Exploring the Biogeography of Microbial Communities on the Surface of Seagrasses

Jenna Morgan-Lang1; Hannah Holland-Moritz1*; Jay Stachowicz1; Jonathan Eisen1
1University of California, Davis

Why Study Seagrass Microbes?

As foundation species, seagrasses play an important role in coastal marine environment health by providing a refuge habitat for small marine fauna. Protecting the coastline from erosion and contributing to coastal nutrient cycling. Biodiversity, these important ecosystems have become threatened by human activities and attempts to restore them have had limited success.

Understanding the microbial communities associated with seagrasses may shine light on the mechanisms behind seagrasses’ important ecological roles, aiding in restoration efforts. Although we have long known about the important roles microbes play in the health of land plants, we still know very little about their role in aquatic systems. The goal of this study is to use culture-independent methods to characterize the microbiome of the seagrass Zostera marina to understand the variation of the microbial communities on the surface of an individual plant.

Conclusions

● Root tip communities suggest a microbiologically unique root environment.
● Distance from vegetative tissue may influence root microbial communities.
● Taxonomic analysis suggests root-associated communities play a role in sulfur-cycling.

Results and Discussion

Community Composition

Methods

1. Collect plants and tissue
2. Cut into sections
3. Wash sections vigorously with sterile water
4. Extract total DNA from root tissue with MoBio extraction kit
5. Prepare PCR reactions with BioStar BioStar
6. Sequence 16s
7. Analyze sequence data with bioinformatics tools

Beta Diversity

Top 10 Sequences

<table>
<thead>
<tr>
<th>Rank</th>
<th>Sequence</th>
<th>Percent Abundance</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Sulfurimonas</td>
<td>0.03</td>
</tr>
<tr>
<td>2</td>
<td>Flavobacteriaceae</td>
<td>0.02</td>
</tr>
<tr>
<td>3</td>
<td>Desulfobulbaceae</td>
<td>0.02</td>
</tr>
<tr>
<td>4</td>
<td>Rhodobacteraceae</td>
<td>0.02</td>
</tr>
<tr>
<td>5</td>
<td>Gammaproteobacteria</td>
<td>0.02</td>
</tr>
<tr>
<td>6</td>
<td>Piscirickettsiaceae</td>
<td>0.02</td>
</tr>
<tr>
<td>7</td>
<td>Chromatiales</td>
<td>0.02</td>
</tr>
<tr>
<td>8</td>
<td>Flavobacteraceae</td>
<td>0.02</td>
</tr>
<tr>
<td>9</td>
<td>Pedobacter</td>
<td>0.02</td>
</tr>
<tr>
<td>10</td>
<td>Arcobacter</td>
<td>0.02</td>
</tr>
</tbody>
</table>

Conclusions

Leaf communities differ from communities associated with the rest of the plant psychrophilic organisms associated with the rest of the plant. Whole roots contain larger amounts of Desulfobulbaceae. Leaf communities contain several taxa whose relative abundance either increases (e.g. Bacteroidales) and decreases (e.g. Acidobacteria) with distance from the leaf. Rhizome root communities are distinct from roots that are closer to the leaf shoot.

Alpha Diversity

Leaf Communities (Genus Level)

- The least diverse leaf is 43%
- The most diverse leaf is 63%

Leaf Communities

- Leaf communities closest to communities associated with the rest of the plant (chloroplast proteins encoded in the plastid, ORFs that are not transcribed).
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Comments?

(If you have any comments or questions, you might have an sticky note here)