Draft Genome Sequence of a Streptomycete Isolated from Potato Common Scab Lesions in the State of Sinaloa, Mexico

Amanda Alejo-Viderique,a Luis Contreras-Castro,a Rubén Félix-Gastélumb, Luis A. Maldonado,c Erika T. Quintanaa

aLaboratorio de Bioprospección en Actinobacterias, Escuela Nacional de Ciencias Biológicas (ENCB), Instituto Politécnico Nacional (IPN), Mexico City, Mexico
bDepartamento de Ciencias Biológicas, Unidad Los Mochis, Universidad de Occidente, Los Mochis, Sinaloa, Mexico
cFacultad de Química, Universidad Nacional Autónoma de México (UNAM), Mexico City, Mexico

ABSTRACT  Streptomyces sp. strain V2 was isolated from potato scab lesions in the state of Sinaloa, Mexico, and appears to be responsible for outbreaks in the area. The thaxtomin cluster was found in the ~10.2-Mb genome; this cluster is associated with potato common scab disease in other potato pathogens.

The genus Streptomyces, class Actinobacteria, currently contains 533 described species, most of them isolated from soil (their primary natural habitat), although there are reports of species recovered from both freshwater and marine environments (1). Among this high number of described species, only a few are considered human and plant pathogens (2, 3).

Some of these plant pathogens cause economically important diseases, such as potato common scab (PCS), which appears as shallow or deep corky blemishes that disfigure the potato skin, which consequently needs excessive peeling (4). Streptomyces scabiei is regarded as the predominant PCS agent worldwide (5), although S. acidiscabies, S. turgidiscabies, S. europaeiscabies, S. stelliscabies, S. luridiscabies, and S. niveiscabies (6–9) have also been recovered from PCS lesions. These pathogenic strains have a polyphyletic nature and have been related by a transmissible pathogenicity island which seems to confer the pathogenic phenotype on some species. The main pathogenic factor of this phenotype is the production of the phytotoxin thaxtomin, a nitrated dipeptide which inhibits cellulose synthesis in expanding plant tissue (10, 11).

Streptomyces sp. strain V2 was recovered as part of a study in the state of Sinaloa, Mexico, of the diversity of PCS lesions related to or associated with bacteria. At the time of writing, this ongoing study has recovered 22 actinobacterial strains identified by nearly complete 16S rRNA gene sequences and includes not only streptomycetes but also rare actinobacteria (i.e., Amycolatopsis and Lentzea spp.). Currently, studies are being conducted to establish either the pathogenic relationship of each isolate to the PCS lesion or its merely saprophytic role within the tubercle (A. Alejo-Viderique, E. Burgueño, L. A. Maldonado, G. Herrera, R. Felix, and E. T. Quintana, unpublished data).

The genome of strain V2 was sequenced by ChunLab (Seoul, South Korea) using the Illumina MiSeq sequencing platform. The obtained reads were assembled with SPAdes 3.1.1 (12). The genome size is 10.2 Mb. The GC content was found to be 71%. Two-way comparison of the average nucleotide identity (ANI) values (13) of S. scabiei and S. acidiscabies indicated values of 82.74% and 93.35%, respectively, suggesting that isolate V2 should constitute a novel species. The genome was annotated with the NCBI Prokaryotic Genome Annotation Pipeline (14). The number of genes was 9,222, with 68 tRNAs, 8 complete rRNAs, 3 noncoding RNAs, and 4 CRISPR arrays. Mining of the genome using antiSMASH 3.0 (15) found 53 potential secondary metabolite-related
clusters. The antiSMASH suite predicted the presence of gene clusters related to the production of albaflavenone, alnumycin, ansamitocin, cahuitamycin, coelbactin, coelcrinel, desferrioxamine B, desotamide, ectoine, furauquinocin A, gamma-butyrolactone, grincamycin, herboxidiene, hopene, informatipeptin, jawsamycin, kanamycin, kedarcidin, lactonamycin, laspartomycin, mensacaricin, nikkomycin, oxazolomycin, pactamycin, pristinamycin, salinamides, skyllamycin, and xantholipin, among others predicted by the Web tool NaPDos (16). It is worth mentioning that the phytotoxin thaxtomin cluster was also found, with over 50% of the genes showing similarity to the cluster of <i>S. scabiei</i>.

**Data availability.** This whole-genome shotgun project has been deposited in GenBank under the accession no. QFDR00000000. The version described in this paper is the first version, QFDR01000000.

**ACKNOWLEDGMENTS**

These actinobacterial diversity studies were part of a collaboration between UNAM (Instituto de Ciencias del Mar y Limnología [L.A.M.]) and IPN (Escuela Nacional de Ciencias Biológicas [E.T.Q.]) under the UNAM code UNAM 32939-2163-16-X-12 (2012 to 2016).

Sequencing expenses were sponsored by Consejo Nacional de Ciencia y Tecnología (CONACyT Mexico) project no. 180692 (to L.A.M.). A.A.V. and L.C.C. were sponsored by Ph.D. scholarships from CONACyT Mexico, no. 246635 and 270230, respectively.

