Thanks for stopping by my poster!

- This is my project website:
 https://www.ufz.de/spp-rhizosphere/index.php?en=46041
- For more experimental details, hover over the images (does not work in browser).
- If you have any questions or suggestions, email me at minh.ganther@ufz.de.



SPATIAL SAMPLING APPROACH TO UNRAVEL THE IMPACT OF SOIL TEXTURE AND ROOT GENOTYPE ON MAIZE ROOT GENE EXPRESSION PROFILES

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INTRODUCTION

Rhizosphere interactions are shaped by soil and plant properties¹. acdS bacteria decrease plant ethylene levels and thereby contribute profoundly to plant health².

We investigated in a soil column experiment how soil types, root genotype, and depth gradients shape gene expression patterns of maize roots and rhizosphere acdS bacterial communities.

EXP. DESIGN soil type depth genotype

DI > D2 >

D3

wildtype loam roothairless sand (rth3)

root gene expression

rhizosphere acdS abundance & community



root genes

RESULTS

acdS bacteria

DRIVERS

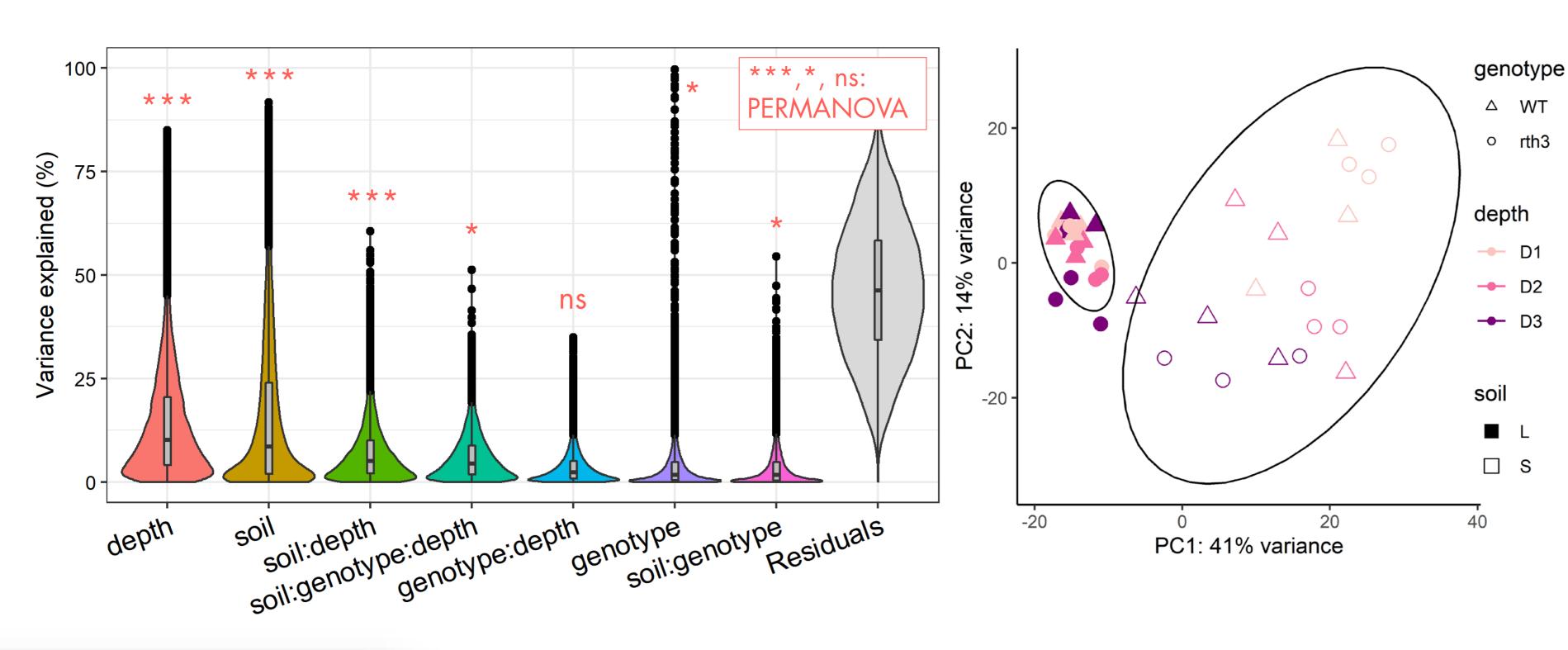
Root expression patterns are mainly explained by soil and depth, but genotype effect is surprisingly minor.

