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

GCEP End of Summer Workshop 2006

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Global Change in the Great Plains

Land use/cover change

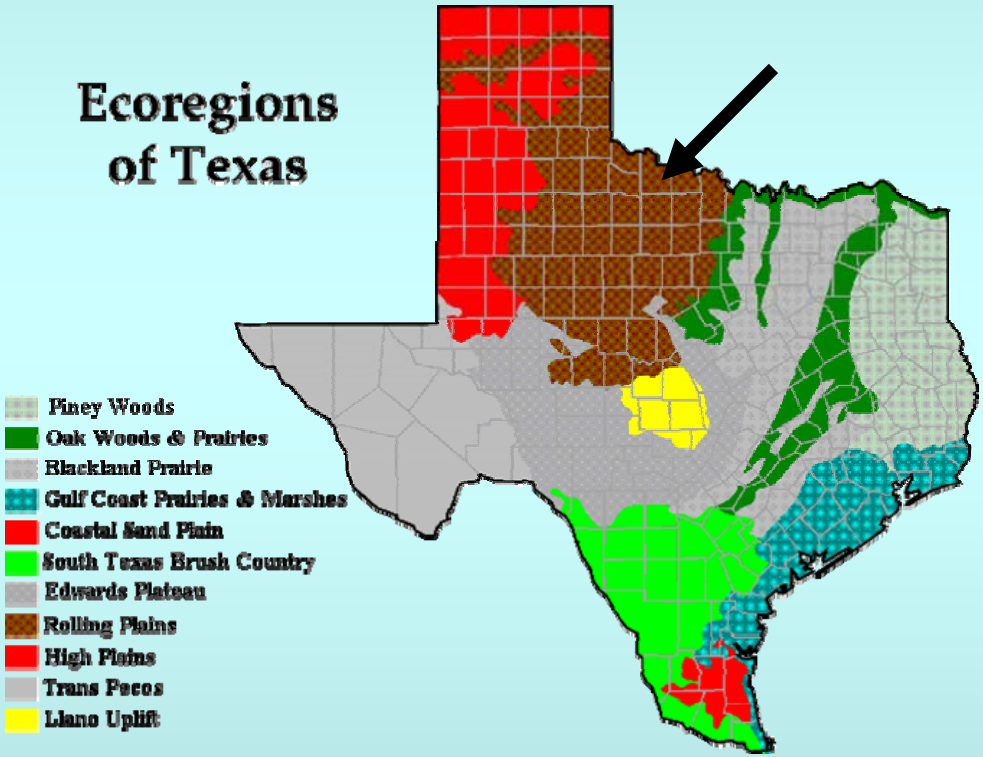
- Agriculture (crops & grazing)
- Fire suppression
- Invasive species
- Woody encroachment
- Urban encroachment

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 **

↓

May be driven by ANPP

Vegetation

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

↓

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

- C_3 perennial grasses
  - Medium stature (25-100 cm)
  - Cool season species
  - Contributes ~30-50% of herbaceous ANPP
  - Dominated by *Nassella leucotricha*




Aboveground players

- C_4 midgrasses
  - Medium stature (30-100+ cm)
  - Warm season growth
  - 2nd 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

