



Holobiont genetic basis of pea root rot resistance

4th Workshop on Implementing Plant-Microbe Interactions in Plant Breeding (19. July 2024)

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Challenge of root rot in pea



Pea root rot complex



Aphanomyces euteiches



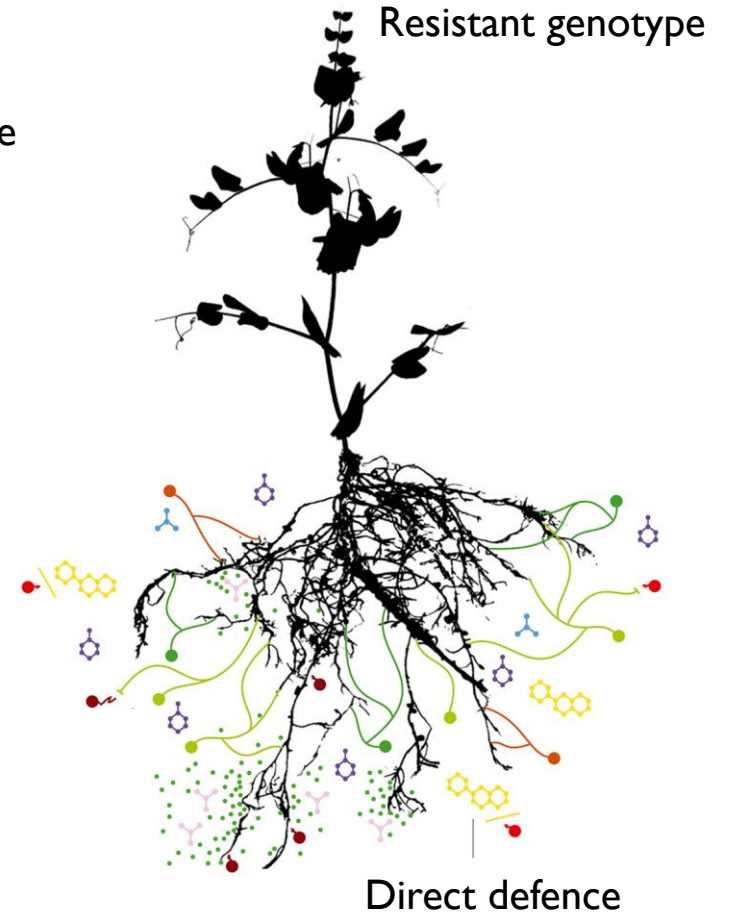
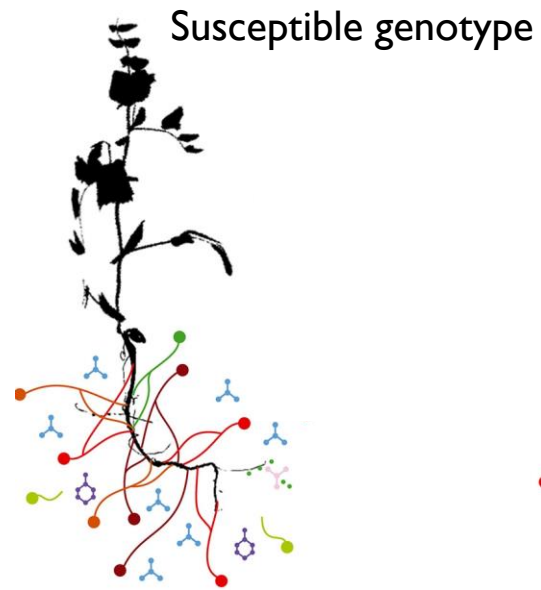
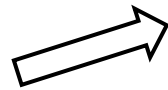
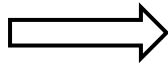
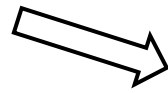
Pythium ultimum



