

exploitation of the plant  
**microbiome**  
for sustainable agriculture

[ Rodrigo Mendes | December 2019 ]



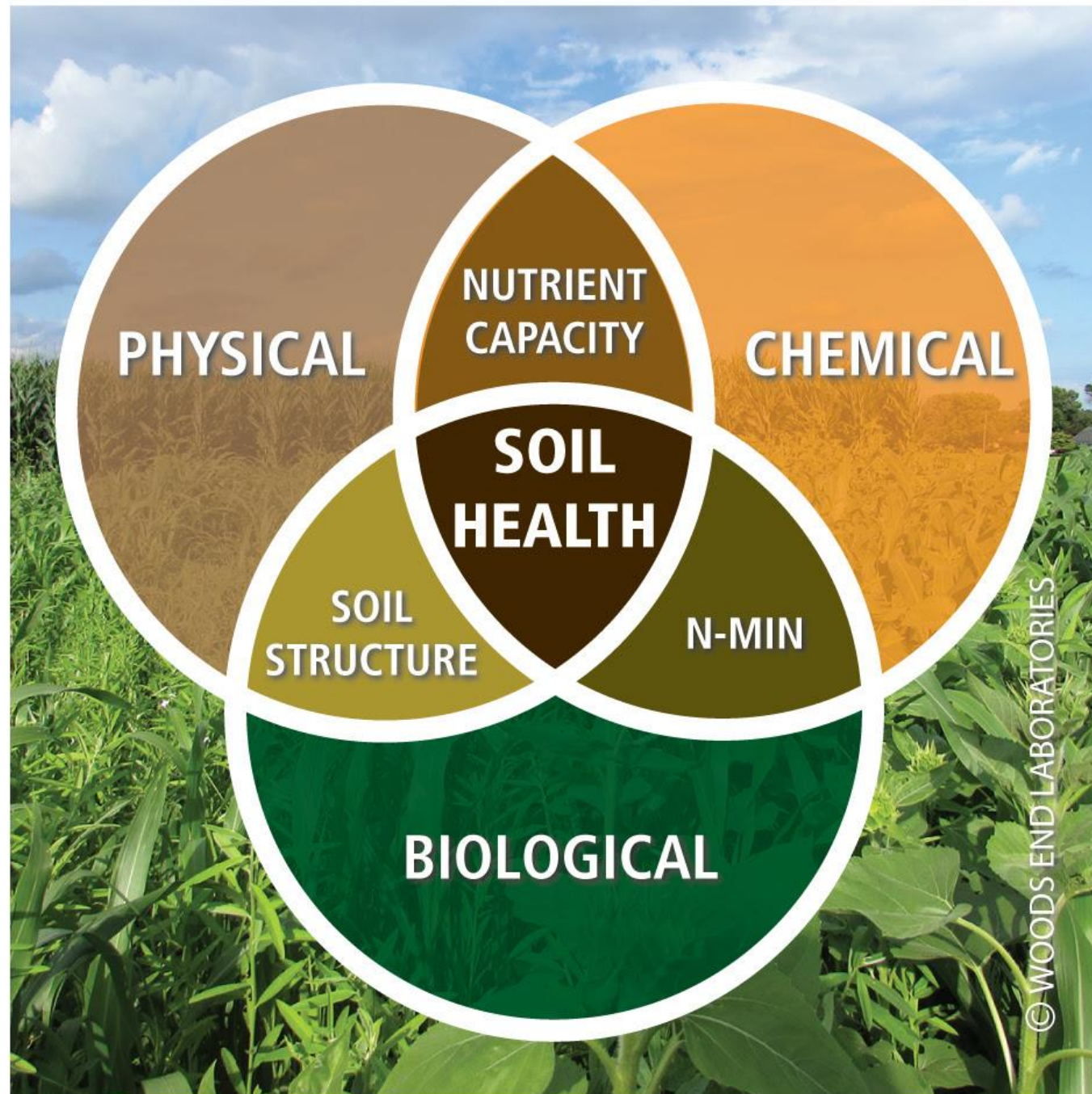
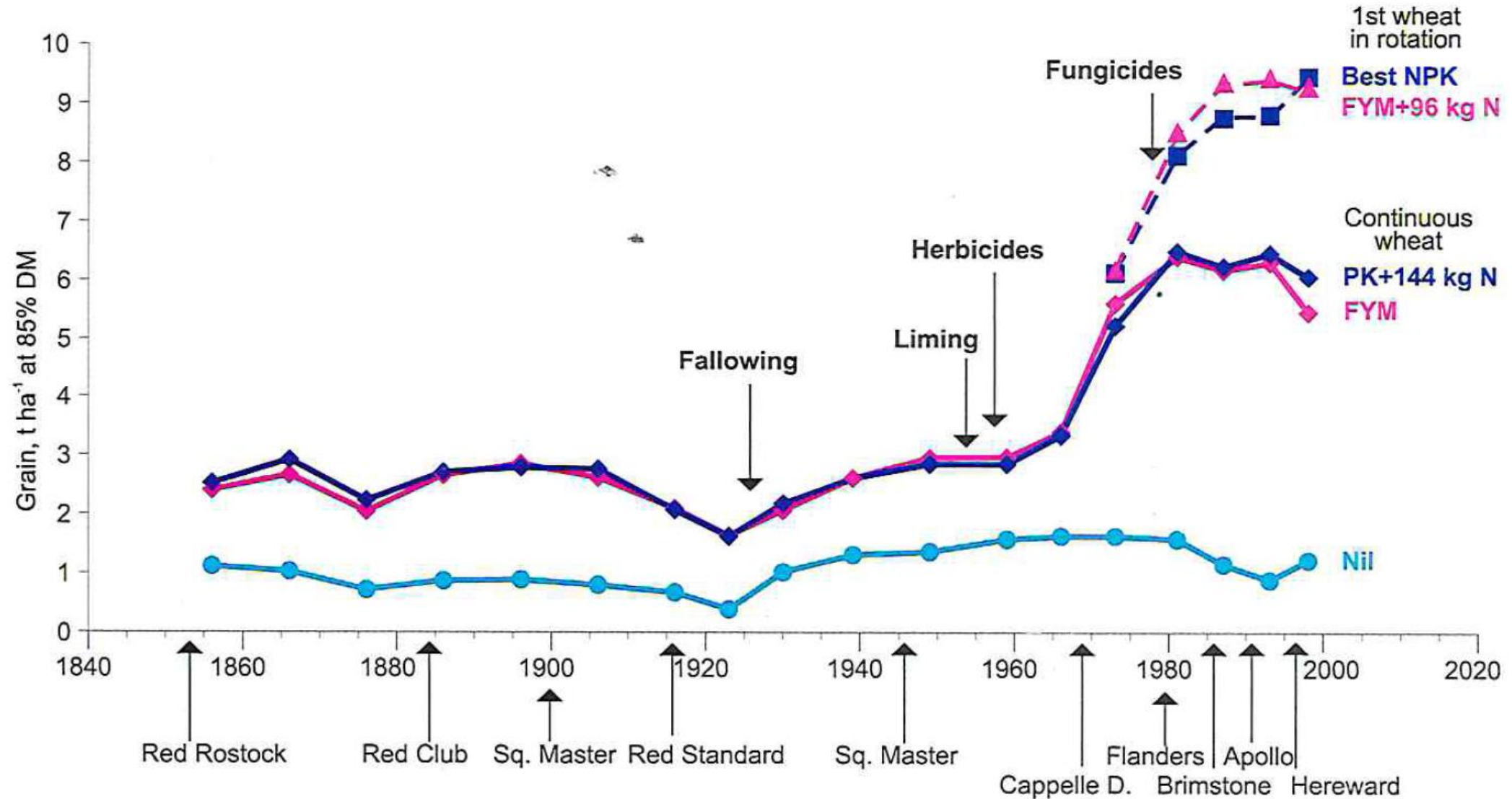




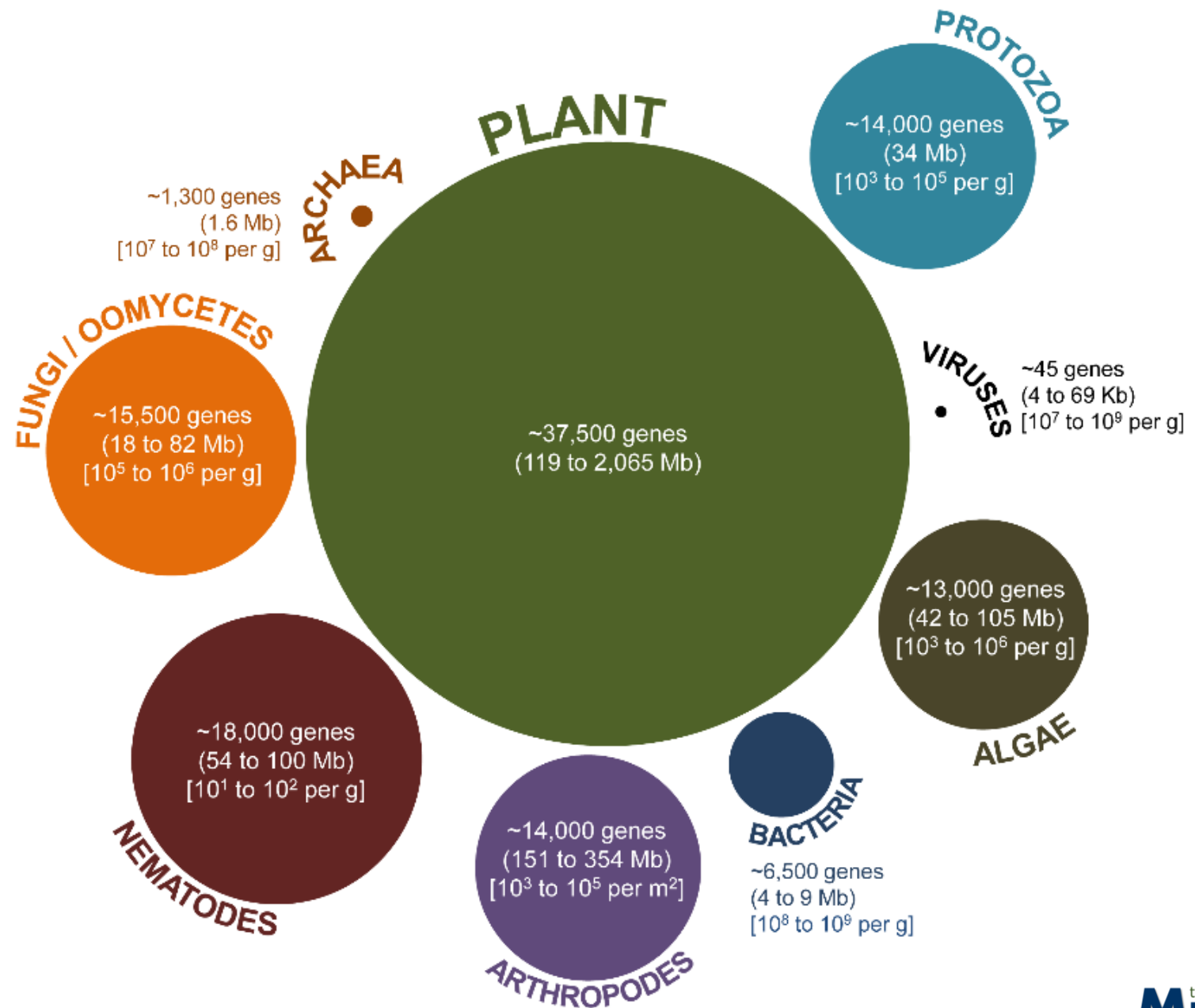




Fig.1 Broadbalk. Mean yields of wheat grain, and changes in husbandry

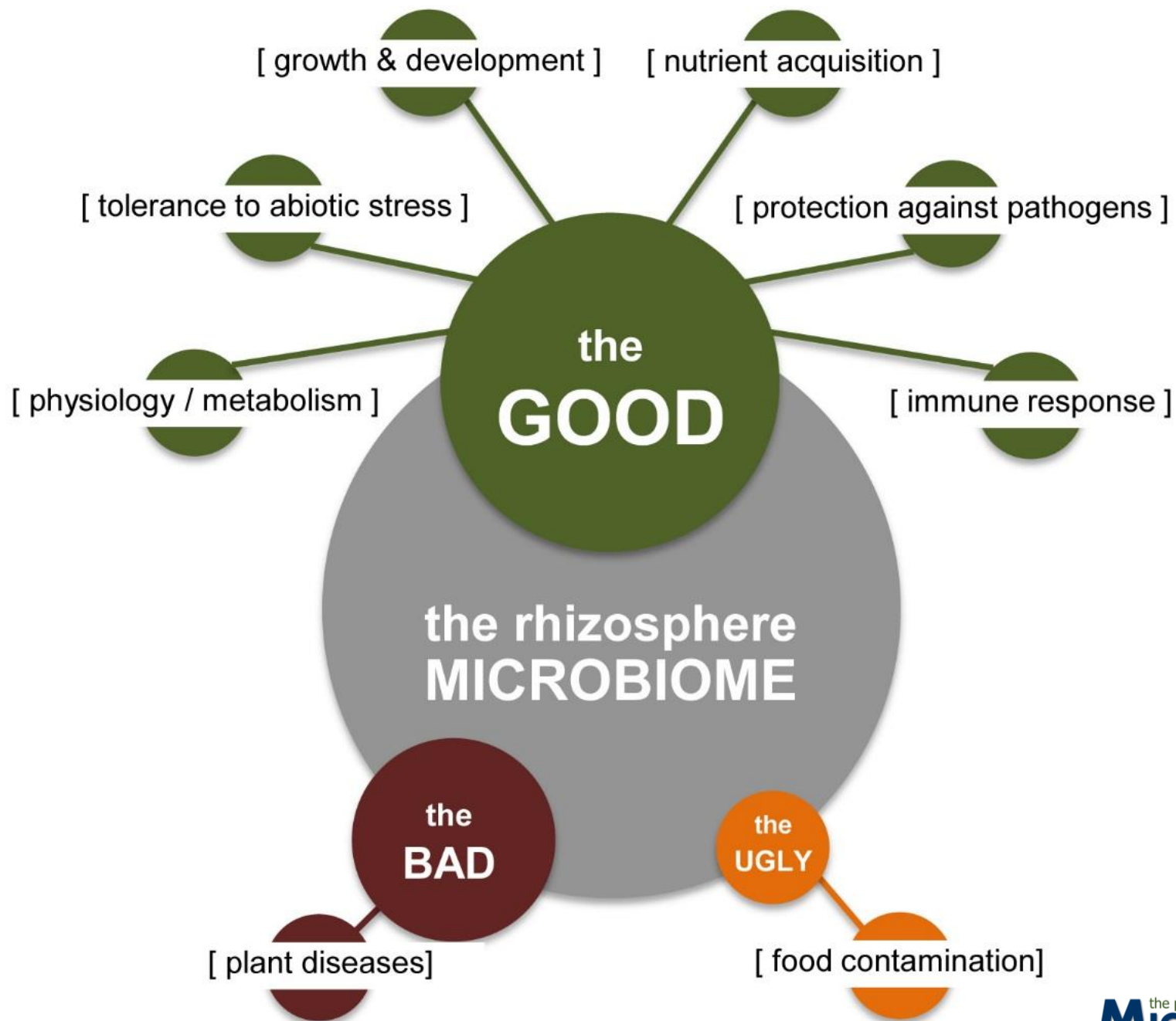
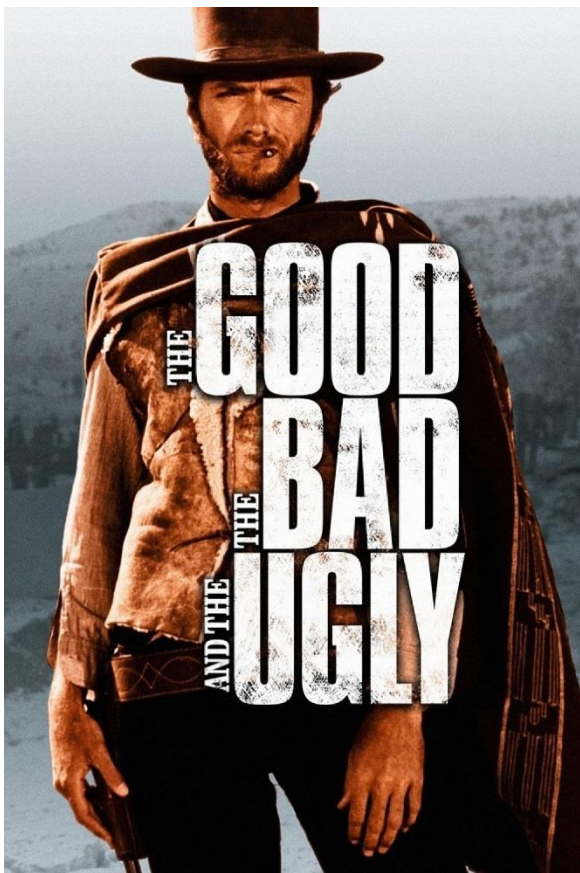




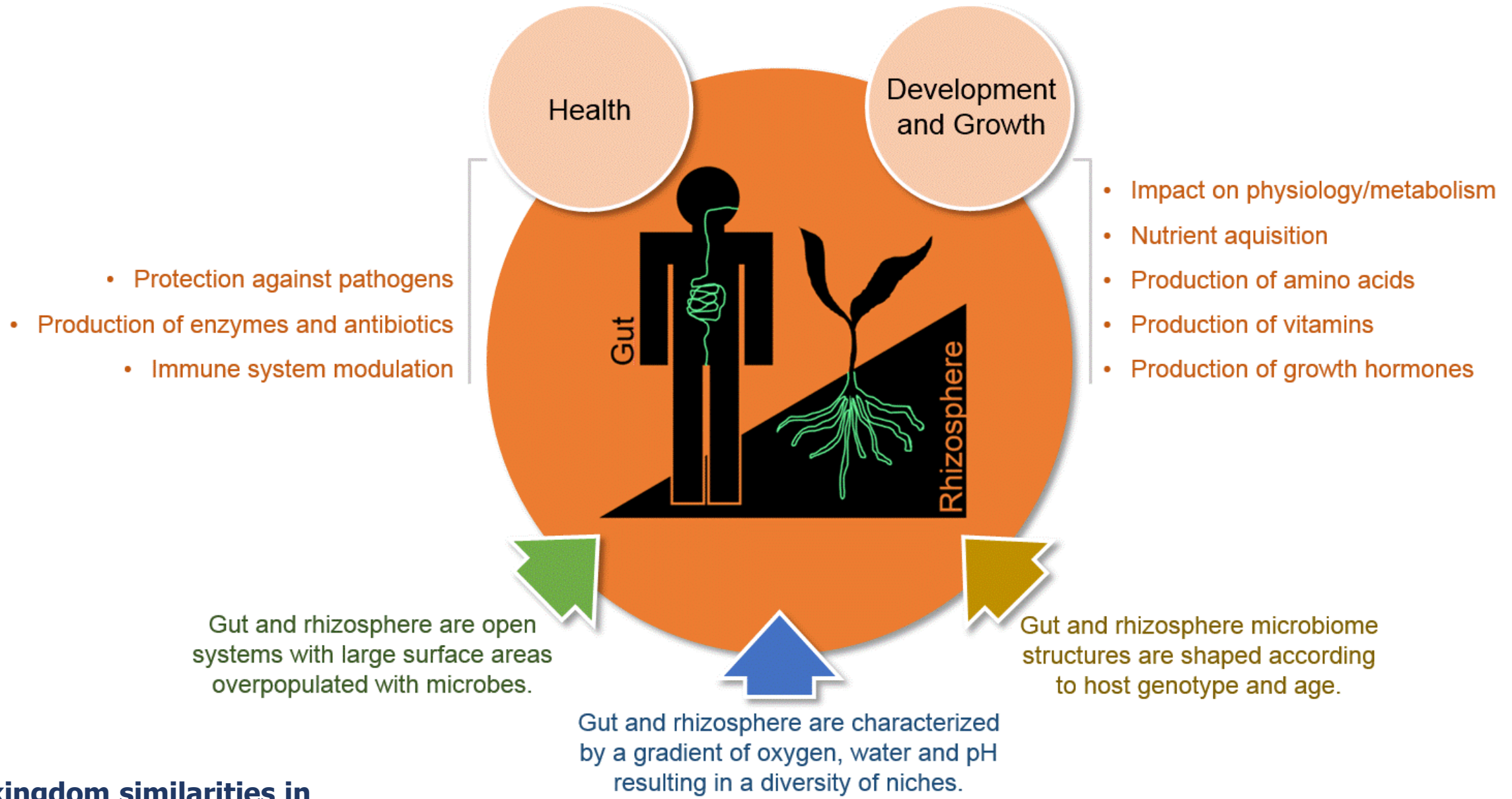


**The rhizosphere microbiome:  
significance of plant beneficial,  
plant pathogenic, and human  
pathogenic microorganisms**

[ Mendes et al., FEMS Microbiol Rev 2013 ]







## Cross-kingdom similarities in microbiome functions

[ Mendes & Raaijmakers, ISME J 2015 ]



[ see Turnbaugh et al., Nature 2006 ]



