

# From Soil to Yield: Unraveling the Role of Microbiome Diagnostics in Enhancing Biofertilizer Efficiency

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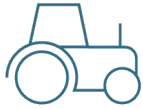
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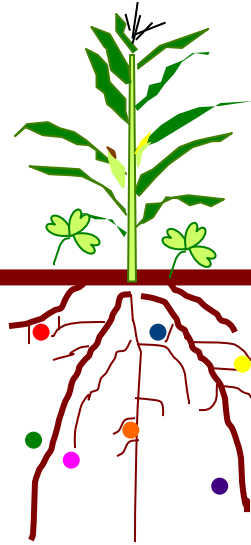


# Sustainable agriculture: lower input, higher microbial diversity



## Soil management

- low till
- mulching



## Plant choice

- Enhanced crop diversity
- Intercropping
- Living mulch
- Plant breeding



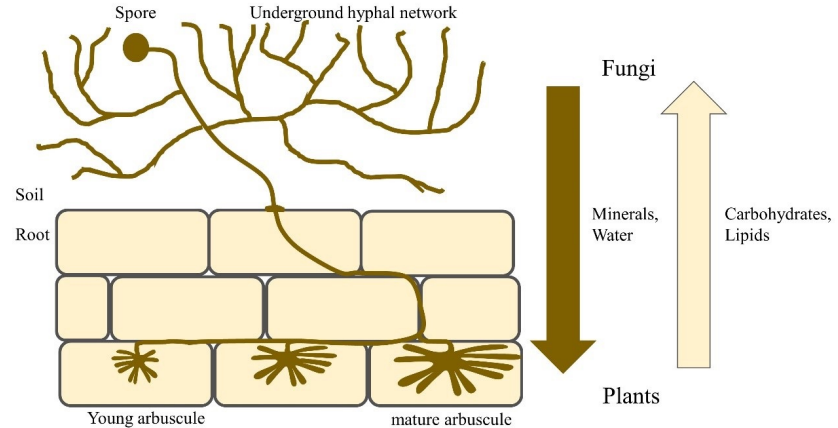
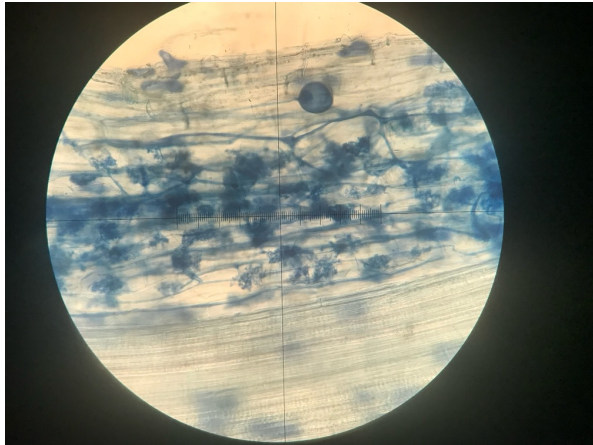
## Microbiome level

- Inoculation with beneficial soil organisms



# Inoculation with Arbuscular Mycorrhizal Fungi (AMF)

- Phylum Glomeromycota
- Symbiosis with 80% plant species
- Exchange of carbohydrates for nutrients including phosphorous
- Characteristic arbuscule



