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Holobiont-based plant breeding

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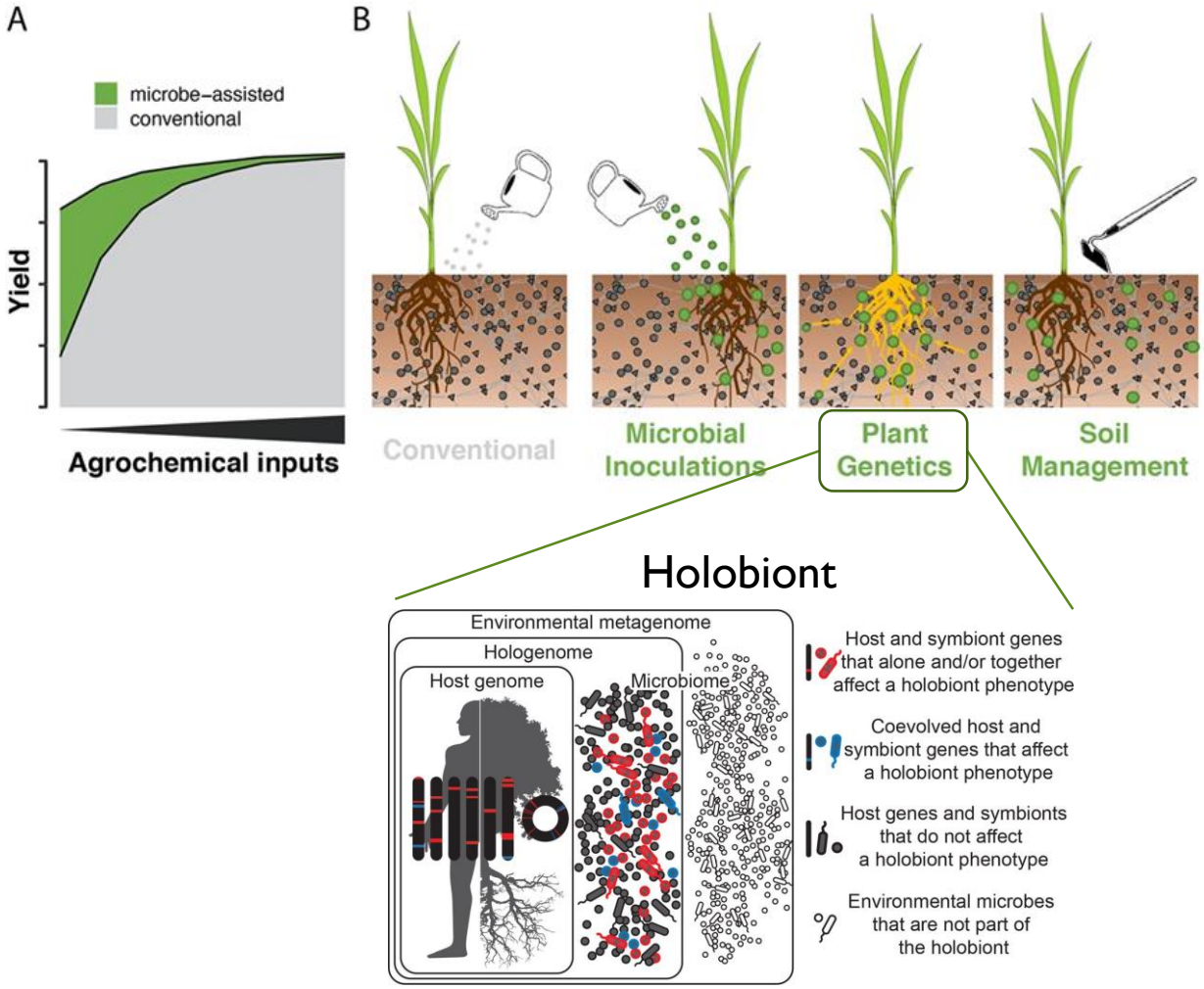
Microorganisms – a solution to maintain yields with reduced inputs



Theis et al. 2016

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Plant genetics of plant-microbe interactions

Is genotypic variation exploitable for breeding?

