

Identification of plant genotype-dependent microbiome recruitment associated with disease resistance against root rot in peas

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Introduction

Peas (*Pisum sativum* L.) are of vital importance due to their nutritional value and their ability to promote soil fertility through symbiosis with nitrogen-fixing rhizobia. Pea cultivation is, however, constrained by various soil-borne pathogens that can trigger soil fatigue and thereby reduce yield. Cultivars resisting this complex of root pathogens are still missing. Harnessing the rhizosphere microbiome for increased resistance poses a possible mechanism to mitigate yield loss. To investigate this microbiome-mediated disease resistance, we compared the root microbiome of 252 pea lines in a controlled soil-based resistance phenotyping assay.

Methods

252 pea lines: 173 landraces (USDA gene bank accessions), 33 registered European cultivars, 46 Swiss breeding lines



Image: LfL

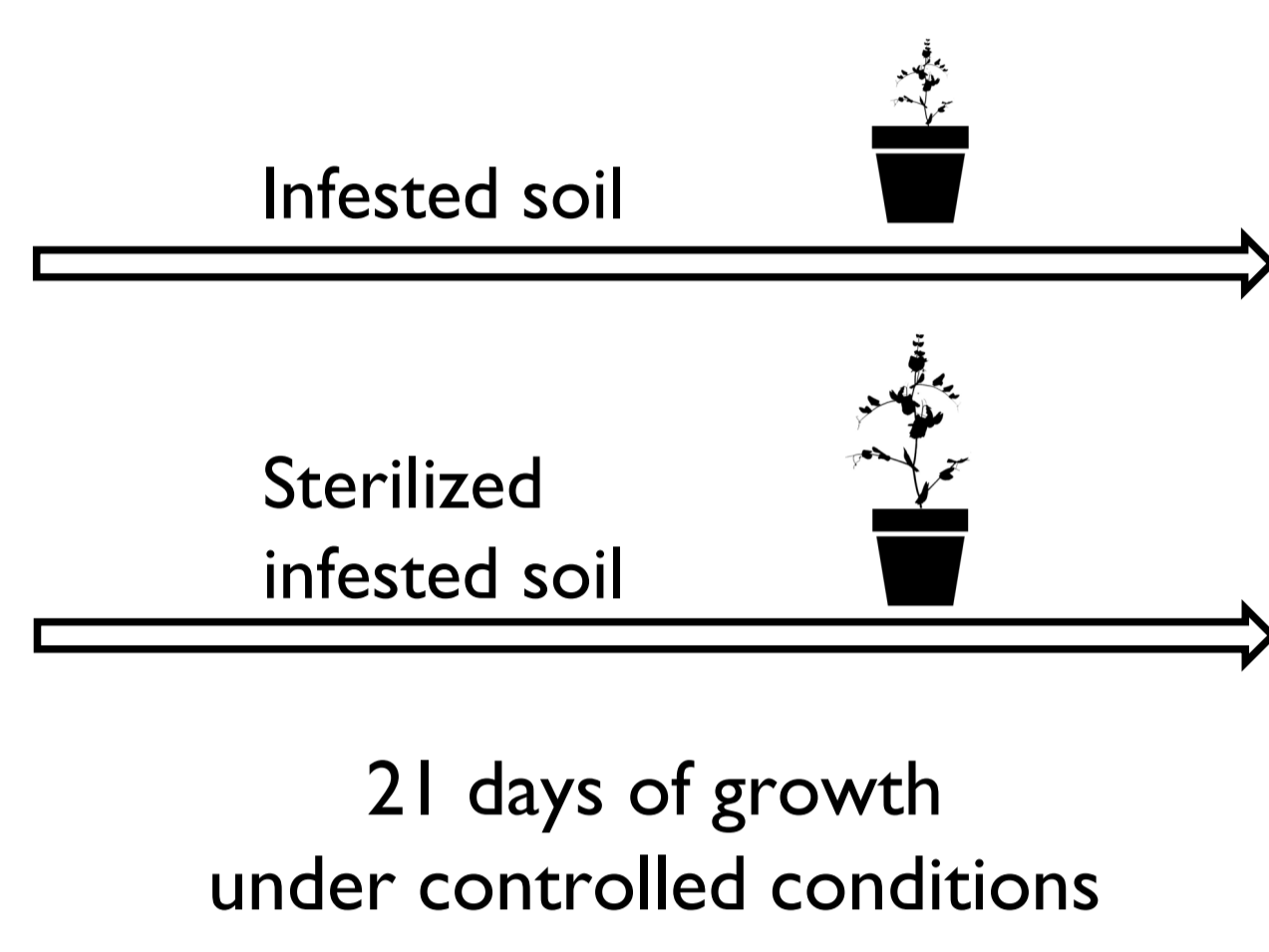


Image: Lukas Wille

Peas were grown in untreated and sterilized infested field soil for 21 days, phenotyped (Wille et. al, 2020), and roots were harvested for microbiome analysis. Root bacteria and fungi were characterized by 16S rRNA and ITS amplicon sequencing, followed by visualization and statistical analysis of different microbiome attributes.