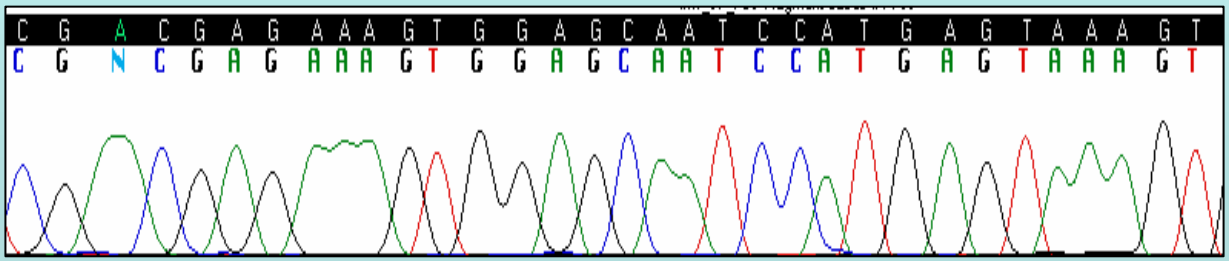
Clone into *E. coli*

Purify cloned DNA

Add fluorescent label

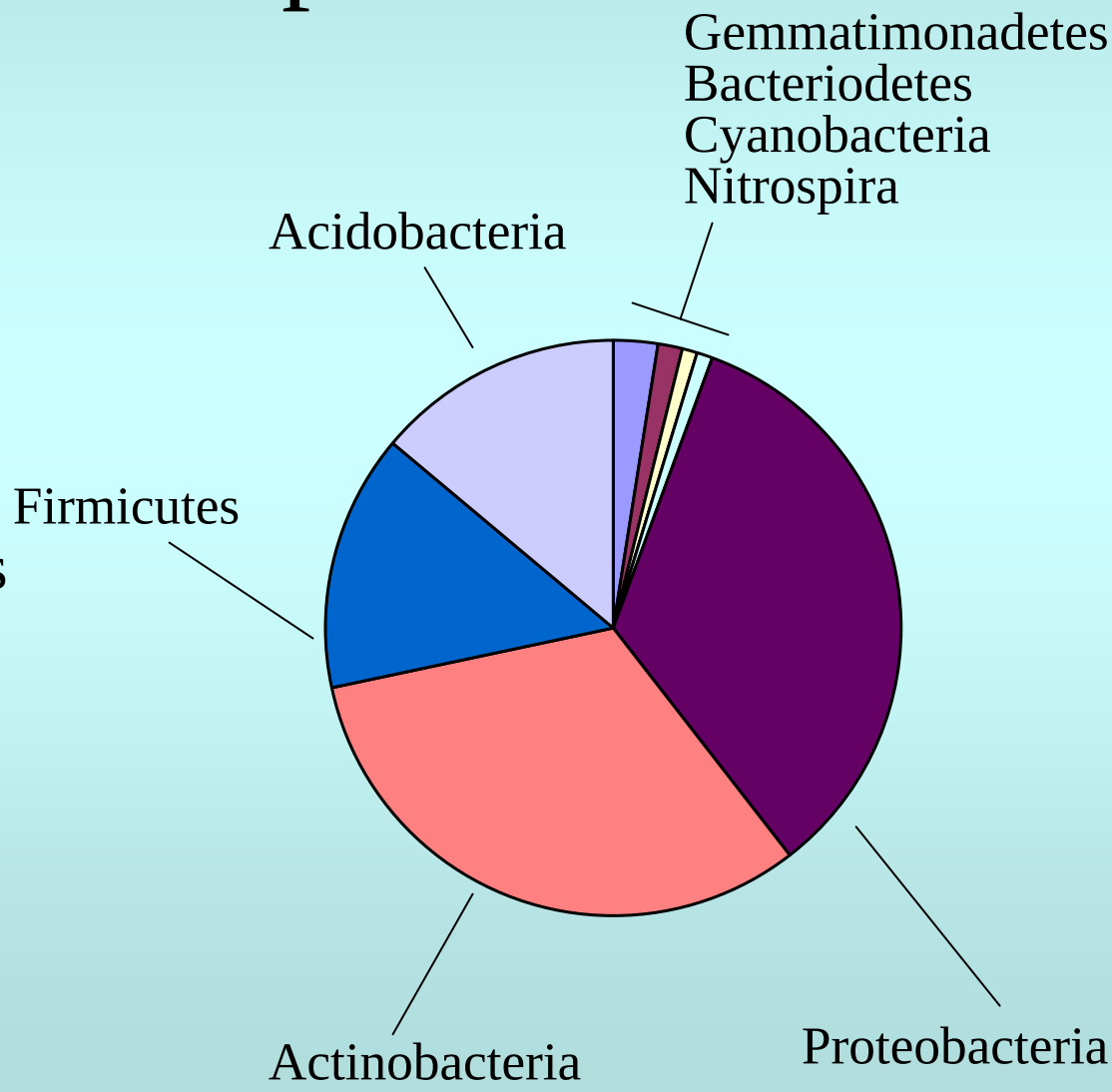
T A C G

Sequence



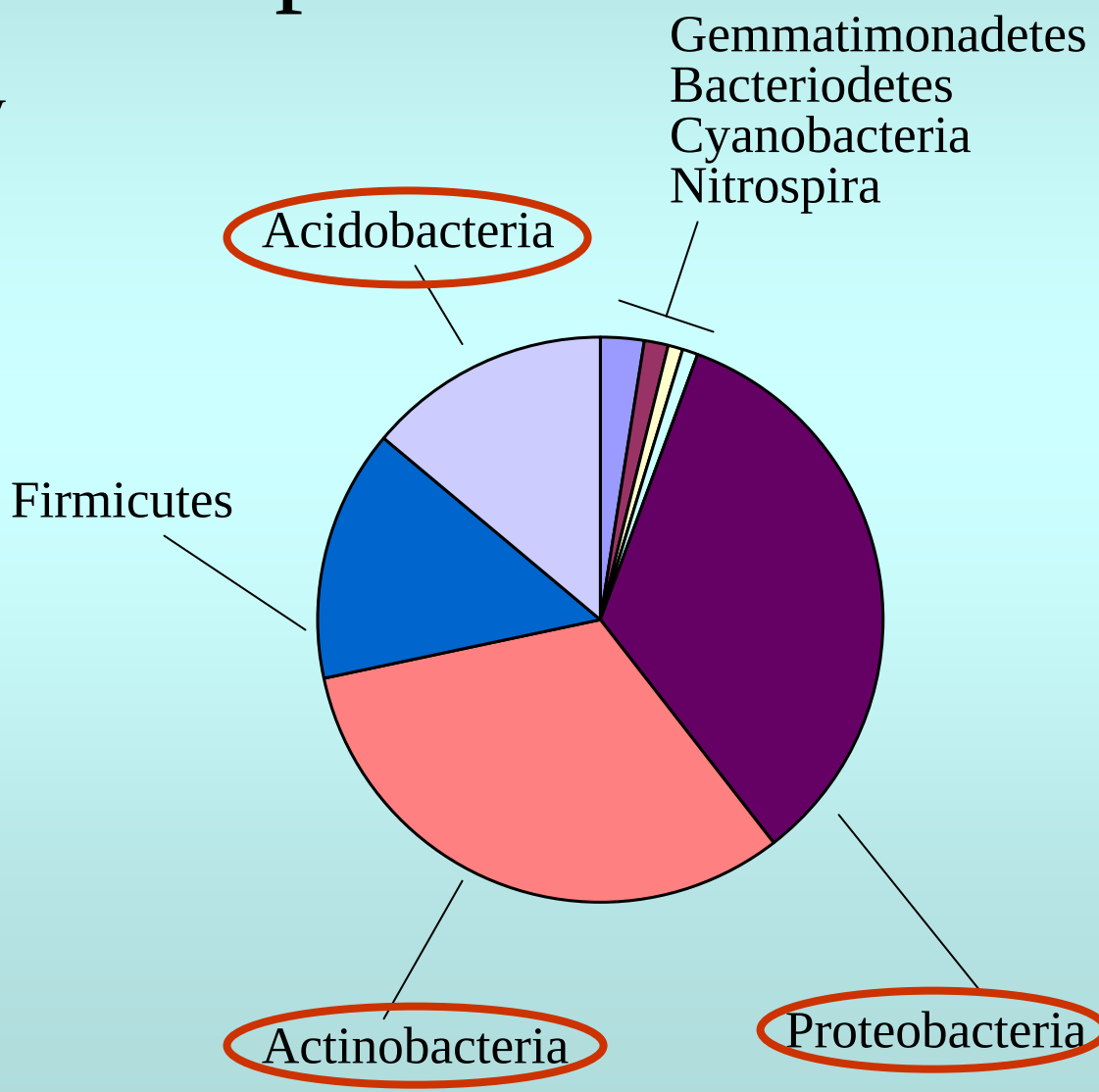
General composition

- 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 C_4 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