Fusarium solani



Rhizoctonia solani



Pea root rot complex



Aphanomyces euteiches



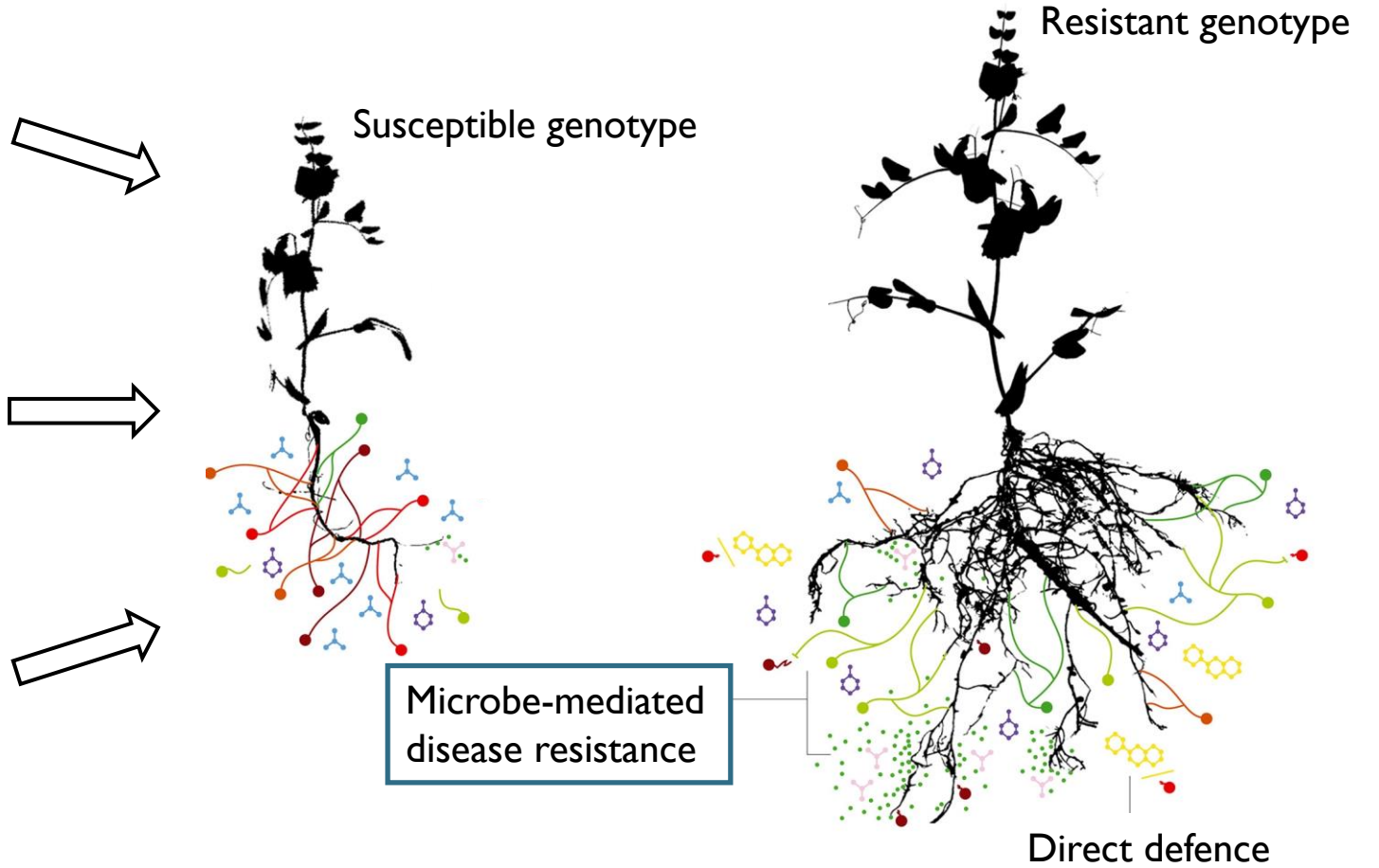
Pythium ultimum



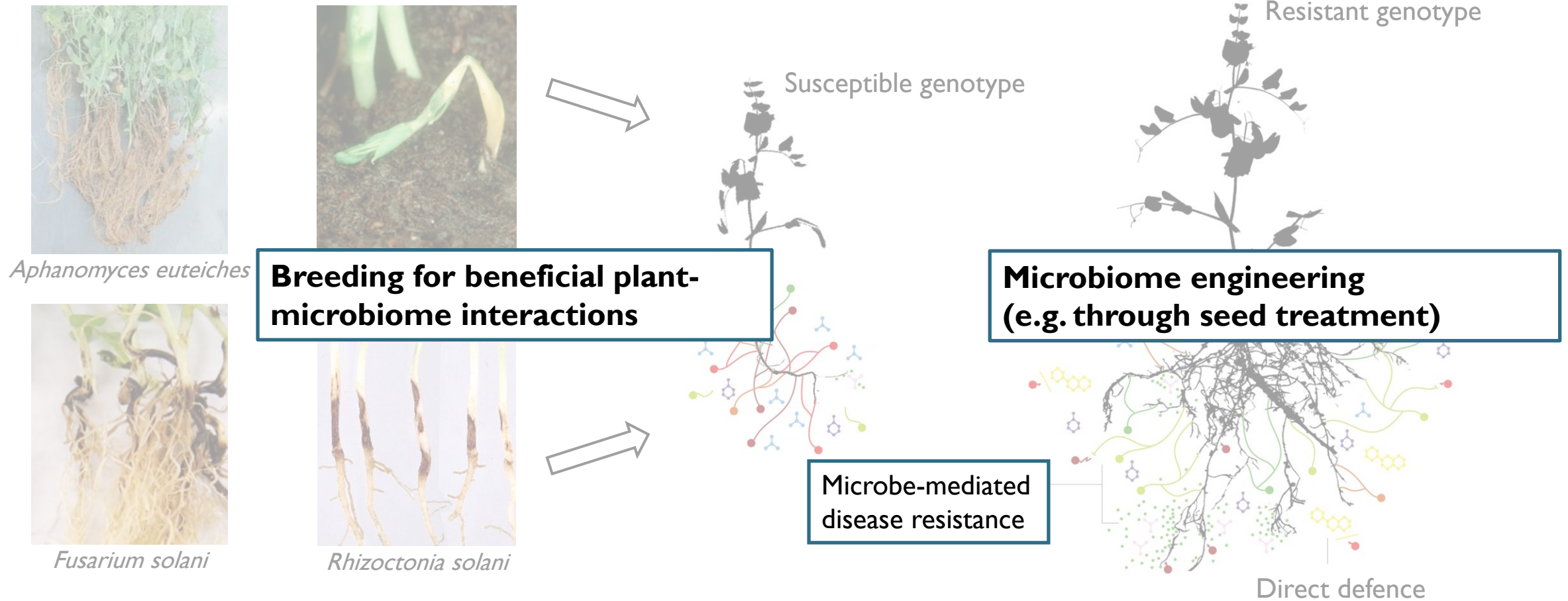
