Do my cropping practices impact soil microbiology?

Lindsay A. Chamberlain & Shawn P. Conley

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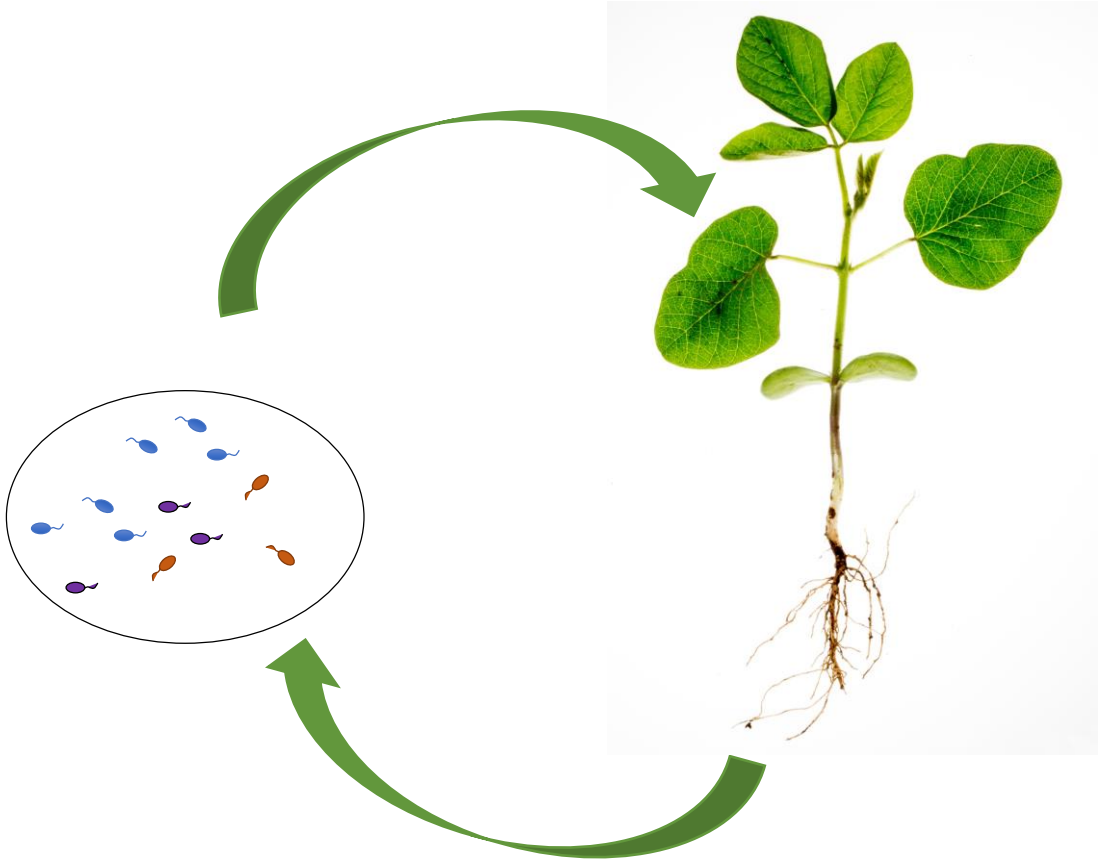
The Soil Microbiome

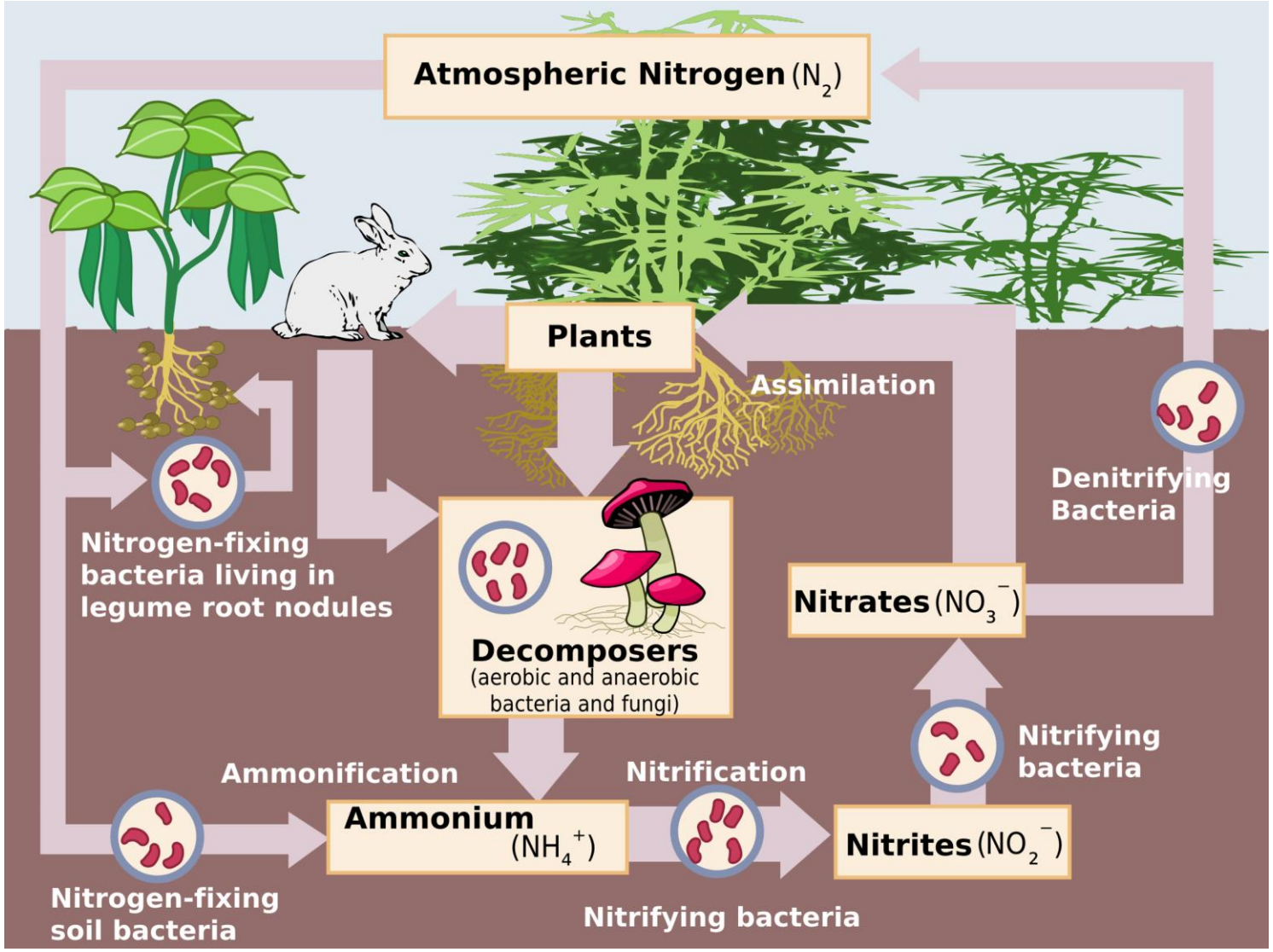
- "Micro"-Biome –
  - Microscopic inhabitants of a specific environment.
  - Fungi, bacteria, archaea, and more!
- The soil microbiome can be influenced by, and have influence on, plants.
- Focusing on bacterial communities today.



(Müller et al., 2016; Fierer, 2017)

Roles of Soil Bacteria

- Nutrient cycling & decomposition
- Competition with disease-causing organisms
- Colonize the rhizosphere



Roles of Soil Bacteria

- Nutrient cycling & decomposition
- Competition with disease-causing organisms
- Colonize the rhizosphere

