

beneficial plant-microbial interactions in agroecosystems: deciphering the rhizosphere microbial community in two field grown crops

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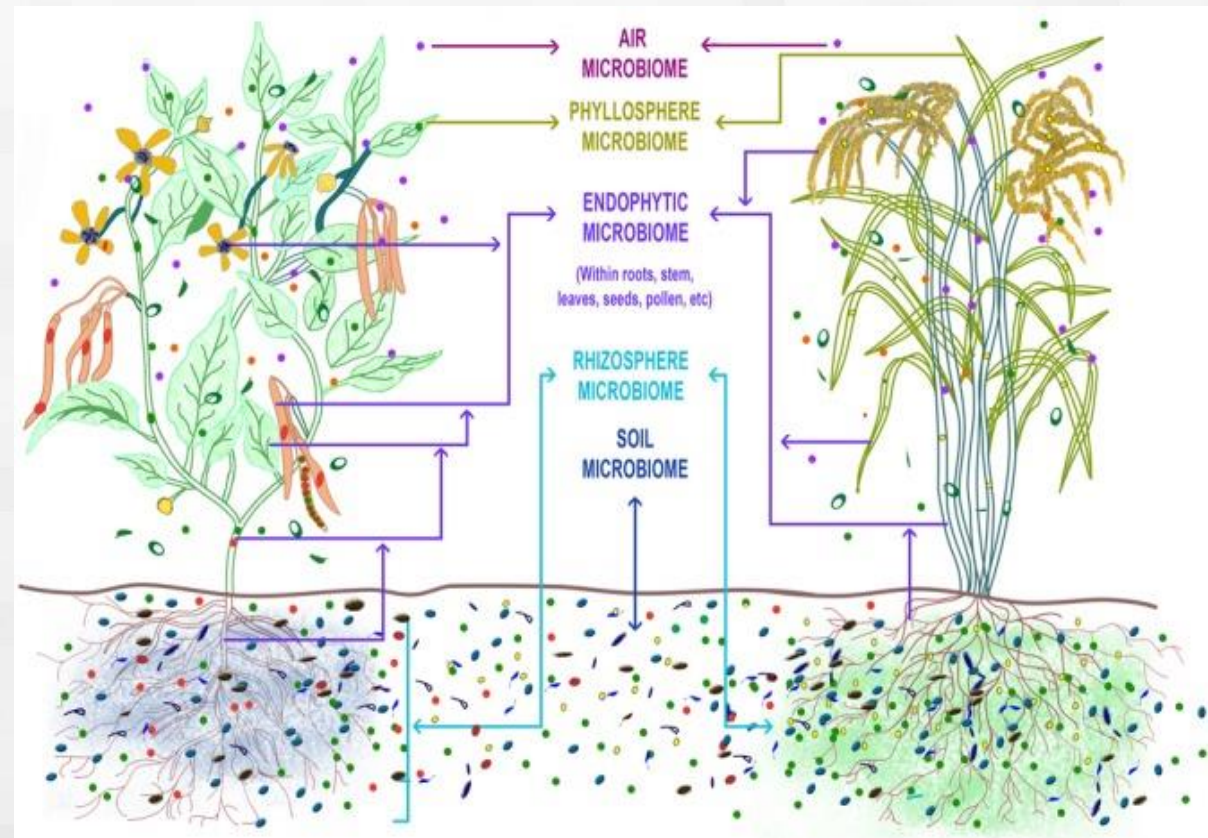
Canola Lines Show Variation in Selecting their Rhizosphere Bacterial Members

