



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

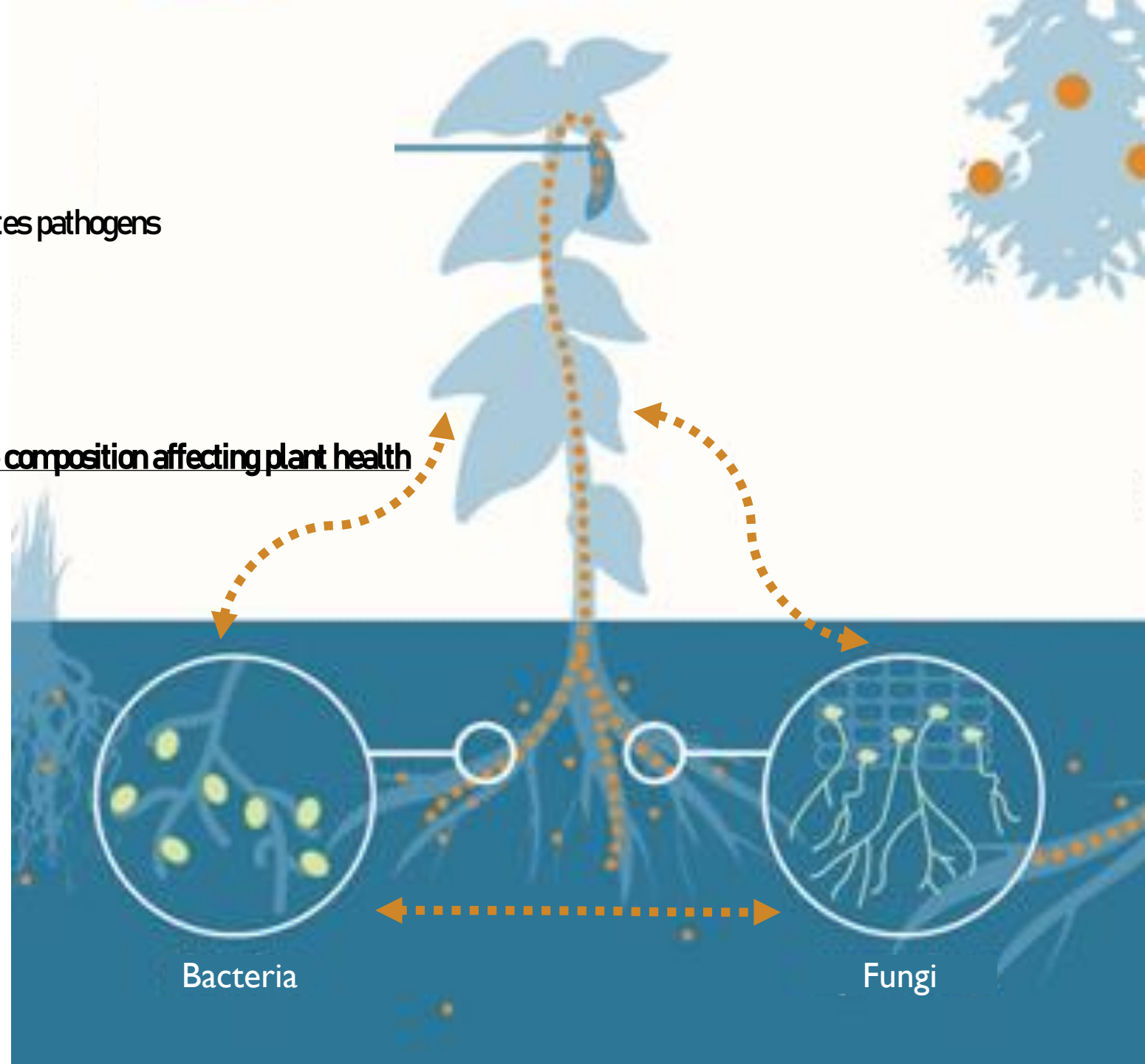
Michael Schneider
21.09.2023

Problem

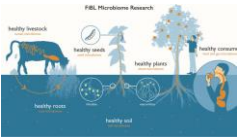
