**Effects of pea breeding history on root microbiome attributes under pea root rot stress**

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The pea root rot complex (PRRC) poses a major threat to pea (*Pisum sativum*), one of the most important crops for plant-based protein production. The co-occurrence of various soil-borne pathogens within a PRRC triggers soil fatigue, and thereby constrains cultivation. Even though resistant cultivars against single pathogens exist, the complexity of interactions among the pathogens can still lead to root infections. In order to make further breeding progress, it is necessary to consider this complexity and link to interactions of the host with the entire root microbial community, including the pathobiome and plant beneficial members. In a previous study, we characterised several known taxa involved in the PRRC (Wille et al., 2021). It is however not known how the PRRC interacts with other members of the microbial community and how these interactions were steered by pea breeding. To shed light on this, we compare the root microbiome of pea landraces and modern European breeding material grown in PRRC-affected field soil. For this, 250 pea genotypes consisting of 174 landraces of the USDA pea core collection, 31 registered cultivars from Europe, and 45 advanced breeding lines from Getreidezüchtung Peter Kunz (CH) were grown for 21 days under controlled conditions in a walk-in climate chamber before roots were harvested for microbiome analysis. Root bacteria and fungi were characterized by 16S- and ITS-amplicon sequencing, respectively. To evaluate potential effect of plant breeding on microbiome characteristics in response to soil infestation, we investigate species richness (alpha diversity), microbial community composition (beta diversity), and potentially network characteristics, such as network complexity. Furthermore, we present potential microbial hubs and individual OTUs associated with breeding history. This will provide valuable information about the selection effects of plant breeding on PRRC-related microbiome attributes and thus help to evaluate the potential of microbe-assisted breeding for disease resistance against pea root rot. In a next step, we aim to exploit genome-wide association studies (GWAS) approaches to seek genetic loci involved in microbe-mediated disease resistance. Markers linked to such loci will be validated in additional genetic material provided by the KWS breeding company. This work could pave the way to microbiome-smart breeding that harnesses beneficial plant-microbiome interactions to promote sustainable agriculture.

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