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Introduction

Plant Microbiome

- Rhizosphere
- Alter soil microbes
- Source of genetic variability



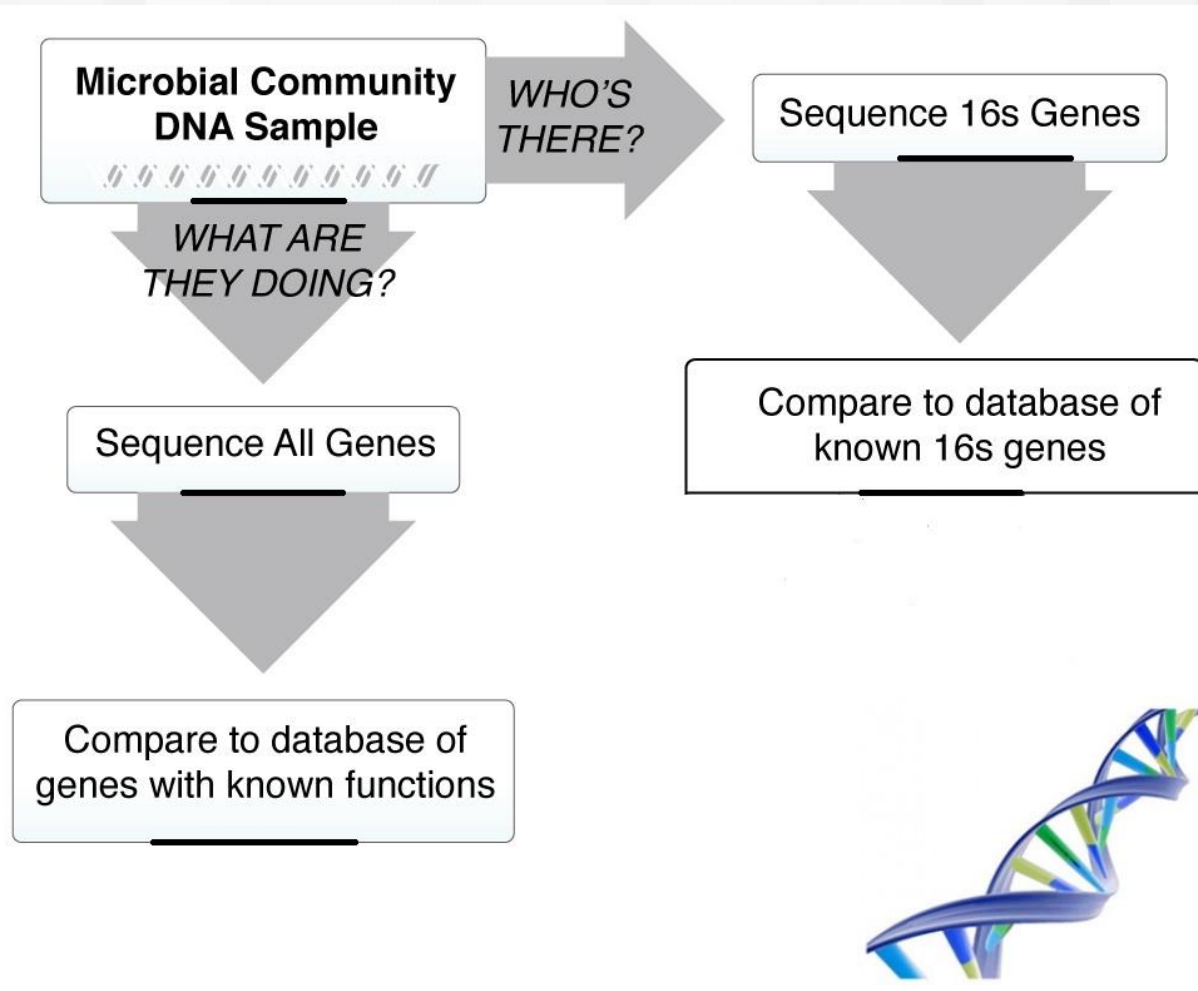
Objectives

- Characterize the core microbiome of *Brassica napus* (Canola).
- Identify bacterial taxa (SNVs) that are differentially abundant among Canola lines.

Methods

How are microbes studied?

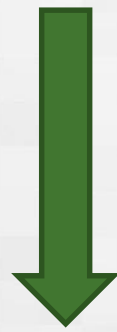
- DNA sequencing
- Samples
- Extraction
- “Universal primers”
- Amplify 16S rRNA
- Gene
- NG Sequencing
- Match to a database



Methods

Processing raw sequence reads

Sequencing Data – High-throughput



Trimomatic (Bolger et al., 2014)

Cutadapt (Marcel, 2011)

DADA2 (Callahan et al., 2016)

Sequence (SNV) and Taxonomy table

Methods

Experimental Design

- Experimental site : Llewelyn Farm near Saskatoon, SK
 - Oilseed ... wheat ... barely ... and fallow
 - Sixteen canola (*Brassica napus*) lines
 - Design: RCBD with three blocks + three reps
 - Sampling: weekly for ten weeks
- 

