

# Environmental Determinants of **Clonal Spread in Whitetop** (*Lepidium draba*) in northeast Colorado

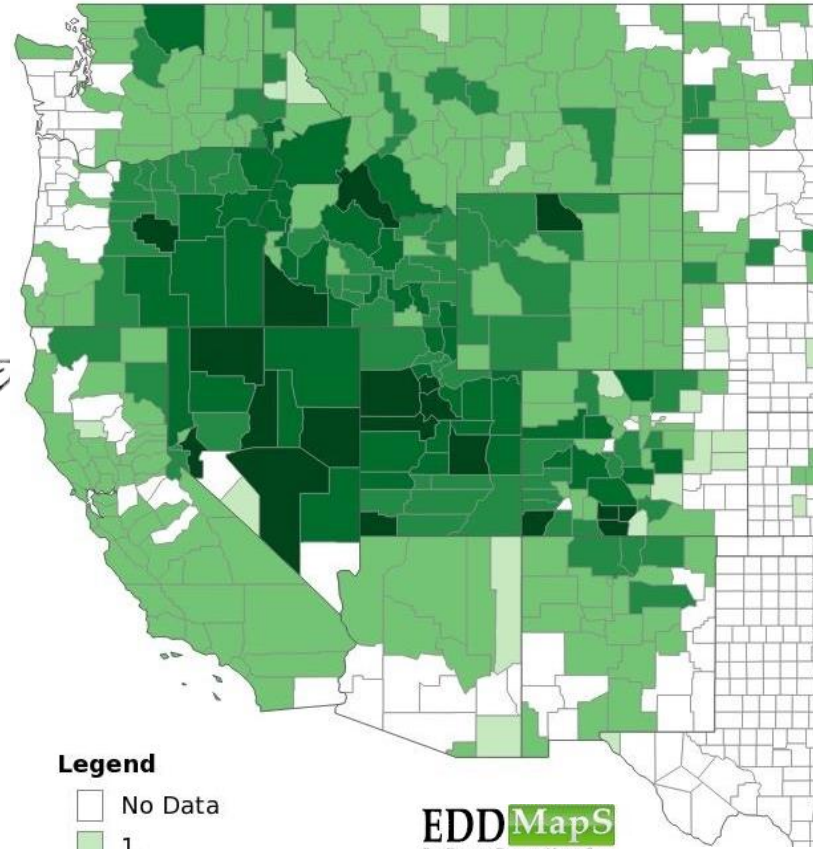
**Amanda Stahlke**, Natalie West, John  
Gaskin

18<sup>th</sup> Annual RiversEdge West  
Riparian Restoration Conference  
Colorado Mesa University  
February 5, 2020





# Whitetop (*Lepidium draba*) aka Hoary Cress



## Legend

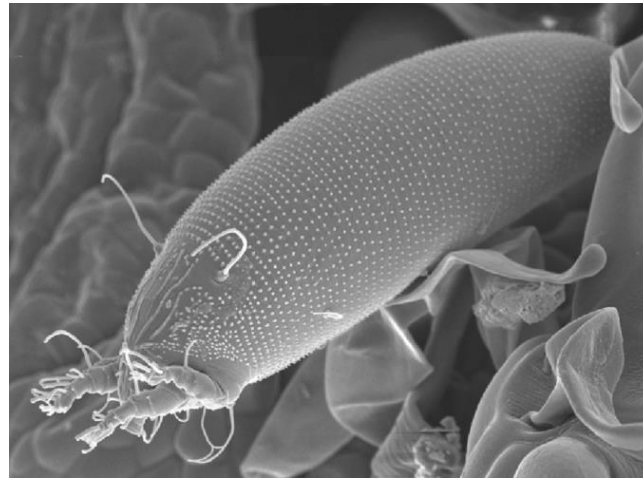
- No Data
- 1
- 2-10
- 11-100
- 101-500
- 501+

**EDDMapS**  
Early Detection & Distribution Mapping System

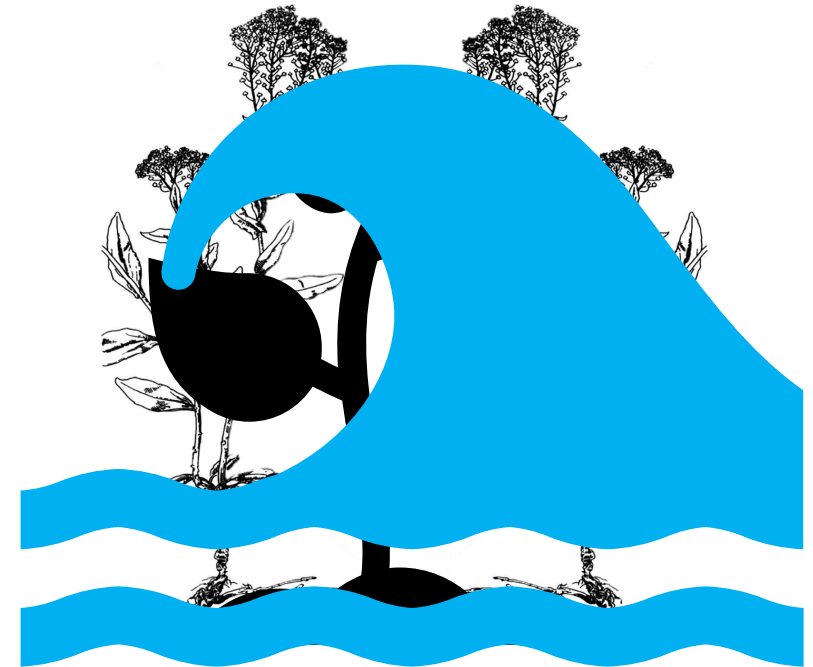


Sexual

Spread, persistence, and efficacy of control are determined in part by reproductive strategies