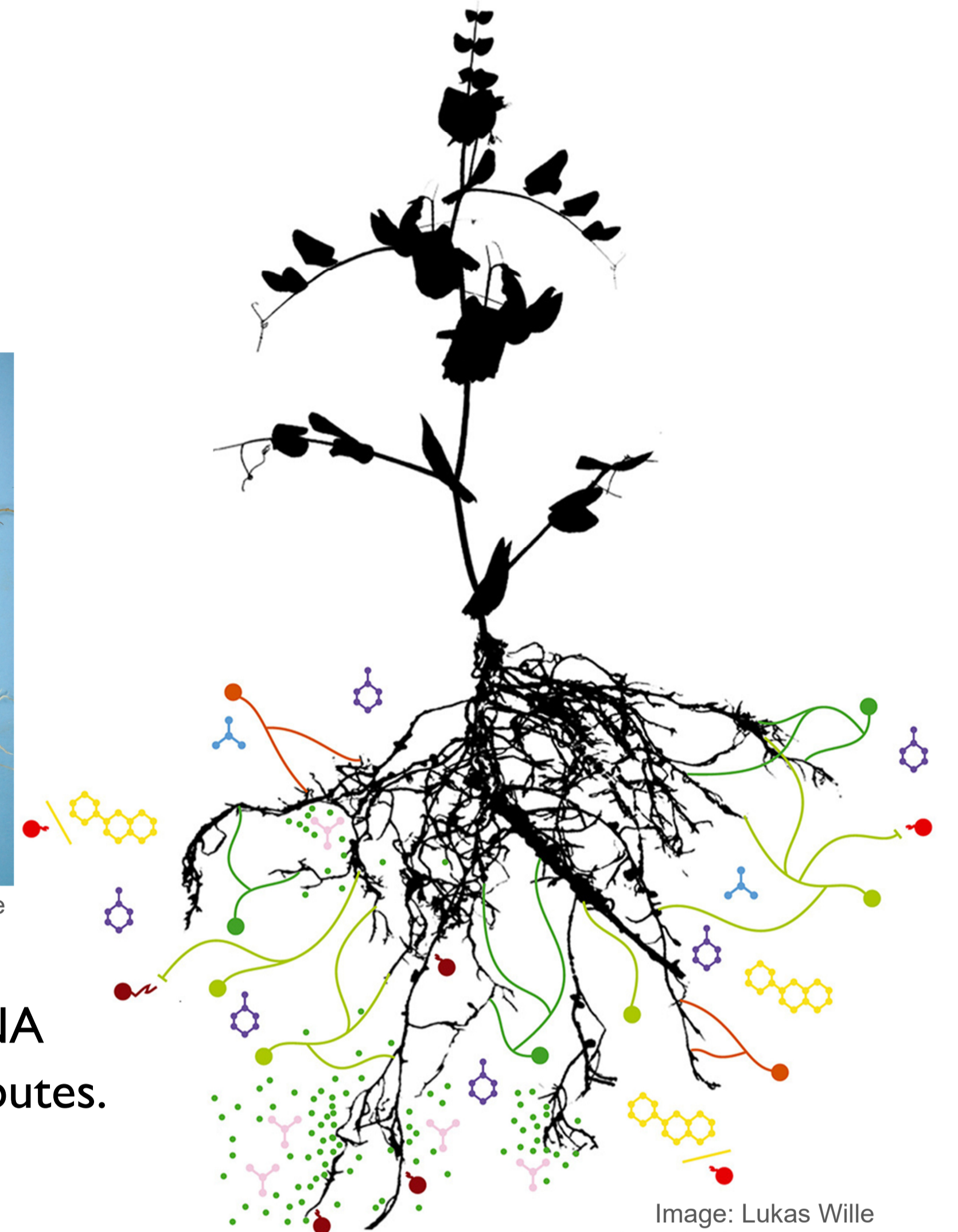


Image: Lukas Wille

Results

- Pea genotype influences the microbial community composition (Fig. 1)
- Microbial community composition is associated with plant resistance (Fig. 1)
- Pea genotypes correlate with potential pathogens and beneficial (Fig. 2)
- Many microbes (OTUs) are heritable (Fig. 3)
- Some of the heritable OTUs associated with disease resistance are highly connected in the microbial network (Fig. 4)
- Host genomic regions are associated with the abundance of potentially beneficial microbial communities and individual microbes (Fig. 5)

Fig. 1 Fungal communities (PCoA, Bray-Curtis)

