GENETIC BASIS OF MICROBIOME RECRUITMENT IN PEA ROOTS CHALLENGED BY ROOT ROT DISEASE

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Legumes play a crucial role in the shift towards more sustainable protein production, but root rot complexes can cause massive yield losses in many legume crops such as pea. The pea root rot complex (PRRC) is caused by various soil-borne pathogens that likely act synergistically and influence the composition of the rhizosphere microbiome (Wille et al., 2021). As there is genotypic variation in the abundance of key PRRC taxa and disease susceptibility, we aimed to investigate the genotype effect on the root microbiome composition affecting plant health. This crucial interaction between the plant genotype and its associated microbiome, also known as the holobiont, has the potential to lead to increased resistance to PRRC.

We obtained genetic markers from 253 diverse pea genotypes using genotyping-by-sequencing (GBS). The genotypes were grown under controlled conditions in diseased farm soil (or its sterilized equivalent), showing root rot symptoms caused by a naturally occurring pathogen complex. Several phenotypic traits, such as emergence rate and root rot index, and root samples were obtained at the seedling stage to correlate early root colonizers with disease phenotypes. Root microbial DNA was extracted from the root samples and sequenced for fungi (ITS) and bacteria (16S V3-V4). Operational taxonomic units (OTUs) were assembled based on 97% identity. OTU abundance was used for a genome-wide association study (GWAS) and genomic prediction (GP). Our objectives were to examine if...

- Genomic loci explain a relevant proportion of the variance in the abundance and presence of individual OTUs in pea roots (QTL detection)
- Identified QTLs for differentially-abundant OTUs reveal QTLs additional to the resistance phenotype QTLs
- Microbiome-mediated disease resistance concepts can be implemented into breeding programs via genomic prediction at the holobiont level

The GWAS of differentially abundant OTUs revealed 50 highly significant QTLs at 19 independent loci on five different chromosomes (**Figure 1).** Most QTL can be associated with more than one OTU, while only four loci are associated with both fungi and bacteria. QTLs on chromosome six co-segregated with QTLs for the shoot dry weight, root rotting, and emergence rates. The genomic heritability reached $h^2 > 0.6$ for some of these differentially abundant OTUs. The relative abundance of several OTUs was strongly correlated with plant health. For instance, a strong effect was observed for OTUs from the genus *Fusarium* (negative) and *Dactylonetria* (positive), with genomic heritabilities above 0.35.

Higher accuracy in predicting resistance to PRRC was obtained using the OTU abundance alone or combined with phenotype QTLs (μ=0.6) in a genomic prediction model. Lower accuracies were obtained using genomic markers for either OTUs or plant phenotypes alone (μ=0.3).

The results obtained indicate that (i) the presence and abundance of microbial taxa are determined (among other factors) by the pea genotype; (ii) the holobiont significantly determines the resistance of the plant to root rot; (iii) the holobiont approach of genomic markers for plant resistance and root microbial recruitment lead to an improved prediction of PRRC resistance compared to predictions based on plant genetics alone.

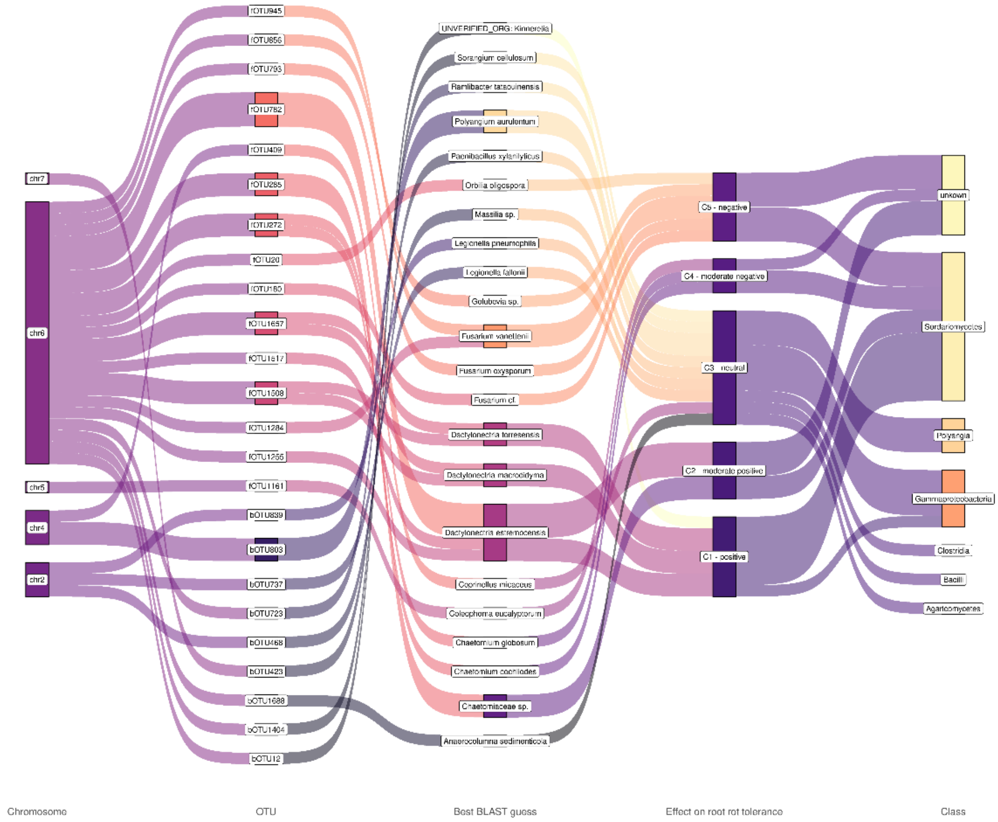

Figure 1. Relationship between pea genetics, root OTU presence and abundance, and resistance to a pea root rot complex. Chromosome refers to the QTL on the pea genome of each OTU. The best BLAST guess is the most similar match against the NCBI genome database. The effect on root rot was categorized into five classes, ranging from negative to positive. The class represents the annotation derived from the curated UNITE database. The most significant QTLs (-log(p) > 9 are presented).

References

Wille, L., Kurmann, M., Messmer, M. M., Studer, B., & Hohmann, P. (2021). Untangling the Pea Root Rot Complex Reveals Microbial Markers for Plant Health. *Frontiers in Plant Science*, *12*, 737820. https://doi.org/10.3389/FPLS.2021.737820/BIBTEX