Global change in the Great Plains: Biodiversity, fire, and ecosystem carbon storage

GCEP End of Summer Workshop 2006

Emily Hollister
Department of Rangeland Ecology & Management
Texas A&M University
Global Change in the Great Plains

Land use/cover change
- Agriculture (crops & grazing)
- Fire suppression
- Invasive species
- Woody encroachment
- Urban encroachment

My Research
- Prescribed fire
- Woody encroachment
- Carbon cycle
- Net primary productivity
- Soil carbon pools and fluxes
- Soil microbial community
Waggoner Ranch Experimental Site

Location: Wilbarger County, TX

Mean Annual Precipitation: 665 mm

Mean Annual Temperature: 16.1 °C

Soil Texture: 16% sand, 52% silt, 32% clay

Soil pH : 7.0-7.21

Vegetation: Mixed grasses and *Prosopis glandulosa*

Fire regime: Repeated winter-only and summer-only fires

Image courtesy of: Texas Parks and Wildlife
Fire and Vegetation are associated with altered nutrient dynamics

**Fire**
- Increased SMB
- Soil organic C
- Soil total N
- MRT of labile C

**Vegetation**
- SMB
- Soil organic carbon
- Soil total N
- Size of slow C pool

May be driven by ANPP

Differences in grasses vs. mesquite
Linking above- and belowground communities

• Do microbial communities vary with vegetation type?
  – Cloning and sequencing approach
  – 4 vegetation types
Aboveground players

• Honey mesquite (*Prosopis glandulosa*)
  – N$_2$ fixing, woody species
  – Subcanopy soils have increased SOC and soil total N
  – Potential microclimate effects
Aboveground players

- C₃ perennial grasses
  - Medium stature (25-100 cm)
  - Cool season species
  - Contributes ~30-50% of herbaceous ANPP
  - Dominated by *Nassella leucotricha*
Aboveground players

- \( \text{C}_4 \) midgrasses
  - Medium stature (30-100+ cm)
  - Warm season growth
  - 2\textsuperscript{nd} largest contributor to herbaceous ANPP
Aboveground players

- $C_4$ shortgrasses
  - Short stature (5-25 cm)
  - Warm season growth
  - Dominated by *Buchloe dactyloides*
Identifying those belowground

Extract DNA from soil → Amplify 16S rRNA → Clone into *E. coli*

Purify cloned DNA → Add fluorescent label → Sequence

```
C G A T C G A T C G A T C G A T
A T A T A T A T A T A T A T A T
G T G T G T G T G T G T G T G T
```
General composition

- Phylum level classification using the Ribosomal Database Project
- RDP estimates the likelihood that membership frequencies are equal
General composition

• Most libraries were very similar, except C4 shortgrass

• What was the nature of these differences?

• How would they affect diversity estimates?
A few words about Diversity…

• Sample effort, size*, and statistics

• Definition of a “species”
  – Humans and primates differ by ~2%
  – Bacterial OTUs are often defined by 3% difference

• Multiple measures
A few words about Diversity…

Multiple measures

- Richness (“species” number)
- Evenness (distribution of abundance)
- Overlap (shared species)
- Structure (species and relative abundance)
- Phylogeny (evolutionary relationships)
### Basic Diversity Measures

<table>
<thead>
<tr>
<th>Vegetation</th>
<th>Sequences analyzed</th>
<th>OTUs classified</th>
<th>Shannon-Wiener</th>
<th>Simpson’s (1/D)</th>
<th>Chao I Richness Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mesquite</td>
<td>90</td>
<td>76</td>
<td>4.25</td>
<td>190.71</td>
<td>314.33</td>
</tr>
<tr>
<td>C₃ grass</td>
<td>55</td>
<td>44</td>
<td>3.71</td>
<td>114.23</td>
<td>118.38</td>
</tr>
<tr>
<td>C₄ Midgrass</td>
<td>67</td>
<td>57</td>
<td>3.97</td>
<td>157.93</td>
<td>261.17</td>
</tr>
<tr>
<td>C₄ Shortgrass</td>
<td>116</td>
<td>98</td>
<td>4.51</td>
<td>277.92</td>
<td>366.15</td>
</tr>
</tbody>
</table>

- Many of these indices are sample size-dependent.
- These don’t tell us how our 4 communities differ.
Comparisons between communities

• Community similarity
  – Composition
    • Shared members
    • Structure (relative abundances)
  – Phylogeny
    • Do communities share a similar phylogenetic (evolutionary) history?
Composition and Overlap

- **SONS** – Shared OTUs and Similarity*
  - Calculates shared richness
  - Calculates community overlap
    - Incidence-based
    - Abundance-based
    - Relative abundance-based

Phylum level composition

- Firmicutes
- Proteobacteria
- Actinobacteria
- Acidobacteria
- Gemmatimonadetes
- Bacteroidetes
- Cyanobacteria
- Nitrospira