2019 keynote discussions:

- Jos Raaijmakers: Beneficial plant-associated microbiomes were indirectly co-selected throughout the history of breeding
- Richard Jefferson: Plant genome-focussed breeding has neglected agile trait contributions from the microbiome

➢ 5-10% of variation of microbiome composition explained by plant genotype

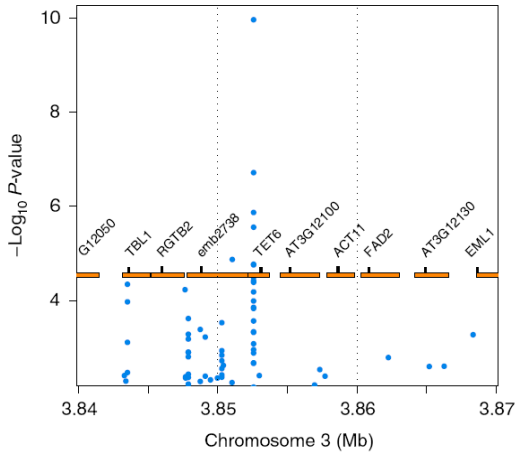
Plant genetics of plant-microbe interactions

Genotypic variation of plant responsiveness to micro(biome)es

- Colonisation success of symbionts
- Recruitment of microbes under stress situations
- Microbe-mediated disease resistance
- Priming effects (readiness of plant to respond to (a)biotic stresses)

Genetic marker (QTL)

- Plant microbiome composition
- Recruitment of specific microbial taxa
- Microbe-induced leaf rust resistance



Horton et al. 2014

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Breeding for plant-microbe interactions

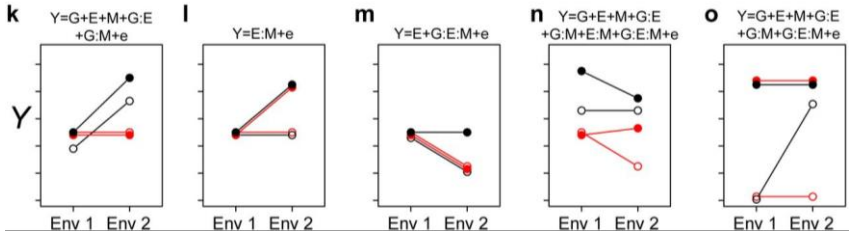
Disentangling the environmental effect:

From G x E to G x E'xMB

G: Host genotype

E': climate and physicochemical soil environment

MB: Soil and/or plant microbiome



Oyserman et al. 2020

- Disentangling MB from E due to its dynamic and evolving nature
- Useful framework to capture ecological interactions
- Enhancing the predictability of microbe-assisted plant breeding

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Opportunities for breeding

- Yield stability and productivity (reduced inputs)
- Tools: High-throughput phenotyping, machine learning and modelling, seed treatments, genetic markers, gene editing
- Monitoring and decision tools for genotype selection, but also for crop selection and agricultural practices
- From controlled conditions to field
  >> farmer participation

