AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Draft Genome Sequences of Pathotype Strains for Three Pathovars Belonging to Three *Xanthomonas* Species

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ABSTRACT We present here the draft genome sequences of type/pathotype strains for three *Xanthomonas* species and pathovars with different host specificities, the *Hedera helix* L. pathogen *Xanthomonas hortorum* pv. *hederae* WHRI 7744 (NCPPB 939T), the rice pathogen *X. oryzae* pv. *oryzicola* WHRI 5234 (NCPPB 1585), and the cotton pathogen *X. citri* subsp. *malvacearum* WHRI 5232 (NCPPB 633).

The genus *Xanthomonas* comprises a diverse and economically important group of bacterial pathogens, some of which are quarantine pathogens that cause bacterial spots, rots, wilts, blights, and cankers of plants, leaves, stems, and fruits on a wide variety of plant species (1, 2). The majority of the pathogenic *Xanthomonas* species reveal high degrees of host specificity, and some are divided into multiple pathovars based on their host specificity. The formal description of each species includes a type strain, and each pathovar has a designated pathotype strain.

Xanthomonas hortorum pv. *hederae* causes bacterial leaf spot and stem canker on English ivy (*Hedera helix* L.), as well as on plants of the genera *Dizygotheca*, *Schefflera*, *Brassaia*, *Polyscias*, and *Fatsia* and on the species *Fatshedera araliaceous*. It was originally described in France in 1920 (3, 4). Vauterin et al. in 1990 (5) proposed the reclassification of this pathovar from *X. campestris* to *X. hortorum* pv. *hederae* based on DNA hybridization, metabolic similarities, and protein profiles. The type strain of the species *X. hortorum* and pathotype strain of *X. hortorum* pv. *hederae* (WHRI 7744 = NCPPB 939 = ICMP 453) originates from the United States in 1943.

Bacterial leaf streak (BLS) caused by *X. oryzae* pv. *oryzicola* was first reported in the Philippines in 1918 and is present in tropical and subtropical Asia, including China, Malaysia, India, and Indonesia, and also in northern Australia and West Africa (6–8). Several studies, based on DNA fingerprinting, revealed high variability among *X. oryzae* pv. *oryzicola* strains (7, 8). The pathotype strain (WHRI 5234 = NCPPB 1585 = ICMP 5743) is from Malaysia from 1964.

X. citri subsp. *malvacearum* causes bacterial blight of cotton plants (9). This is one of the most devastating bacterial diseases that plague cotton plants worldwide. *X. citri* subsp. *malvacearum* has a wide range of aggressiveness depending on the host species (10, 11), and 19 physiological races have been identified. Race 1 is widespread in Australia, India, and the United States, and race 18 is present in Australia, Nicaragua, and India. Races 6, 7, and 10 were reported in Nigeria, and races 1, 2, 8, 21, 26, and 32 were reported in Syria (9). The pathotype strain (WHRI 5232 = NCPPB 633 = ICMP 5739) is from Sudan and was obtained in 1958.

The *Xanthomonas* strains were routinely grown in nutrient agar broth (peptone A, 6.0 g/liter; beef extract, 1.0 g/liter; yeast extract, 2.0 g/liter; sodium chloride, 5.0 g/liter; pH, ~7.3) with aeration (180 rpm) at 28°C. The genomic DNA was extracted according to bacterial genomic DNA isolation using cetyltrimethylammonium bromide (12). The

Received 3 July 2018 **Accepted** 2 September 2018 **Published** 27 September 2018

Citation Michalopoulou VA, Vicente JG, Studholme DJ, Sarris PF. 2018. Draft genome sequences of pathotype strains for three pathovars belonging to three *Xanthomonas* species. Microbiol Resour Announc 7:e00923-18. https://doi.org/10.1128/MRA.00923-18.

Editor Iddo Friedberg, Iowa State University

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genomes of the three above-mentioned strains were sequenced using the Illumina MiSeq next-generation sequencing platform in the University of Exeter Sequence Centre (http://sequencing.exeter.ac.uk) to generate 2.6 million, 1.5 million, and 1.6 million pairs of 300-nucleotide reads, respectively, for *X. hortorum* pv. *hederae*, *X. oryzae* pv. *oryzicola*, and *X. citri* subsp. *malvacearum*.

The sequences were trimmed with TrimGalore (https://github.com/FelixKrueger/TrimGalore), which is a wrapper around CutAdapt version 1.15 (https://cutadapt.readthedocs.io/en/latest), and assembled using the SPAdes version 3.11.1 (13). Total lengths of the three assemblies were 5.52 Mb, 5.24 Mb, and 4.68 Mb. The N_{50} contig lengths were 41.6 kb, 81.4 kb, and 61.1 kb. The numbers of contigs were 444, 283, and 179. G+C contents of each genome assembly were 64, 63, and 64%. The assembled sequences were annotated by the NCBI Prokaryotic Genome Annotation Pipeline (14).

Data availability. These genome assemblies and the raw sequence reads have been deposited in DDBJ/EMBL/GenBank and in the Sequence Read Archive under the accession numbers PYJG00000000 and SRR7643104, respectively, for *X. hortorum* pv. *hederae* WHRI 7744; PYJI00000000 and SRR7643312, respectively, for *X. oryzae* pv. *oryzicola* WHRI 5234; and PYJH00000000 and SRR7642345, respectively, for *X. citri* subsp. *malvacearum* WHRI 5232.

ACKNOWLEDGMENTS

V.A.M. was supported by the General Secretariat of Research and Technology (GSRT) and by the Hellenic Foundation for Research and Innovation (ELIDEK) through a fellowship for her Ph.D. thesis (number KA 4776). P.F.S. and D.J.S. were supported by the Gatsby Foundation, United Kingdom.

We are grateful to Karen Moore and colleagues in the Exeter Sequencing Service for expert technical support.

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