acdS bacteria community composition

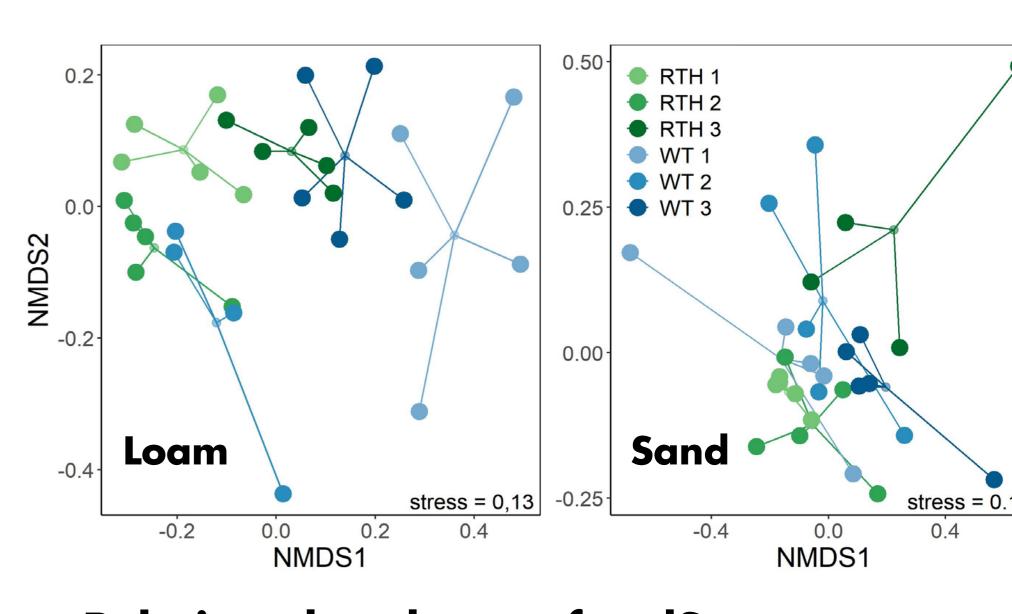
is also driven by soil and depth.

NMDS of acdS genes in the rhizosphere

VariancePartioning / PERMANOVA



PCA

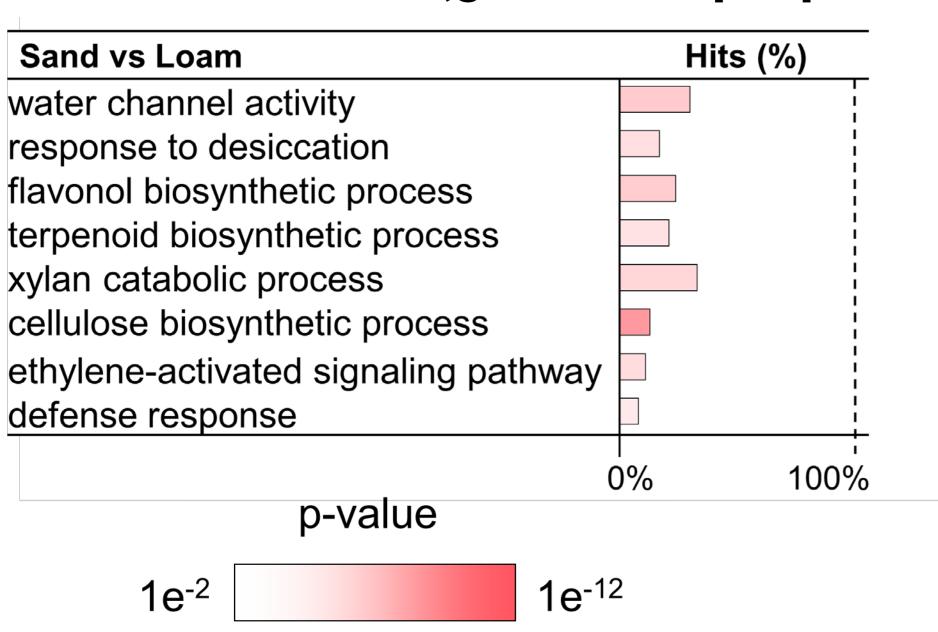


Relative abundance of acdS genes at the order level

FUNCTIONS

Differentially expressed genes comprise various interesting functions and pathways:

GO term analysis (genes with padj <0.05, >2-fold differential expression)