*Few significant differences between samples*
## Composition and Overlap

<table>
<thead>
<tr>
<th>Vegetation pair</th>
<th>Shared members (OTUs)</th>
<th>Community similarity (structure and relative abundance)</th>
</tr>
</thead>
<tbody>
<tr>
<td>M-C₃</td>
<td>0.156</td>
<td>0.263</td>
</tr>
<tr>
<td>M-C₄ Mid</td>
<td>0.197</td>
<td>0.261</td>
</tr>
<tr>
<td>M-C₄ Short</td>
<td>0.222</td>
<td>0.136</td>
</tr>
<tr>
<td>C₃-C₄ Mid</td>
<td>0.274</td>
<td>0.215</td>
</tr>
<tr>
<td>C₃-C₄ Short</td>
<td>0.510</td>
<td>0.191</td>
</tr>
<tr>
<td>C₄ Mid-C₄ Short</td>
<td>0.240</td>
<td>0.143</td>
</tr>
</tbody>
</table>
## Composition and Overlap

<table>
<thead>
<tr>
<th>Vegetation pair</th>
<th>Shared members (OTUs)</th>
<th>Community similarity (structure and relative abundance)</th>
</tr>
</thead>
<tbody>
<tr>
<td>M-C₃</td>
<td>0.156</td>
<td>0.263</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.277</td>
</tr>
<tr>
<td>M-C₄ Mid</td>
<td>0.197</td>
<td>0.261</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.128</td>
</tr>
<tr>
<td>M-C₄ Short</td>
<td>0.222</td>
<td>0.136</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.110</td>
</tr>
<tr>
<td>C₃-C₄ Mid</td>
<td>0.274</td>
<td>0.215</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.141</td>
</tr>
<tr>
<td>C₃-C₄ Short</td>
<td>0.510</td>
<td>0.191</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.170</td>
</tr>
<tr>
<td>C₄ Mid-C₄ Short</td>
<td>0.240</td>
<td>0.143</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.137</td>
</tr>
</tbody>
</table>
Phylogeny

- **TreeClimber**
  - Asks: Do two or more communities share a common level of phylogenetic diversity?
  - Independent of species similarity
### Phylogeny

<table>
<thead>
<tr>
<th>Vegetation pair</th>
<th>Parsimony score</th>
<th>Random vs. Perturbed</th>
</tr>
</thead>
<tbody>
<tr>
<td>M-C₃</td>
<td>36</td>
<td>0.136</td>
</tr>
<tr>
<td>M-C₄ Mid</td>
<td>45</td>
<td>0.284</td>
</tr>
<tr>
<td>M-C₄ Short</td>
<td>38</td>
<td>0.034</td>
</tr>
<tr>
<td>C₃-C₄ Mid</td>
<td>37</td>
<td>0.466</td>
</tr>
<tr>
<td>C₃-C₄ Short</td>
<td>34</td>
<td>0.047</td>
</tr>
<tr>
<td>C₄ Mid-C₄ Short</td>
<td>40</td>
<td>0.041</td>
</tr>
</tbody>
</table>

![Phylogenetic tree diagram]
### Phylogeny

<table>
<thead>
<tr>
<th>Vegetation pair</th>
<th>Parsimony score</th>
<th>Random vs. Perturbed</th>
</tr>
</thead>
<tbody>
<tr>
<td>M-C$_3$</td>
<td>36</td>
<td>0.136</td>
</tr>
<tr>
<td>M-C$_4$ Mid</td>
<td>45</td>
<td>0.284</td>
</tr>
<tr>
<td>M-C$_4$ Short</td>
<td>38</td>
<td>0.034</td>
</tr>
<tr>
<td>C$_3$-C$_4$ Mid</td>
<td>37</td>
<td>0.466</td>
</tr>
<tr>
<td>C$_3$-C$_4$ Short</td>
<td>34</td>
<td>0.047</td>
</tr>
<tr>
<td>C$_4$ Mid-C$_4$ Short</td>
<td>40</td>
<td>0.041</td>
</tr>
</tbody>
</table>
Phylogeny

Why does the $C_4$ shortgrass community stand apart from the rest?

<table>
<thead>
<tr>
<th>Vegetation pair</th>
<th>Parsimony score</th>
<th>Random vs. Perturbed</th>
</tr>
</thead>
<tbody>
<tr>
<td>M-$C_3$</td>
<td>36</td>
<td>0.136</td>
</tr>
<tr>
<td>M-$C_4$ Mid</td>
<td>45</td>
<td>0.284</td>
</tr>
<tr>
<td>M-$C_4$ Short</td>
<td>38</td>
<td>0.034</td>
</tr>
<tr>
<td>$C_3$-$C_4$ Mid</td>
<td>37</td>
<td>0.466</td>
</tr>
<tr>
<td>$C_3$-$C_4$ Short</td>
<td>34</td>
<td>0.047</td>
</tr>
<tr>
<td>$C_4$ Mid-$C_4$ Short</td>
<td>40</td>
<td>0.041</td>
</tr>
</tbody>
</table>
Potential underlying causes

- Ecosystem patterning
  - Spatial and temporal
  - Above and belowground
Potential underlying causes

- Ecosystem patterning
- Microclimate
Potential underlying causes

- Ecosystem patterning
- Microclimate
- Plant tissue chemistry
Thank You

– Department of Energy
  • GCEP
  • Microbial Ecology and Physiology group at ORNL
– Boutton lab
– Texas Agricultural Experiment Station
– Pat Schloss (DOTUR, TREECLIMBER, SONS)
– Samuel Roberts Noble Foundation