Vegetation	Sequences analyzed	OTUs classified	Shannon-Wiener	Simpson's (1/D)	Chao I Richness Estimate
Mesquite	90	76	4.25	190.71	314.33
C_3 grass	55	44	3.71	114.23	118.38
C_4 Midgrass	67	57	3.97	157.93	261.17
C_4 Shortgrass	116	98	4.51	277.92	366.15

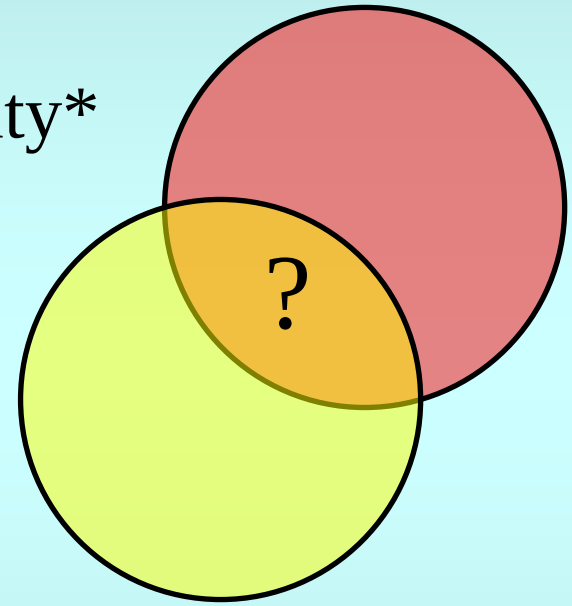
- Many of these indices are sample size-dependent.
- These don't tell us *how* our 4 communities differ.