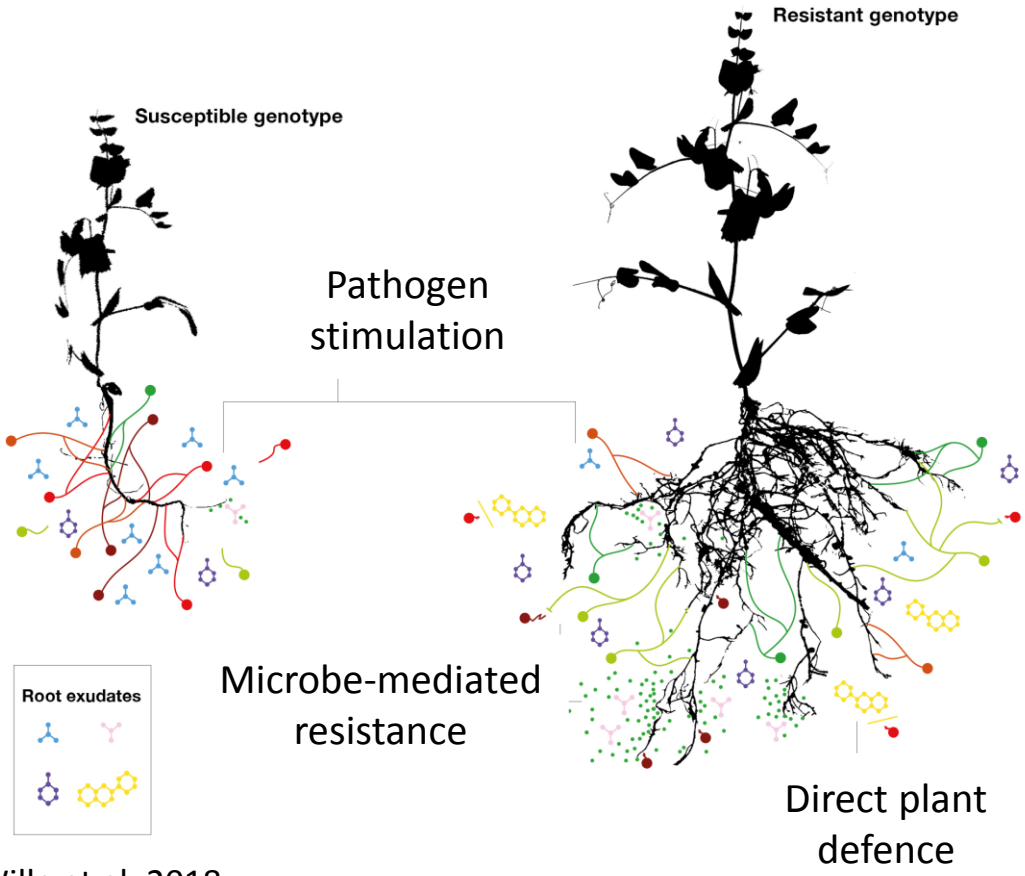
Advancing pea resistance breeding

STIFTUNG MERCATOR SCHWEIZ

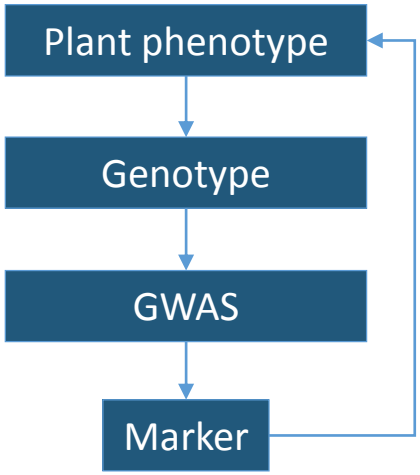
LIVESEED

Lukas Wille

Improving disease resistance of pea through selection at the plant-soil interface



Wille et al. 2018



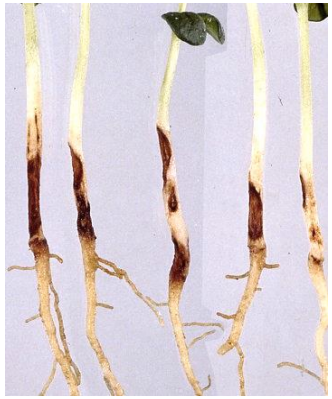
Advancing pea resistance breeding

Pea is affected by a complex of fungal and oomycete pathogens, e.g.:

Aphanomyces euteiches

Pythium ultimum

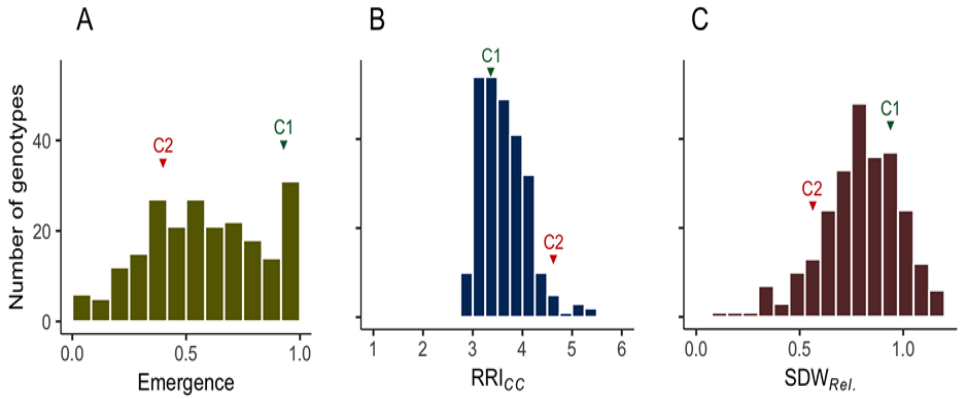
Fusarium solani



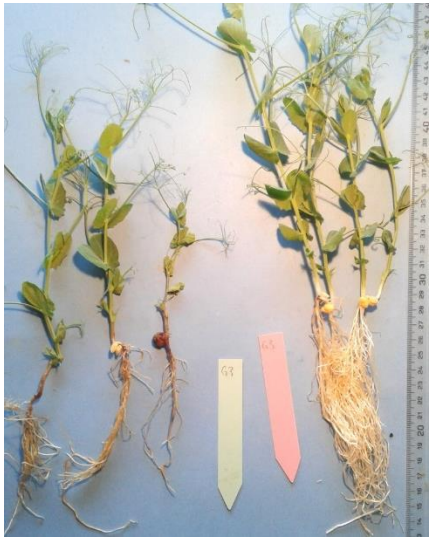
Rhizoctonia solani

Advancing pea resistance breeding

Heritable variation for resistance against a root rot complex



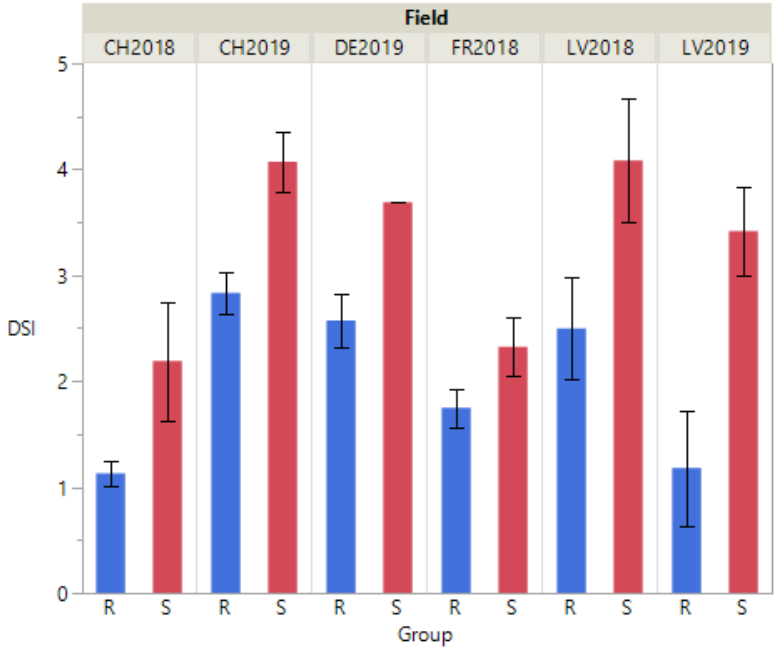
Wille et al. 2020



Advancing pea resistance breeding

Heritable Variation in Pea for Resistance Against a Root Rot Complex

Validated in 6 field environments



Advancing pea resistance breeding

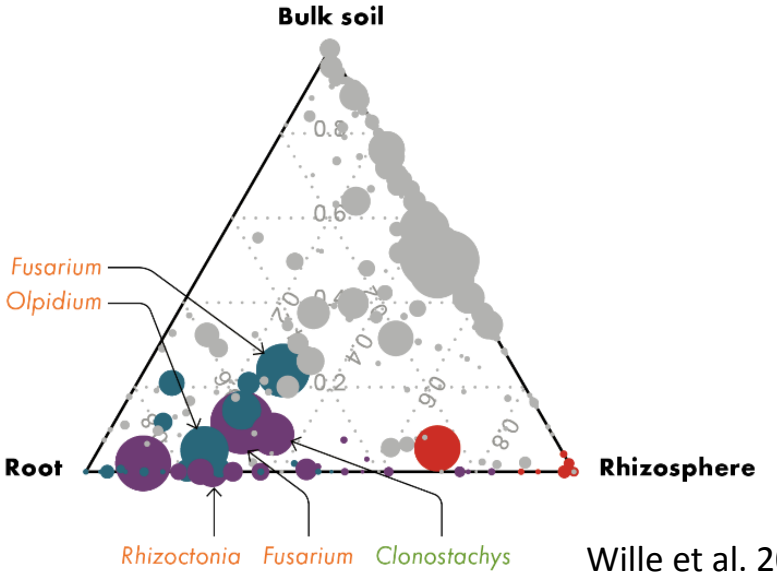
Heritable Variation in Pea for Resistance Against a Root Rot Complex