Functional Redundancy

When multiple organisms in the soil can carry out the same function

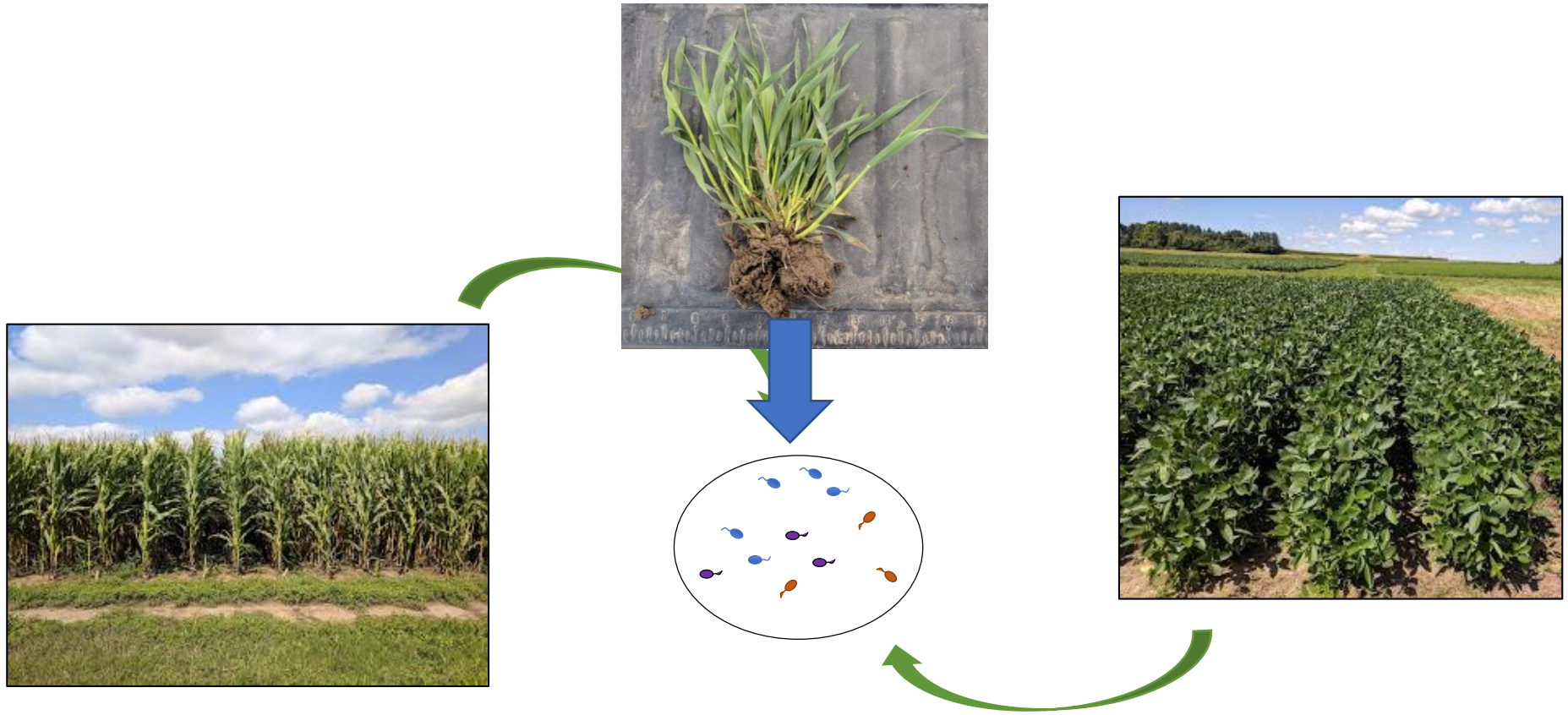
Can we manipulate soil microbiomes?

- Probiotic:
  - Inoculation of living microorganisms that benefit the host

- Prebiotic:
  - Specific substrates to “feed” the good microbes

(Foo, 2017)

Could cropping practices manipulate the soil microbiome?



Methods to estimate the microbial diversity

- Biomarkers:
  - Highly conserved, but variable
  - Cell membranes
  - DNA

- Phospholipid fatty acid (PLFA)
  - Fungal to bacterial ratios
  - Microbial biomass
- Whole genome shotgun sequencing
  - Looks at the WHOLE genome and set of genes in the community
- Amplicon sequencing of a marker gene

(Goodrich, 2014)

Amplicon sequencing

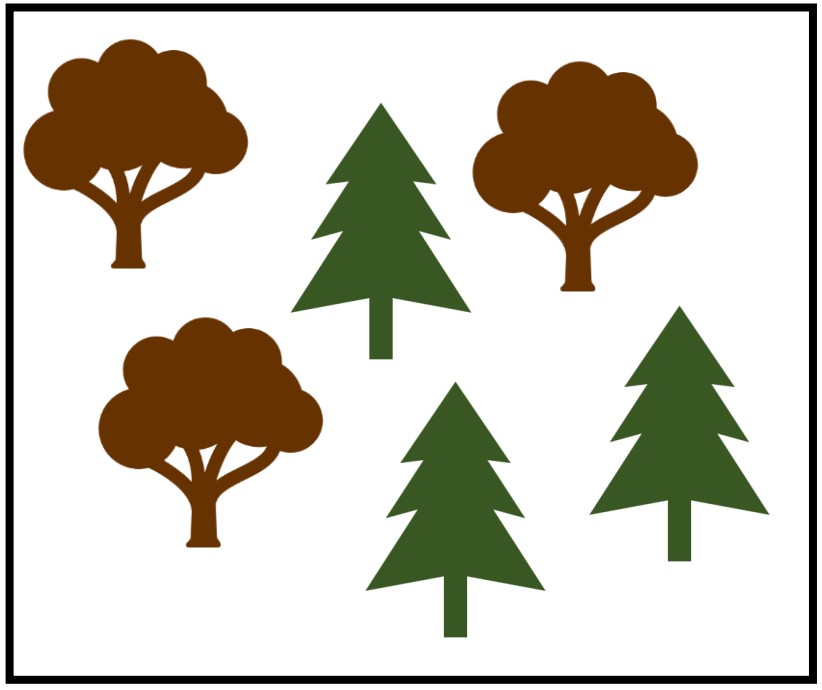
- What can we determine?
  - Taxonomic census
  - “Who” is present
  - Relative abundance
- Alpha diversity
  - Total number of different taxa
- Beta diversity
  - Variation in the types of species present in two different environments

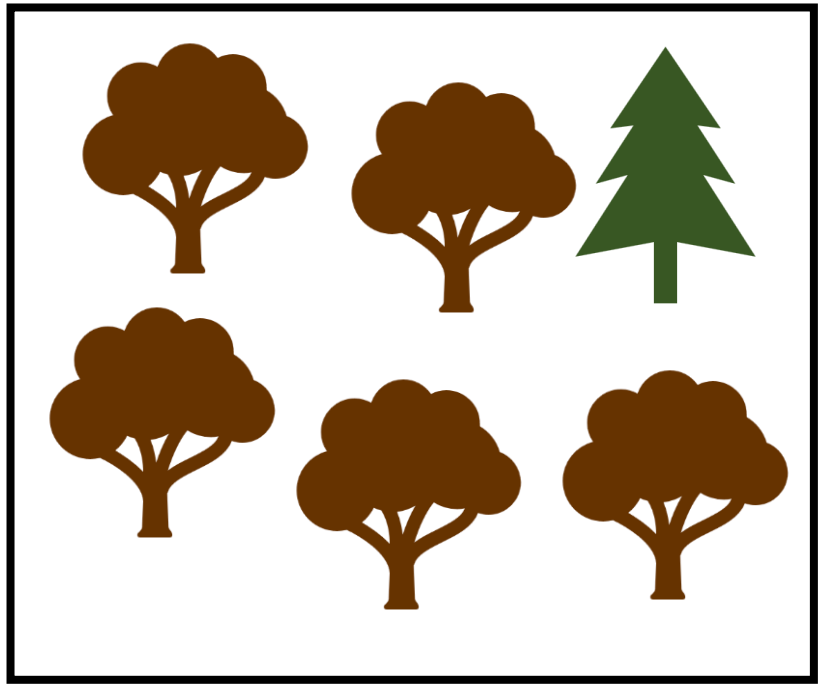
(Goodrich, 2014)