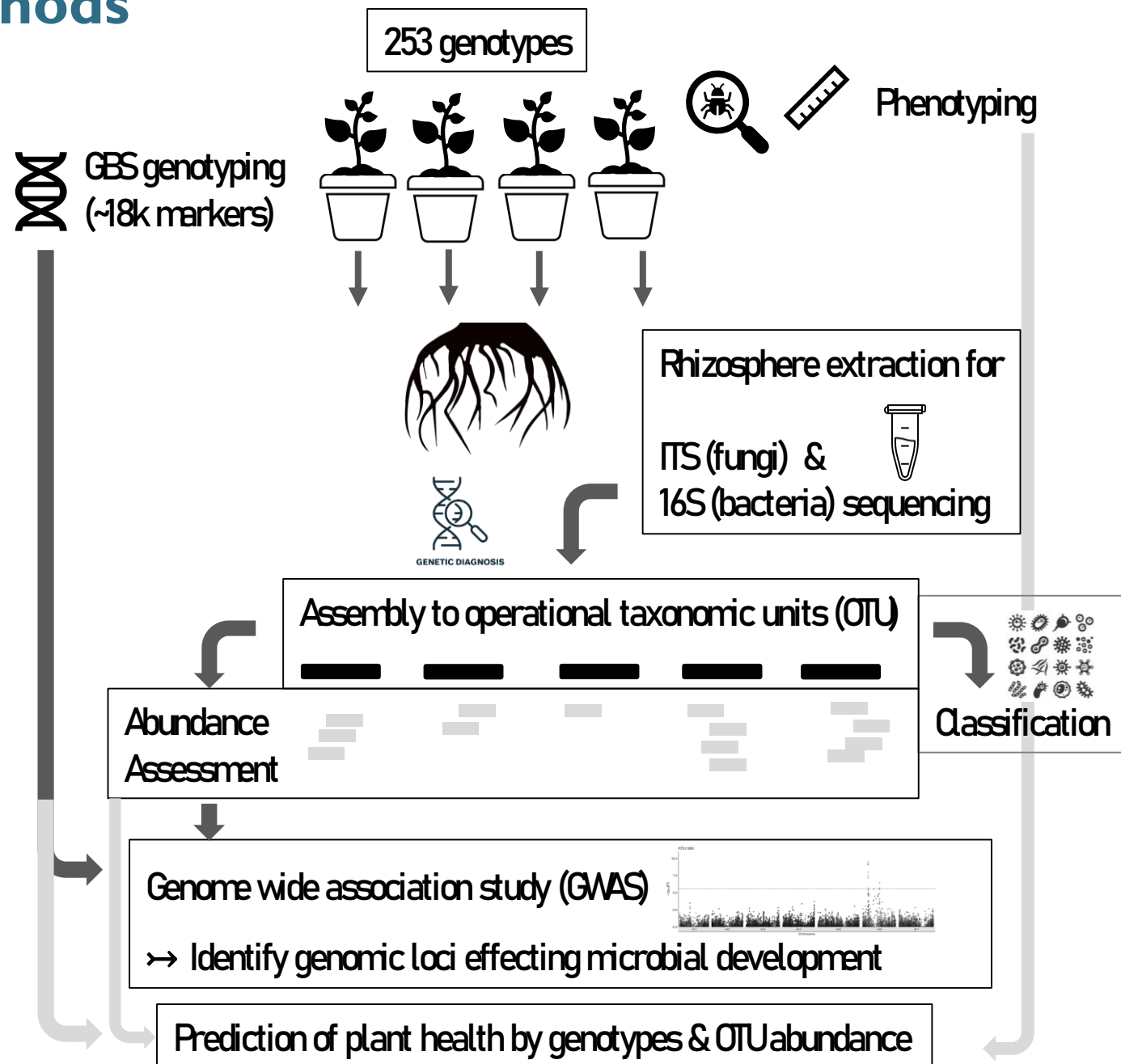
- Pea root rot complex results in massive yield declines
- The rot complex consists of bacterial, fungi and oomycetes pathogens