Methods

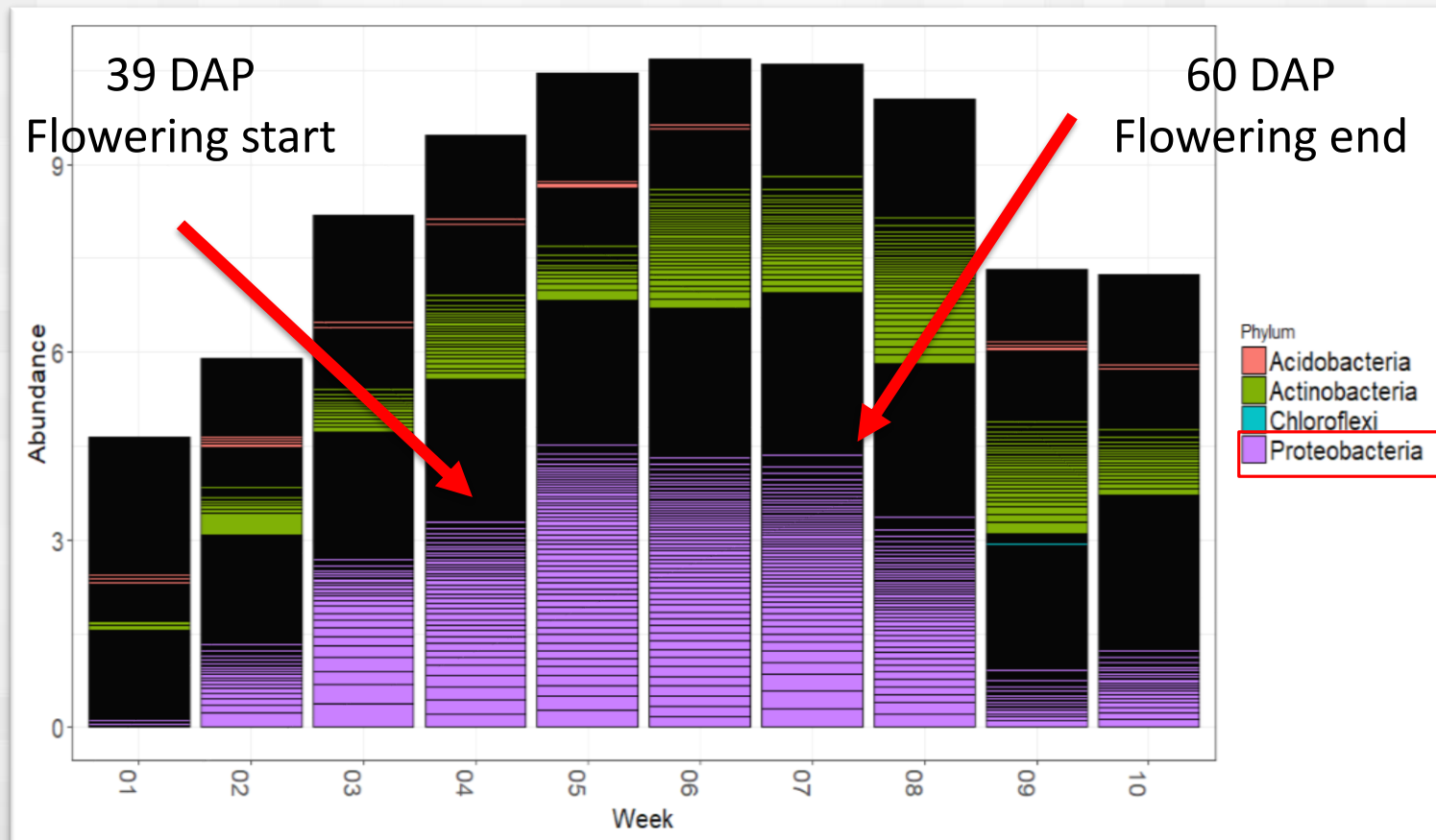
Statistical Analysis

- Core Microbiome:
 - Phyloseq R package (McMurdie and Holmes, 2013)
 - Microbiome R package (Leo et al., 2017)
 - Detection threshold of 0.1 and prevalence 50 to 95 %
- Differential abundance
 - DESEQ2: phyloseq extention (Love, Huber, and Anders 2014)
 - Generalized linear model with negative binomial distribution
 - False discovery rate of 1% (alpha value of 0.01)
 - P value :Benjamini-Hochberg (BH) adjustment (Benjamini and Hochberg 1995)

