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Ecosystem Science and Management

UWYO SOIL MICROBIAL ECOLOGY LAB

# Assessing soil microbial community functional response to non-native *Bromus inermis* presence and restoration efforts in the Sagebrush Steppe of Grand Teton National Park

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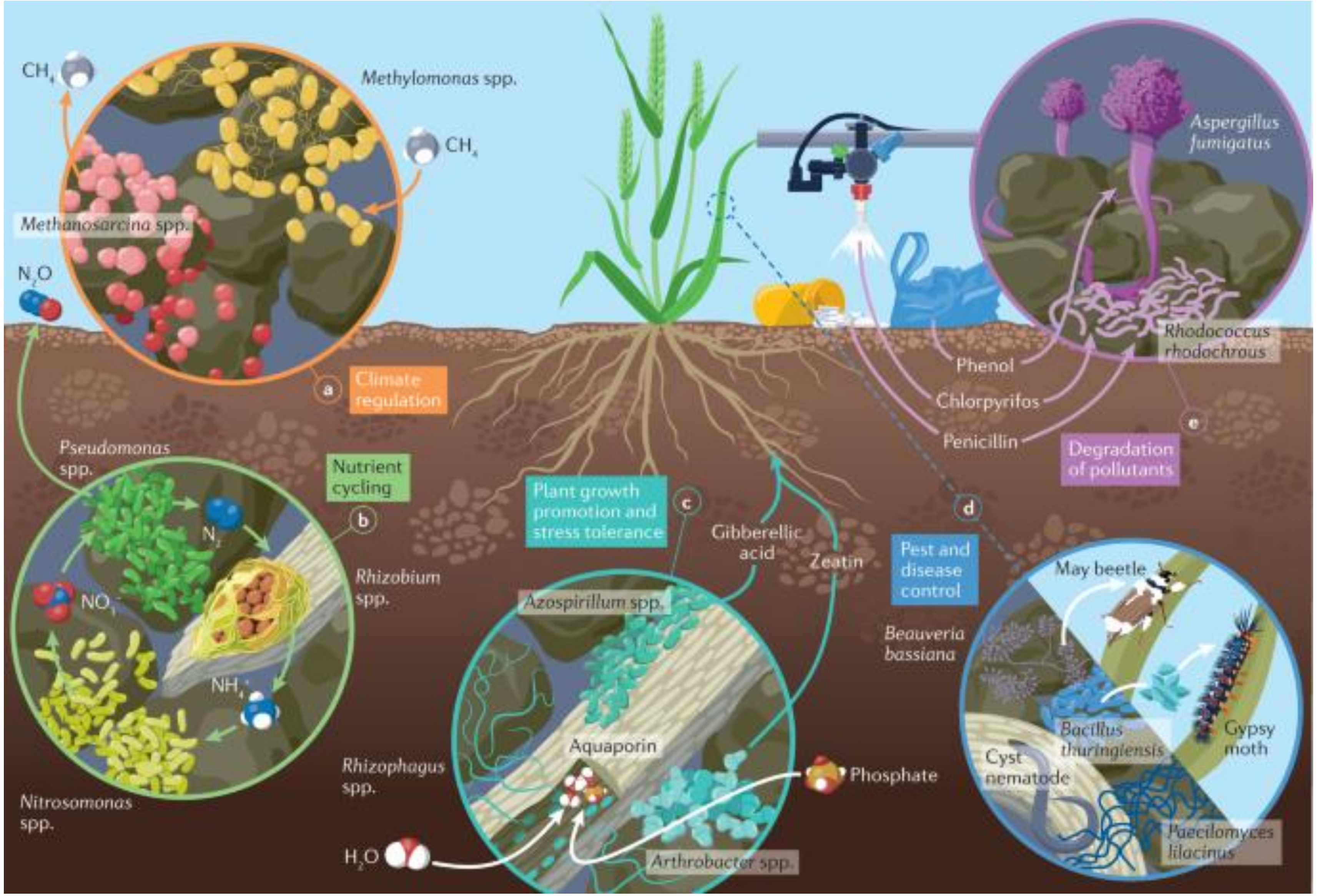
# Why do we care about soil microbes?

(Hartmann and Six, 2022)

- Establish the conditions for plant growth
  - Nutrient cycling & availability
  - Soil Structure
- Associations with plants
  - Plant growth promotion (i.e., mycorrhizae)
- Succession



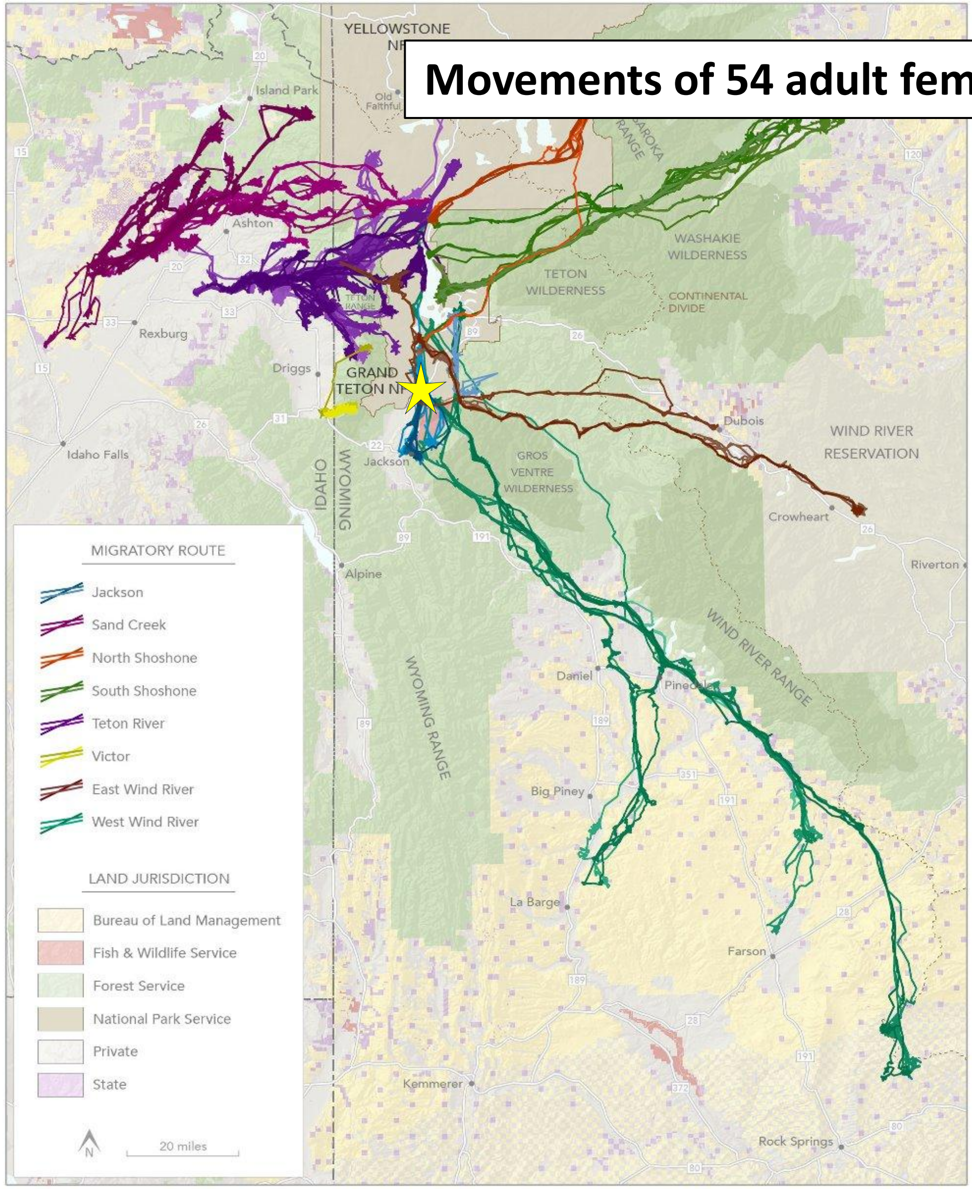

# Sagebrush steppe ecosystem services: fauna

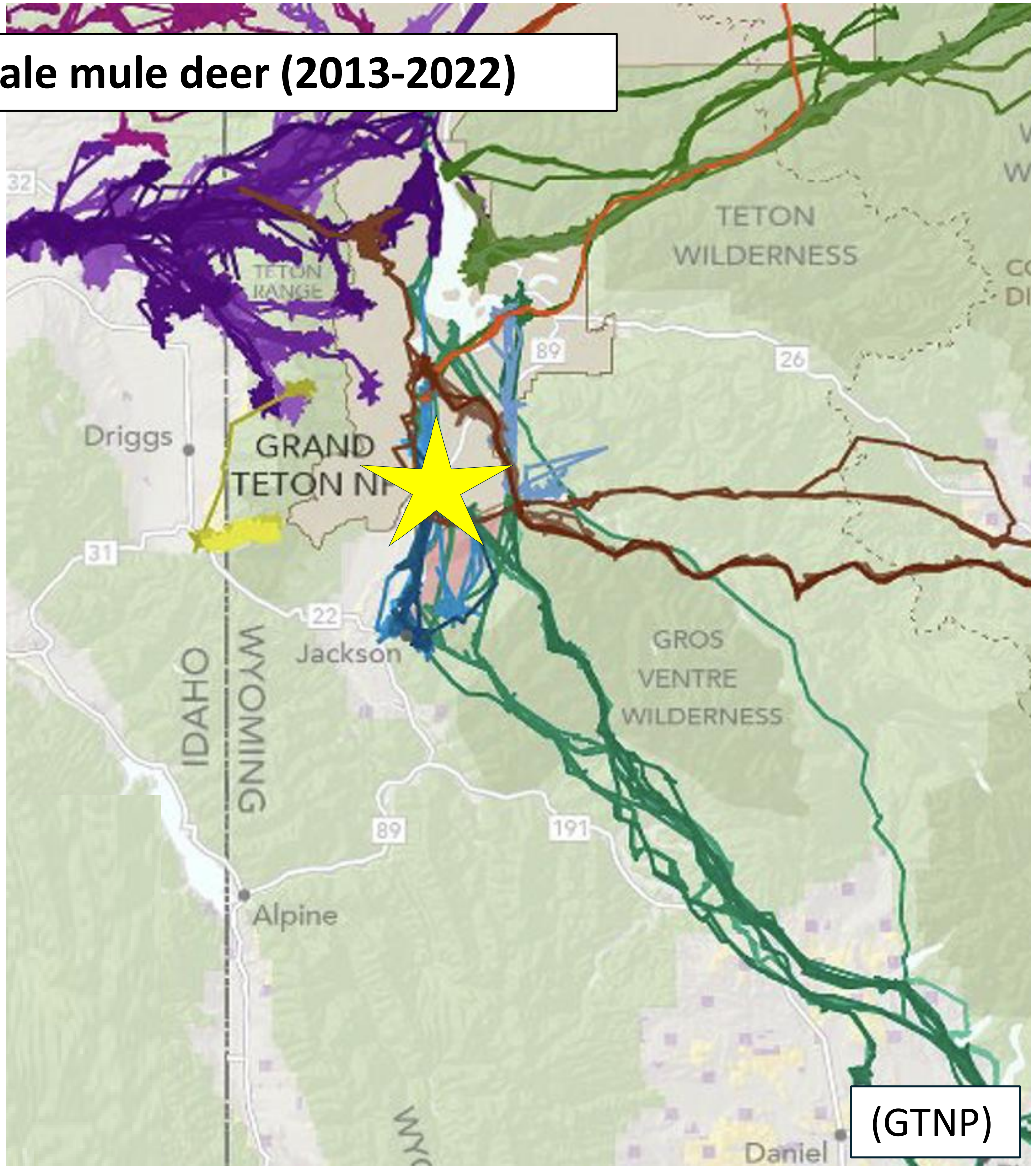




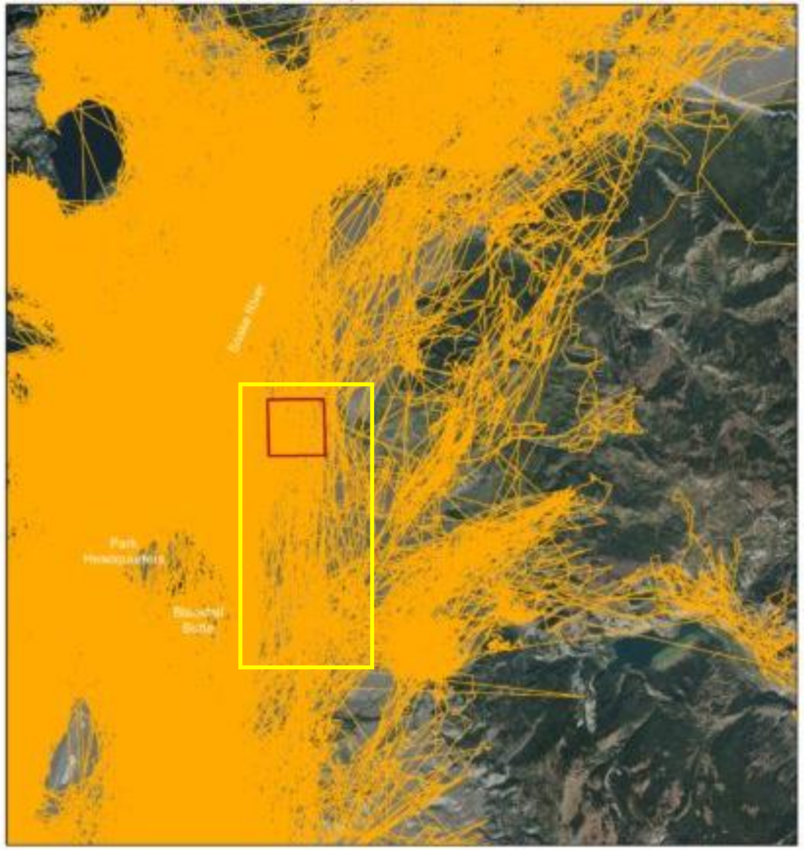
# GTNP → critical bottleneck for ungulate migration

