CHARACTERIZATION OF A POPULATION OF *FUSARIUM OXYSPORUM*, FROM SUGAR BEET, USING THE POPULATION STRUCTURE OF PUTATIVE PATHOGENICITY GENES

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ABSTRACT

Sugar beet (*Beta vulgaris* L.) Fusarium yellows is caused by *Fusarium oxysporum* f. sp. *betae* and leads to reductions in root yield, sucrose percentage, and juice purity and storability for sugar beet producers. *F. oxysporum* f. sp. *betae* can be highly variable in growth, pigmentation, conidial production, and in virulence. Additionally many *F. oxysporum* isolated from symptomatic sugar beet are non-pathogenic. Identifying pathogenicity factors and their diversity in the *F. oxysporum* f. sp. *betae* population, could lead to further understanding of how this pathogen causes disease on sugar beet and provide molecular markers to rapidly identify pathogenic from non-pathogenic isolates. Many methods have been used to characterize the genetic diversity of *F. oxysporum* f. sp. *betae* from sugar beet however these technologies have done little to describe regional populations of *F. oxysporum* f. sp. *betae* and are mostly unable to differentiate between pathogenic *F. oxysporum* f. sp. *betae* and non-pathogenic isolates of *F. oxysporum*. *F. oxysporum* utilizes a wide array of secreted molecules, called effectors, and pathogenicity genes, which encode host determining factors that are used by the pathogen to cause disease in sugar beet. Utilizing these target effectors, it is possible to utilize patterns of nucleotide diversity (both within and among populations) to infer the molecular basis of pathogen relatedness. In this work, we obtained the nucleotide sequence for thirteen previously described fungal pathogenicity genes (*Fmk1*, *Fow1*, *Pda1*, *PelA*, *PelD*, *Pep1*, *Prt1*, *Rho1*, *Sge1*, *Six1*, *Six6*, *Snf1*, and *Ste12)* to use as genetic markers to characterize the diversity of a population of 26 pathogenic and non-pathogenic isolates of *F. oxysporum* originally isolated from symptomatic sugar beet. Using this information, we characterized the pathogen population by "clade" and "pathogenicity" to 1) determine the genetic diversity of the *F. oxysporum* population from symptomatic sugar beet and 2) determine if this diversity could be correlated to "pathogenicity" or "clade" designations of *F. oxysporum* f. sp. *betae*. Of the genes investigated, 6 were present in all *F. oxysporum* isolates from sugar beet (*Fmk1*, *Fow1*, *PelA*, *Rho1*, *Snf1*, and *Ste12*), and 7 were found to be dispersed within the population (*Pda1*, *PelD*, *Pep1*, *Prt1*, *Sge1*, *Six1*, and *Six6*). Of these, *Fmk1*, *Fow1*, *PelA*, *Rho1*, *Sge1*, *Snf1*, and *Ste12* were significant in describing clade designations while *PelD* and *Prt1* were significant for describing pathogenicity in *F. oxysporum* f. sp. *betae.*