

Improving disease resistance of pea through selection at the plant-soil interface

Mercator Research Program acronym: resPEAct

Background

Pea (*Pisum sativum*) belongs to the legume family (*Fabaceae*). Legumes form a mutualistic symbiosis with nitrogen-fixing rhizobacteria and are able to improve soil fertility (Fig. 1). They represent ecologically important crops for agriculture – especially in organic farming systems, where the application of fertilisers is highly regulated. Besides their ecological function, grain legumes, in general, represent a sustainable protein source for humans.¹ In temperate climate, the cultivation of pea is an ecologically worthwhile alternative to soybean imports.¹

Despite their ecological and economic importance, legume cultivation remains below expectations due to low and unstable yields. For pea, this is mainly due to a high susceptibility to a complex of soil-borne diseases that accumulate with recurrent pea cultivation. This phenomenon is called “soil fatigue” leading to wilting and root rot of infected plants (Fig. 2).² Such infestation can lead to total crop failure.



Fig. 1 Top left: Flowering pea plant. Top right: Mature pea pods. Bottom: Nodules on pea roots. The right nodule was cut transversally. Note the typical red colour of the nodules. Bar represents 1 mm.

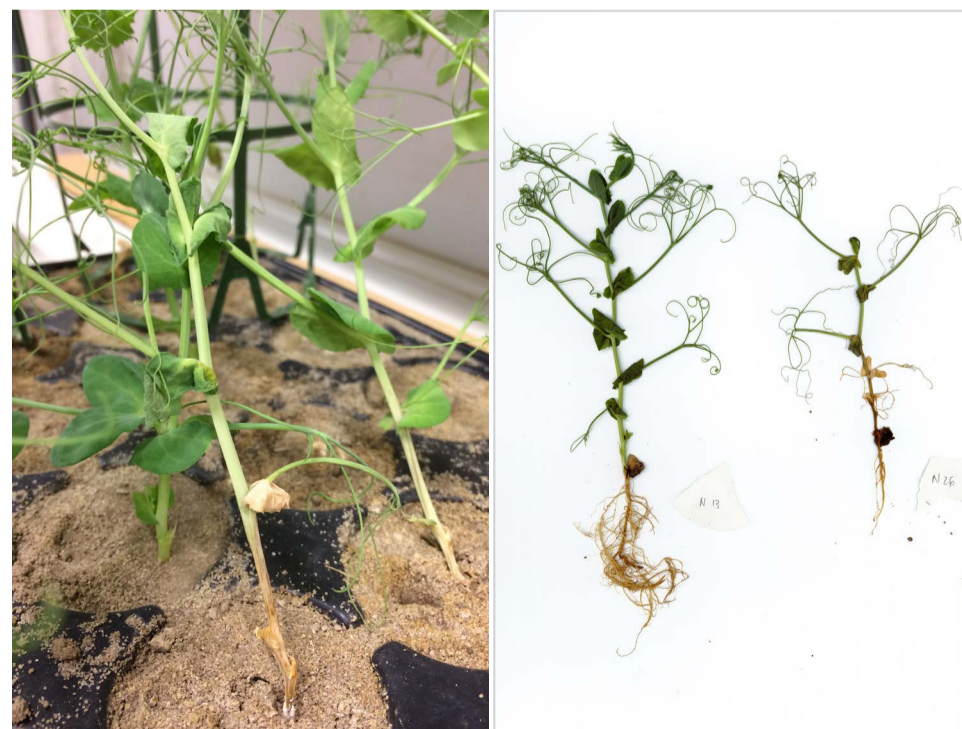


Fig. 2 Twenty-four days old pea plants (cv. Nitouche). Left: Plants before excavation growing in an experimental tray system. Note the honey-brown colour on the stem indicating foot rot. Right: Infested (right) and uninfested (left) plant after excavation.

Expected outcomes

- › Develop a screening tool for resistance against root rot in pea
- › Improve resistance of pea against soil-borne diseases
- › Develop a HPTLC method to profile resistance-related root exudates of pea lines
- › Enhance the understanding of soil microbe-plant interactions within the soil-fatigue framework
- › Elucidate the genetic basis of polygenic resistance of pea against fungal pathogens
- › Provide the knowledge base to breed for superior cultivars for organic and other sustainable agricultural systems

Objectives

The overall goal of this project is to improve the resistance of pea against soil-borne diseases. 300 pea lines (varieties, advanced breeding material and SNP-genotyped genebank accessions) will be screened for resistance in standardised growth chamber experiments and on-farm. We will investigate resistance-associated quantitative trait loci via genome-wide association study to set the foundation for a marker-assisted breeding programme for pea.³ Breeding efforts will be in collaboration with the organic breeder *Getreidezüchtung Peter Kunz, Switzerland*.

Key fungal pathogens and beneficial fungi (e.g. mycorrhizal fungi) in infested soils will be characterised and compared among pea lines with contrasting resistance levels. We will elucidate the role of root exudates in shaping the plants' own detrimental or beneficial microbial community in the rhizosphere.

Acknowledgements

The authors would like to thank the Mercator Research Program of the ETH Zurich World Food System Center and the ETH Zurich Foundation for supporting this project. We thank CAMAG, Switzerland for training on high-performance thin-layer chromatography and technical support.

References

- ¹ Rubiales & Mikic Crit. Rev. in Plant Science 2015 34: 2-3.
- ² Fuchs et al. Applied Soil Ecology 2014 79: 26-36.
- ³ Desgroux et al. BMC Genomics 2016 17: 124.