

De nova genome sequence of Karnal bunt pathogen (*Tilletia indica*) of wheat

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Karnal bunt of wheat is a serious quarantine disease caused by hemibiotrophic fungus, *Tilletia indica*. Despite its economic importance, little knowledge is known about molecular pathogenesis including various pathogenic determinants and avirulence factors. Besides studies are complicated as reported genes of *T. indica* do not share high degree of homology with other closest basidiomycete fungi. *T. indica* genome was sequenced employing hybrid approach of PacBio Single Molecule Real Time (SMRT) and Illumina HiSEQ 2000 sequencing platforms (1). The genome was assembled into 10,957 contigs, 7,87 scaffolds with total size of 31.83 Mbp. We predicted 11,535 putative genes, which were annotated employing Gene Ontology databases. The improved draft version of the assembly was achieved using Metaassembler, (v.1.5), by merging draft monoteliosporic sequence-based assemblies from DAOM 236416 and RAKB_UP_1 isolates with the improved and reassembled hybrid assembly. Repeated genome assembly, gap filling and polishing on merged assembly employing Gapfiller tool (V.1.10) resulted in an improved coverage of 107 x. Secretome analysis of pathogen and the predicted putative Functional annotation of Karnal bunt pathogen genome and classification of identified effectors into protein families revealed interesting functions related to pathogenesis. Several biological, cellular and molecular functions were detected that include some related to pathogenesis, which include mating, zoospore development, host surface attachment, cell wall degrading enzyme, translocation and several others. Work is in progress to improve genome coverage and identification of potential effectors that could serve as molecular targets for development of diagnostic markers and new fungicide markers.

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Reference

1. Kumar A., Mishra P., Maurya R., Mishra A.K., Vijai K., Pramod W., Marla S. (2018) Improved draft genome sequence of a monoteliosporic culture of the karnal bunt (*Tilletia Indica*) pathogen of wheat. Genome Announc. 6:e00015-18. <https://doi.org/10.1128/genomeA.00015-18>.