

Draft Genome Sequence of the Plant-Pathogenic Fungus *Stemphylium*

lycopersici Strain CIDEFI-216

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Stemphylium lycopersici is a pathogenic fungus that provokes the leaf spot disease on over 30 host genera worldwide, among them Tomato. Here we report the draft genome sequence of *S. lycopersici* strain CIDEFI-216. Total genomic DNA was isolated from a monosporic culture using the DNeasy Plant Mini Kit (Qiagen) and was used to construct 100 bp paired-end libraries, which were then sequenced by Illumina HiSeq 2000 technology. Reads were assembled using SOAPdenovo2 software at Macrogen (Korea). Gene prediction was performed by Fgenesh software (Softberry), functional annotation was carried out with Blast2GO software (BioBam) and tRNAs and rRNAs were predicted using tRNAscan-SE and HMM-rRNA tools from WebMGA server. The paired-end libraries produced 31117554 reads with a total of 3142872954 bp,

25 representing an average coverage of 77.39 X. The genome was assembled into 419
26 scaffolds with a total length of 35.18 Mbp (1000 bp; N50=498048 bp) and an overall
27 G+C content of 50.5 %. A total of 8998 protein-coding genes were predicted, whose
28 functional annotation is discussed. Additionally, 94 tRNAs and 44 rRNAs were found.
29 This draft genome sequence, the first available for *S. lycopersici*, represents a new
30 resource for further research into the taxonomy, biology and phytopathology of this plant
31 pathogen.