ASSUMPTIONS

**Superorganism**  
**Outsourced** **Microbiome**  
**services** **modulation**



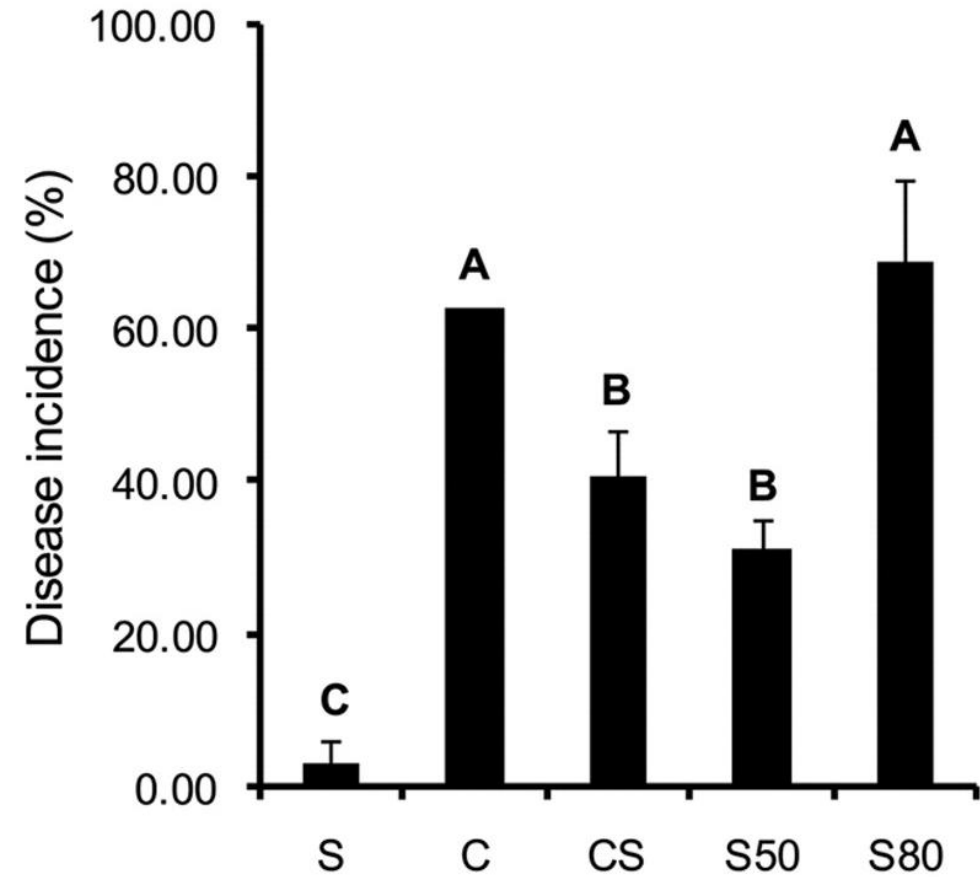






## Sugarbeet

*Rhizoctonia solani*



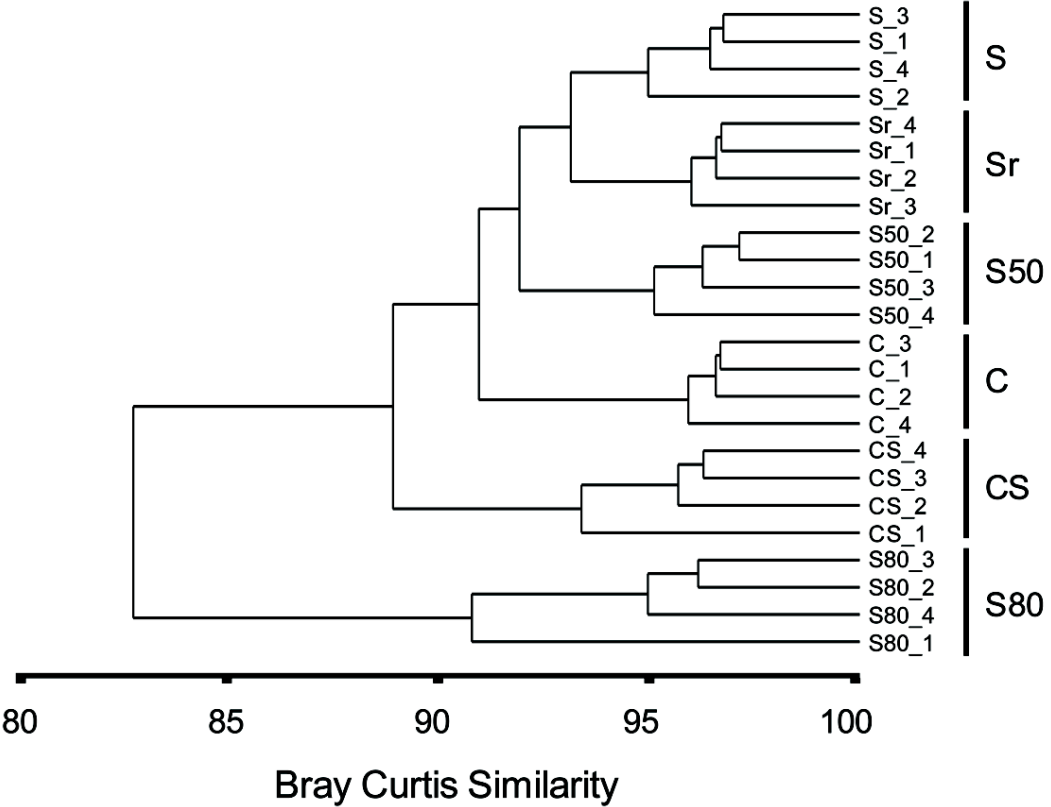
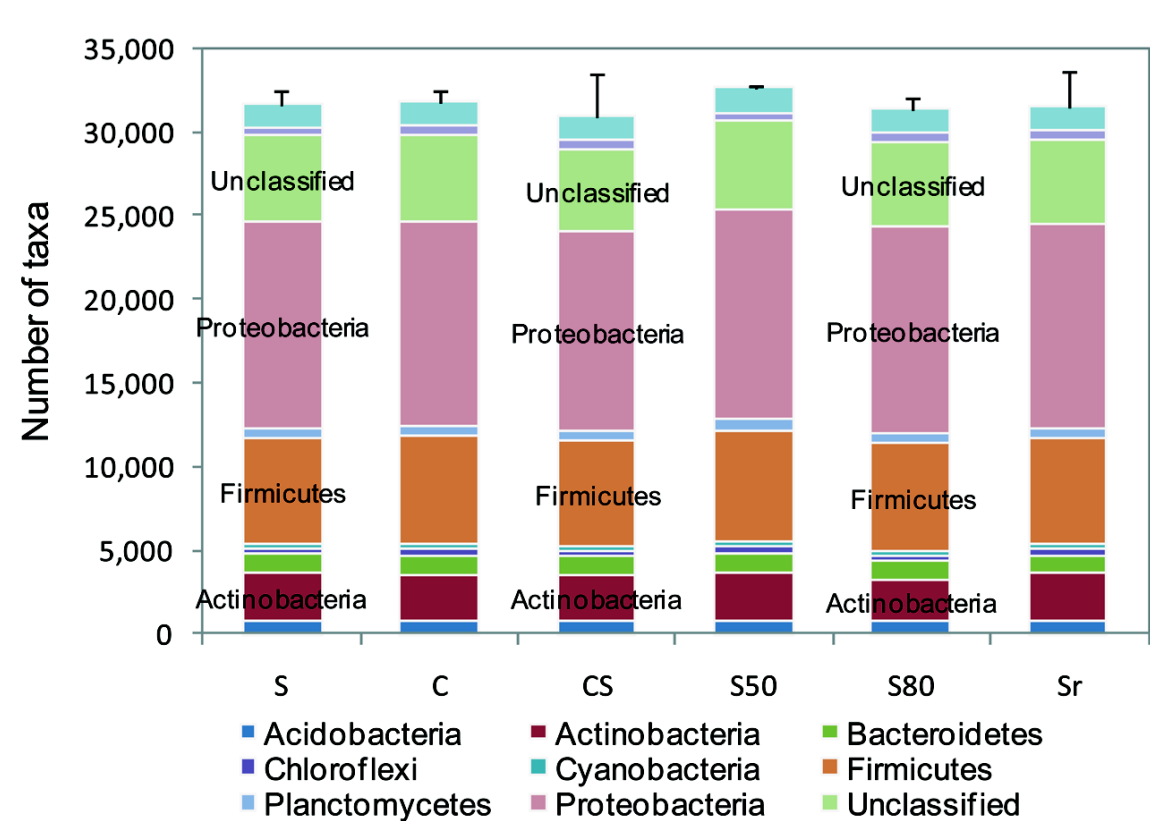
**Deciphering the rhizosphere microbiome for disease-suppressive bacteria**

[ Mendes et al., Science 2011 ]



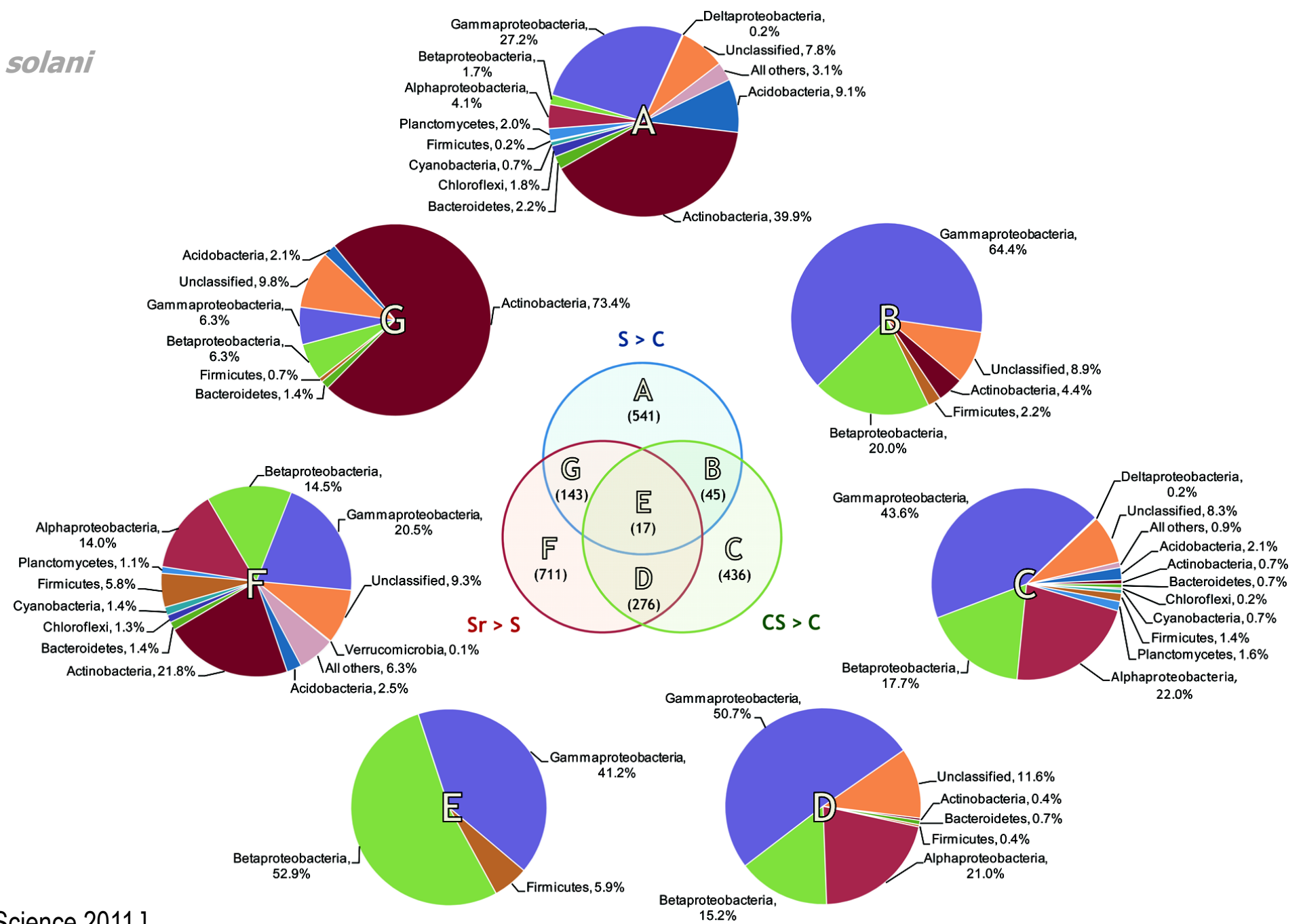


Sugarbeet  
*Rhizoctonia solani*



# Sugarbeet

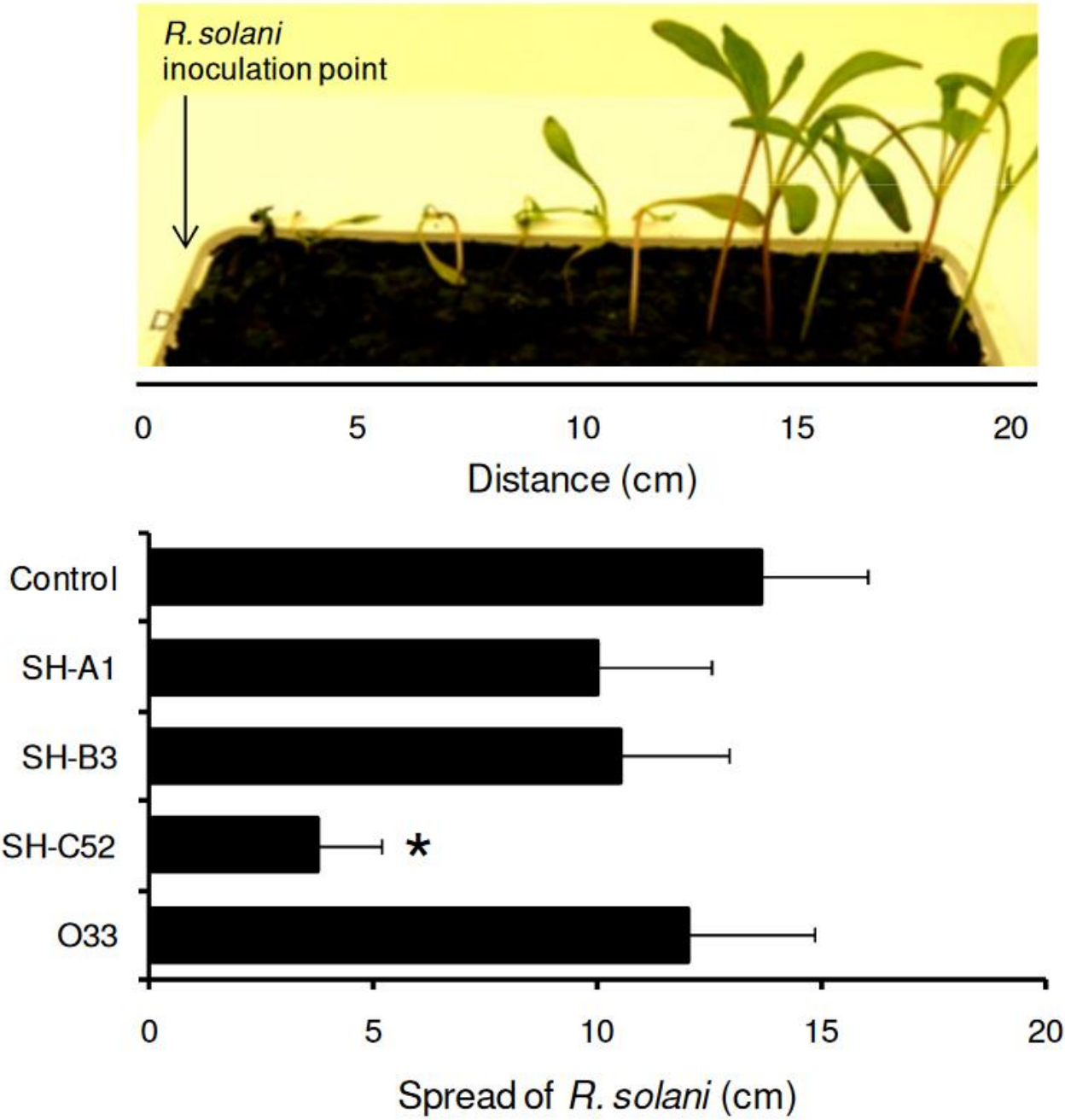
## *Rhizoctonia solani*



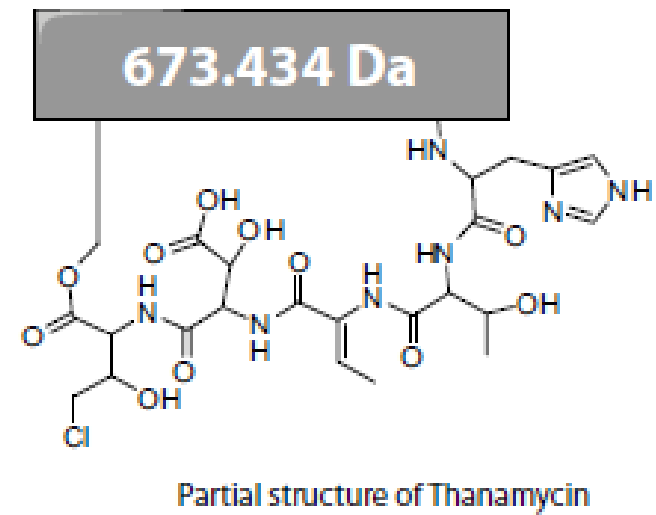
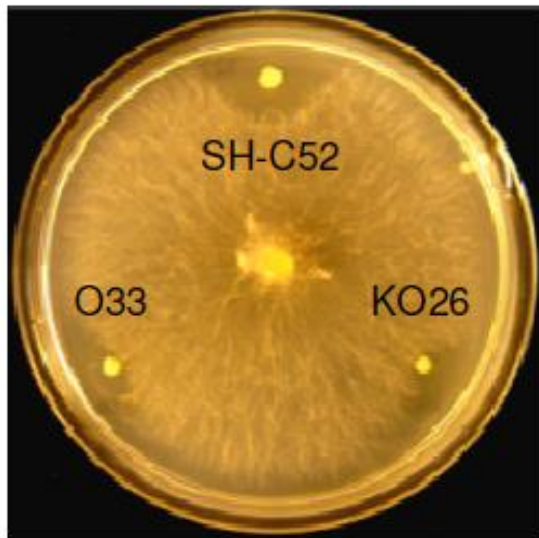
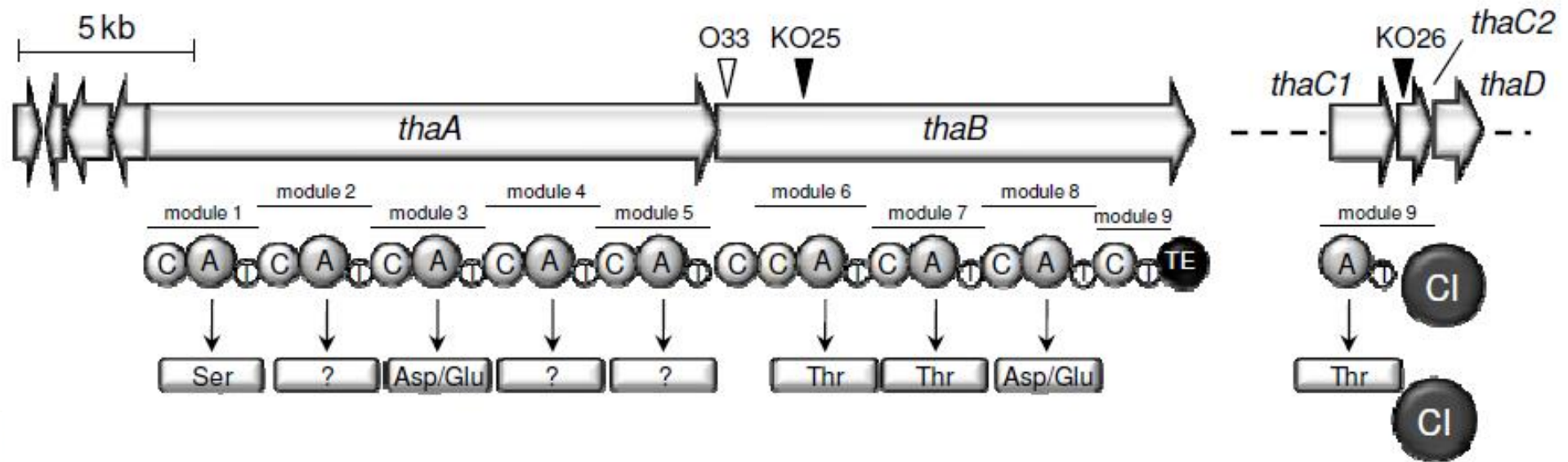


Sugarbeet

*Rhizoctonia solani*



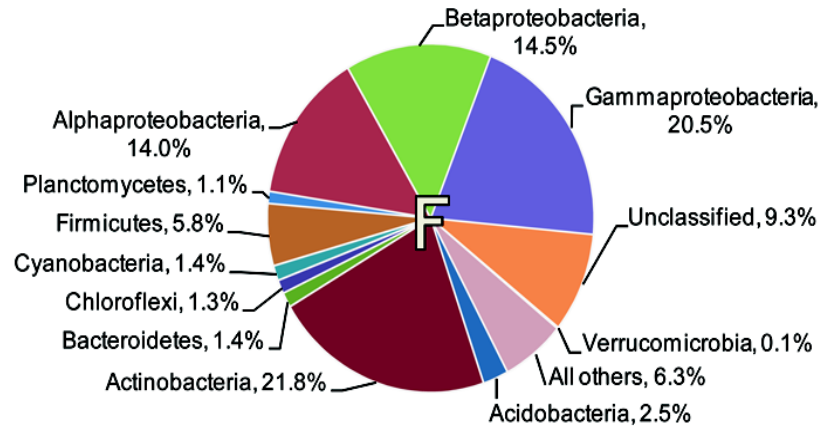
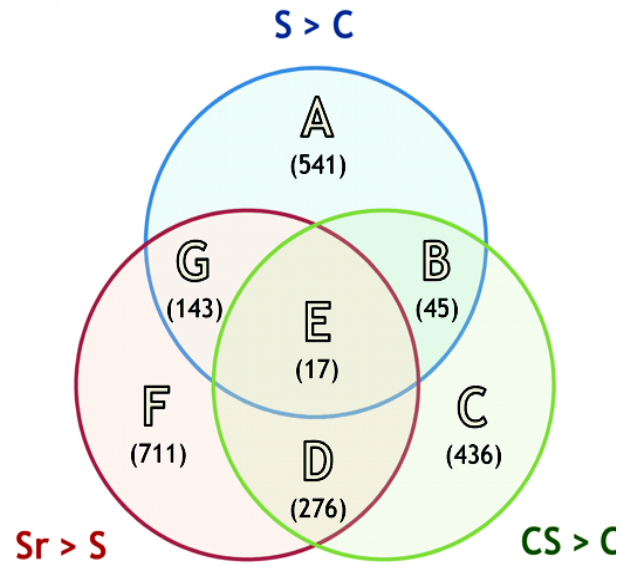
[ Mendes et al., Science 2011]