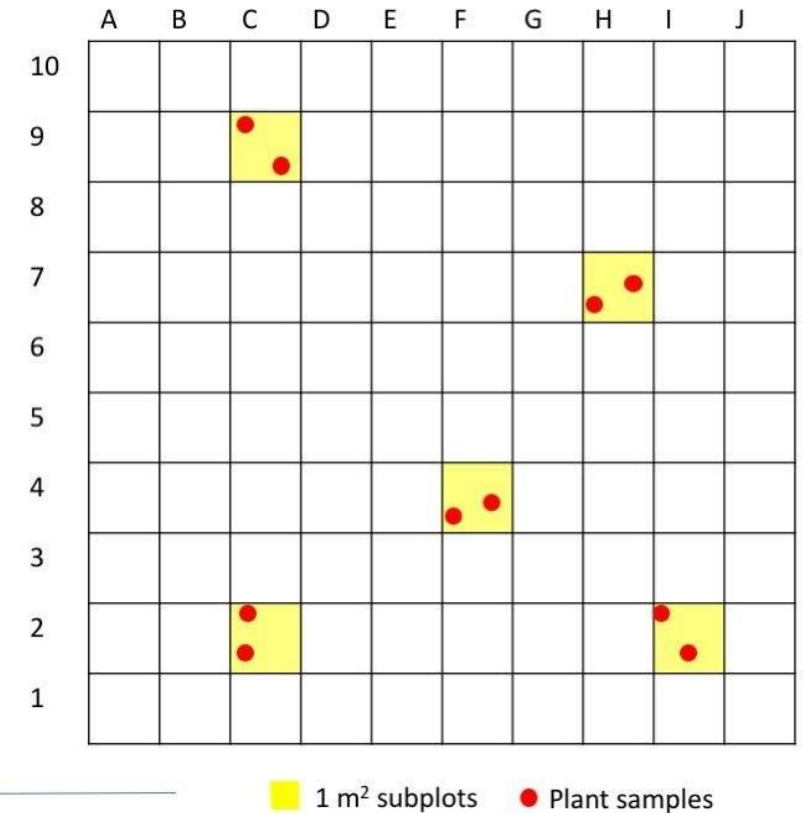
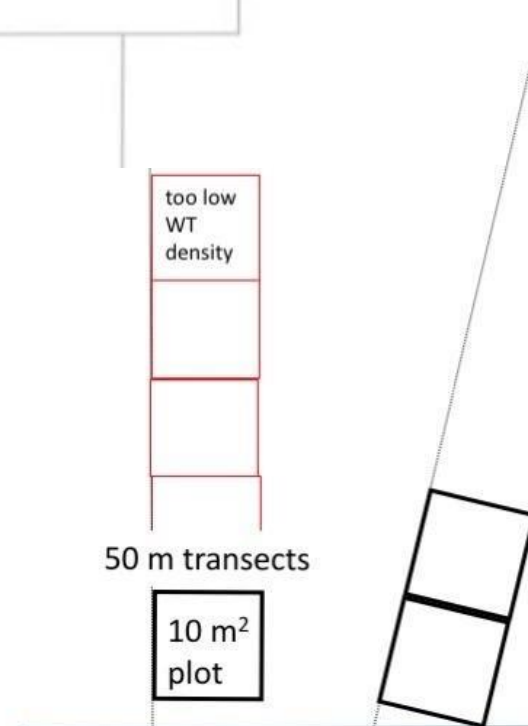
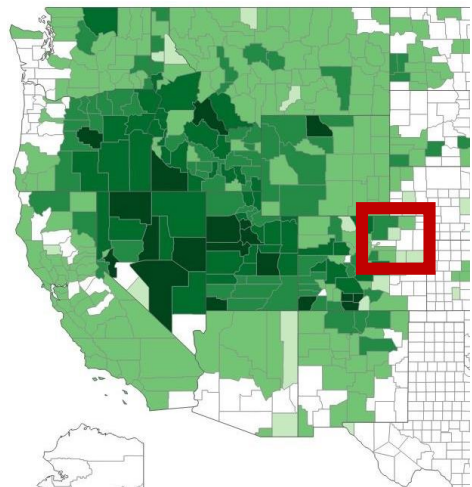


K<sup>N</sup> N  
N P K<sup>N</sup> P  
P K P





We examined the relationship between **clonality** and **environmental variables** in the South Platte River Basin









A person wearing a blue shirt and dark pants is standing in a field of tall grass and shrubs, holding a long