Alpha Diversity

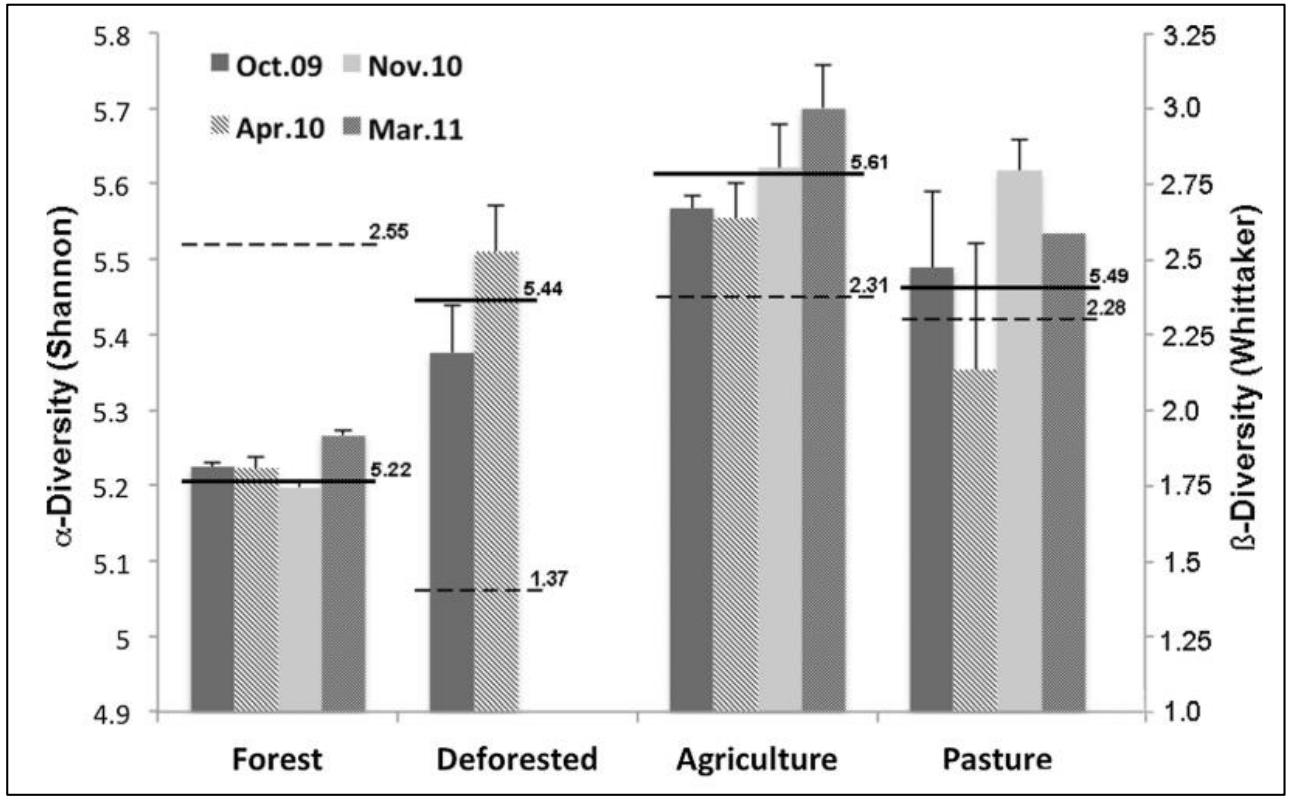
Richness: number of taxa
Evenness: distribution of taxa

Shannon's diversity is an index that incorporates richness AND evenness





Do cropping practices impact Alpha Diversity?



(Mendes et al., 2015)

- Forested land had LOWER diversity than cultivated land (Mendes et al., 2015)

Fig. 1 Levels of alpha diversity based on Shannon index for the different land-use systems across four sampling times. The *black lines* represent the alpha diversity average. The *dashed lines* represent the beta diversity

Do cropping practices impact Alpha Diversity?

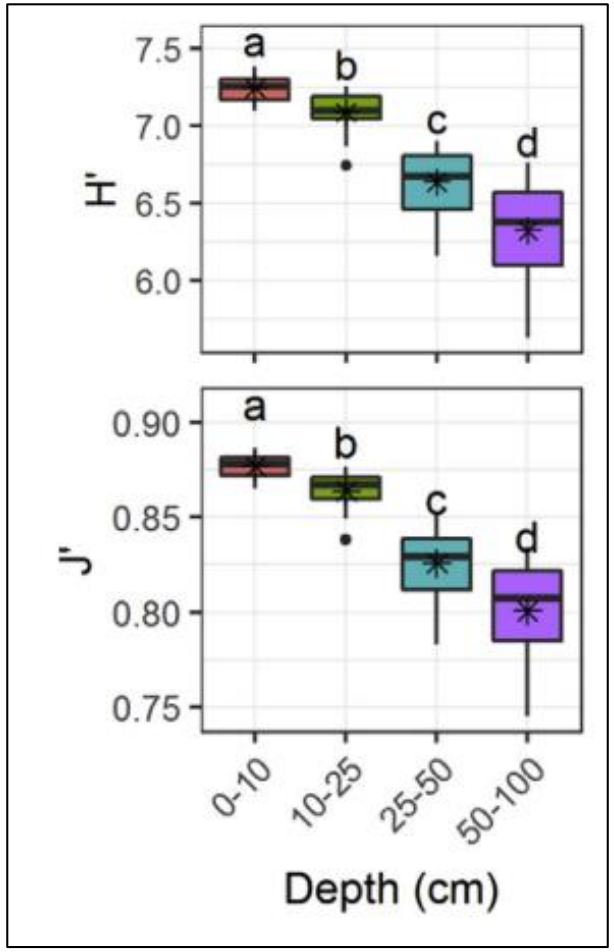
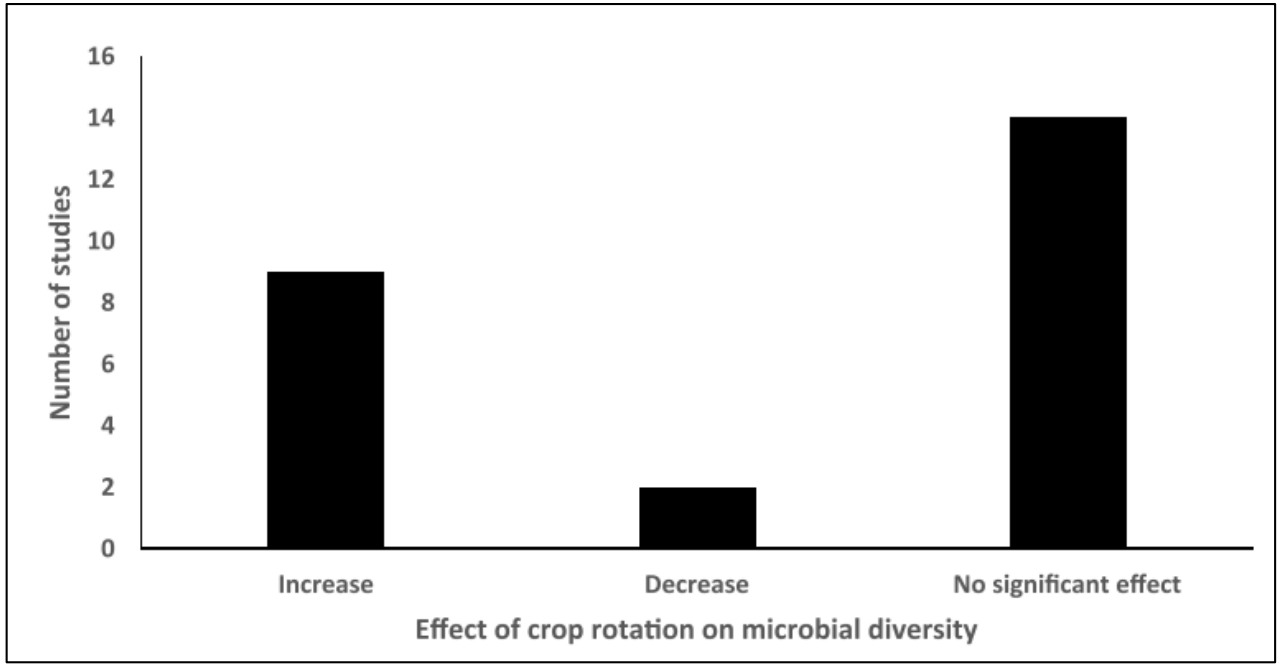


Fig. 2. Comparisons of bacterial diversity indexes among soil depths and among crops at the depth of 10–25 cm. The four crop abbreviations are defined in Table 1. Letters indicate the ANOVA grouping among depths and crops ($\alpha = 0.05$). Explanation of boxes and stars as for Fig. 1. S_{obs}, observed number of OTUs; H′, Shannon diversity index; J′ Pielou's evenness index.

- Forested land had LOWER diversity than cultivated land (Mendes et al., 2015)
- Diversity decreases with depth in the soil profile (Zhang et al., 2017)