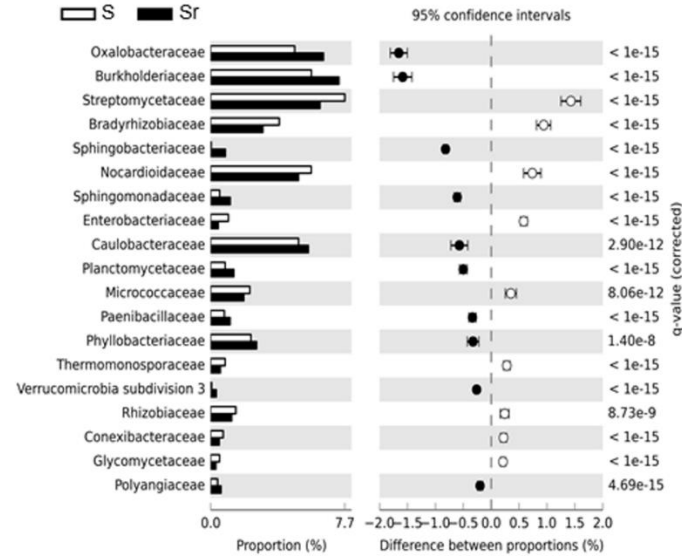


# Sugarbeet

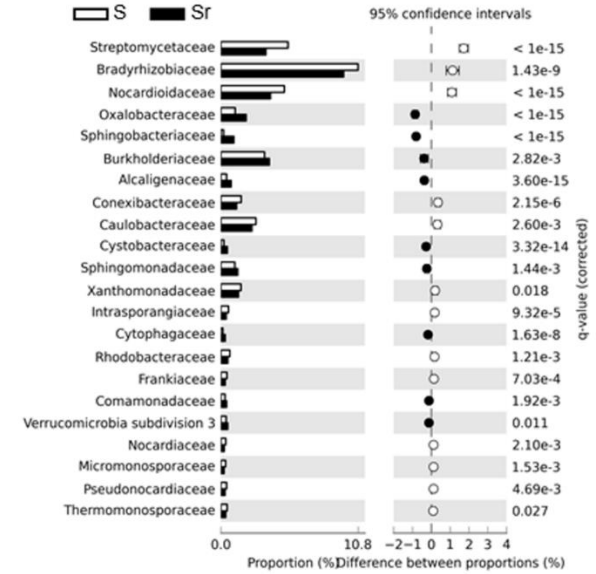
## *Rhizoctonia solani*



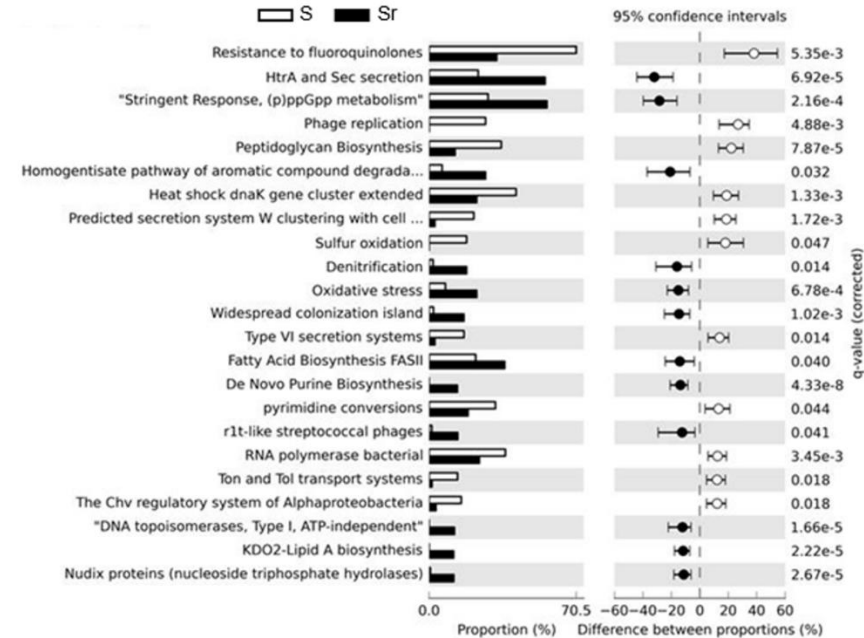
### A rRNA (taxonomy)



### B mRNA (taxonomy)

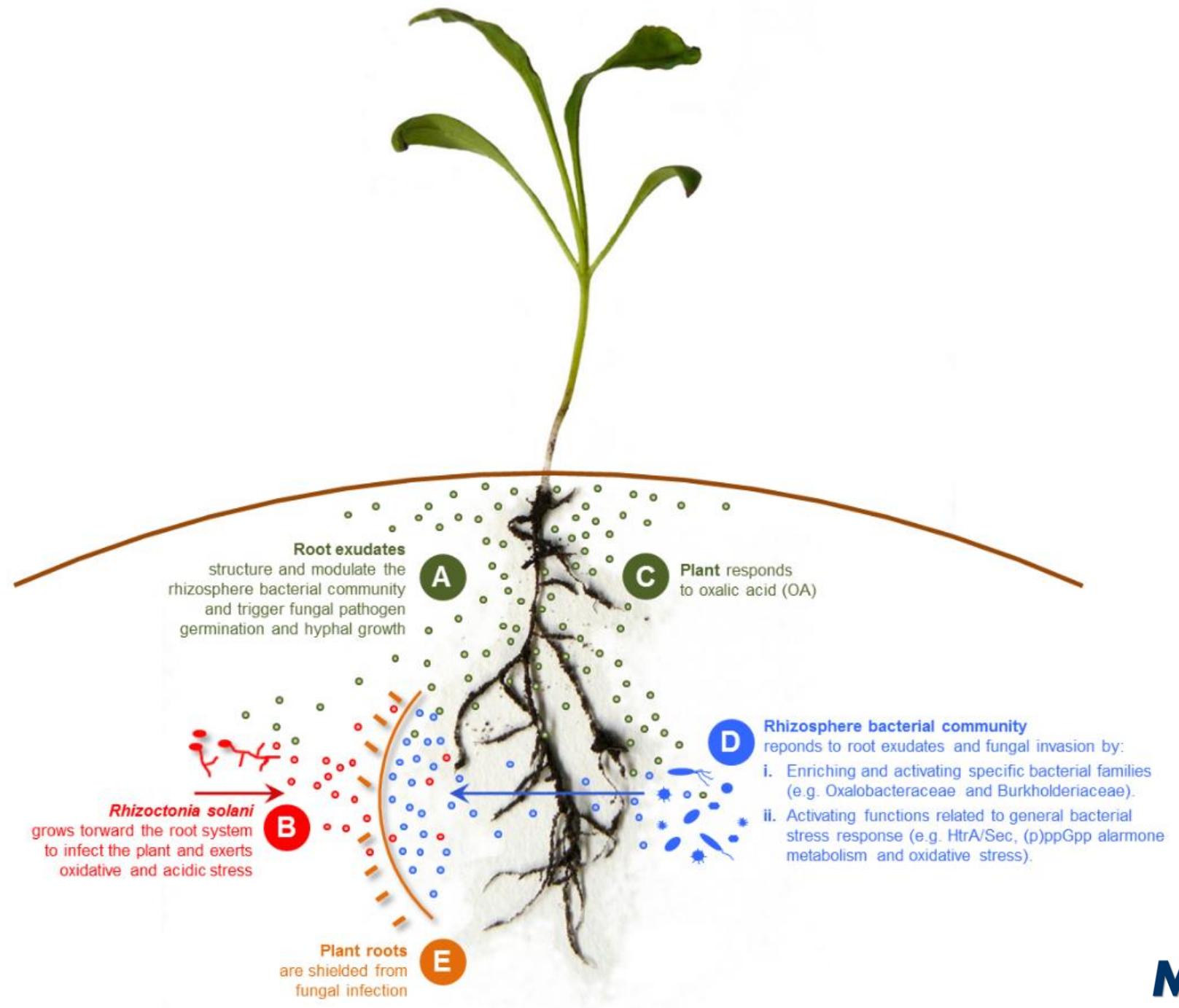


### C mRNA (functions)



# Sugarbeet

## *Rhizoctonia solani*

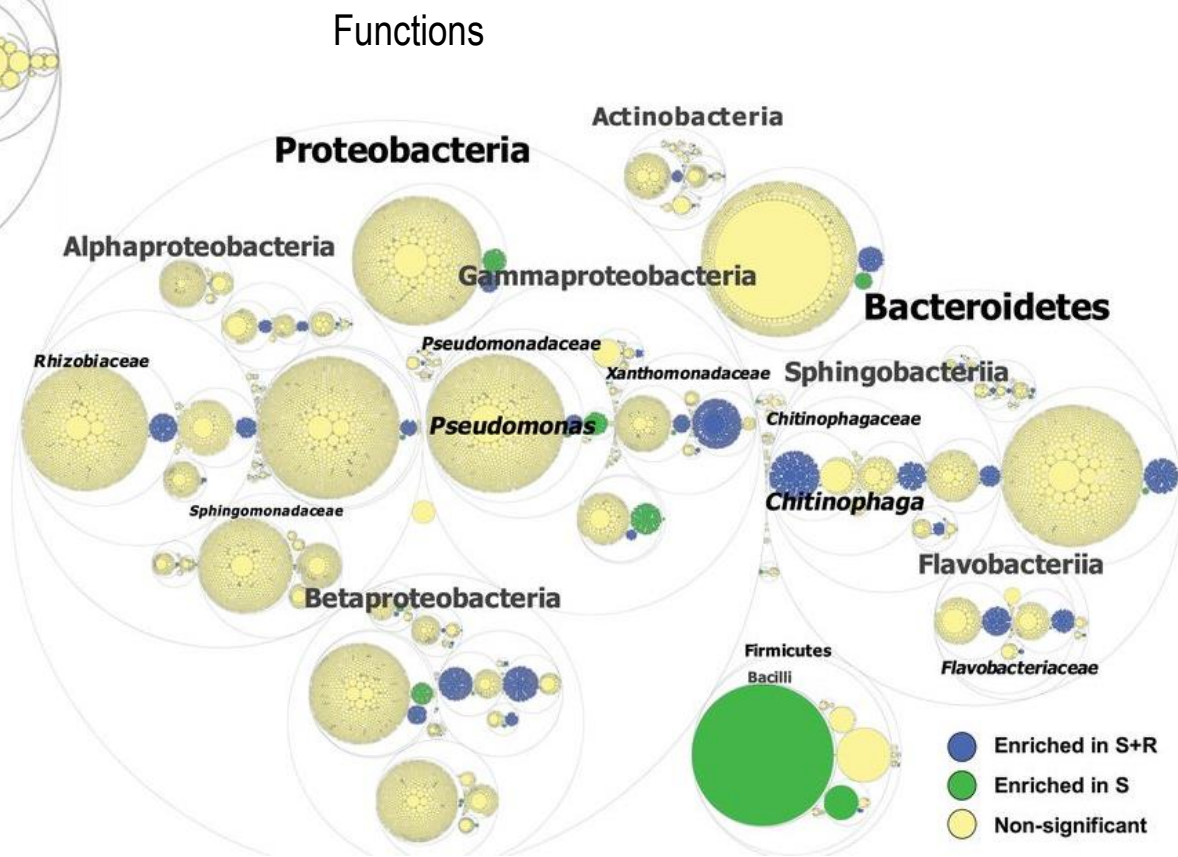
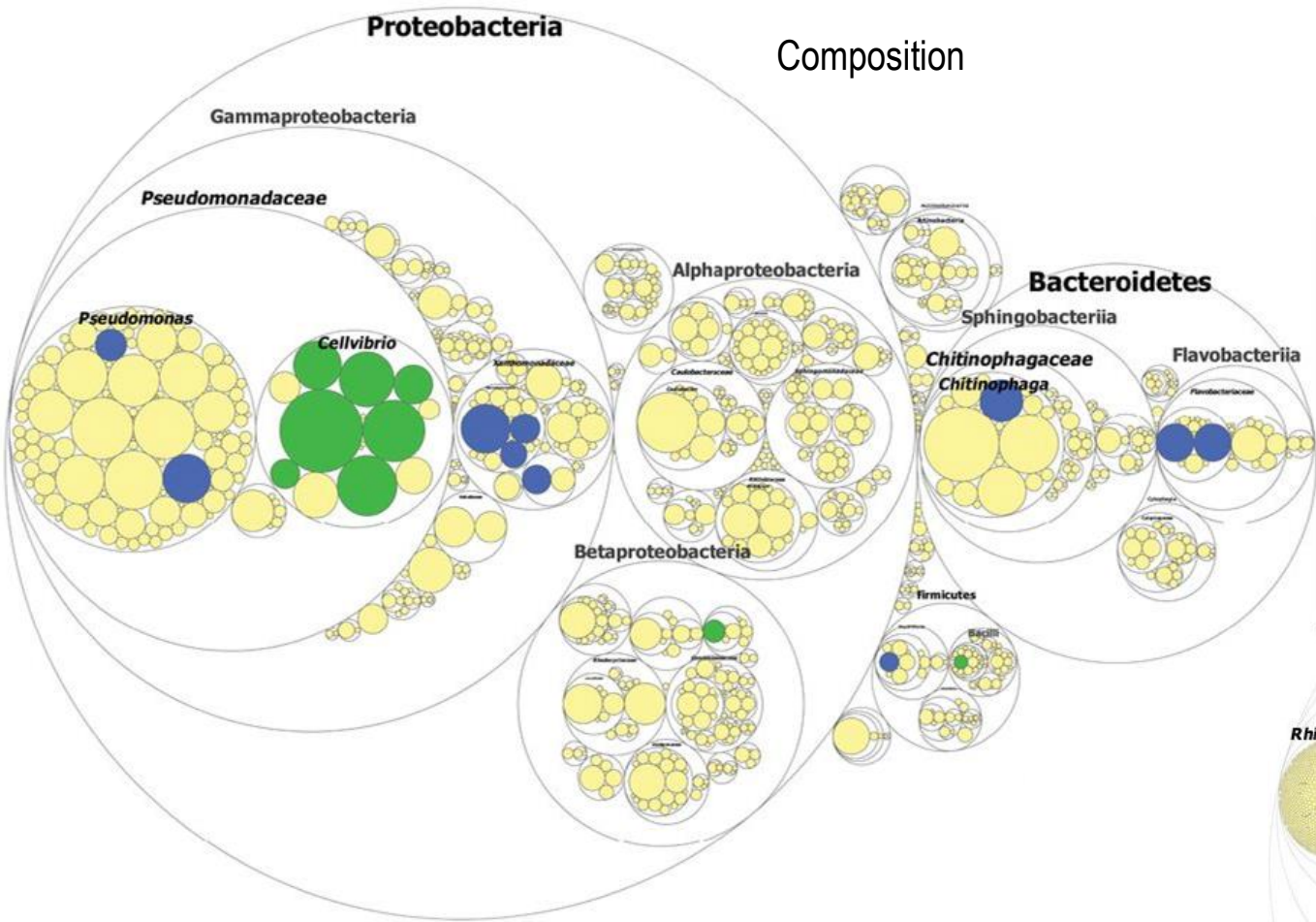


## Fungal invasion of the rhizosphere microbiome

[ Chapelle et al., ISME J 2016 ]



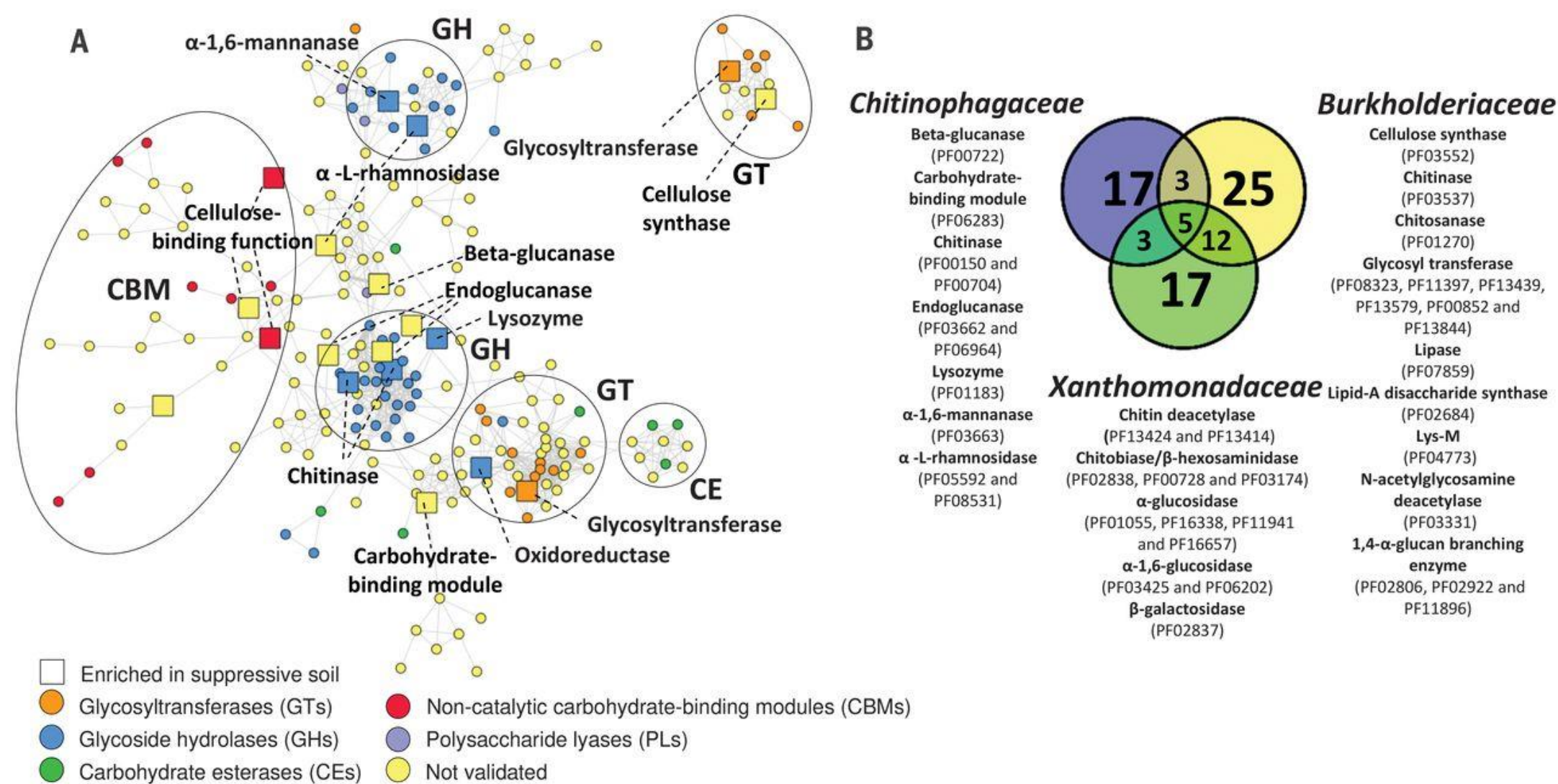
Sugarbeet  
*Rhizoctonia solani*



Pathogen-induced activation  
of disease-suppressive  
functions in the endophytic  
root microbiome  
[ Carrión et al., Science 2019 ]

