

Uncovering Host Genetic Determinants of Protective Plant-Microbe Interactions

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Abstract

Plant-associated microbial communities play an important role in plant health, including protection against bacterial pathogens. Although commensal bacteria can suppress pathogen-induced disease, the extent to which plant host influences these protective interactions remains poorly understood. Previous work in our lab identified natural variation among *Arabidopsis thaliana* accessions in their ability to benefit from the protective commensal *Pseudomonas* strain p3.A9 during infection with the pathogenic strain p4.C9. A genome-wide association (GWAS) study identified several candidate host loci and single-nucleotide polymorphisms (SNPs) associated with variation in commensal-mediated protection. In this study, we investigate the genetic basis of this protection by screening homozygous T-DNA insertion mutants in candidate host genes for altered responses to p3.A9 and p4.C9 co-inoculation. By comparing pathogen-induced disease in the presence and absence of the commensal, we aim to identify host genes required for effective commensal-mediated protection. This work will provide insight into the molecular mechanisms underlying beneficial plant-microbe interactions and identify host genetic factors that could be leveraged to enhance microbiome-mediated disease resistance in crops.

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