

Master Thesis at FiBL Plant Breeding Group

Title	Analysis of the rhizosphere microbiome of pea infected by soil-borne fungal pathogens
Context	Soil-borne diseases in legumes, especially in pea, cause severe damage and can lead up to total yield loss. The lack of adequate resistance in current pea varieties against a complex of different soil-borne diseases impede pea cultivation worldwide. Root-associated microbial communities plays a crucial part in the expression of important plant traits, including disease resistance (Berendsen et al. 2012, Hartmann et al. 2014, Yu et al. 2012). Microbial shifts at the community level have been linked to disease resistance. Plants have the ability to influence the microbial structure in the rhizosphere. It has been demonstrated that not only different plant species, but also different genotypes within the same species can modify the rhizosphere microbiome (e.g. Berg et al. 2006, Peiffer et al. 2013). Two genotypes have been identified that show different responses to the infection of soil-borne pea pathogens.
Procedure/ Method	The aim of the MSc project is to establish the ITS amplicon sequencing workflow and get first insights in the rhizosphere microbiome of pea grown in a naturally-infested agricultural soil.
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Starting period	Immediately
Location	FiBL, Frick, Kanton Aargau, Switzerland, www.fibl.org Genetic Diversity Centre, ETH, Zurich, Switzerland
Language	English or German
Literature	Berendsen RL, Pieterse CMJ and Bakker PAHM (2012). Trends in Plant Science 17(8): 478–86. Berg G, Opelt K, Zachow C, Lottmann J, Götz M, Costa R and Smalla K (2006). FEMS Microbiology Ecology 56(2): 250–61. Hartmann M, Frey B, Mayer J, Mäder P and Widmer F (2014). The ISME Journal 9: 1177–94. Peiffer JA, Spor A, Koren O, Jin Z, Green S and Dangl JL (2013). PNAS 110(16): 6548–53. Yu L, Nicolaisen M, Larsen J and Ravnskov S (2012). Plant and Soil 357(1): 395–405.