Fusarium solani



Rhizoctonia solani



Pea root rot complex (PRRC)



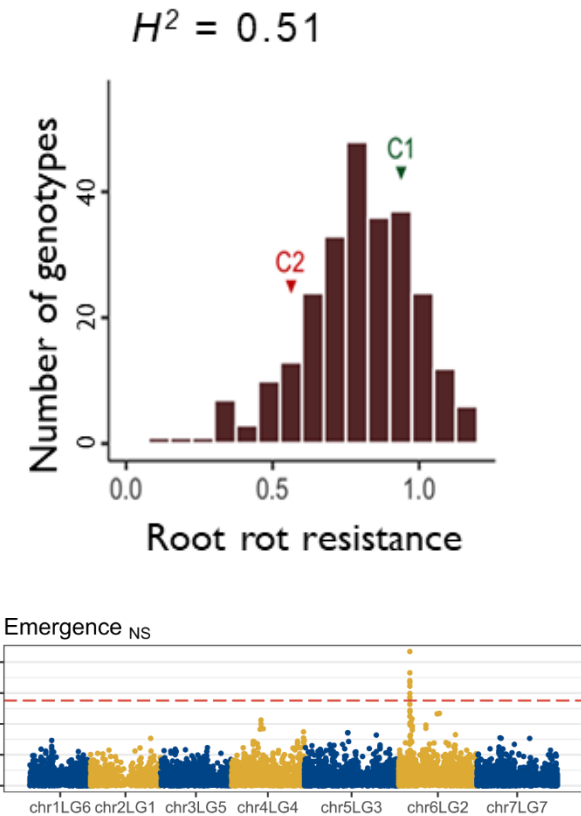
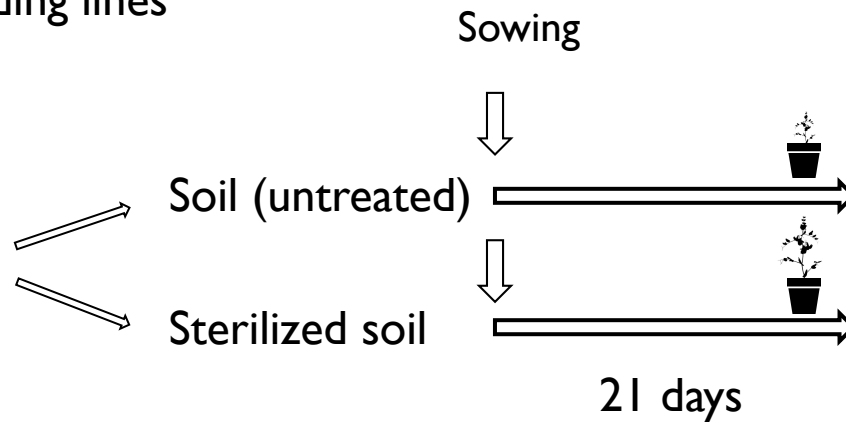
Heritable variation of root rot resistance

