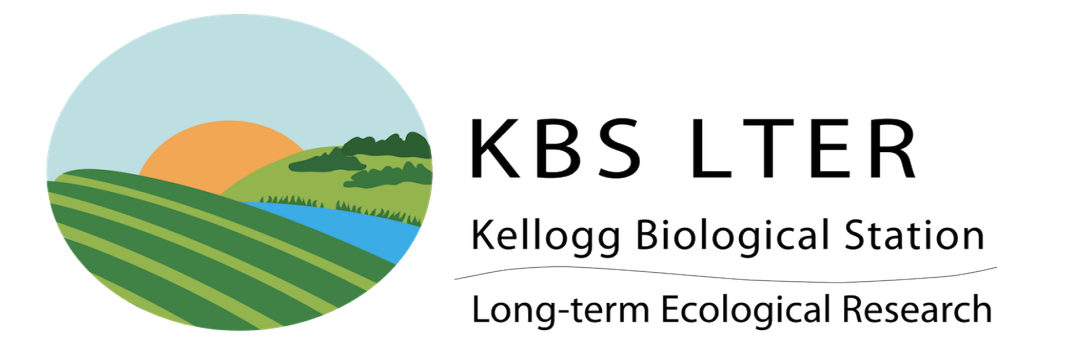# Microbial community composition of wheat among four land management strategies

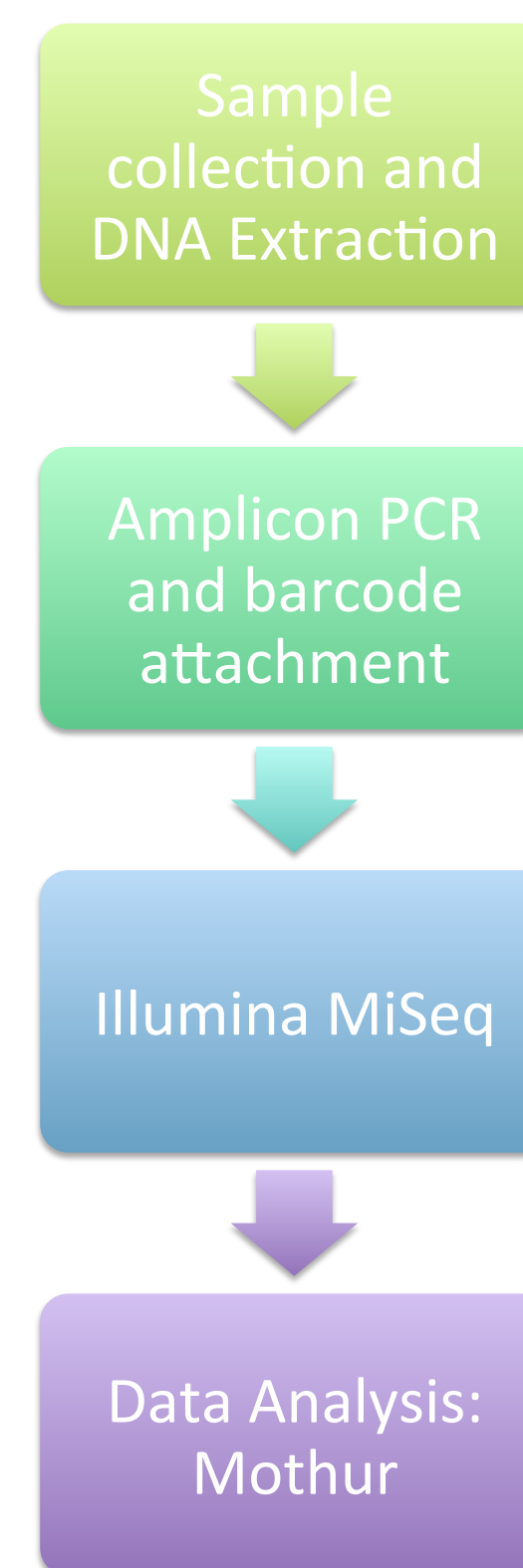Kristi Gdanetz MacCready[1] and Frances Trail[1,2]