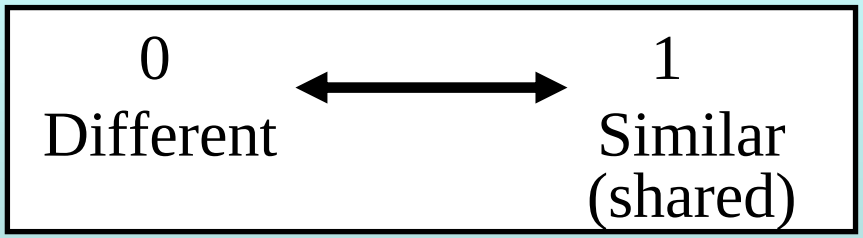
Comparisons between communities

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

Composition and Overlap

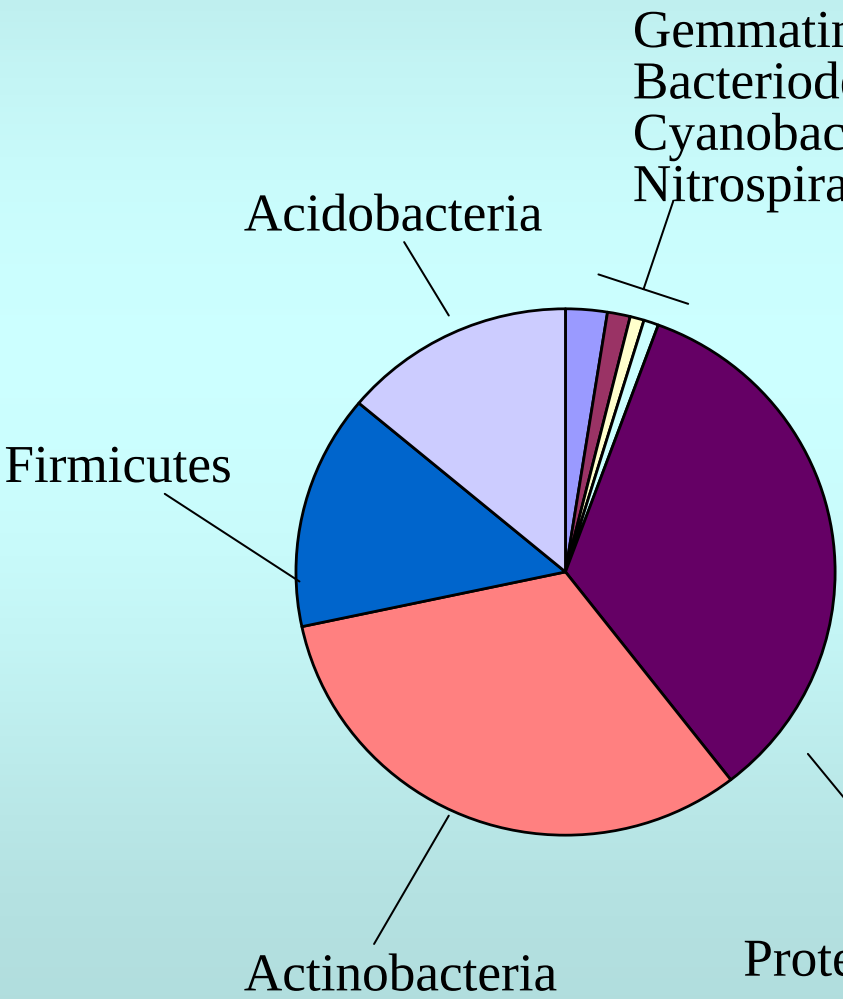
- SONS – Shared OTUs and Similarity*
  - Calculates shared richness
  - Calculates community overlap
    - Incidence-based
    - Abundance-based
    - Relative abundance-based





*Schloss, PD and Handelsman J. 2006. Introducing SONS, a tool for OTU-based comparisons of membership and structure between microbial communities. *Applied and Environmental Microbiology*.