252 pea lines (genotypes)

- 173 landraces: USDA gene bank accessions
- 33 registered European cultivars
- 46 Swiss breeding lines



Infested field soil



How does the PRRC interact with the root microbiota?

Does the information on the microbiota increase prediction ability of pea genotype resistance?

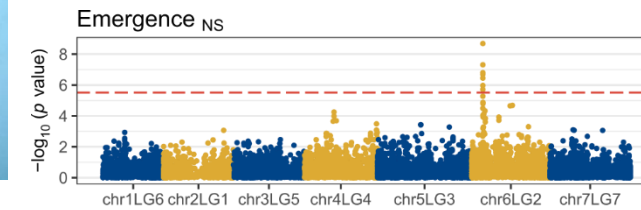
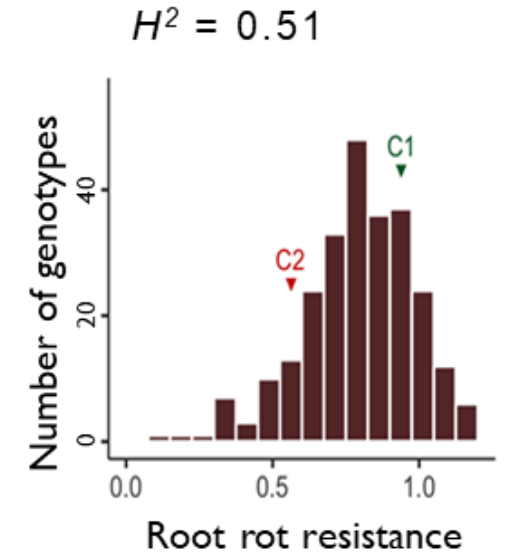
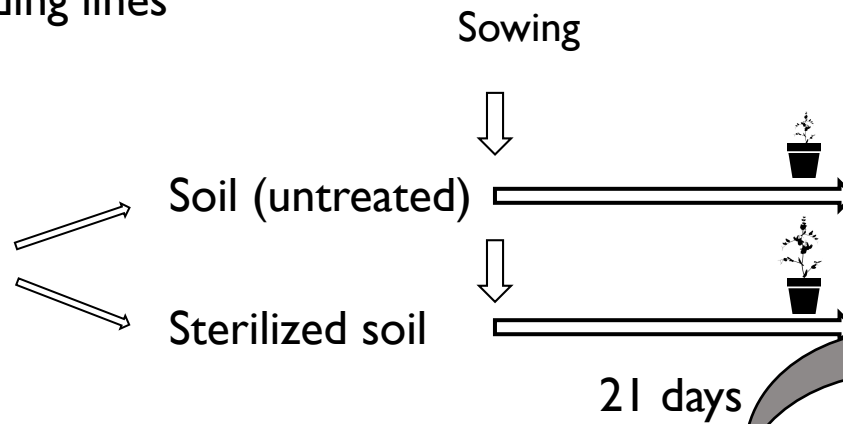
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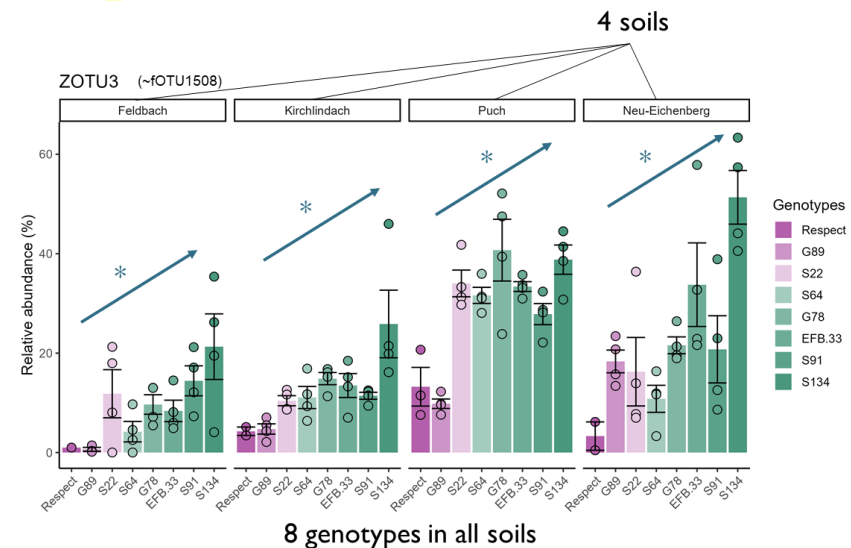
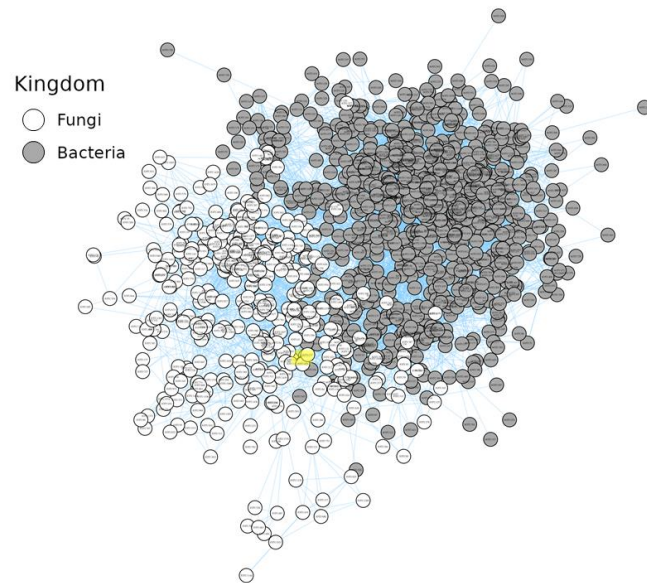
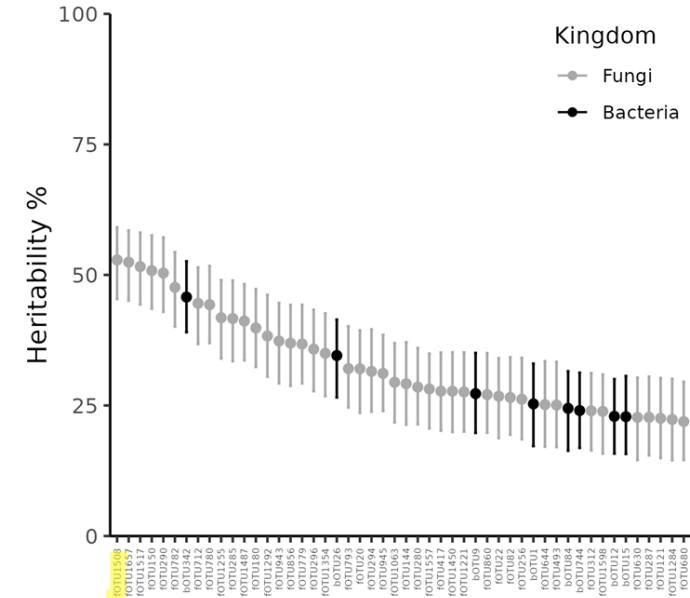
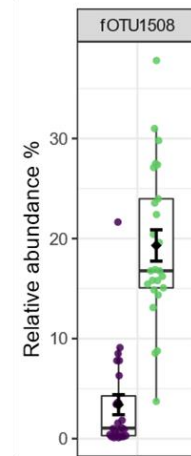
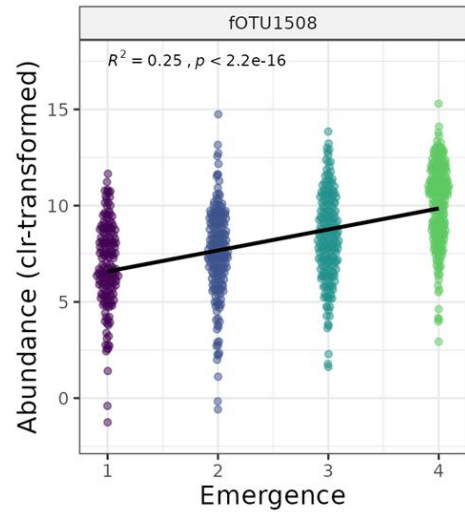
Infested field soil



