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Abstract

The bacterial plant pathogen *Xanthomonas hyacinthi* is the causal agent of yellow disease of *Hyacinthus* and other ornamental plant genera. There is no available complete genome for *X. hyacinthi*, limiting basic research for this pathogen. Here, we release a high-quality complete genome sequence for the *X. hyacinthi* type strain, CFBP 1156. Single-molecule real-time (SMRT) sequencing with a mean coverage of 306× revealed two contigs of 4,918,645 and 44,381 bp in size. This was the first characterized plant-disease-causing species of *Xanthomonas* and this genome provides a resource to better understand the biology of yellow disease of hyacinth.

Resource Announcement

Xanthomonas hyacinthi is a plant-pathogenic bacteria that causes yellow disease in *Hyacinthus*, *Scilla*, and other related ornamental plant genera (Janse and Miller 1983; Van Tuyl and Toxopeus 1980). *X. hyacinthi* was first isolated in 1883 by J. H. Wakker, who was among the first plant pathologists to recognize bacteria as a possible cause of plant disease (Beijer 1966; Wakker 1883). Because of its ability to cause severe symptoms, *X. hyacinthi* threatens production of ornamental bulbous plants. The type strain is available in culture collections as CFBP 1156, LMG 739, NCPPB 599, ICMP 189, ATCC 19314, and DSM 19077 (Vauterin et al. 1995). A low-quality draft genome of *X. hyacinthi* strain DSM 19077 was provided in 2015, with 15× coverage Illumina HiSeq data assembled into 1,415 contigs (Naushad et al. 2015). This draft and other incomplete genomic information allowed researchers to previously develop nucleic acid-based diagnostic methods for detecting *X. hyacinthi* (Back et al. 2015; van Doorn et al. 2001). A newer draft genome was recently generated with Illumina HiSeq data, with 104 contigs assembled representing 100× coverage (NCBI BioProject Accession PRJNA338630) (Merda et al. 2017). However, short-read

sequencing is not sufficient for assembly of *Xanthomonas* transcription activator-like effector (TALE) genes (Peng et al. 2016). Here, we report the complete genome sequence for *X. hyacinthi* strain CFBP 1156 generated by long-read sequencing.

X. hyacinthi strain CFBP 1156 was isolated from *Hyacinthus orientalis* in the Netherlands in 1958 and deposited in the French Collection for Plant-associated Bacteria (CIRM-CFBP) in 1969. From lyophilized stock preserved at CIRM-CFBP, a single colony was isolated and grown on rich nutrient agar media. Genomic DNA was extracted using the Genomic DNA buffer set and Genomic-tips following the manufacturer's instructions (Qiagen, Valencia, CA, U.S.A.). DNA was sheared three times with a Covaris g-TUBE at 5,500 rpm for 2 min to 8- to 30-kb fragments and sequenced using long-read single-molecule real-time (SMRT) sequencing on a PacBio Sequel I, and the genome was assembled with HGAP v4 (Pacific Biosciences, Menlo Park, CA, U.S.A.). QUAST 5.0.2 was used to assess genome quality (Gurevich et al. 2013). NCBI Prokaryotic Genome Annotation Pipeline version 4.9 was used for functional annotation of genes (Haft et al. 2018). SignalP 5.0 was used to identify genes with predicted signal peptides (Almagro Armenteros et al. 2019). AnnoTALE 1.4.1 was used to detect and annotate TALE genes (Grau et al. 2016).

Mean coverage for the *X. hyacinthi* strain CFBP 1156 genome was 306×. The genome was assembled into two contigs of 4,918,645 and 44,381 bp in size—a chromosome and a plasmid, respectively—with a total G+C content of 68.0%. The N_{50} and L_{50} were 4,918,645 and 1, respectively. Of the 4,392 genes predicted, 4,011 encoded proteins, 63 encoded functional RNAs, and 318 were considered pseudogenes. Genes encoding predicted secretion system (SS) proteins were identified, including T1SS, T2SS, T3SS, and T4SS. In all, 10 genes were annotated as type III effectors or avirulence genes, including one locus (FZ025_20815) encoding a TALE previously undetected in draft genomes. The TALE was assigned to a novel class by AnnoTALE and designated as TalHQ1. Signal peptides for Sec/SPI, Sec/SPII, and Tat/SPI were detected in 496, 87, and 207 genes, respectively (Supplementary Table S1).

Raw reads and the complete genome were uploaded to NCBI Sequence Read Archive and GenBank under BioProject accession PRJNA562936.

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