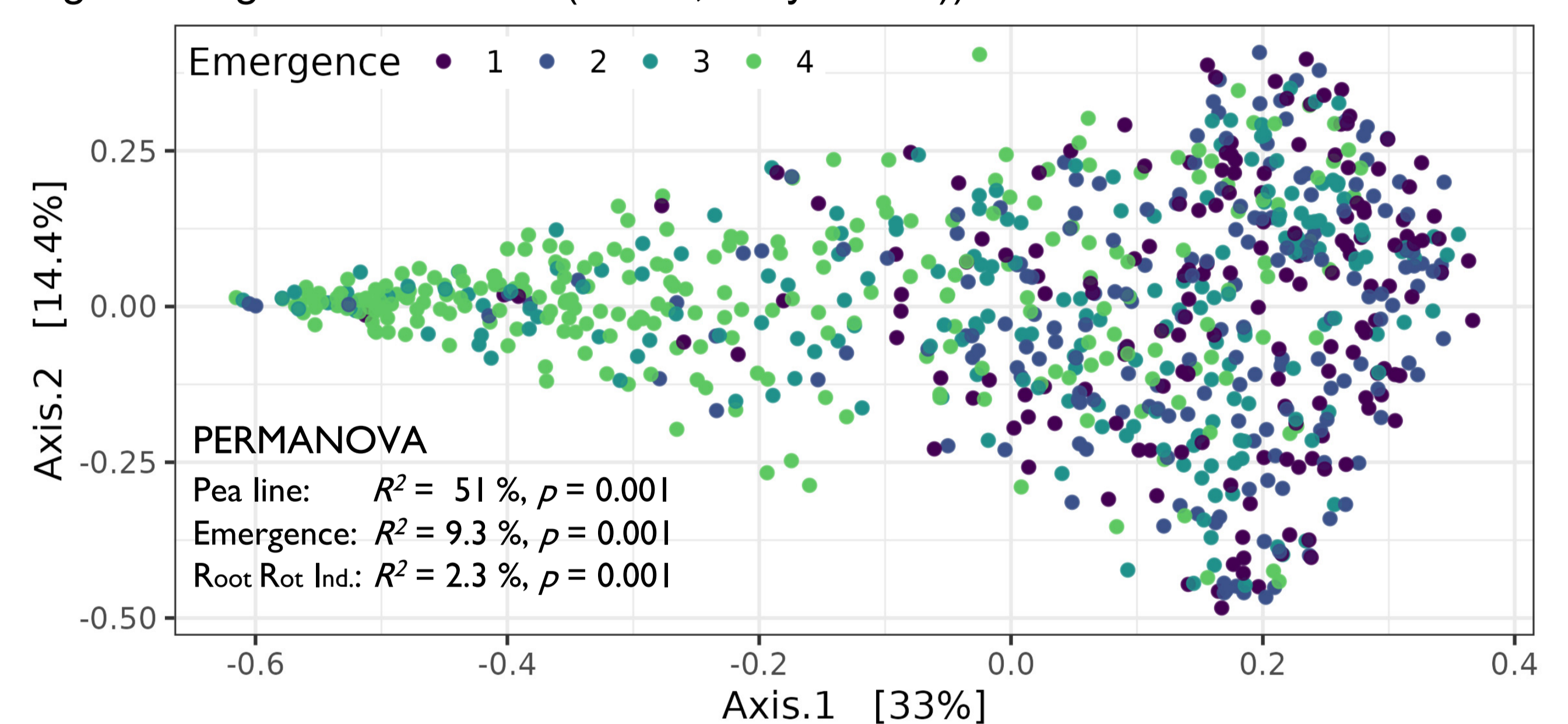


Fig. 4 Network