# Sugarbeet

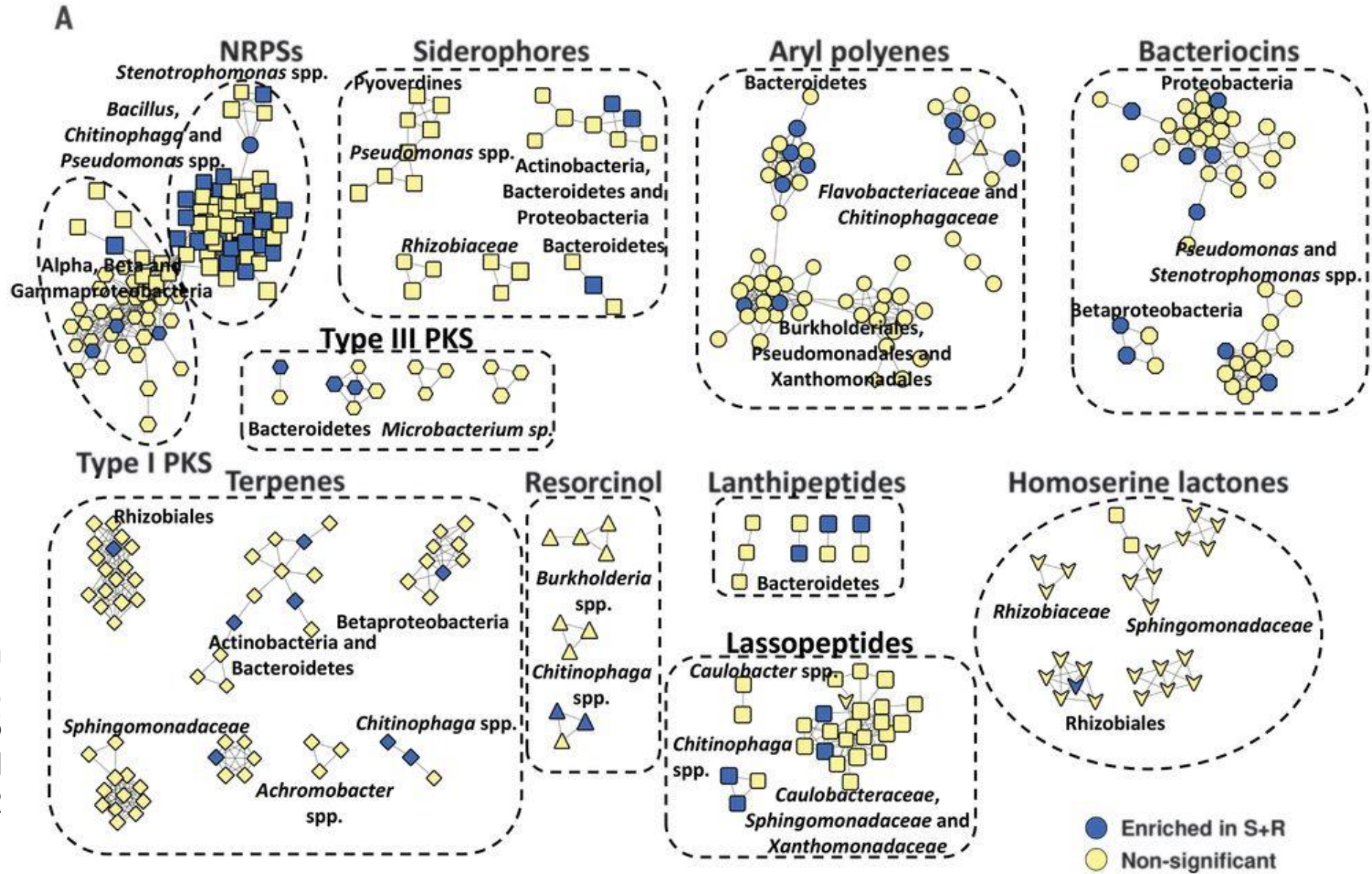
*Rhizoctonia solani*





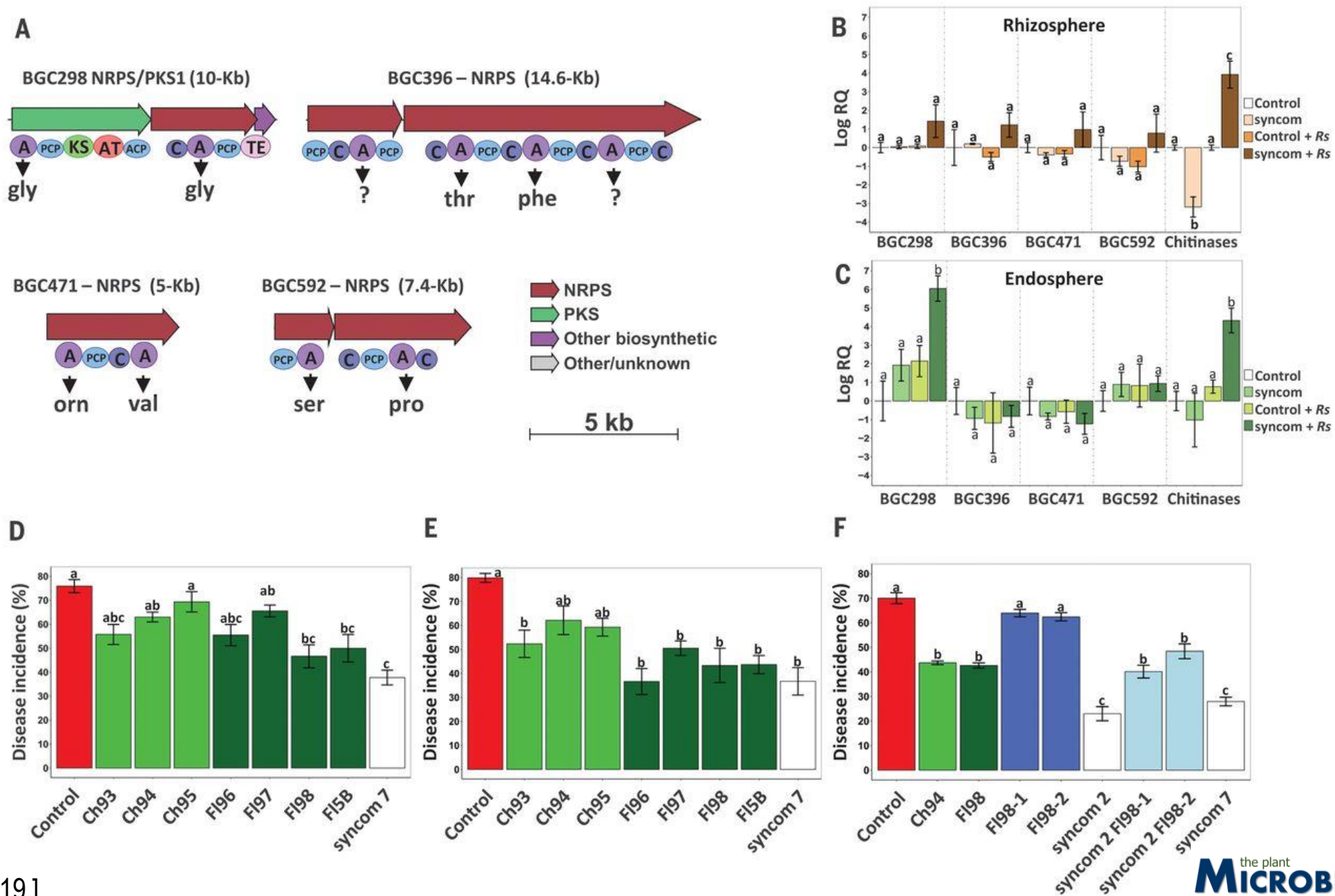
# Sugarbeet

*Rhizoctonia solani*



From the 730 BGCs identified in the metagenome by antiSMASH, 157 were found in a set of 25 metagenome-assembled genomes (MAGs) and only 12 were previously described.

Sugarbeet  
*Rhizoctonia solani*



[ Carrion et al., Science 2019 ]



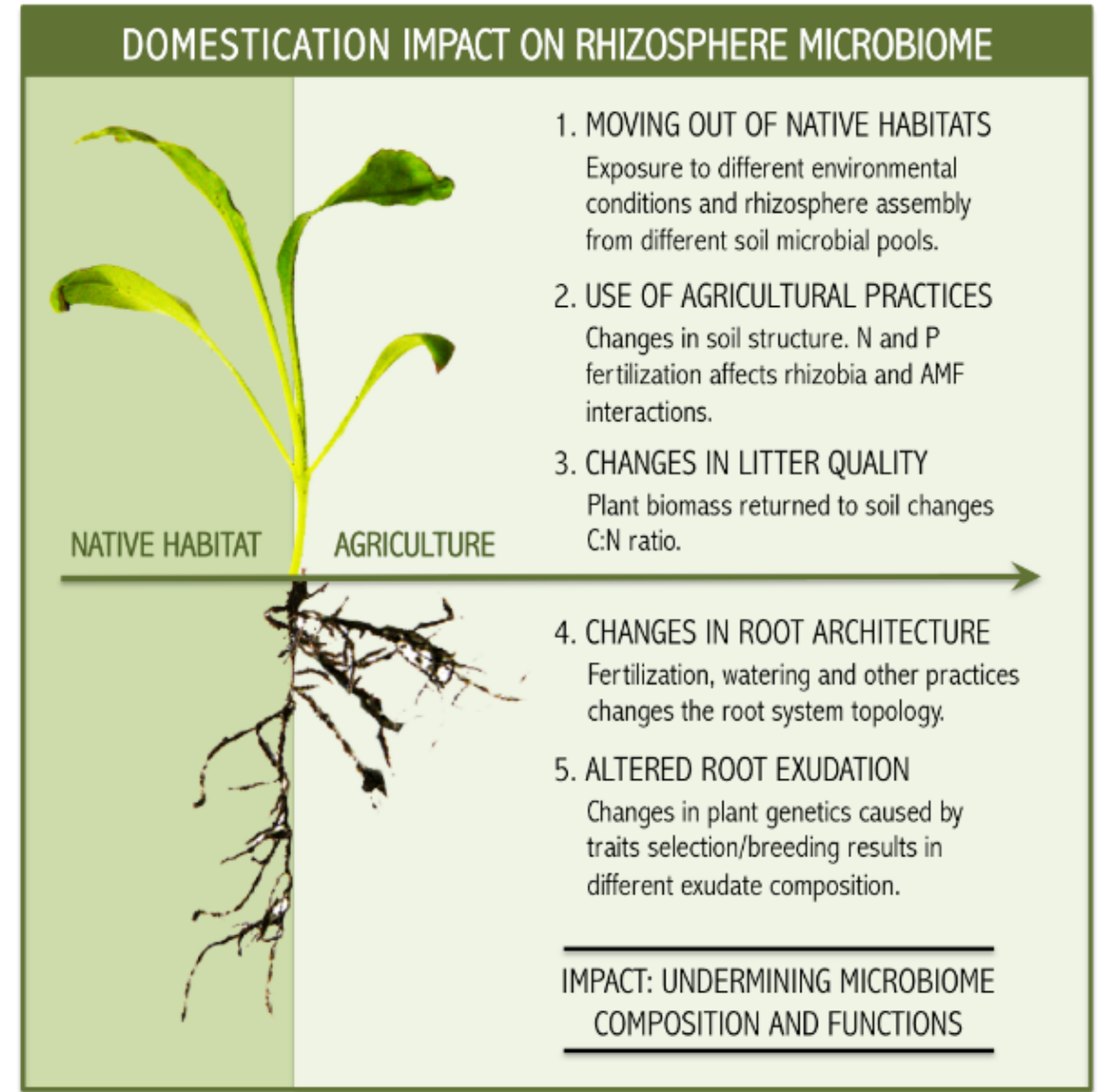
PLANT MICROBIOME  
and **Ancestrality**  
**Protection**  
**Nutrition**

# Back to the Roots

*“Domestication of plant species has substantially contributed to human civilization, but also caused a strong decrease in the genetic diversity of modern crop cultivars that may have affected the ability of plants to establish beneficial associations with rhizosphere microbes.”*

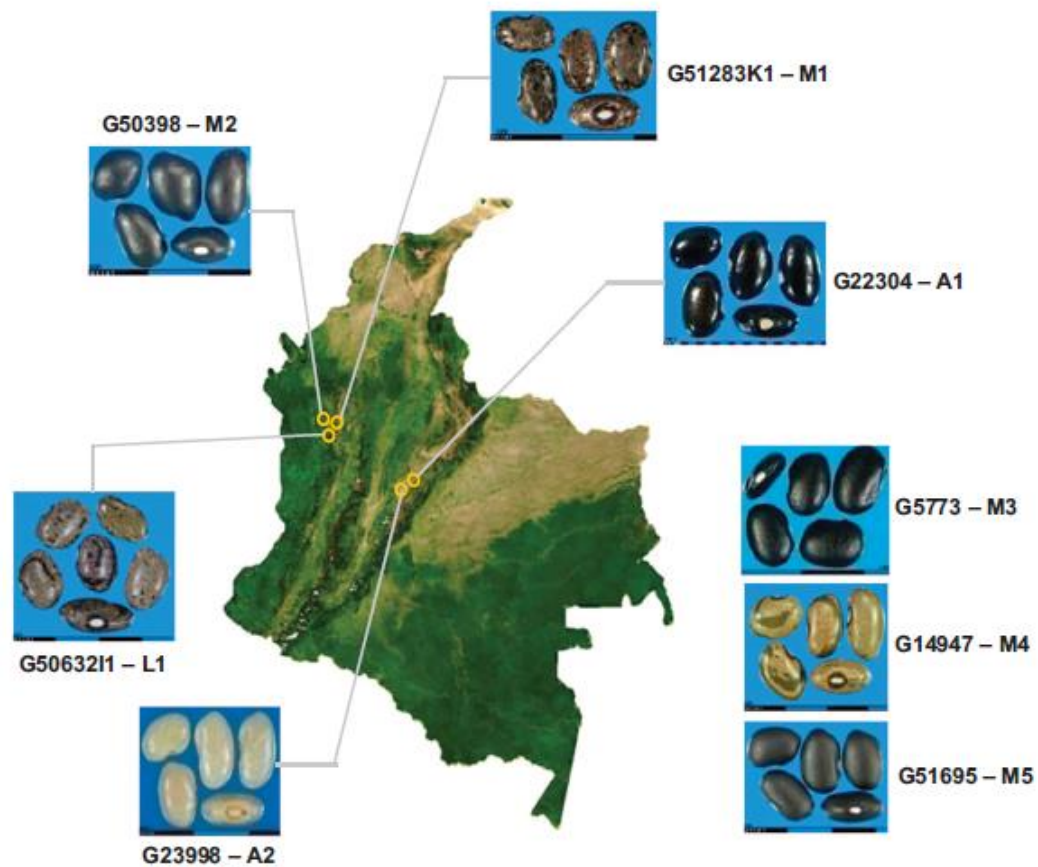
## Impact of plant domestication on rhizosphere microbiome assembly and functions

[ Perez-Jaramillo et al., Plant Mol Biol 2016; see also <http://backrootsproject.wixsite.com/backroots> ]



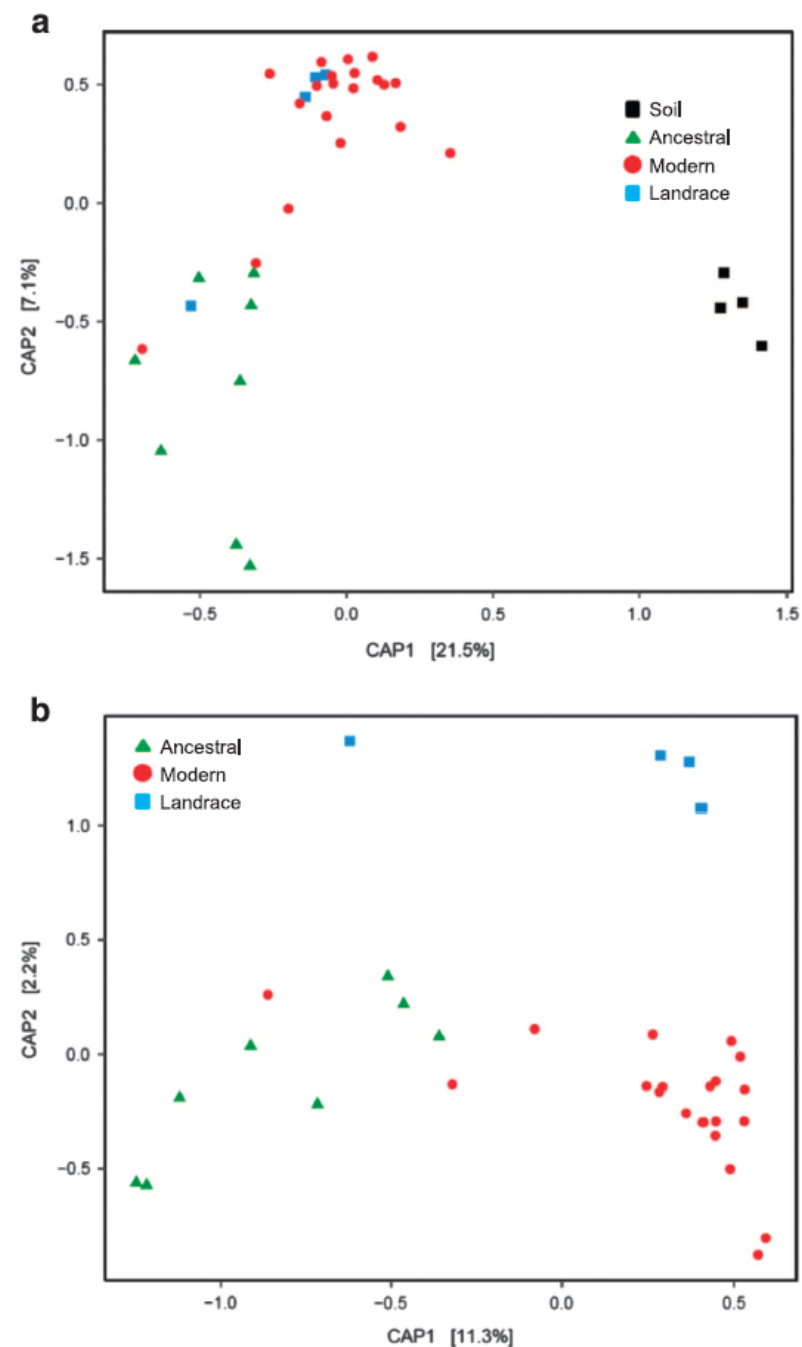


## Ancestrality

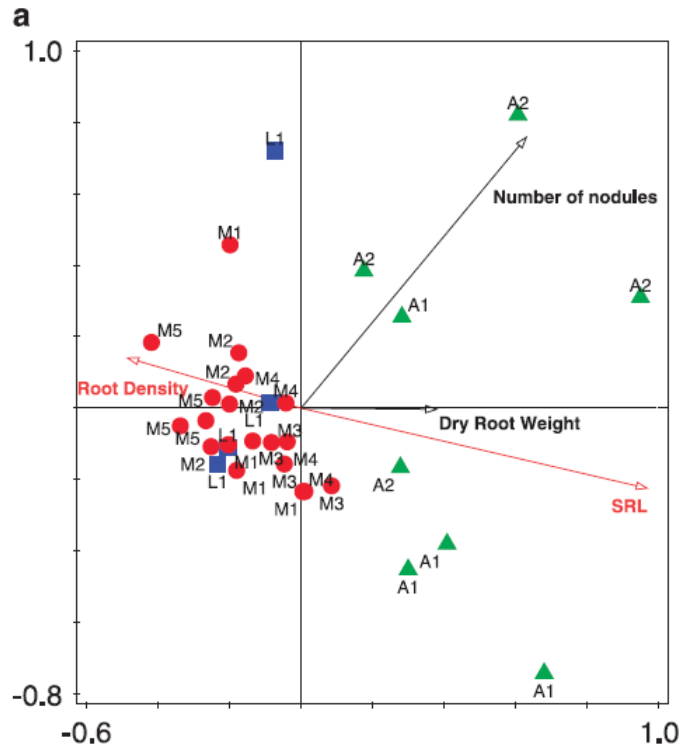


**Linking rhizosphere microbiome composition of wild and domesticated *Phaseolus vulgaris* to genotypic and root phenotypic traits**

[ Perez-Jaramillo et al., ISME J 2017 ]

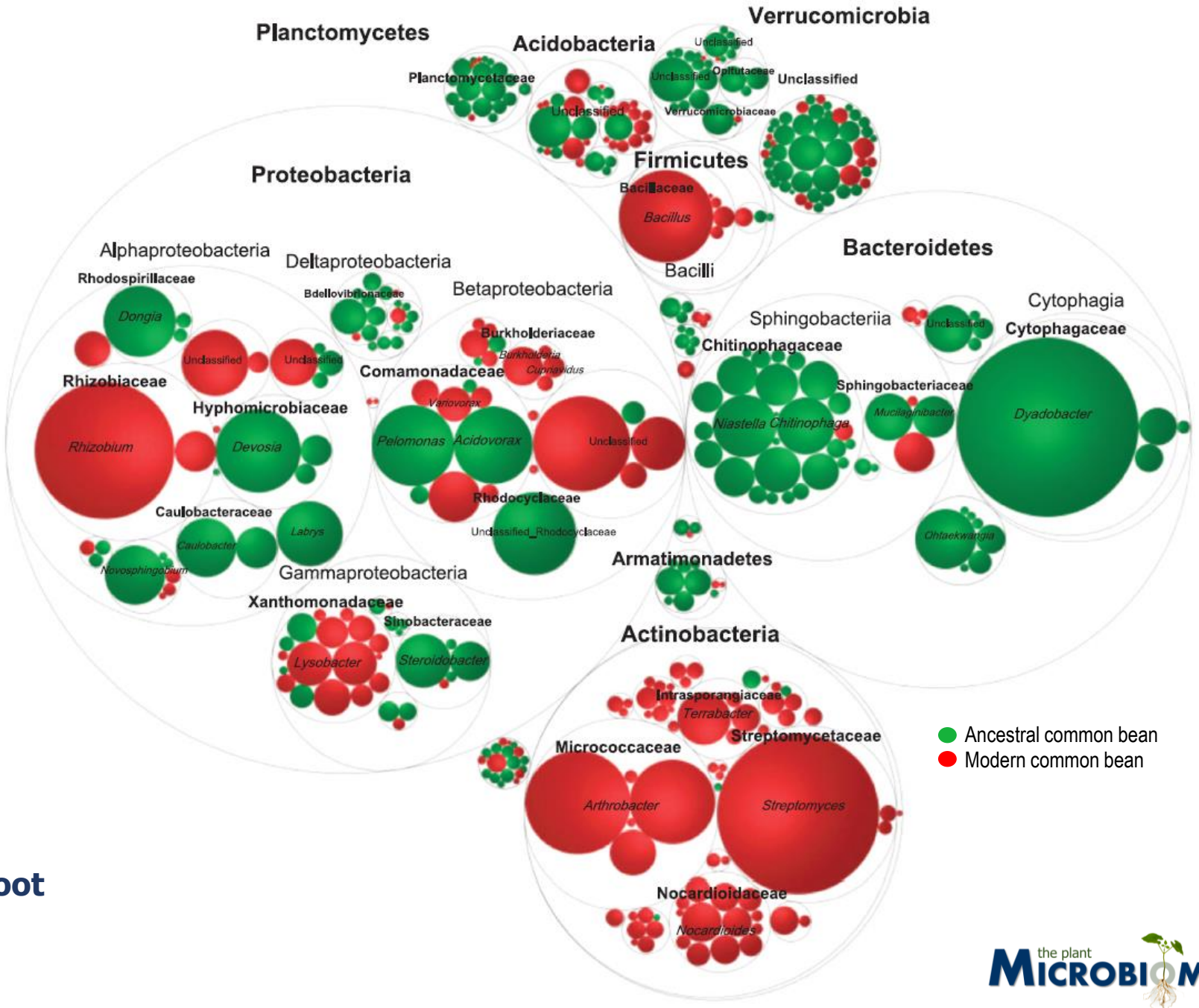


# Ancestrality



# Linking rhizosphere microbiome composition of wild and domesticated *Phaseolus vulgaris* to genotypic and root phenotypic traits

[ Perez-Jaramillo et al., ISME J 2017 ]





