Thursday, September 25, 11:00-11:30 a.m.

"Proteomic and functional analyses of plant immune signaling"

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The plant innate immune system is capable of recognizing conserved microbial patterns as well as pathogen effector proteins. Intracellular immune receptors typically contain nucleotide-binding leucine rich repeats (NB-LRRs) and recognize specific pathogen effectors delivered inside plant cells. Surface localized immune receptors consist of a variety of receptor like kinases (RLKs) or receptor like proteins that recognize conserved microbial patterns or damage associated molecular patterns. We have used quantitative proteomics coupled with RNAseq to profile changes occurring over time at the Arabidopsis plasma membrane upon activation of the RLK FLS2 and the intracellular NB-LRR RPS2. We were able to quantify >4,000 proteins per time point and 1,500 phosphorylated peptides. Protein kinases represent the largest class of differentially regulated proteins and our data highlight the importance of specific phosphorylated residues. Functional analyses of the cysteine rich RLKs (CRKs) will be reported. Phosphorylation of serine and threonine residues were identified in several CRKs and five sites are conserved across multiple members. The role of specific phosphorylated and cysteine residues for CRK function will be reported. These results provide one of the largest analyses of the plasma membrane proteome and highlight multiple areas for further hypothesis driven research.