analysis

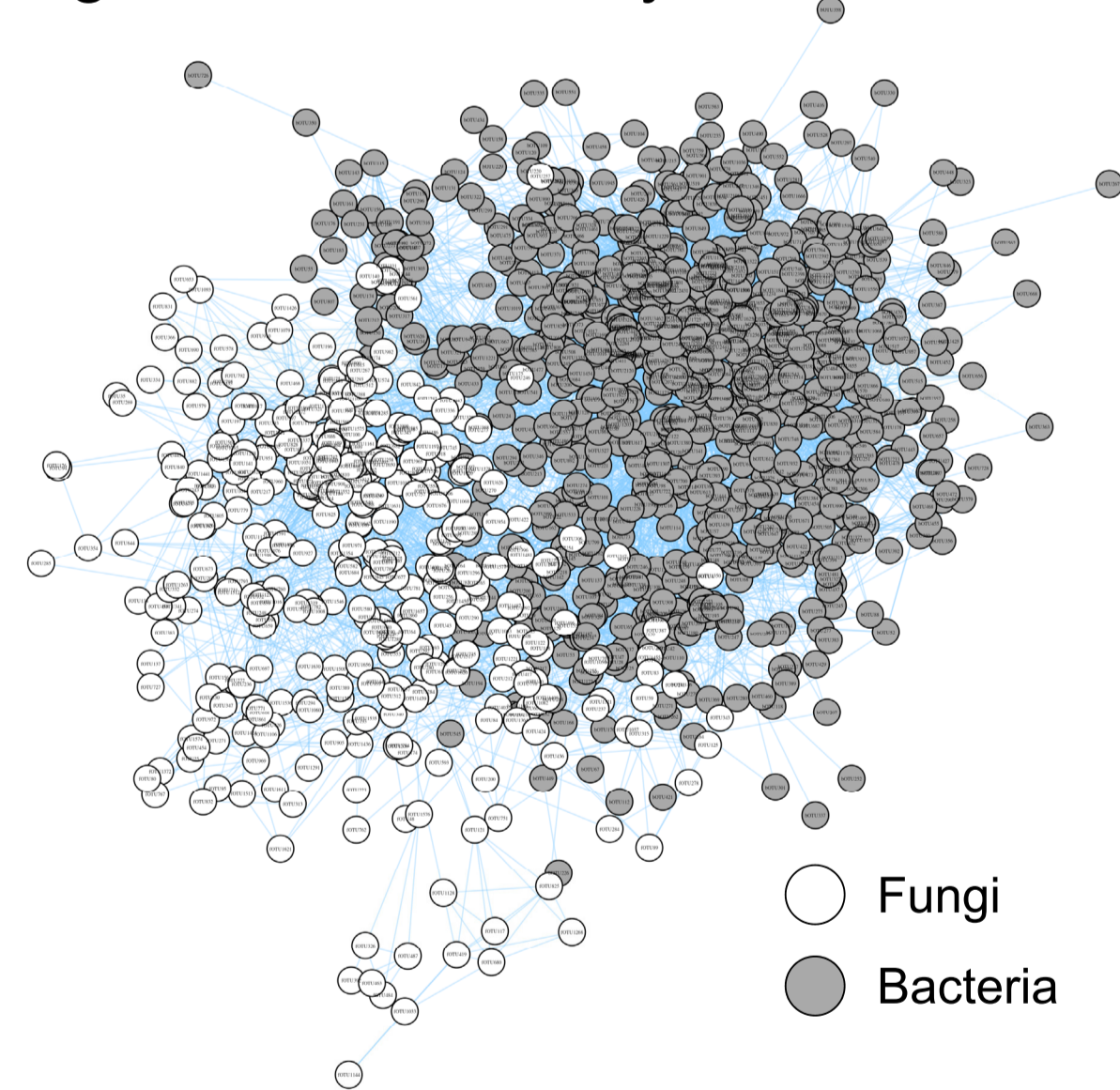