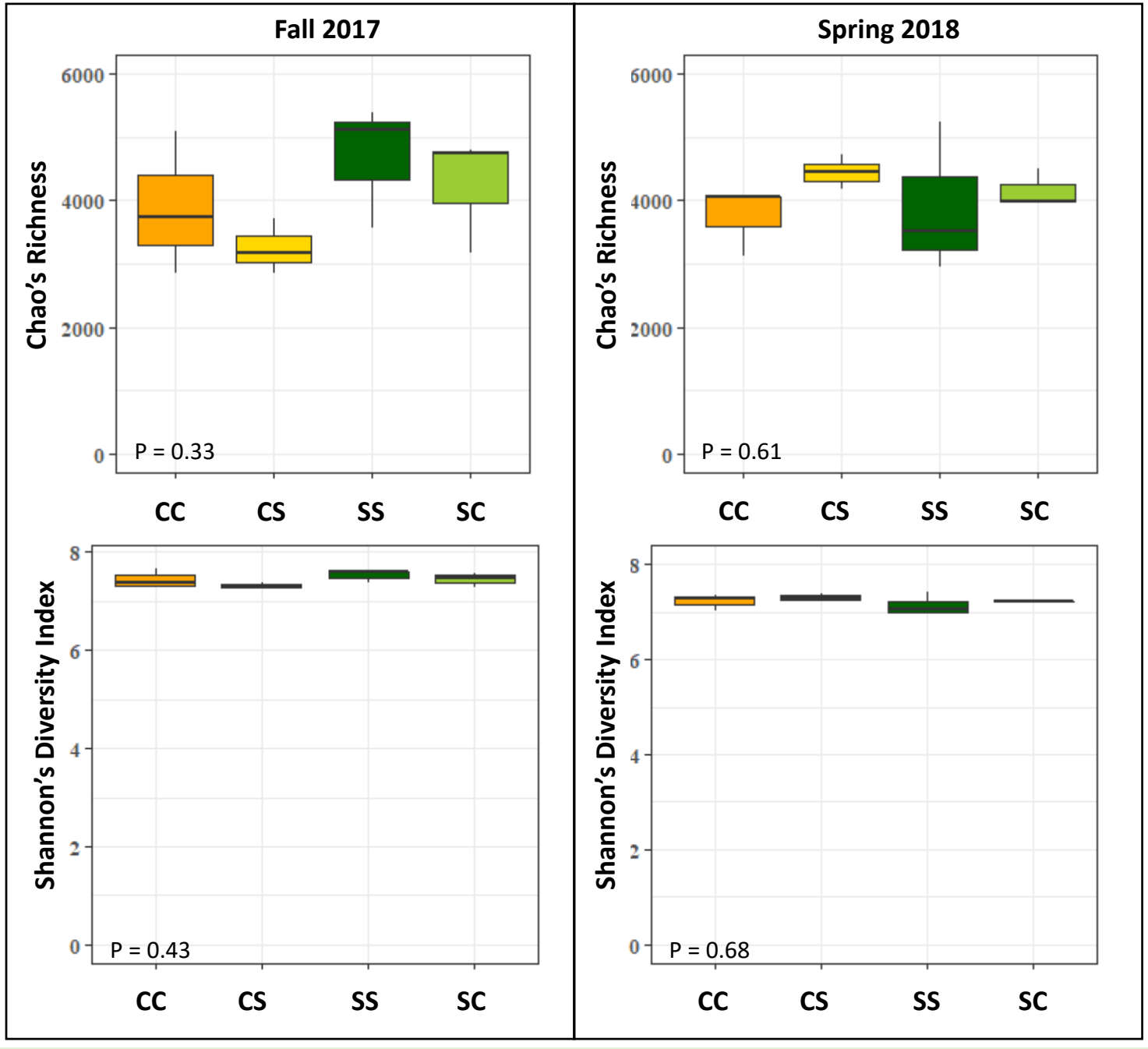
Do cropping practices impact Alpha Diversity?



(Venter et al., 2016)

Fig. 1. Number of studies (including studies that did not meet the quality criteria for data extraction) that show a significant increase, decrease or neutral soil microbial diversity with an increase in crop diversity.

- Forested land had LOWER diversity than cultivated land (Mendes et al., 2015)
- Diversity decreases with depth in the soil profile (Zhang et al., 2017)
- Mixed results on the effect of crop rotation on diversity (Venter et al., 2016)



Rotational Treatments

- **CC** Continuous corn
- **CS** Annual corn
- **SS** Continuous soybean
- **SC** Annual soybean

Functional Redundancy

When multiple organisms in the soil can carry out the same function

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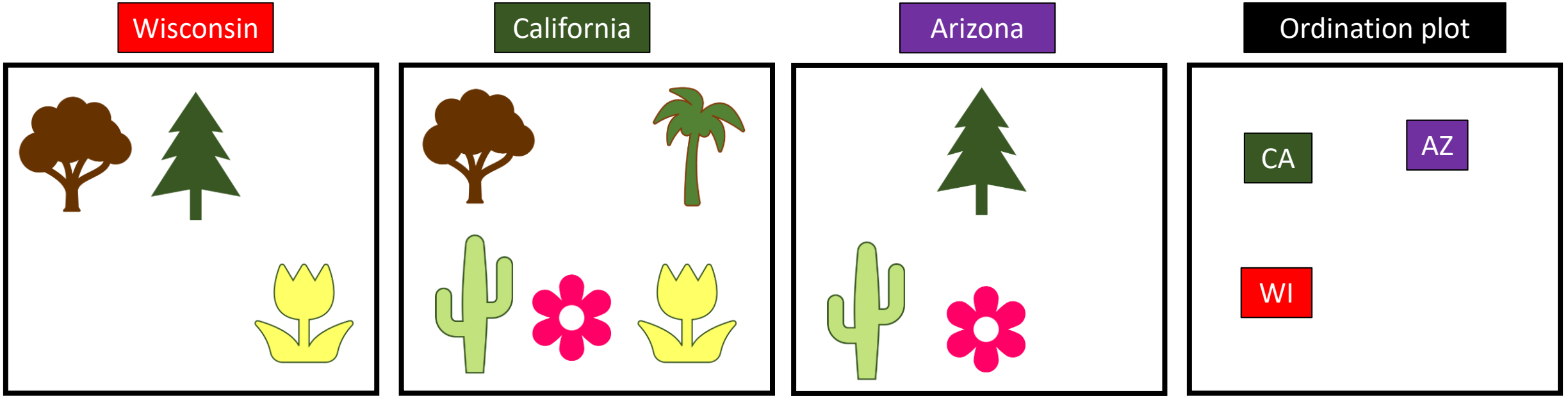
Beta Diversity

Variation in the types of species present in two different environments



Do cropping practices impact Beta Diversity?

- Tilled and no-till fields had distinct bacterial communities (Smith et al., 2016)

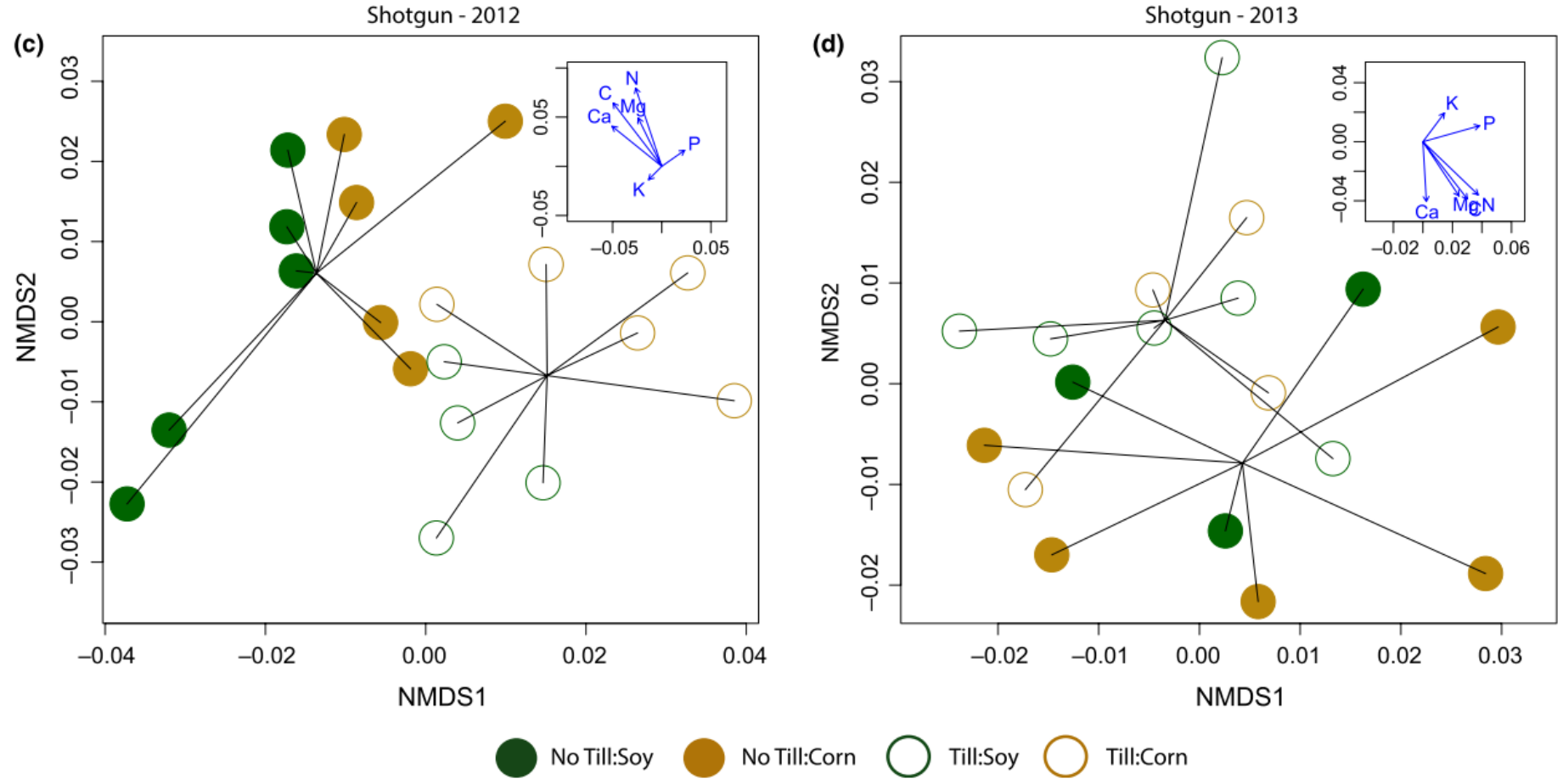


FIGURE 1 Ordination (NMDS) plots of communities for each year and using 16S rRNA amplicons (a, b) and functional shotgun annotations (c, d). Insets show correlations of axes with soil nutrients. There was a statistically significant difference between tilled and untilled fields in all years and across both data types (16S rRNA and shotgun); crop type was only statistically significant for shotgun/function in 2012 (Appendix Table S8). Soil nutrients tend to increase in the direction of no-tillage fields in all four panels (Appendix Figure S4)

