The role of secondary metabolites in the composition of root microbiome of Arabidopsis

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Plants are vital to human life



Grape

Maize

Coffee

Plants produce secondary metabolites



Secondary metabolites contribute to host fitness

- Primary metabolites are essential for growth and development
- Secondary metabolites are a biproduct of metabolism and are not essential for growth but contribute to the fitness of the host



Plants produce secondary metabolites









Arabidopsis can be used to study how secondary metabolites are made and why they're important

Arabidopsis is a "model organism" for studying plant genetics

- A member of the Brassicaceae family
- Easy to grow
- Genome is small (114.5 Mb) and already sequenced
- Genetically tractable
- **Mutant libraries**















Secondary metabolites modulate the root microbiome

Triterpenes (a secondary metabolite) are secreted by Arabidopsis roots







Root microbiome has a diverse composition

What is root microbiome?

- The community of microorganisms that reside in and around plant roots
- Includes bacteria, fungi, archaea, and viruses
- Commonly consists of Proteobacteria, Actinobacteria, and Bacteriodetes



Healthy root microbiome is beneficial to the plant

How does it affect the plant?

- PGP (plant growth promoting) services
- Competes for resources against pathogens



There are different compartments of root microbiome



CYP702A genes are associated with phytosteroid production



CYP702A genes are associated with phytosteroid production

phytosteroid

Acetyl-CoA Labelled with mevalonate-D3 Campesterol CYP702A-derived C28H48O cyp702a5cyp70a6 (CRISPR-Cas9) Chr. 1 Chr. 4 Mevalonate C₂₈H₄₈O C₂₈H₄₈O₂ cyp702a1 cyp702a2 cyp702a3 cyp702a5 cyp702a6 CD3 GK-047B01 SALK_008925 GK-634A06 GK-697G04 SALK-097493 ∇ C₂₈H₄₄O C₂₈H₄₆O₂ C₂₈H₄₆O₂ C₂₈H₄₈O₃ ∇ ∇ CYP702A1 CYP702A2 CYP702A3 CYP702A5 CYP702A6 0.5kb C₂₈H₄₂O C₂₈H₄₄O₂ C₂₈H₄₄O₂ C₂₈H₄₆O₃ AT1G65670 AT4G15393 AT4G15396 AT4G15300 AT4G15310 A5 • A5 Campesterol C₂₈H₄₈O A5/A6 C₂₈H₄₂O₂ C₂₈H₄₄O₃ A5 A5 normalized intensity C28H42O3 β-Sitosterol C29H50O Stigmasterol C₂₉H₄₈O β-Sitosterol ő Stigmasterol C₂₉H₄₈O C₂₉H₅₀O₂ . C₂₉H₅₀O C₂₉H₄₆O C₂₉H₄₈O₂ C₂₉H₅₀O₃ C₂₉H₄₄O C₂₉H₄₆O₂ C₂₉H₄₆O₂ C₂₉H₄₆O₃ [0]-C29H44O2 C_29H_46O_3 C_n oxyphytosteroids 100 C₂₀ oxyphytosteroids C29H44O3 0 15 30 20 25 Retention time

CYP702As (cytochromes P450)

CYP702A genes are associated with phytosteroid production



T-DNA lines:

cyp702a1-TD-GK-697G04 cyp702a2-TD-SALK-097493 cyp702a3-TD-GK-047B01 cyp702a5-TD-SALK-008925 cyp702a6-TD-GK-634A06

Knockout lines:

cyp702a5cyp702a6 cyp702a1cyp702a5cyp702a6 cyp702a2cyp702a3cyp702a5cyp702a6 cyp702a1cyp702a2cyp702a3cyp702a5cyp702a6 (Quintuple mutant)

Knockdown lines:

CYP702A2 in *cyp702a5cyp702a6* CYP702A3 in *cyp702a5cyp702a6* CYP702A2CYP702A3 in *cyp702a5cyp702a6* CYP702A2 in *cyp702a1cyp702a5cyp702a6* CYP702A3 in *cyp702a1cyp702a5cyp702a6* CYP702A2CYP702A3 in *cyp702a1cyp702a5cyp702a6*

No consistent phenotype!



Do phytosteroids produced by the CYP702 enzymes affect the Arabidopsis root microbiome?

Experimental Design

2 types of soil

8 Arabidopsis genotypes

4 replicates

1 developmental stage





2 types of soil from Jingke's garden (A and B)



- 1. WT
- 2. CYP702 quintuple mutant
- 3. CYP702A5 overexpression
- 4. CYP702A6 overexpression
- 5. CYP87 mutant
- 6. CYP87 CDS2 overexpression
- 7. CYP87 CDS3 overexpression
- 8. DpCYP87 overexpression



- 64 pots total
- 32 with soil A
- 32 with soil B
- 8 pots per genotype 5 plants per pot

Pots labelled A1, A2, B1, B2, etc.



Harvest after 4-6 weeks

4 types of collection

- 1. Bulk soil
- 2. Rhizosphere
- 3. Endosphere
- 4. Total root

Microbiome sampling



DNA collection



Validation of the DNA extraction protocol

Standardization protocol starting with ~100 mg of soil or ~100 mg of roots





- 2 Rhizosphere 3 - Endosphere
- 4 Total Root

Plant growth progress (3 weeks)





Soil type A

Soil type B

- 1. WT
- 2. CYP702 quintuple mutant
- 3. CYP702A5 overexpression
- 4. CYP702A6 overexpression
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- 7. CYP87 CDS3 overexpression
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