Genome Sequence of *Xanthomonas axonopodis* pv. punicae Strain LMG 859

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We report the 4.94-Mb genome sequence of *Xanthomonas axonopodis* pv. punicae strain LMG 859, the causal agent of bacterial leaf blight disease in pomegranate. The draft genome will aid in comparative genomics, epidemiological studies, and quarantine of this devastating phytopathogen.

*Xanthomonas axonopodis* pv. punicae is one of the numerous host-specific pathovars of phytopathogenic xanthomonads, a highly evolved group of bacteria. This pathovar was first reported in India on pomegranate (4). It has now emerged as a destructive pathogen in pomegranate-cultivating areas of India, the biggest producer of pomegranates in the world. *X. axonopodis* pv. punicae has become a serious threat to pomegranate cultivation and also to the tremendous export potential such cultivation represents because of the effect of its disease on the quality and quantity of the fruit. As India is an area where *X. axonopodis* pv. punicae infections are presently endemic, the species is also a potential threat to pomegranate-growing areas of the world where such infections are not endemic. In this context, sequencing of the genome of *X. axonopodis* pv. punicae is an urgent requirement to gain deeper insights into its phylogeny and taxonomy and also to study the genomic determinants of its virulence.

To begin with, we sequenced the genome of LMG 859, the reference strain of *X. axonopodis* pv. punicae, using the Roche 454 GS (FLX Titanium) pyrosequencing platform (Macrogen, Republic of Korea). The shotgun sequencing yielded 664,349 reads amounting to 278,291,163 bases and ~55-fold coverage. The GS De Novo Assembler (version 2.3) yielded 217 contigs (over 500 bp) with an average contig size of 22,795 kb and largest contig of 166,069 kb. The proportion of bases called that had a quality score of 40 or above was 99.99%. The genome of strain LMG 859 has G+C content of 64.9%, and annotation using the RAST (Rapid Annotation using Subsystem Technology) pipeline (7) and RNAmmer 1.2 (5) with further manual inspection revealed 4,385 predicted coding regions (CDSs) and 50 tRNA and 3 rRNA genes.

BLAST analysis revealed that the 16S rRNA and complete rpoB gene sequences of *X. axonopodis* pv. punicae are >99% identical to those of *Xanthomonas axonopodis* pv. citri, the causal agent of citrus canker. Further phylogenomics analysis using highly conserved housekeeping genes described earlier for xanthomonads (2) confirmed its close relationship with *X. axonopodis* pv. citri. Interestingly, the diseases caused by *X. axonopodis* pv. punicae and also *X. axonopodis* pv. citri were first noticed in India, which may also be the region of origin of these bacteria (3, 4, 6). Moreover, the hosts of these pathovars also grow wild and are cultivated on a large scale in India. Hence, these highly related phytopathogens may be dynamically exchanging their gene pools for fitness and virulence capabilities. Studies have shown that *X. axonopodis* pv. citri has spread from Asia to other countries (3, 6), and *X. axonopodis* pv. punicae is already on its way, as can be noted in recent reports (1, 8). Hence, the demand of the hour is to quarantine *X. axonopodis* pv. punicae, with special attention to its striking relationship with *X. axonopodis* pv. citri. The availability of the genome sequence of reference strain of *X. axonopodis* pv. punicae is certain to be an important resource in epidemiological and quarantine studies. It will also be interesting as well as necessary to undertake studies to achieve a detailed understanding of evolutionary relationships by sequencing the genomes of large sets of *X. axonopodis* pv. punicae and also *X. axonopodis* pv. citri strains to obtain greater insights into their origins and pathogenicities.

**Nucleotide sequence accession numbers.** Sequences from this whole-genome shotgun project have been deposited at EMBL under accession numbers CAGJ01000001 to CAGJ01000217.

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