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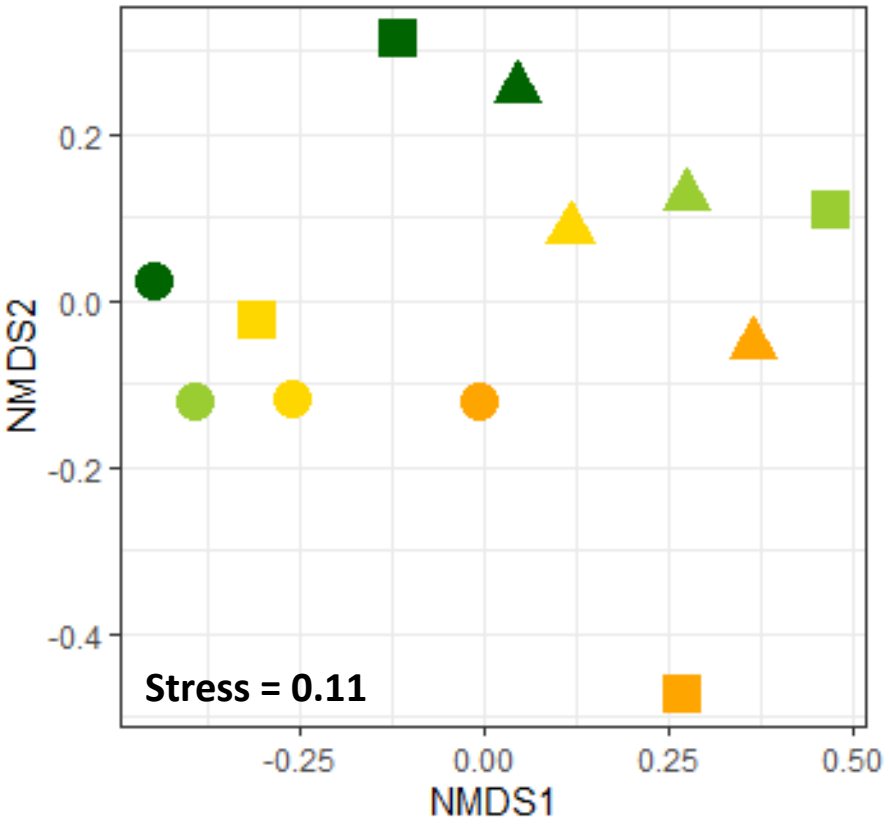
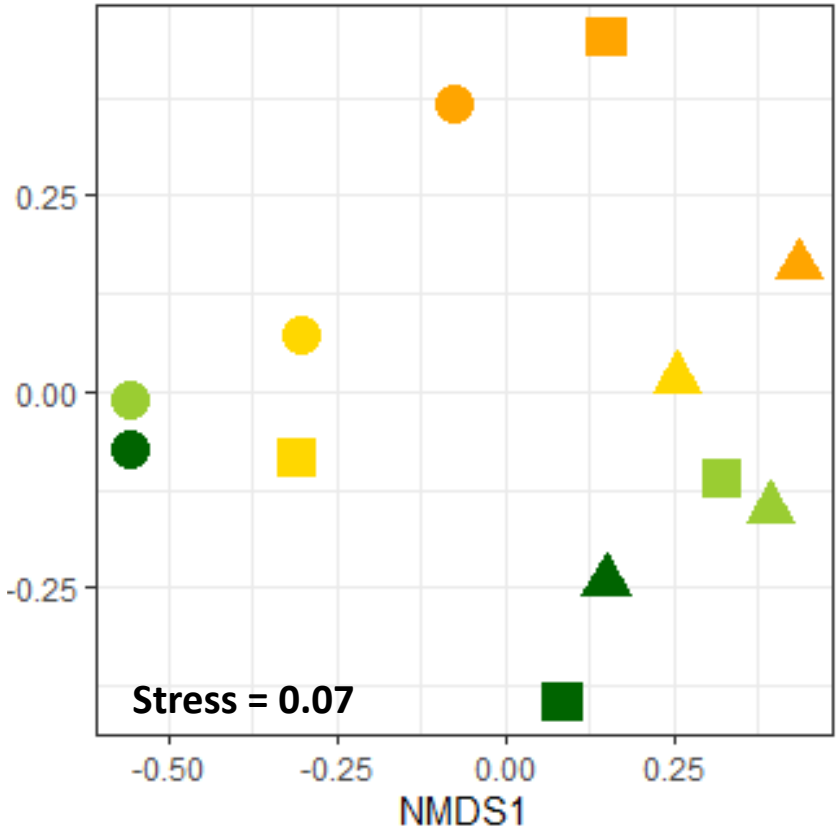
Crop rotation had an impact on Beta Diversity

Fall 2017



Spring 2018



Rotational Treatments

- Continuous corn
- Annual corn
- Continuous soybean
- Annual soybean

Block

- 1
- 2
- 3

	R^2	P-value
Fall 2017	0.28	0.017
Spring 2018	0.30	0.006

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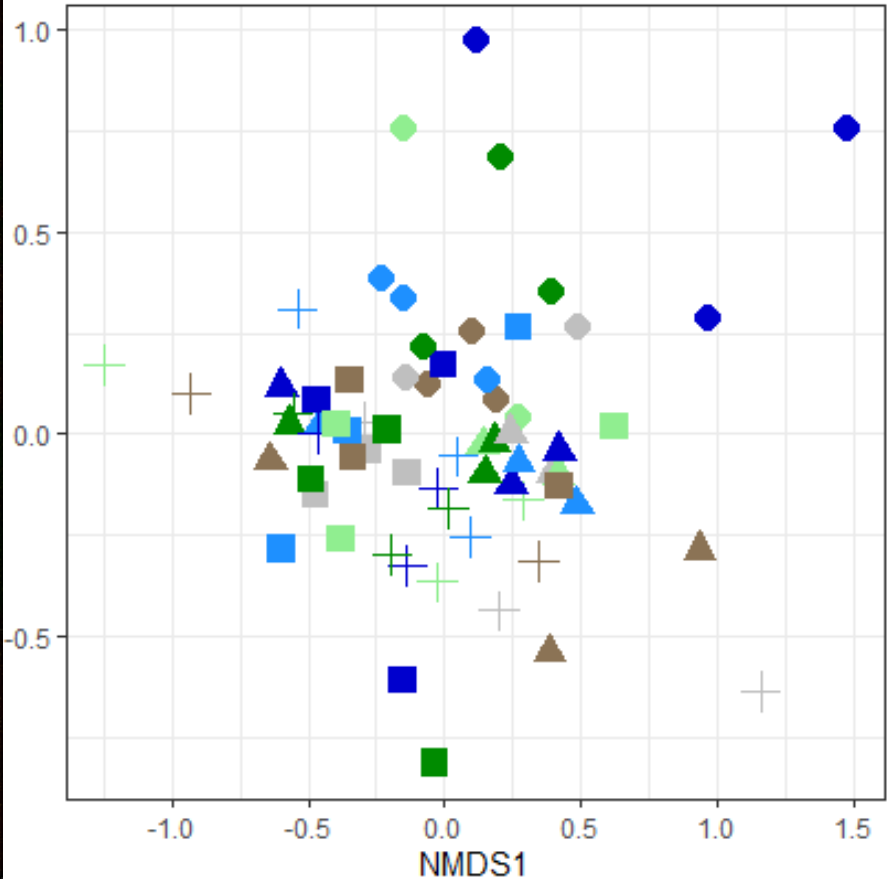
Crop rotation effects: direct? Or indirect?