white pole. The background shows a line of trees under a cloudy sky.

## Environmental data

Community  
composition,  
Soil texture,  
Soil nutrients,  
Stem counts

90 subplots across 6  
sites

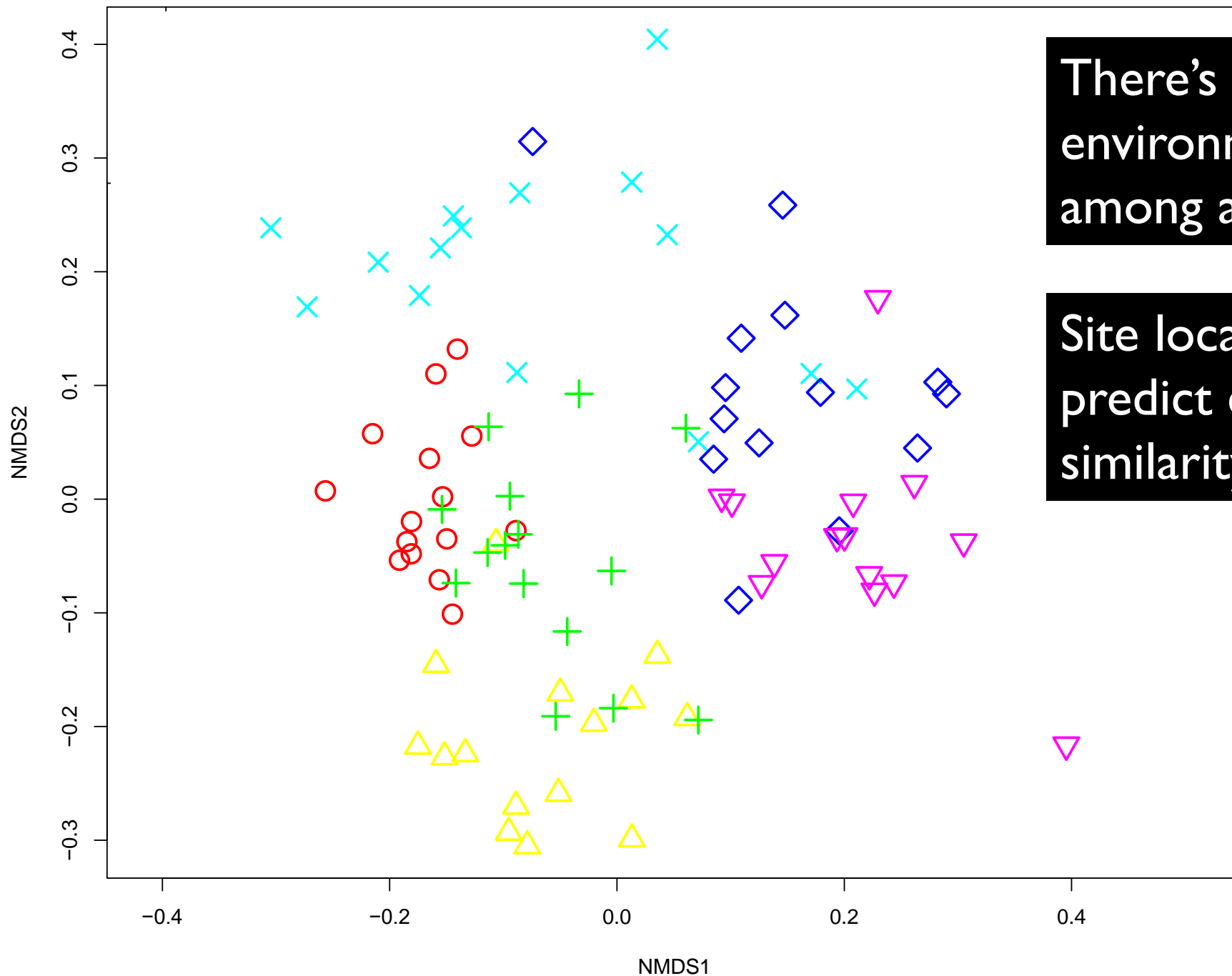
A person wearing a white lab coat and blue gloves is working in a laboratory, handling a sample in a rack. The background shows laboratory equipment and a person's head.

