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Improving disease resistance of pea – clues from plant-microbe interactions

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Introduction

Pea (*Pisum sativum* L.) is a valuable protein source for food and feed. Like other legume plants, peas form an intimate mutualistic symbiosis with nitrogen fixing rhizobacteria, and, thereby, are able to significantly improve soil fertility.

Pea is highly prone to soil-borne pathogens and rotation breaks of up to ten years are recommended to avoid the build-up of high pathogen loads in the field. This stands in conflict with efforts to increase acreage of pea to strengthen low input farming systems and meet the protein demand of a growing world population.

Pea cultivars resistant against individual pathogen species exist, but not against pathogen complexes present under field conditions. Incorporating the microbial complexity present in the rhizosphere into plant variety testing is a potential means to harness beneficial plant-microbe interactions for resistance breeding programs (Fig.1).

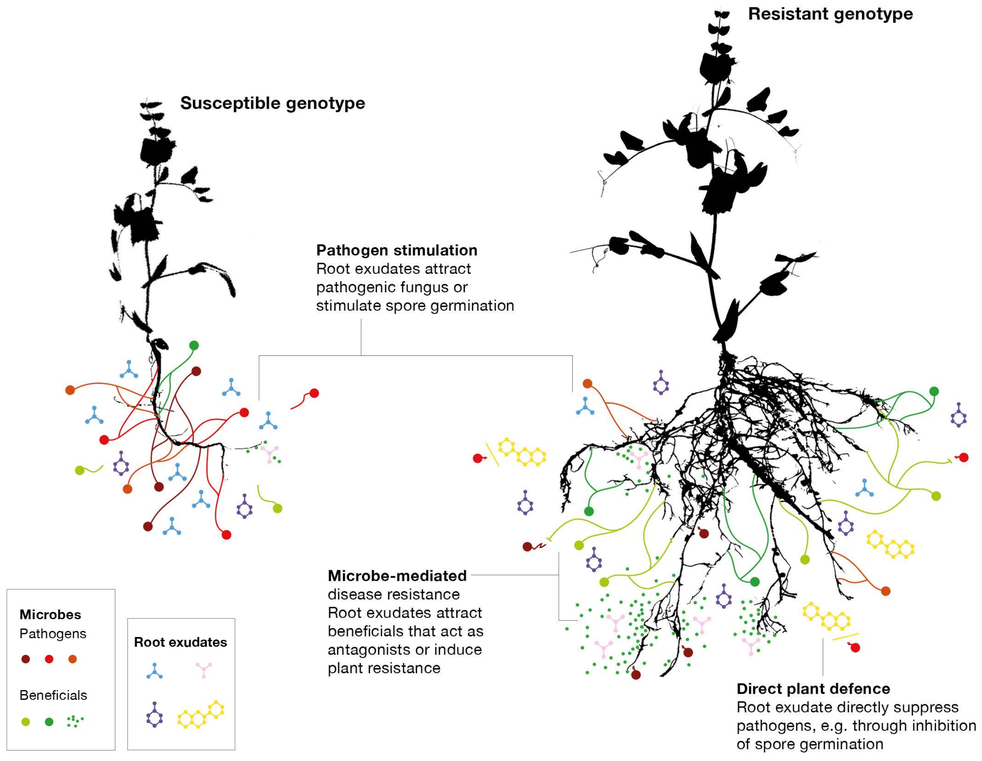

Fig. 1 - Schematic representation of plant genotype-dependent interactions in the rhizosphere. Four hypothetical root exuded compounds, three pathogenic and three beneficial microbial species are represented. Mainly fungal pathogens are attracted by the susceptible genotype, and the plant is heavily infected. The resistant genotype exudes either compounds that suppress pathogens directly or compounds that attract beneficial microbes. Figure adapted from Wille *et al.* 2018.

