**Sequencing of K60, Type Strain of the Major Plant Pathogen *Ralstonia solanacearum***

Benoit Remenant,a Lavanya Babujee,a* Aurélie Lajus,b Claudine Médigue,b Philippe Prior,c and Caitilyn Allena

Department of Plant Pathology, University of Wisconsin—Madison, Madison, Wisconsin, USA; Laboratoire d’Analyse Bio-informatique en Génomique et Métabolisme CNRS-UMR 8030, Commissariat à l’Energie Atomique (CEA), Institut de Génomique, Genoscope, Evry, France; and UMR Peuplements Végétaux et Bioagresseurs en Milieu Tropical, INRA-CIRAD, Saint Pierre, La Réunion, France

*Corresponding author. E-mail: lac@plantpath.wisc.edu

**R. solanacearum** is a widespread and destructive plant pathogen. We present the genome of the type strain, K60 (phylogenotype IIA, sequevar 7). Sequevar 7 strains cause ongoing tomato bacterial wilt outbreaks in the southeastern United States. K60 generally resembles *R. solanacearum* CFBP2957, a Caribbean tomato isolate, but has almost 360 unique genes.

**R. solanacearum** is a major plant pathogen that causes bacterial wilt disease of over 200 species, primarily in tropical and warm-temperate zones (1). Strains of this generally soilborne betaproteobacterium form a heterogeneous species complex. Distribution patterns and phylogenetic analyses suggest that it has associated with plants for over 160 million years (6, 8). *R. solanacearum* strains from Asia, Africa, South America, and the Caribbean have been sequenced (3, 9–11). However, no strain from the southeastern United States had been sequenced, although the organism was first isolated there, and bacterial wilt is an important disease in the area (2, 12, 13). We therefore sequenced the *R. solanacearum* type strain, K60 (synonyms CFBP2047, NCPPB325, and ATCC 11696), which was isolated from a wilted “Marglobe” tomato in Raleigh, NC, in November 1953 (7). K60 belongs to phylogenotype IIA, sequevar 7 (8), historically classified as race 1, biovar 1. The biology of K60 is well characterized (1), and it is typical of sequevar 7 strains (8). Sequence typing found little difference between K60 and five 2010 isolates from wilting tomatoes in Virginia, indicating that K60 resembles current outbreak strains.

The K60 genome was obtained using Illumina and 454 technologies, resulting in 604,336 reads and 218,382,588 bases. Raw data were assembled into 547 contigs and 28 scaffolds by using Newbler. Contigs were organized in two replicons by using the genome of strain CFBP2957 (phylogenotype IIA, sequevar 36), the fully sequenced strain most closely related to K60. The chromosome and the megaplasmid contain 14 and 6 scaffolds, respectively, representing 3,717,547 and 1,772,932 bp. Unassembled contigs (109,631 bp) were added at the end of the chromosome. Strong orthologs (>85% identity over >80% of coding sequence [CDS] length) were automatically annotated using the manually curated CDSs of *R. solanacearum* CMR15 and CFBP2957 (10). The remaining 1,035 genes were manually curated.

The overall G+C content of the K60 genome is 66.5%. It contains 5,342 predicted CDSs, similar to the species complex average of 5,213. CDSs on the chromosomes of K60 and CFBP2957 were 81% syntenic. The megaplasmid is usually less conserved in bacteria with two replicons, but the K60 and CFBP2957 megaplasmids share more than 88% synteny, indicating a very close relationship (4, 5). The K60 megaplasmid is 371 kb shorter than that of CFBP2957, notably lacking a 250-kb region from 1.42 to 1.67 Mb, which encodes uncharacterized proteins or proteins of extrachromosomal origin (phages and transposons). However, many genes present in this region of CFBP2957 are found in the unassembled K60 contigs.

Almost 360 genes were unique to strain K60. Among these newly detected genes in the species complex pangenome, 82% encode uncharacterized proteins and 9% encode proteins of extrachromosomal origin. These genes and other genomic differences between CFBP2957, which is adapted to Caribbean conditions, and K60, which is native to the warm-temperate southeastern United States, can be used to test hypotheses about the contrasting biologies of the two strains.

**Nucleotide sequence accession number.** The K60 genome EMBL database accession number is CAGT01000001. Assembled sequences and annotations are also available in the RalstoniaScope database at http://www.genoscope.cns.fr/agc/microscope/ralstoniascope.

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**REFERENCES**