## Genetic data

96 AFLPs  
(Amplified fragment length  
polymorphisms)  
Clones differ by  $<4$   
markers

180 samples in 90  
subplots

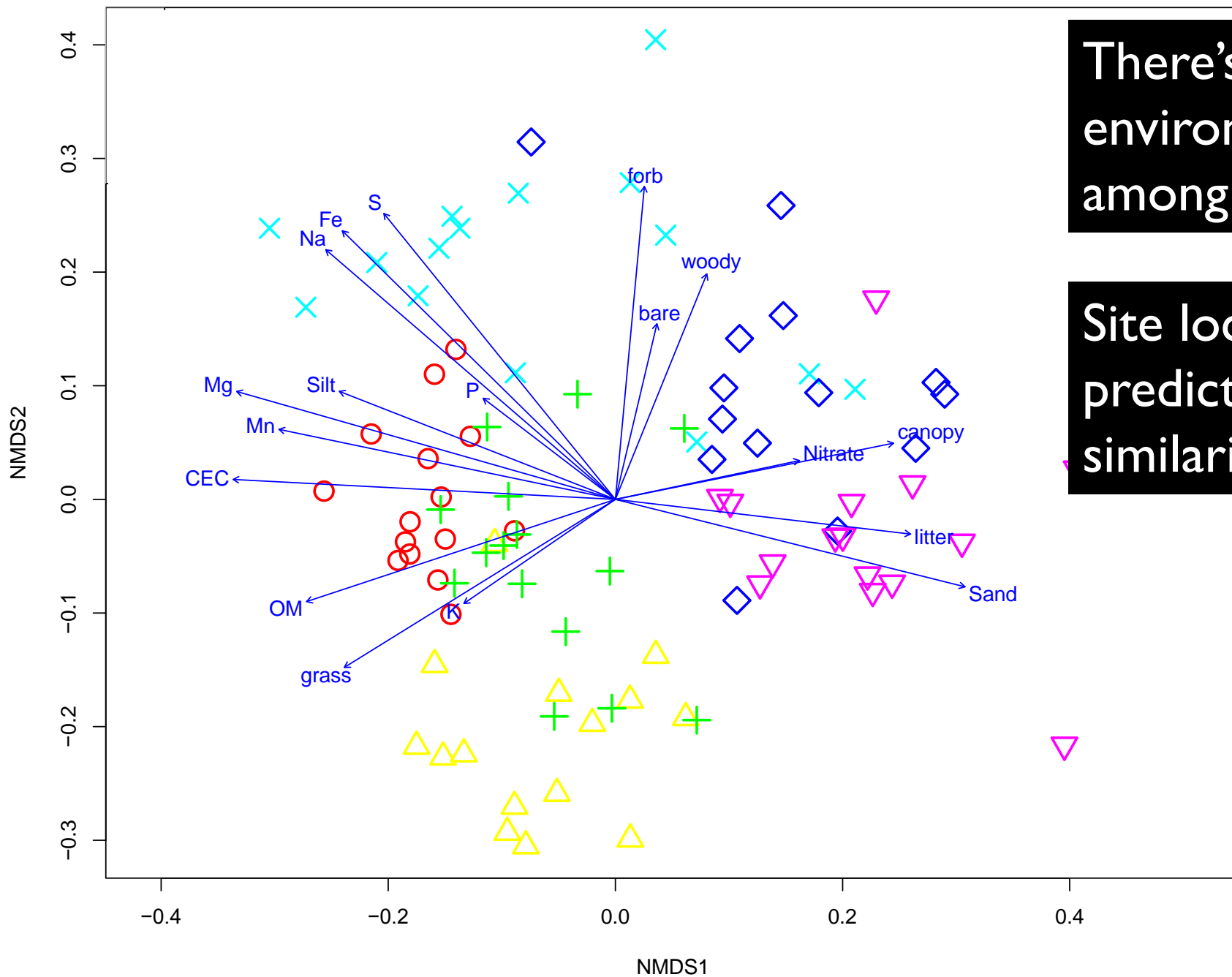
- 1
- △ 2
- + 3
- × 4
- ◇ 5
- ▽ 6



There's lots of  
environmental variation  
among and within sites

Site location does not  
predict environmental  
similarity

- 1
- △ 2
- + 3
- × 4
- ◇ 5
- ▽ 6

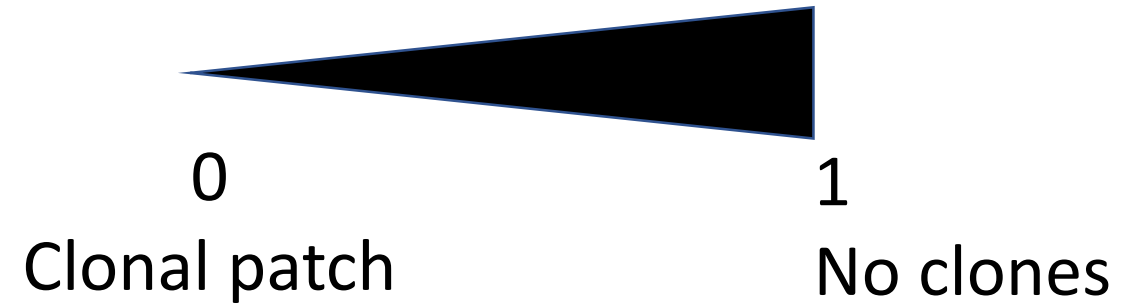


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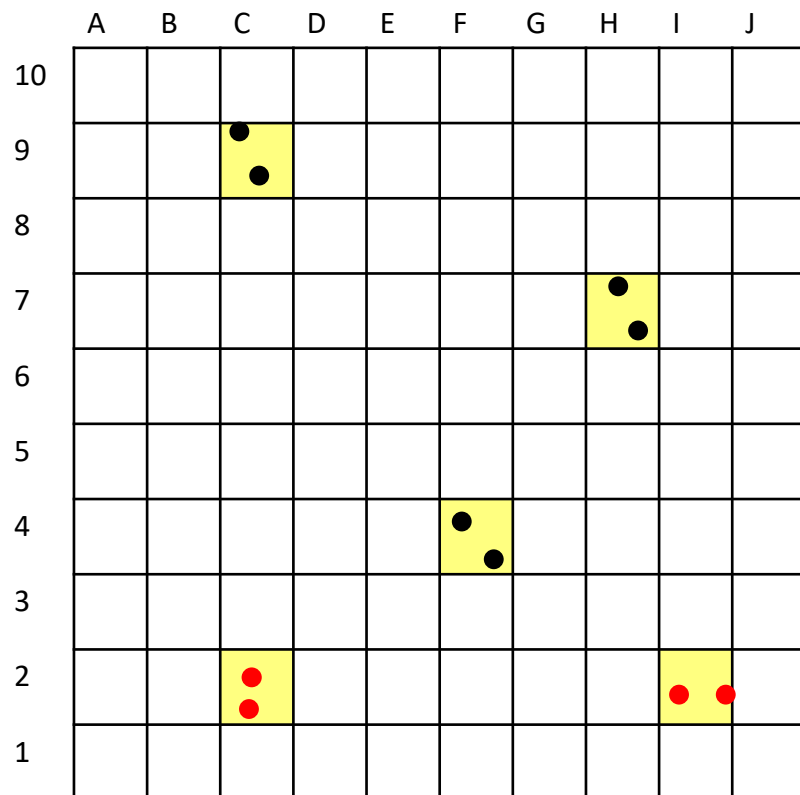
$$\frac{1 \text{ Genet}}{3 \text{ Samples (N)}} = .33$$



Site	N	G	MLG/N
○ 1	30	20	0.7
△ 2	30	13	<b>0.4</b>
+ 3	30	20	0.7
× 4	30	15	0.5
◇ 5	30	15	0.5
▽ 6	30	24	<b>0.8</b>

