Molecular profiling of the sugar beet pathogen *Fusarium secorum*

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Fusarium yellowing decline caused by the fungal pathogen *Fusarium secorum* has become an emerging problem in the sugar beet industry. Since *F. secorum* is not closely related to other *Fusarium* pathogens of sugar beet, little is known of the virulence mechanisms of this pathogen. To that end, we utilized whole-genome sequencing of the pathogen, xylem sap mass spectrometry, and transcriptome analysis of *F. secorum* infected-sugar beet plants to understand the molecular basis of virulence of this pathogen. *Fusarium secorum* showed an increased genome size due to an increased number of introns and repetitive elements. Additionally, we successfully developed a CRISPR-Cas9 ribonucleoprotein mediated gene-editing technique to disrupt target genes encoding candidate effector proteins in the pathogen. There were five gene targets, and among them, one gene target (*Fsec2*) was identified as a virulence factor of *F. secorum*. This study provides valuable genomic resources and a better understanding of the virulence strategies of an important pathogen of sugar beet.