- Corn harvested for grain leaves behind 3 times more biomass than soybean.
- Corn residue has a much higher C:N ratio than soybean residue.

(Buyanovsky and Wagner, 1986; Kaboneka et al., 1997)

Cover crop did not impact bacterial Beta Diversity

Spring 2018



Cover Crop Treatments

- Untreated control
- Oat aerially seeded
- Oat drilled
- Oat/Rye alternating
- Rye aerially seeded
- Rye drilled

Rotational Treatments

- Continuous Corn
- Annual Corn
- Annual Soybean
- Continuous Soybean

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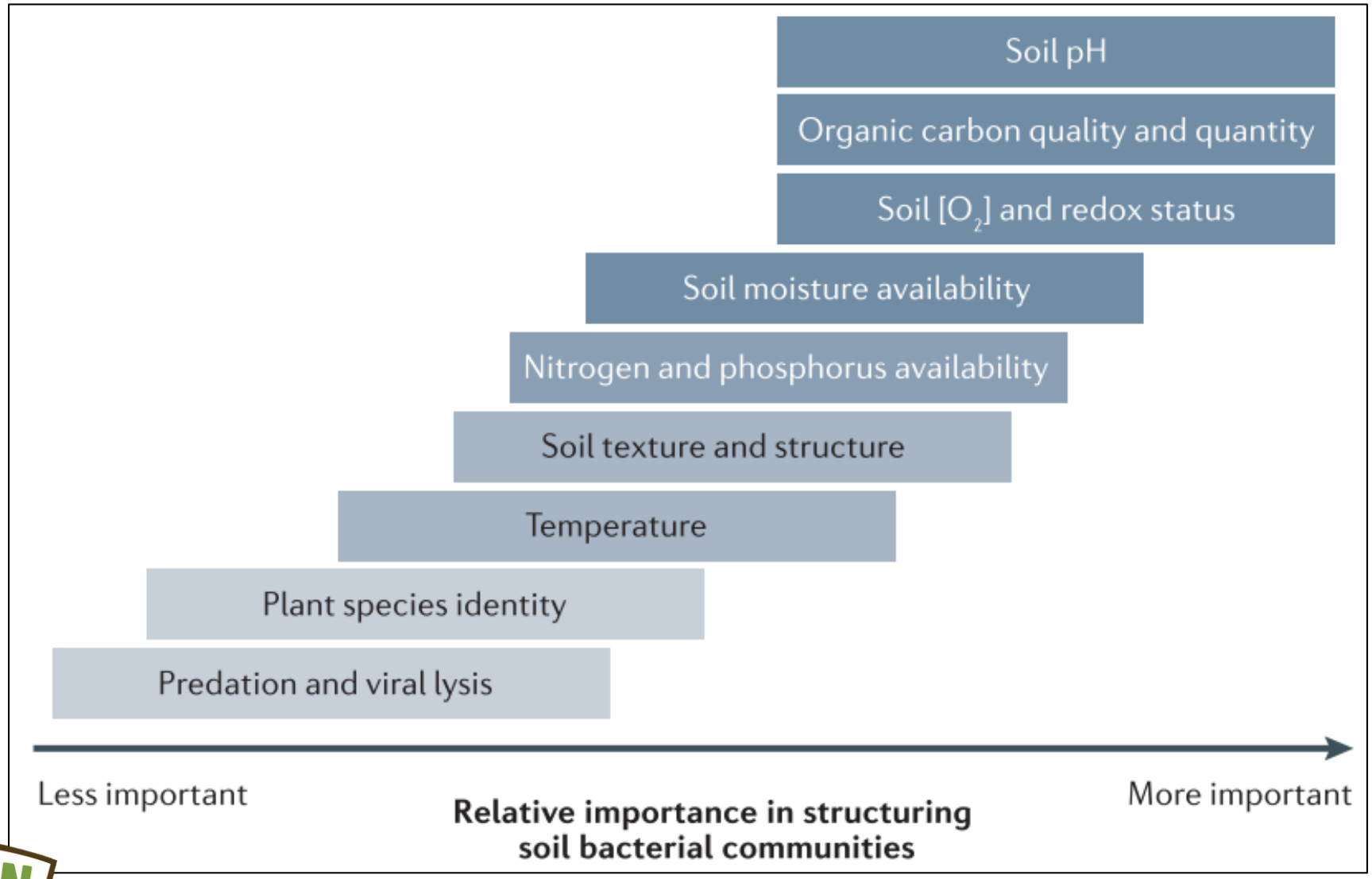
Plant species is less important than other factors



(Fierer, 2017)

Yes – cropping practices DO impact soil microbiology

*Especially practices that alter soil properties like organic matter, nutrients, and soil structure.

Future Studies to look out for:

- Corn/soy rotation impact on soil fungi
- Repeated foliar fungicide use on soil fungi
- Soil health in soybean systems (Recruiting!)

Do you grow soybeans? Are you interested in soil health?

- Recruiting for a variety of management practices and locations.
- Requirements: spring soil sampling, field history survey, report yields.

Contact Lindsay Chamberlain

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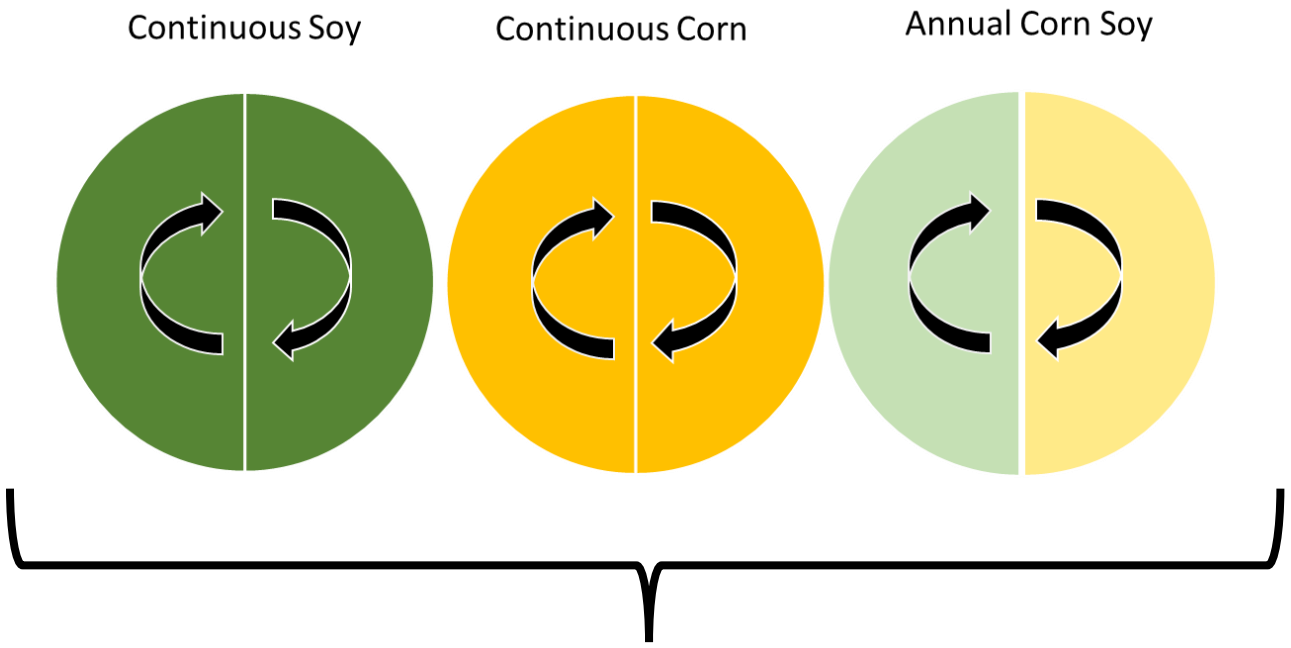
Methods: Long Term Crop Rotation Study



Six cover crop treatments per rotation scheme, established in 2017

- Established 2002
- RCBD with 3 replications
- Main plot: crop rotation
- Split plot: cover crops