*Credit: Florence Sessoms*

# Inoculation is more often successful under controlled conditions than in the field

Credit: Franz Bender



control

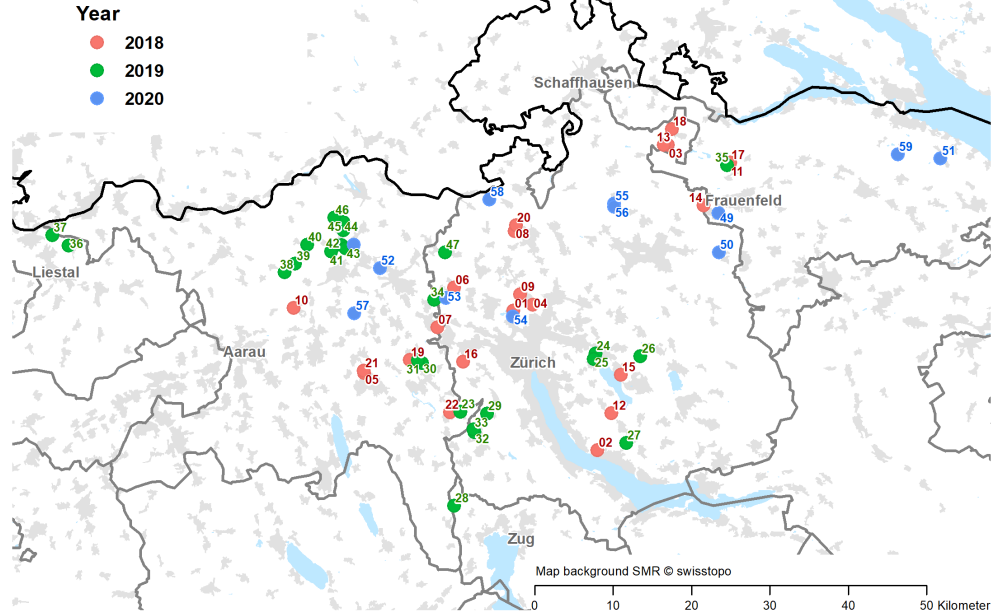
inoculated

Context dependency

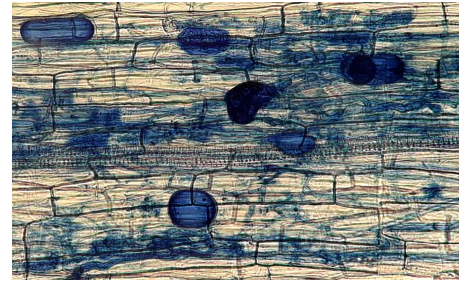
1. identity of plant host
2. identity of the fungi
3. soil fertility
4. biotic complexity of the soil

Hoeksema et al. Ecology letters (2010)

