PRACTICAL RISK PREDICTION TO SUPPORT MANAGEMENT AND VARIETY TRIALS: DEALING WITH VARIATION IN *FUSARIUM OXYSPORUM* F. SP. *VASINFECTUM* INOCULUM DENSITY

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Abstract

This work concerns the emergence of *Fusarium oxysporum* f. sp. *vasinfectum* (FOV) with new or changing virulence on cotton in the region of west Texas, assumed to be FOV race 4. Overall aims of the work are to develop and implement inoculum density quantification methods, to support research on the movement of inoculum and on temporal dynamics of inoculum density, and to support interpretation of variety trial data by providing a quantitative estimate of disease pressure in experimental fields. Spatially variable in-field inoculum density can be quantified to enhance variety trials, by providing disease pressure estimates useful when rating plants, and by providing a pre-experiment projection of disease pressure across space so that experimental design may take this into account. An alternative approach to addressing variable inoculum density is to randomize across the variation, but the spatial variability of both Fusarium wilt and FOV4 inoculum density are high to a degree that the number of samples required to randomize would be large. Thus, this work will increase the efficiency of ongoing variety trials in west Texas while also building practical knowledge of FOV's ecology in the region. A real-time PCR method of FOV genomic DNA quantification was developed and confirmed to preferentially amplify inoculum from the west Texas region *vs.* other regions of TX and the greater cotton belt of the United States. Performance of this method was assessed by creating standards composed of FOV tissues added to environmental soil samples, and testing the method's ability to estimate these known amounts of tissue. Results indicate appreciable spatial variability in inoculum density within experimental fields. Study of the relationships of inoculum density to disease occurrence in these fields is ongoing.