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ABSTRACT

Fusarium oxysporum is serious threat to sugar beet production worldwide. Although certain sugar beet lines appear to have resistance against *F. oxysporum*, little is understood about the basis for that resistance. Examination of *F. oxysporum*-induced protein changes in the sugar beet will serve two purposes: to identify candidate genes for use in marker-assisted selection and to elucidate mechanisms responsible for resistance. Sugar beet genotype C1200.XH024, with resistance to *F. oxysporum* isolate F-19, was analyzed at 2- and 5-days post pathogen challenge and compared to mock-inoculated beets. These times correlate with initial infection and vascular tissue penetration, respectively. A total of approximately 950 proteins were reproducibly detected in the sugar beet leaf and root protein extracts using multidimensional liquid chromatography. One hundred twenty-one proteins were differentially expressed during resistance to F-19. Fourteen were only expressed during initial infection, forty-three once the vascular system was penetrated and forty-nine were expressed at both points. Fifteen proteins were repressed in F-19 challenged tissue in comparison to the mock inoculated control. Seventy protein peaks were analyzed by matrix-assisted laser desorption ionization time-of-flight mass spectrometry, the remaining protein peaks were below the level of detection. This analysis lead to the identification of proteins associated with salicylic acid-dependent resistance, the oxidative burst, signal transduction, photosynthesis, respiration and gene expression and regulation.