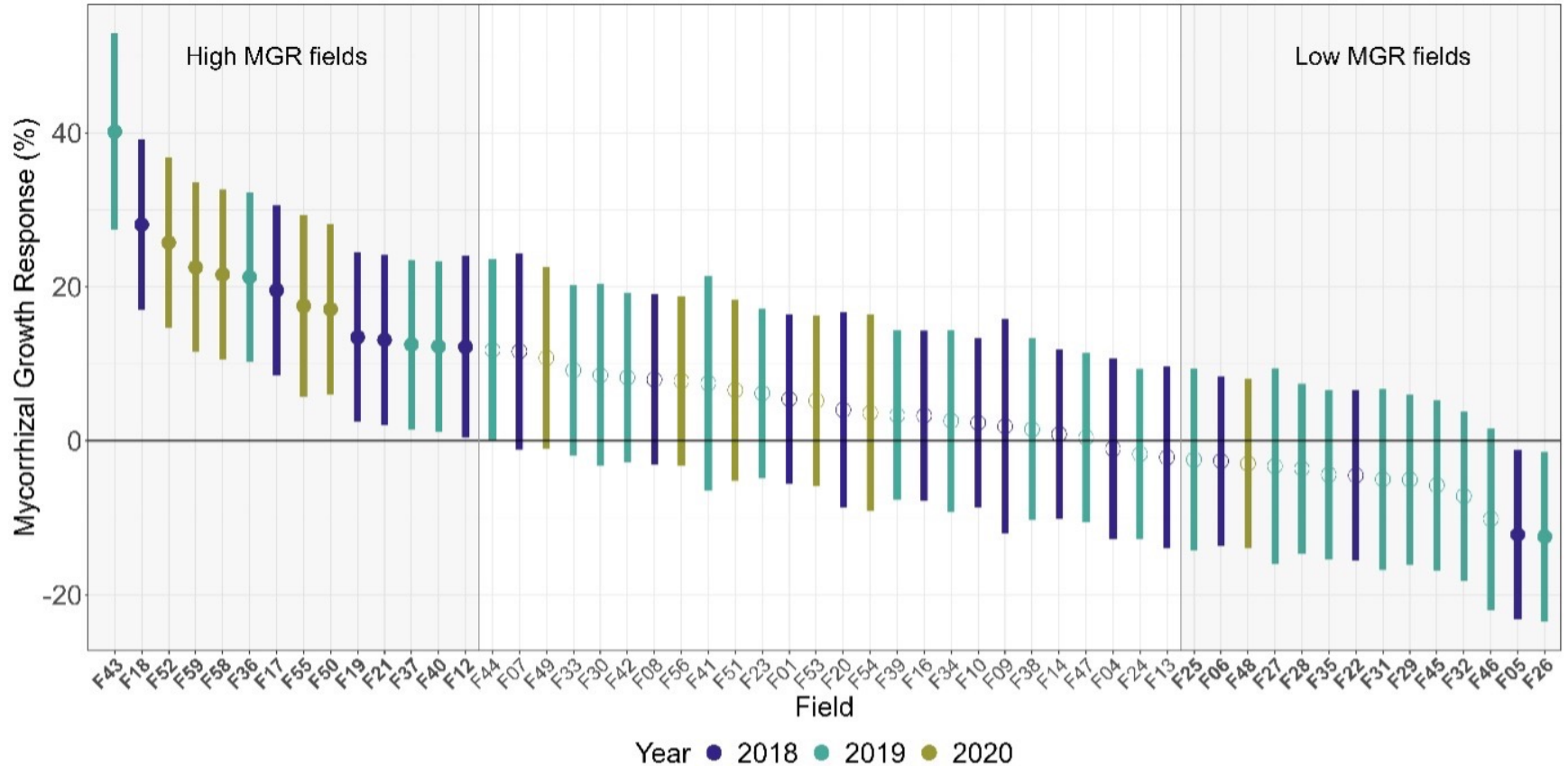
# 54 on farm field experiments with maize