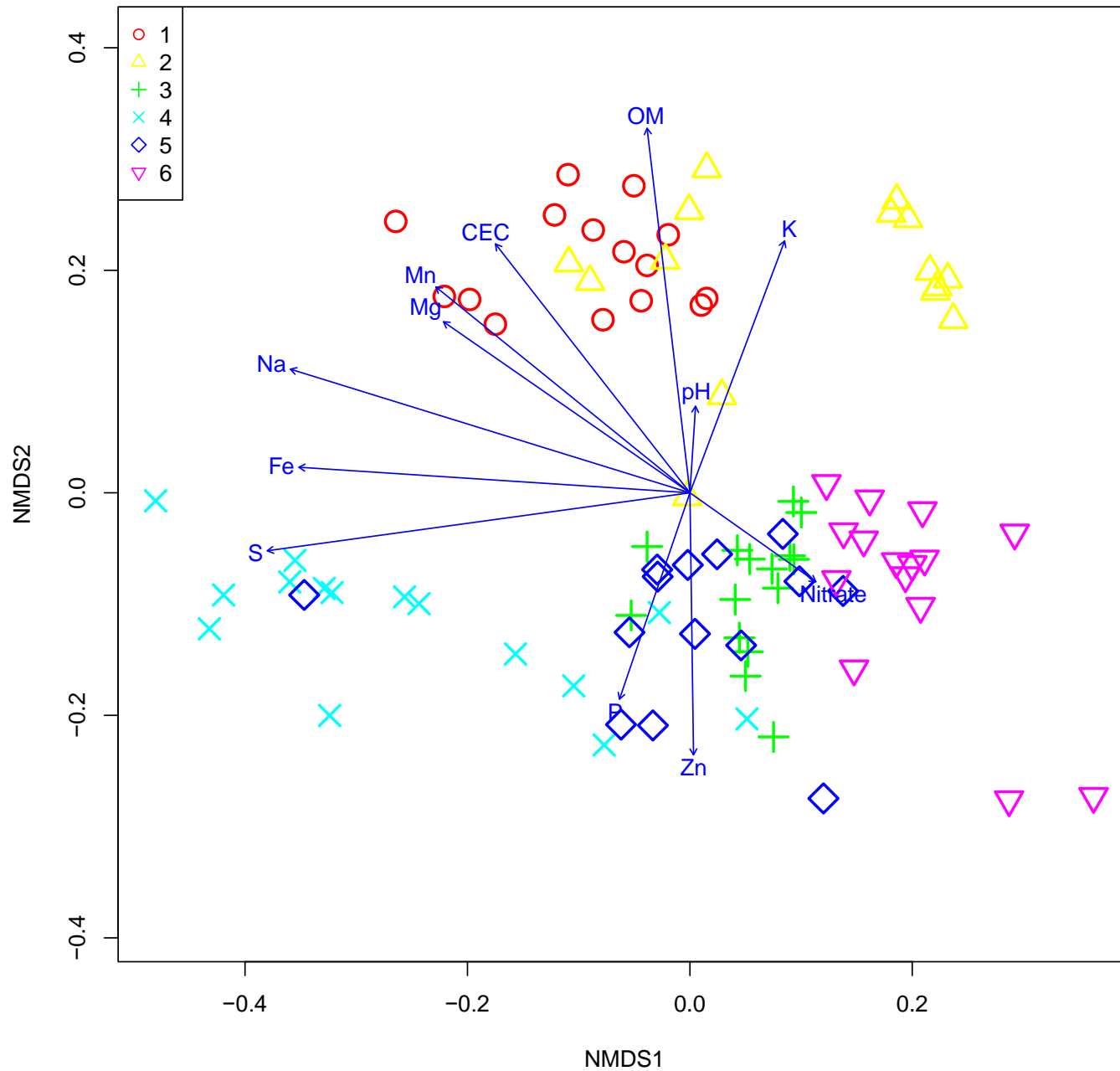


Subplot clonal incidence  
 reflects clonal richness  
 across sites



Site	N	G	MLG/N	Clones in subplots	Subplot clones
○ 1	30	20	0.7	7	0.47
△ 2	30	13	<b>0.4</b>	9	0.60
+ 3	30	20	0.7	8	0.53
× 4	30	15	0.5	12	<b>0.80</b>
◇ 5	30	15	0.5	7	0.47
▽ 6	30	24	<b>0.8</b>	0	<b>0.00</b>

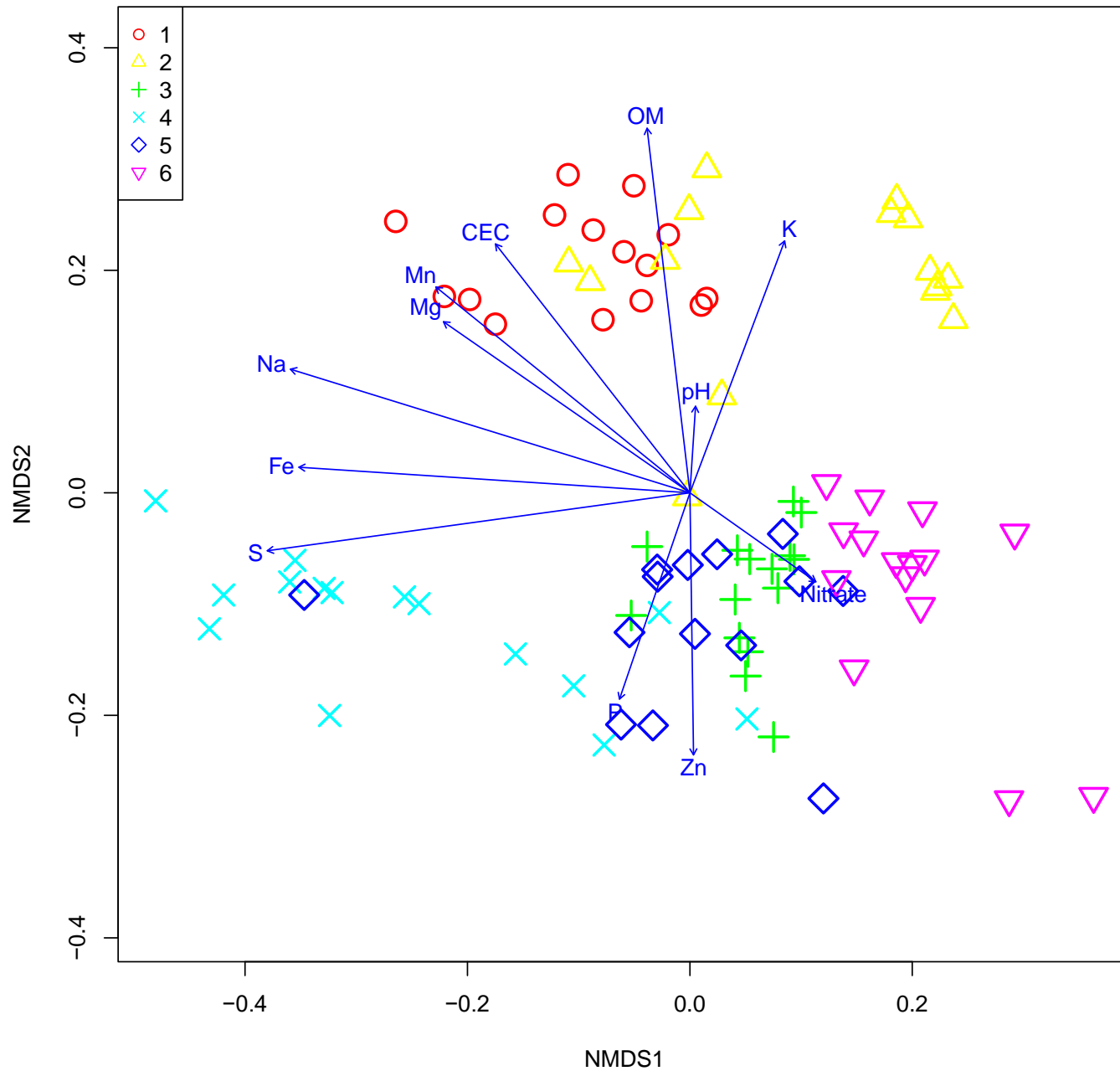




Which factors explain subplot clonality and stem count?

