**Novel Adaptive Physiology for Salinity Tolerance in Transgressive Segregants of Rice**

Isaiah Pabuayon1, Md Mamunur Rashid2, Ai Kitazumi1, Habtom Ressom2, Benildo de los Reyes1

1 Department of Plant and Soil Science, Texas Tech University, Lubbock, TX, USA

2 Department of Oncology, Genomics, and Epigenomics Shared Resource, Lombardi Comprehensive Cancer Center, Georgetown University Medical Center, Washington, DC, USA

The effects of salinity stress are primarily mitigated by reducing the uptake of toxic Na+ and Cl- ions from essential tissues particularly the photosynthesizing leaves, hence often the focus of genetic analysis. However, prolonged exposure to saline conditions eventually overpowers the ion exclusion mechanisms regardless of capacity. We identified a salinity super-tolerant transgressive recombinant inbred line FL510 from an F8 population derived from a cross between IR29 (sensitive, *indica*) and Pokkali (tolerant, *aus*). This recombinant possesses multiple auxiliary mechanisms that enhance its tolerance to saline conditions despite the overaccumulation of Na+ ions in tissues. FL510 displayed a unique morphology that reduces osmotic stress effects by virtue of modulated transpiration rate and stomatal conductance. We identified two regulatory genes, *TAC3* and *OsIBH1*, as potential hubs of cytokinin and brassinosteroid genetic networks. These networks appear to be critical to the unique, non-parental morphology of the transgressive segregant. The architectural novelty appeared to be due to the positive complementation of the genetic potential of the *indica* and *aus* genomes, and the unique epigenomic landscape of outlier recombinants, which translated to novel regulatory networks and gain of physiological functions. In this presentation, we will discuss the consequences of recombination between two phylogenetically distant genomes (genomic shock) in terms of morphology, metabolome, and transcriptome, and the overall impacts to salinity tolerance potential.