*Rhizoglomus irregulare* SAF22

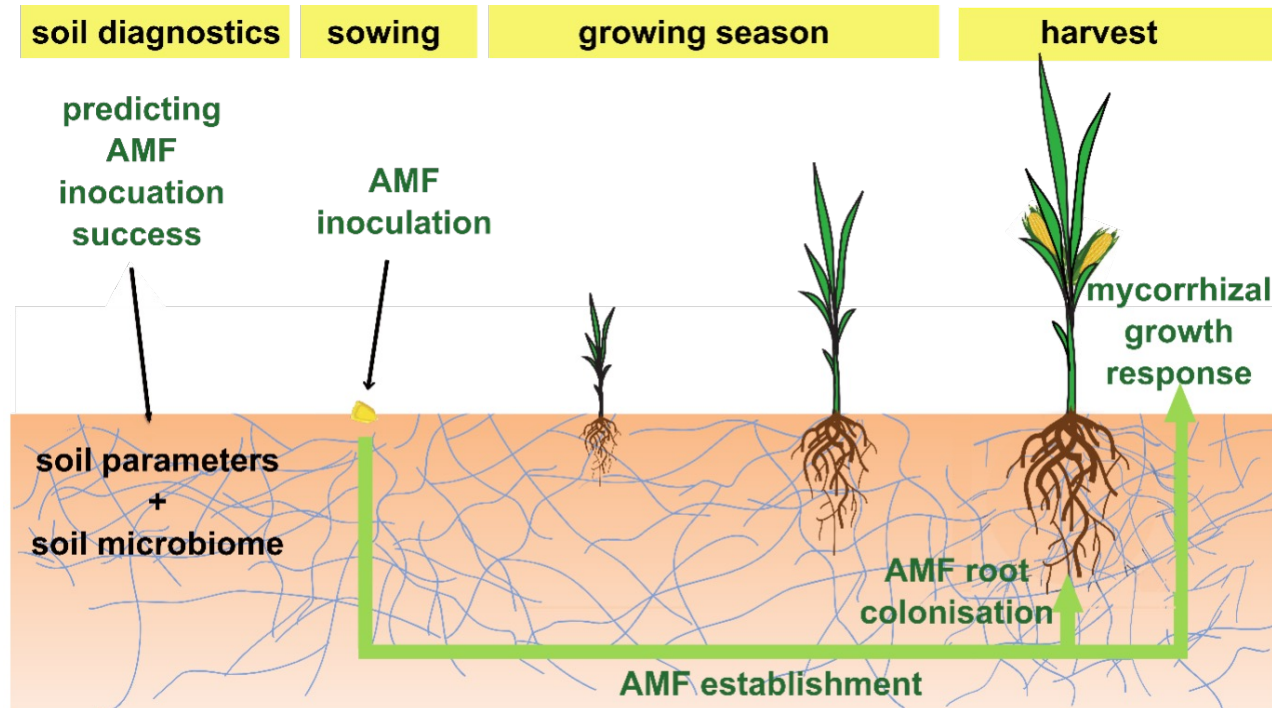


# 25% of the fields have positive mycorrhizal growth response



# Can we predict successful AMF inoculation based on:

AMF establishment?  
Soil properties?  
Soil microbiome?



# Does mycorrhizal growth response depend on establishment ?

inoculation → establishment → mycorrhizal growth response

microscopy



“magnified intersection method”  
McGonigle et al 1990

sequencing



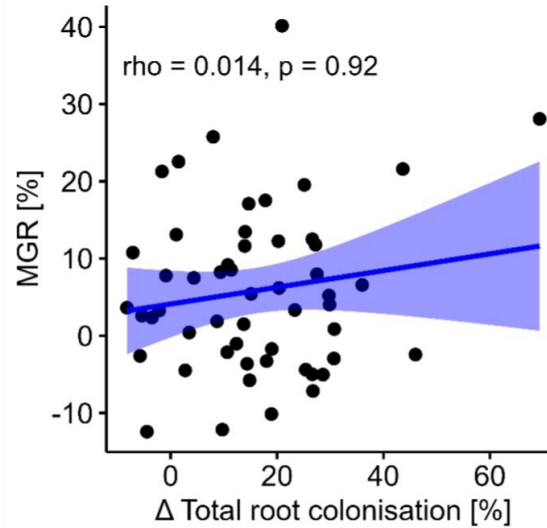
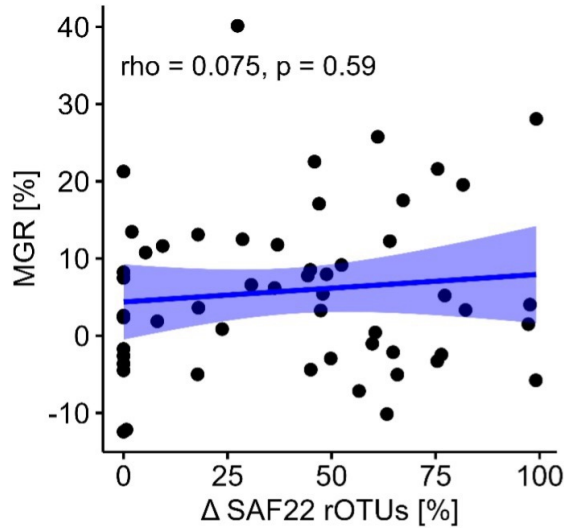
Pacbio sequencing

