Complete Genome Sequence of the African Strain AXO1947 of Xanthomonas oryzae pv. oryzae

J. C. Huguet-Tapia,a Z. Peng,b B. Yang,c Z. Yin,d S. Liu,a F. F. Whitea

Department of Plant Pathology, University of Florida, Gainesville, Florida, USA; Department of Plant Pathology, Kansas State University, Manhattan, Kansas, USA; Department of Genetics, Development and Cell Biology, Iowa State University, Ames, Iowa, USA; Temasek Life Sciences Laboratory, National University of Singapore, Singapore, Republic of Singapore

Xanthomonas oryzae pv. oryzae is the etiological agent of bacterial rice blight. Three distinct clades of X. oryzae pv. oryzae are known. We present the complete annotated genome of the African clade strain AXO194 using long-read single-molecule PacBio sequencing technology. The genome comprises a single chromosome of 4,674,975 bp and encodes for nine transcriptional activator-like (TAL) effectors. The approach and data presented in this announcement provide information for complex bacterial genome organization and the discovery of new virulence effectors, and they facilitate target characterization of TAL effectors.

Received 21 December 2015 Accepted 22 December 2015 Published 11 February 2016


ACKNOWLEDGMENTS
This work was supported by National Science Foundation research award IOS-1238189 (S.L., F.F.W., B.Y.) and the Grand Challenges Explorations Phase II grant OPP1068450 from the Bill & Melinda Gates Foundation (S.L., F.F.W., B.Y.). PacBio and Illumina sequencing services were provided by the Yale Center for Genome Analysis at Yale University and the Integrated Genomic Facility at Kansas State University, respectively.

FUNDING INFORMATION
This work was supported by National Science Foundation research award IOS-1238189 (S.L., F.F.W., B.Y.) and the Grand Challenges Explorations Phase II grant OPP1068450 from the Bill & Melinda Gates Foundation (S.L., F.F.W., B.Y.).

REFERENCES

January/February 2016 Volume 4 Issue 1 e01730-15 Genome Announcements genomea.asm.org 1