Profiling of root
fungi (ITS) and
bacteria (16S rRNA)

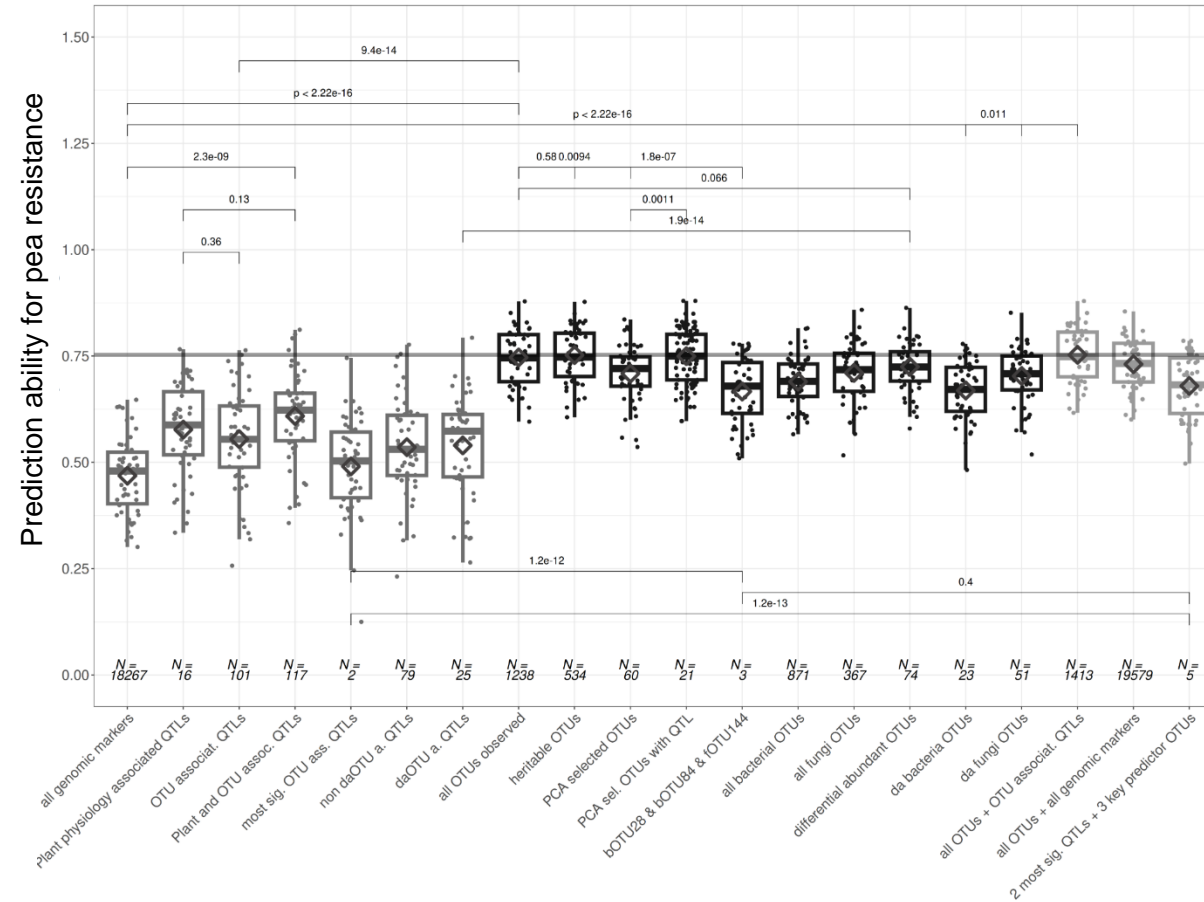
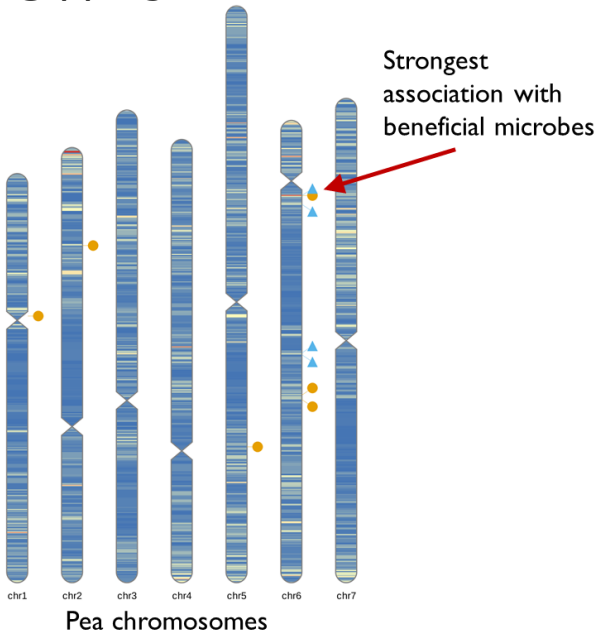
Wille et al. 2020,
Ariza-Suarez in prep, 2024