Fig. 3 Heritability of individual OTUs

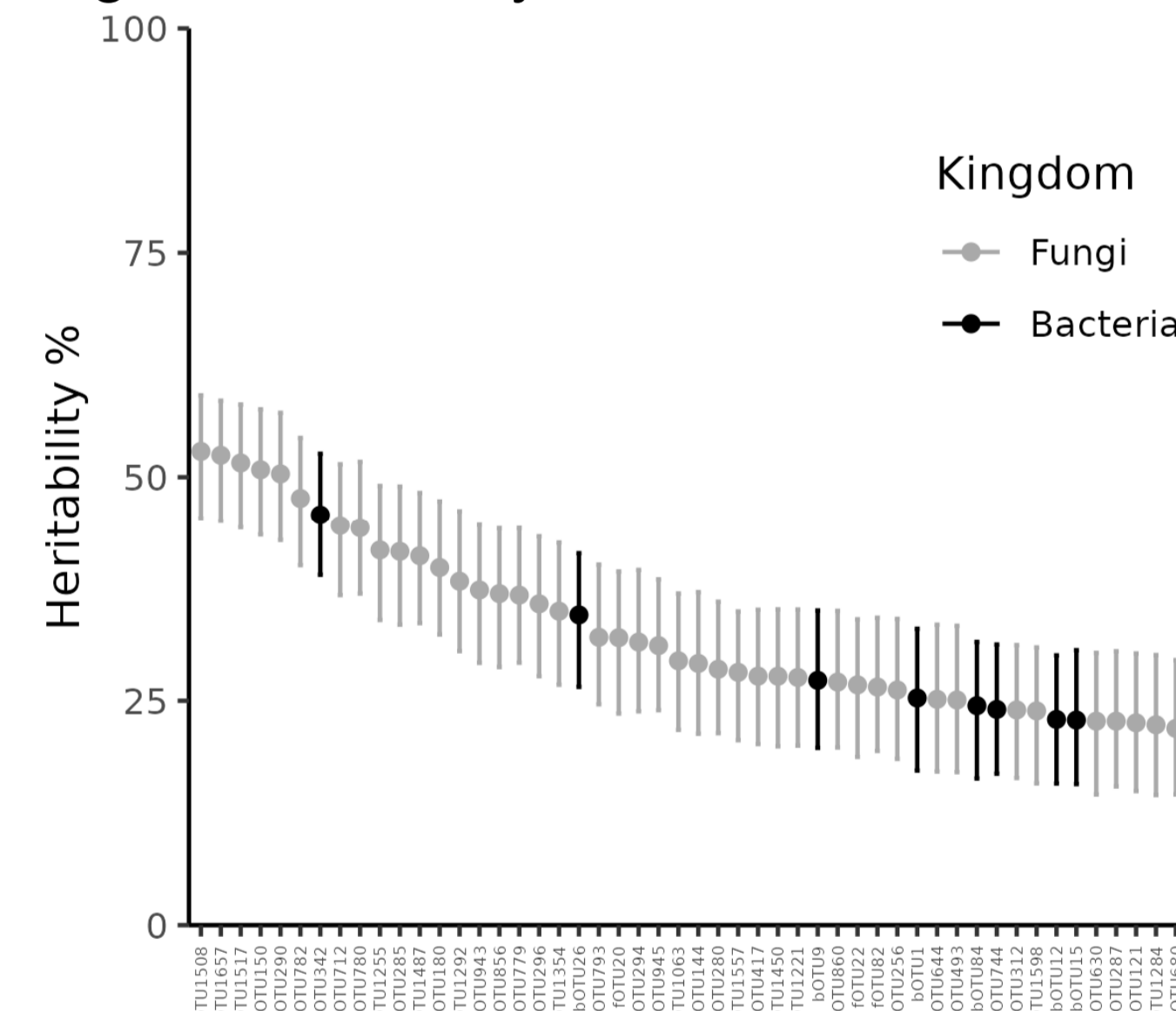
