



HAL
open science

Genome Sequence of *Bacillus velezensis* P1, a Strain Isolated from a Biofilm Captured on a Pig Farm Building

Virgile Guéneau, Jean-Christophe Piard, Bastien Frayssinet, Valentin Loux, Hélène Chiapello, Julia Plateau-Gonthier, Mathieu Castex, Romain Briandet

► **To cite this version:**

Virgile Guéneau, Jean-Christophe Piard, Bastien Frayssinet, Valentin Loux, Hélène Chiapello, et al.. Genome Sequence of *Bacillus velezensis* P1, a Strain Isolated from a Biofilm Captured on a Pig Farm Building. *Microbiology Resource Announcements*, 2022, 10.1128/mra.01219-21 . hal-03555762

HAL Id: hal-03555762

<https://hal.inrae.fr/hal-03555762v1>

Submitted on 1 Mar 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



Genome Sequence of *Bacillus velezensis* P1, a Strain Isolated from a Biofilm Captured on a Pig Farm Building

Virgile Guéneau,^{a,b} Jean-Christophe Piard,^a Bastien Frayssinet,^b Valentin Loux,^{c,d} Hélène Chiapello,^c Julia Plateau-Gonthier,^b Mathieu Castex,^b  Romain Briandet^a

^aUniversité Paris-Saclay, INRAE, AgroParisTech, Micalis Institute, Jouy-en-Josas, France

^bLallemand SAS, Blagnac, France

^cUniversité Paris-Saclay, INRAE, MalAGE, Jouy-en-Josas, France

^dUniversité Paris-Saclay, INRAE, Bioinformatics Facility, Jouy-en-Josas, France

ABSTRACT The genome of the *Bacillus velezensis* P1 strain isolated from a biofilm on the wall of a pig farm was sequenced. The strain harbors many surface colonization genes involved in surfactant, matrix, and antibacterial synthesis.

Surface communities on the wall inside a pig farm building were sampled by using coupons installed on the surface for 31 days. Biofilms were recovered by scratching using a pipette cone and 30 mL of saline solution, and the bacterial suspension was treated for 10 min at 80°C to select heat-resistant spores. Plating the treated suspension on Trypticase soy (TS) agar at 30°C for 24 h allowed isolation of the P1 strain forming highly structured colonies on agar.

From a –80°C glycerol stock, the P1 strain was cultured in TS under agitation at 37°C overnight (~16 h). Genomic DNA was extracted and purified using the Monarch genomic DNA purification kit (New England Biolabs, Ipswich, MA, USA). DNA sequencing (DNA-seq) was performed at the GeT-PlaGe core facility (INRAE, Toulouse, France; www.genotoul.fr/en/). DNA-seq libraries were prepared according to Illumina's protocols using the TruSeq Nano DNA high-throughput (HT) library kit (Illumina, San Diego, CA, USA). Briefly, DNA was fragmented by sonication, size selection was performed using sample purification beads (SPBs) (kit beads), and adaptors were ligated to be sequenced. Library quality was assessed using the Agilent DNF-474 high-sensitivity (HS) next-generation sequencing (NGS) fragment kit (Agilent Technologies, Santa Clara, CA, USA), and libraries were quantified by quantitative PCR (qPCR) using the Kapa library quantification kit (Roche, Basel, Switzerland). DNA-seq experiments were performed on an Illumina NovaSeq 6000 system, using a paired-end read length of 2 × 150 bp with the Illumina NovaSeq 6000 reagent kits (Illumina). Verification of the libraries was done using NanoDrop quantification (NanoDrop 8000; Thermo Scientific, Waltham, MA, USA). The reads (5,299,802 sequences, sequence length of 150 bp) were analyzed using tools available in Galaxy with default parameters (<https://galaxy.migale.inrae.fr/>) (1). *De novo* assembly was performed using Unicycler (Galaxy version 0.4.8.0) with quality control done with Quast (Galaxy version 5.0.2 + Galaxy 3) (2, 3), and genome annotation was performed using the Prokaryotic Genome Annotation Pipeline (PGAP, annotation software revision 5.2) (4). The percent genome coverage is 201, and the size of the assembly is 3,901,648 bp, made of 26 contigs with a GC content of 47% and an N_{50} value of 564,796 nucleotides. A total of 3,766 predicted protein-coding genes were detected with 78 tRNAs, 3 rRNAs, and 5 noncoding RNAs (ncRNAs). The bacterial species identified with more than 99.9% identity is *Bacillus velezensis* as determined by a BLAST search of the genome of 100 kb, using the nucleotide database collection of *Bacillus* (taxid: 1386) optimized for highly similar sequences. The Staramr tool (Galaxy version 0.7.2 + Galaxy 0) revealed that *B. velezensis* P1 does not harbor antibiotic resistance genes (<https://github.com/phac-nml/staramr>) and that no plasmids were predicted.

Editor Steven R. Gill, University of Rochester School of Medicine and Dentistry

Copyright © 2022 Guéneau 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 Romain Briandet, romain.briandet@inrae.fr.