**Movements of 54 adult female mule deer (2013-2022)**

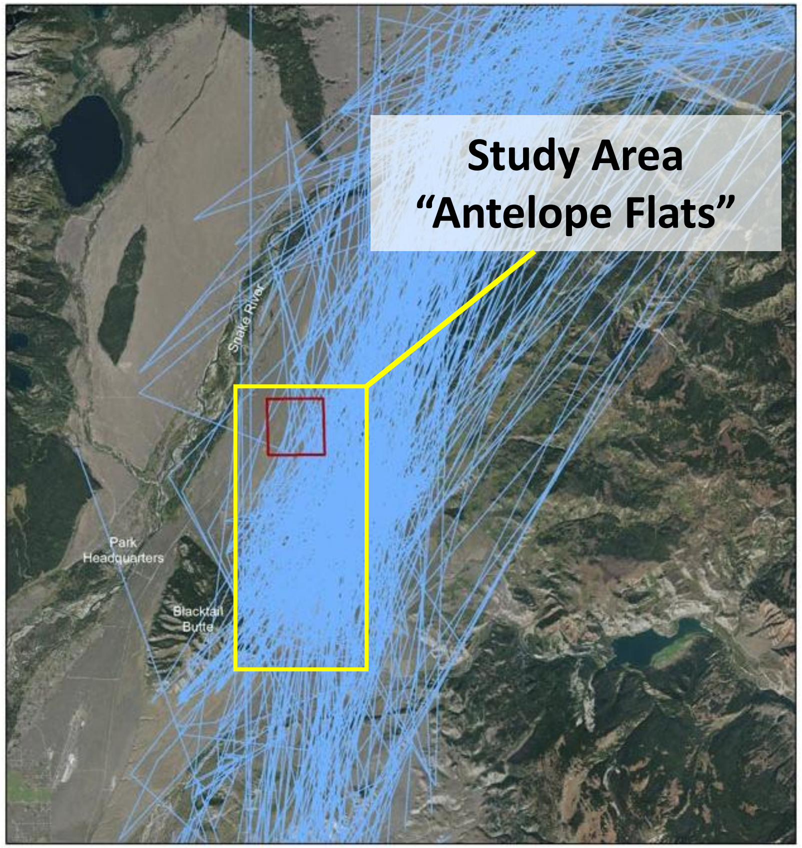


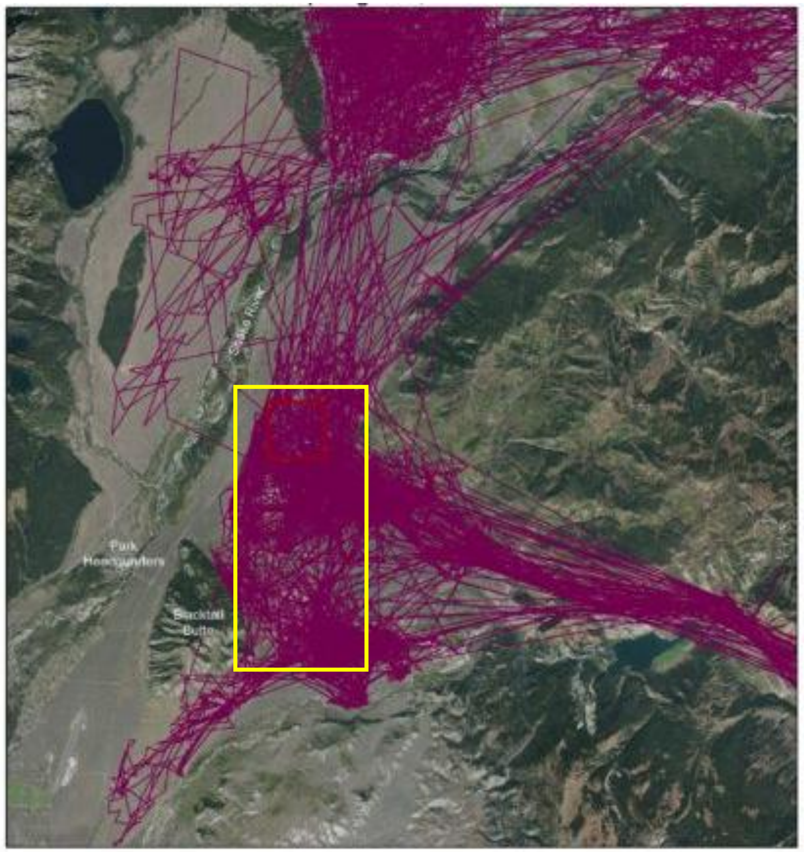
# GTNP → critical bottleneck for ungulate migration



Movements of 111 individual elk (2006-2015)




Movements of 35 individual bison (1997-2007)



Movements of 21 individual pronghorn (1997-2007)

(GTNPF)

# Haying in Antelope Flats

**Settler activities**

- Clear cut ~4,500ac native shrubland
- Plant *Bromus inermis* as forage for cattle
- Dig extensive ditch systems

*B. inermis* and *thlaspi arvensii*

(NPS)

# Smooth brome invasiveness

- Highly competitive → alters soil chemistry[1]
- Changes in soil properties select for **taxonomically and functionally distinct microbial community**[2]
- Smooth brome is rarely studied in shrublands

causes

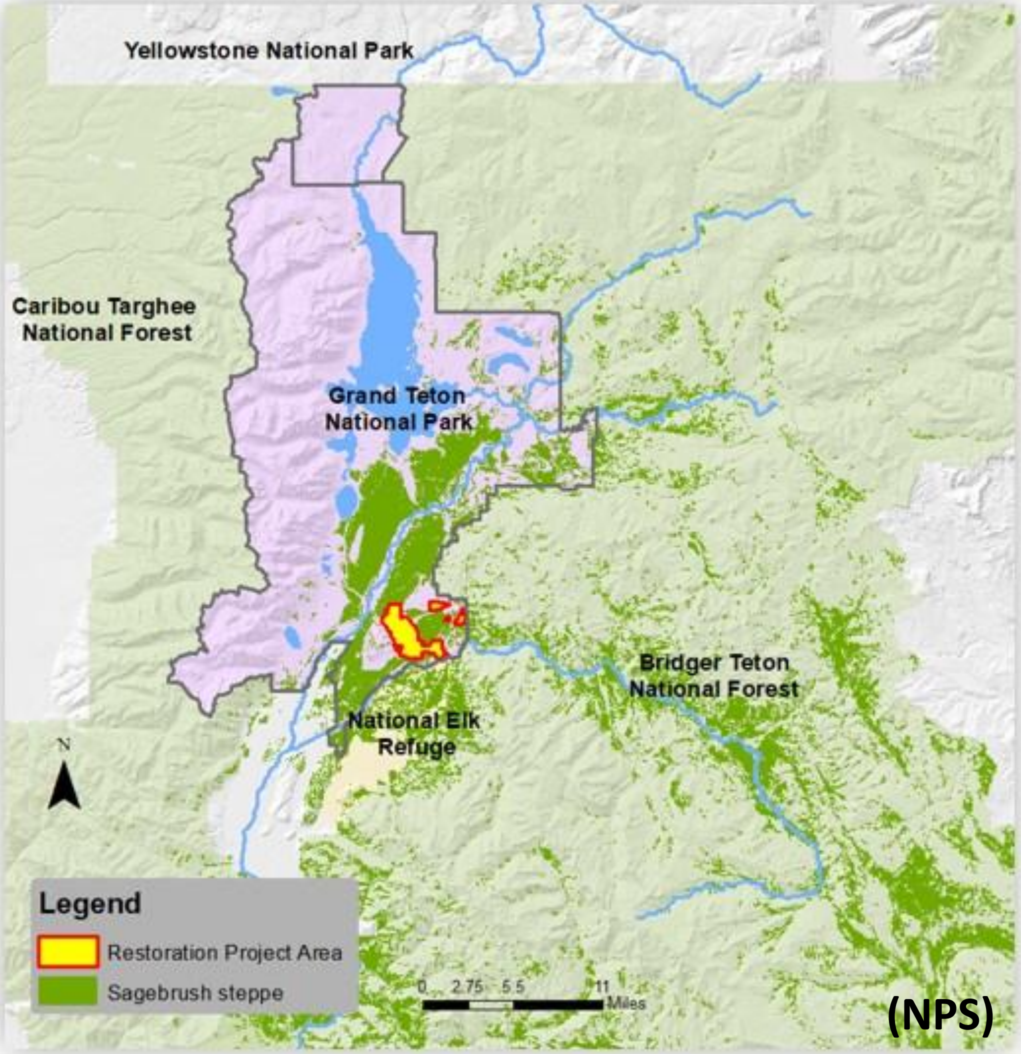
**↑N, ↑C, ↑OM, ↑WHC, ↓pH**

drives

**microbial community shift**

supports


# GTNP restoration initiative





- Began in 2009
- Smooth brome removal – fire + herbicide
- Reseed with collected park seed

# GTNP restoration protocol*

**Year 1:**

Early spring: **controlled burn** of smooth brome hayfield

Mid-late summer: **glyphosate** application

**Year 2:**

Mid-late summer: **glyphosate** application

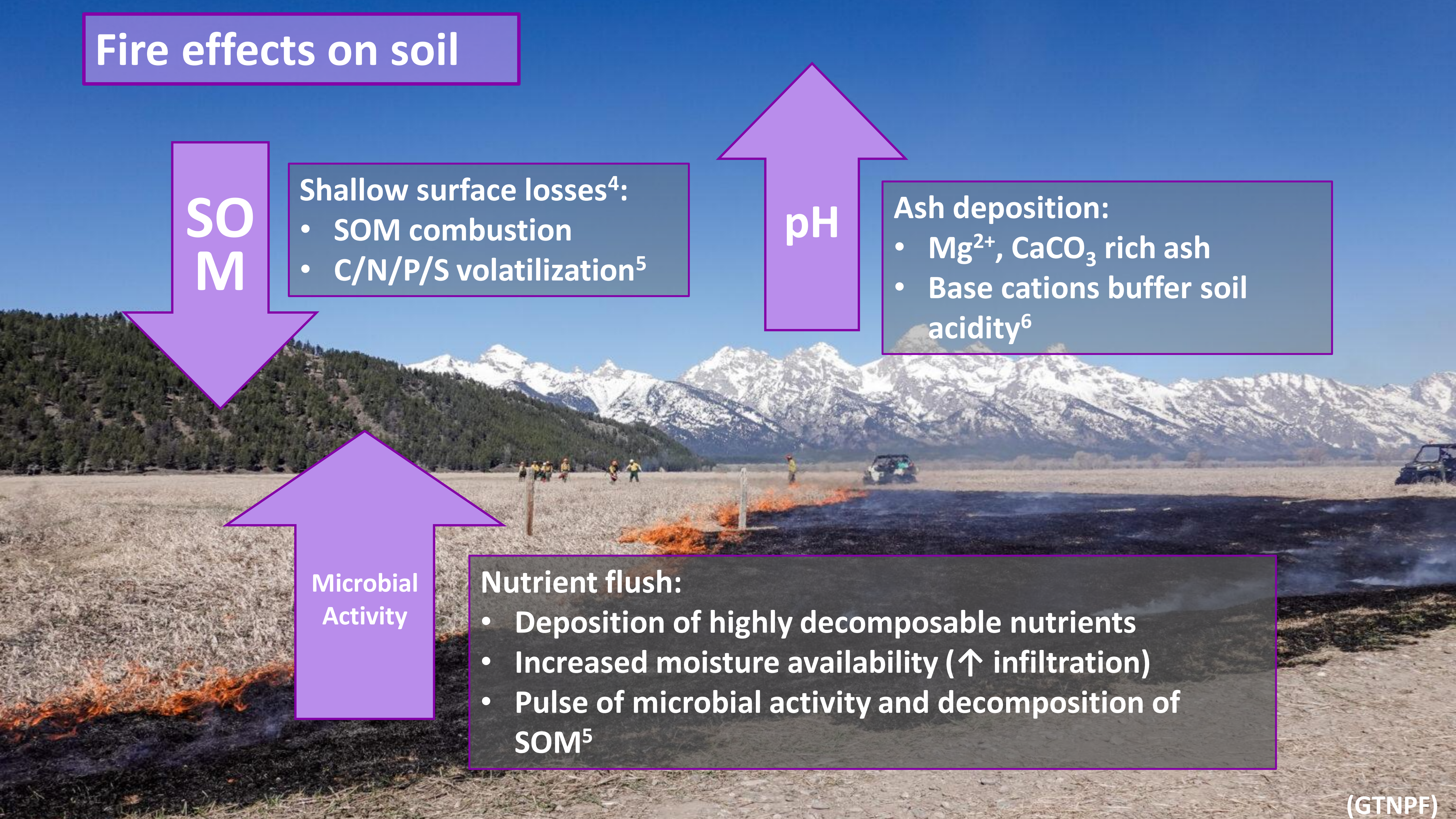
Fall: **seed** with native seed mix

**Combination treatment most effective for smooth brome removal[3] (Moeney, 2008).*

(NPS)


