Description of *Rummeliibacillus stabekisii* gen. nov., sp. nov. and reclassification of *Bacillus pycnus* Nakamura et al. 2002 as *Rummeliibacillus pycnus* comb. nov. *Int J Syst Evol Microbiol* 59: 1094–1099. <http://dx.doi.org/10.1099/ijs.0.006098-0>.
2. Vollú RE, Jurelevicius D, Ramos LR, Peixoto RS, Rosado AS, Seldin L. 2014. Aerobic endospore-forming bacteria isolated from Antarctic soils as

- producers of bioactive compounds of industrial interest. *Polar Biol* 37: 1121–1131. <http://dx.doi.org/10.1007/s00300-014-1505-y>.
3. Chin C-S, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. *Nat Methods* 10:563–569. <http://dx.doi.org/10.1038/nmeth.2474>.
 4. Tatusova T, Ciufu S, Federhen S, Fedorov B, McVeigh R, Neill K, Tolstoy I, Zaslavsky L. 2015. Update on RefSeq microbial genomes resources. *Nucleic Acids Res* 43:D599–D605. <http://dx.doi.org/10.1093/nar/gku1062>.
 5. Richter M, Rosselló-Móra R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. *Proc Natl Acad Sci USA* 106: 19126–19131. <http://dx.doi.org/10.1073/pnas.0906412106>.