Aim

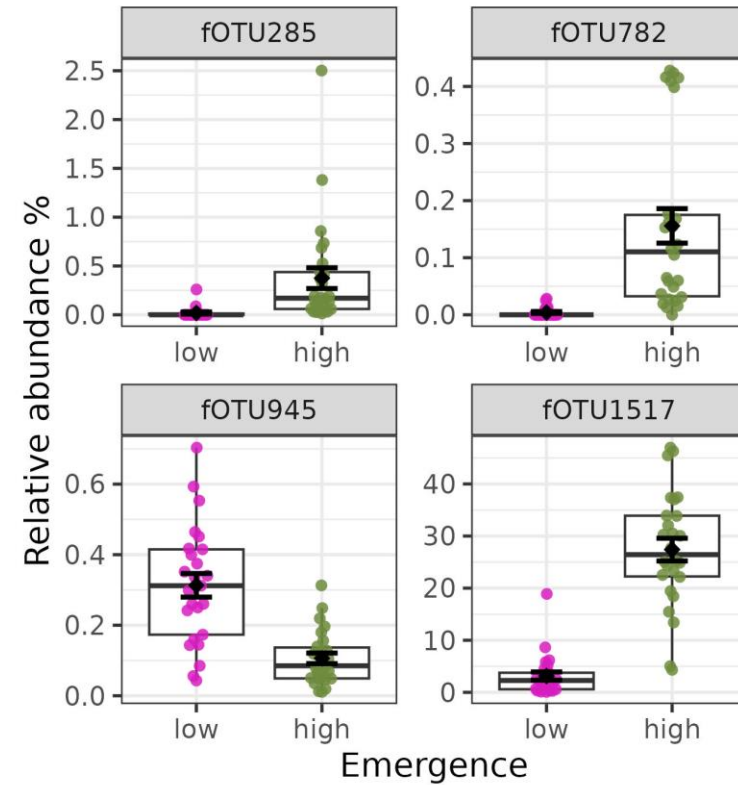
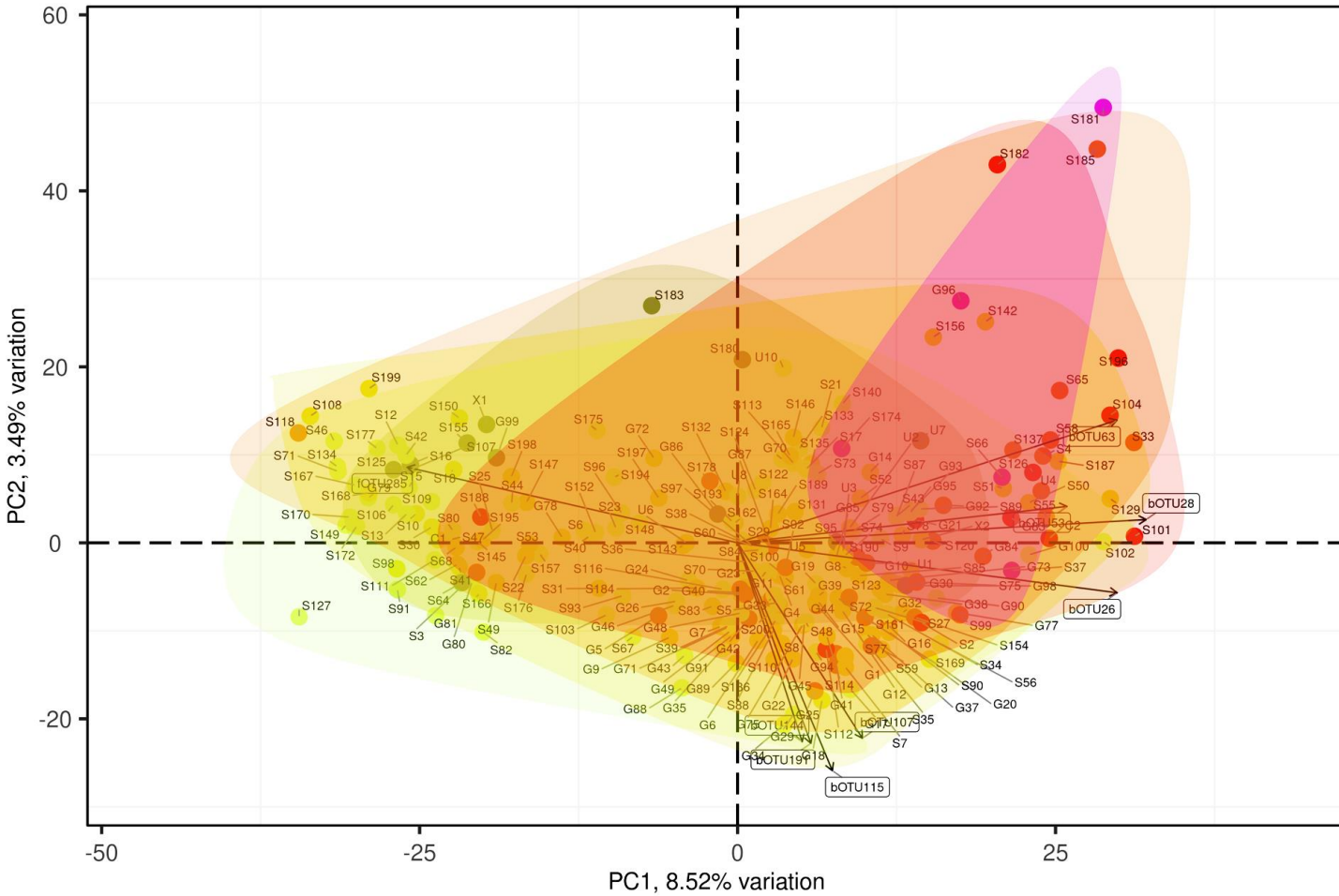
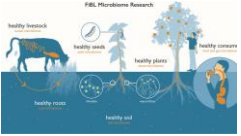
- investigate the genotype effect on the root microbiome composition affecting plant health
- potential to lead to increased resistance to PRRC
- Application in breeding



