Complete Genome Sequence of *Streptomyces albus* SM254, a Potent Antagonist of Bat White-Nose Syndrome Pathogen *Pseudogymnoascus destructans*

Jonathan P. Badalamenti,*a* Joshua D. Erickson,*b* Christine E. Salomon*b*

BioTechnology Institute, University of Minnesota, Saint Paul, Minnesota, USAa; Center for Drug Design, University of Minnesota, Minneapolis, Minnesota, USA

* Present address: Joshua D. Erickson, Rebiotix Inc., Roseville, Minnesota, USA.

We sequenced and annotated the complete 7,170,504-bp genome of a novel secondary metabolite-producing *Streptomyces albus* strain, *Streptomyces albus* SM254, isolated from copper-rich subsurface fluids at ∼220-m depth within the Soudan Iron Mine (Soudan, MN, USA).

White-nose syndrome (WNS) is a devastating disease caused by the psychrophilic fungus *Pseudogymnoascus destructans* which affects bats in the United States and Canada (1). One approach toward disease treatment or prevention is the development of microbial biological control agents for application on or near bats and roost areas (2, 3). We isolated bacteria and fungi from bat swabs, roosts, and other subterranean surfaces near hibernacula areas and screened for antifungal activities in direct competition assays. One *Streptomyces* isolate obtained from high copper sediments in the Soudan Iron Mine exhibited potent antagonistic activity against *P. destructans*. We initiated studies of the genome of *S. albus* SM254 to identify the potential biosynthetic pathways responsible for producing antifungal metabolites.

Sediments were collected from a shallow pool on level 10 of the Soudan Mine (∼220-m depth). Samples were diluted in artificial seawater (ASW), vortexed, and plated onto ISP2 media made with Soudan Mine (~220-m depth). Samples were diluted in artificial pathways responsible for producing antifungal metabolites. *S. albus* genome of *tagonistic activity against copper sediments in the Soudan Iron Mine exhibited potent an-

Like other *Streptomyces* spp., the *S. albus* SM254 genome is replete with biosynthetic genes for secondary metabolites (antiSMASH v3), including terpene, lantipeptide, bacteriocin, nonribosomal peptide synthetase, and polyketide synthase gene clusters.

**Nucleotide sequence accession numbers.** Sequences have been deposited in GenBank under accession number CP014485. Raw Illumina and PacBio reads, as well as base modification data, have been deposited to the NCBI Sequence Read Archive under BioProject PRJNA295319.

**ACKNOWLEDGMENTS**

Illumina sequencing was performed at the University of Minnesota Genomics Center and computational analyses were performed at the Minnesota Supercomputing Institute. We thank Karl Oles (Mayo Clinic Bioinformatics Core) for performing PacBio library preparation and sequencing. We thank Christopher Gelbmann for isolation of the strain and Michael Wilson for antifungal testing with *Pseudogymnoascus destructans*. We are grateful to Jim Essig and the Soudan Mine State Park staff for field assistance.

**FUNDING INFORMATION**

This work, including the efforts of Jonathan Badalamenti and Christine E. Salomon, was funded by Minnesota Environment and Natural Resources Trust Fund (M.L.2013CHF.52SCC2SUBD3F).

This work was supported in part by the Center for Drug Design.
REFERENCES

1. Blehert DS, Hicks AC, Behr M, Meteyer CU, Berlowski-Zier BM, Buckles EL, Coleman JTH, Darling SR, Gargas A, Niver R, Okoniewski JC, Rudd RJ, Stone WB. 2009. Bat white-nose syndrome: an emerging fungal pathogen? Science 323:227. http://dx.doi.org/10.1126/science.1163874.

2. Cornelison CT, Keel MK, Gabriel KT, Barlament CK, Tucker TA, Pierce GE, Crow SA. 2014. A preliminary report on the contact-independent antagonism of Pseudogymnoascus destructans by Rhodococcus rhodochrous strain DAP96253. BMC Microbiol 14:246. http://dx.doi.org/10.1186/s12866-014-0246-y.

3. Hoyt JR, Cheng TL, Langwig KE, Hee MM, Frick WF, Kilpatrick AM. 2015. Bacteria isolated from bats inhibit the growth of Pseudogymnoascus destructans, the causative agent of white-nose syndrome. PLoS One 10: e0121329. http://dx.doi.org/10.1371/journal.pone.0121329.

4. 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.

5. Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakhikumar S, Cuomo CA, Zeng Q, Wortman J, Young SK, Earl AM. 2014. Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. PLoS One 9:e112963. http://dx.doi.org/10.1371/journal.pone.0112963.

6. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. http://dx.doi.org/10.1093/bioinformatics/btu153.

7. Oden S, Brocchieri L. 2015. Quantitative frame analysis and the annotation of GC-rich (and other) prokaryotic genomes: an application to Anaeromyxobacter dehalogenans. Bioinformatics 31:3254–3261. http://dx.doi.org/10.1093/bioinformatics/btv339.

8. Suzuki T, Miyachi K. 2010. Discovery and characterization of tRNAlle lysidine synthetase (TIlS). FEBS Lett 584:272–277. http://dx.doi.org/10.1016/j.febslet.2009.11.085.