Compared factors in a multi-model framework with a generalized linear model:

- Soil nutrients
- % sand
- % cover
- % bare ground
- Site as random effect (or not)

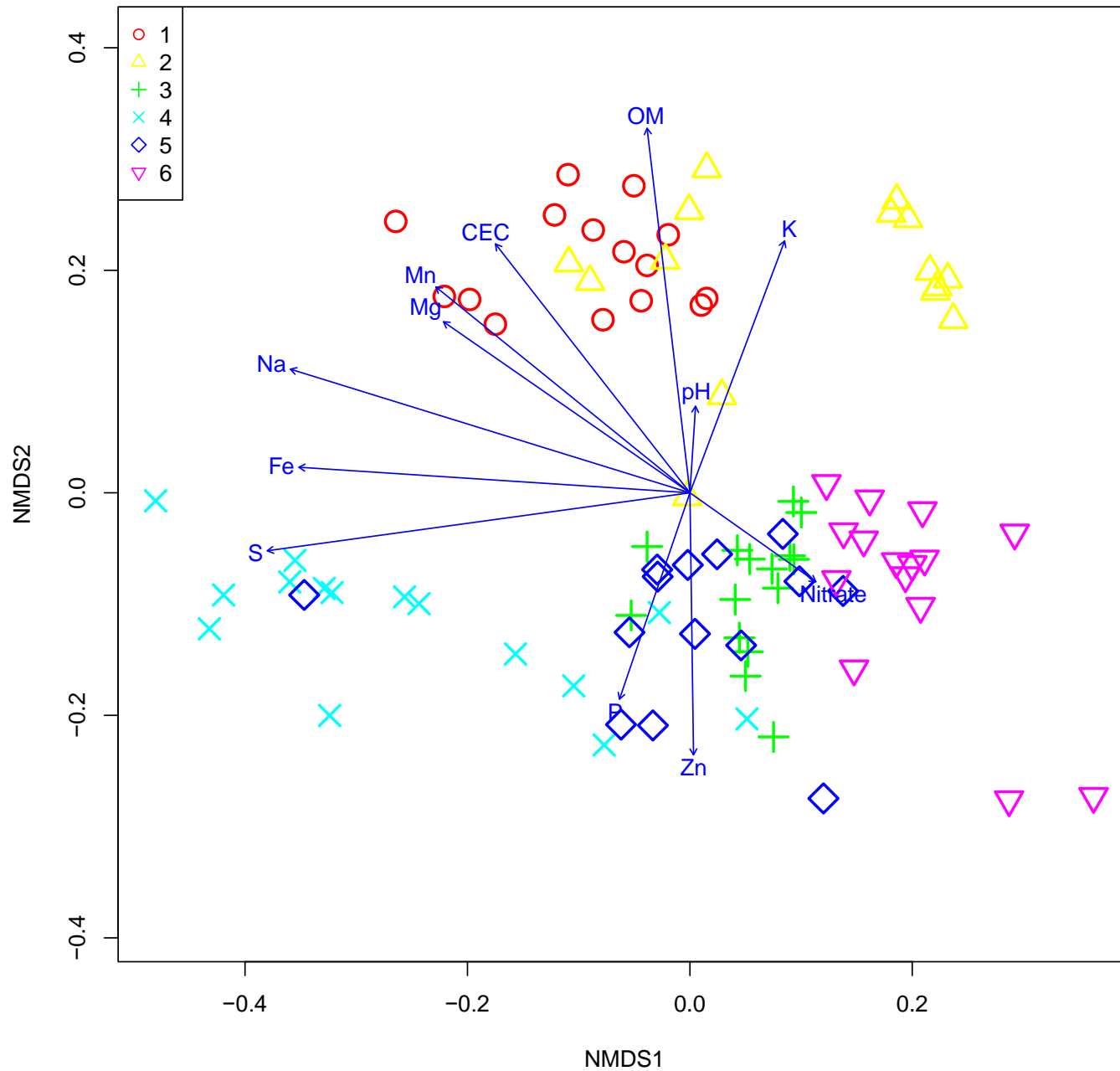


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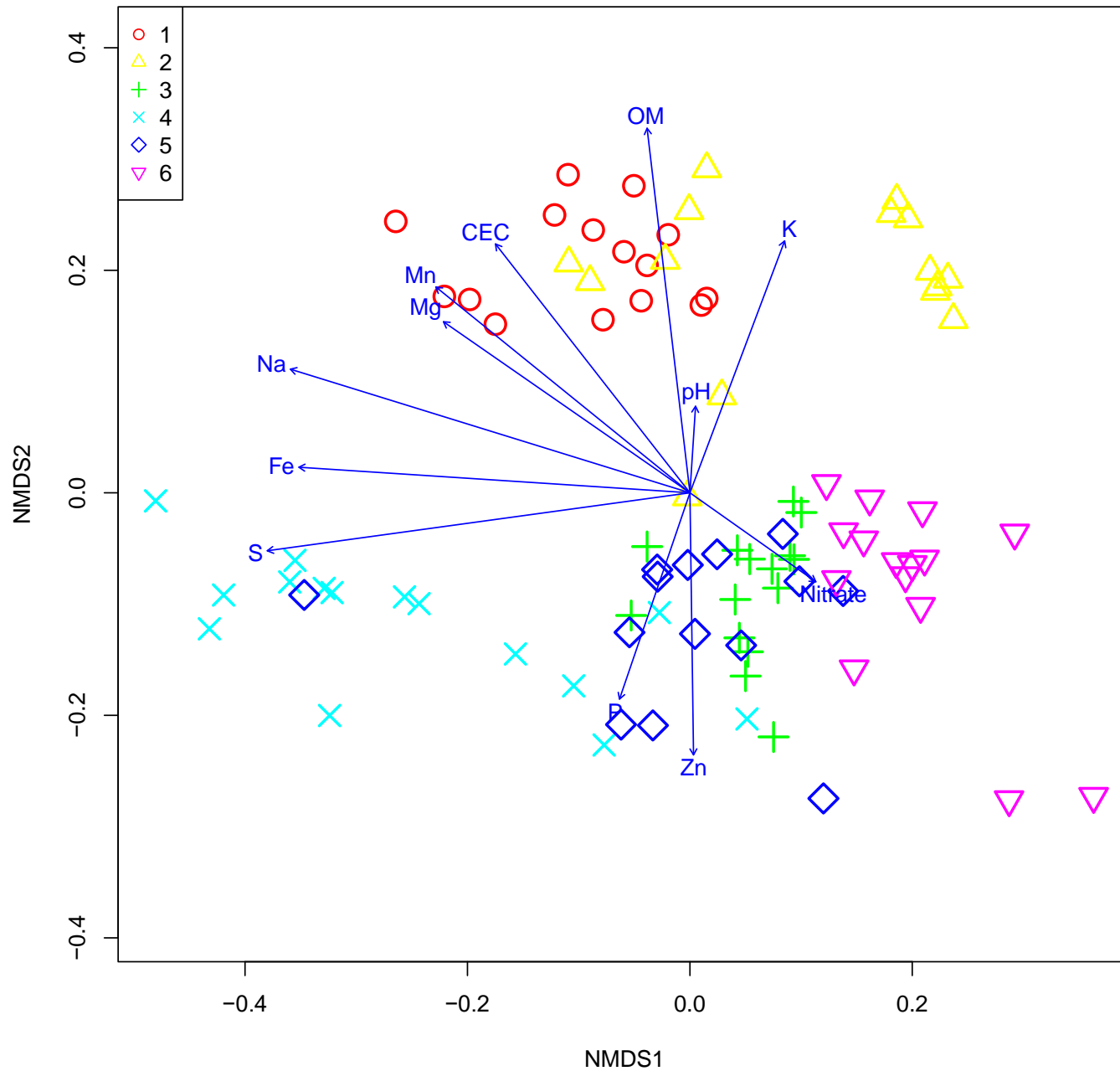