Objectives

- **Identify pea lines resistant to soil-borne pathogen complexes**
- **Elucidate the genetic basis of polygenic resistance of pea against fungal pathogens**
- **Improve our understanding of plant-microbe interactions conferring resistance to pathogens**
- **Provide the knowledge base to breed for superior cultivars for organic agricultural systems**

Pot-based resistance screening & field evaluation: Significant differences in resistance level among pea lines

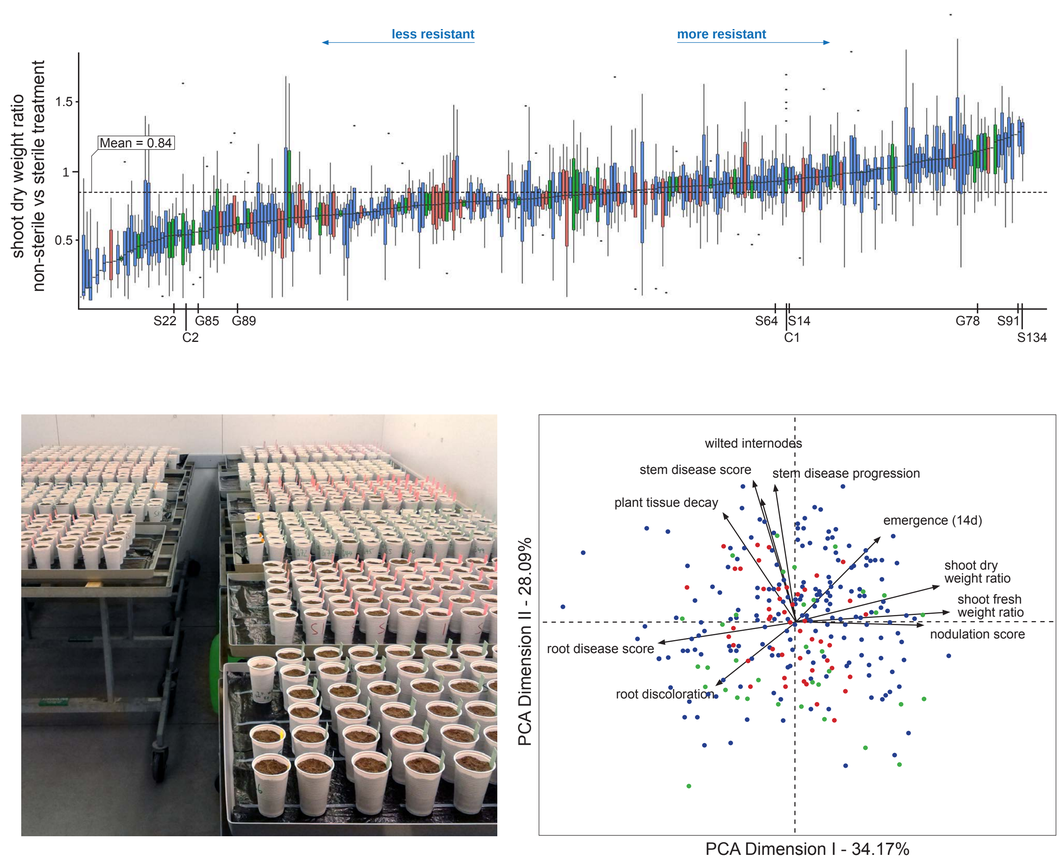

Fig. 2 - Top: Biomass ratios of 312 pea lines grown on infested field soil and X-ray sterilized soil (4 replications) under controlled conditions. Ten genotypes included in the field evaluation of 2018 are indicated. Bottom left: Impression from the growth chamber experiment. Bottom right: PCA biplot showing genotype and variable factor map on the first two principal component axes, representing a total of 62.26% of the observed variance. Six disease assessment variables, two biomass assessment variables, nodulation score and emergence are represented. In the histogram and biplot the genotypes are colored according to their origin: Green = cultivars; blue = gene bank accessions; red = advanced breeding material.

