



Category: Metagenomics

Draft genome sequence of *Sclerospora graminicola*, the pearl millet downy mildew pathogen

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Abstract

Sclerospora graminicola pathogen is the most important biotic production constraints of pearl millet in India, Africa and other parts of the world. We report a *de novo* whole genome assembly and analysis of pathotype 1, one of the most virulent pathotypes of *S. graminicola* from India. The whole genome sequencing was performed by sequencing of 7.38 Gb with 73,889,924 paired end reads from the paired-end library, and 1.15 Gb with 3,851,788 reads from the mate pair library generated from Illumina HiSeq 2500 and Illumina MiSeq, respectively. A total 597,293 filtered sub reads with average read length of 6.39 Kb was generated on PACBIO RSII with P6-C4 chemistry. Assembled draft genome sequence of *S. graminicola* pathotype 1 was 299,901,251 bp in length, N50 of 17,909 bp with a minimum of 1 Kb scaffold size. The GC content was 47.2 % consisting of 26,786 scaffolds with longest scaffold size of 238,843 bp. The overall coverage was 40X. The draft genome sequence was used for gene prediction using AUGUSTUS which resulted in 65,404 genes using *Saccharomyces cerevisiae* as a model. A total of 52,285 predicted genes found homology using BLASTX against nr database and 38,120 genes were observed with a significant BLASTX match with E-value cutoff of 1e-5 and 40% identity percentage. Out of 38,120 genes annotated a set of 11,873 genes had UniProt entries, while 7,248 were GO terms and 9,686 with KEGG IDs. Of the 7,248 GO terms, 2,724 were associated with the biological processes. The genome information of downy mildew pathogen is available in the NCBI GenBank database. The *Sclerospora graminicola* whole genome shotgun (WGS) project has the project accession MIQA00000000. This version of the project (02) has the accession number MIQA02000000, and consists of sequences MIQA02000001-MIQA02026786, with BioProject ID PRJNA325098 and BioSample ID SAMN05219233. This study may help understand the evolutionary pattern of pathogen and aid elucidation of effector evolution for devising effective durable resistance breeding strategies in pearl millet.

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