Results

Major Bacterial Taxa in Canola Rhizosphere

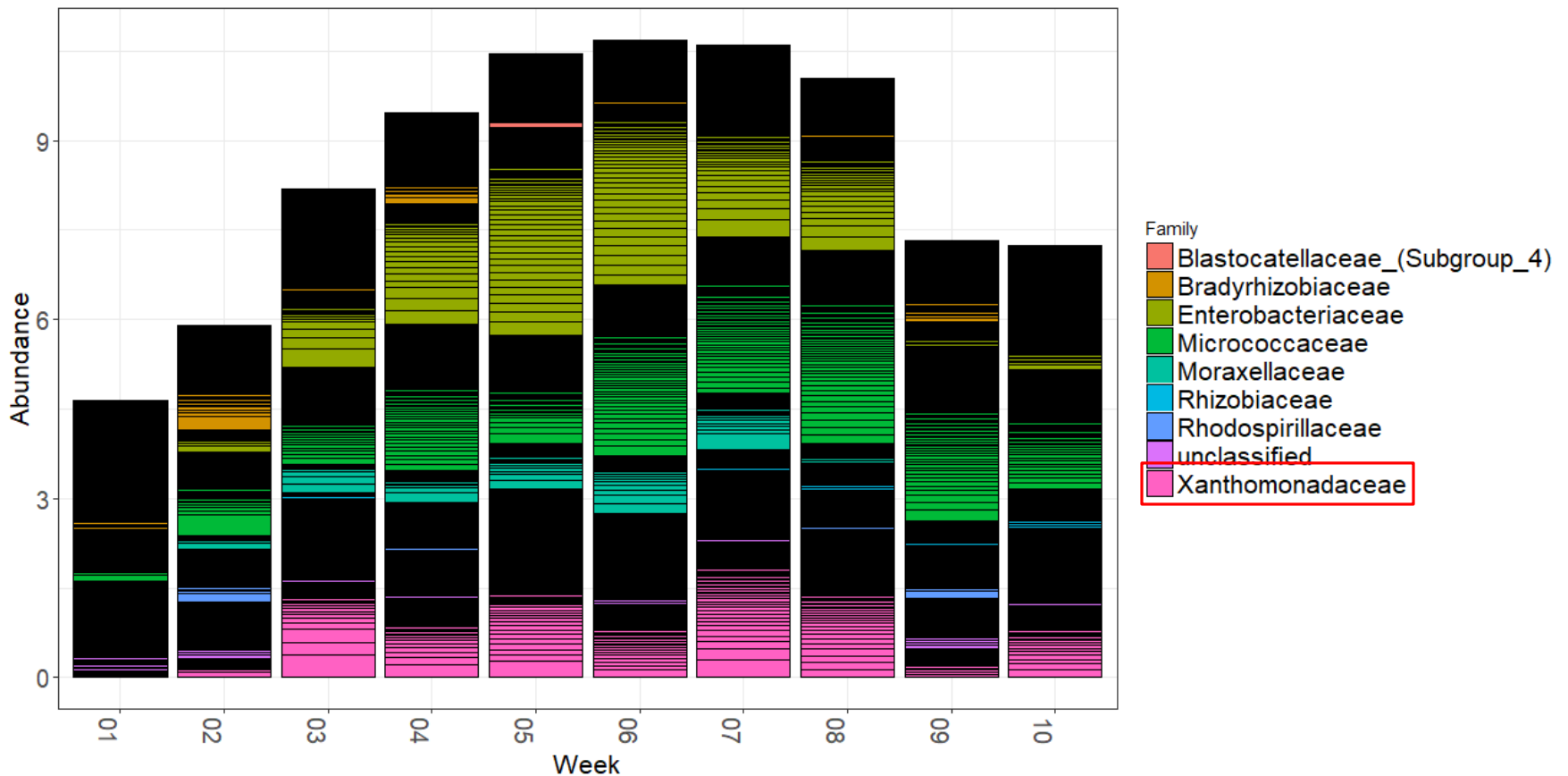
- 49526 taxa in 6 taxonomic ranks



Results

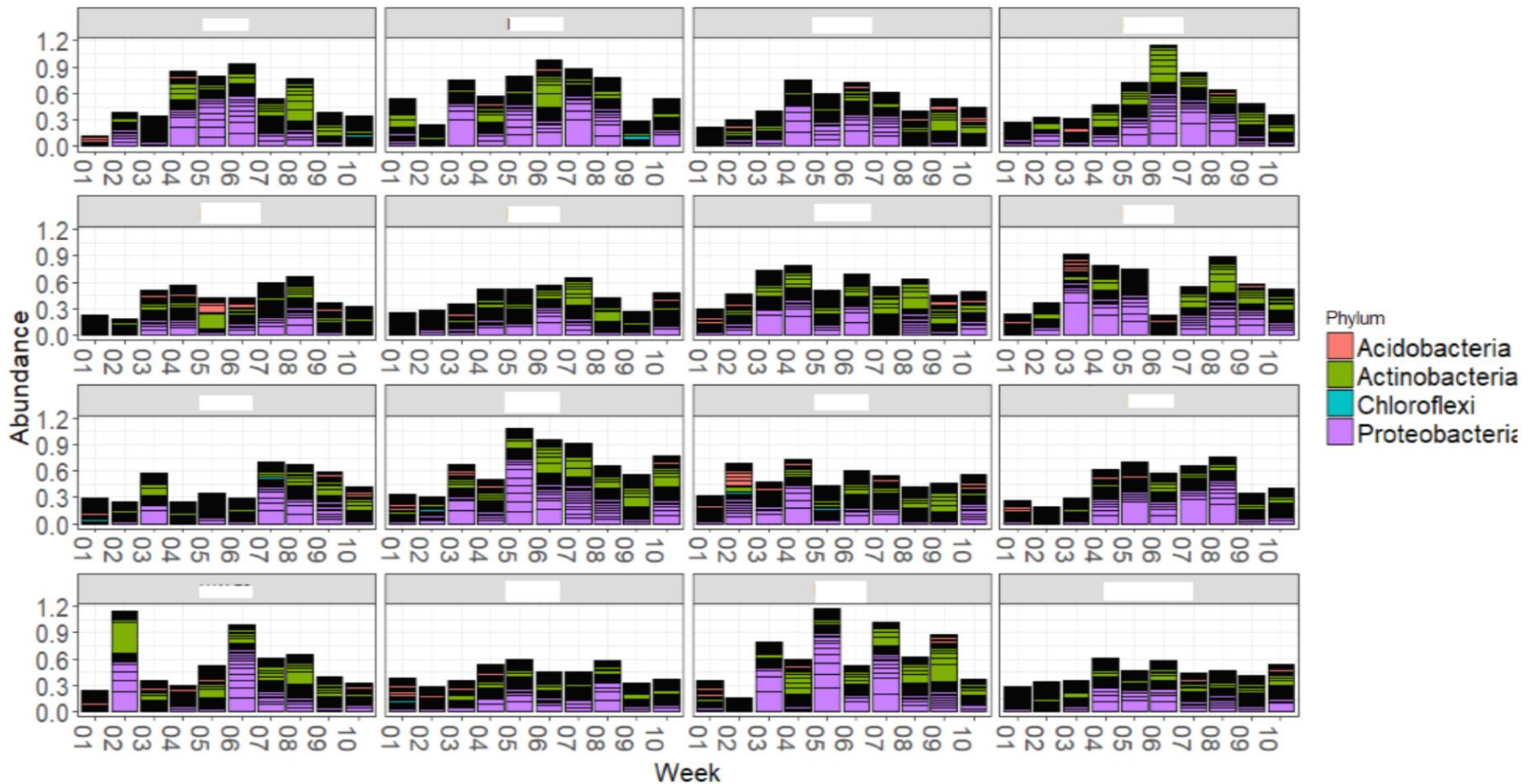
Major Bacterial Taxa in Canola Rhizosphere

- 49526 taxa in 6 taxonomic ranks



Results


Major Bacterial Taxa in Canola Rhizosphere by Canola Line



Results

Core Microbiome of Canola

- Of observed 49526 taxa




Prevalence	50	60	65	75	80	85	90	95
# Core taxa	39	23	16	8	5	4	2	1

- At 90%:
 - Pseudarthrobacter (Actinobacteria)
 - Bradyrhizobium (Proteobacteria)

Results

Core Microbiome of Canola (75%)



Phylum	Genus
Proteobacteria	Stenotrophomonas
Proteobacteria	Bradyrhizobium
Proteobacteria	Skermanella
Proteobacteria	Skermanella
Actinobacteria	Pseudarthrobacter
Actinobacteria	Arthrobacter
Actinobacteria	unclassified
Acidobacteria	unclassified

