ᵃ | Bacteriology | Announcement

Draft genome sequence of type strain *Streptomyces brasiliscabiei* IBSBF 2867ᵀ

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ABSTRACT Here, we report the draft genome sequence of *Streptomyces* IBSBF 2867ᵀ, associated with potato scab in Brazil. Genome analysis using the antiSMASH bioinformatics tool showed the presence of phytopathogenic biosynthetic pathways.

Potato scab, caused by phytopathogenic *Streptomyces*, is a complex disease that affects the crop with widespread occurrence in the main producing regions of Brazil and the world (1, 2). The symptoms are characterized by lesions on the tuber surface, which decrease its commercial value or even prevent commercialization, both for consumption and to serve as seeds (3, 4).

Potato tubers exhibiting scab lesions, from production area in Santa Catarina State, Brazil, were disinfected with 1.5% NaOCl/1 min and rinsed with sterile distilled water. After cutting, the scab lesions were placed in a tube with sterile water, incubated at 55°C/30 min, and then macerated in a microscope slide with sterile water. A drop of this suspension was streaked onto water agar medium, and the plates were incubated at 28°C/10 d. Characteristic colonies of *Streptomyces* were picked, transferred to ISP 2 medium at 28°C/14 d (5), and subsequently identified as *S. brasiliscabiei* IBSBF 2867ᵀ. The type strain showed morphological, physiological, and biochemical characteristics very similar to *S. scabiei*, bacterial species widely distributed in the world, as well as the main pathogenicity factors: taxtomin, *nec* 1, and tomatinase, but with different genomic features (1).

DNA extraction of *S. brasiliscabiei* IBSBF 2867ᵀ was performed according to Corrêa et al. (6), and the genome sequencing was carried out by Biotecnologia Pesquisa e Inovacão, Botucatu, Brazil, using the Illumina HiSeq 2500 next-generation sequencing platform with a 2×100 bp paired-end protocol. The sequencing library was prepared using the TruSeq DNA library preparation kit with the standard Illumina DNA protocol. The raw reads were quality trimmed (including adapters removal) using Seqyclean software and *de novo* assembled using SPAdes 3.14.1 (7) in "isolate" mode. The SSPACE_basicv2.pl script (8) was used to improve the scaffold pre-assembled contigs using the paired-end library, and the quality of the genome assembly was assessed using QUAST (9). The draft genome, genes, and proteins were annotated with the DFAST web-based genome annotation tool (10). Default parameters were used for all software unless otherwise specified.

The whole-genome sequencing resulted in, approximately, 2.1 Gb raw reads. *De novo* genome was assembled into 1,319 scaffolds (N_{50}, 40,518 bp), comprising a total of 10,846,379 bp with a GC content average of 71.3%. The draft genome annotation predicted a total of 9,179 putative genes, 3 rRNAs, 89 tRNAs, and 1 CRISPR annotated. The highest percentage of genes is involved in catalytic activity (~15%) and in metabolic processes within the category of biological process.

Analysis using antiSMASH 6.0 online tool showed 42 biosynthetic clusters associated with different secondary metabolites were also identified. Two predicted pathways showed high homology to biosynthetic plant pathology gene clusters: *thaxtomin D/thaxtomin A/thaxtomin C/thaxtomin B* gene clusters showed 83% similarity with *Streptomyces scabiei* 87.22, and the *concanamicin A* gene cluster showed 82% similarity with *Streptomyces neyagawaensis*.

ACKNOWLEDGMENTS

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FUNDING

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DATA AVAILABILITY

The whole-genome sequence has been deposited at DDBJ/ENA/GenBank under the accession number PRJNA632639, for the assembly JABRXD000000000.1, and reads in SRA SRX8353089. The version described in this paper is the first version.

REFERENCES

1. Corrêa DBA, do Amaral DT, da Silva MJ, Destéfano SAL. 2021. *Streptomyces brasiliscabiei*, a new species causing potato scab in South Brazil. Antonie Van Leeuwenhoek 114:913–931. https://doi.org/10.1007/s10482-021-01566-y

2. Destéfano SAL, Vitor L, Corrêa DBA, Tomaseto AA, Monteiro R dos S. 2021. Streptomyces spp. associadas à Sarna DA Batata. RAPP 27:91–117. https://doi.org/10.31976/0104-038321v270005

3. Dees MW, Wanner LA. 2012. In search of better management of potato common scab. Potato Res 55:249–268. https://doi.org/10.1007/s11540-012-9206-9

4. Jansky S, Douches D, Haynes K. 2018. Release: three tetraploid potato clones with resistance to common scab. Am. J. Potato Res 95:178–182. https://doi.org/10.1007/s12230-017-9624-y

5. Shirling EB, Gottlieb D. 1966. Methods for characterization of *Streptomyces* species. International Journal of Systematic Bacteriology 16:313–340. https://doi.org/10.1099/00207713-16-3-313

6. Corrêa DBA, Salomão D, Rodrigues-Neto J, Harakava R, Destéfano SAL. 2015. Application of PCR-RFLP technique to species identification and phylogenetic analysis of *Streptomyces* associated with potato scab in Brazil based on partial atpD gene sequences. Eur J Plant Pathol 142:1–12. https://doi.org/10.1007/s10658-014-0584-5

7. 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

8. Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W. 2011. Scaffolding pre-assembled Contigs using SSPACE. Bioinformatics 27:578–579. https://doi.org/10.1093/bioinformatics/btq683

9. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. https://doi.org/10.1093/bioinformatics/btt086

10. Tanizawa Y, Fujisawa T, Nakamura Y. 2018. DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. Bioinformatics 34:1037–1039. https://doi.org/10.1093/bioinformatics/btx713