Schlaeppli et al. 2016

Primers Cf and Br  
amplify Glomeromycota



# Mycorrhizal growth response does **not** depend on abundance of *Rhizoglopus irregulare* SAF22

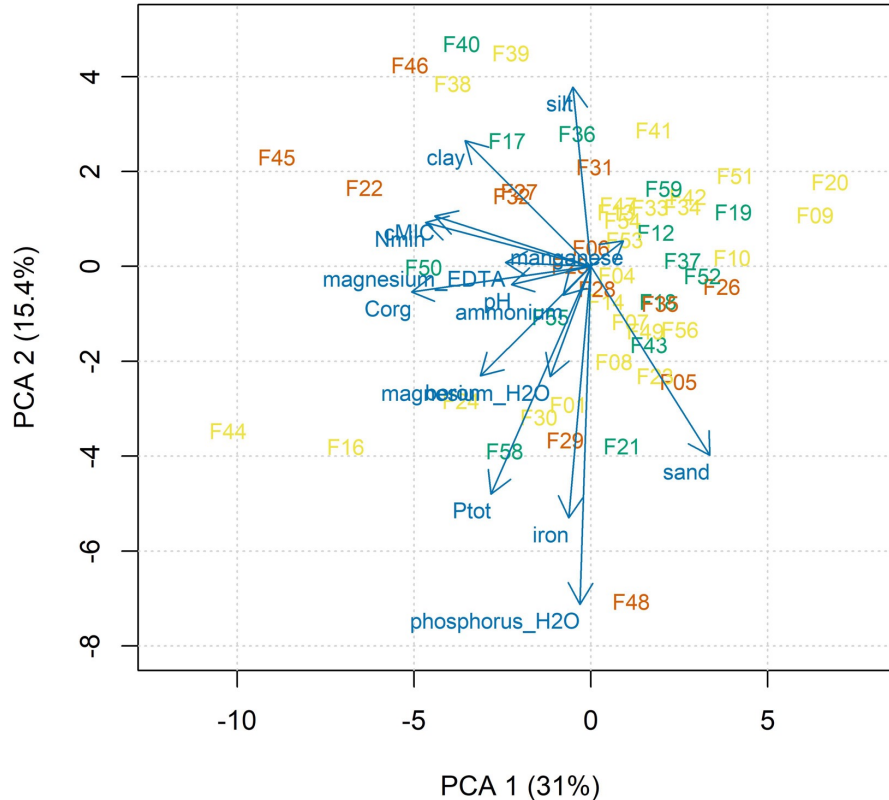


# Does mycorrhizal growth response depend on soil parameters ?



physical	chemical	biological
soil texture	pH	microbial biomass
water holding capacity	extractable nutrients (P, N, K, ..)	microbial respiration
soil structure	soil organic matter (humus)	

# Principle Component Analysis of 15 soil variables



MGR ● High ● Medium ● Low

No grouping of samples by the mycorrhizal growth response

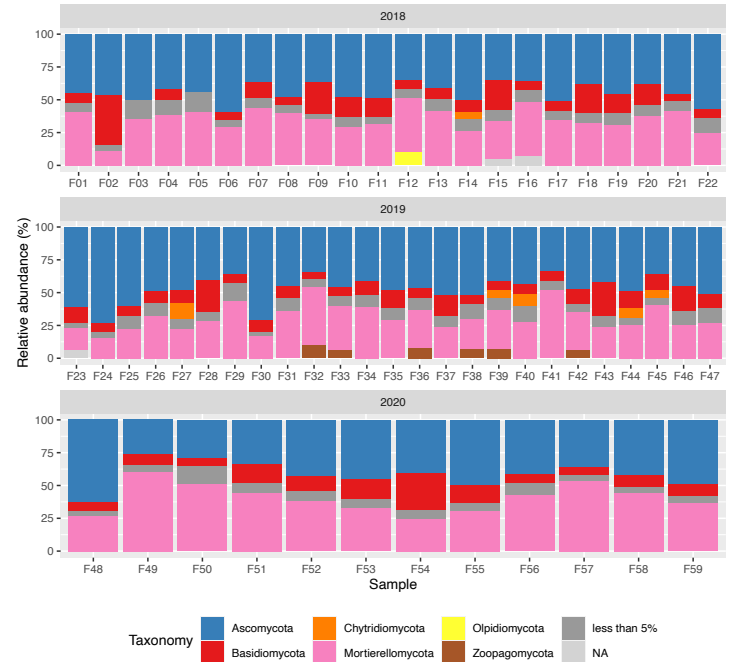
# Does mycorrhizal growth response depend on soil microbiome ?



