DISSECTING THE DISEASE MECHANISM OF *FUSARIUM OXYSPORUM* F. SP. *VASINFECTUM* RACE 4 (*FOV4*) IN COTTON

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Abstract

Fusarium wilt disease of cotton (*Gossypium* spp.), caused by soil-borne fungal pathogen *Fusarium oxysporum* f. sp. *vasinfectum* (*Fov*), has been a continuing problem causing cotton losses worldwide. This pathogen is particularly difficult to control in cotton as the hyphae reside in the woody vascular tissues and is thus protected from fungicides with overwintering structures that can survive in soils forever. *Fov* race 4 (*Fov4*), identified in the U.S. in 2003, was known to be distributed only in California previously, but was identified in Texas in 2017. Resistance to *Fov4* was originally identified in commercial Pima cotton (*G. barbadense* L.), 'Phytogen 800', and originated-pool germplasm, 'Pima S-6'. However, so far, resistance in upland cotton (*G. hirsutum* L.) has not been identified and commercial varieties are not available. Thus, there is a critical need to further understand the disease mechanism and cotton response to *Fov4* and develop upland cotton germplasm and cultivars with resistance to *Fov4*. To assist the strategic development of effective disease controls, we have performed the live-cell imaging analysis to monitor the fungal attachment, penetration and colonization in the cotton vascular bundles through the course of infection period using green fluorescent protein (GFP)-tagged Texas *Fov4* strains in cottons. In addition, we are establishing platforms for the whole genome-sequencing of *Fov* field isolates by Oxford Nanopore MinION portable sequencing devices to reveal the genetic diversity. The recent progresses on these perspectives will be presented during the meeting.