[1]Department of Plant Biology, [2]Department of Plant, Soil and Microbial Sciences, Michigan State University, 612 Wilson Rd, East Lansing, MI, 44824.
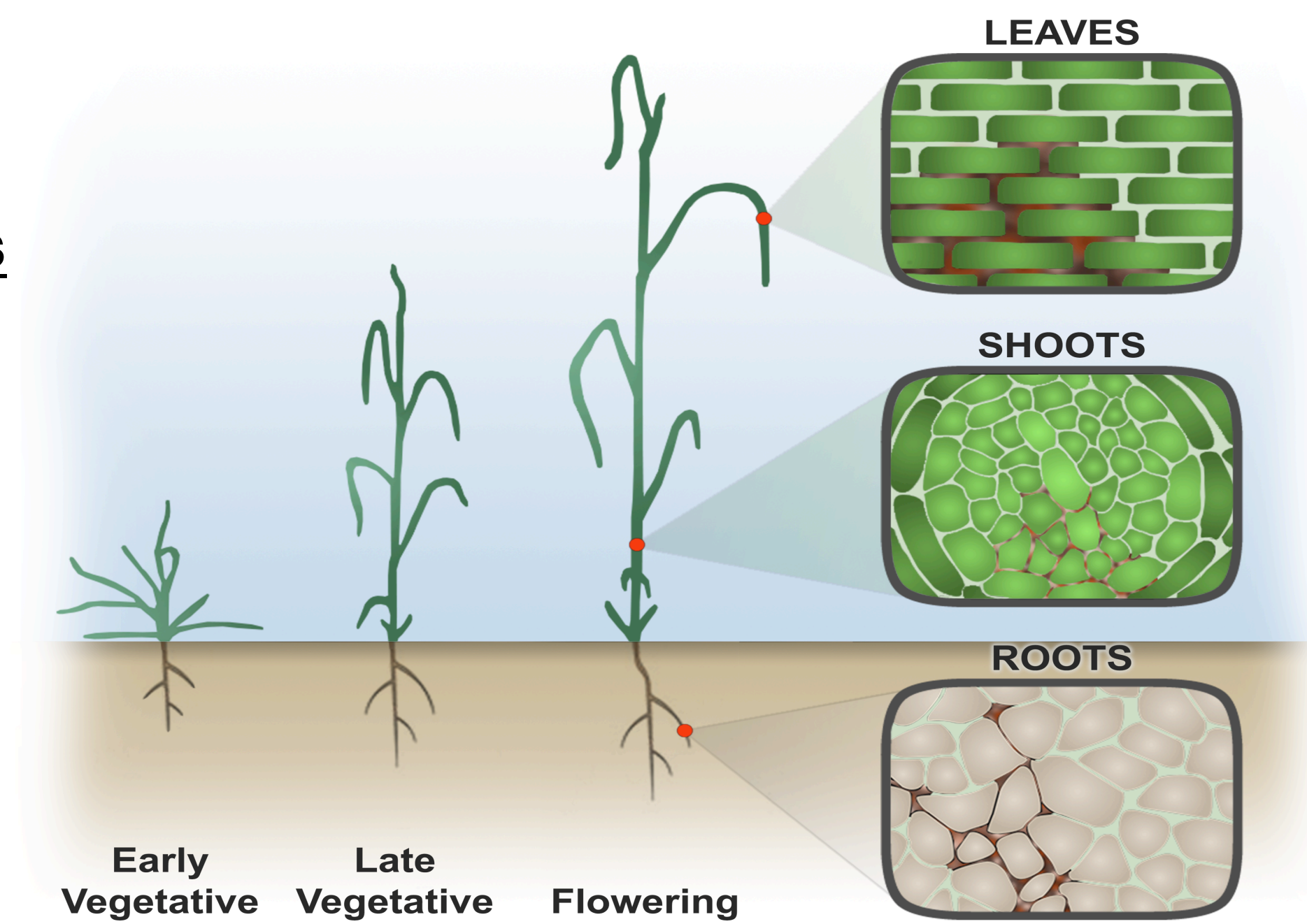
Introduction:

Recent research has indicated that the microbes associated with a crop can influence the crop's susceptibility to disease. Several studies have been conducted to investigate the differences in rhizosphere microbiota between crops or land management strategies, but less information is known about the microbiota inhabiting the vegetative tissues of plants. The wheat fungal and bacterial phytobiome composition was assessed using plants from the Kellogg Biological Station Long-Term Ecological Research wheat/ maize/soybean crop rotation site. Barcoded primers were used to tag samples from four land management strategies (conventional till, no-till, reduced nitrogen input, or organic), three growth stages (vegetative, flowering, senesced), and three tissue types (leaf, stem, or root). The outcome of this study will describe the tissue-specific communities associated with each plant developmental stage and across all land management strategies. In the future hope to combine these data with disease incidence data to determine if there is a disease-associated phytobiome.

