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Draft Genome Sequence of *Xylella fastidiosa* subsp. *fastidiosa* Strain Stag's Leap

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***Xylella fastidiosa* subsp. *fastidiosa* causes Pierce's disease of grapevine. Presented here is the draft genome sequence of the Stag's Leap strain, previously used in pathogenicity/virulence assays to evaluate grapevine germplasm bearing Pierce's disease resistance and a phenotypic assessment of knockout mutants to determine gene function.**

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Xylella fastidiosa is a Gram-negative xylem-limited bacterium (1, 2) comprising multiple subspecies causing disease in a wide variety of horticultural and landscape perennials (3). Pierce's disease (PD) of grapevine is caused by strains of *X. fastidiosa* subsp. *fastidiosa*. Over the past 15 years, considerable effort has been devoted toward understanding mechanisms of *X. fastidiosa* subsp. *fastidiosa* pathogenicity and interactions with the grapevine host (4). Temecula1 (accession no. NC_004556.1) was the first strain of the subspecies to be completely sequenced (5); this sequence serves as a reference for PD research. The complete genome of *X. fastidiosa* subsp. *fastidiosa* strain M23 (accession no. NC_010577.1), isolated from almonds in San Joaquin Valley, CA, also was sequenced (6) and is highly similar to that of Temecula1. A third strain of *X. fastidiosa* subsp. *fastidiosa*, Stag's Leap (isolated from grapevine in Napa Valley, CA) (7), has been used to evaluate PD resistant germplasm and in knockout/pathogenicity/virulence assays to elucidate gene function (8). This study fills a critical knowledge gap, the draft genome sequence of strain Stag's Leap.

For sequencing, Stag's Leap was cultured in periwinkle wilt medium (9) at 28°C for 14 days. Cells were collected; total genomic DNA was extracted according to a standard procedure (10). Whole-genome sequencing was performed on the Illumina MiSeq platform (Illumina, Inc., San Diego, CA); 6.59×10^6 paired-end reads (301 bp average length) were generated. Sequence reads were assembled *de novo* with CLC Genomics Workbench (version 7.5), yielding 99 contigs >1,000 bp. The same sequence reads were then mapped to the M23 complete genome using Bowtie 2 version 2.2.6 (11), generating 20 contigs. Finally, contigs from both *de novo* and mapping methods were combined manually. The final assembled draft genome (750× mean coverage) had a G+C content of 51.7%, with 2,510,798 bp distributed among 15 contigs ranging in size from 1,307 bp to 731,756 bp. All sequences were annotated using the RAST server (http://rast.nmpdr.org/) (12). The chromosomal sequence had 2,756 open reading frames (ORFs) and 55 RNA genes. The Stag's Leap draft chromosomal sequence corresponds to 99.0% of the M23 genome (2,535,690 bp) and 99.6% of the Temecula1 genome (2,519,802 bp).

Nucleotide sequence accession numbers. The *X. fastidiosa* subsp. *fastidiosa* strain Stag's Leap whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. LSMJ00000000. The version described in this paper is version LSMJ00000000.1.

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