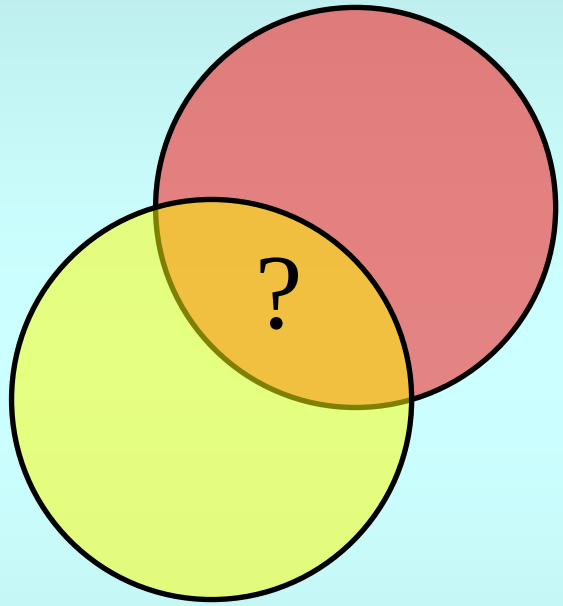
Phylum level composition



*Few significant differences between samples

Composition and Overlap

Vegetation pair	Shared members (OTUs)		Community similarity (structure and relative abundance)
M-C_3	0.156	0.263	0.277
M-C_4 Mid	0.197	0.261	0.128
M-C_4 Short	0.222	0.136	0.110
C_3-C_4 Mid	0.274	0.215	0.141
C_3-C_4 Short	0.510	0.191	0.170
C_4 Mid-C_4 Short	0.240	0.143	0.137



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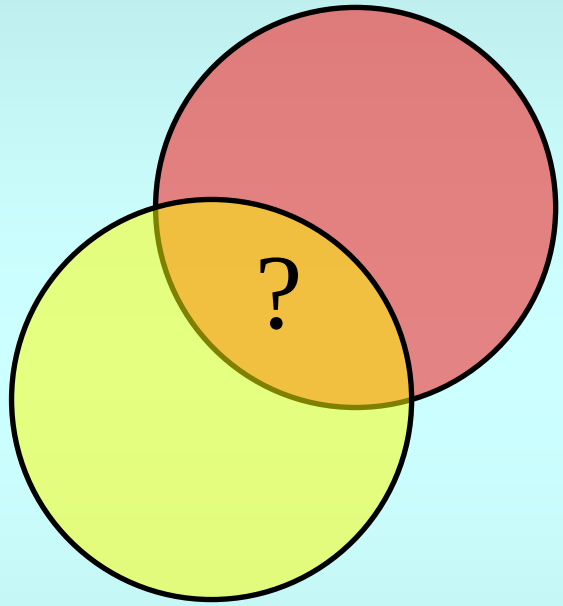
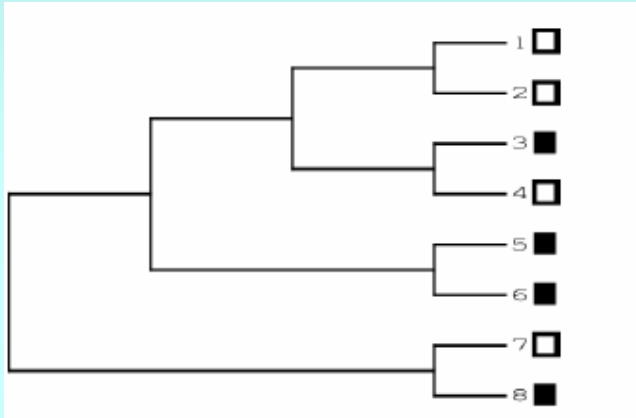


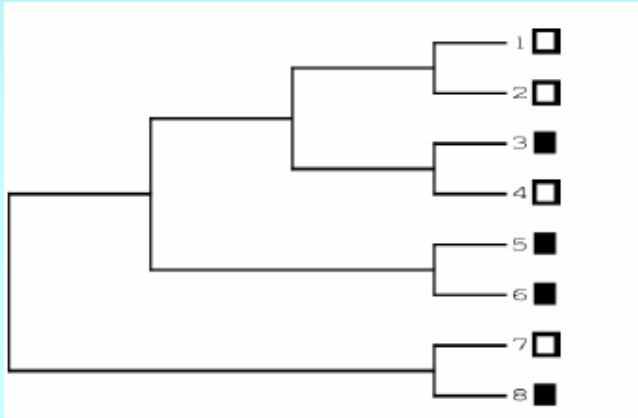
Phylogeny

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



Phylogeny

Vegetation pair	Parsimony score	Random vs. Perturbed
M-C_3	36	0.136
M-C_4 Mid	45	0.284
M-C_4 Short	38	0.034
C_3-C_4 Mid	37	0.466
C_3-C_4 Short	34	0.047
C_4 Mid-C_4 Short	40	0.041



