

Dr. Longfu Zhu, got his PhD in Huazhong Agriculture University in 2005. He is the dean of College of Plant Science and Technology, Huazhong Agriculture University and a member of the International Verticillium Steering Committee. He once visited Texas Tech University in 2008 and Wageningen University in 2014 and collaborated with Dr. Hong Zhang and Dr. Bart Thomma. Verticillium wilt and Fusarium wilt caused by *Verticillium dahliae* and *Fusarium oxysporum* f.sp.vasinfectum, respectively, are the most devastating diseases for cotton (*Gossypium hirsutum*) production worldwide. His research interest focuses on elucidating plant immune signaling pathways and virulence factors from these fungi involved in cotton-pathogen interaction through genomic, functional genomic, genetic, biochemical and bioinformatic approaches with the resistant germplasm in *G. hirsutum* and *G. barbadense* and the dominant aggressive strains. In addition, plant immunity is inextricably linked with plant development and environmental stresses. They are also interested in understanding the signaling crosstalk that orchestrates plant development and immune response. *GhFov7*, the R gene in *G. hirsutum* resistant to *F. oxysporum* race 7, has been identified through genome-wide associated mapping and genome editing. Meanwhile, many key genes involved in cotton immune system, like *GhSSN*, *GbWRKY1*, *GhLac1*, have been illustrated. Their research work has been published in *Advanced Science*, *Nature Communications*, *Plant Physiology*, etc. The genes, like *GhFov7*, have been applied in genome selection to improve cotton resistance to fungus.