## Ancestrality

agricultural soil

native soil

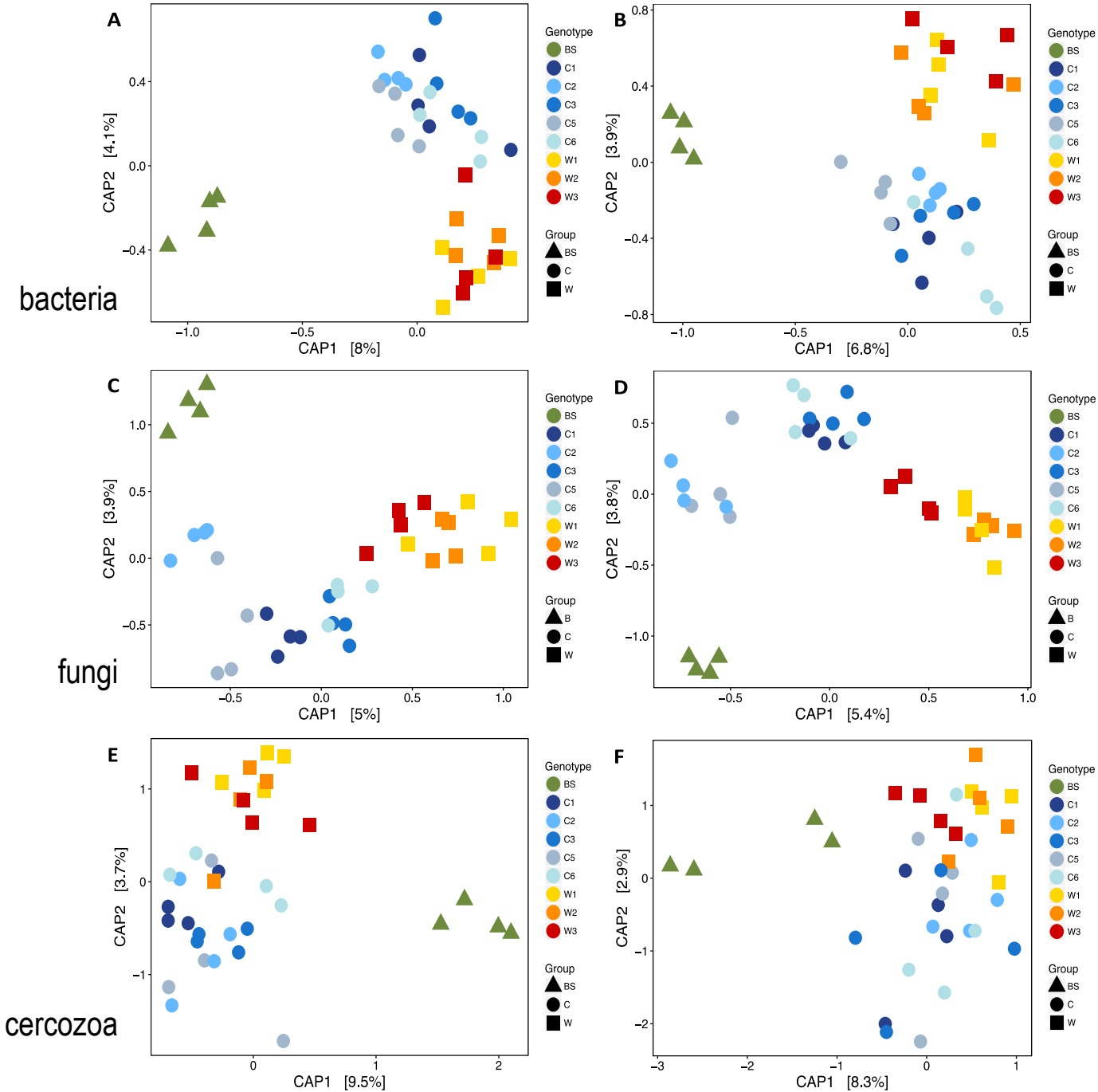
**Deciphering rhizosphere microbiome assembly of wild and modern common bean (*Phaseolus vulgaris*) in native and agricultural soils from Colombia**

[ Perez-Jaramillo et al., Microbiome 2019 ]

Ancestrality

Wheat domestication impacts on rhizosphere microbiome assembly

[ Rossmann et al., under review ]



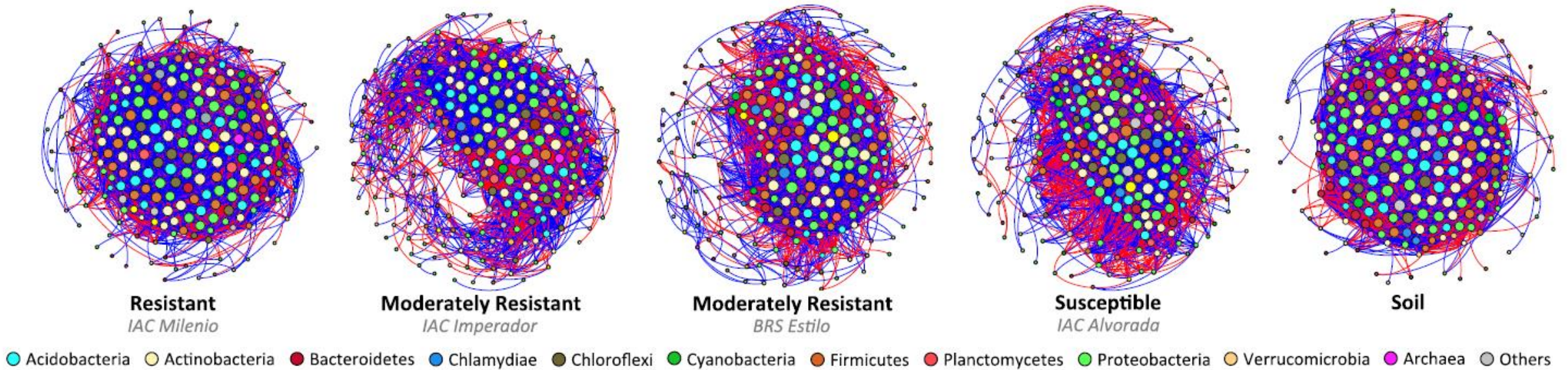






## Protection

Common bean  
*Fusarium oxysporum*



### In the resistant genotype

More Pseudomonadaceae, Bacillaceae, Solibacteraceae and Cytophagaceae  
More genes related to antifungal phenazines and rhamnolipids  
More complex and highly connected bacterial community

**Influence of resistance breeding  
in common bean on rhizosphere  
microbiome composition and function**

[ Mendes et al., ISME J 2017 ]

**Breeding for soil-borne pathogen  
resistance impacts active rhizosphere  
microbiome of common bean**

[ Mendes et al., ISME J 2018 ]





John A. Kelley, USDA Natural Resources Conservation Service

FOOD

# The next big war might be over phosphorus

By [Nathanael Johnson](#) on May 11, 2015

## The role of common bean rhizosphere bacterial communities on phosphorus mobilization

[ Chiaramonte et al., in prep. ]

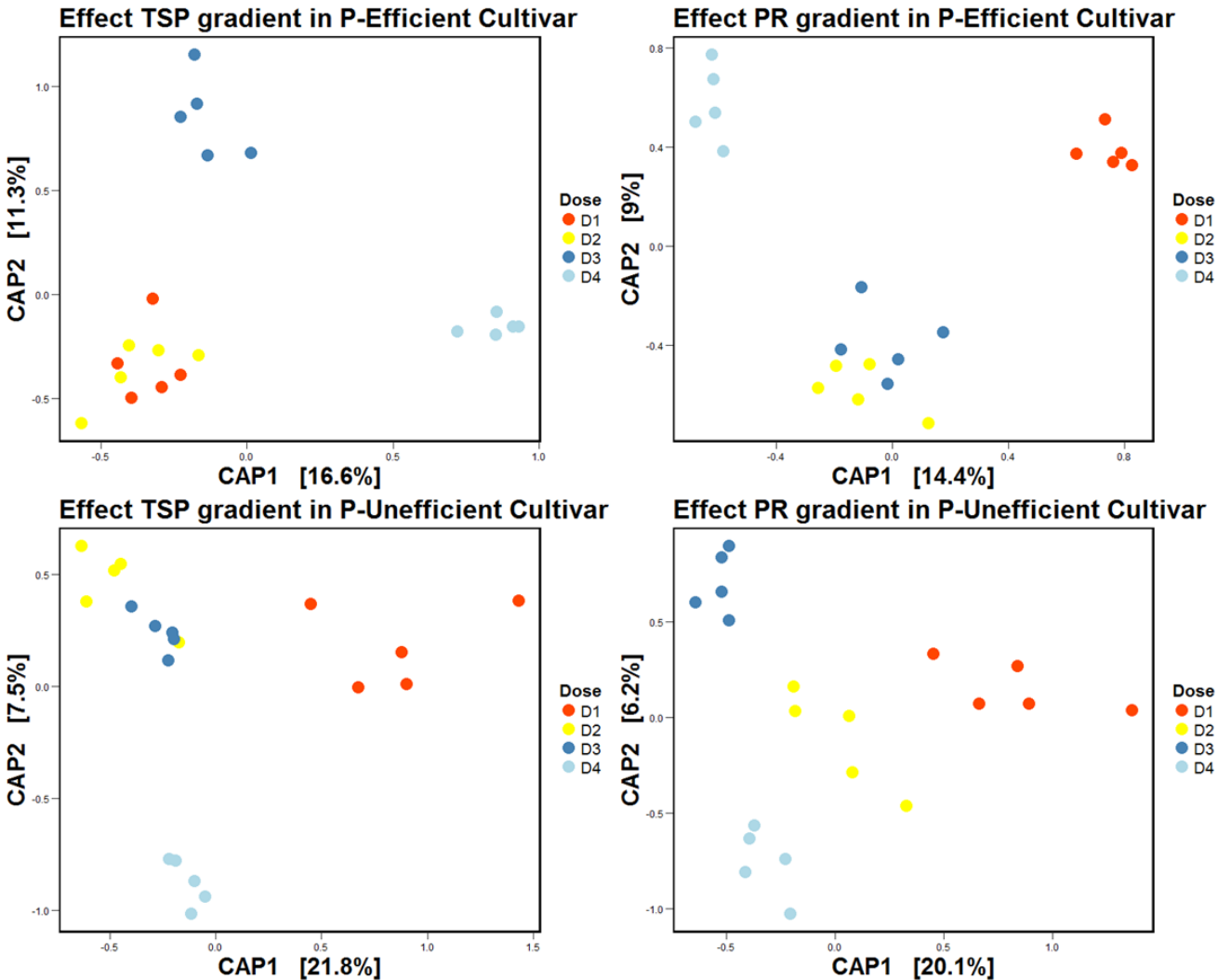
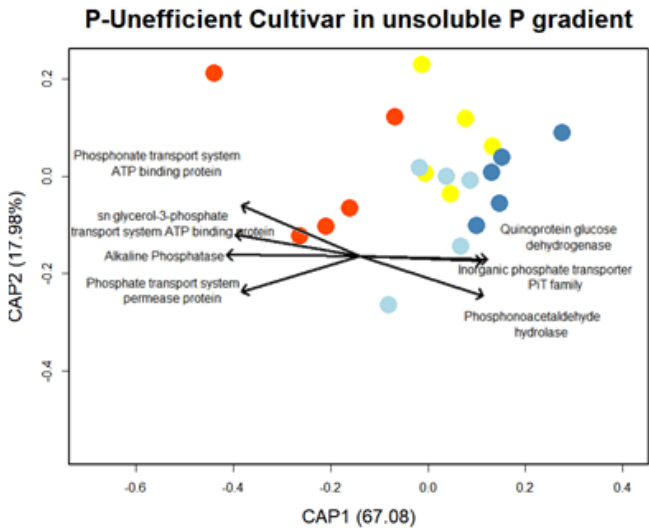
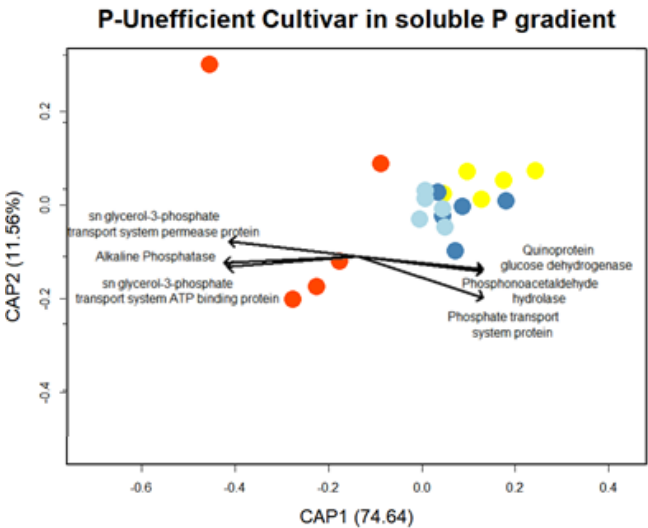
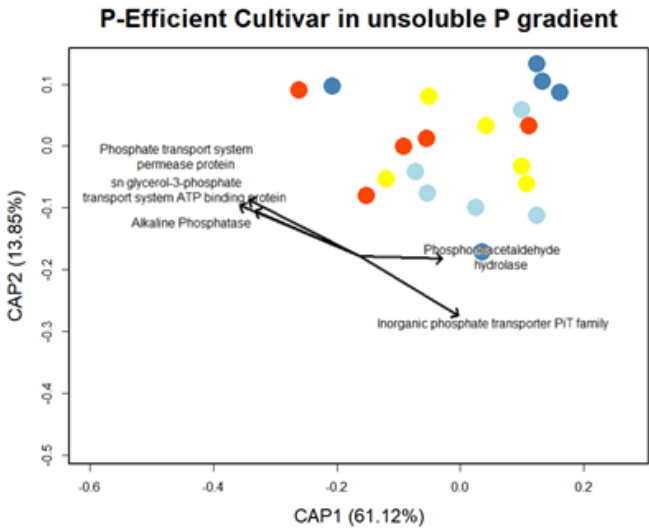
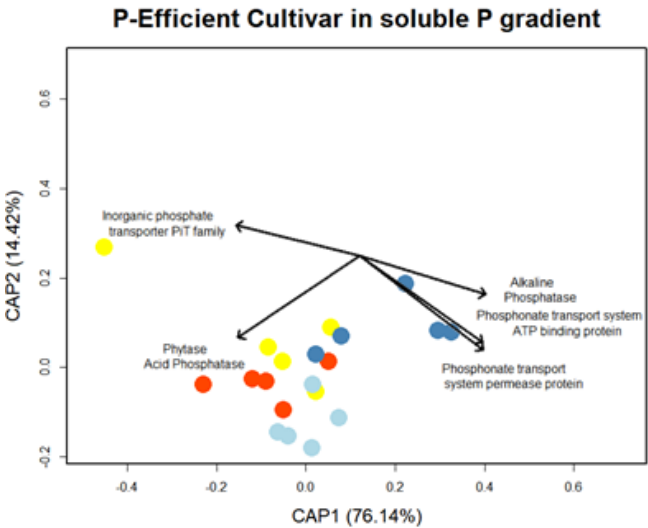




Foto: Maria Carolina Pezzo Kmit



The role of common bean rhizosphere bacterial communities on phosphorus mobilization

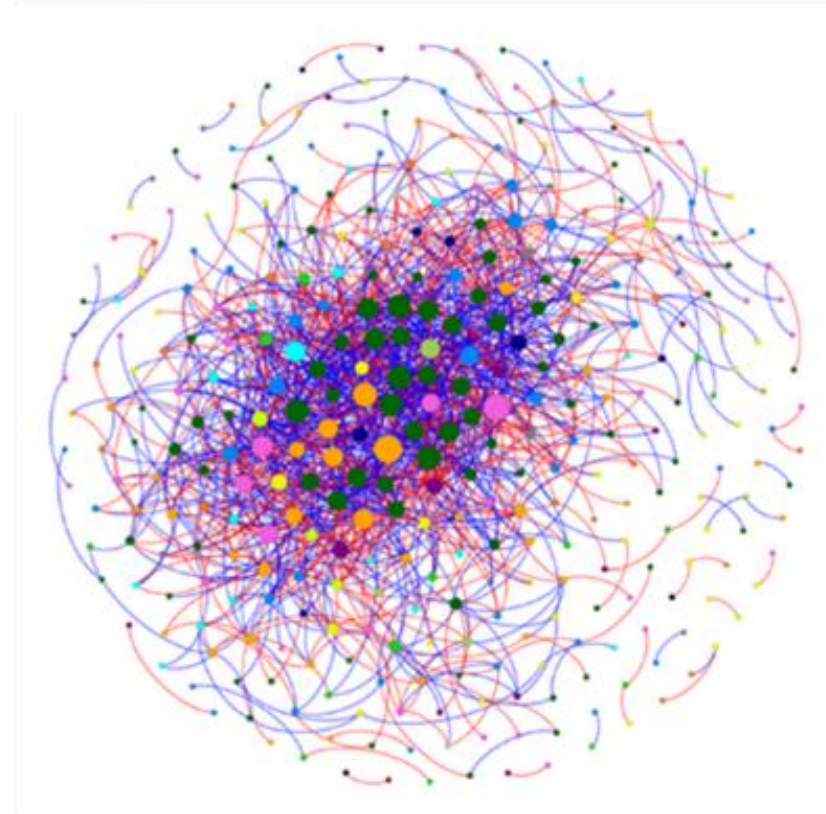
[ Chiaramonte et al., in prep. ]



IAC Imperador  
[P-efficient]



Dor-364  
[P-inefficient]



**The role of common bean rhizosphere  
bacterial communities on phosphorus  
mobilization**

[ Chiaramonte et al., in prep. ]





**Embrapa** Embrapa Environment | Brazil  
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 Maíke Rossmann  
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 Lilian Abreu Soares Costa  
 Maria Carolina Pezzo Kmit  
 Miriam Rabelo Faria  
 Juliana Carvalho

Embrapa Wheat | Brazil  
 Tammy A. M. Kiihl  
 Ricardo L. de Castro  
 José Pereira da Silva

 Rothamsted Research | England  
 Tim Mauchline  
 Penny Hirsch  
 Ian Clark  
 Vanessa Nessner Kavamura

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 Lucas William Mendes (CENA)  
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 University of Dundee | Scotland  
 Davide Bulgarelli  
 Rodrigo Alegria

 Universidad de Antioquia | Colombia  
 Camilo Ramirez

 NIOO | The Netherlands  
 Jos Raaijmakers  
 Juan Perez-Jaramillo  
 Victor Carrion

**Embrapa**

**FAPESP**

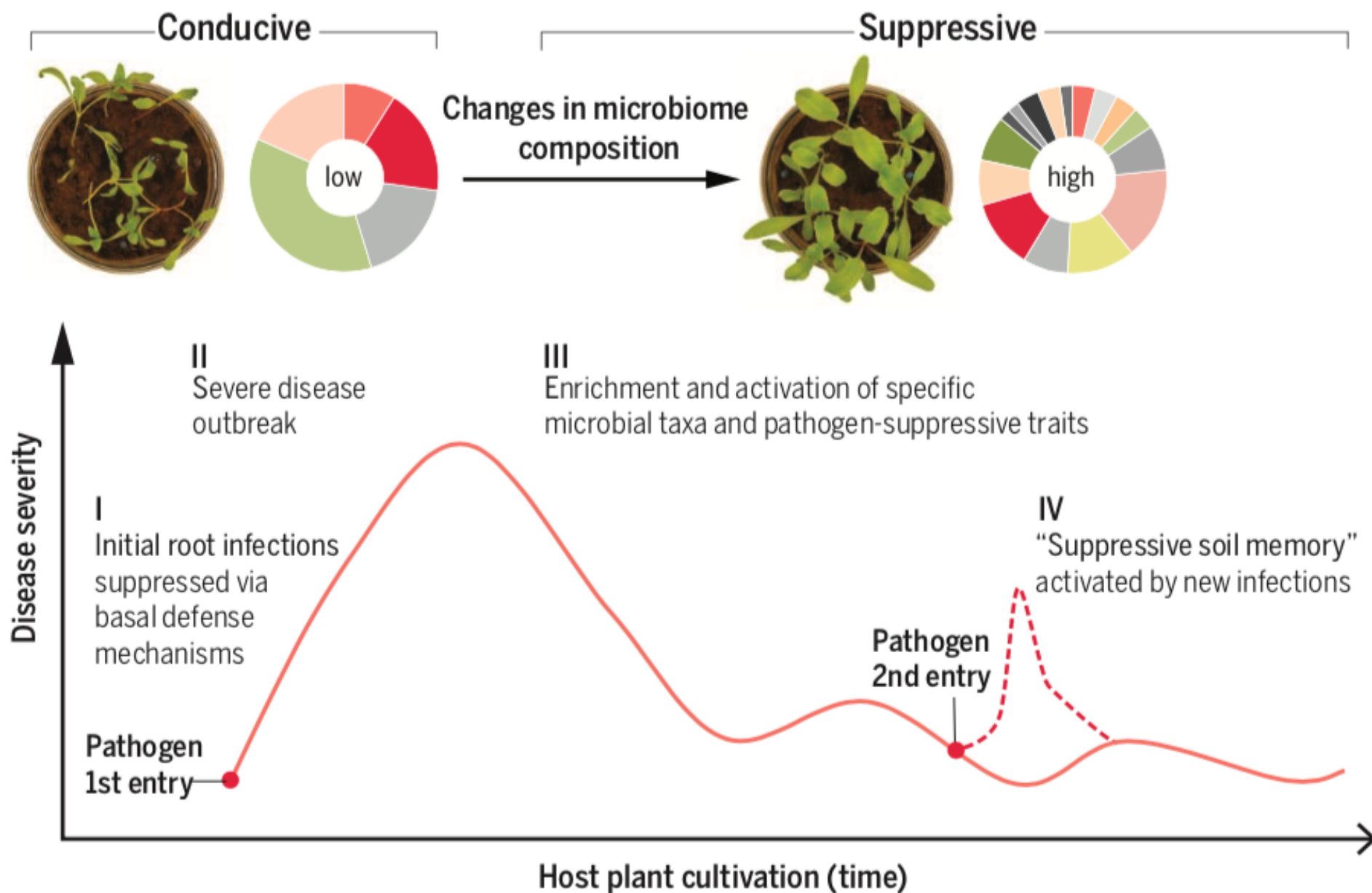
**CNPq**

**BBSRC**  
 bioscience for the future

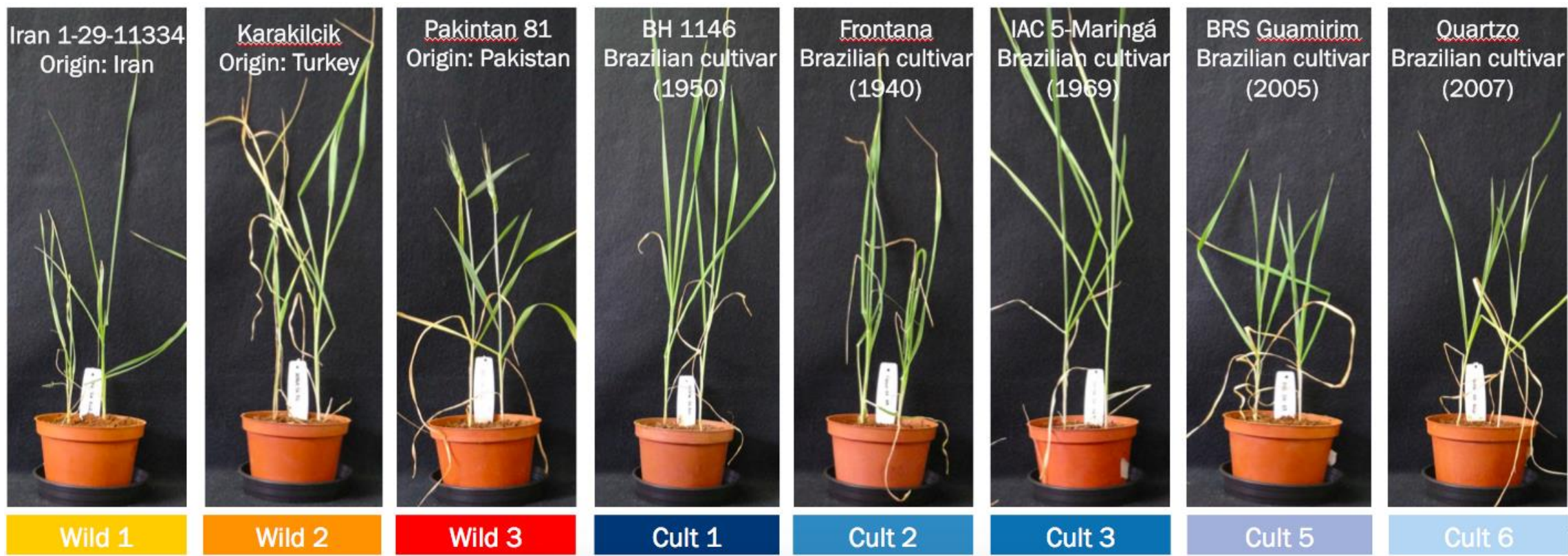
# The plant's first line of defense

*“Selection pressure imposed by soilborne pathogens may favor a different defense strategy - namely, plants with the ability, during monoculture, to support and respond to populations of rhizosphere microorganisms antagonistic to their pathogens.”*