# How are soils impacted by these practices?

# Fire effects on soil



**SOM** ↓

Shallow surface losses[4]:
- SOM combustion
- C/N/P/S volatilization[5]

**pH** ↑

Ash deposition:
- $Mg^{2+}$, $CaCO_3$ rich ash
- Base cations buffer soil acidity[6]

**Microbial Activity** ↑

Nutrient flush:
- Deposition of highly decomposable nutrients
- Increased moisture availability (↑ infiltration)
- Pulse of microbial activity and decomposition of SOM[5]

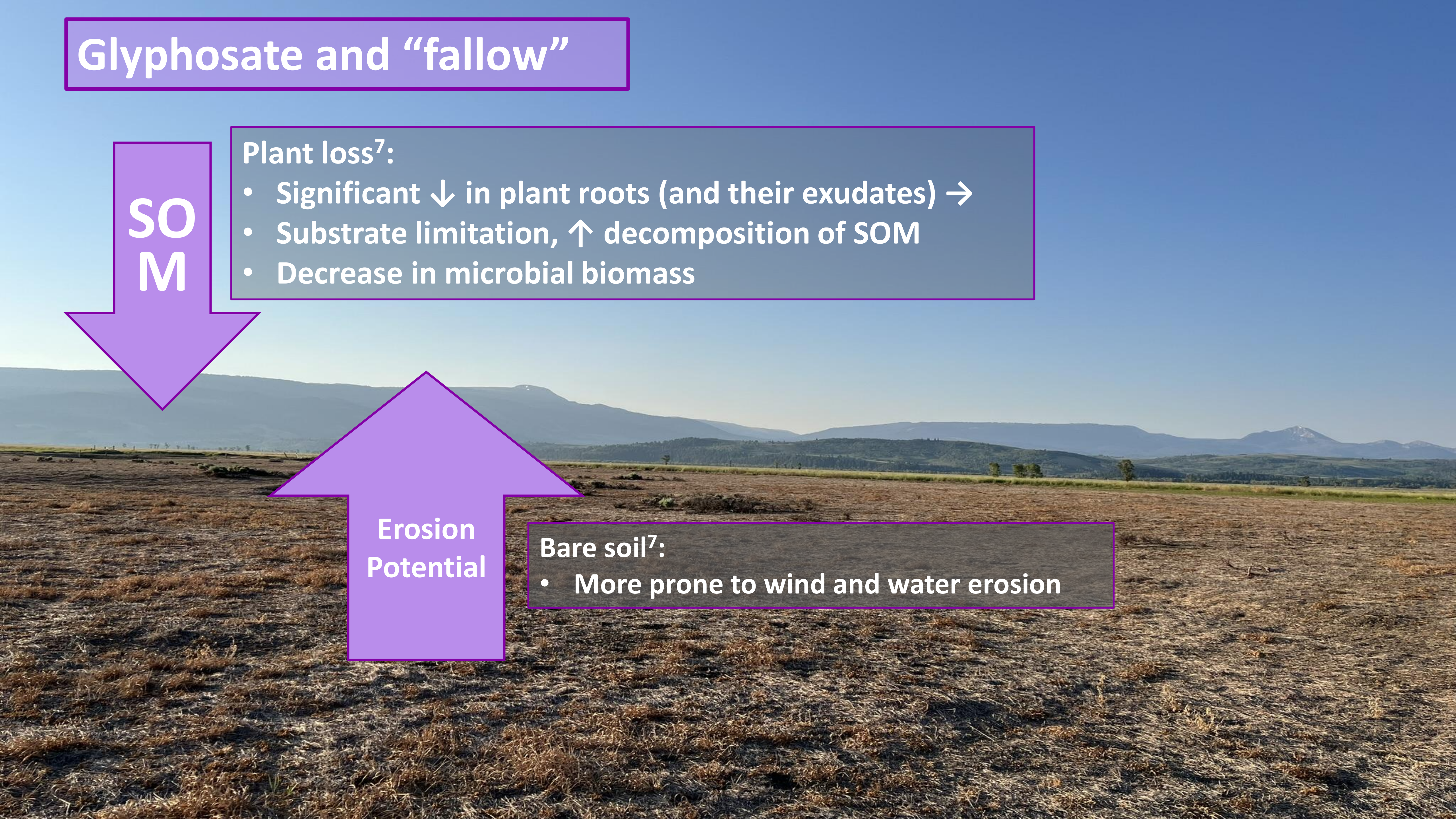
(GTNPF)

# Glyphosate and “fallow”

# Glyphosate and “fallow”

**Plant loss[7]:**

- Significant ↓ in plant roots (and their exudates) →
- Substrate limitation, ↑ decomposition of SOM
- Decrease in microbial biomass




**Bare soil[7]:**

- More prone to wind and water erosion

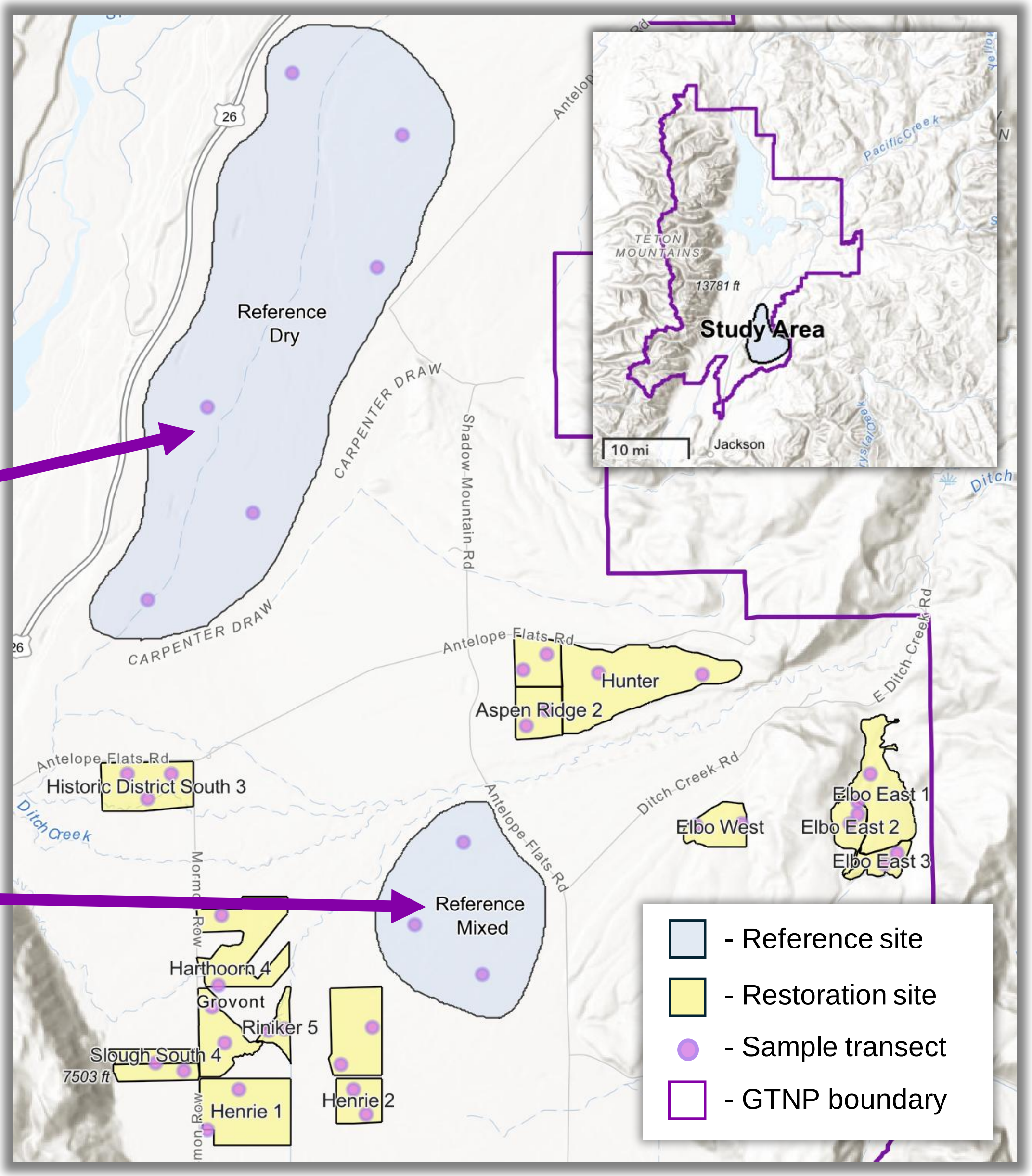
## Questions:

1) How does restoration impact soil chemical properties in Antelope Flats?
2) How are soil microbial communities responding to restoration in Antelope Flats?

# Study Area

- **2 reference sites**
  - Dry – sagebrush dominated shrubland
  - Mixed – sagebrush/antelope bitterbrush

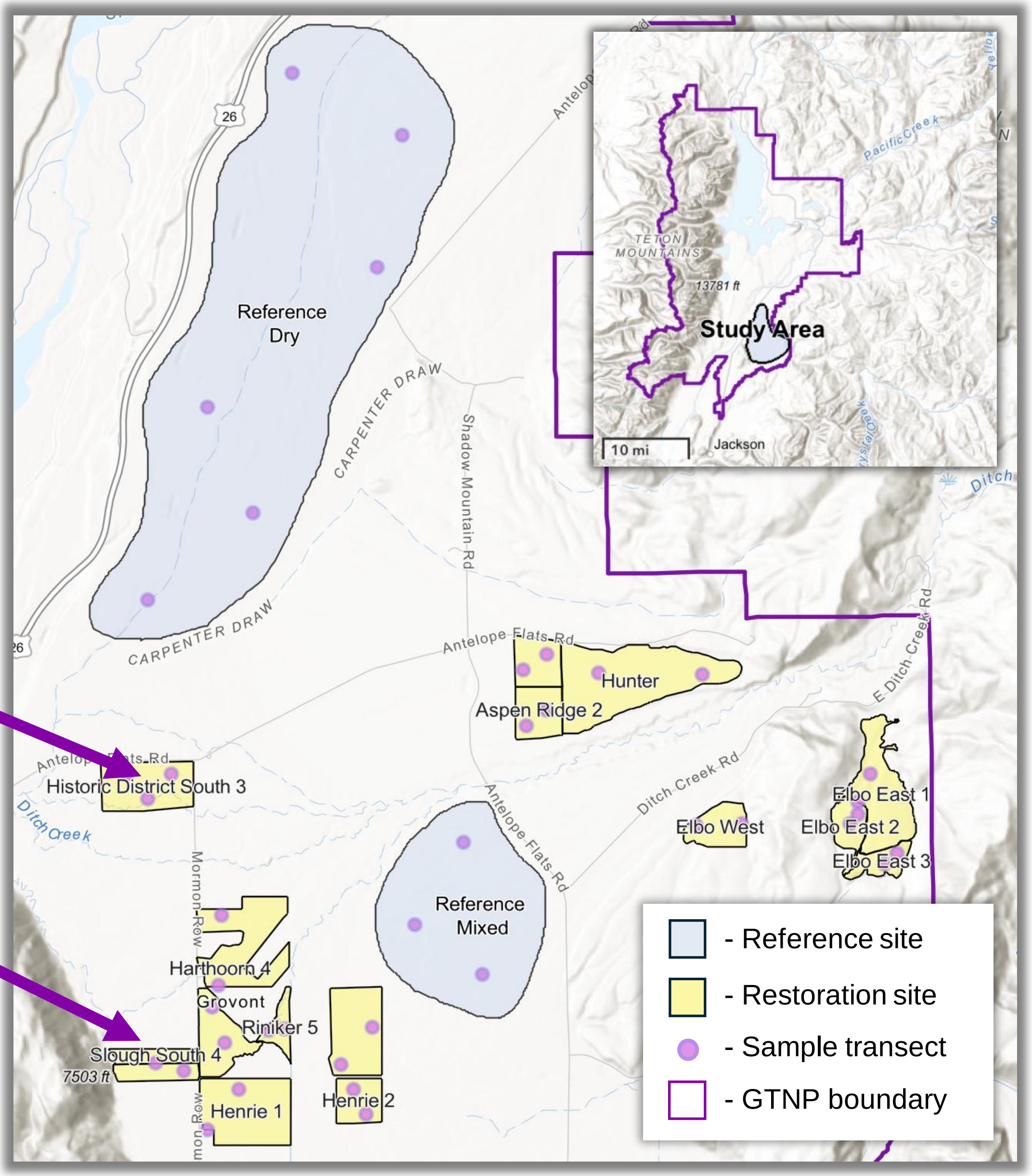




# Study Area

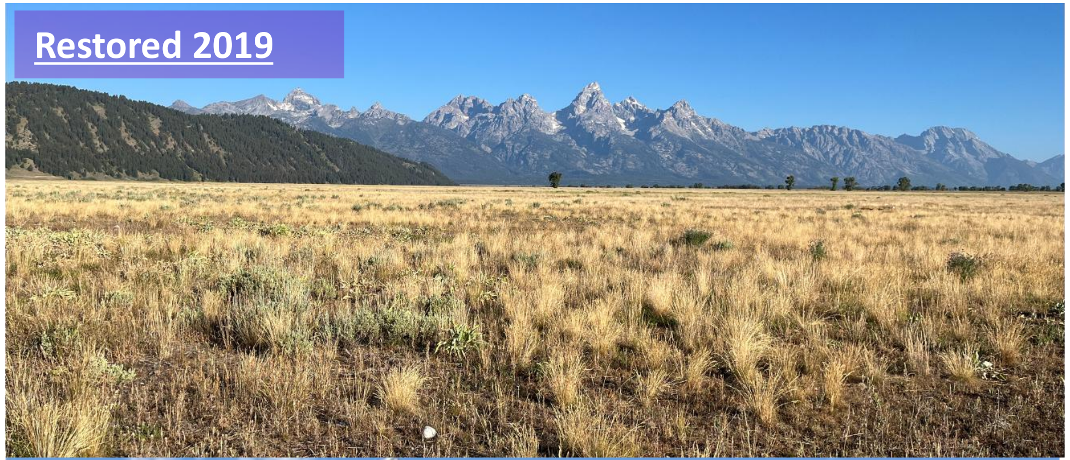
- 1 unrestored site – smooth brome hayfield
- 1 prepped, unseeded site