Workflow:

Sample collection and DNA Extraction

Amplicon PCR and barcode attachment

Illumina MiSeq

Data Analysis: Mothur

Plot Treatment Abbreviations

Conventional till	Trt 1
No-till	Trt 2
Low Input	Trt 3
Organic	Trt 4

Outline of sample processing and workflow (Left). Samples were collected from the KBS LTER Main Cropping Rotation Site. Three tissues and three stages of wheat development were sampled (Right).
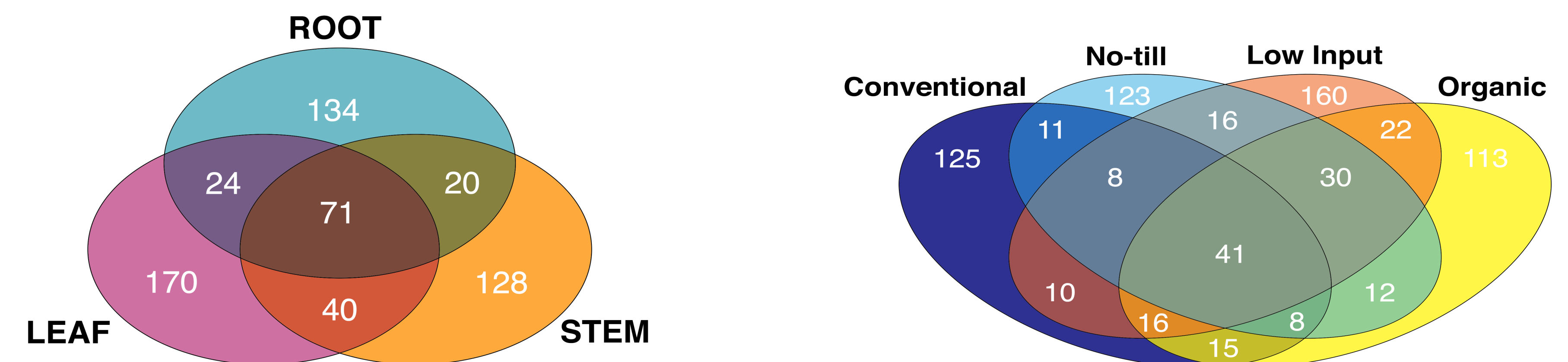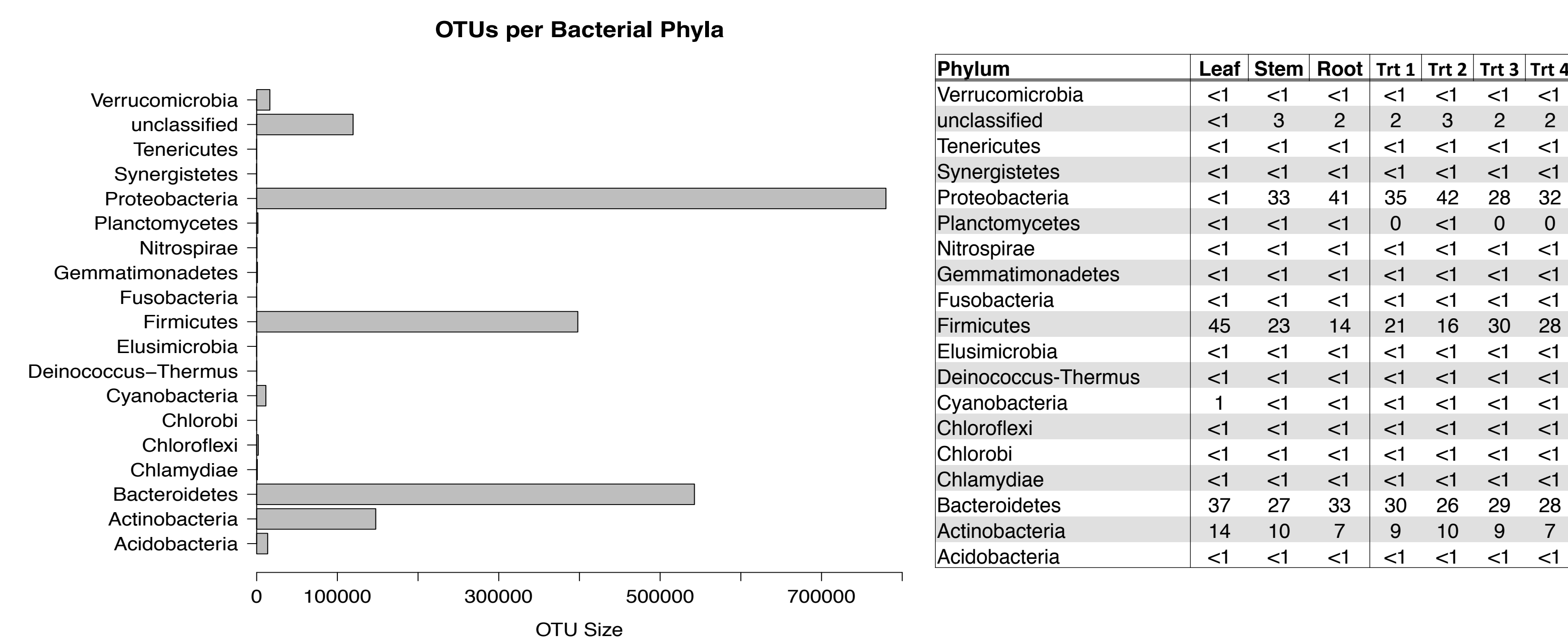
Results:

Phylum	Leaf	Stem	Root	Trt 1	Trt 2	Trt 3	Trt 4
Verrucomicrobia	<1	<1	<1	<1	<1	<1	<1
unclassified	<1	3	2	2	3	2	2
Tenericutes	<1	<1	<1	<1	<1	<1	<1
Synergistetes	<1	<1	<1	<1	<1	<1	<1
Proteobacteria	<1	33	41	35	42	28	32
Planctomycetes	<1	<1	<1	0	<1	0	0
Nitrospirae	<1	<1	<1	<1	<1	<1	<1
Gemmatimonadetes	<1	<1	<1	<1	<1	<1	<1
Fusobacteria	<1	<1	<1	<1	<1	<1	<1
Firmicutes	45	23	14	21	16	30	28
Elusimicrobia	<1	<1	<1	<1	<1	<1	<1
Deinococcus−Thermus	<1	<1	<1	<1	<1	<1	<1
Cyanobacteria	1	<1	<1	<1	<1	<1	<1
Chloroflexi	<1	<1	<1	<1	<1	<1	<1
Chlorobi	<1	<1	<1	<1	<1	<1	<1
Chlamydiae	<1	<1	<1	<1	<1	<1	<1
Bacteroidetes	37	27	33	30	26	29	28
Actinobacteria	14	10	7	9	10	9	7
Acidobacteria	<1	<1	<1	<1	<1	<1	<1

Figure 1. Total number of OTUs recovered from different bacterial phyla (Left). Percentage of OTUs from a specific phylum found within each tissue or treatment (Right).

Figure 2. Shared unique OTUs between plant tissue type or between four plot treatments.

Figure 3. Clustering of individual OTUs (red) and segregation to communities (polygons).

Table 1. AMOVA significance of clustering visualized in NMDS plots.

Tissue Source	Degrees of Freedom	Mean Square	F-statistic	Significance
Leaf-Root-Stem	95	0.195119	16.4387	<0.001*
Leaf-Root	63	0.192187	24.0671	<0.001*
Root-Stem	63	0.197875	19.5358	<0.001*
Leaf-Stem	63	0.195296	5.79374	0.003*
Treatment Source	**Degrees of Freedom**	**Mean Square**	**F-statistic**	**Significance**
Conventional-Low-input-No-till-Organic	95	0.249762	2.11263	0.024*
Conventional-No-till	59	0.274714	1.13644	0.33
Conventional-Low-input	53	0.260614	3.51423	0.014
Conventional-Organic	53	0.250701	2.86683	0.036
No-till-Organic	41	0.235655	1.84793	0.109
Low-input-No-till	41	0.248542	1.74771	0.16
Low-input-Organic	35	0.207198	1.1304	0.335

Conclusions:

- Communities were dominated by several different phyla.
- Few unique OTUs were shared by all tissues or treatments.
- Communities segregated by tissue type, each significantly different from the others.
- No clear clustering of communities by plot treatment was observed.
- Management strategies of wheat crops do not have an impact on community similarity. Host plant tissue type is a stronger influence on community structure.