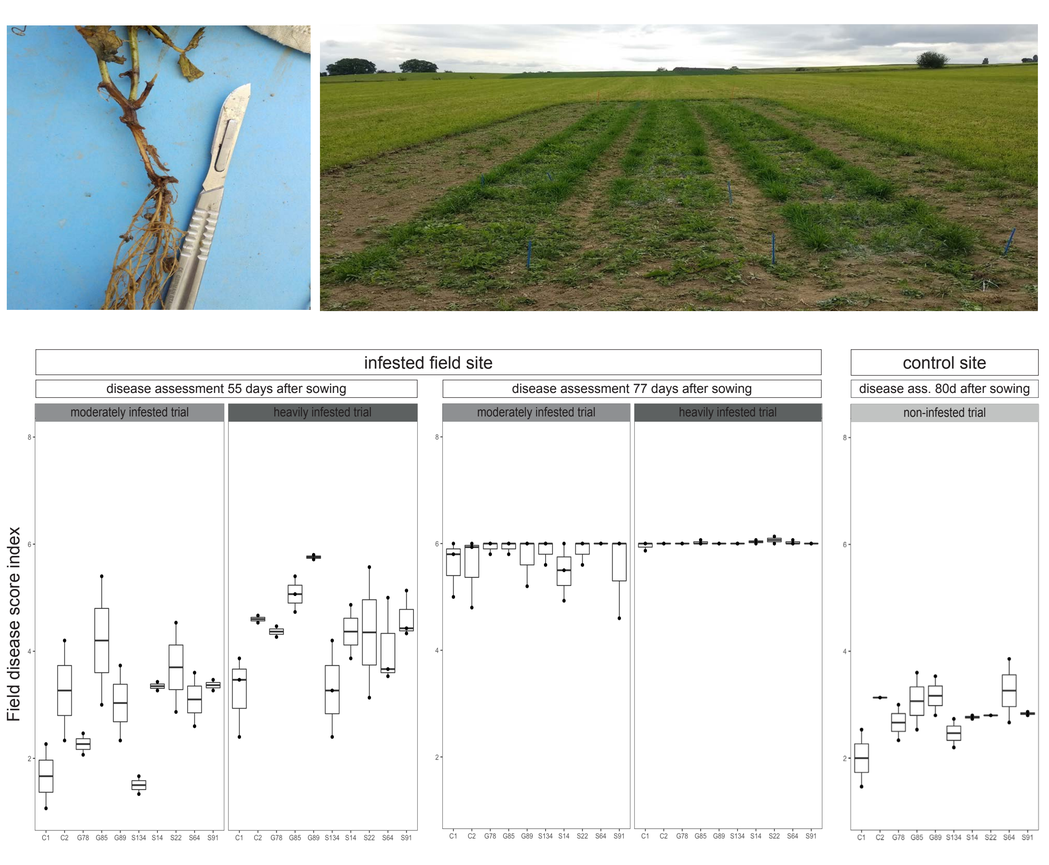

Fig. 3 - Ten pea lines were evaluated in 2018 in trials `I` and `II` in Kirchlindach (Kt. Bern) and trial `III` in Feldbach (Kt. Zürich). Trial `I` was on soil heavily infested and trial `II` on soil moderately infested with fungal pathogens. Trial `III` was on non-infested soil (control trial). Pea lines were evaluated in 1.5 x 1.5 m plots with 3 replication per trial in a randomized complete block design. Top left: Diseased pea sample, with dark brown discoloration of the root and lower stem. Top right: Impression from trial `I` in Kirchlindach, 2018. Bottom: Disease score index (DSI; 1-8) assessed 55 days and 77 days after sowing at theinfested filed site and after 80 days at the control site: DSI 1 = no disease symptoms on root and lower stem; DSI 8 = total root-rot, plant dead.

Current work & next steps

- The evaluated pea genotypes are currently being genotyped by sequencing (GBS). The genetic marker data set will be used for a genome-wide association study in order to identify genetic regions in the pea genome significantly associated with disease resistance.
- Major root-rot pathogens are being identified in the roots of diseased pea using quantitative real time PCR. This will shed light on different microbial compositions among resistant and susceptible pea genotypes.

Partner Getreidezüchtung Peter Kunz Verein für Kulturpflanzenentwicklung; CAMAG World Leader in Planar Chromatography

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