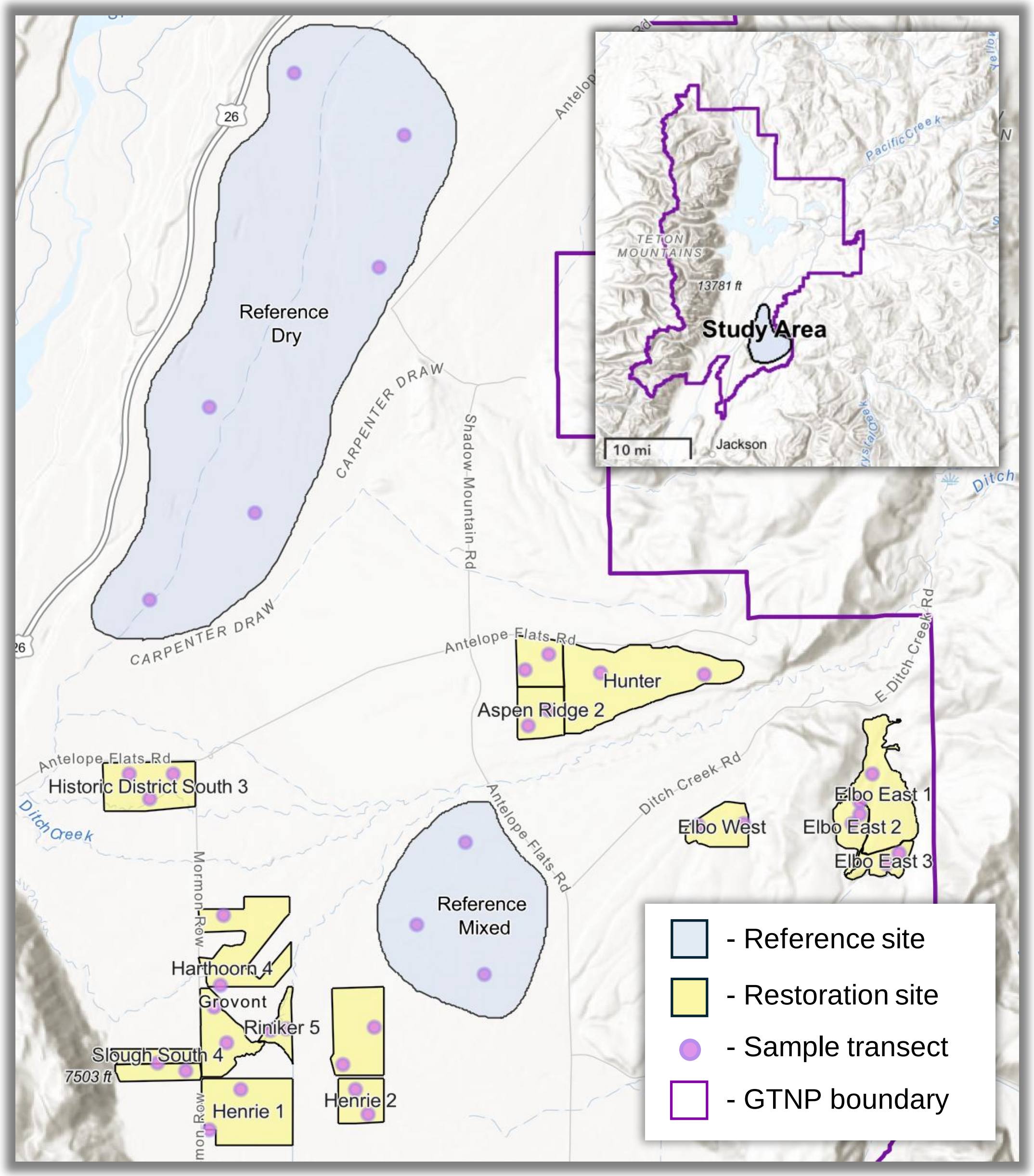


# Study Area

- 17 restoration sites (2009-2024)

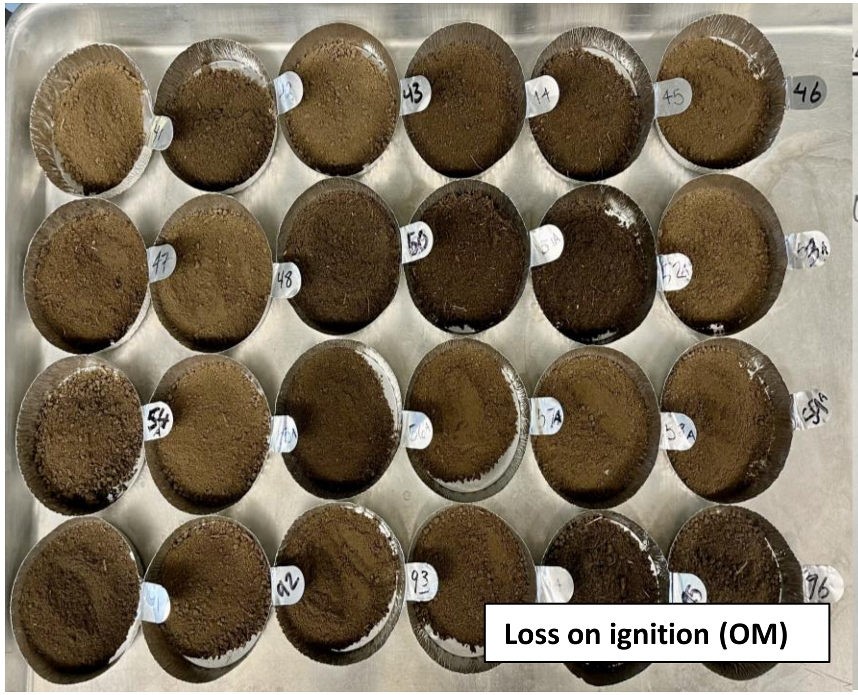






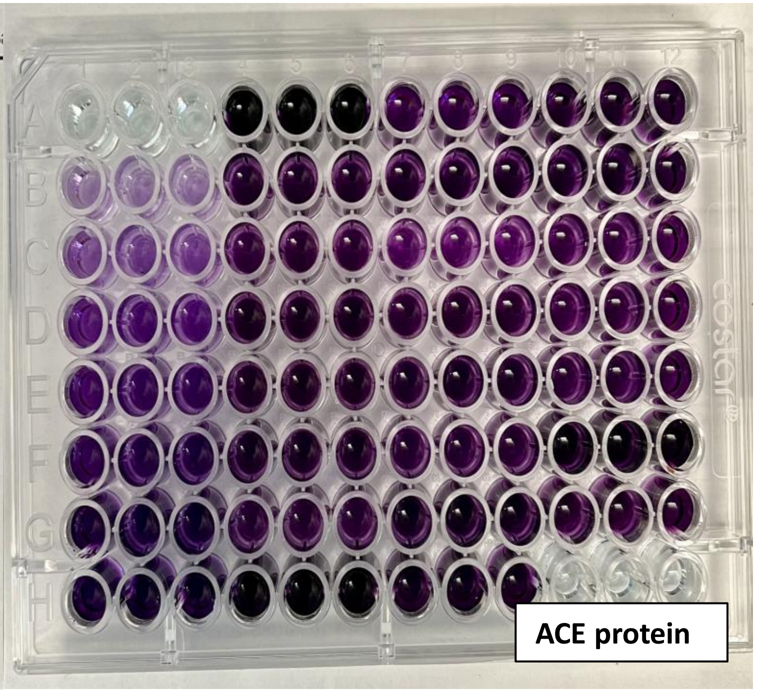
1) Assess changes in soil chemistry between sites

- C cycle –
  - Soil organic matter → "stable" C
  - Permanganate oxidizable carbon (POXC) → active C
- N cycle –
  - Acid citrate extractable (ACE) protein → organic, available N



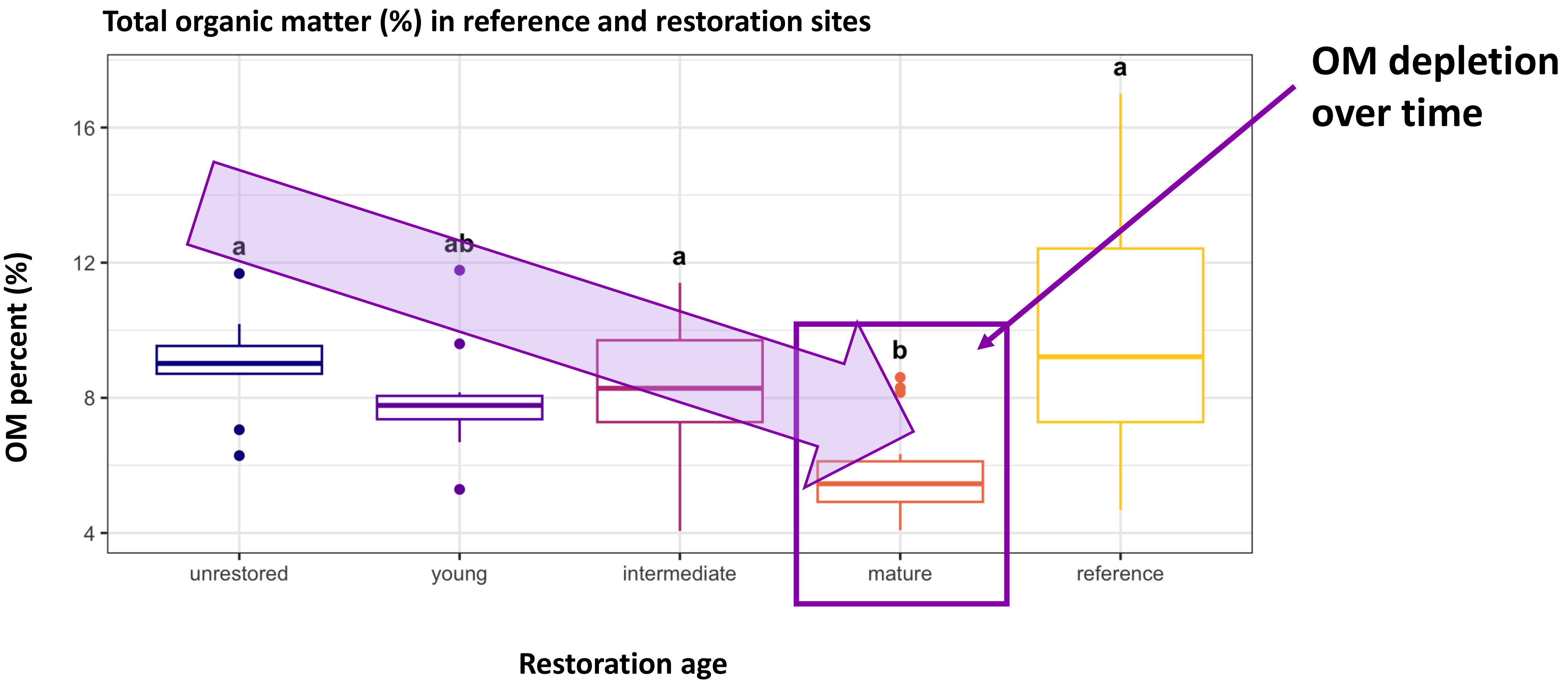
Loss on ignition (OM)