Material and Methods

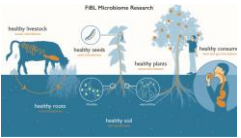
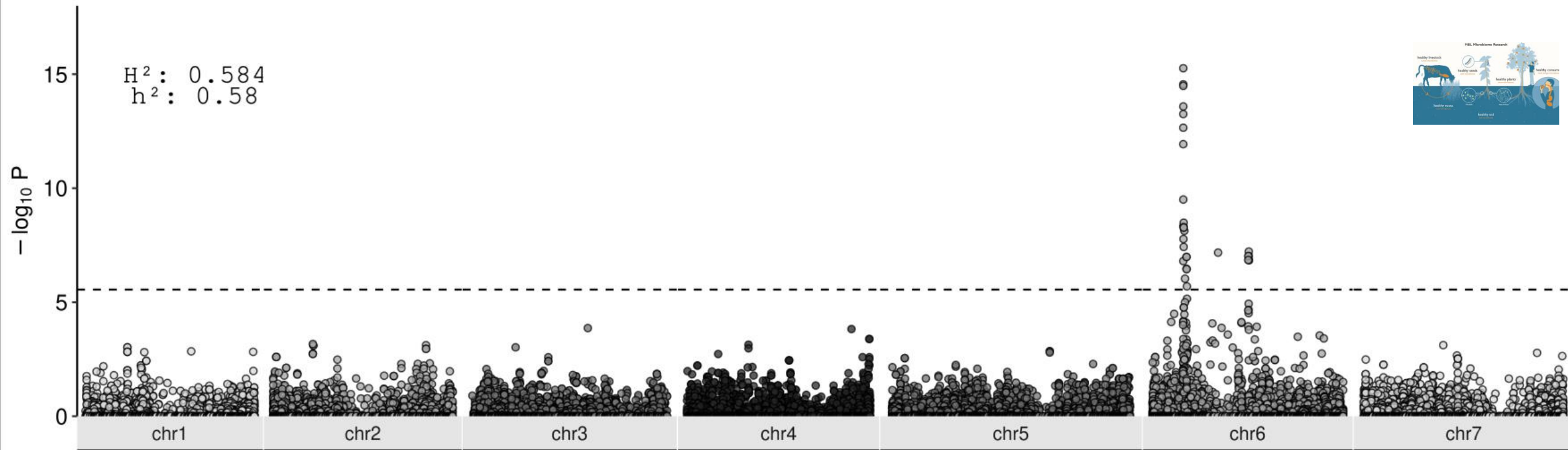