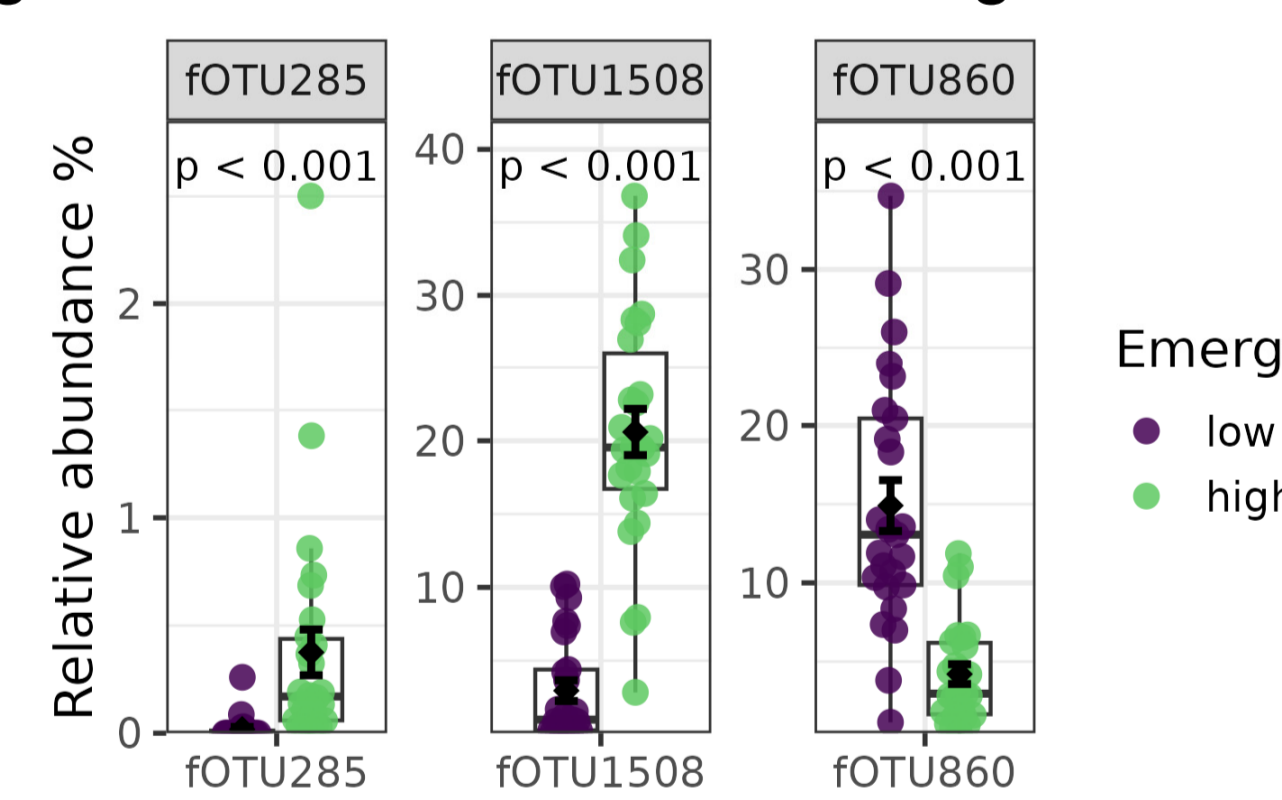