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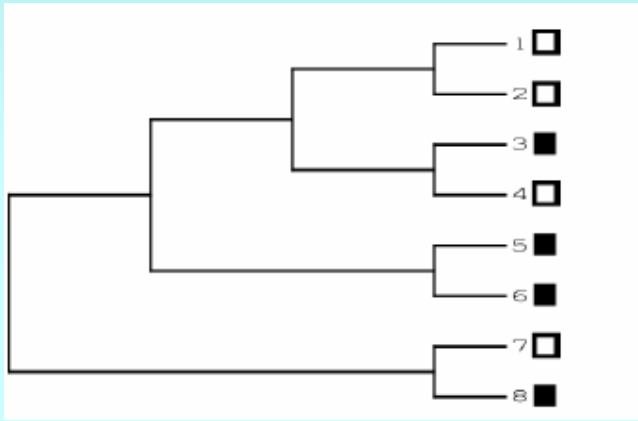

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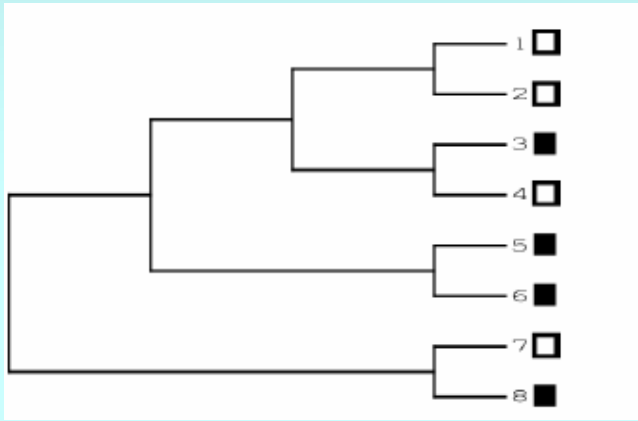
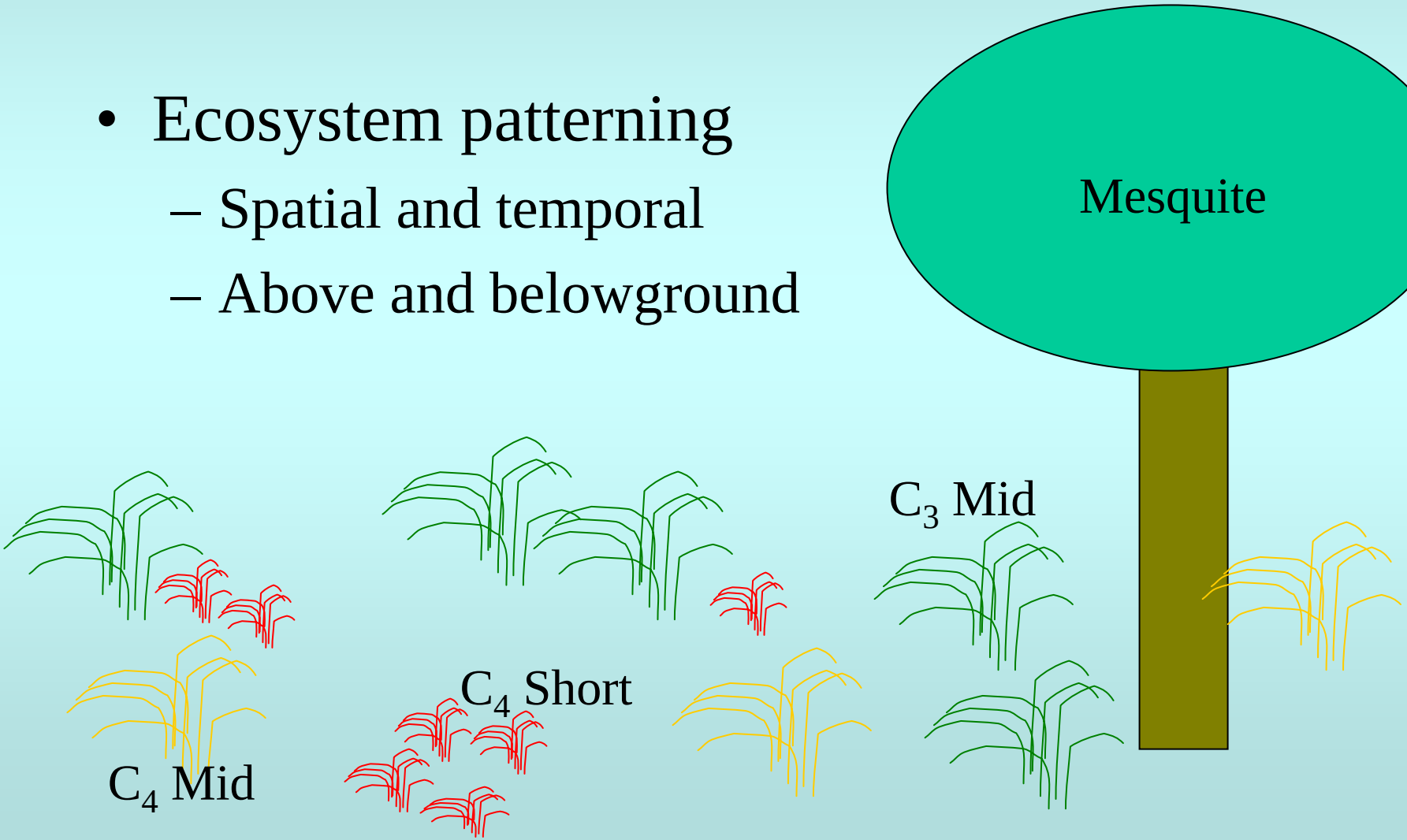


