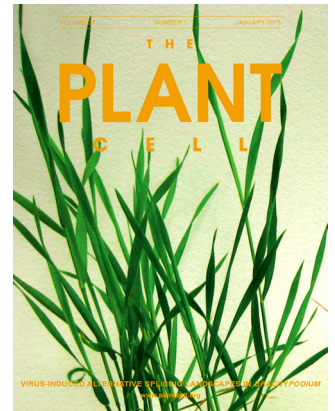


PLANT GENOMICS, MOLECULAR BIOLOGY, AND BIOTECHNOLOGY PROGRAM

Kranthi Kiran Mandadi, Ph.D., Assistant Professor
Department of Plant Pathology and Microbiology
Texas A&M AgriLife Research and Extension Center at Weslaco

RESEARCH

Pathogens, insects, and environmental stresses cause major losses in yield and quality of crops globally. At the Texas A&M AgriLife Research and Extension Center at Weslaco, we are using the latest “Omics,” molecular and genetic approaches to advance the fundamental and translational research related to diverse agricultural crop stresses. Using high-throughput next-generation sequencing (NGS) and phenotyping technologies, we are establishing genotype-to-phenotype knowledge bases for diverse abiotic and biotic stress conditions. The knowledge bases are valuable resources for discovery of gene modules and molecular markers useful for crop improvement via biotechnology and breeding, as well as to advance the fundamental knowledge of plant stress phenology.



The Plant Cell, 2015
Vol. 27: 71–85

IMPROVING BIOENERGY GRASSES THROUGH GENOMICS

Sugarcane, energycane, and switchgrass are important sources of sugar-based ethanol and lignocellulosic biomass feedstocks globally. However, diseases and environmental stresses such as cold, salinity, and drought can result in yield losses greater than 50% and are major impediments to attaining maximum bioenergy yield potential.



Brachypodium

At the Weslaco Center, we employ the latest NGS, bioinformatics, and genetic tools to discover and study novel genes that confer resistance to diseases (viral, fungal, and bacterial) and environmental stresses (cold, salinity, and drought) in bioenergy grasses. We conduct fundamental studies to understand resistance mechanisms in model bioenergy grasses such as *Brachypodium* and *Setaria*, as well as translational research to improve sugarcane and energycane using biotechnology and breeding.



Sugarcane smut

COMBATING INSECT-VECTORED DISEASES OF VEGETABLE AND FRUIT CROPS

It is estimated that 30%–40% of yield losses caused by plant diseases are due to the effect of pathogens transmitted by insect pests. For example, the tomato/potato psyllid, *Bactericera cockerelli*, is a vector of *Candidatus Liberibacter solanacearum* — a bacterial pathogen of solanaceous plants and the causative agent of the potato zebra chip disease, tomato vein-greening, and pepper variegated disease. Zebra chip disease is responsible for millions of dollars in losses to the potato industry. Similarly, citrus greening or huanglongbing (HLB) disease, caused by the *Candidatus Liberibacter asiaticus*, is the most devastating disease of citrus that is threatening citrus production worldwide. HLB is transmitted by an insect vector, the Asian citrus psyllid (*Diaphorina citri*).

At the Weslaco Center, through collaborations with breeders and entomologists, we are identifying novel sources of resistance against insect-vectored diseases. Using systems-biology approaches, we are studying the multi-component (host-vector-pathogen) interactions that occur during disease transmission, as well as interactions with the environment. The overall goal is to identify novel sources of resistance, genes, and markers that could be used to develop disease- and pest-resistant vegetables (tomato and potato) and fruits (citrus) using biotechnology and breeding approaches.



DEVELOPING NOVEL TECHNOLOGIES FOR DISEASE RESISTANCE AND ANTIMICROBIAL SCREENING

A major bottleneck in studying pathogens such as *Candidatus* spp. is the inability to culture them *in vitro*, outside the host plants, as they are obligate pathogens of plants. At the Weslaco Center, we are developing novel microbial hairy root systems to help propagate fastidious pathogens *in vitro*. Further, the microbial hairy root systems enable transformative, high-throughput screening and characterization of insect-resistance genes, anti-microbial genes, antibiotics, and small molecules.



Hairy roots

EXTENDING CURRENT CAPABILITIES AND EXPERTISE

The goal of our program is to use the latest genomics, genetics, and phenotyping tools to speed discovery and characterization of plant stress resistance mechanisms toward crop improvement. The framework and technologies we established can be readily leveraged to improve several agronomic high-value crops and combat their diseases, pests, and environmental stresses. To fulfill these goals, we are open for multi-disciplinary and multi-institutional partnerships and collaborations.