

Resistant and susceptible pea lines harbour different root-rot pathogens and antagonistic fungi

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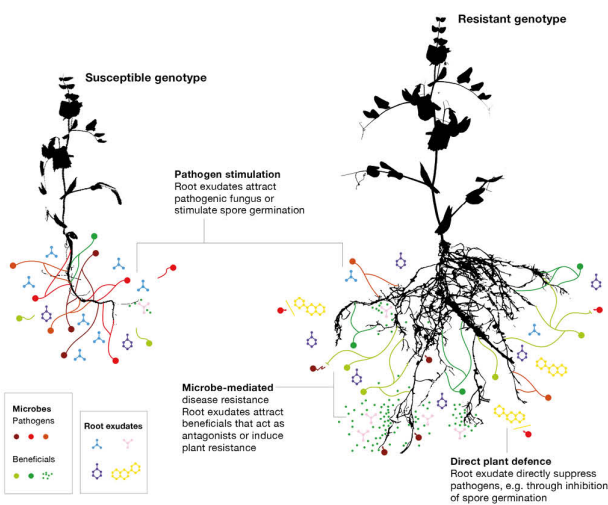
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Abstract

Pea (*Pisum sativum* L.) is a valuable protein source and important crop in low-input farming systems. Fungal root diseases threaten cultivation, and resistance in current pea varieties against multiple pathogens is lacking. To fully acknowledge the rhizosphere microbiome as a part of the plant environment, eight pea genotypes with contrasting root rot resistance levels were selected and tested on four soils with different disease pressure. Our controlled conditions pot experiment showed a significant genotype x soil type interaction for root disease index. Furthermore, the quantification of pathogens and one potential antagonist suggests different roles of these fungi in pea root disease.



Microbes are important for plant health

Recent studies on plant resistance have shown that the plant associated microbiome plays a crucial role for plant health. There is evidence that the plant genotype determines the composition of the plant associated microbial community. Plants release a variety of chemical compounds from their roots; these root exudates encompass defence molecules and compounds that attract certain microbes. Whereas many microbes are pathogenic to plants and cause economically important diseases, as many can be beneficial promoting plant growth or resistance. Understanding the interactions between plants and microbes poses a leverage point for resistance breeding. Incorporating the plant microbiome in plant breeding could be a sustainable solution for improved, resistant crop varieties.

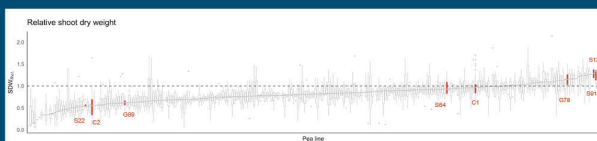
Further reading: Wille et al. (2019) Insights to plant-microbe interactions provide opportunities to improve resistance breeding against root diseases in grain legumes. *Plant, Cell & Environment*.



Breeding superior cultivars for sustainable agricultural systems

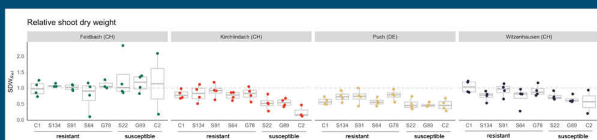
- We conducted large trials on infested soil to identify pea lines resistant to root rot pathogens
- We confirmed our controlled conditions screenings in on-farm trials
- We verified the resistance ranking of the pea lines on four different soils
- We quantify pathogens and antagonists by quantitative real-time PCR (qPCR) in diseased roots
- We compare root microbiome profiles of different pea lines with different levels of root rot resistance
- We currently genotype 312 pea lines by GBS to perform a genome-wide association study

Screening on infested soil allows to differentiate between resistant and susceptible pea lines



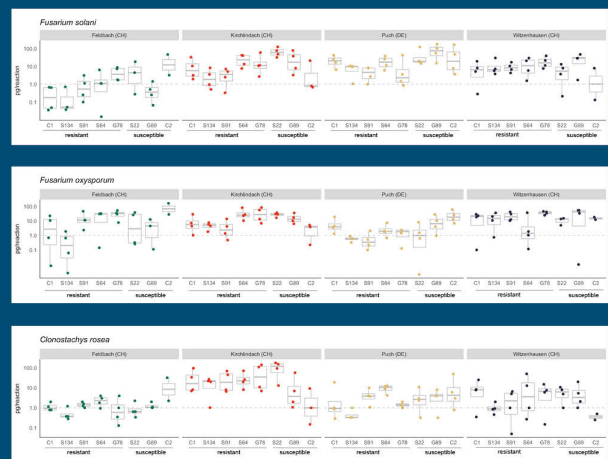
Growth performance of 261 pea lines grown on infested field soil ('Kirchhündach' soil) and X-ray sterilised soil (4 replications) under controlled conditions. Plants were assessed 21 days after sowing. The shoot dry weight of the infested soil treatment was divided by the shoot dry weight of the corresponding sterilised soil treatment to obtain relative shoot dry weight (SDW_{Root}). SDW_{Root} served as a proxy for plant performance. The range of SDW_{Root} was 0.03 - 2.14 (mean = 0.82); Broad-sense heritability was 51%. Eight genotypes assessed in subsequent resistance screenings are highlighted in orange.

Confirmation of resistance ranking on four soils



Growth performance of eight selected pea lines with contrasting levels of disease susceptibility. Pea lines were grown on three infested field soils (Kirchhündach, Puch and Witzzenhausen) and a healthy soil (Feldbach). Plants were assessed 28 days after sowing. SDW_{Root} was significantly higher in 'Feldbach' soils than in the three infested soils (1.1 versus 0.7, 0.6 and 0.5, respectively), indicating the 'healthy' status of this soil. Results from 'Kirchhündach' soil confirms the resistance ranking obtained in the initial screening of 261 lines (Spearman rank correlation $r_s = 0.62$, p -value < 0.01).

Quantification of fungal pathogens and an antagonistic species in diseased pea roots



Quantification of two fungal pathogens (*Fusarium solani* and *F. oxysporum*) and one potential antagonist (*Clonostachys rosea*) by quantitative real-time PCR (qPCR). The fungal species were quantified in diseased roots of 28 days old pea plants grown on three infested soils ('Kirchhündach', 'Puch' and 'Witzzenhausen') and one 'healthy' soil ('Feldbach'). Total genomic DNA was extracted from freeze-dried roots. The amount of fungal DNA (in pg/reaction) was obtained by comparing the sample Ct to a standard curve (absolute quantification). A serial dilution of 1000, 100, 10 and 1 pg/μl fungal DNA was used to calculate the standard curve for each fungal species.