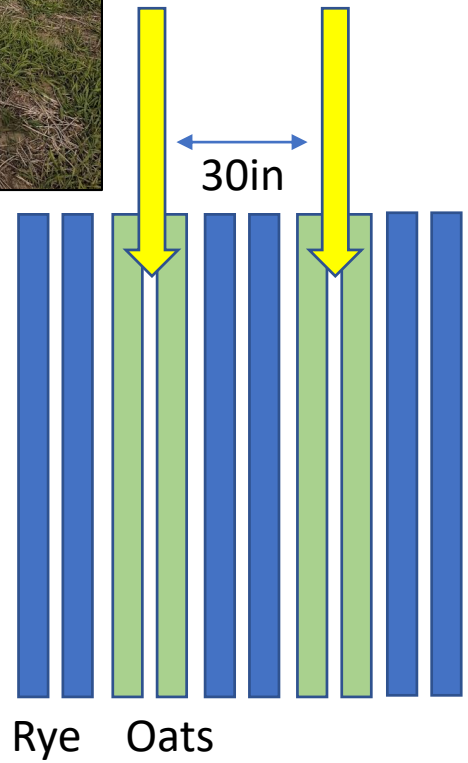
Methods: Cover Crops

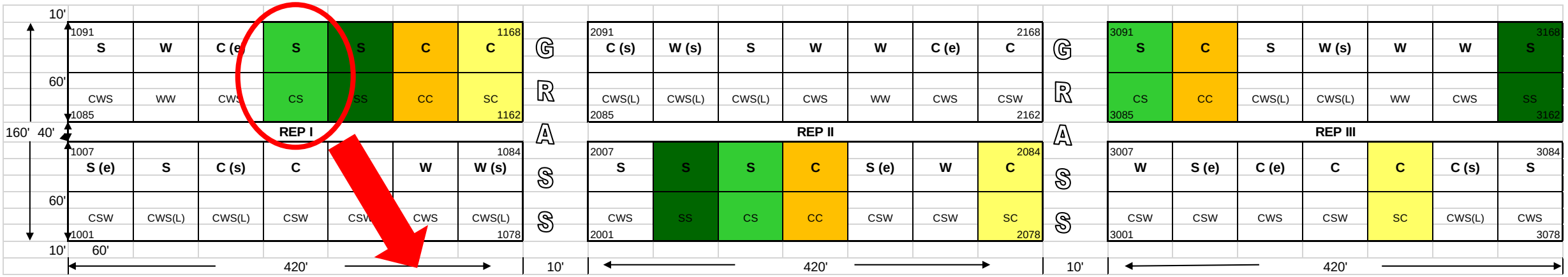
- Split-plots, established 2017

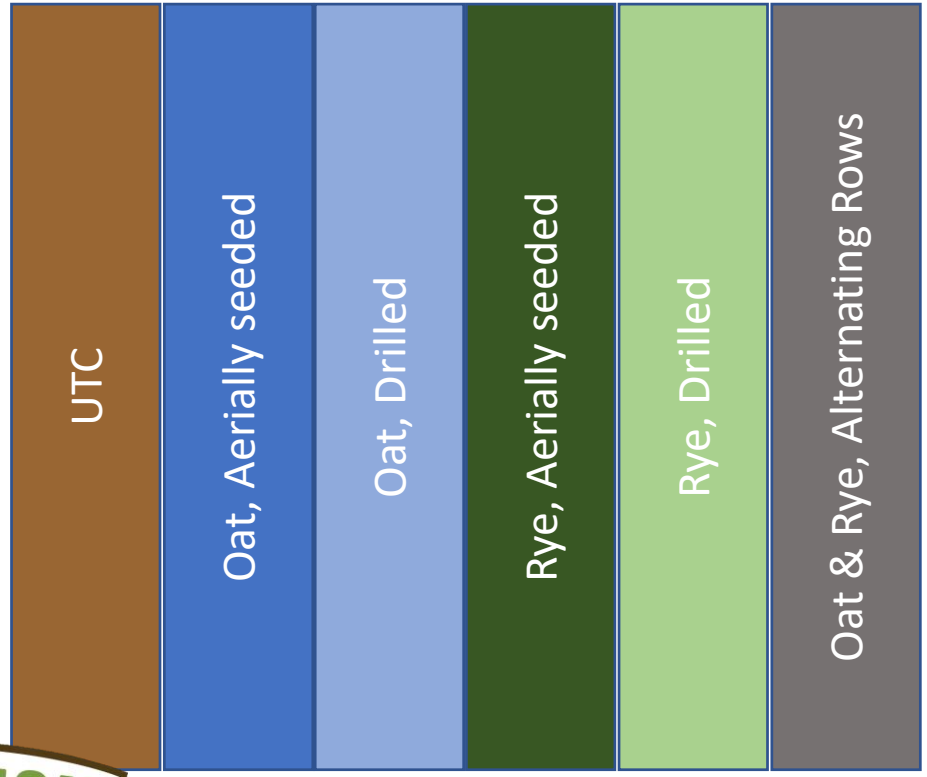
- Aerially seeded (September):
  - Cereal Rye (*Secale cereale*)
  - Oat (*Avena sativa*)

- Drilled post-harvest (October):
  - Cereal Rye (*Secale cereale*)
  - Oat (*Avena sativa*)
  - Oat/Rye alternate rows

- Untreated Control

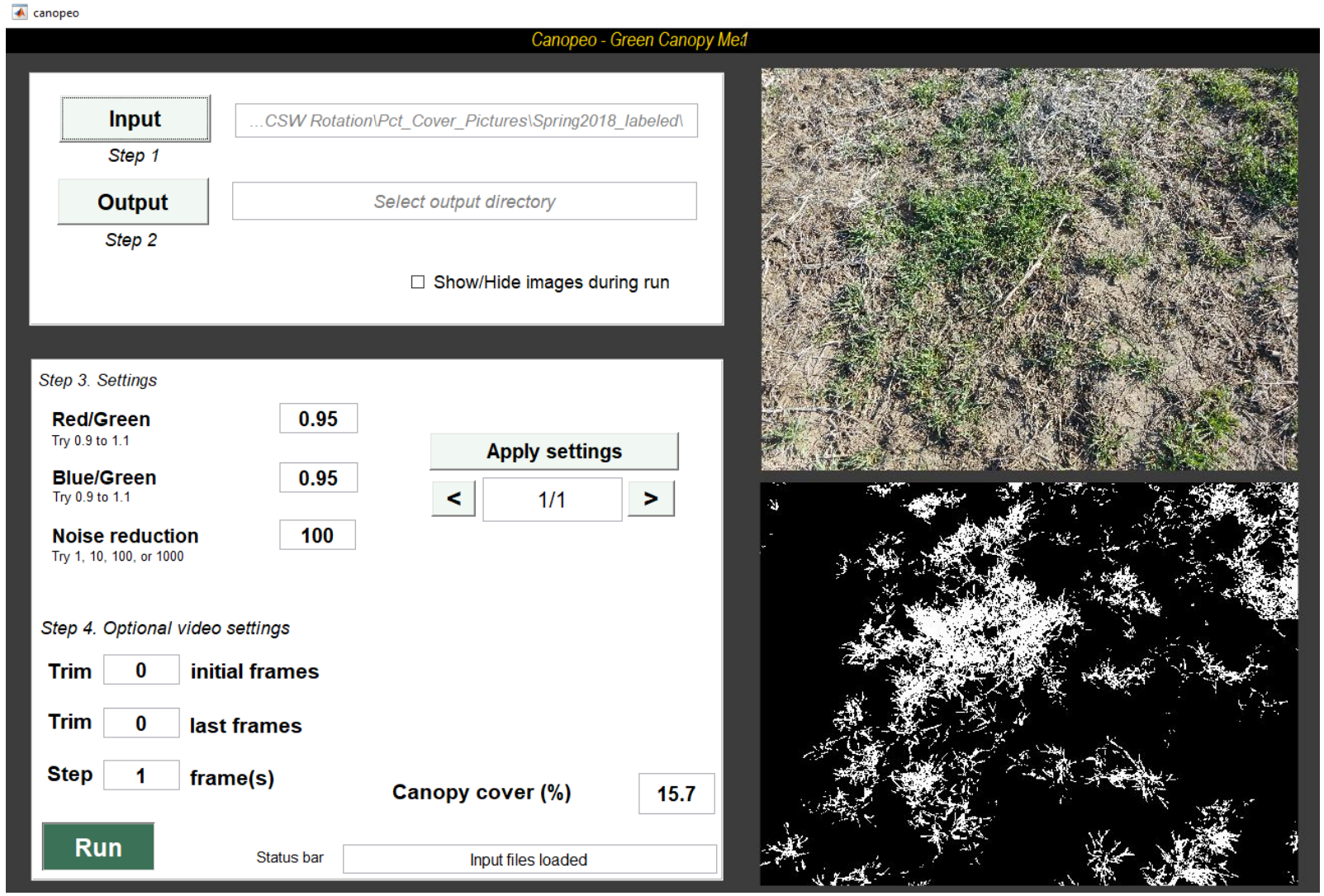



10'
160'
40'
60'
60'
10'
REP I
REP II
REP III
GRASS
1091 S W C (e) S S C 1168 C
CWS WW CWS CS SS CC SC
1085 1162
1007 S (e) S C (s) C W W (s) 1084
CSW CWS(L) CWS(L) CSW CSW CWS CWS(L)
1001 1078
2091 C (s) W (s) S W W C (e) C 2168
CWS(L) CWS(L) CWS(L) CWS WW CWS CSW
2085 2162
2007 S S S C S (e) W C 2084
CWS SS CS CC CSW CSW SC
2001 2078
3091 S C S W (s) W W S 3168
CS CC CWS(L) CWS(L) WW CWS SS
3085 3162
3007 W S (e) C (e) C C C (s) S 3084
CSW CSW CWS CSW SC CWS(L) CWS
3001 3078
420'
420'
420'


