Drivers of plant microbial community composition

Susannah Green Tringe
DOE Joint Genome Institute
Phytobiomes 2015
Talk outline

• A model plant: Arabidopsis
  – Drivers of microbial community composition
  – Seeking endophyte genomes

• A non-model plant: Agave
  – Impact of location and cultivation on bacterial and fungal communities
Talk outline

• A model plant: *Arabidopsis*
  – Drivers of microbial community composition
  – Seeking endophyte genomes

• A non-model plant: *Agave*
  – Impact of location and cultivation on bacterial and fungal communities
Plant microbiome

1) Rhizosphere / endophyte microbes
   - provide nutrients
   - protect from pathogens and stress
   - influence growth
   - sequester carbon

2) Challenges
   - soil microbial communities are notoriously complex
   - plant genomes are complex
   - crosses multiple disciplines and programs
   - statistical rigor requires high sample numbers

Jeff Dangl, UNC
Are there unique communities in each compartment? Does the plant control access?
The Arabidopsis Microbiome

Identifying the major determinants of microbial community assembly

Host factors

Root-associated microbial communities

Variables investigating:
- Soil type – Mason Farm vs. Clayton
- Sample fraction – Bulk soil vs. rhizosphere vs. endophyte
- Plant age – bolting (young) vs. senescent (old)
- Genotype – 8 ecotypes
- Individual – Aim for 10 individuals per condition

Full factorial design
1117 samples
16S pyrotag profiles

Dangl lab, UNC
The Arabidopsis microbiome

The endophyte community is unique and reproducible and similar across soil types.

Lundberg Nature 2012

Rhizosphere/Soil 1

Rhizosphere/Soil 2

Endophyte
The *Arabidopsis* Microbiome

Dangl lab, UNC
Woyke lab, JGI

Cultured isolates

“Plate scrape” metagenomes

Single cells

Flow-sorted “mini-metagenomes”

STREPTOMYCES
OTU 14834

SPHINGOBACTERIALES
OTU 2324

PSEUDONOCARIAE
OTU 13797
An endophyte genome catalog

99 isolates and 130 SAGs
fully sequenced
>50% of target OTUs
### Genomic signatures of plant association

<table>
<thead>
<tr>
<th>Taxon</th>
<th>Phylum</th>
<th># PA genomes</th>
<th># NPA genomes</th>
<th># total genes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bacillus</td>
<td>Firmicutes</td>
<td>28</td>
<td>141</td>
<td>852,695</td>
</tr>
<tr>
<td>Paenibacillus</td>
<td>Firmicutes</td>
<td>11</td>
<td>29</td>
<td>226,631</td>
</tr>
<tr>
<td>Burkholderiales</td>
<td>Proteobacteria</td>
<td>60</td>
<td>144</td>
<td>1072,509</td>
</tr>
<tr>
<td>Pseudomonas</td>
<td>Proteobacteria</td>
<td>152</td>
<td>77</td>
<td>1,242,490</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rhizobiales</td>
<td>Proteobacteria</td>
<td>93</td>
<td>19</td>
<td>433,488</td>
</tr>
<tr>
<td>Xanthomonadaceae</td>
<td>Proteobacteria</td>
<td>170</td>
<td>152</td>
<td>1,717,437</td>
</tr>
<tr>
<td>Sphingomonas</td>
<td>Proteobacteria</td>
<td>7</td>
<td>12</td>
<td>73,946</td>
</tr>
<tr>
<td>Microbacteriaceae</td>
<td>Actinobacteria</td>
<td>18</td>
<td>27</td>
<td>140,326</td>
</tr>
<tr>
<td>Micrococcaceae</td>
<td>Actinobacteria</td>
<td>13</td>
<td>22</td>
<td>117,775</td>
</tr>
<tr>
<td>Nocardiaceae</td>
<td>Actinobacteria</td>
<td>13</td>
<td>37</td>
<td>315,053</td>
</tr>
<tr>
<td>Streptomyces</td>
<td>Actinobacteria</td>
<td></td>
<td>229</td>
<td></td>
</tr>
</tbody>
</table>