Results

Core Microbiome of Canola



Core Microbiome

Co-occurrence Pattern

Microbial hub

Result

Differential Abundant Bacterial Taxa

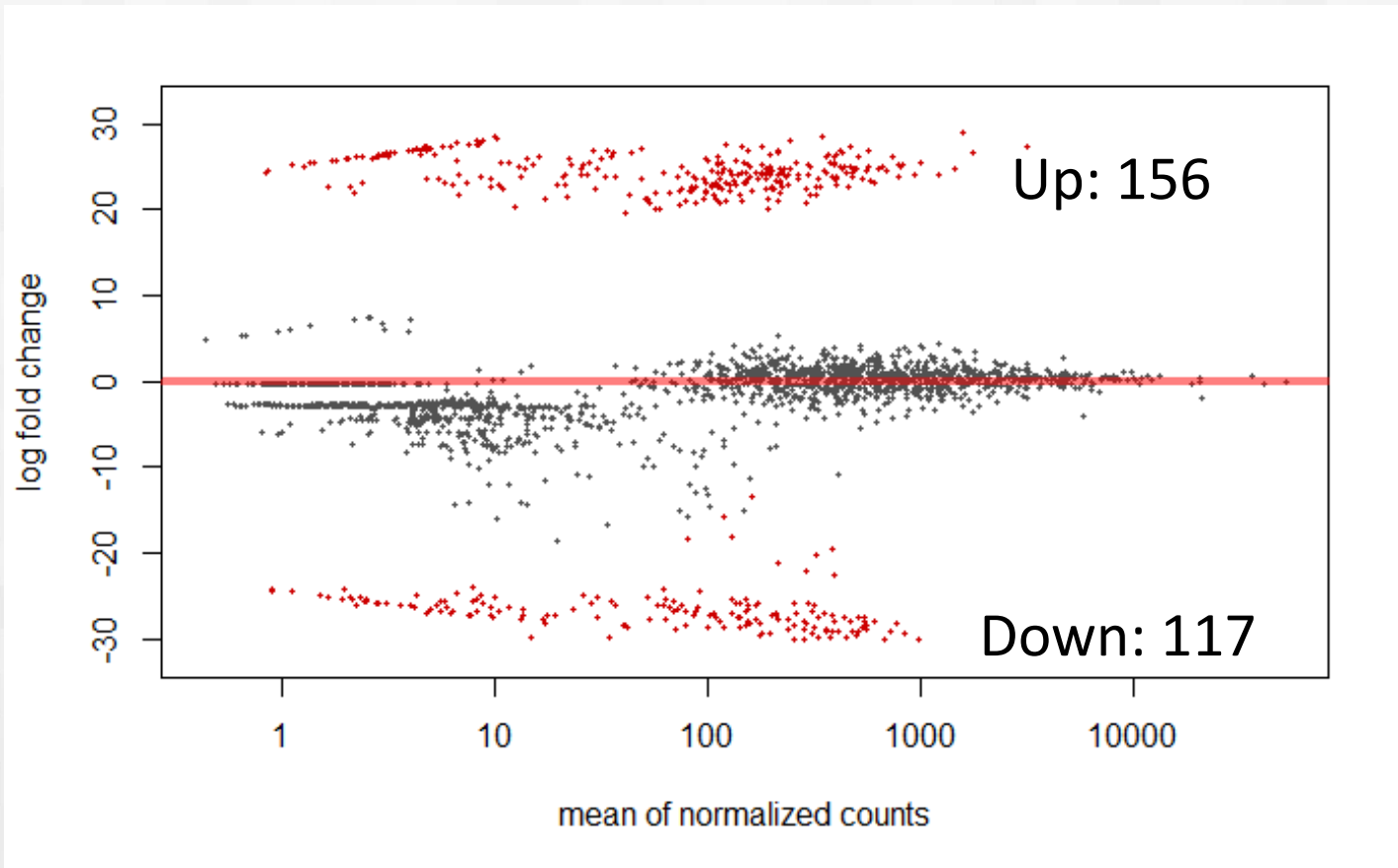
- Number of differentially abundant taxa in fifteen Canola lines compared with the reference line
- False discovery rate of 1% (Adj. p value < 0.01)