Why does the C_4 shortgrass community stand apart from the rest?

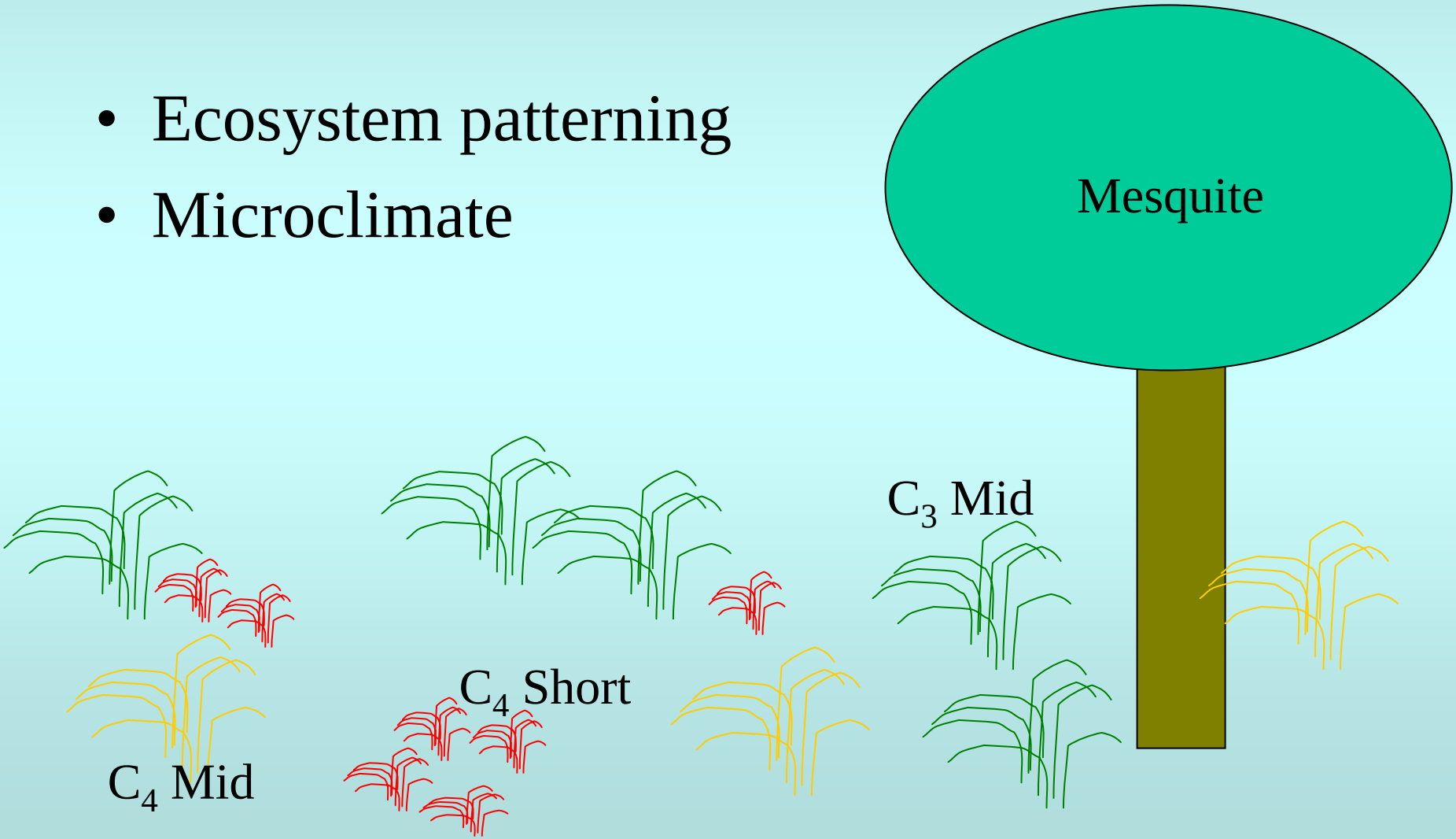
Potential underlying causes

- Ecosystem patterning