Comparative genomics revealed plant-associated genes and operons involved in chemotaxis, carbohydrate metabolism, and secondary metabolite biosynthesis.
Recolonization and RNA-seq

Inoculation with root-associated microbes reverses low P phenotype
Conclusions / Next steps

• Phase I conclusions
  – Endophytic and rhizosphere communities assemble in a predictable manner
  – “Core microbiome” is very small (at OTU level)

• Phase II
  – Is there a “functional core”?
  – How do microbes affect plant phenotypes?
  – How do plants influence microbes?
Talk outline

• A model plant: *Arabidopsis*
  – Drivers of microbial community composition
  – Seeking endophyte genomes

• A non-model plant: *Agave*
  – Impact of location and cultivation on bacterial and fungal communities
Biofuels in semi-arid lands?

Is biofuel production possible in arid and semi-arid lands?

(Adapted from: Dale et al. 2010 in Biofuels and Sustainability Reports. Ecological Society of America and Wright, L. L., 1994.. Biomass & Bioenergy 6: 191-209.)
Numerous species of Agave are native to arid regions of Mexico

(Adapted from: Garcia-Moya et al., 2011. GCB Bioenergy.)
Agave microbiome across time and space

6 Sample Types x
9 Sub-regions x
2 Seasons x
3 Reps
= ~300 Samples

Devlin Coleman-Derr
Factors driving microbial community composition

Prokaryotes
- Inside/Outside Plant: Axis 1: 13.7%, Axis 2: 6.8%
- Anosim = 0.511 *

Fungi
- Inside/Outside Plant: Axis 1: 11.4%, Axis 2: 7.8%
- Anosim = 0.237 *

Above/Below Ground: Axis 1: 13.7%, Axis 3: 6.4%
- Anosim = 0.300 *

Legend for Endosphere
- Soil
- Episphere
- Endosphere

Legend for SampleClass
- Soil
- Root
- Aerial

PCoA distance measure: 0.0 - 0.4

Devin Coleman-Derr
Factors driving microbial community composition

Prokaryotes

- Axis 1: 13.7%
- Axis 2: 6.8%

- Region: 6.8%

Fungi

- Axis 1: 11.4%
- Axis 2: 6.9%

- AnoSim = 0.188 *
- AnoSim = 0.624 *

Species

- Axis 1: 13.7%
- Axis 2: 7.8%

- AnoSim = 0.262 *
- AnoSim = 0.633 *

Legend:
- California
- Mexico
- A_deserti
- A_salmiana
- A_tequiliana

(* = p<0.001)
Low diversity communities in cultivated Agave

Prokaryotes ~ Rhizosphere

Cultivated Agave

Prokaryotes ~ Bulk Soil
Low diversity communities in cultivated Agave

Prokaryotes ~ Rhizosphere

Shannon’s Diversity

Prokaryotes ~ Leaf Episphere

Cultivated Agave

Devon Coleman-Derr
Agave Microbiome: Conclusions

- Fungal communities are more influenced by sampling location / host species; bacterial communities are more influenced by sampling type.

- Bacterial diversity is greater for epispheres of wild Agaves than for cultivated Agave.

- Specific bacterial and fungal genera differentiate the Agave microbiome from surrounding soils, and from the microbiomes of other desert plants.
Community Sequencing Program

Focus areas:
- Functional genomics and microbiomes of DOE JGI Flagship Plants
- Function-driven microbial genomics
- Extreme environments
- DNA synthesis

JGI “Flagship” plant genomes

Expanding to a cross-species Plant Microbiome Project
Acknowledgments

- **Dangl lab, UNC Chapel Hill**
  - Derek Lundberg
  - Sarah Lebeis
  - Sur Herrera-Paredes
  - Natalie Breakfield
  - Scott Yourstone

- **Cornell**
  - Ruth Ley
  - Jason Peiffer
  - Zhao Jin

- **DOE-JGI**
  - Scott Clingenpeel
  - Julien Tremblay
  - Devin Coleman-Derr
  - Tanja Woyke
  - Axel Visel
  - Stephen Gross

- **CINVESTAV**
  - Laila Partida
Thanks!