	L2	L3	L4	L5	L6	L7	L8	L9	L10	L11	L12	L13	L14	L15	L16
L1	273	476	193	375	223	214	274	239	220	274	226	230	244	279	204

Result

Differential Abundant Bacterial Taxa

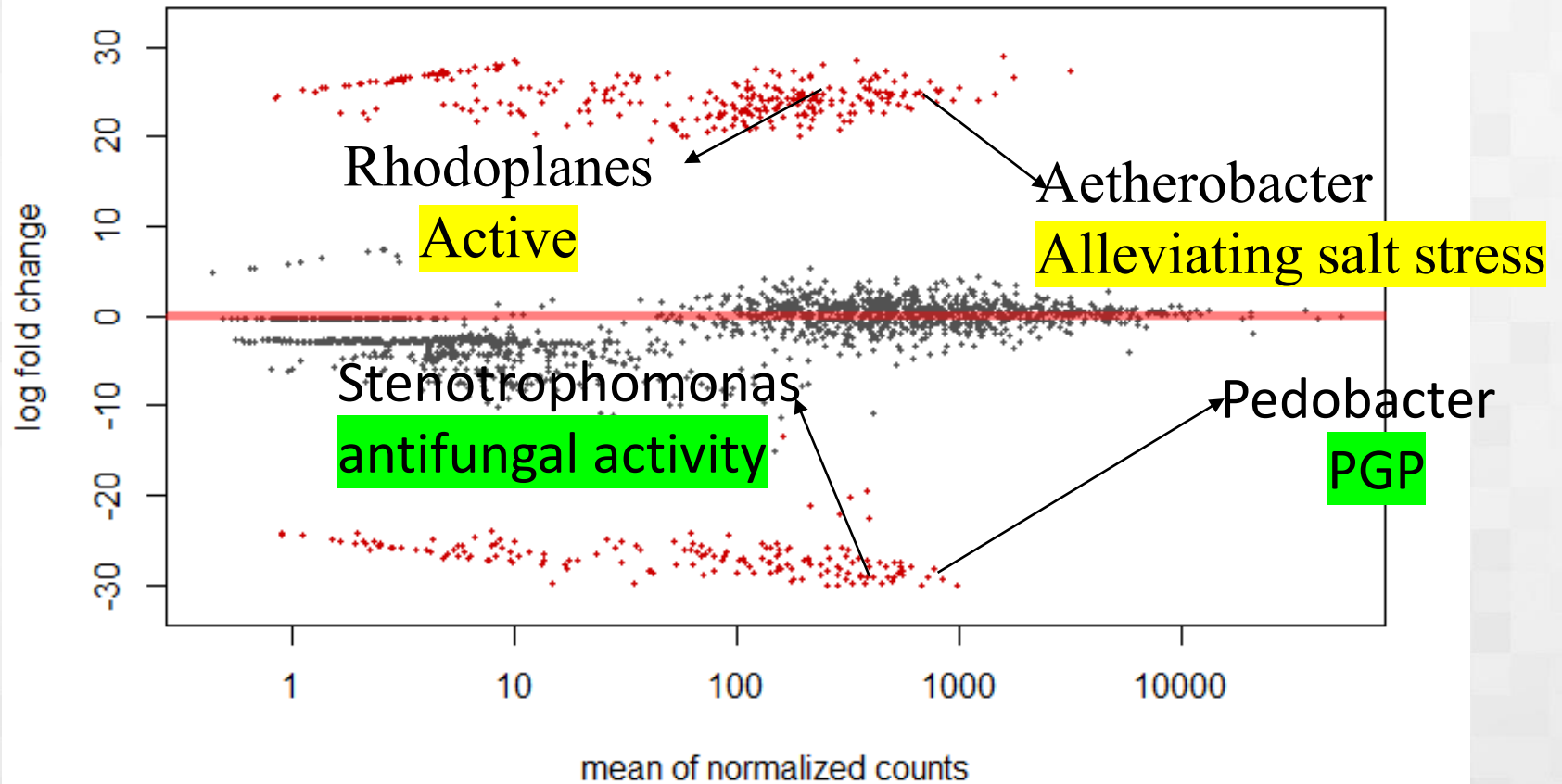
- Significantly differential abundant bacterial taxa in Line 2 at a false discovery rate of 1 %



Result

Differential Abundant Bacterial Taxa

- Significantly differential abundant bacterial taxa in Line 2 at a false discovery rate of 1 %



Take Home Message

- Rhizosphere Microbiome can be potential source of genetic variability need for breeding the next generation Canola varieties.

THANK YOU



Questions?