Exploring plant-microbiome-pathogen triangular interactions in the leaf phyllosphere

Shanice S. Webster[1,2], Yulin Sun[1], Xu Jin[3], Tao Chen[1], Sheng Yang He[1,2]

[1]*Department of Biology, Duke University, Durham, NC*
[2]*Howard Hughes Medical Institute, Chevy Chase, MD*
[3]*University of Florida, Gainesville, FL*
[4]*Whitehead Institute, MIT, Boston, MA.*

Plants are colonized by a diverse range of microbes that are important for plant health and fitness. Given this array of commensals, pathogens and symbionts found on plants, how do plants assemble a correct microbiome to maximize the benefits of beneficial species and minimize the impacts of harmful ones? Work from our group shows that a healthy microbiome composition is characterized by a balance between Proteobacteria and Firmicutes. However, the underline mechanisms that link plant-derived signals to phyllosphere microbiome composition are unclear. Here, we hypothesize that heathy plants secrete a distinct profile of metabolites that impact the microbiome transcriptome and thereby impact the plant's microbiome composition. We found that a *mfec* plant mutant which shows a dysbiotic microbiome composition and associated tissue damages, shows an altered metabolite signature and a dysbiotic microbiome transcriptome. Through binary interaction studies, we show that *a Proteobacterium* inhibits *Firmicute sp.* in a metal-dependent manner, and *Proteobacterium* mutants defective in metal uptake reduces the inhibition. These data begin to provide a mechanistic explanation for the proliferation of Proteobacteria and reduction of Firmicutes observed in plants with a dysbiotic microbiome composition. Our studies highlight a potential mechanism wherein healthy plants regulate levels of apoplastic ions and possibly other metabolites to maintain a healthy microbiome composition in the phyllosphere.