Screen implementation at gzpk Biodynamische Pflanzenzüchtung

© Christine Schreiner

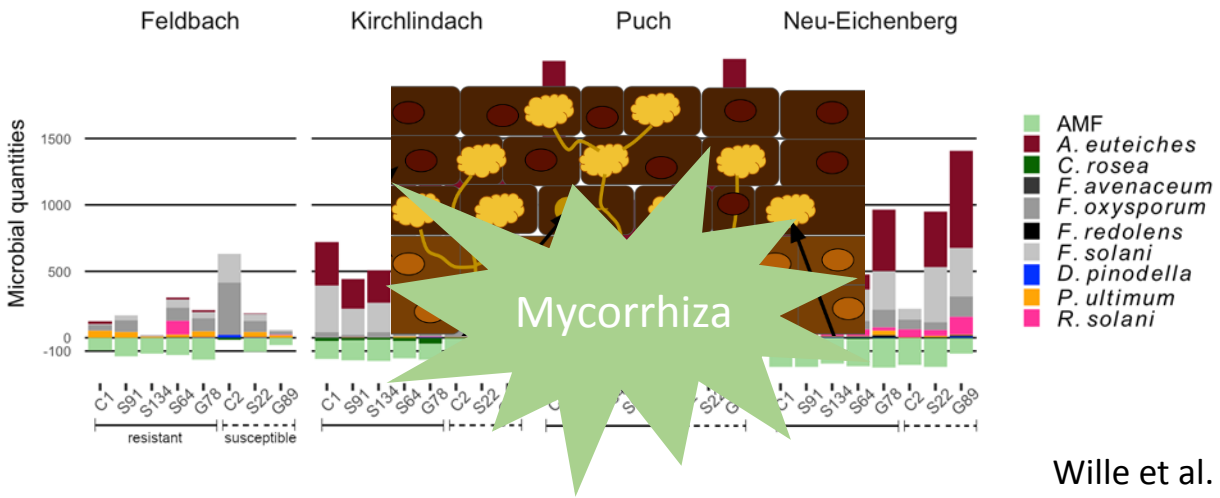
Advancing pea resistance breeding

Verification of the complexity of pea root rot



Wille et al. 2018

Microbial markers for resistance breeding



Wille et al. in prep

Advancing pea resistance breeding

WISSENSCHAFT. BEWEGEN
GEBERT RÜF STIFTUNG

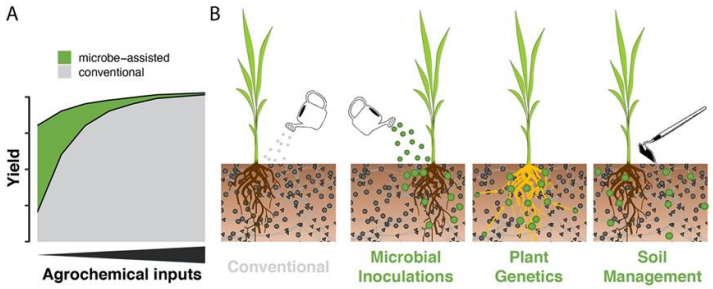
AGRIBIOME – Plant microbiome recruitment for superior agricultural systems

Three genome-wide association studies related to disease resistance:

1. Standard plant genetic markers based on disease phenotype
2. Advanced plant genetic markers for functional microbiome diversity and the recruitment of microbial key taxa
3. Holobiont genetic markers: combined action of plant+microbiome markers

Outlook

FEMS MICROBIOLOGY ECOLOGY perspective article



Main Research priority:

Identify genetic determinants that steer beneficial plant-microbiome interactions

Key targets:

- Bridge fundamental knowledge and application
- Understand functioning within complex microbial communities and holobiont interactions
- Improve efficacy predictions
- Link beneficial functions of indiv. microbes or entire microbiomes with plant traits

Thank you for your attention!

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Main partner:

ETH zürich

INRAE

gzpk biodynamische Pflanzenzüchtung

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Schweizerische Eidgenossenschaft
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ReMIX Species mixtures for redesigning European cropping systems

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