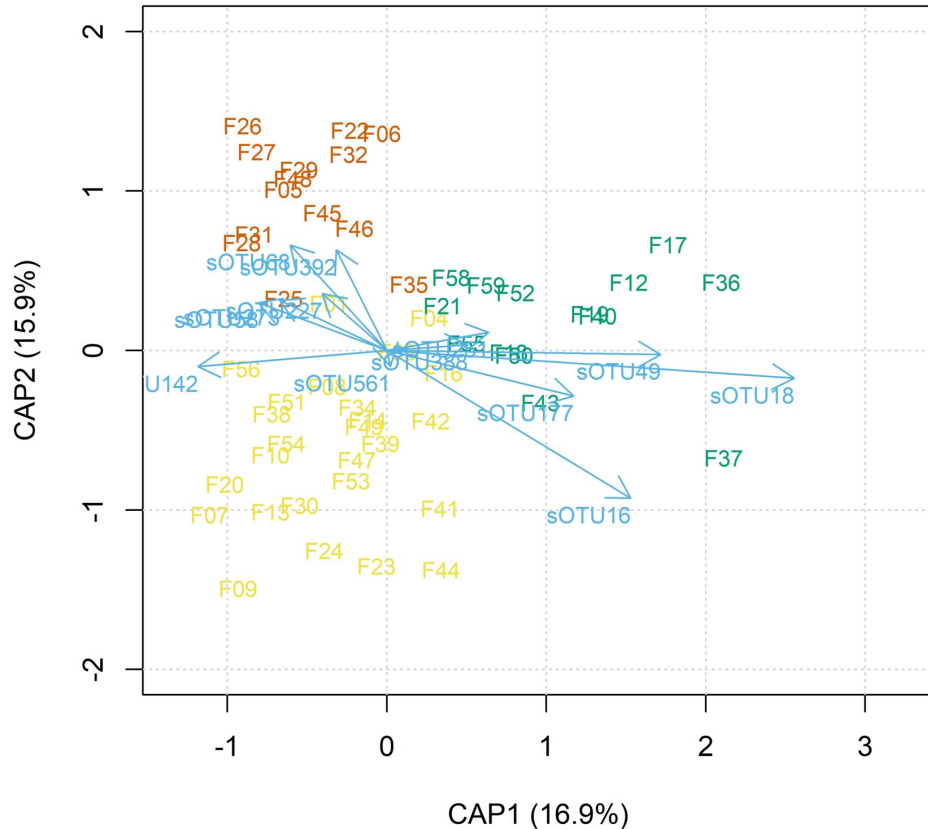
Pacbio sequencing

Bodenhausen et al. 2023

Primers ITS1F and ITS4  
amplify Ascomycota,  
Basidiomycota and  
Mortierellomycota



# Community composition of the soil microbiome



MGR ● High ● Medium ● Low

Clear grouping of samples by the mycorrhizal growth response.