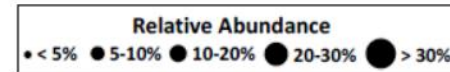
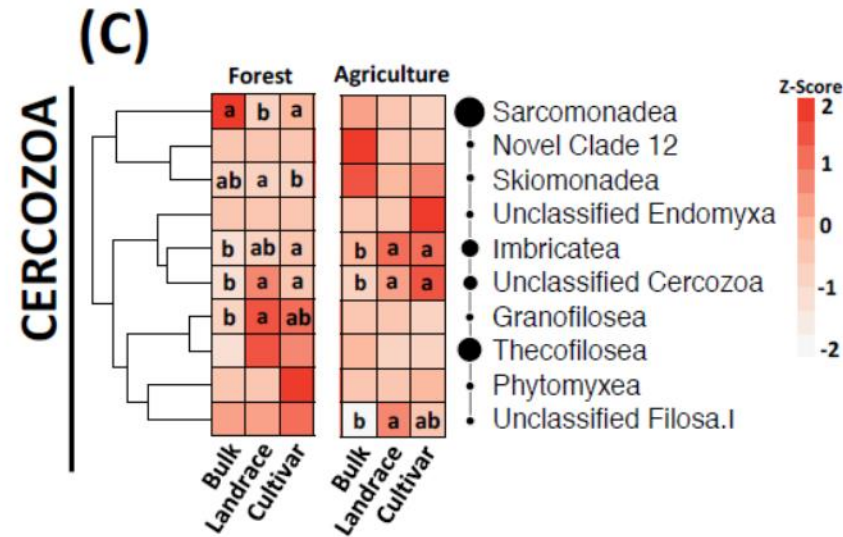
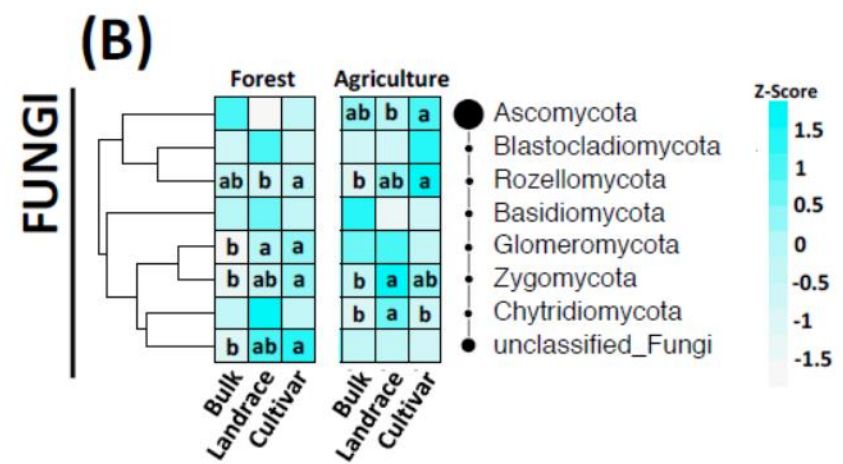
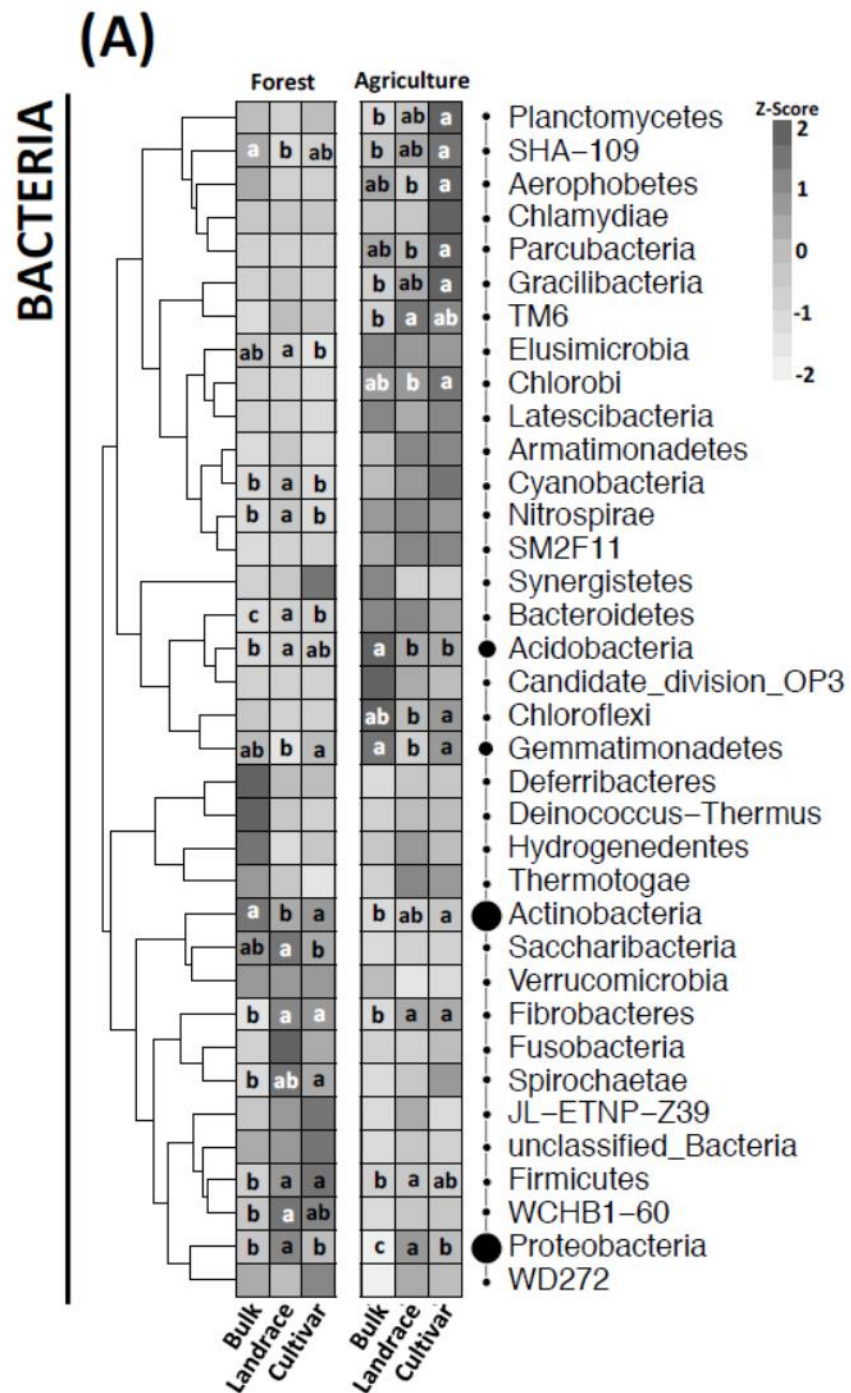


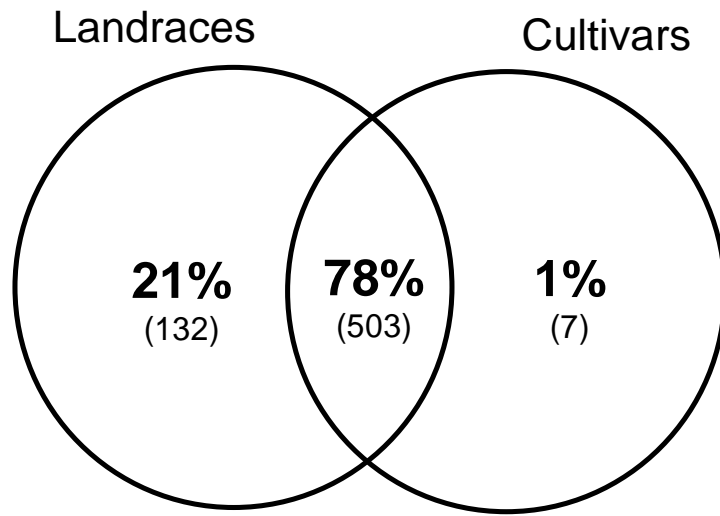


## Wheat domestication impacts on rhizosphere bacterial community assembly

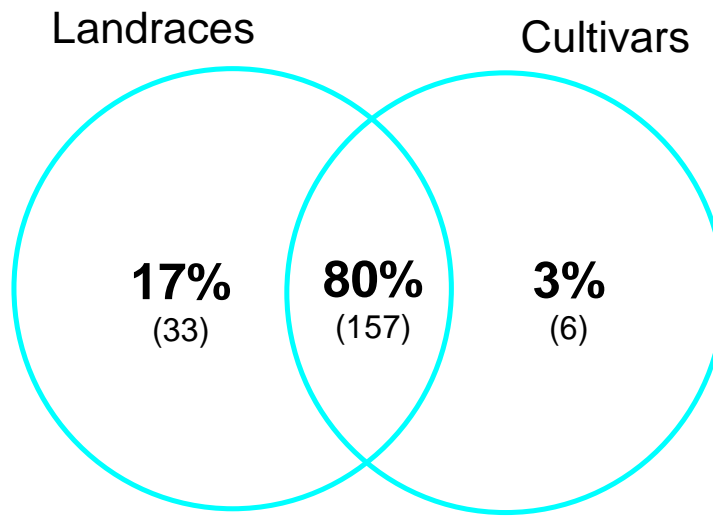
[ Rossmann et al., in prep. ]



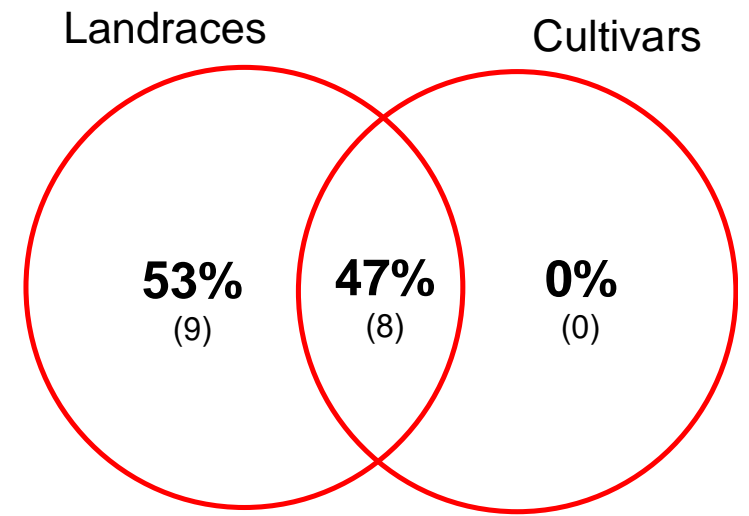




Bacterial Community  
8,964 OTUs

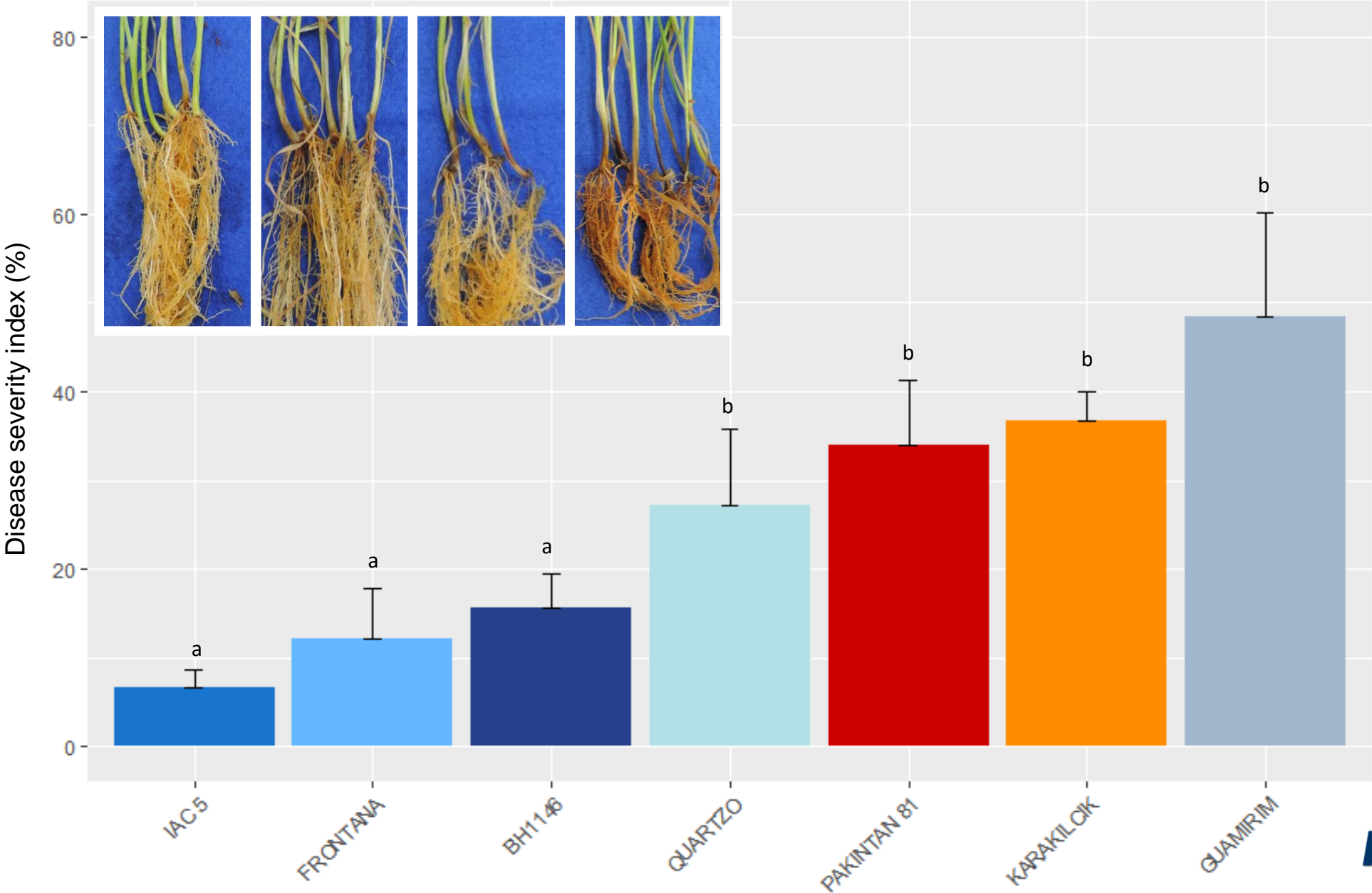


Fungal Community  
4,043 OTUs



Cercozoa Community  
1,934 OTUs

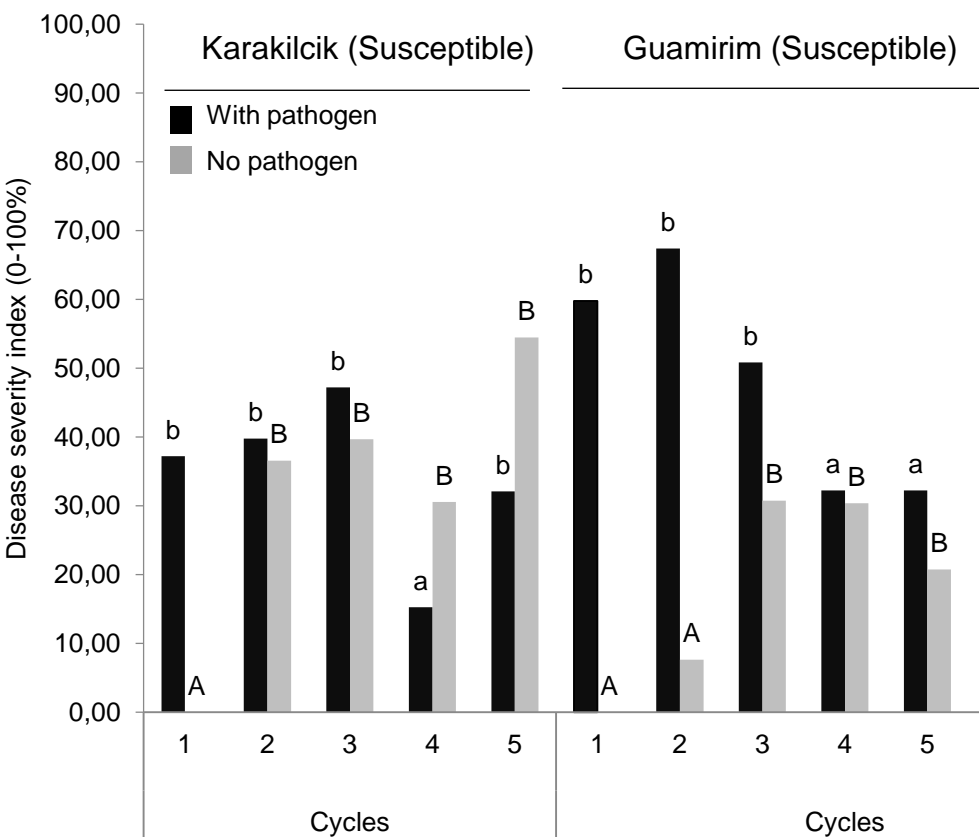
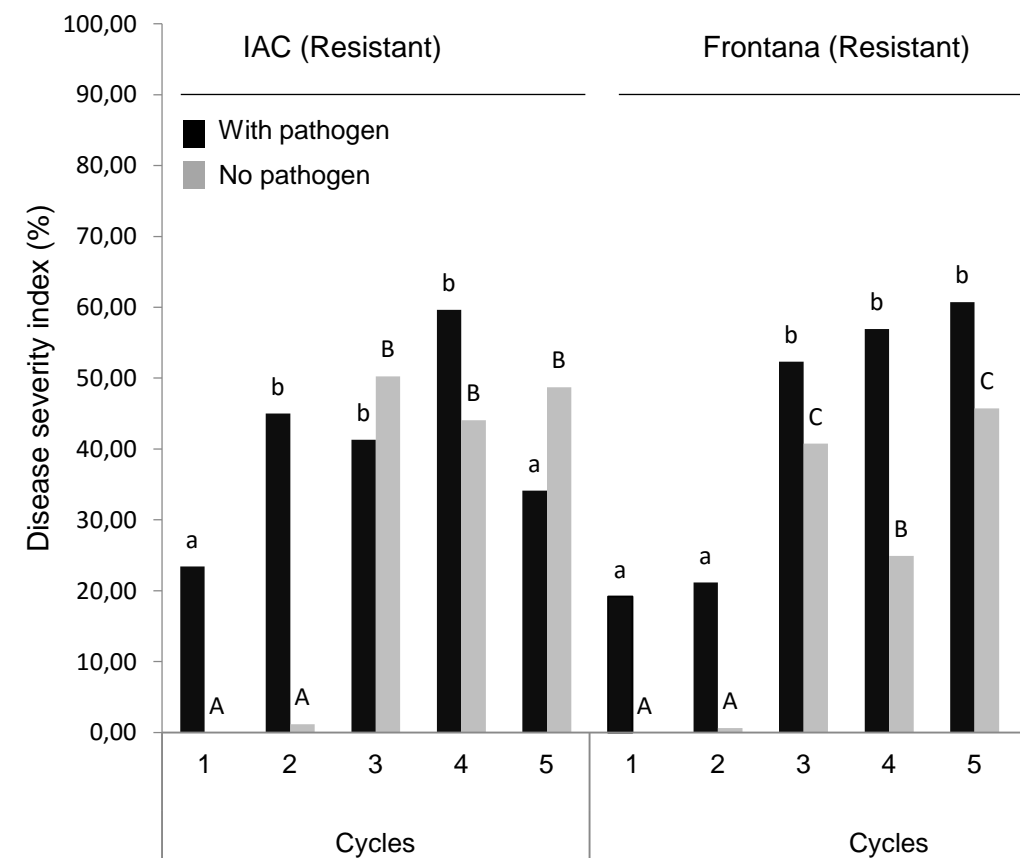
Wheat  
*Bipolaris sorokiniana*





