

MARTYN, R. D.*, E. A. DILLARD, and C. M. RUSH. Dept. of Plant Pathology and Microbiology, Texas A&M University, College Station, TX 77843. - Host specific and nonhost specific isolates of *Fusarium oxysporum* recovered from sugar beet, spinach, and red-root pigweed.

Sugar beet (*Beta vulgaris* L.) and spinach (*Spinacia oleracea* L.) are members of the Chenopodiaceae plant family. Red-root pigweed (*Amaranthus retroflexus*) is a cosmopolitan weed pest in the Amaranthaceae family. A wilt disease caused by formae speciales of *Fusarium oxysporum* has been described on each of these plants. In this study, 20 isolates of *F. oxysporum* recovered from diseased plants were cross-inoculated onto each of the three species by three different inoculation procedures in an attempt to determine host specificity of the isolates. Analysis of the inoculation tests defined several levels of host specificity and aggressiveness among the isolates; however, the inoculation method had little effect on the results. Isolates specific to sugar beet and to spinach were identified as well as isolates that were pathogenic to both hosts. In addition, pigweed isolates were highly aggressive to sugar beet, but not to spinach. Of the three plant species tested, pigweed was the most tolerant to *Fusarium* wilt. That there are isolates of *F. oxysporum* pathogenic to more than one plant species suggests that there is a continuum of pathogenicity within a given forma specialis.

MARTYN, R. D.*, D. H. KIM, E. A. DILLARD, and C. M. RUSH. Dept. of Plant Pathology and Microbiology, Texas A&M University, College Station, TX 77843. - Isozyme relatedness and mtDNA RFLP groups of *Fusarium oxysporum* from sugar beet, spinach, and red-root pigweed.

Twenty isolates of *Fusarium oxysporum* recovered from diseased sugar beet, spinach, and red-root pigweed plants were examined by isozyme profiles and mtDNA RFLP patterns to determine their relatedness. Five enzymes (G-6-PD, MDH, CAD, PGI, and ADH) were electrophoresed in polyacrylamide gels. Isozyme bands were scored as binomial data and subjected to a cluster analysis program to generate matching distances between isolates. When analyzed individually, each enzyme separated the isolates into three main groups that correlated with host specificity. When all five enzymes were analyzed together, each main group separated into subgroups that corresponded to aggressiveness of the isolates. Genomic DNA from each isolate was probed with an mtDNA PstI polyprobe (pFON-1-pFON9) constructed from *F. o. f. sp. niveum* and examined for polymorphisms. Six RFLP groups were identified. Group I contained the crossover isolates, group II contained host-specific sugar beet isolates, and group III contained host-specific spinach isolates. The remaining three groups separated out on the basis of reduced aggressiveness.