

Breeding for symbioses – Mycorrhizae as a case study

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Plant associated soil microbes are known to play an important role in the expression and stability of certain plant traits such as nutrient use efficiency and disease resistance. Arbuscular mycorrhizal fungi (AMF) form one of the primary mutualistic plant-microbe symbioses. Besides known benefits such as improved nutrient mobilisation (mainly phosphorus and zinc) and tolerance against abiotic stresses (mainly drought), an increasing number of studies highlight a significant role of AMF in the mediation of disease resistances and priming mechanisms. Individual reports have shown enhanced levels of defence-related compounds (such as glucanases, chitinases and phenolics) in mycorrhizal plants, and there is first evidence of certain phytohormone pathways (in particular jasmonate signalling) to be involved in mycorrhiza-mediated disease resistance.

The level of mycorrhisation (formation of mycorrhizae on the roots) and mycorrhizal responsiveness (response to AMF) can vary widely between plant species and also among genotypes within the same species, indicating a genetic basis for the regulation of this symbiosis. Genotypic differences in mycorrhizal responsiveness have been observed in various crops and quantitative trait loci (QTL) that govern plant growth responses to AMF have been reported for maize, barley and onion. However, little is known about the heritability of mycorrhiza-mediated disease resistance. Mycorrhizal responsiveness (when based on biomass) is negatively correlated with available soil P content. Breeding under high P conditions might therefore indirectly select for poor AMF hosts. We hypothesise that a reduced mycorrhizal dependency also affects other benefits elicited by AMF such as disease resistance. We therefore pledge to include factors other than biomass to estimate mycorrhizal responsiveness (i.e. disease resistance, PUE and drought tolerance) to obtain a more comprehensive differentiation of the plant-AMF interaction. The authors also propose to complement mycorrhizal responsiveness with an additional measure called mycorrhizal efficiency since mycorrhization and mycorrhizal responsiveness on their own might not indicate an optimum cost-benefit ratio of this symbiosis. We will present initial results on genotypic variation in mycorrhization, mycorrhizal responsiveness and mycorrhizal efficiency of SNP-genotyped accessions of pea (*Pisum sativum* L.). Eventually, these SNP-genotyped accessions can be used to identify QTL that govern mycorrhiza-mediated disease resistance and exploit genotypic differences, e.g., via marker-assisted selection.

Another research project has been initiated to investigate the role of flavonoids in defence mechanisms of pea and their possible function in microbe-mediated disease resistance. Variation in microbial composition has been attributed to a differential exudation of compounds that stimulate or suppress particular members/groups of the microbial community. The complex group of flavonoids has been shown to play a signalling and/or direct role in plant defence mechanisms, but also to influence the interaction with symbionts including mycorrhizal fungi (and also plant-symbiotic rhizobia). Overall, current and future research activities of our group aim to better understand and make use of plant-microbe interactions in plant breeding for an improved expression and stability of important plant traits.