POXC



ACE protein

# 1) Assess changes in soil chemistry between sites: **C-cycling**

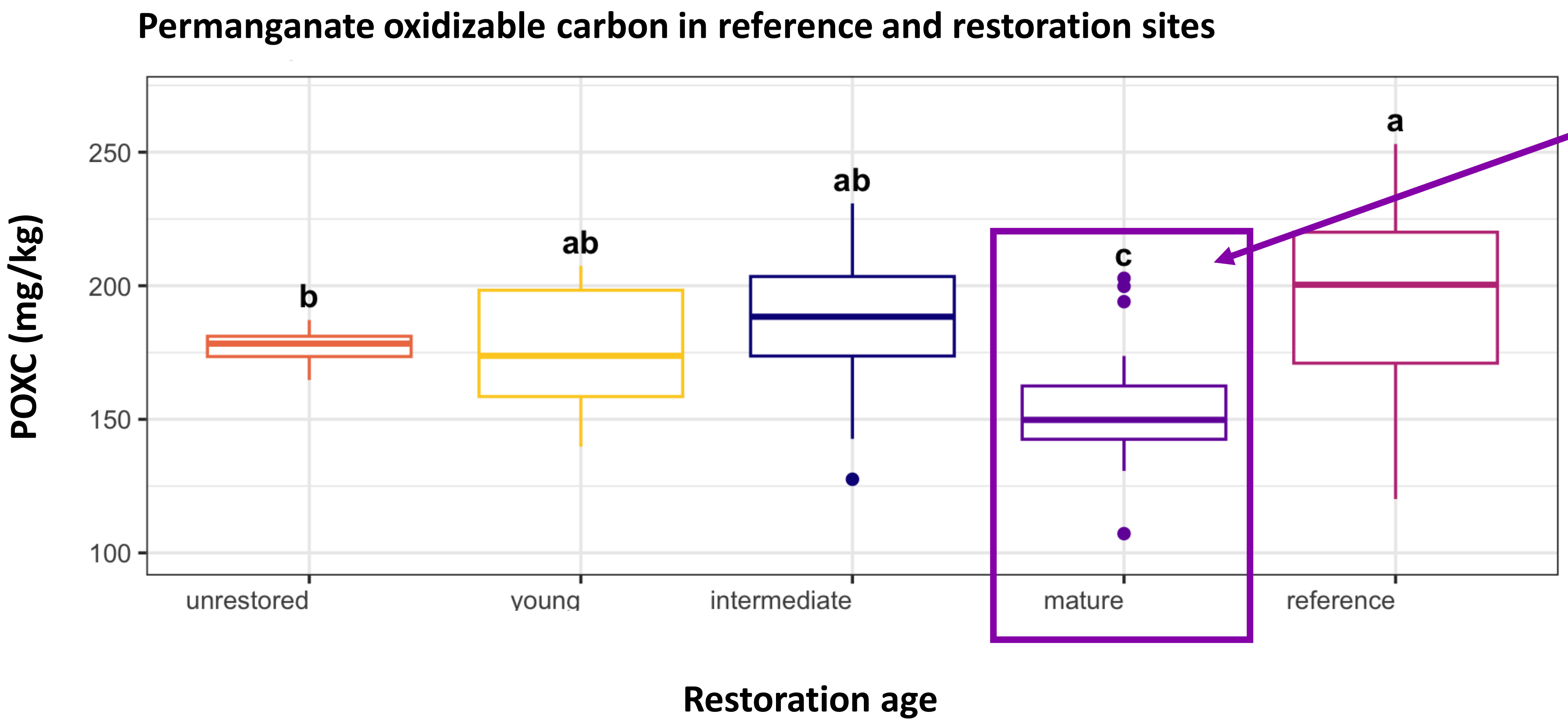


# 1) Assess changes in soil chemistry between sites: **C-cycling**


**OM depletion over time**

**Smooth brome monoculture + shrub reference have ~ SOM**

# 1) Assess changes in soil chemistry between sites: **C-cycling**

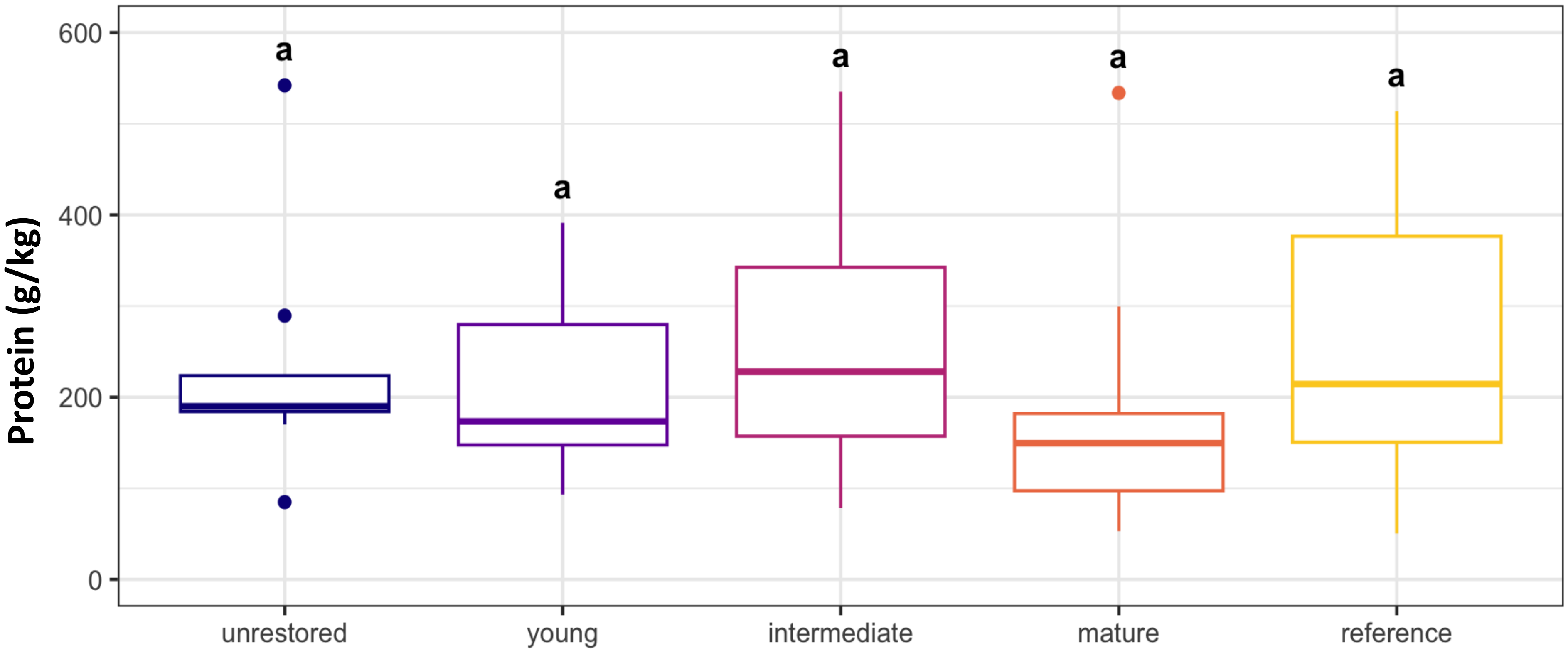



**POXC depletion in mature sites**

**Smooth brome has less active C than ref**

# 1) Assess changes in soil chemistry between sites: **N-cycling**

**Acid citrate extractable protein in reference and restoration sites**




**Restoration age**

**No observed effects**

2) Assess <u>microbial community response</u> to restoration

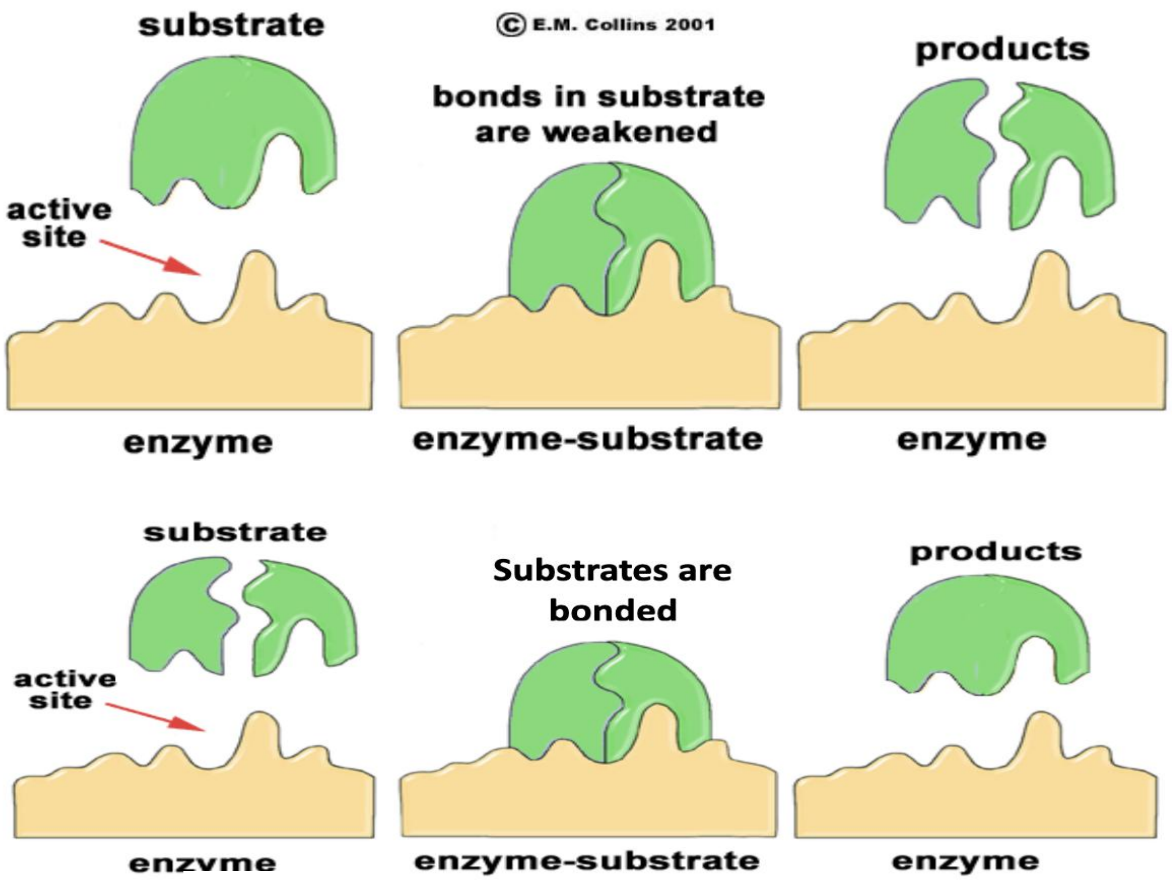
- Function – extracellular enzyme assay (EEA)
- Structure – DNA extraction

**Structure → who's there?**

**Function → what are they doing?**

## 2) Assess microbial community response to restoration

- Function – extracellular enzyme assay (EEA)
- Structure – DNA extraction




F ... "Lock and Key" Enzyme Mechanisms
(Image from E.M. Collins 2001)

- Specific enzymes serve **specific functions**
- Critical for **organic matter degradation/nutrient cycling**
- Transformation of N/P/S to plant available forms
- Soil enzyme activities help us understand how microbes…
  - **function** in the soil
  - **respond** to environmental change

2) Assess microbial community response to restoration

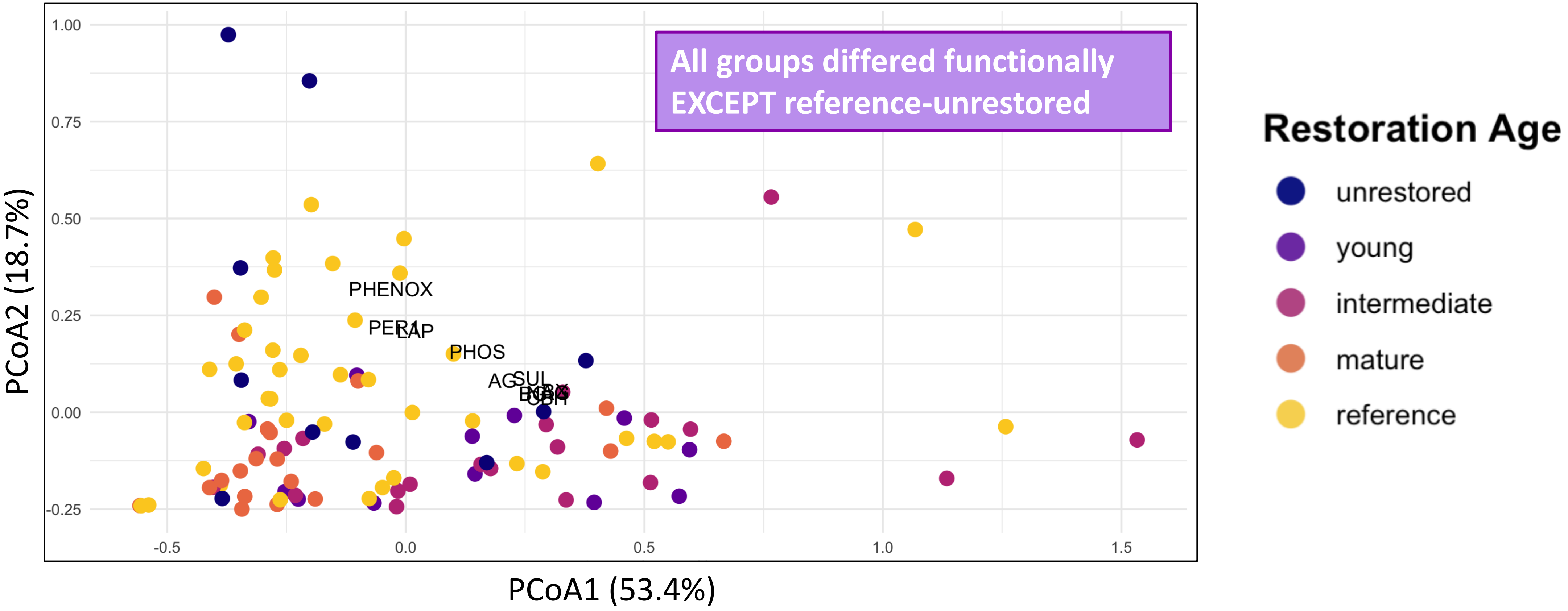
- Function – extracellular enzyme assay (EEA)
- Structure – DNA extraction



| Enzyme | Nutrient cycle | Role |
| --- | --- | --- |
| β-glucosidase (BG) | Carbon | Cellulose (simple) |
| Cellobiohydrolase (CBH) | Carbon | Cellulose (complex) |
| α-glucosidase (AG) | Carbon | Starch |
| N-acetyl-β-glucosaminidase (NAG) | Carbon | Chitin (insect/fungal cell walls) |
| β-xylosidase (BX) | Carbon | Hemicellulose |
| Leucine aminopeptidase (LAP) | Nitrogen | Polypeptides |
| Acid phosphatase (PHOS) | Phosphorus | Phosphate esters |
| Arylsulfatse (SUL) | Sulfur | Ester sulfates |
| Phenol oxidase (PHENOX) | Carbon | Organic matter |
| Peroxidase (PEROX) | Carbon | OM/lignin/humic substances |

