Draft Genome Sequences of Two Strains of Xanthomonas arboricola
pv. celebensis Isolated from Banana Plants

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We report here the annotated draft genome sequences of strains Xanthomonas arboricola pv. celebensis NCPPB 1832 and NCPPB 1630 (NCPPB, National Collection of Plant Pathogenic Bacteria), both isolated from Musa species in New Zealand. This will allow the comparison of genomes between phylogenetically distant xanthomonads that have independently converged with the ability to colonize banana plants.

The bacterial genus Xanthomonas contains pathogens and commensals that collectively infect hundreds of plant species (1). Within the genus, the ability to colonize banana (Musa species) has evolved at least three times. Xanthomonas campestris pv. musacearum is responsible for banana Xanthomonas wilt in Africa (2), Xanthomonas arboricola pv. celebensis has been found in India and Indonesia (including Sulawesi) and causes drooping and chlorotic and necrotic stripes on banana leaves; bacteria can spread through the vascular system and attack the rhizome (1). It may cause rotting of the rhizome and fruit. Milder chronic infections sometimes follow acute epidemics with severe attacks, resulting in death of the plant (3). This pathogen has been described as “Xanthomonas muscicola” and as “Xanthomonas celebensis” (1, 3). Finally, Xanthomonas strains have been isolated from bananas in eastern and western Samoa that were not assigned to a named species. Genome sequences are already available for X. campestris pv. musacearum (4, 5) and for two Samoan Xanthomonas strains (6) but not for X. arboricola pv. celebensis. Genomic comparisons of these three phylogenetically disparate xanthomonads might yield insights into common strategies for colonizing bananas; therefore, we sequenced the genomes of two strains of X. arboricola pv. celebensis. Genome sequences (7–11) are available for several other strains and pathovars within the species X. arboricola, offering the possibility of identifying genomic features unique to the banana-pathogenic X. arboricola pv. celebensis.

Strains NCPPB 1630 and NCPPB 1832 were obtained from the National Collection of Plant Pathogenic Bacteria (NCPPB) at York in the United Kingdom. Both were originally isolated in 1960 by D. W. Dye from Musa species in New Zealand. The pathotype strain is NCPPB 1832 and is synonymous with LMG 677, ATCC 19045, PDGCC 1488, and ICPB XCl45. We used the Illumina HiSeq to generate 9.7 million pairs of 100-bp reads for NCPPB 1630 and 2 million pairs of 100-bp reads for NCPPB 1832; raw data are available in the Sequence Read Archive (12). De novo assembly with Velvet version 1.2.10 (13) resulted in 3 scaffolds comprising a total of 75 contigs for NCPPB 1832. For the NCPPB 1630 assembly, there were 7 scaffolds, comprising a total of 121 contigs. The contig \( N_{50} \) lengths for NCPPB 1832 and NCPPB 1630 were 172,772 and 80,994 bp, respectively. Both genomes were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (14) version 2.6 (rev. 439576).

Nucleotide sequence accession numbers. These whole-genome shotgun projects have been deposited in DDBJ/ENA/GenBank under the accession numbers JPHC00000000 (pathotype strain NCPPB 1832) and JPH00000000 (strain NCPPB 1630). The versions described in this paper are the first versions, JPHC01000000 and JPH01000000, respectively.

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REFERENCES

1. Bradbury JF. 1986. Guide to plant pathogenic bacteria (A CAB International publication). Oxford University Press, Oxford, United Kingdom.
2. Biruma M, Pillay M, Tripathi L. 2007. Banana Xanthomonas wilt: a
review of the disease, management strategies and future research directions. Afr J Biotechnol 6:953–962.

3. Elliott C. 1951. Manual of bacterial plant pathogens, 2nd ed. Chronica Botanica Company, Waltham, MA.

4. Wasukira A, Tayebwa J, Thwaites R, Paszkiewicz K, Aritua V, Kubiriba J, Smith J, Grant M, Studholme DJ. 2012. Genome-wide sequencing reveals two major sub-lineages in the genetically monomorphic pathogen Xanthomonas campestris pathovar musacearum. Genes (Basel) 3:361–377.

5. Studholme DJ, Kemen E, MacLean D, Schornack S, Aritua V, Thwaites R, Grant M, Smith J, Jones JDG. 2010. Genome-wide sequencing data reveals virulence factors implicated in banana Xanthomonas wilt. FEMS Microbiol Lett 310:182–192. http://dx.doi.org/10.1111/j.1574-6968.2010.02065.x.

6. Studholme DJ, Wasukira A, Paszkiewicz K, Aritua V, Thwaites R, Smith J, Grant M. 2011. Draft genome sequences of Xanthomonas sacchari and two banana-associated xanthomonads reveal insights into the Xanthomonas group 1 clade. Genes (Basel) 2:1050–1065.

7. Ignatov AN, Kyrova EI, Vinogradova SV, Kamionskaya AM, Schaad NW, Luster DG. 2015. Draft genome sequence of Xanthomonas arboricola strain 3004, a causal agent of bacterial disease on barley. Genome Announc 3(1):e01572-14. http://dx.doi.org/10.1128/genomeA.01572-14.

8. Ibarra Caballero J, Zerillo MM, Snelling J, Boucher G, Tisserat N. 2013. Genome sequence of Xanthomonas arboricola pv. corylina, isolated from Turkish filbert in Colorado. Genome Announc 1(3):e00246-13. http://dx.doi.org/10.1128/genomeA.00246-13.

9. Garita-Cambronero J, Serna-Vélez M, Palacio-Bielsa A, Cubero J. 2014. Draft genome sequence of Xanthomonas arboricola pv. pruni strain Xap33, causal agent of bacterial spot disease on almond. Genome Announc 2(3):e00440-14. http://dx.doi.org/10.1128/genomeA.00440-14.

10. Pereira UP, Gouran H, Nascimento R, Adaskaveg JE, Goulart LR, Dandekar AM. 2015. Complete genome sequence of Xanthomonas arboricola pv. juglandis 417, a copper-resistant strain isolated from Juglans regia L. Genome Announc 3(5):e01126-15. http://dx.doi.org/10.1128/genomeA.01126-15.

11. Higuera G, González-escalona N, Véliz C, Vera F. 2015. Draft genome sequences of four Xanthomonas arboricola pv. juglandis strains associated with walnut blight in Chile. Genome Announc 3(5):e01160-15. http://dx.doi.org/10.1128/genomeA.01160-15.

12. Leinonen R, Sugawara H, Shumway M, International Nucleotide Sequence Database Collaboration. 2011. The Sequence Read Archive. Nucleic Acids Res 39:D19–D21. http://dx.doi.org/10.1093/nar/gkq1019.

13. Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res 18:821–829. http://dx.doi.org/10.1101/gr.074492.107.

14. Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thompson N, White O. 2008. Toward an online repository of Standard Operating Procedures (SOPs) for (meta)genomic annotation. OMICS 12:137–141.