Plenary Lecture:

“Integrative Plant Genomics: From Botanical Discovery to Agricultural Transformation”

Speaker 1 (focusing on monocots; agronomic crops):

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Decoding Rice: Linking Natural Variation to Genes, Traits, and Agricultural Transformation

Abstract: Rice (*Oryza sativa* L.) occupies a unique position in plant science as both a globally important crop and a powerful model for investigating plant diversity, adaptation, and trait evolution. Its extensive natural variation, shaped by domestication, ecological adaptation, and farmer selection, provides an exceptional framework for linking biodiversity to gene function and crop performance. Integrative genomics has increasingly enabled this diversity to be translated into biological insight and breeding value. Using Thai rice germplasm as a case study, recent studies have combined population genomics, genome-wide association studies (GWAS), QTL-seq, transcriptomics, and functional validation to dissect the genetic basis of key adaptive and agronomic traits. These efforts have led to the identification of genomic regions and candidate genes associated with stomatal density, a trait closely related to water use and gas exchange; F-box genes linked to ethylene responsiveness and root growth under soil constraints; and *NAL1* and *OsOFP19* as additive regulators of tiller number, with direct implications for plant architecture and yield improvement. Additional work has identified *OsSAMHD1* as a causal gene underlying a novel white-striped leaf phenotype, and has revealed alternative resistance-associated components such as *RIR1b* in bacterial leaf streak resistance beyond the well-known *xa5* pathway. Together, these examples illustrate how natural variation in rice can be mechanistically decoded and translated into useful knowledge for crop improvement. Rice therefore provides a compelling model for bridging botanical discovery with functional genomics, molecular breeding, and the development of climate-resilient crops.