UTC
Oat, Aerially seeded
Oat, Drilled
Rye, Aerially seeded
Rye, Drilled
Oat & Rye, Alternating Rows
60 ft
10 ft

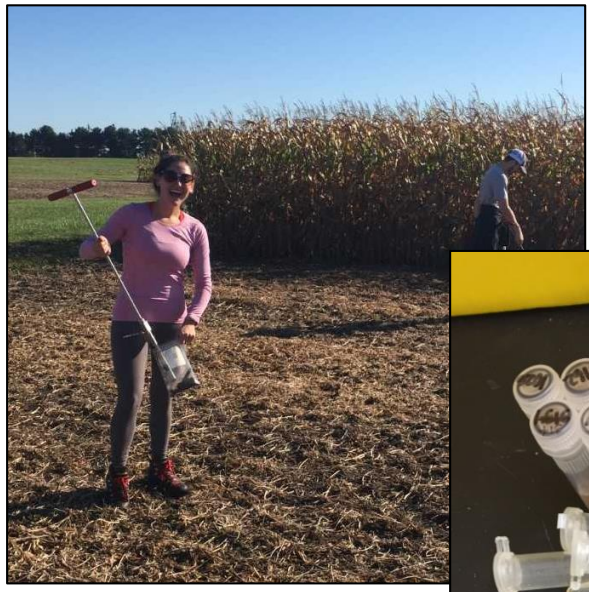
Methods: Cover Crop Percent Ground Cover

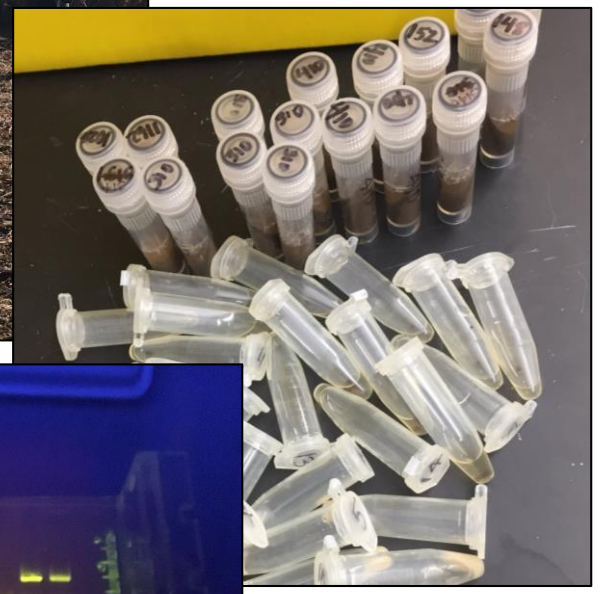
- Estimation of cover crop vigor
- Canopeo app
- Took photos:
  - Fall 2017 before frost
  - Spring 2018 before termination

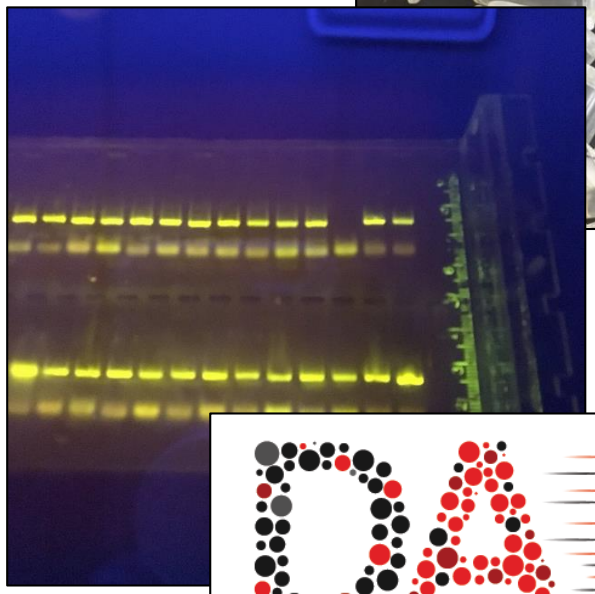


Methods: Microbiome

1. Collected bulk soil samples
   - Fall 2017 (Harvest)
   - Spring 2018 (Planting)
2. Extracted DNA
3. Sequenced V3V4 region of 16S gene
   - Bacterial barcode-like gene
   - Illumina MiSeq
4. Processed amplicon data
   - DADA2 package in R
   - CHTC







DADA2
Amplicon Sequencing. Exactly. Version 1.10

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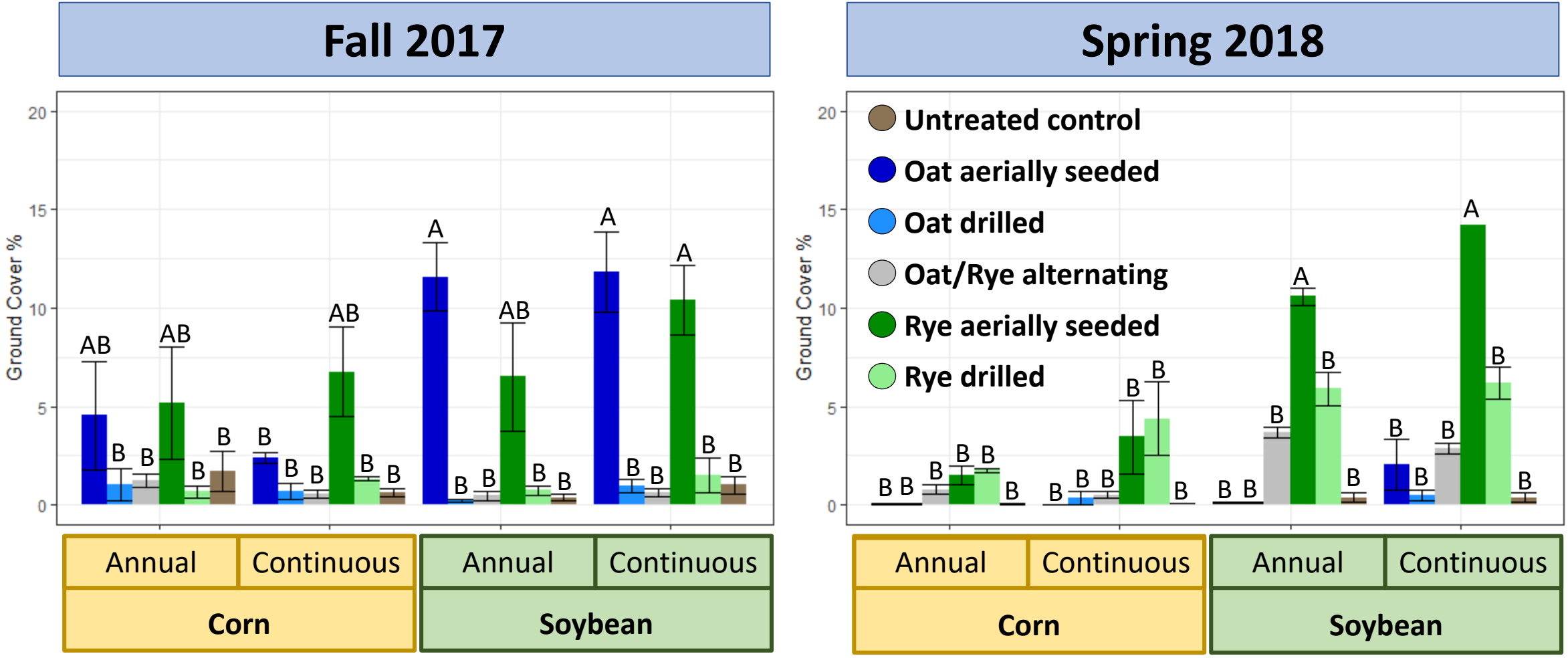
Limited cover crop growth in establishment year



Organic matter, pH, and nutrients have an impact on bacterial communities

Fall 2017		
	R^2	p-value
pH	0.08	0.001
OM %	0.05	0.001
P	--	0.555
K	0.03	0.008
NH_4	--	0.050
NO_3	0.03	0.002

Spring 2018		
	R^2	p-value
pH	0.12	0.001
OM %	0.08	0.001
P	0.02	0.023
K	0.03	0.010
NH_4	0.03	0.005
NO_3	0.06	0.001

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