Results 1 - microbiome diversity



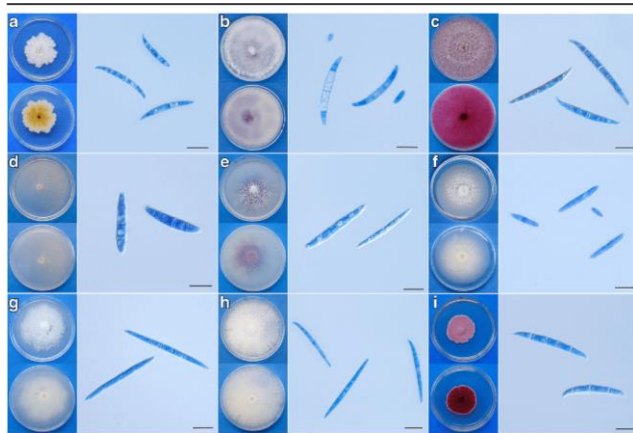
Emergence
 ● low
 ● high

Results 2 - GWAS

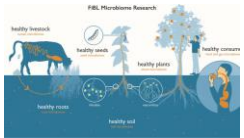
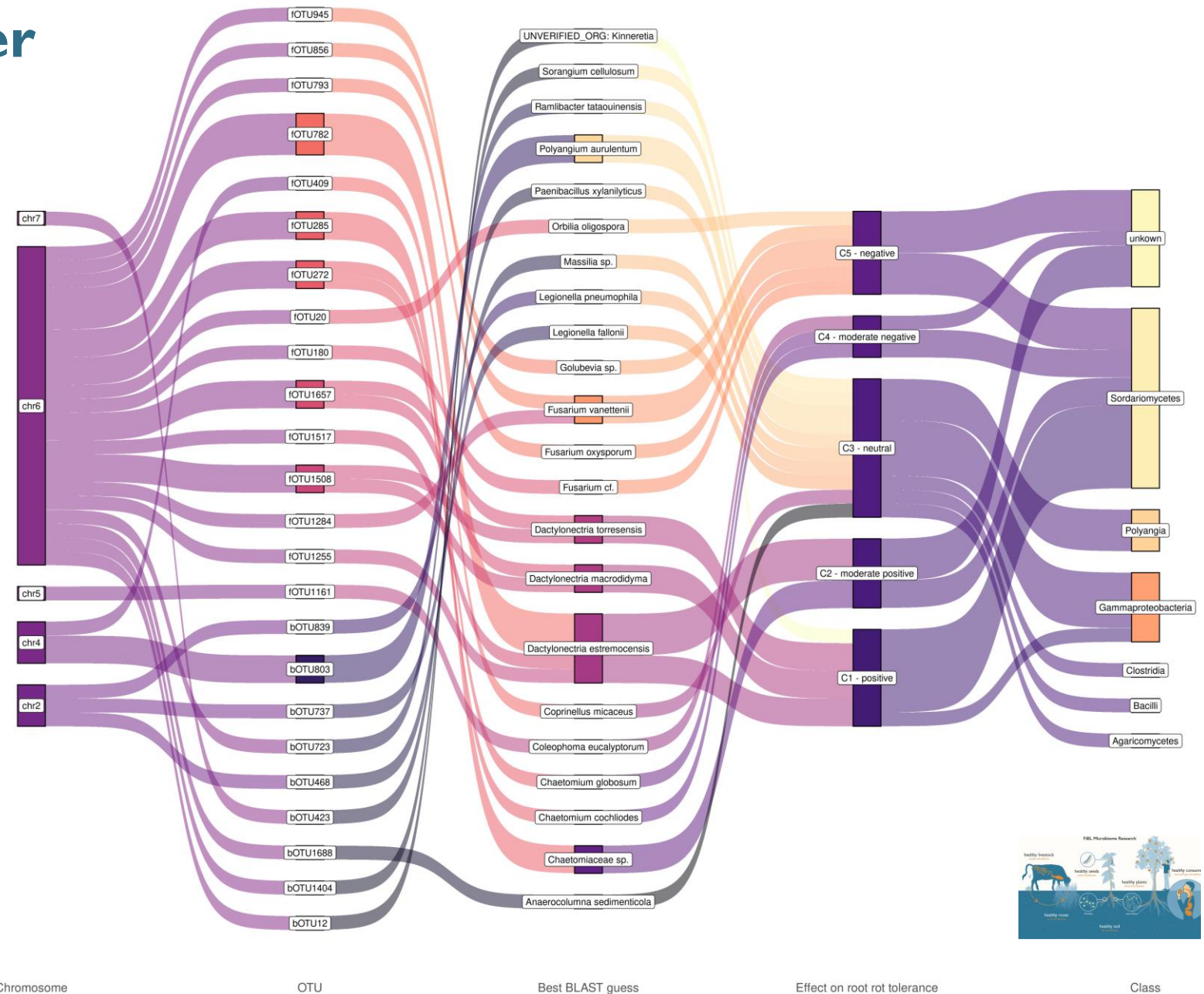


Combining all together

OTU	ExpVarTotal (%)	QTLs detected
<i>fOTU782</i>	57.68	10
<i>fOTU1517</i>	38.51	2
<i>fOTU285</i>	37.79	6
<i>fOTU1255</i>	30.07	1
<i>fOTU793</i>	27.48	2
<i>fOTU945</i>	26.88	4
<i>fOTU296</i>	26.29	4
<i>fOTU856</i>	25.17	2
<i>fOTU1657</i>	24.52	2

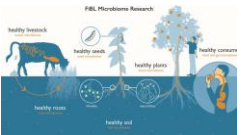


Chang et al. 2018



Conclusion

- the presence and abundance of **microbial taxa** are **determined** (among other factors) **by the pea genotype**
- the **holobiont** significantly **determines** the **resistance** of the plant to root rot
- 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



Results 3 - Prediction of the root rot in pea genotypes

Use in resistance breeding:

- 2 markers equal to all markers
- OTU abundance is a much better predictor