The authors declare no conflict of interest.

Received 21 December 2021

Accepted 9 January 2022

Published 27 January 2022

Different genes involved in biofilm formation were detected in the genome (i.e., *eps*, *sps*, *cap*, *tapA*→*tasA*, *bslA*) (5–7). Using the antiSMASH genome analysis tool, 5 antibacterial genes were detected, encoding with a coverage of more than 98% bacillibactin, macrolactin, bacillaene, diffidin, and bacilysin (8, 9).

The biofilm formation and antimicrobial secretion properties of *B. velezensis* P1 are assumed to confer significant fitness to live and persist in the livestock building surface biotope.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [JAHLGR000000000](https://www.ncbi.nlm.nih.gov/assembly/JAHLGR000000000) and in the NCBI Sequence Read Archive (SRA) under BioProject accession number [PRJNA736682](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA736682). The draft genome assembly and annotation can be found under BioProject number [PRJNA736682](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA736682) and BioSample number [SAMN19656044](https://www.ncbi.nlm.nih.gov/biosample/SAMN19656044), respectively.

ACKNOWLEDGMENTS

This study was funded by Lallemand Animal Nutrition, INRAE, and the Association Nationale de la Recherche et de la Technologie (ANRT) as part of Virgile Guéneau's Ph.D.

We are grateful to the INRAE MIGALE bioinformatics facility (<https://migale.inrae.fr/>) for providing technical support.

REFERENCES

- Afgan E, Baker D, Batut B, van den Beek M, Bouvier D, Cech M, Chilton J, Clements D, Coraor N, Grüning BA, Guerler A, Hillman-Jackson J, Hiltemann S, Jalili V, Rasche H, Soranzo N, Goecks J, Taylor J, Nekrutenko A, Blankenberg D. 2018. The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update. *Nucleic Acids Res* 46:W537–W544. <https://doi.org/10.1093/nar/gky379>.
- Wick RR, Judd LM, Gorrie CL, Holt KE. 2017. Unicycler: resolving bacterial genome assemblies from short and long sequencing reads. *PLoS Comput Biol* 13:e1005595. <https://doi.org/10.1371/journal.pcbi.1005595>.
- Mikheenko A, Prjibelski A, Saveliev V, Antipov D, Gurevich A. 2018. Versatile genome assembly evaluation with QUAST-LG. *Bioinformatics* 34:i142–i150. <https://doi.org/10.1093/bioinformatics/bty266>.
- Li W, O'Neill KR, Haft DH, DiCuccio M, Chetverin V, Badretdin A, Coulouris G, Chitsaz F, Derbyshire MK, Durkin AS, Gonzales NR, Gwadz M, Lanczycki CJ, Song JS, Thanki N, Wang J, Yamashita RA, Yang M, Zheng C, Marchler-Bauer A, Thibaud-Nissen F. 2021. RefSeq: expanding the Prokaryotic Genome Annotation Pipeline reach with protein family model curation. *Nucleic Acids Res* 49:D1020–D1028. <https://doi.org/10.1093/nar/gkaa1105>.
- Diehl A, Roske Y, Ball L, Chowdhury A, Hiller M, Molière N, Kramer R, Stöppler D, Worth CL, Schlegel B, Leidert M, Cremer N, Erdmann N, Lopez D, Stephanowitz H, Krause E, van Rossum B-J, Schmieder P, Heinemann U, Turgay K, Akbey Ü, Oschkinat H. 2018. Structural changes of TasA in biofilm formation of *Bacillus subtilis*. *Proc Natl Acad Sci U S A* 115:3237–3242. <https://doi.org/10.1073/pnas.1718102115>.
- Eichenberger P, Fujita M, Jensen ST, Conlon EM, Rudner DZ, Wang ST, Ferguson C, Haga K, Sato T, Liu JS, Losick R. 2004. The program of gene transcription for a single differentiating cell type during sporulation in *Bacillus subtilis*. *PLoS Biol* 2:e328. <https://doi.org/10.1371/journal.pbio.0020328>.
- Earl C, Arnaouteli S, Bamford NC, Porter M, Sukhodub T, MacPhee CE, Stanley-Wall NR. 2020. The majority of the matrix protein TapA is dispensable for *Bacillus subtilis* colony biofilm architecture. *Mol Microbiol* 114:920–933. <https://doi.org/10.1111/mmi.14559>.
- Blin K, Shaw S, Steinke K, Villebro R, Ziemert N, Lee SY, Medema MH, Weber T. 2019. antiSMASH 5.0: updates to the secondary metabolite genome mining pipeline. *Nucleic Acids Res* 47:W81–W87. <https://doi.org/10.1093/nar/gkz310>.
- Chen XH, Koumoutsis 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, Borriss R. 2007. Comparative analysis of the complete genome sequence of the plant growth-promoting bacterium *Bacillus amyloliquefaciens* FZB42. *Nat Biotechnol* 25:1007–1014. <https://doi.org/10.1038/nbt1325>.