

77. Genome-wide association study for resistance of pea against a complex of root rot pathogens

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Fungal root diseases severely narrow yield in pea (*Pisum sativum* L.) cultivation, threatening this highly valuable protein source and important crop in low input-farming systems. Adequate resistance in current pea varieties against various root pathogens is largely lacking. The control of these pathogens is challenging, as they occur as pathogen complexes in the field, themselves embedded in entangled interactions in the rhizosphere. Plants have the ability to actively shape their root-associated microbiome and genetic variation for rhizosphere related traits exists that can potentially be harnessed in resistance breeding [1]. Results from a controlled pot-based resistance screening of 312 pea cultivars, advanced breeding lines and gene bank accessions on naturally infested soil will be presented. Based on different disease assessments, significant differences in resistance level between pea lines were identified. Validation of a subset of most contrasting lines in the field confirmed significant differences for diseases susceptibility. ITS amplicon sequencing of the fungal rhizosphere community showed a root community of evenly abundant fungal taxonomic units not dominated by a few taxa. This finding points at complex interactions within the fungal community. Along the microbiome sequencing approach, quantitative real-time PCR assays targeting the most important pathogen species are being implemented for the analysis of pot and field rhizosphere samples. Finally, first results of a genome-wide association study on resistance to root rot will be presented.

References:

[1] Wille, L. et al., 2018, PCE, Special issue on legumes, doi: 10.1111/pce.13214, Epub ahead of print

Organisers