# 2) Assess microbial community response: **function → Enzyme assay**

**Principle coordinates analysis of enzyme activities in reference and restoration sites (Euclidian distance)**



2) Assess microbial community response:
**function → Enzyme assay**

**Canonical correlation analysis to determine effects of OM and POXC on enzyme activities (Euclidian distance)**


CCA1 (2.3%)

# Soil C does not explain variation between sites

2) Assess microbial community response:
**function → Enzyme assay**

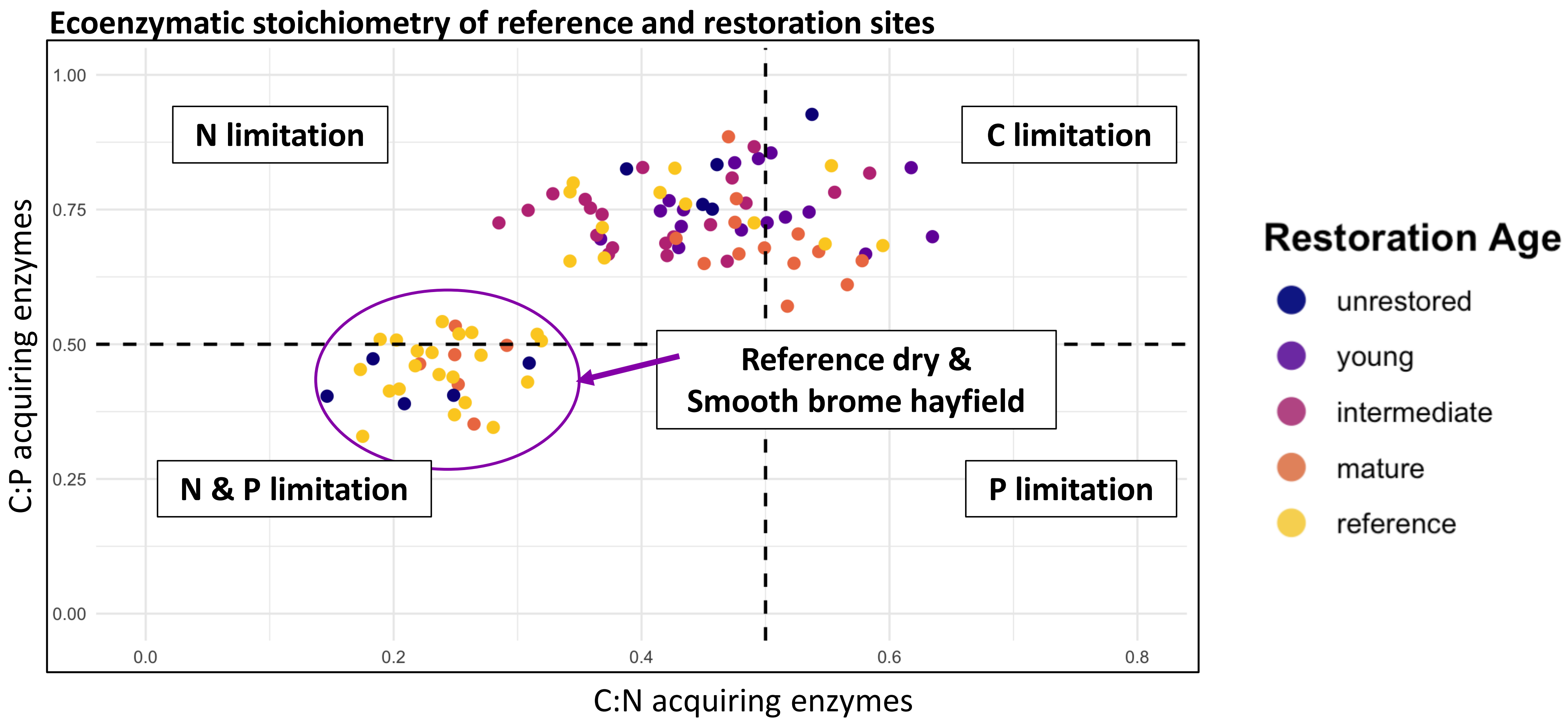
**Ecoenzymatic stoichiometry of reference and restoration sites**

- Comparing the *relative* activities of C related enzymes to N and P related enzymes can help us understand **which nutrients might be limiting microbial metabolism** in the soil;
- Higher activity → greater metabolic requirement (i.e., **limitation**)
- Lower activity → lower metabolic requirement (i.e., **adequate supply**)

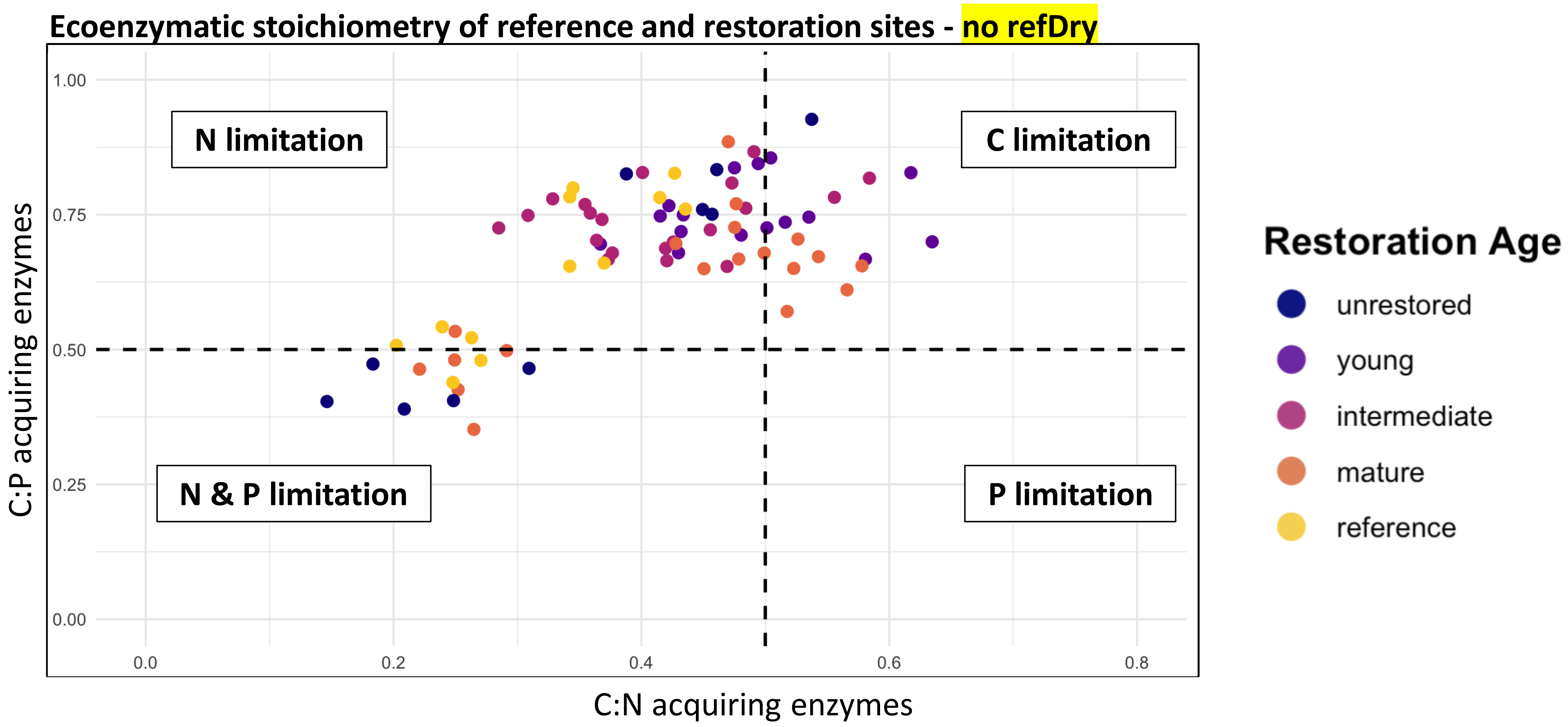
**↑C:N/P ~ ↑ C limitation**

2) Assess microbial community response:

