Leveraging Omics to ask and answer big biological questions

Wei Zhang

Department of Plant Pathology, Kansas State University

Plant pathogens cause dramatic crop losses every year. Plant-pathogen interactions, like any other infections, are complex interactions between two organisms where molecules continuously flow in both directions. A central goal of studying host-pathogen interaction is to understand how host and pathogen manipulate each other to promote their own fitness in a pathosystem. Omics technologies have thriven with the fast development of next generation sequencing and mass spectrometry together with continuously growing computing power. Omics technologies are high-throughput biochemical assays that measure whole-genome molecular behaviors comprehensively and simultaneously from a biological sample. Integrated omics approaches allow to snapshot physical or functional interactions among DNA, RNA, proteins, and small molecules and uncover the organizing principles within a cell, an organism, even an ecosystem. We apply omics-based approaches on Arabidopsis-*B. cinerea pathosystem* to test how natural genetic variation impacts plant host and fungal pathogen interact from gene expressions (transcriptomic level) to disease symptoms (phenotypic level). We use co-transcriptomic approaches to simultaneously analyze dual transcriptomes during infection and provide a systematic map of the cross-kingdom communication between two species. At epigenomic level, we demonstrate how chemical modification of lysine residues on the histone H3, which helps organize and control DNA usage, play an important regulatory role in *Magnaporthe oryzae*, a model fungal pathogen causing rice blast disease.