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Draft Genome Sequence of *Xylella fastidiosasubsp. multiplex* Strain Griffin-1 from *Quercus rubra* in Georgia

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The draft genome sequence of *Xylella fastidiosa* subsp. *multiplex* strain Griffin-1, isolated from a red oak tree (*Quercus rubra*) in Georgia, is reported here. The bacterium has a genome size of 2,387,314 bp, with a G+C content of 51.7%. The Griffin-1 strain genome contains 2,903 predicted open reading frames and 50 RNA genes.

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Xylella fastidiosa is a Gram-negative, xylem-limited plant-pathogenic bacterium (1) causing many economically important diseases, including oak leaf scorch disease in the eastern United States (2–4). Due to nutritional fastidiousness, characterization of X. fastidiosa has been difficult, and many biological issues related to X. fastidiosa strains remain to be investigated. Both complete genome (5–8) and whole-genome shotgun (9, 10) sequences of X. fastidiosa are currently available. Three subspecies of X. fastidiosa (subspecies fastidiosa, subspecies multiplex, and subspecies pauca) have been proposed (11). The taxonomic statuses of X. fastidiosa strains from oak trees have not been evaluated. An early study based on a random amplified polymorphic DNA analysis showed that X. fastidiosa strains from turkey oak (Quercus laevis) in Florida and red oak (Quercus rubra) in Georgia were highly similar (12).

In the summer of 2006, a strain of X. fastidiosa was isolated from a symptomatic red oak tree (Q. rubra) in Griffin, Georgia (33°15’38.07”N, 84°16’48.69”W), and it has been maintained in our laboratory in California. This bacterial strain was triple cloned and designated Griffin-1. To obtain genomic DNA, Griffin-1 was cultured in periwinkle wilt (PW) broth (13) at 28°C for 10 days. Bacterial cells were collected by centrifugation; the total genomic DNA was extracted by a standard procedure (14). Genome sequencing was carried out on a 454 GS-FLX system using Titanium chemistry (Roche) (15). Paired-end reads were assembled with the Newbler software (Roche Diagnostics). The Griffin-1 genome consists of 2,387,314 bp (~30X coverage, G+C content of 51.7%) assembled into 84 contigs ranging from 523 bp to 142,581 bp. Annotation was performed by the RAST server (http://rast.nmpdr.org/) (16), which utilizes the GeneMark, Glimmer, and tRNAscan-SE databases. The Griffin-1 genome was predicted to have a total of 2,903 open reading frames (ORFs) and 50 RNA genes. Using BLAST analyses (17), the sequences of ssr (16S rRNA) and four housekeeping genes, gyrB (DNA gyrase subunit B), dnaK (chaperone protein), rpoD (RNA polymerase sigma factor), and tonB (outer membrane receptor), were selected and compared to the corresponding gene sequences of X. fastidiosa subspp. multiplex strain M12 (5), X. fastidiosa subspp. fastidiosa strains M23, GB514, and Temecula (5, 6, 8), and X. fastidiosa subspp. pauca strain 9a5c (14). For all five loci, X. fastidiosa subspp. multiplex Griffin-1 is 100% identical to strain M12, indicating that the oak strain is a member of X. fastidiosa subspp. multiplex.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. AVGA00000000. The version described in this paper is version AVGA01000000.

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