genomeA
Journals.ASM.org

Draft Genome Sequences of Four *Streptomyces* Isolates from the *Populus trichocarpa* Root Endosphere and Rhizosphere

Dawn M. Klingeman,[a] Sagar Utturkar,[b] Tse-Yuan S. Lu,[a] Christopher W. Schadt,[a,b] Dale A. Pelletier,[a,b] Steven D. Brown[a,b]

Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA[a]; Graduate School of Genome Science and Technology, University of Tennessee, Knoxville, Tennessee, USA[b]

D.M.K. and S.U. contributed equally to this work.

Draft genome sequences for four *Actinobacteria* from the genus *Streptomyces* are presented. *Streptomyces* is a metabolically diverse genus that is abundant in soils and has been reported in association with plants. The strains described in this study were isolated from the *Populus trichocarpa* endosphere and rhizosphere.

Received 28 September 2015 **Accepted** 30 September 2015 **Published** 12 November 2015

Citation Klingeman DM, Utturkar S, Lu T-YS, Schadt CW, Pelletier DA, Brown SD. 2015. Draft genome sequences of four *Streptomyces* isolates from the *Populus trichocarpa* root endosphere and rhizosphere. Genome Announc 3(6):e01344-15. doi:10.1128/genomeA.01344-15.

Copyright © 2015 Klingeman et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Steven D. Brown, brownsd@ornl.gov.

The *Actinobacteria* phylum contains genera of astonishing diversity of form and function (1). Its members include pathogens of plants, humans and other mammals, nitrogen fixers (*Frankia*), and *Corynebacterium glutamicum* for industrial amino acid production. Genera such as the *Streptomyces* are rich sources for natural products (e.g., antibiotics) and can form endophytic relationships (1–3). *Actinobacteria* are Gram-positive bacteria that usually have high G+C DNA content and are typically filamentous. Our recent bacterial analyses of root microbiomes from mature *Populus deltoides* in Tennessee and North Carolina based on 16S rRNA analyses have identified *Actinobacteria* at the operational taxonomic unit level as, similar to the genus *Streptomyces*, common and often dominant within the endosphere (4). Genome sequences for a number of bacteria isolated from the rhizosphere and endosphere of *P. deltoides* have been reported (5, 6); however, to date, genome sequences for *Streptomyces* isolated from *Populus* have not been reported.

To better understand plant-microbe interactions and to further investigate the role of *Streptomyces* in association with *Populus*, draft genome sequences for three *Streptomyces* strains isolated from the *Populus trichocarpa* endosphere (OK006, OK074, OV320) and one strain from the rhizosphere (OV450) were generated. The strains were isolated from two different common gardens located in Oregon, USA. Strains with the designation OV were collected from Corvallis, and strains designated OK were from Clatskanie.

DNA sequence data were obtained from Illumina paired-end and mate-pair libraries with average insert sizes of 500 bp and 4 kb, respectively; each was sequenced using a MiSeq instrument in 2 × 151-bp configuration according to manufacturer's protocols. For each genome, multiple assembly approaches were tested as described previously (7), and the SPAdes version 3.1 assembly algorithm (8) gave the best results. Draft genome sequences for strains OV320, OK006, OK074, and OV450, comprised 38, 291, 318, and 390 contigs (>500 bp), respectively. The estimated genome sizes ranged from approximately 9.2 to 11.9 Mb, and the N_{50} statistics ranged from 50 to 627 kb. Gene predictions were based on the Prodigal algorithm (9), and the annotations were performed as part of an ORNL annotation pipeline, used previously (7). An analysis of the 16S rDNA sequences revealed that strains OK006, OK074, OV320, and OV450 were 99% identical to cognate sequences from *Streptomyces* sp. JL164 (accession no. AF101414), *Streptomyces lincolnensis* strain cfcc3132 (accession no. GQ258686), *Streptomyces rishiriensis* strain 1706 (accession no. KC336416), and *Streptomyces* sp. 10-1 (accession no. AB222068), respectively. The 16S rDNA sequences from strains OK006, OV320, and OV450 were 97% identical to the 16S rDNA sequence from the model *Streptomyces coelicolor* A3(2), and strain OK074 was 96% identical.