Fig. 2 Differential abundant fungi



Differential abundant bacteria

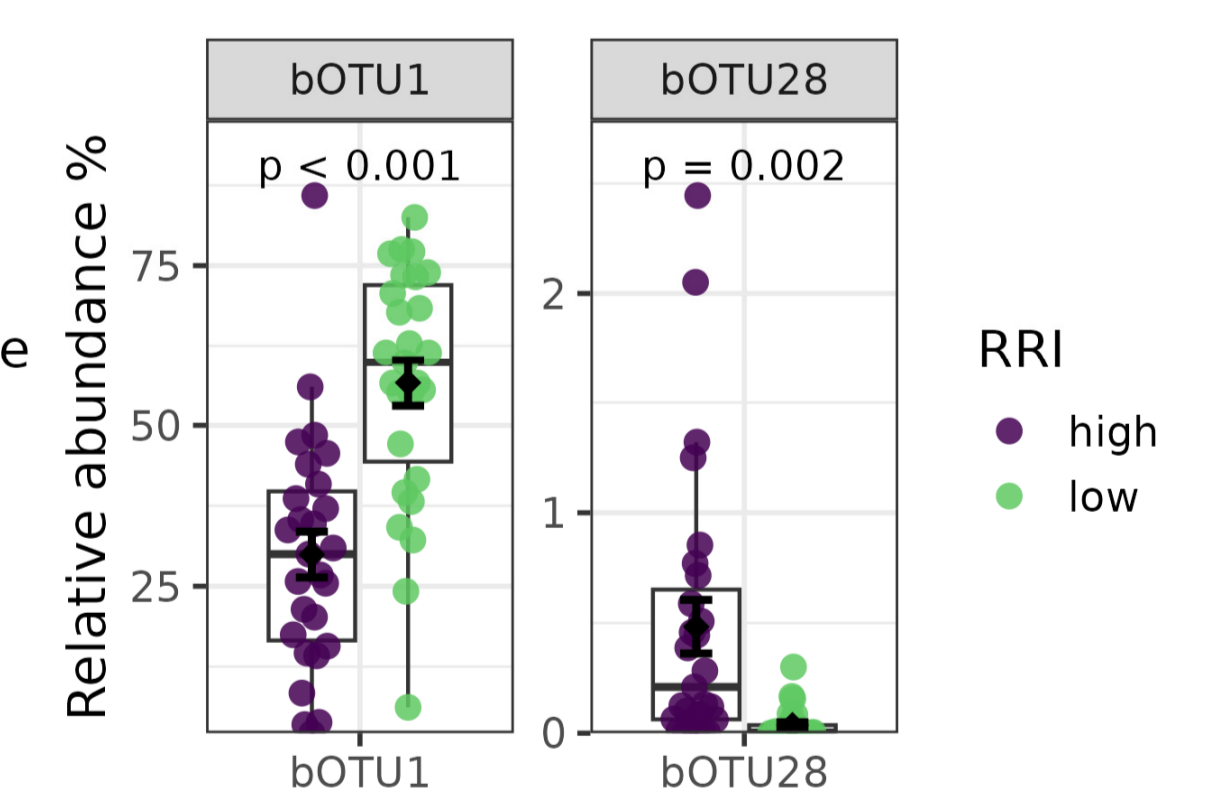
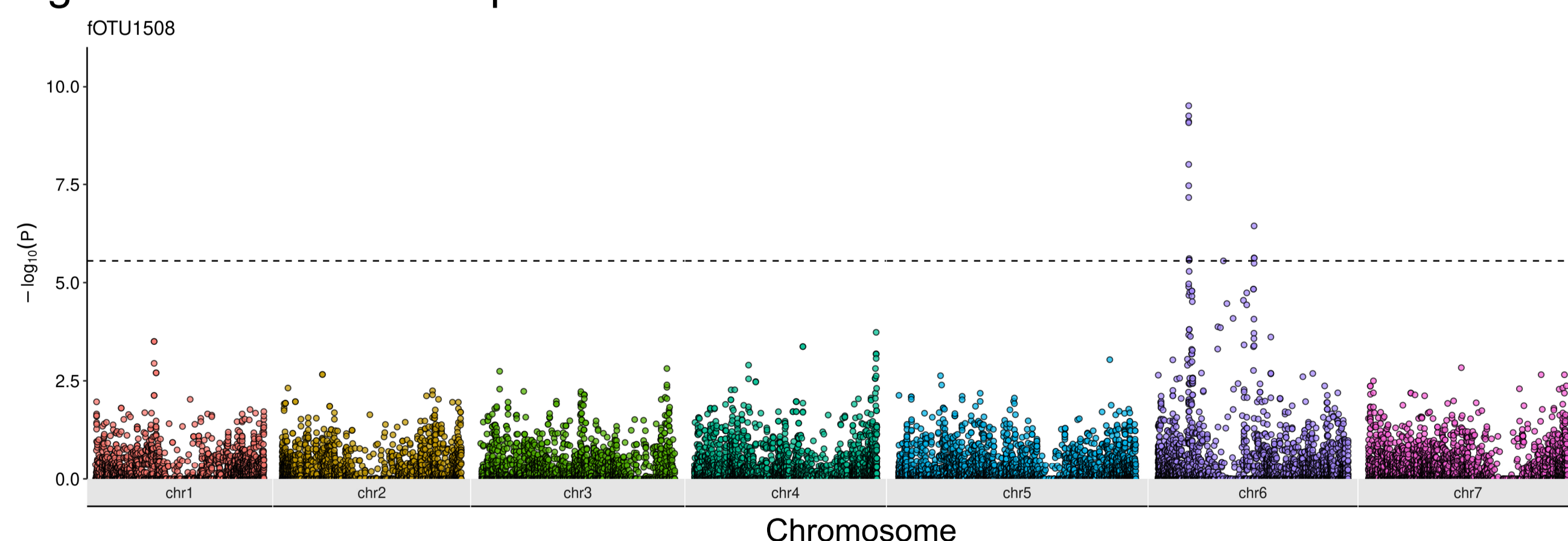


Fig. 5 GWAS on one representative resistance-associated OTU



Discussion

- We show that plant genotype-specific root microbiome attributes are associated with root rot resistance in peas
- The identified genetic markers will now be used to select pea breeding material for field validation of microbiome-mediated resistance against the pea root rot complex
- This work demonstrates the potential of microbiome-assisted breeding to promote sustainable farming practices

Affiliations

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Reference

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Partner



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