AGRONOMY SEMINAR SERIES
SPRING 2025

Monday, March 10, 2025
2:30 p.m.   LILY 2-425

Attend virtually via Zoom
Seminar links will be posted at: purdue.ag/agryseminars

DR. LING LI

ASSOCIATE PROFESSOR, DEPARTMENT OF BIOLOGICAL SCIENCES
MISSISSIPPI STATE UNIVERSITY

Faculty Host: Dr. Cankui Zhang

Dr. Li is an Associate Professor in the Department of Biological Sciences at Mississippi State University. She obtained her B.S. in biology and M.S. in Botany from Peking University in 1997 and 2000, and her Ph.D. in Genetics (minor in Statistics) from Iowa State University in 2006. She has been an Associate Professor from 2023 (Assistant Professor 2017-2023). Dr. Li has been developing an integrated experimental/biocomputational approach to identify the factors (including orphan genes and proteins with obscure features) that regulate plant metabolism and plant adaptation to environmental changes, bridging basic research from Arabidopsis and application in crops.

PURDUE UNIVERSITY | Agronomy

From Arabidopsis to Crops: A molecular tool to increase protein content and disease resistance

Deficiency in dietary protein is globally one of the most severe health problems; the ability to optimize protein productivity of plant-based foods has far-ranging impact on world health and sustainability. Crop plants must integrate signals from the environment and prioritize responses to stresses that may occur individually/simultaneously throughout the growing season. Stress responses can adversely affect plant growth and quality traits such as protein and starch. Plant diseases each year cause major losses to crop production. The Arabidopsis species specific QQS (Qua-Quine Starch) orphan gene binds to Nuclear Factor Y subunit C4 (NF-YC4) in Arabidopsis and its homologs in crops; overexpression of QQS or NF-YC4 increases protein content of leaves and seeds at the expense of carbohydrates. Mutants overexpressing QQS or NF-YC4 have also significantly increased resistance to plant pathogens and pests. We detected several conserved motifs predicted to be bound by repressors in the promoters of rice and soybean NF-YC4 genes. Using CRISPR/Cas9 to edit the promoters of rice and soybean NF-YC4 genes, we deleted promoter fragments harboring repressor binding motifs. Those deletions resulted in decreased repressor binding, increased NF-YC4 expression, increased protein and decreased carbohydrates. Gene-edited plants showed up to 48% higher leaf protein and 15% increased seed protein. Moreover, we exemplify a general approach for upregulating gene expression through targeted genomic deletions.