



Pseudomonas fluorescens Induces Strain-Dependent and Strain-Independent Host Plant Responses in Defense Networks, Primary Metabolism, Photosynthesis, and Fitness

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Background

- The root-rhizosphere harbors numerous microbial associates that shape host plant performance. The mechanisms mediating these interactions are largely unknown.

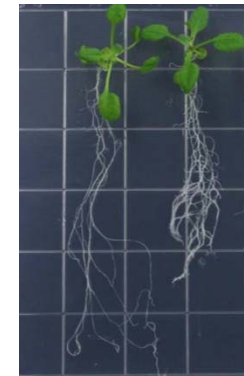
Science

- Using *Arabidopsis* plants as a model, *Populus deltoides* bacterial isolate GM30 was found to be a plant-growth-promoting rhizobacterium (PGPR) increasing lateral root growth and protecting the plant host against disease.
- Root colonization of *Arabidopsis* by GM30 elicits a systemic defensive response that was elucidated by network modeling of gene expression and metabolite pathway analysis.

Significance

- This work identifies a specific gene network driving the systemic response in plant-PGPR interactions.
- This work also provides a baseline network for understanding the roles of multiple microbial associates and host plant genotypes.

Resulting Plant Phenotype



Control GM-30



8.08 (1.03)

Control



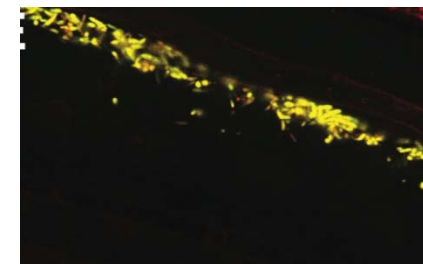
1.08 (0.64)

GM-30

Numbers are lesions per plant and (SE) after pathogen challenge



Host plant metabolism (network modeling & physiology)



GM30 associated with plant root

Weston et al., (Accepted for publication). *Molecular Plant-Microbe Interactions*, Vol. 25, doi:10.1094/MPMI -09-11-0253

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Abstract:

Colonization of plants by nonpathogenic *Pseudomonas fluorescens* strains can confer enhanced defense capacity against a broad spectrum of pathogens. Few studies, however, have linked defense pathway regulation to primary metabolism and physiology. In this study, physiological data, metabolites, and transcript profiles are integrated to elucidate how molecular networks initiated at the root–microbe interface influence shoot metabolism and whole-plant performance. Experiments with *Arabidopsis thaliana* were performed using the newly identified *P. fluorescens* GM30 or *P. fluorescens* Pf-5 strains. Co-expression networks indicated that Pf-5 and GM30 induced a subnetwork specific to roots enriched for genes participating in RNA regulation, protein degradation, and hormonal metabolism. In contrast, only GM30 induced a subnetwork enriched for calcium signaling, sugar and nutrient signaling, and auxin metabolism, suggesting strain dependence in network architecture. In addition, one subnetwork present in shoots was enriched for genes in secondary metabolism, photosynthetic light reactions, and hormone metabolism. Metabolite analysis indicated that this network initiated changes in carbohydrate and amino acid metabolism. Consistent with this, we observed strainspecific responses in tryptophan and phenylalanine abundance. Both strains reduced host plant carbon gain and fitness, yet provided a clear fitness benefit when plants were challenged with the pathogen *P. syringae* DC3000.