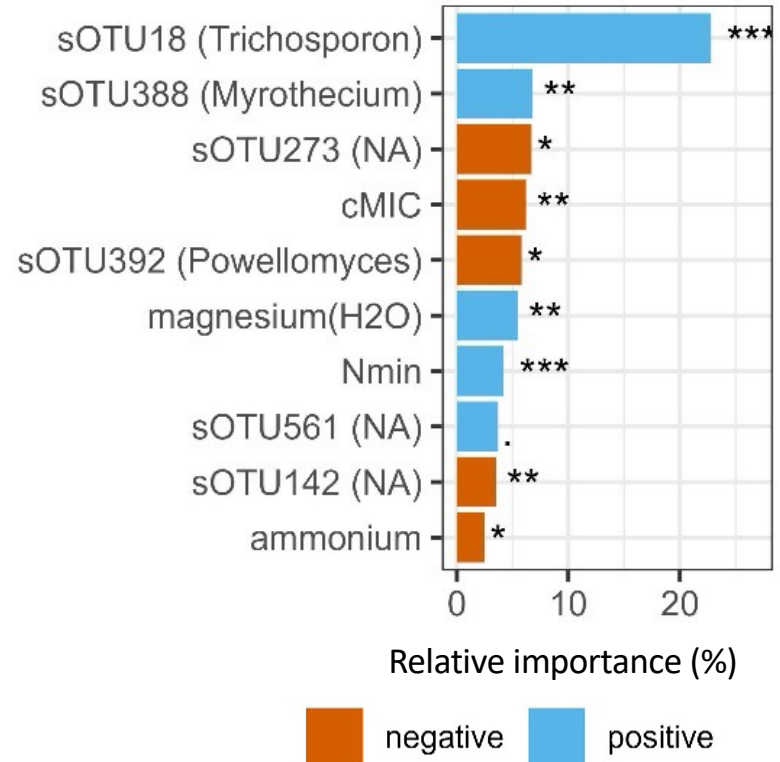
# Modeling mycorrhizal growth response

Reduced model

$r^2=0.683$ ,  $p<0.001$

Soil OTUs explain most of the variation in MGR

Soil variables are less important



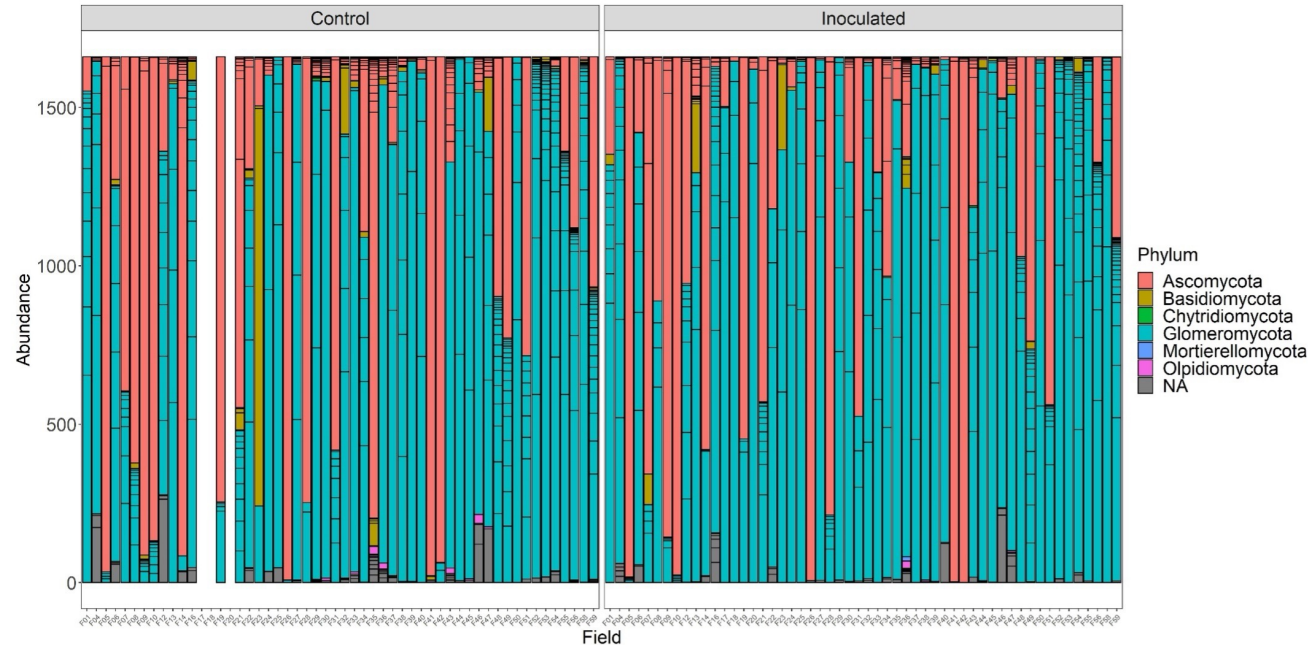
# Pacbio sequencing of the root microbiome