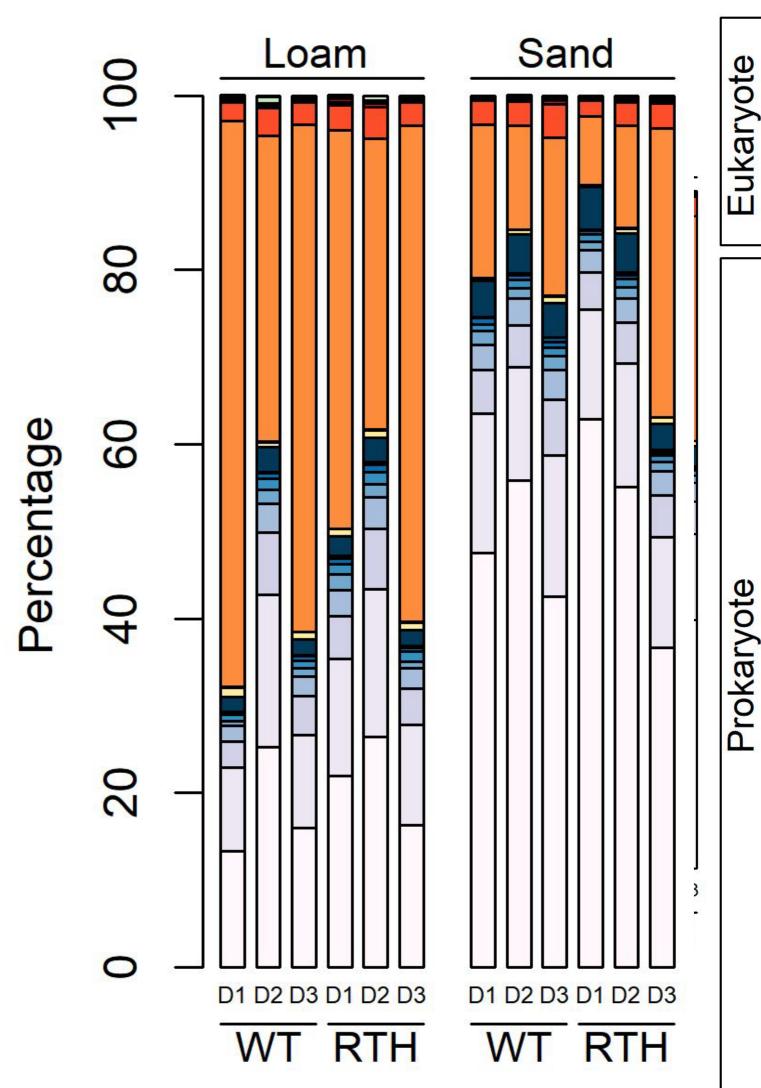


Hits (%) rth3 vs Wildtype androstan-3-alpha,17-beta-diol DH diterpene phytoalexin biosynthesis nitrite transport nitrate transmembrane transporter **D3 vs D1** Hits (%) response to ethylene respiratory burst involved in defense ethylene-activated signaling pathway plant-type cell wall organization xyloglucan metabolic process anthocyanin compound biosytnehsis

References

1 Berg G, Smalla K (2009) FEMS Microbiol Ecol 68: 1-13.

2 Glick BR (2014) Microbiol Res 169: 30-39.



Oomycetes Peronosporales Sordariomycetes

■ Glomerellales

□ Sordariales ***

unclassified bacteria Alphaproteobacteria

Sphingomonadales

Rhodospirillales

Rhodobacterales Rhizobiales ***

Betaproteobacteria ■ Burkholderiales ***

Gammaproteobacteria

unclassified

Enterobacterales Pseudomonadales *

Actinobacteria

unclassified ***

Nakamurellales

Micromonosporales

Geodermatophilales Propionibacteriales *

Corynebacteriales **

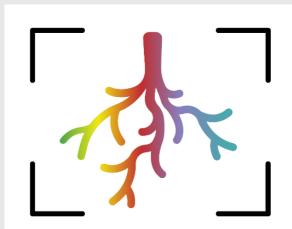
Pseudonocardiales **

□ Micrococcales *** ☐ Streptomycetales ***

CONCLUSION

- Soil and Depth are main drivers for both root gene expression and acdS bacteria community composition
- Differentially expressed genes relate to multiple functional categories such as: growth, water/nutrient uptake, secondary metabolism, stress, and phytohormone signaling.
- In Loam, acdS relative abundance is shifted towards proteobacteria, whereas in Sand, actinobacteria are more abundant.





RHIZOSPHERE **SPATIOTEMPORAL ORGANISATION**

