The impacts of microbial genes on plant development

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Outline

- Introduction
- Impact of *iacA* on *Arabidopsis* gene expression over time
- Future directions

Microbial impact on plants

PGPB

- Pseudomonas
- Burkholderia
- Bacillus
- Azospirillum

Effects

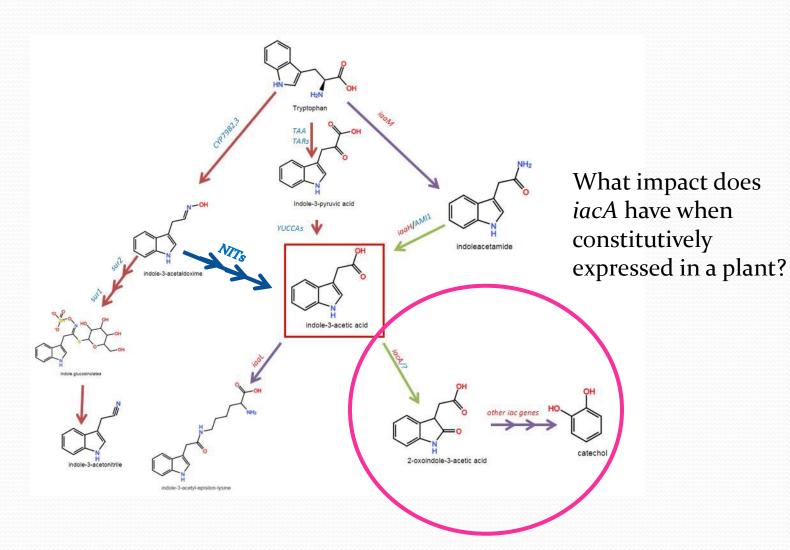
- Biocontrol
 - Antagonism
 - Predation
 - Signal interference
- Fertilization
 - N₂ fixation
- Phytostimulation
 - Stress control
 - Hormone metabolism

Pseudomonas putida 1290

- Environmental bacterium
- Capable of indole-3 acetic acid (IAA) degradation
- Possesses 10-gene *iac* cluster
- Grows on IAA as a sole carbon and nitrogen source

Indole-3 Acetic Acid (IAA)

- What is it?
 - Plant Hormone
 - Produced by plants and some plant pathogens
- Why is it important to plants?
 - Root development
 - Shoot development
 - Embryogenesis
 - Flowering
 - Gravitropism



Naming Clarification

- Col-o: Wild type "Columbia" Arabidopsis thaliana
- pMD1iacA: A. thaliana constitutively (from a 35S promoter) expressing P. putida 1290 gene iacA (Columbia background)
- pMD1iacA5 and pMD1iacA8 are independent transformants both constitutively expressing *iacA*.

Does iacA expression impact:

- Root Phenotype?
 - Delayed root growth in young plants (9 days post sowing)
- Disease Resistance?
 - No significant difference in response to *Pseudomonas syringae pv. tomato DC*3000
- Root Transcriptome?

Impact of *iacA* on *Arabidopsis* transcriptome?

Differentially Expressed Genes

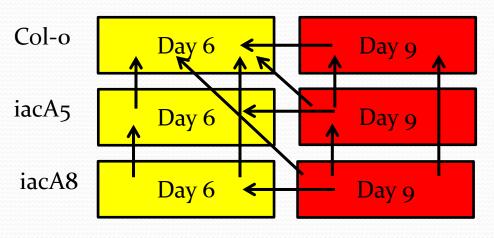
- Nutrient Metabolism?
- Hormone regulation/transport?
- Disease response?
- Stress response?

Methods

- Trizol RNA extraction from Arabidopsis roots
 - Grown on sterile Hoagland media
 - Samples taken at 6 and 9 days post-germination
 - ~40 plants pooled/biological replicate
 - 4 biological reps, 3 cultivars, 2 time points (24 samples total)
- RNA Clean-up
 - Zymo kit (DNAse step very important)
- Bioanalyzer
 - Measure RNA integrity (RIN)
 - Ratio of 28S:18S RNA
- Poly-A Enrichment
 - Select for mRNA
- Library Preparation, sequencing, and analysis

Transcriptional Comparisons

How do the mutants compare to wild type within each time point? How do the mutants and wildtype compare between time points? How do the mutants and wildtype compare to each other between time points?



- Look at genes that are differentially expressed by at least a factor of 1.5
- p value < .05

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