**REFERENCES**

1. Kämper P. 2015. <i>Streptomyces</i>. In Whitman WB, Rainey F, Kämper P, Trujillo M, Chun J, DeVos P, Hedlund B, Dedysh S (ed), Bergey’s manual of systematics of archaea and bacteria. John Wiley & Sons, New York, NY.
2. Quintana ET, Wierzbicka K, Mackiewicz P, Osman A, Fahal AH, Hamid ME, Zakrzewska-Czerwinska J, Maldonado LA, Goodfellow M. 2008. <i>Streptomyces sudanensis</i> sp. nov., a new pathogen isolated from patients with actinomycetoma. Antonie Van Leeuwenhoek 93:305–313. https://doi.org/10.1007/s10482-007-9205-z.
3. Tomihama T, Nishi Y, Sakai M, Ikemata M, Okubo T, Ikeda S. 2016. Draft genome sequences of <i>Streptomyces scabiei</i> SS9, <i>Streptomyces turgidiscabies</i> T45, and <i>Streptomyces acidiscabies</i> a10, the pathogens of potato common scab, isolated in Japan. Genome Announc 4:e00062-16. https://doi.org/10.1128/genomeA.00062-16.
4. Leiminger J, Frank M, Wenk C, Poschenrieder G, Kellermann A, Schwarzfelscher A. 2013. Distribution and characterization of <i>Streptomyces</i> species causing potato common scab in Germany. Plant Pathol 62:611–623. https://doi.org/10.1111/j.1365-3059.2012.02659.x.
5. Lambert DH, Loria R. 1989. <i>Streptomyces scabies</i> sp. nov., norm. rev. Int J Syst Bacteriol 39:387–392. https://doi.org/10.1099/00207713-39-4-387.
6. Lambert DH, Loria R. 1989. <i>Streptomyces acidiscabies</i> sp. nov. Int J Syst Bacteriol 39:393–396. https://doi.org/10.1099/00207713-39-4-393.
7. Miyajima K, Tanaka F, Takeuchi T, Kuninaga S. 1998. <i>Streptomyces turgidiscabies</i> sp. nov. Int J Syst Bacteriol 48:495–502. https://doi.org/10.1099/00207713-48-2-495.
8. Bouchech-Mechiche K, Gardan L, Normand P, Jouan B. 2000. DNA relatedness among strains of <i>Streptomyces</i> pathogenic to potato in France: description of three new species, <i>S. europaeiscabiei</i> sp. nov., and <i>S. stelliscabiei</i> sp. nov. associated with common scab, and <i>S. reticulisabiei</i> sp. nov. associated with netted scab. Int J Syst Evol Microbiol 50:91–99. https://doi.org/10.1099/00207713-50-1-91.
9. Park DH, Kim JS, Kwon SW, Wilson C, Yu YM, Hur JH, Lim CK. 2003. <i>Streptomyces luridiscabiei</i> sp. nov., <i>Streptomyces puniciscabiei</i> sp. nov. and <i>Streptomyces niveiscabiei</i> sp. nov., which cause potato common scab disease in Korea. Int J Syst Evol Microbiol 53:2049–2054. https://doi.org/10.1099/ijs.0.02629-0.
10. Loria R, Kers J, Joshi M. 2006. Evolution of plant pathogenicity in <i>Streptomyces</i>. Annu Rev Phytopathol 44:469–487. https://doi.org/10.1146/annurev.phyto.44.032905.091147.
11. Loria R, Bignell DRD, Moll S, Huguet-Tapia JC, Joshi MV, Johnson EG, Seipke RF, Gibson DM. 2008. Thaxtomin biosynthesis: the path to plant pathogenicity in the genus <i>Streptomyces</i>. Antonie Van Leeuwenhoek 94:3–10. https://doi.org/10.1007/s10482-008-9240-4.
12. Bankевич A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenski SI, Pham S, Prijelbski AD, Pyshkin AV, Sirotkin AV, Vyakhni 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.
13. Rodriguez-R LM, Konstantinidis KT. 2016. The enveomics collection: a toolbox for specialized analyses of microbial genomes and metagenomes. PeerJ Preprints 4:e1900v1. https://doi.org/10.7277/peerj.preprints.1900v1.
14. Ivanova N, Jakovljevic V, Dettenberger K, Tettelin H, Tiedje JM, Kyrpides NC. 2012. PATRIC: a multifaceted database and analysis resource for pathogenic bacteria. Nucleic Acids Res 40:D533–D541. https://doi.org/10.1093/nar/gkr441.
15. de la Fuente J, Fariñas A, Alcalde TF, García-Donausquía D, García-Carbonero L, de la Peña M, et al. 2015. A global survey of antimicrobial resistance in Spain: the SENTRY antimicrobial surveillance program. PLoS One 10:e0137111. https://doi.org/10.1371/journal.pone.0137111.
16. Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyakhni 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.
17. Rodriguez-R LM, Konstantinidis KT. 2016. The enveomics collection: a tool-box for specialized analyses of microbial genomes and metagenomes. PeerJ Preprints 4:e1900v1. https://doi.org/10.7277/peerj.preprints.1900v1.
18. Tatusova T, DiCuccio M, Badretdin A, Chevtserina V, Ciufo S, Li W. 2013. Prokaryotic genome annotation pipeline. The NCBI handbook [Internet]. 2nd ed. NCBI, Bethesda, MD. https://www.ncbi.nlm.nih.gov/books/NBK174280.
19. Weber T, Blin K, Duddela S, Krug D, Kim HU, Brucoceri R, Lee SY, Fischbach MA, Müller R, Wohleben W, Breitling R, Takano E, Medema MH. 2015. <i>antiSMASH 3.0</i>—a comprehensive resource for the genome mining of biosynthetic gene clusters. Nucleic Acids Res 43:W237–W243. https://doi.org/10.1093/nar/gkv437.
20. Ziemert N, Podell S, Penn K, Badger JH, Allen E, Jensen PR. 2012. The natural product domain seeker NaPDos: a phylogeny based bioinformatic tool to classify secondary metabolite gene diversity. PLoS One 7:e34064. https://doi.org/10.1371/journal.pone.0034064.

Volume 7 Issue 5 e00827-18 mra.asm.org 2