Composition and Diversity of Soil Microbial Communities Following Vegetation Change from Grassland to Woodland: An Assessment Using Molecular Methods

I.B. Kantola, T.W. Boutton, T.J. Gentry, and E.C. Martin

1Department of Ecosystem Science and Management, Texas A&M University
2Department of Soil and Crop Sciences, Texas A&M University

BACKGROUND

Many grass-dominated ecosystems around the world have experienced woody plant encroachment during the past century due to livestock grazing, fire suppression, and/or changes in climate and atmospheric chemistry. Our prior research in the Rio Grande Plains of Texas shows that subtropical thorn woodlands dominated by N-fixing tree legumes have largely replaced grasslands, resulting in increased above- and belowground productivity, soil C and N storage, and the size and activity of the soil microbial biomass pool. These profound changes in ecosystem structure and function are likely to influence the composition and function of soil microbial communities.

OBJECTIVE

To assess the impact of grassland to woodland transitions and topoedaphic variation on the bacterial biodiversity of soil microbial communities in a subtropical savanna landscape using molecular identification techniques for soil DNA.

RESEARCH AREA

Research was conducted at the La Copita Research Area in southern Texas (MAP=715mm; MAT=22.4°C). Topography consists of nearly level uplands which grade (1-3% slopes) into lower-lying drainage woodlands. Sandy loam uplands (Typic Argustolls and Pachic Haplustolls) are covered with remnant grasslands interspersed with small, discrete clusters of woody plants, which may coalesce to form larger groves of woody vegetation. Lower-lying, closed-canopy drainage woodlands have finer-textured clay loam soils (Pachic Argisols). Prosopis glandulosa, an N2-fixing tree legume, dominates all woody landscape elements. Playas are basins with no external drainage that occupy the lowest portions of the landscape and have no external drainage, and consist of relatively open grassland with scattered mesquite trees.

METHODS

1. Soil samples (0-10 cm) were collected in remnant grasslands and in four different woody community types (discrete clusters, groves, drainage woodlands, and playas) in a subtropical savanna parkland in southern Texas.

2. Ages of woody plant stands were determined by dendrochronology.

3. Microbial DNA was extracted from whole soil using a MoBio PowerMax Soil DNA isolation kit and purified by gel electrophoresis.

4. The 16S-23S ribosomal intergenic spacer region was amplified by polymerase chain reaction (PCR) with a fluorescently-labeled primer.

5. The resulting fragment length diversity of the intergenic spacer region was analyzed by automated ribosomal intergenic spacer analysis (ARISA).

6. Different fragment lengths were assumed to be different bacterial species.

7. The Shannon diversity index (H) and evenness calculations (E) were used to quantify the diversity of soil microbial communities.

CONCLUSIONS

1. Bacterial species richness decreased by 48% from 144 species in remnant grasslands to approximately 75 species in each of the four wooded landscapes.

2. The Shannon index decreased from 4.38 in grasslands to 3.68 in wooded areas.

3. The evenness component of diversity was comparable across all sites.

4. Bray-Curtis ordination revealed that microbial community composition of grasslands was significantly different from that of all woody plant community types.

5. There was no relationship between any of the bacterial diversity indices and the age of the woody plant stands (data not shown).

6. We hypothesize that the lower bacterial diversity in wooded areas may be a consequence of reduced diversity of organic matter substrates resulting from lower plant species diversity in wooded areas.

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La Copita Research Area, Ben Bolt, Texas

Figure 1. Principal component analyses of bacterial community composition in different landscape elements in a subtropical savanna parkland.

Table 1. Comparison of number of species, diversity (Shannon index), and community evenness for soil bacteria from five landscape elements.

<table>
<thead>
<tr>
<th>Landscape Element</th>
<th>Number of Species (S)</th>
<th>Shannon Diversity Index ((H))</th>
<th>Evenness ((E))</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grassland</td>
<td>144 ± 56</td>
<td>4.38 ± 0.34</td>
<td>0.89 ± 0.02</td>
</tr>
<tr>
<td>Cluster</td>
<td>88 ± 29</td>
<td>4.04 ± 0.28</td>
<td>0.91 ± 0.01</td>
</tr>
<tr>
<td>Grove</td>
<td>70 ± 14</td>
<td>3.68 ± 0.41</td>
<td>0.87 ± 0.10</td>
</tr>
<tr>
<td>Drainage Woodland</td>
<td>75 ± 25</td>
<td>3.80 ± 0.33</td>
<td>0.89 ± 0.04</td>
</tr>
<tr>
<td>Playa</td>
<td>68 ± 15</td>
<td>3.72 ± 0.33</td>
<td>0.89 ± 0.04</td>
</tr>
</tbody>
</table>

\(H = -\Sigma p_i \ln p_i\), \(E = H/\ln S\)

Table 2. Analysis of similarity between bacterial communities in soils from different landscape elements. Numbers are Bonferroni-corrected p-values. Asterisks indicate significant p-values.

<table>
<thead>
<tr>
<th>Landscape Element</th>
<th>Grassland</th>
<th>Cluster</th>
<th>Grove</th>
<th>Drainage Woodland</th>
<th>Playa</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Cluster</td>
<td>Grove</td>
<td></td>
<td>Drainage Woodland</td>
<td>Playa</td>
</tr>
<tr>
<td>Cluster</td>
<td>0.005*</td>
<td>1.000</td>
<td></td>
<td>0.001*</td>
<td>1.000</td>
</tr>
<tr>
<td>Grove</td>
<td></td>
<td>0.000*</td>
<td>1.000</td>
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<tr>
<td>Drainage Woodland</td>
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<tr>
<td>Playa</td>
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<td>0.009*</td>
<td>0.440</td>
</tr>
</tbody>
</table>

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