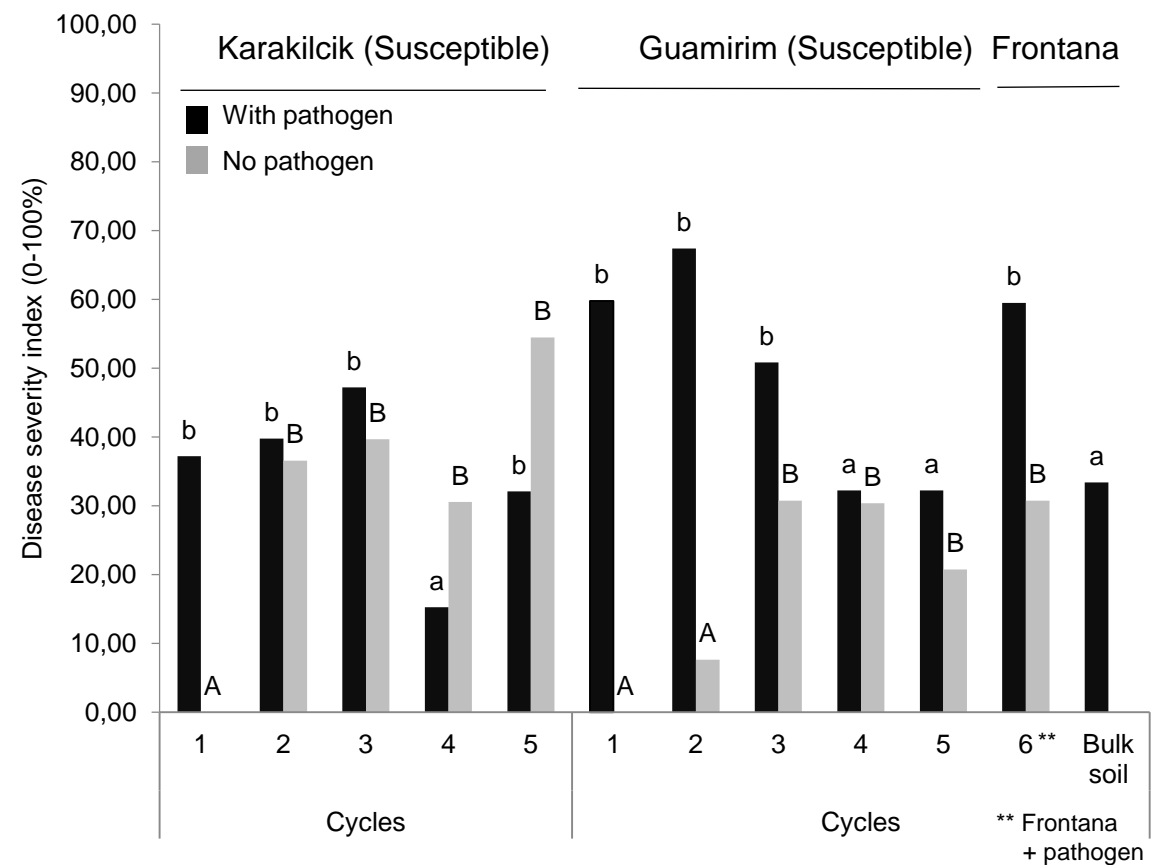
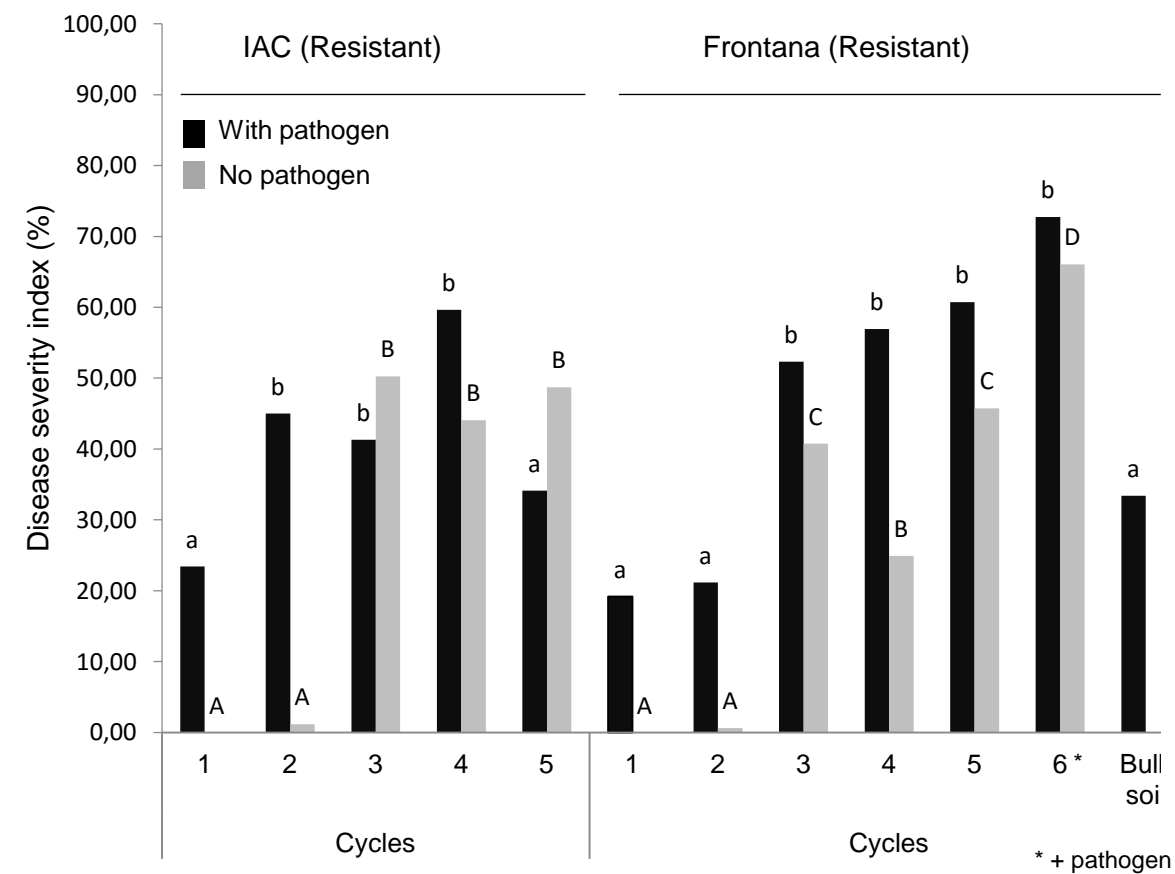
# Wheat