Pacbio sequencing

Schlaeppli et al. 2016

Primers Cf and Br  
amplify Glomeromycota

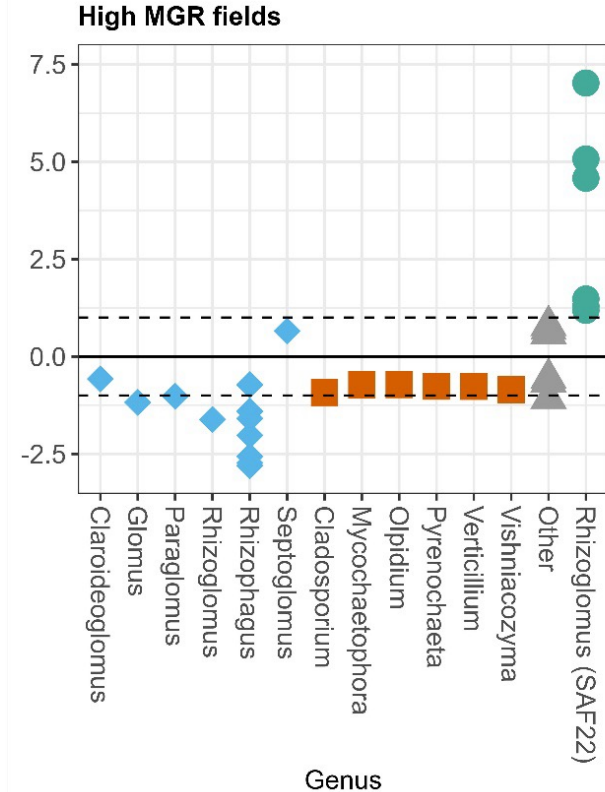
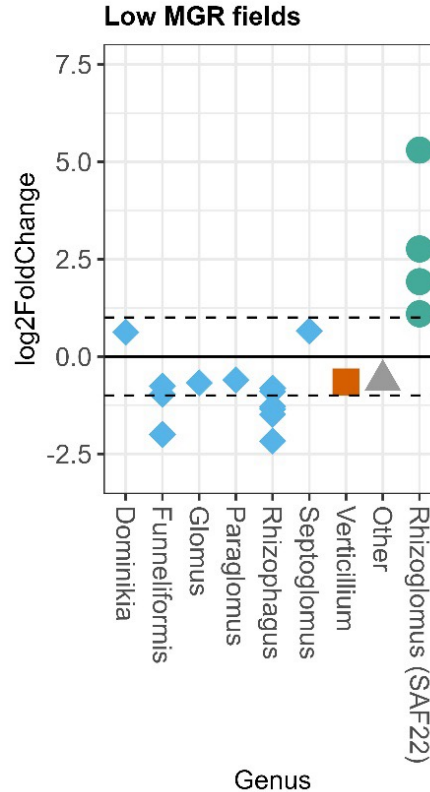
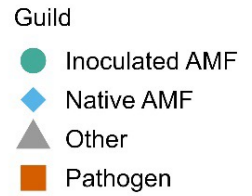
and other fungal  
sequences, as well!



# Differential abundance analysis

*Rhizoglyphus irregulare*  
SAF22 largely replaces  
native AMF

High MGR fields: the  
relative abundance of  
several plant pathogenic  
taxa reduced.





# Conclusions

- Soil fungal OTUs are good predictors of inoculation success
- AMF protect plant roots against colonization by plant pathogens.
- Possible mechanisms:
  - improved plant nutrition
  - induced systemic resistance
  - competition for root space

<https://doi.org/10.1038/s41564-023-01520-w>

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nature microbiology

Article

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## Soil microbiome indicators can predict crop growth response to large-scale inoculation with arbuscular mycorrhizal fungi

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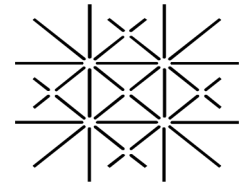
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