  - Spatial and temporal
  - Above and belowground



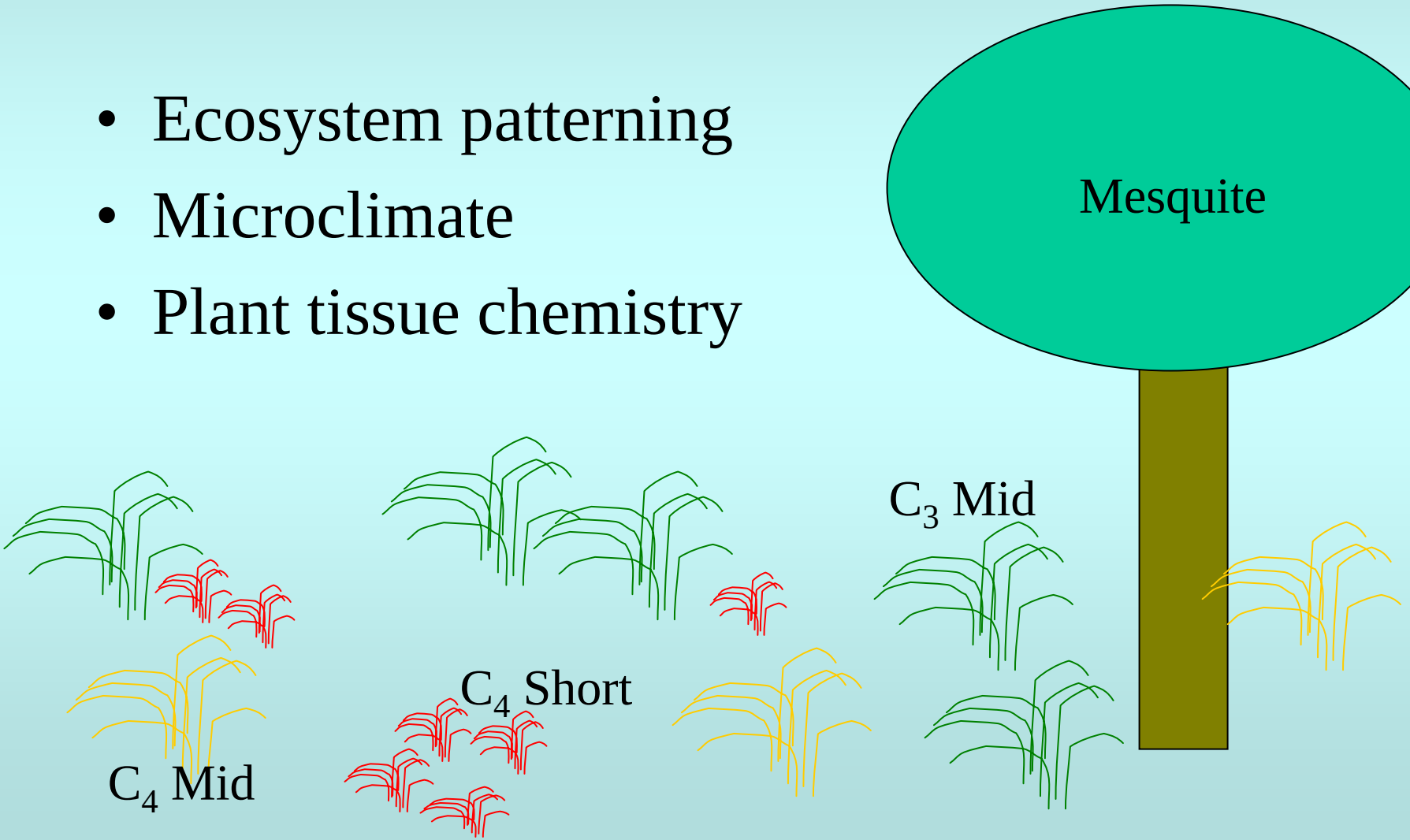
Potential underlying causes

- 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