The new *Streptomyces* spp. genomes all encode for cytochrome P450s, which are important enzymes involved in drug metabolism and bioactivation (10), secondary metabolism genes (e.g., polyketide synthases), mono- and dioxygenases, and genes for the breakdown of various cell wall components (e.g., chitinases, endo-1,4-beta-xylanases, endo-1,4-beta-glucanases). The availability of these new bacterial genome sequences, along with those reported previously, and the plethora of genome sequences from ongoing studies will facilitate a deeper understanding of plant-microbe interactions and insights into the *Streptomyces*.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers LJCU00000000, LJCV00000000, LJCW00000000, and LJCX00000000 for strains OK006, OK074, OV450, and OV320, respectively. The versions described in this report are the first versions, LJCU01000000, LJCV01000000, LJCW01000000, and LJCX01000000.

ACKNOWLEDGMENTS

We thank Miriam Land (ORNL) for maintaining the microbial genome annotation pipeline.

This research was sponsored by the Genomic Science Program, U.S. Department of Energy, Office of Science, Biological and Environmental Research, as part of the Plant Microbe Interfaces Scientific Focus Area

Downloaded from http://genomea.asm.org/ on September 6, 2016 by Oak Ridge Nat'l Lab

(http://pmi.ornl.gov). Oak Ridge National Laboratory is managed by UT-Battelle LLC, for the U.S. Department of Energy under contract DEAC05-00OR22725.

REFERENCES

1. **Chandra G, Chater KF**. 2014. Developmental biology of *Streptomyces* from the perspective of 100 actinobacterial genome sequences. FEMS Microbiol Rev **38:**345–379. http://dx.doi.org/10.1111/1574-6976.12047.
2. **Golinska P, Wypij M, Agarkar G, Rathod D, Dahm H, Rai M**. 2015. Endophytic actinobacteria of medicinal plants: diversity and bioactivity. Antonie Van Leeuwenhoek **108:**267–289. http://dx.doi.org/10.1007/s10482-015-0502-7.
3. **Hopwood DA**. 2006. Soil to genomics: the *Streptomyces* chromosome. Annu Rev Genet **40:**1–23. http://dx.doi.org/10.1146/annurev.genet.40.110405.090639.
4. **Shakya M, Gottel N, Castro H, Yang ZK, Gunter L, Labbé J, Muchero W, Bonito G, Vilgalys R, Tuskan G, Podar M, Schadt CW**. 2013. A multifactor analysis of fungal and bacterial community structure in the root microbiome of mature *Populus deltoides* trees. PLoS One **8:**e76382. http://dx.doi.org/10.1371/journal.pone.0076382.
5. **Brown SD, Klingeman DM, Lu T-S, Johnson CM, Utturkar SM, Land ML, Schadt CW, Doktycz MJ, Pelletier DA**. 2012. Draft genome sequence of *rhizobium* sp. strain PDO1-076, a bacterium isolated from *Populus deltoides*. J Bacteriol **194:**2383–2384. http://dx.doi.org/10.1128/JB.00198-12.
6. **Brown SD, Utturkar SM, Klingeman DM, Johnson CM, Martin SL, Land ML, Lu T-S, Schadt CW, Doktycz MJ, Pelletier DA**. 2012. Twenty-one genome sequences from *Pseudomonas* species and 19 genome sequences from diverse bacteria isolated from the rhizosphere and endosphere of *Populus deltoides*. J Bacteriol **194:**5991–5993. http://dx.doi.org/10.1128/JB.01243-12.
7. **Utturkar SM, Klingeman DM, Land ML, Schadt CW, Doktycz MJ, Pelletier DA, Brown SD**. 2014. Evaluation and validation of *de novo* and hybrid assembly techniques to derive high-quality genome sequences. BioInformatics **30:**2709–2716. http://dx.doi.org/10.1093/bioinformatics/btu391.
8. **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. http://dx.doi.org/10.1089/cmb.2012.0021.
9. **Hyatt D, Chen G, LoCascio PF, Land ML, Larimer FW, Hauser LJ**. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinformatics **11:**119. http://dx.doi.org/10.1186/1471-2105-11-119.
10. **Kelly SL, Kelly DE**. 2013. Microbial cytochromes P450: biodiversity and biotechnology. Where do cytochromes P450 come from, what do they do and what can they do for us? Philos Trans R Soc B Biol Sci **368:**20120476. http://dx.doi.org/10.1098/rstb.2012.0476.

Downloaded from http://genomea.asm.org/ on September 6, 2016 by Oak Ridge Nat'l Lab