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GENOME ANNOUNCEMENT

Genome Sequence of *Xanthomonas citri* pv. mangiferaeindicae Strain LMG 941

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We report the 5.1-Mb genome sequence of *Xanthomonas citri* pv. mangiferaeindicae strain LMG 941, the causal agent of bacterial black spot in mango. Apart from evolutionary studies, the draft genome will be a valuable resource for the epidemiological studies and quarantine of this phytopathogen.

Xanthomonas citri pv. mangiferaeindicae is one of the important pathovars belonging to the *Xanthomonas axonopodis* species complex. Even though this phytopathogen was first reported in South Africa in mango in 1915 (2), the disease was known much earlier in India (8, 9). It is a serious problem in mango cultivation and export in regions in which this pathogen is endemic. Moreover, the taxonomic relationship between *X. citri* pv. mangiferaeindicae and other closely related pathovars that infect citrus and other fruit crops is controversial. Hence the genome sequence of *X. citri* pv. mangiferaeindicae is an urgent requirement for gaining deeper insights into its phylogeny and taxonomy and also for identifying the determinants of its virulence.

In this direction, we have sequenced the genome of LMG 941, the reference strain of *X. citri* pv. mangiferaeindicae, using the Roche 454 GS (FLX Titanium) pyrosequencing platform (Macrogen, Republic of Korea). The shotgun sequencing yielded 770,765 reads amounting to 345,463,238 bases and ~69-fold coverage. The GS de novo assembler (version 2.6) yielded 195 contigs of ≥500 bp with an average contig size of 26.213 kb and a largest contig of 169.379 kb. The percentage of bases that have a quality score of 40 or above was 99.98%. The genome of strain LMG 941 has a G+C content of 64.85%, and annotation using the rapid annotation using subsystem technology (RAST) pipeline (7) and RNAmmer 1.2 (5) with further manual inspection revealed 4,521 predicted coding regions (CDSs), 51 tRNA genes, and 3 rRNA genes.

BLAST analysis revealed that the 16S rRNA and complete *rpoB* gene sequences of *X. citri* pv. mangiferaeindicae are >99% identical to those of *X. axonopodis* pv. citri, the causal agent of citrus canker, and *X. axonopodis* pv. punicae, the causal agent of bacterial leaf blight in pomegranate (11). Further phylogenomic analysis using highly conserved housekeeping genes described earlier for xanthomonads (1) confirmed its close relationship with *X. axonopodis* pv. citri and *X. axonopodis* pv. punicae. Interestingly, the diseases caused by *X. citri* pv. mangiferaeindicae, *X. axonopodis* pv. citri, and *X. axonopodis* pv. punicae were all first noticed in India, which may also be the region of origin of these pathovars (3, 4, 6, 8, 9, 10, 11). Moreover, the hosts of these pathovars also grow wild and are cultivated at a large scale in India. Hence, as hypothesized previously (11), this group of highly related phytopathogens may be dynamically exchanging their gene pool for fitness and virulence capabilities. The availability of the genome sequence of the reference strain of *X. citri* pv. mangiferaeindicae, along with those of *X. axonopodis* pv. punicae and *X. axonopodis* pv. citri, will greatly aid in epidemiological/quarantine studies and in gaining understanding on their origin and evolution.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at EMBL under the accession numbers CAHO01000001 to CAHO01000195.

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