*Bipolaris sorokiniana*

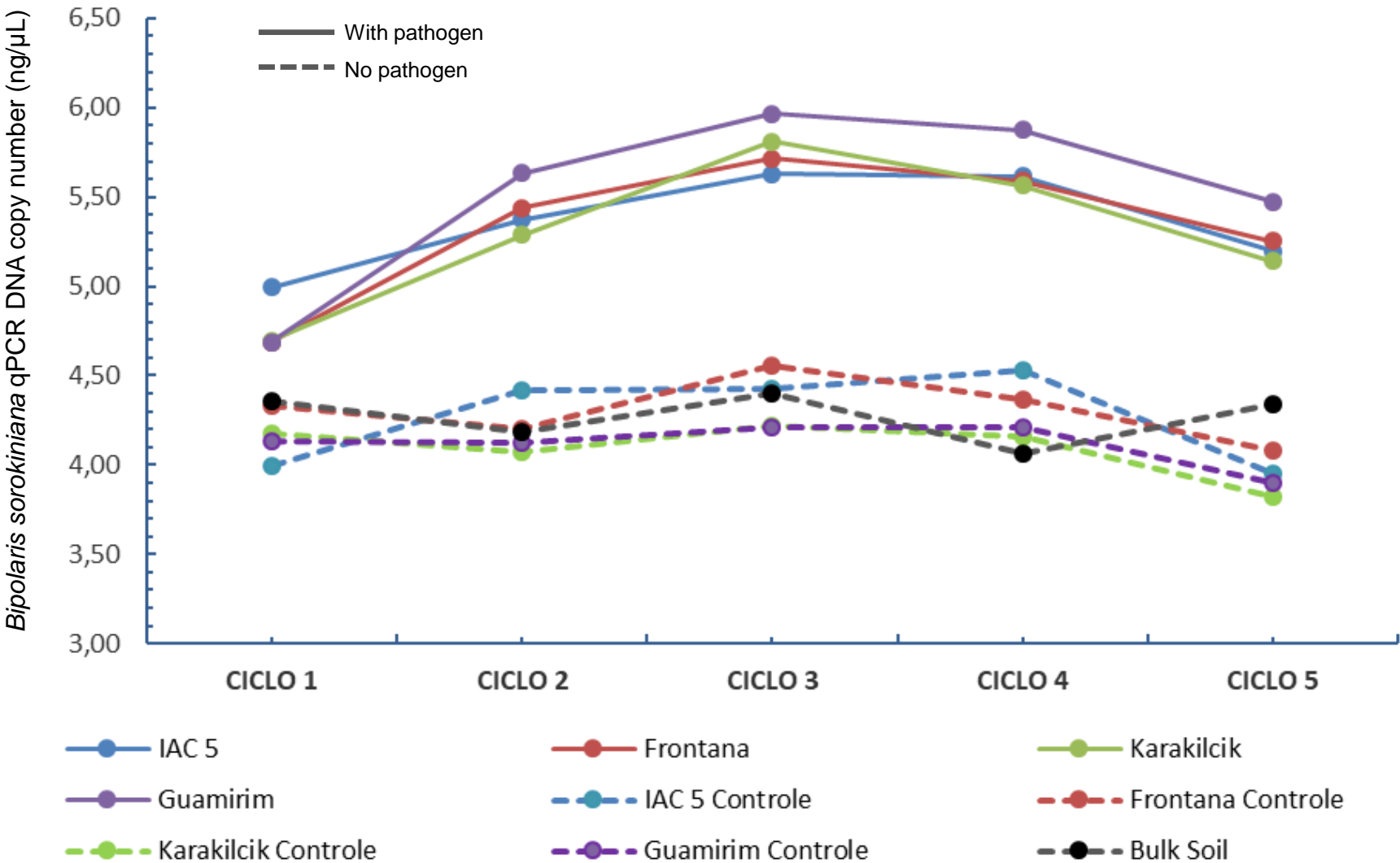


# Wheat

## *Bipolaris sorokiniana*



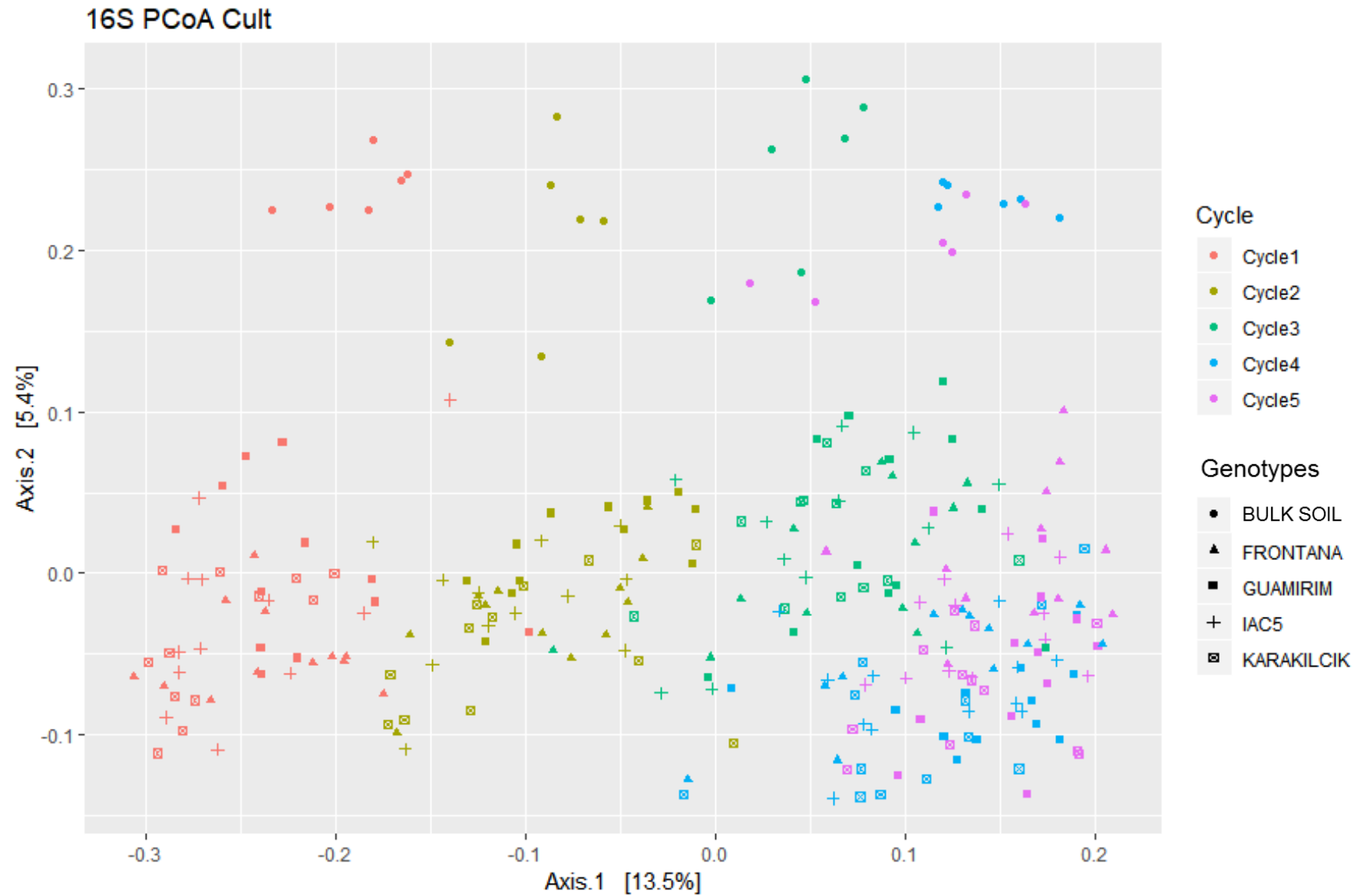
Wheat  
*Bipolaris sorokiniana*



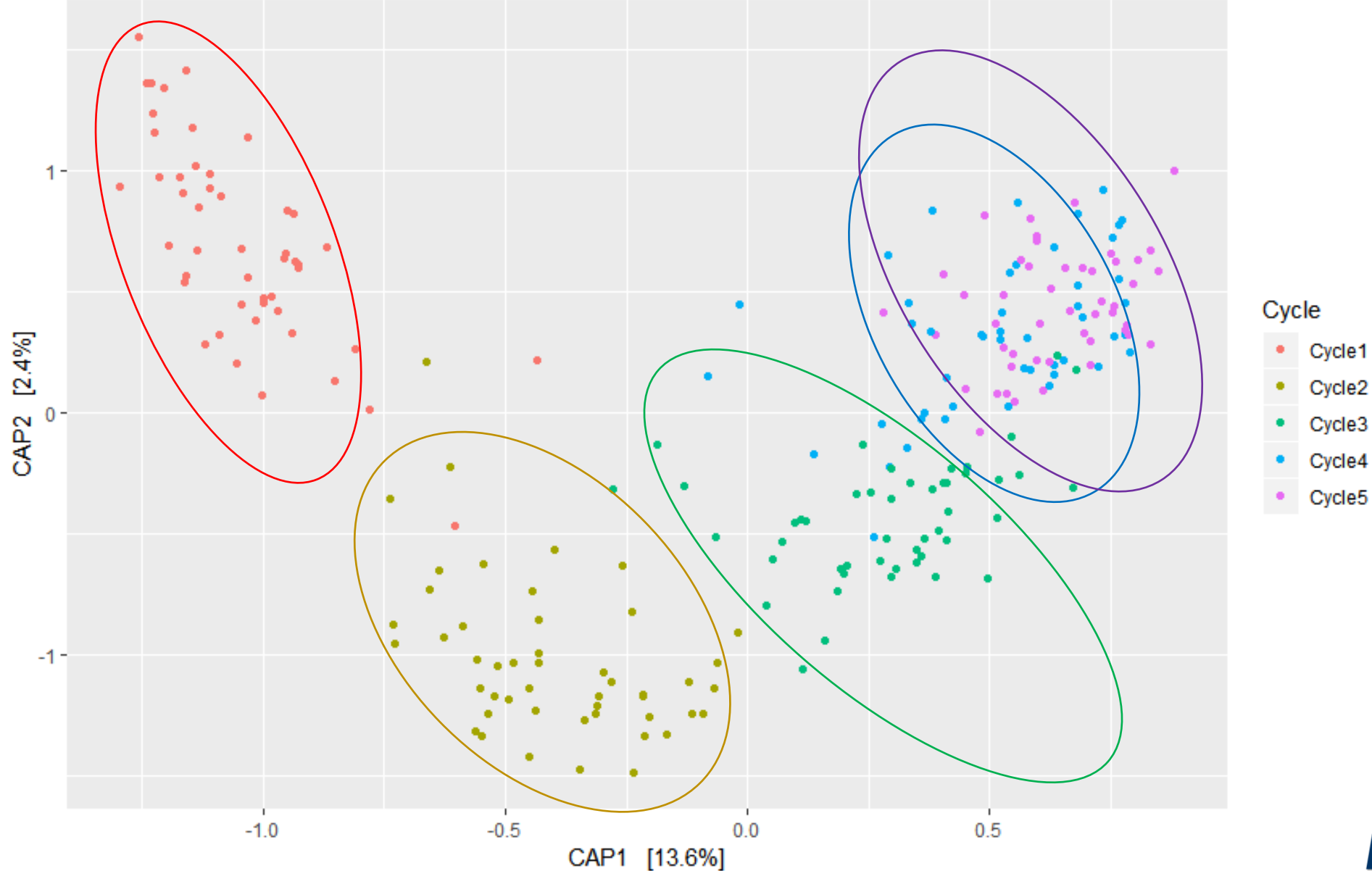


# Wheat

## *Bipolaris sorokiniana*

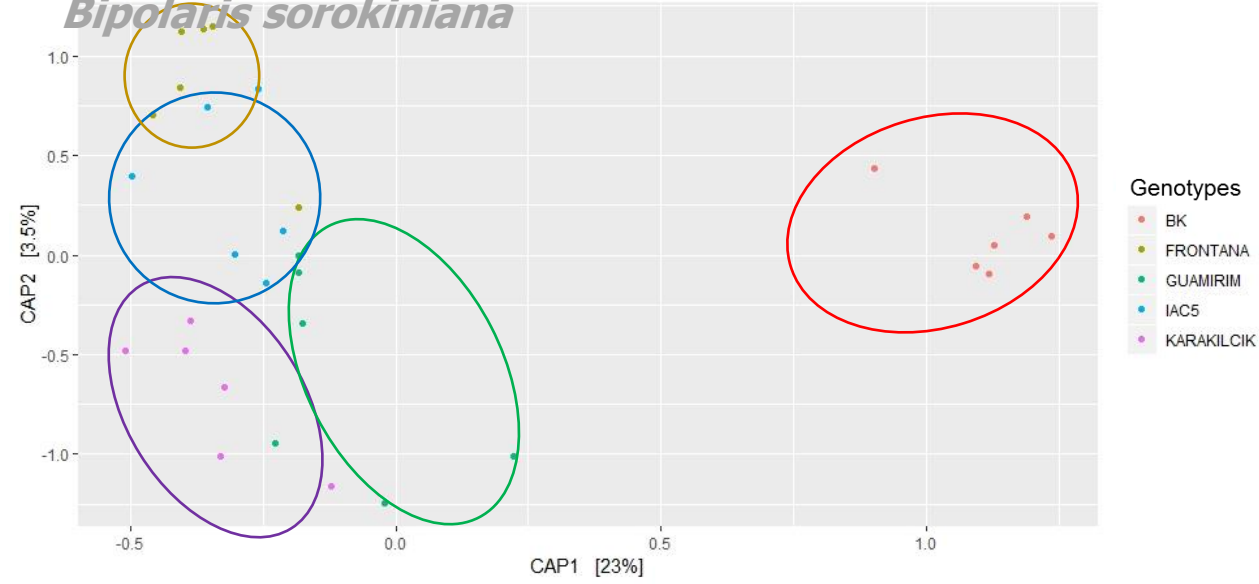


Wheat  
*Bipolaris sorokiniana*

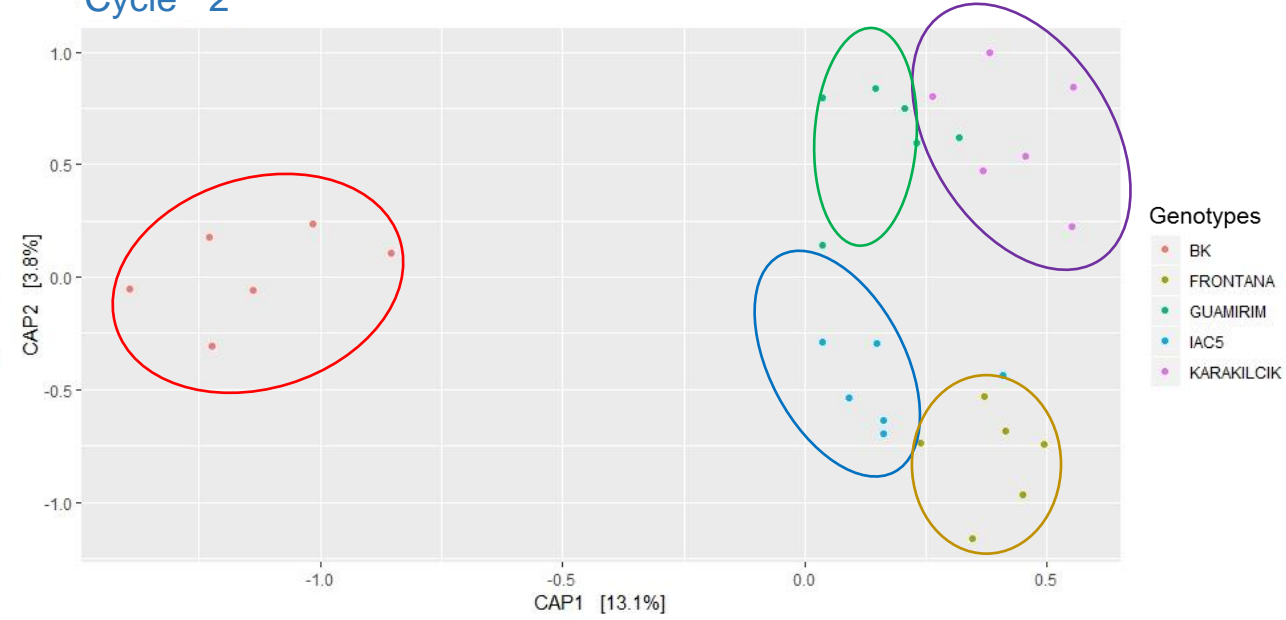


# Wheat Cycle 1

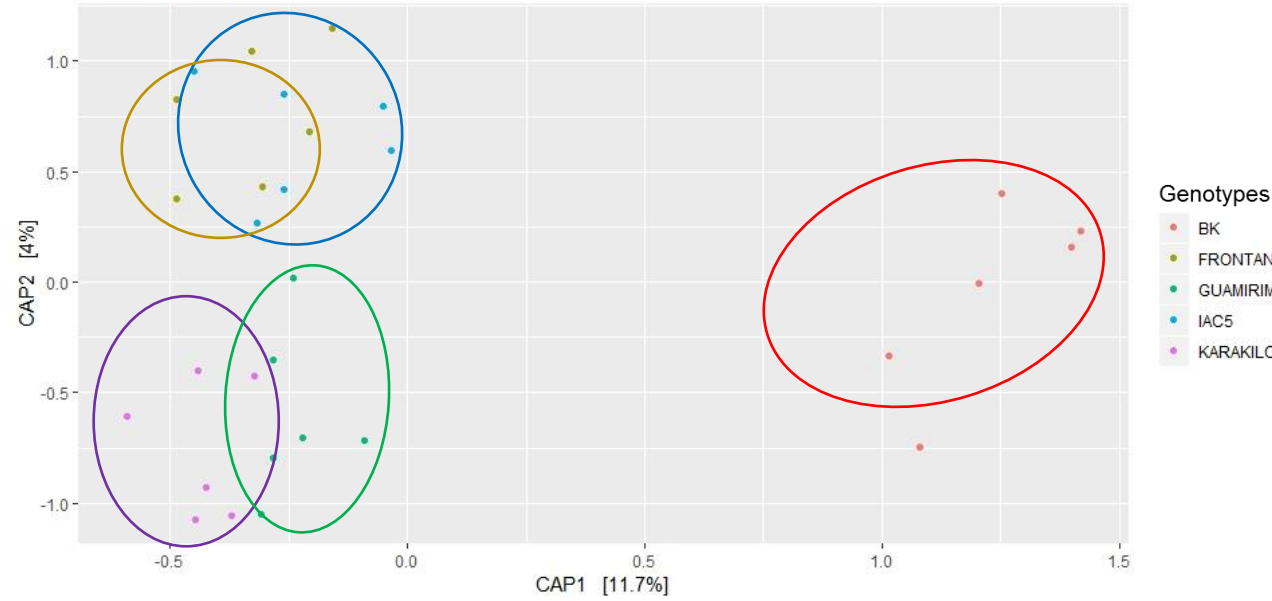
## *Bipolaris sorokiniana*



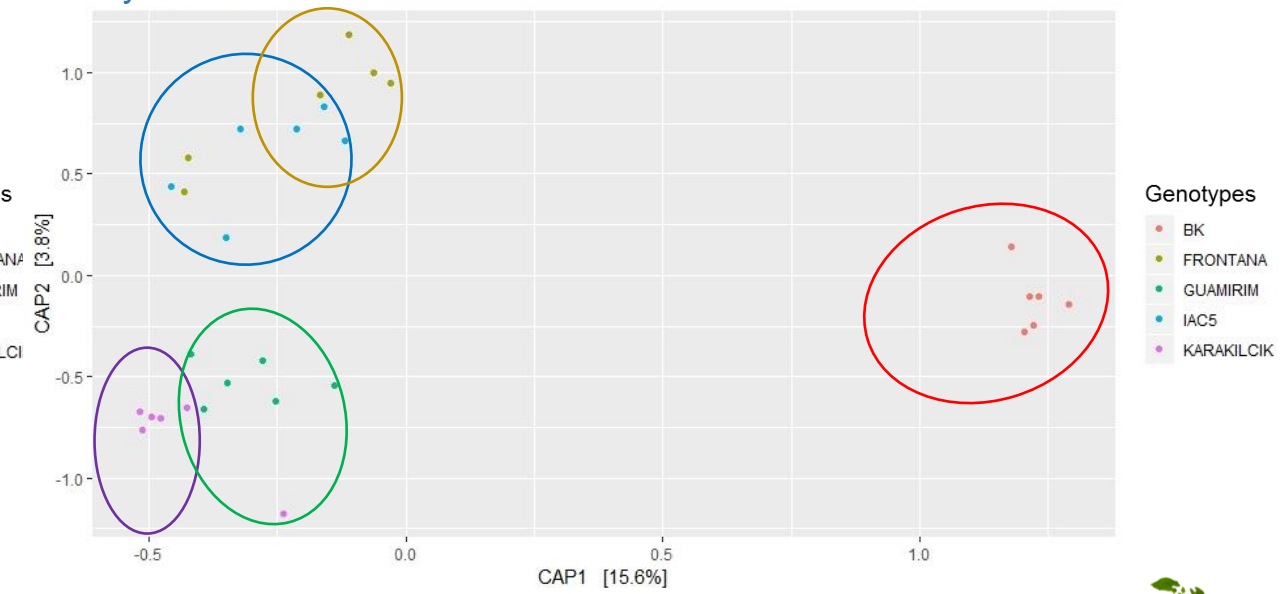
# Cycle 2



# Cycle 3

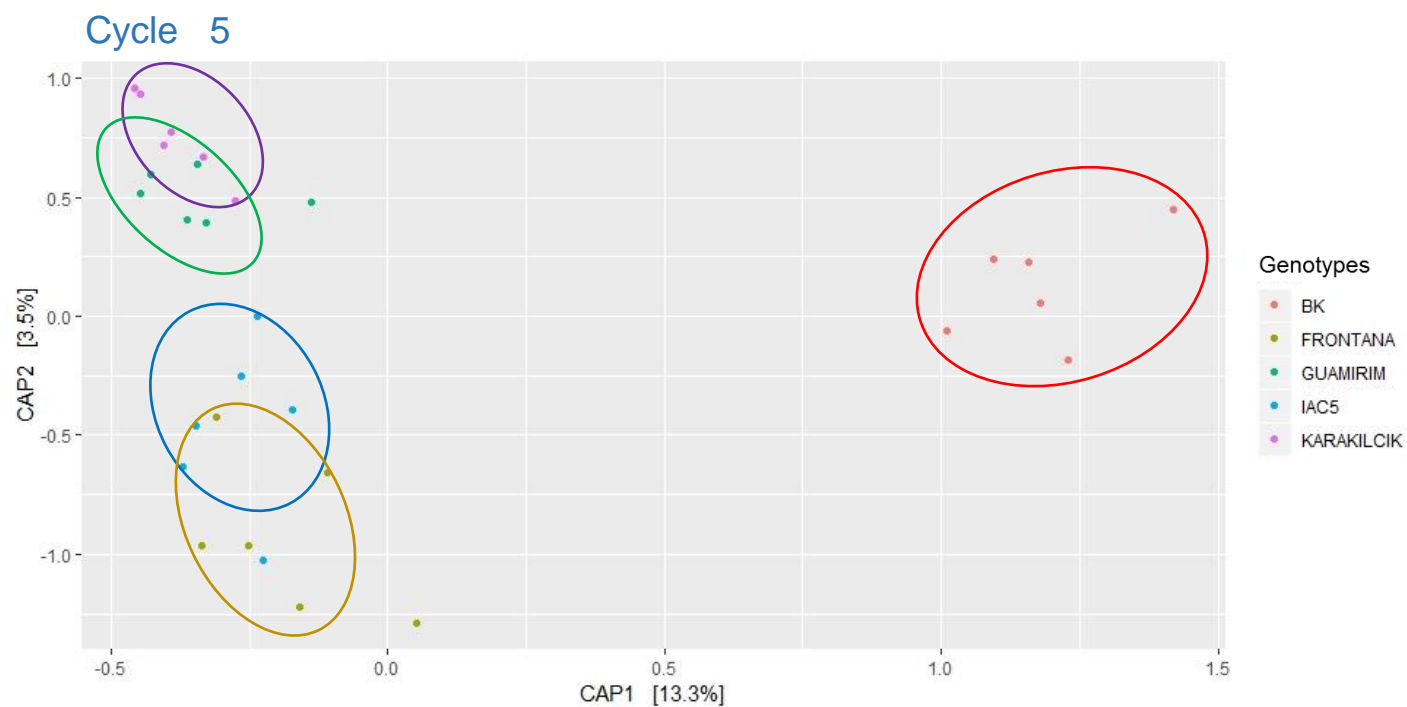


# Cycle 4

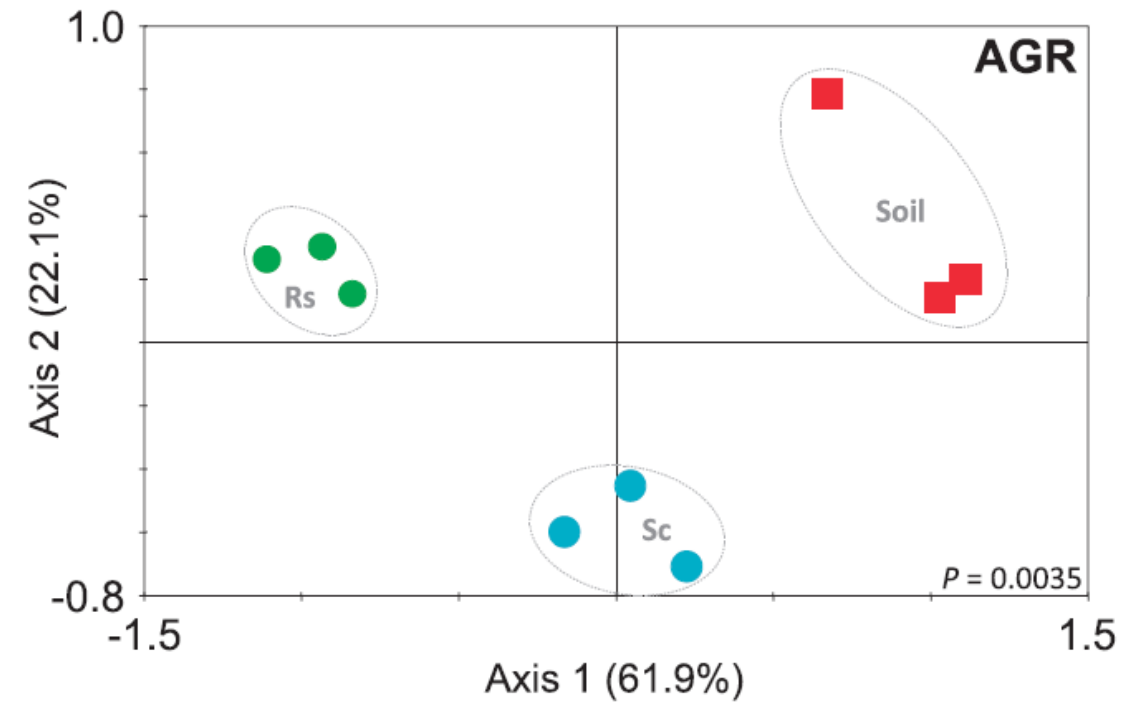
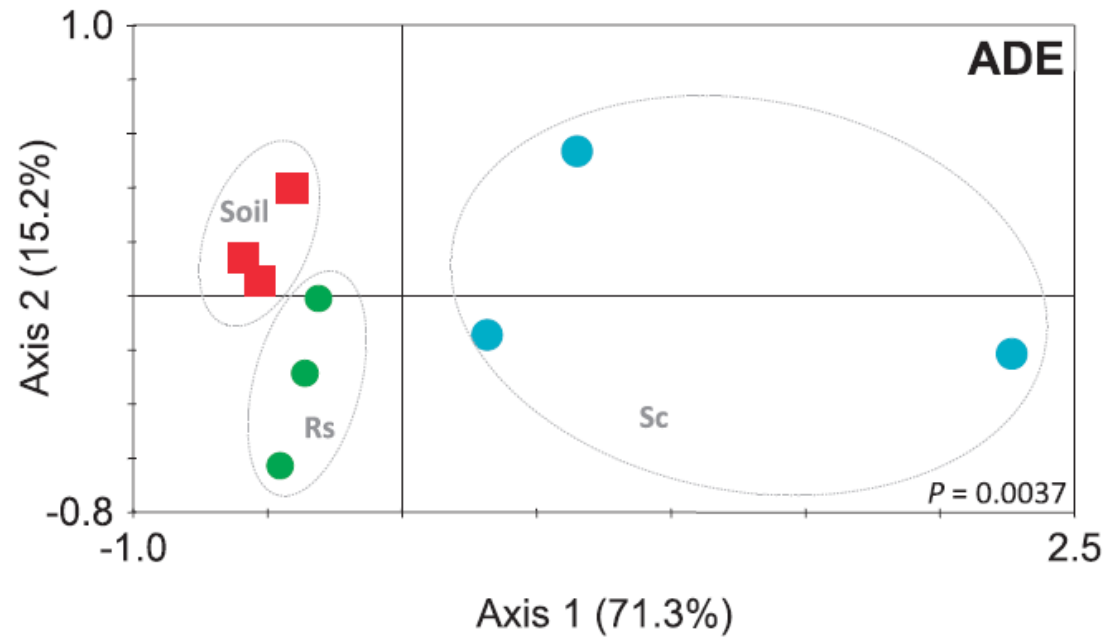




Wheat  
*Bipolaris sorokiniana*



Identificação (16S)	Código do isolado	Origem*	Prod. de AIA	Solub. de P	Antag. (Fusarium)	Fix. de N
<i>B. megaterium</i>	CMAA 1743	W1-5/7	+	+	-	+
<i>Lysinibacillus</i>	CMAA 1742	W2-5/1	+	+	-	+
<i>Paenarthrobacter</i>	CMAA 1740	C6-3/11	+	+	-	+
<i>Paenibacillus</i>	CMAA 1739	W2-3/5	+	+	+	+
<i>Pseudomonas</i>	CMAA 1741	W2-3/2a	+	+	-	+
<i>Streptomyces</i>	CMAA 1738	W1-2/2	+	+	+	-



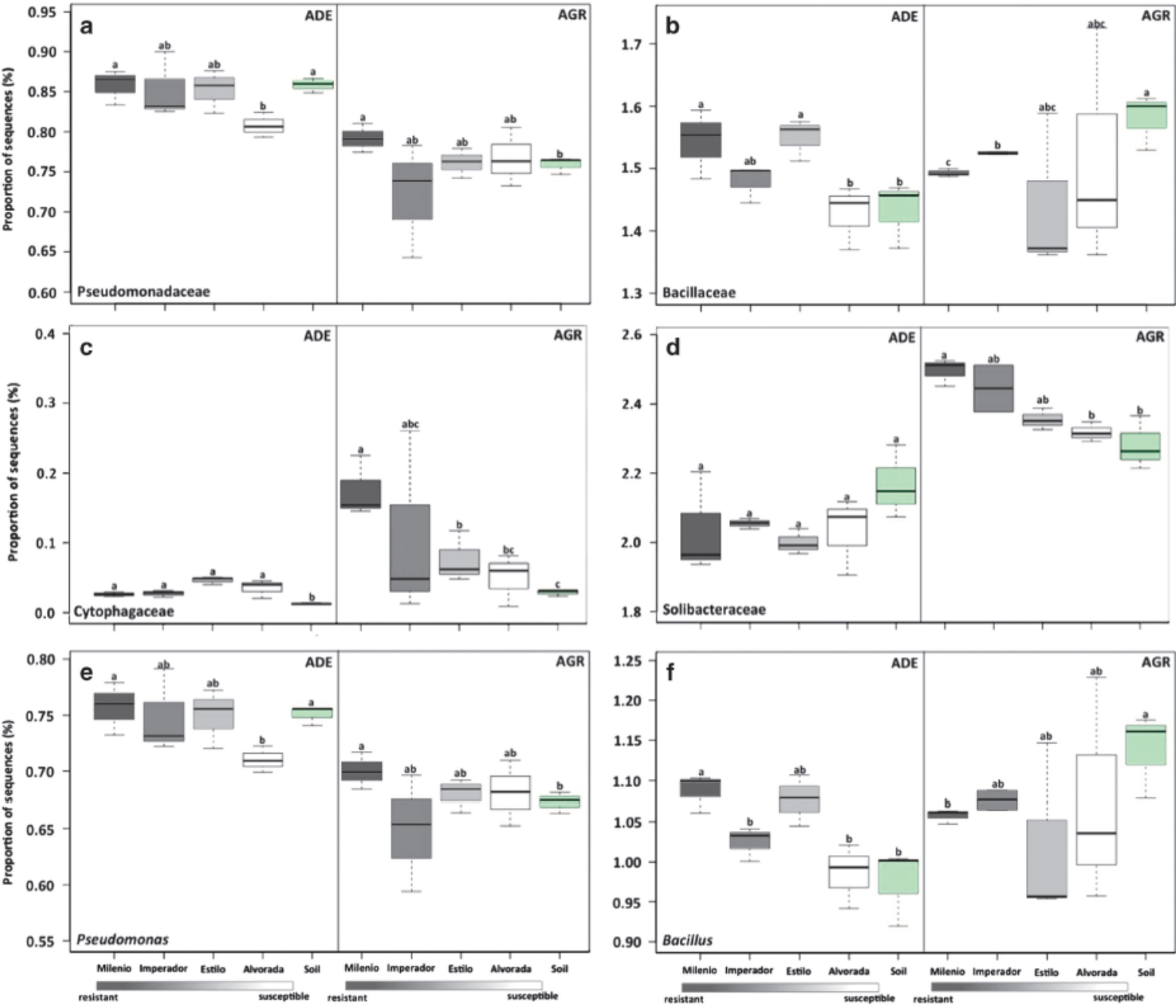
## Influence of resistance breeding in common bean on rhizosphere microbiome composition and function

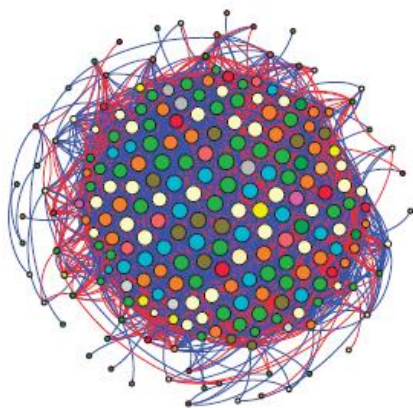
[ Mendes et al., ISME J 2017 ]



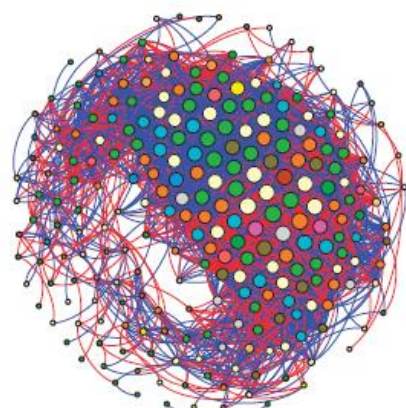
**Influence of resistance breeding in common bean on rhizosphere microbiome composition and function**

[ Mendes et al., ISME J 2017 ]

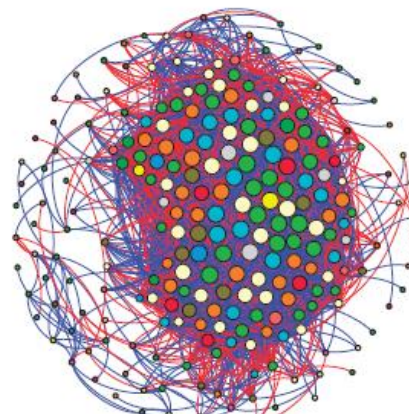




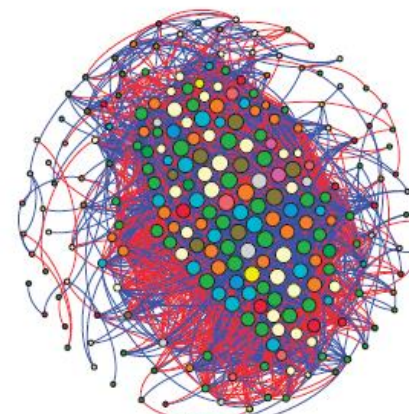
**Resistant**  
*IAC Milenio*



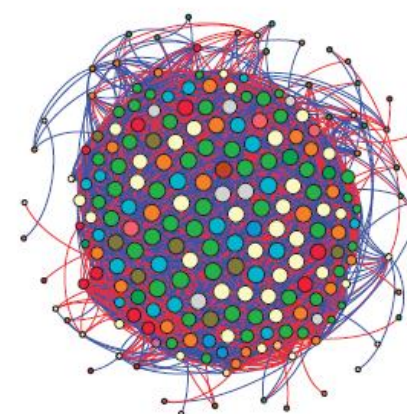
**Moderately Resistant**  
*IAC Imperador*



**Moderately Resistant**  
*BRS Estilo*



**Susceptible**  
*IAC Alvorada*



**Soil**

● Acidobacteria ● Actinobacteria ● Bacteroidetes ● Chlamydiae ● Chloroflexi ● Cyanobacteria ● Firmicutes ● Planctomycetes ● Proteobacteria ● Verrucomicrobia ● Archaea ● Others

## Influence of resistance breeding in common bean on rhizosphere microbiome composition and function

[ Mendes et al., ISME J 2017 ]