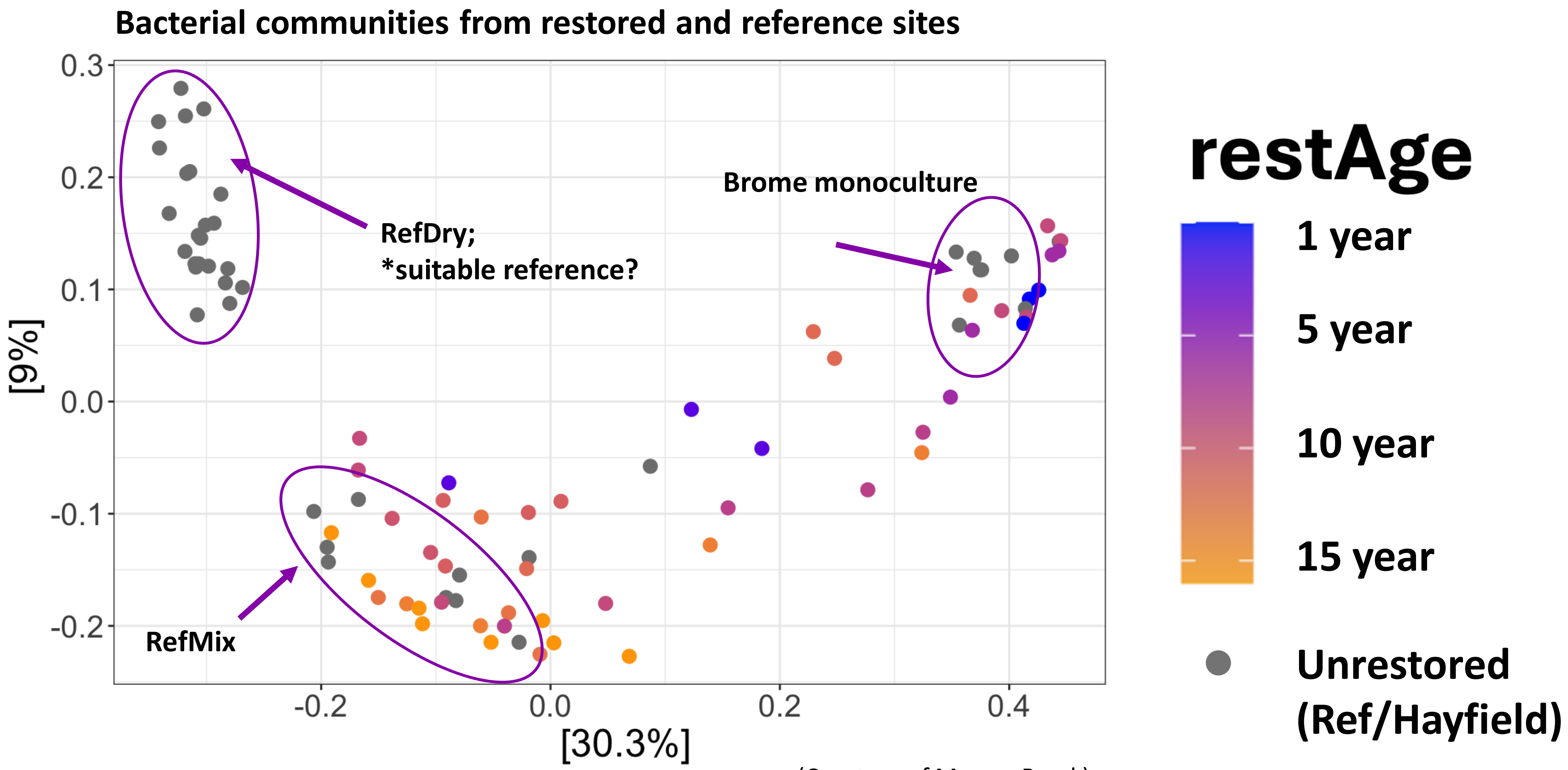
**function → Enzyme assay**



# 2) Assess microbial community response: **function → Enzyme assay**

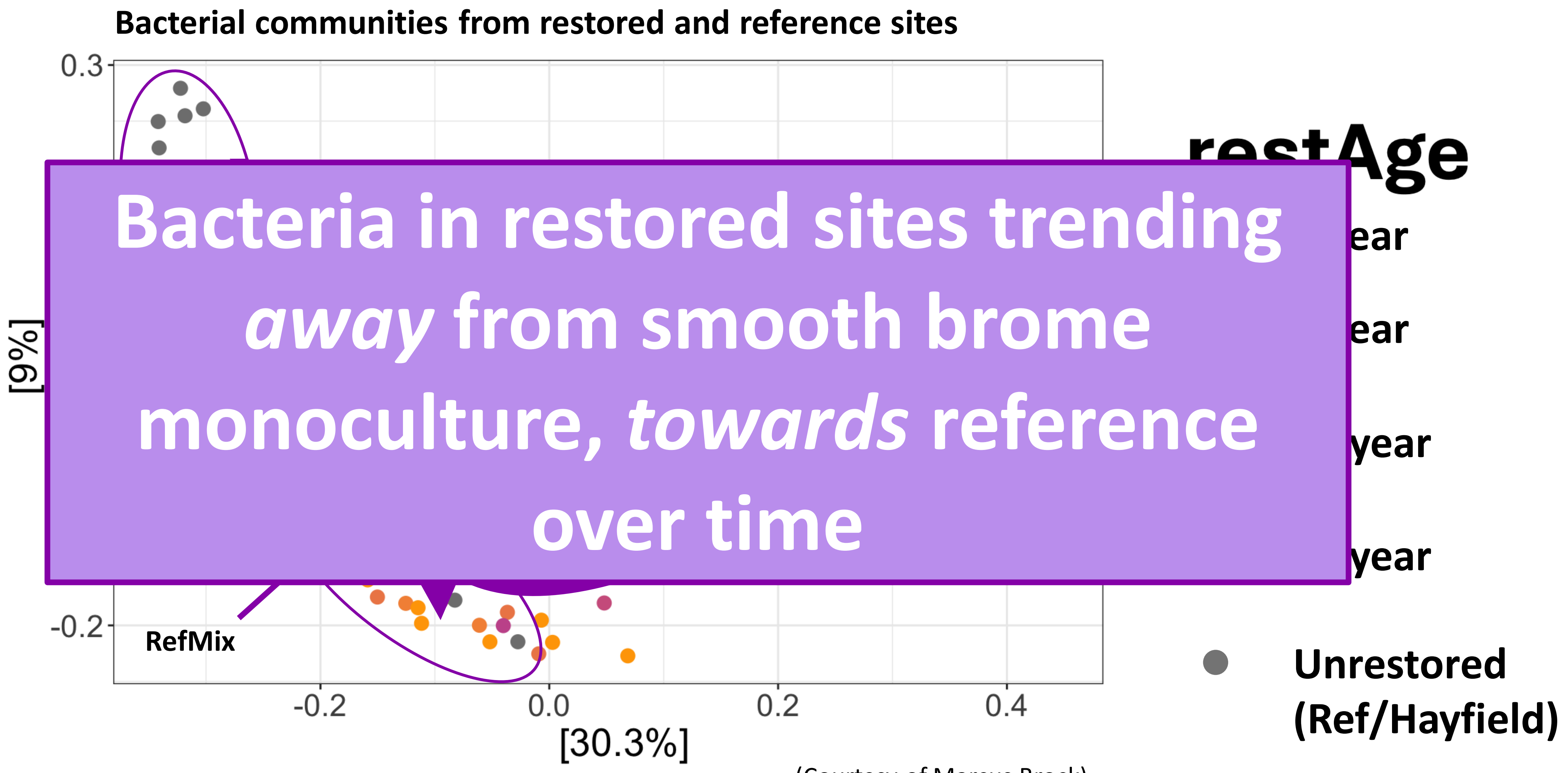


2) Assess microbial community response:
**structure → DNA extraction**




(Courtesy of Marcus Brock)

2) Assess microbial community response:
**structure → DNA extraction**




**Bacteria in restored sites trending *away* from smooth brome monoculture, *towards* reference over time**

(Courtesy of Marcus Brock)

# Conclusions

1) Differences in plant community don’t seem to be driving differences in soil chemistry

- Reference and smooth brome hayfields were equivalent in all soil chemistry metrics
- Soil C gradually declined over 15 years
- Likely due to **smooth brome removal protocol** and initial **productivity lag** when site is in active restoration

# Conclusions

2) Form does not follow function

- The oldest restored sites have similar bacterial communities to the reference, but are still functionally distinct → function will likely recover as soil chemistry (especially C) recovers
- Smooth brome hayfields have a drastically different bacterial community, but equivalent function to reference sites

# Conclusions

3) Soil recovery takes time

- Soil C is lagging behind plant community recovery → **long lived species and dry conditions** hinder biomass production and **slow OM accumulation**
- Decline in productivity and effects on soil are **unavoidable consequences** of effective smooth brome removal in this system

# Conclusions

4) Soil microbiota *may* provide a valid means of assessing the validity of a reference site

- Dry reference site is clearly distinct in ecoenzymatic stoichiometry and bacterial community composition relative to reference, restored, and unrestored sites
- Indicative of **unrealistic restoration target?**

# Next steps

- Differentiate into organic matter fractions
  - Particulate organic matter (POM)
  - Mineral associated organic matter (MAOM)

- Soil fungal communities

★ **Continued collaboration with GTNP**

# Acknowledgements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University of Wyoming
College of Agriculture, Life Sciences and Natural Resources
Ecosystem Science and Management

National Park Service

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Grand Teton National Park Foundation

# In loving memory of Dr. Linda van Diepen

## References

[1]Palit, R., & DeKeyser, E. S. (2022). Impacts and drivers of smooth brome (Bromus inermis Leyss.) invasion in native ecosystems. *Plants*, *11*(10), 1340.

[2]Piper, C. L., Siciliano, S. D., Winsley, T., & Lamb, E. G. (2015). Smooth brome invasion increases rare soil bacterial species prevalence, bacterial species richness and evenness. *Journal of Ecology*, *103*(2), 386-396

[3]Moeney, J. C. (2008). Control of smooth brome and restoration of native plant communities in the Kelly Hayfields of Grand Teton National Park (Doctoral dissertation, New Mexico State University).

[4]Binkley, D., Richter, D., David, M.B. and Caldwell, B. (1992), Soil Chemistry in a Loblolly/Longleaf Pine Forest with Interval Burning. Ecological Applications, 2: 157-164.

[5]DiCosty, R. J., & Callaham, M. A.. 2008. Fire effects on soils – overview. Encyclopedia collection — forest encyclopedia network.

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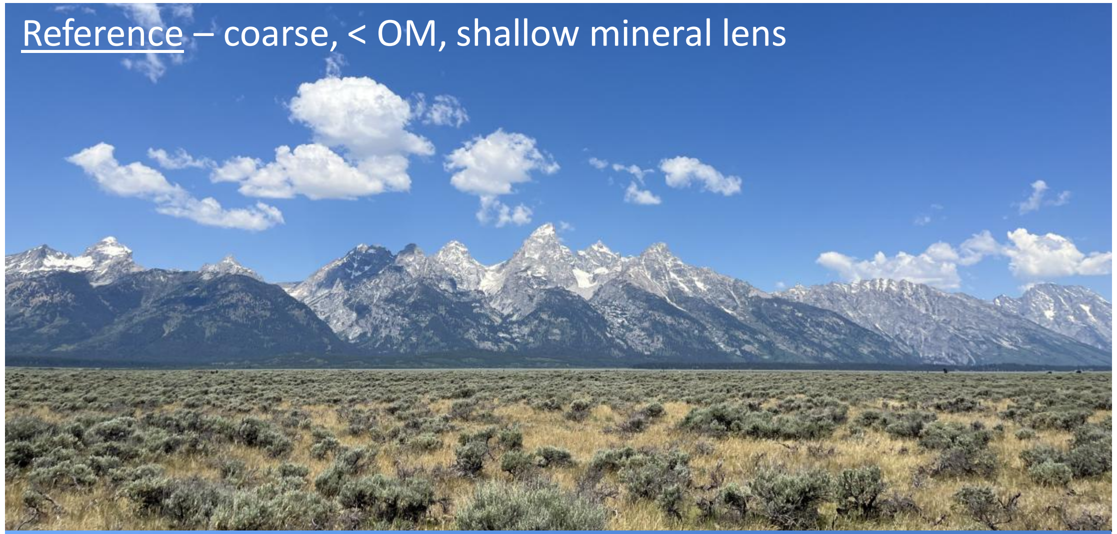
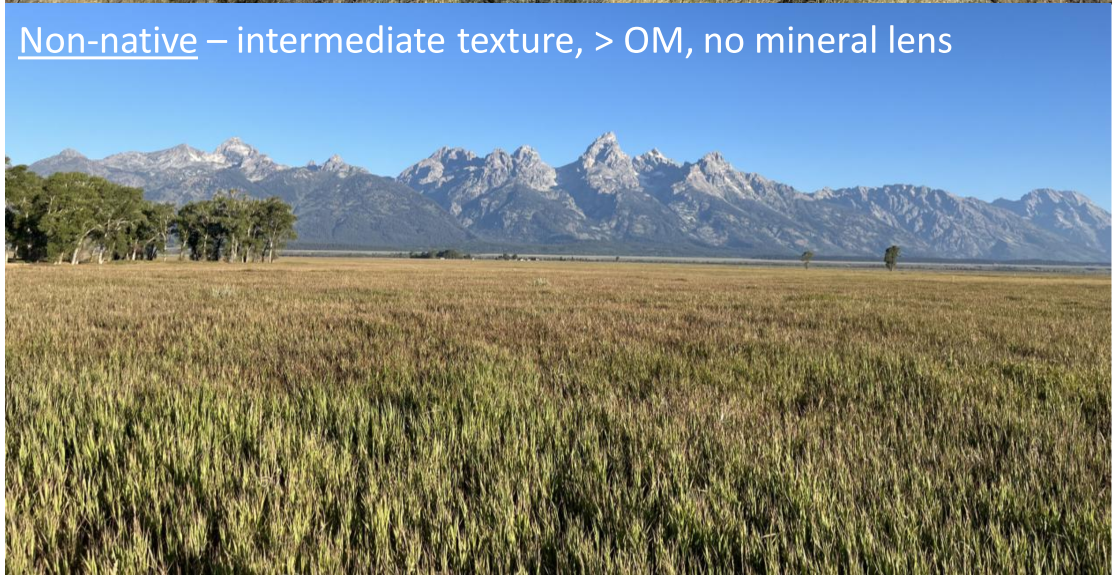
[7]Nielsen, D. C., & Calderón, F. J. (2011). Fallow effects on soil. Soil management: Building a stable base for agriculture, 287-300.


Questions?


Supplemental

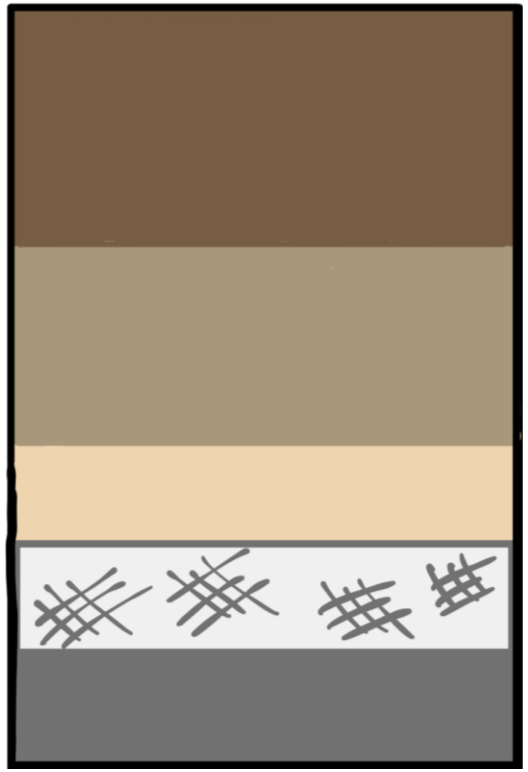
# Reference Conundrum




refDry

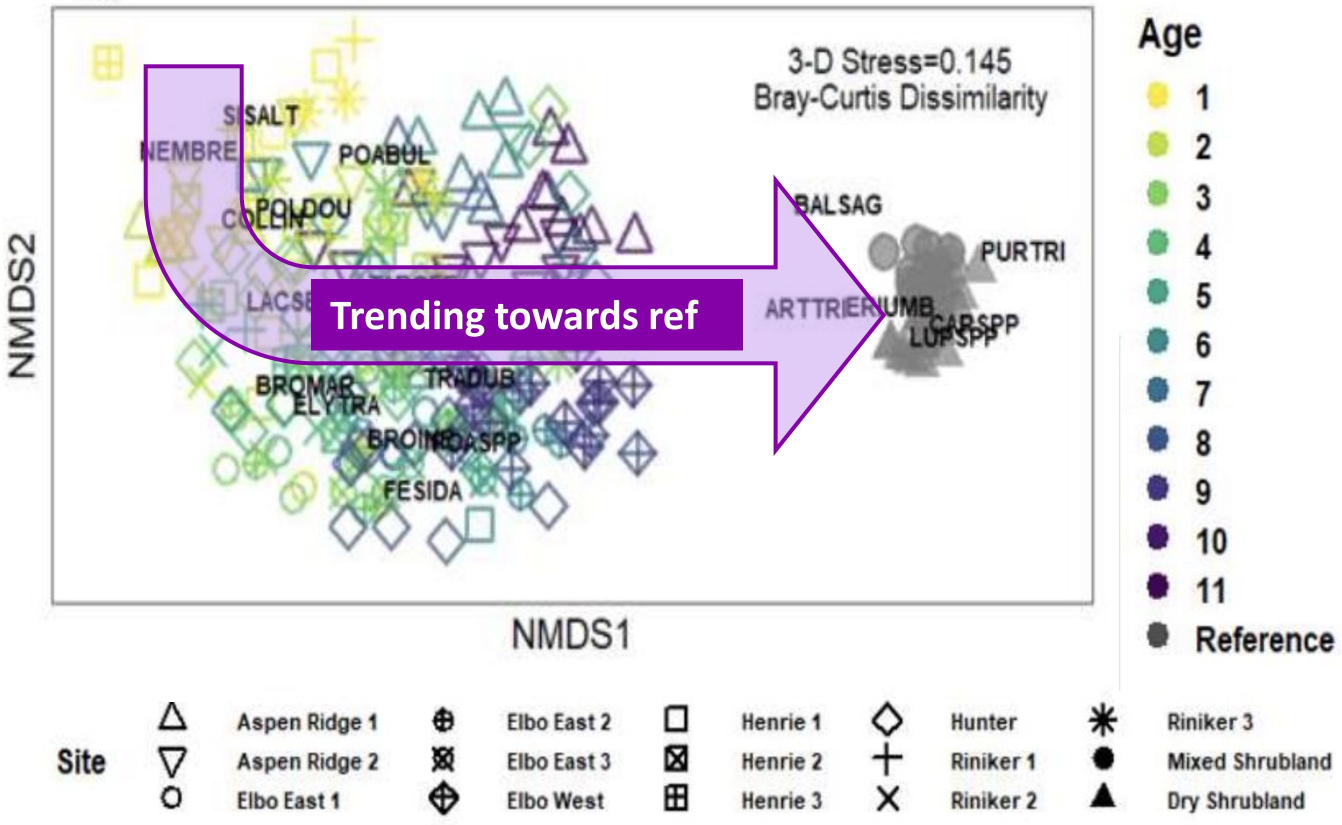

Non-native/restored/
refMix



Hypothesized refDry and NN/restored/refMix soil profiles based on sampling observations.