Some resistance-associated OTUs are heritable, microbial hubs and common across soils



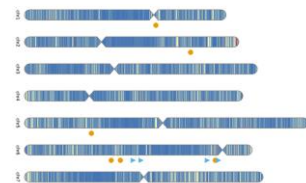
Holobiont marker concept

GWAS

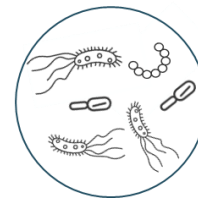


“Hologenomic” prediction
Including information on
microbiota increases the
prediction ability of a
genotype’s resistance

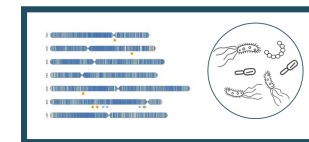
Genomic plant markers



OTU abundance markers



Mix



Validation of potential **resistance loci** and **beneficial microbes**

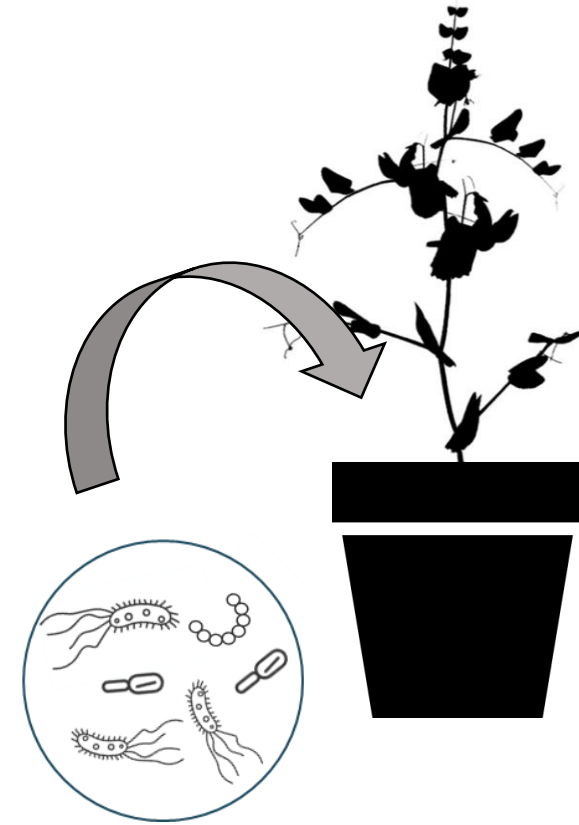
Introgression of resistant genetics into breeding germplasm



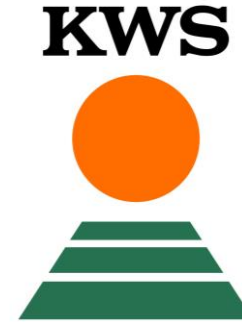
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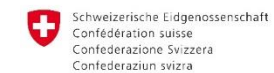
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Acknowledgements



**WISSENSCHAFT.
BEWEGEN**
GEBERT RUF STIFTUNG



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