



HOSTED BY PLANTS3D'S
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INTERACTIONS BETWEEN HOST
GENETICS AND THE MICROBIOME
THAT SUPPRESS PLANT PATHOGENS



In agriculture, microbial disease outbreaks are often associated with the emergence and spread of single pathogenic lineages. Evidence suggests that wild plant populations are more resistant to this type of outbreak. I will describe work that aims to identify factors in wild plant populations that provide protection from pathogen spread. Focusing on interactions between the widespread plant bacterial pathogen *Pseudomonas syringae* and wild populations of *Arabidopsis thaliana*, we used microbiome surveys of host populations to determine the spatial distributions of *Pseudomonas* pathogens. Comparative genomics of more than 1,500 *Pseudomonas* strains and subsequent pathology testing revealed extensive phenotypic and genetic variation in the pathogen populations, and genotype x genotype interactions with the *A. thaliana* immune system. We further found evidence that interactions with other microbiota and phages in wild populations prevent single strains of *Pseudomonas* from spreading broadly. Overall, our results suggest that a combination of host genetic diversity and competition with complex microbial communities suppress *Pseudomonas* spread.

**FRIDAY, MAY
12TH**

**GENOMICS AUDITORIUM
12PM - 1PM**

Coffee Hour @ 11:30am



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