# Mixed restoration outcomes in GTNP

**Plant community composition from 11yrs monitoring**




(Wessel, 2022)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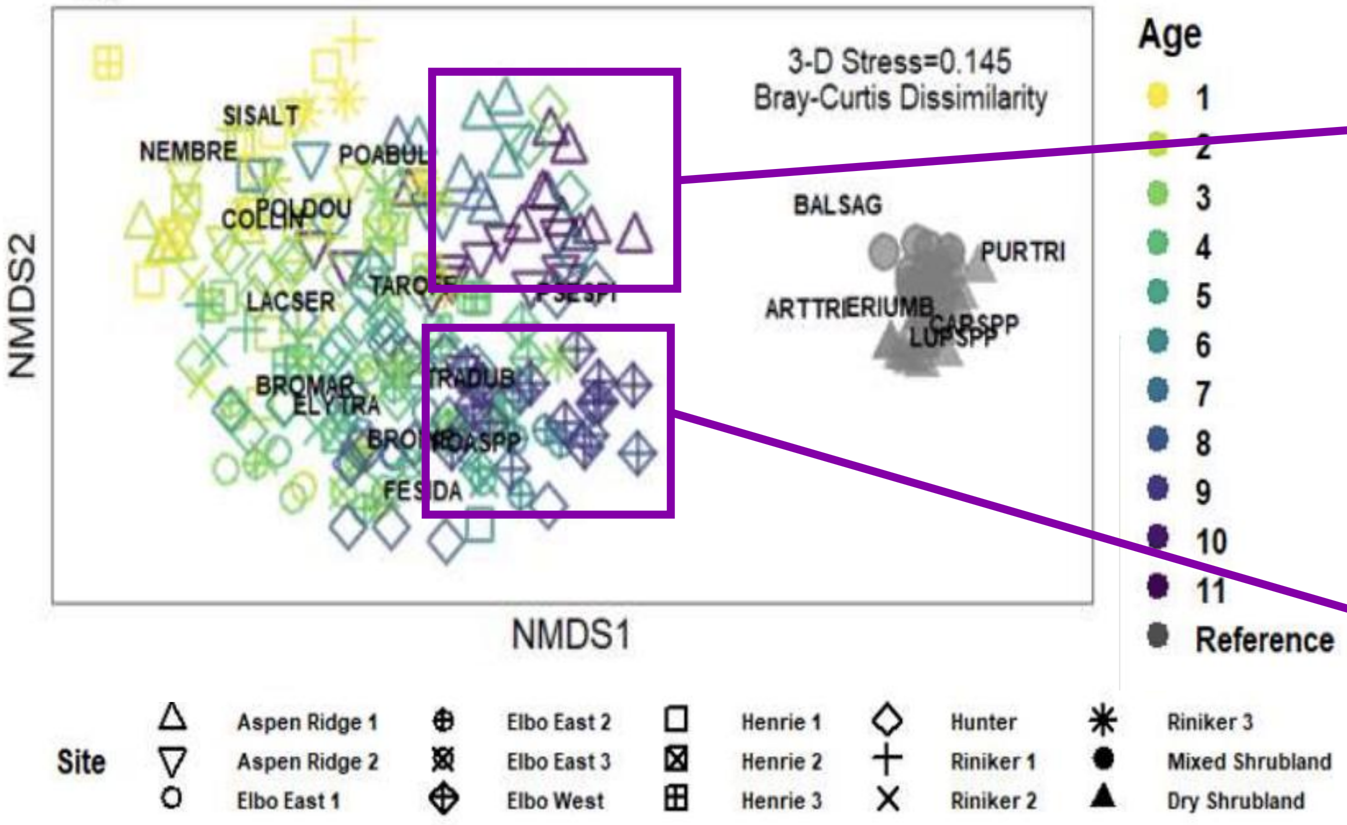


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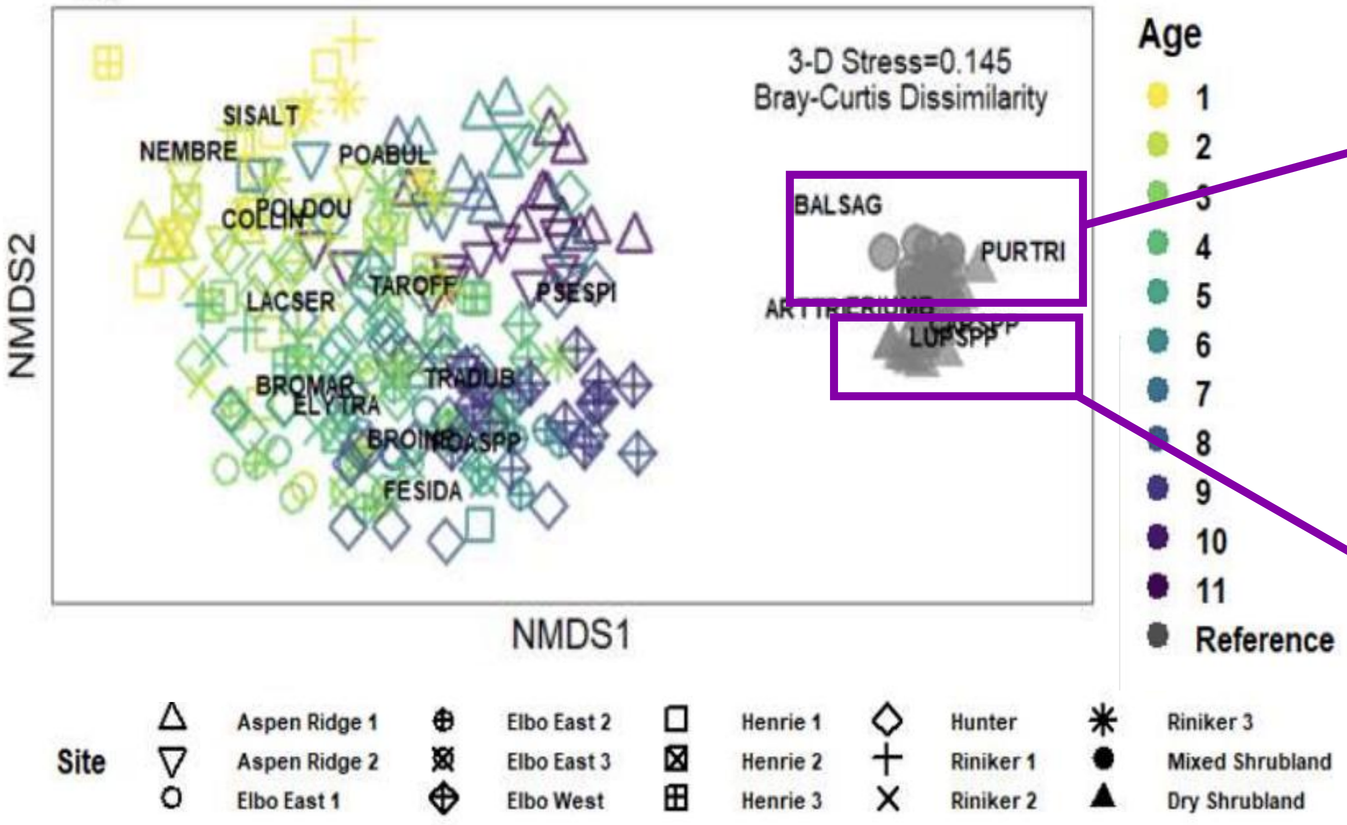
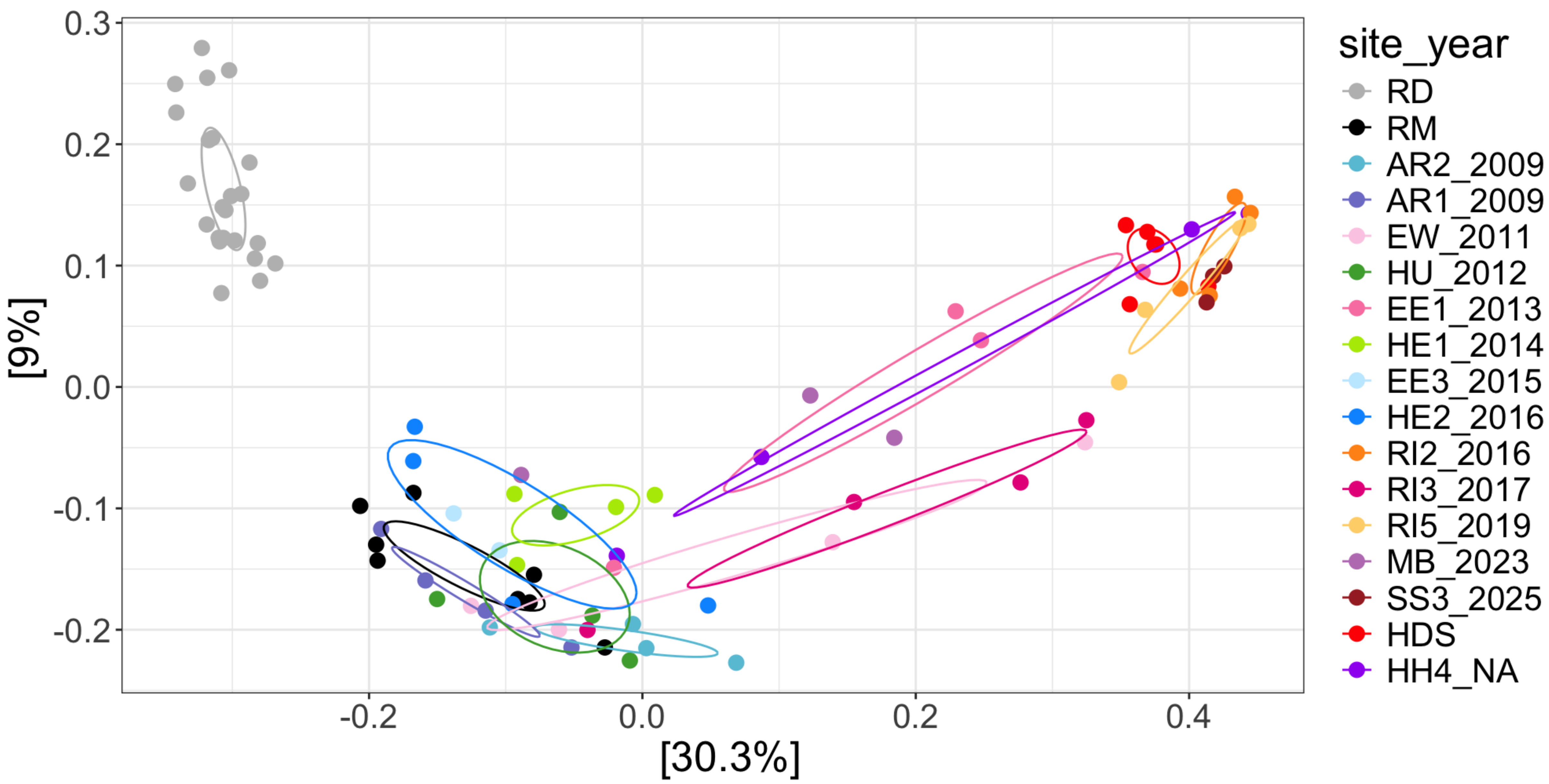



(Wessel, 2022)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0.1
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-0.1
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0.4
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site_year
RD
RM
AR2_2009
AR1_2009
EW_2011
HU_2012
EE1_2013
HE1_2014
EE3_2015
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RI2_2016
RI3_2017
RI5_2019
MB_2023
SS3_2025
HDS
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