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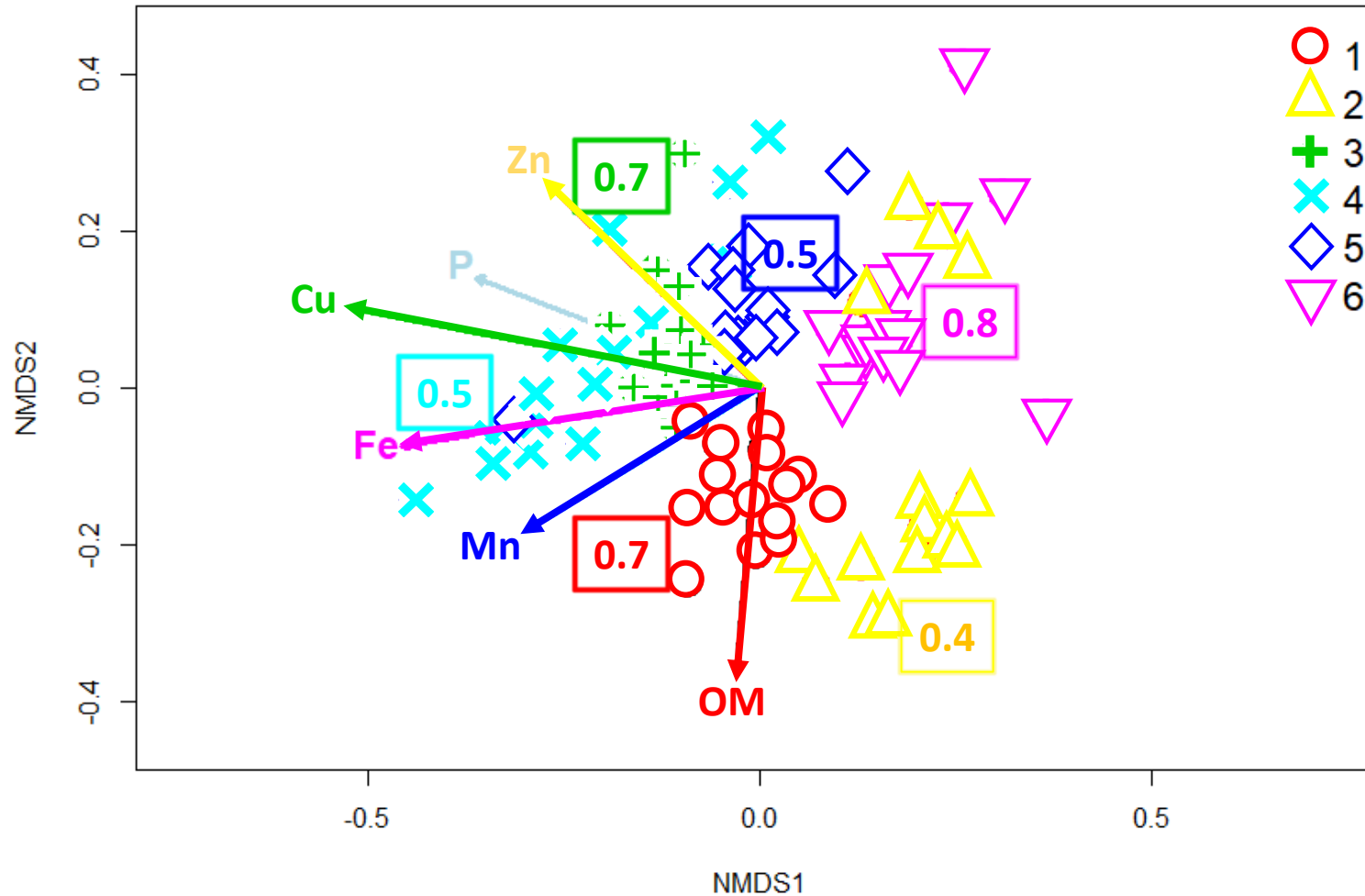
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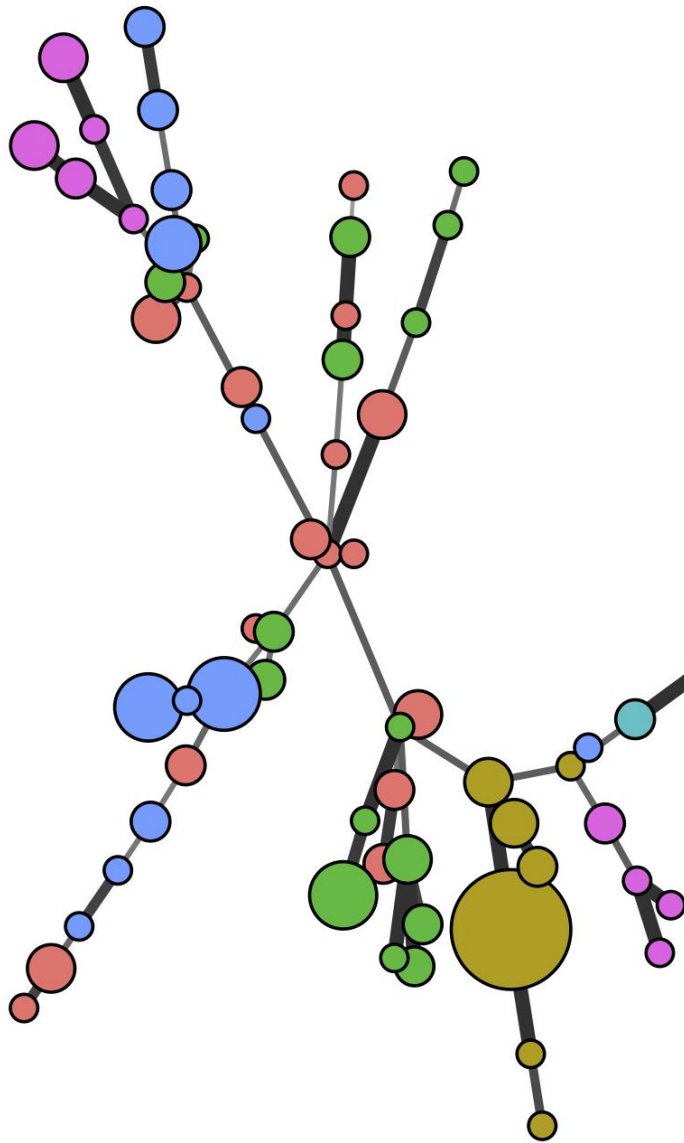
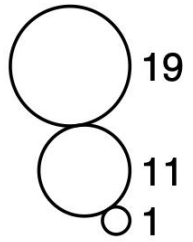
# Soil characters that distinguish sites not necessarily correlated with clonality\*



