Host genotype shapes the root rot resistance-associated microbiome of pea

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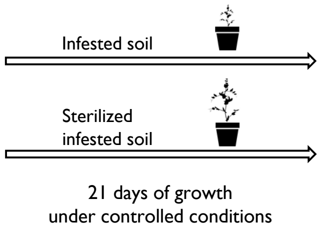
Introduction

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 microbiomes 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



Infested soil

Sterilized infested soil

21 days of growth under controlled conditions

Image: Lukas Wille

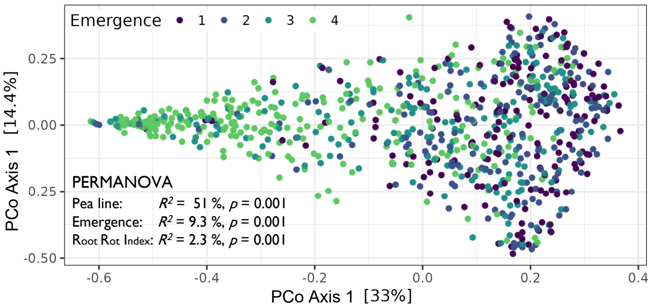
Peas were grown in untreated and sterilized infested field soil for 21 days, phenotyped (Wille et. al, 2020), and roots were harvested for microbiome analysis. Root bacteria and fungi were characterized by 16S rRNA and ITS amplicon sequencing, followed by visualization and statistical analysis of different microbiome attributes. To validate genotype-microbiome associations, a subset of 8 genotypes were grown in three additional soils.

Image: Lukas Wille

Results

- Pea genotype influences the microbial community composition (Fig. 1)
- Microbial community composition is associated with plant resistance (Fig. 1)
- The resistance of pea genotypes correlates with the abundance of potentially beneficial microbes (OTUs) (Fig. 2)
- Some microbes, including potential beneficials, are highly heritable (Fig. 3)
- Some of the heritable and resistance-associated OTUs were validated in three additional soils (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))



PERMANOVA

Pea line: $R^2 = 51\ \%$, $p = 0.001$

Emergence: $R^2 = 9.3\ \%$, $p = 0.001$

Root Rot Index: $R^2 = 2.3\ \%$, $p = 0.001$

Fig. 4 Pea genotype-OTU interaction in different soils

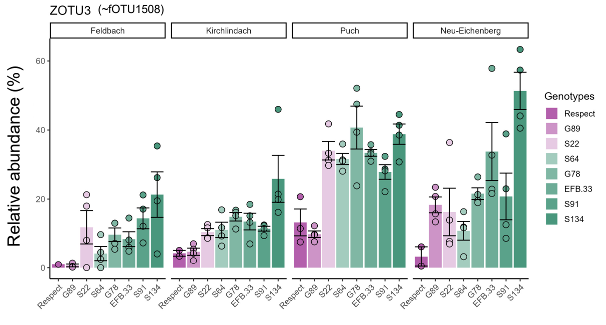


Fig. 3 Heritability of OTUs

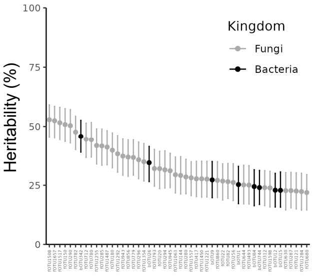


Fig. 2 Differential abundant fungi

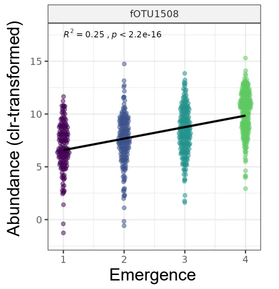
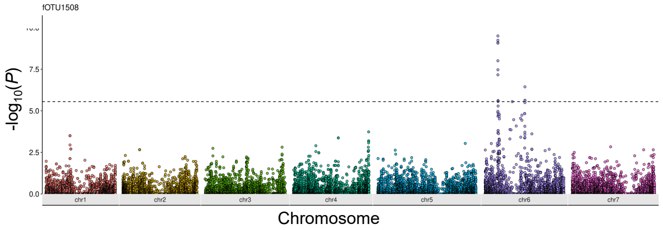


Fig. 5 GWAS on one representative resistance-associated OTU



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 root rot
- This work demonstrates the potential of microbiome-assisted breeding to promote sustainable farming practices

Affiliations

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Reference

Wille L, Messmer MM, Bodenhausen N, Studer B, Hohmann P. 2020. Heritable Variation in Pea for Resistance Against a Root Rot Complex and Its Characterization by Amplicon Sequencing. *Frontiers in Plant Science* **11**.

Partner

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