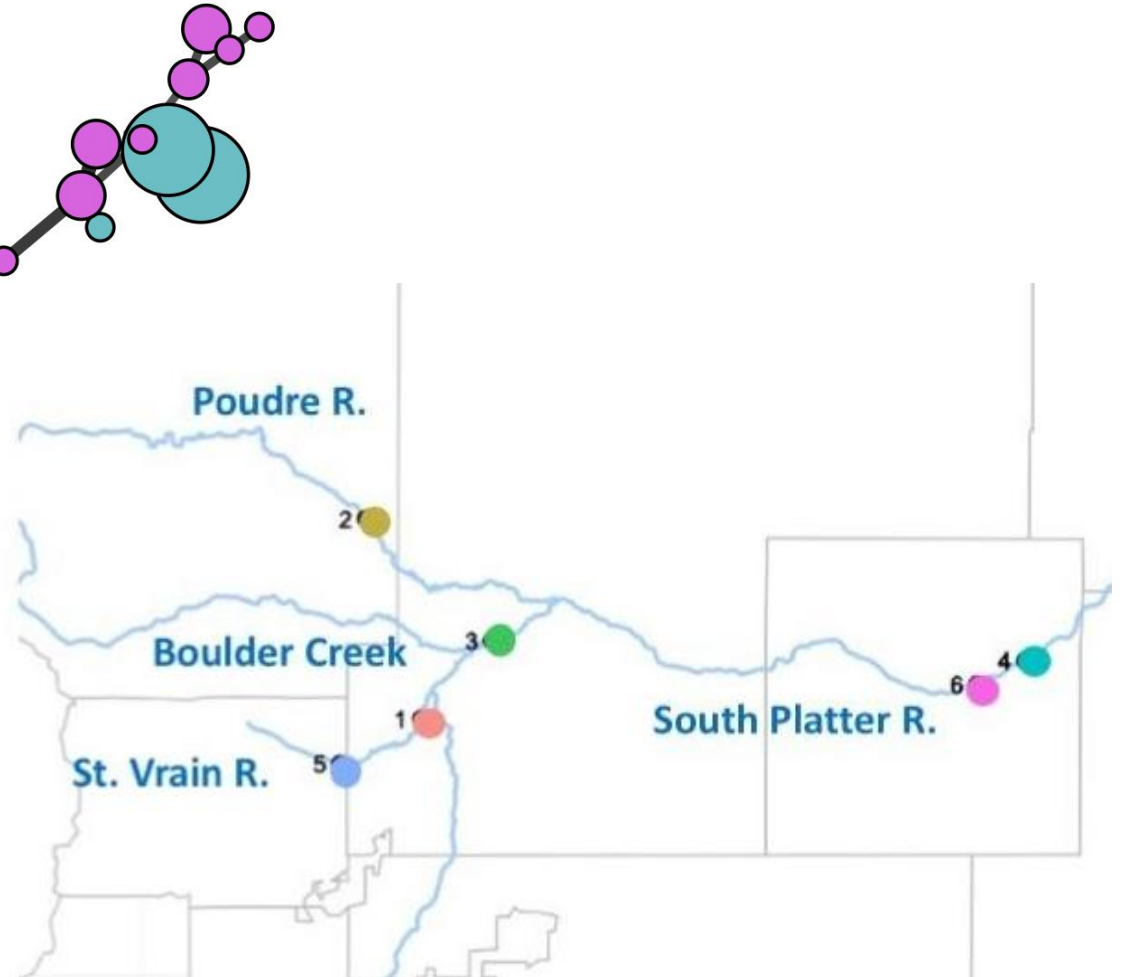
Populations

- 1
- 2
- 3
- 4
- 5
- 6

Samples/Node



Genetic similarity reflects river travel, a possible mechanism of dispersal





- Clonality was associated with K, **Mn**, **OM** & CEC
- Can measure clonality across sites at the subplot scale; Spread within site may be largely clonal, across site by seed
- If mite feeds on stems, belowground spread within site may not be contained
- Common gardens and more sites across bigger gradients in the works





# Thanks!

- Colorado Parks & Wildlife State Wildlife Area Owners
- Andrew Norton (CSU)
- Kim Mann (USDA-ARS NPARL)
- Tessa Hill (USDA-ARS NPARL)
- Kathleen McCully (USDA-ARS NPARL)
- Dora Alvarez de Srygley (USDA-ARS NPARL)
- RiversEdge West
- Bioinformatics and Computational Biology Fellowship (University of Idaho)

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