

Improving disease resistance of pea - clues from plant-microbe interactions

Lukas Wille^{1,2} (lukas.wille@fibl.org), Pierre Hohmann², Monika Messmer², Bruno Studer¹

¹Institute of Agricultural Sciences – Molecular Plant Breeding, ETH Zürich

²Department of Crop Sciences – Plant Breeding and Variety Testing, Research Institute for Organic Agriculture (FiBL)



1) Introduction

Pea (*Pisum sativum* L.) is a valuable protein source for food and feed. Like other legume plants, peas form an intimate mutualistic symbiosis with nitrogen fixing rhizobacteria, and, thereby, are able to significantly improve soil fertility. Pea is highly prone to soil-borne pathogens and rotation breaks of up to ten years are recommended to avoid the build-up of high pathogen loads in the field. This stands in conflict with efforts to increase acreage of pea to strengthen low input farming systems and meet the increasing protein demand of a growing world population.

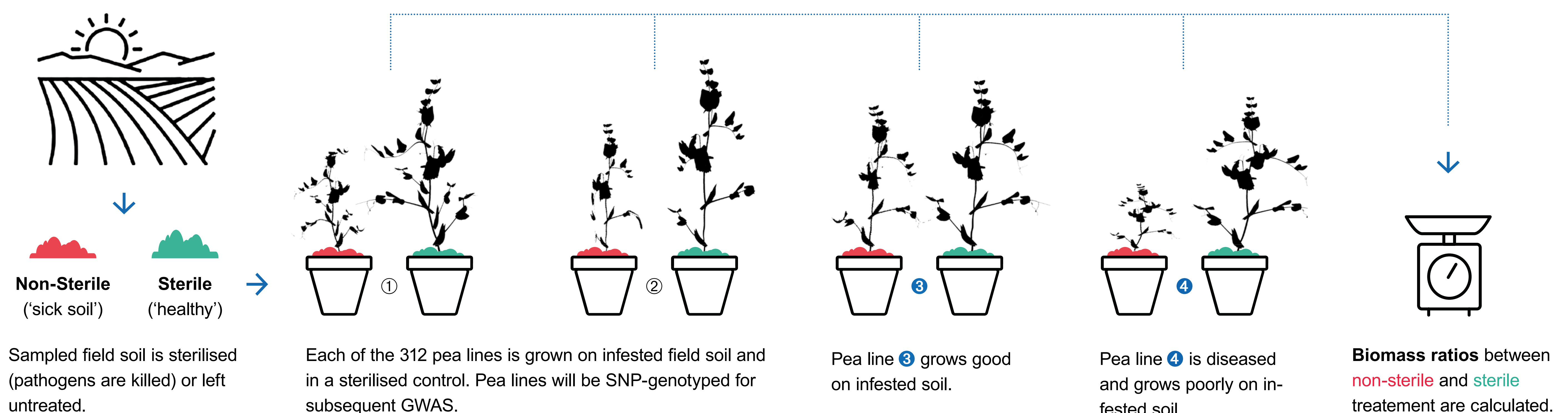
2) Objectives

- Identify pea lines resistant to soil-borne pathogen complexes.
- Elucidate the genetic basis of polygenic resistance of pea against fungal pathogens.
- Improve our understanding of plant-microbe interactions conferring resistance to pathogens.
- Provide the knowledge base to breed for superior cultivars for organic and other forms of sustainable agricultural systems.

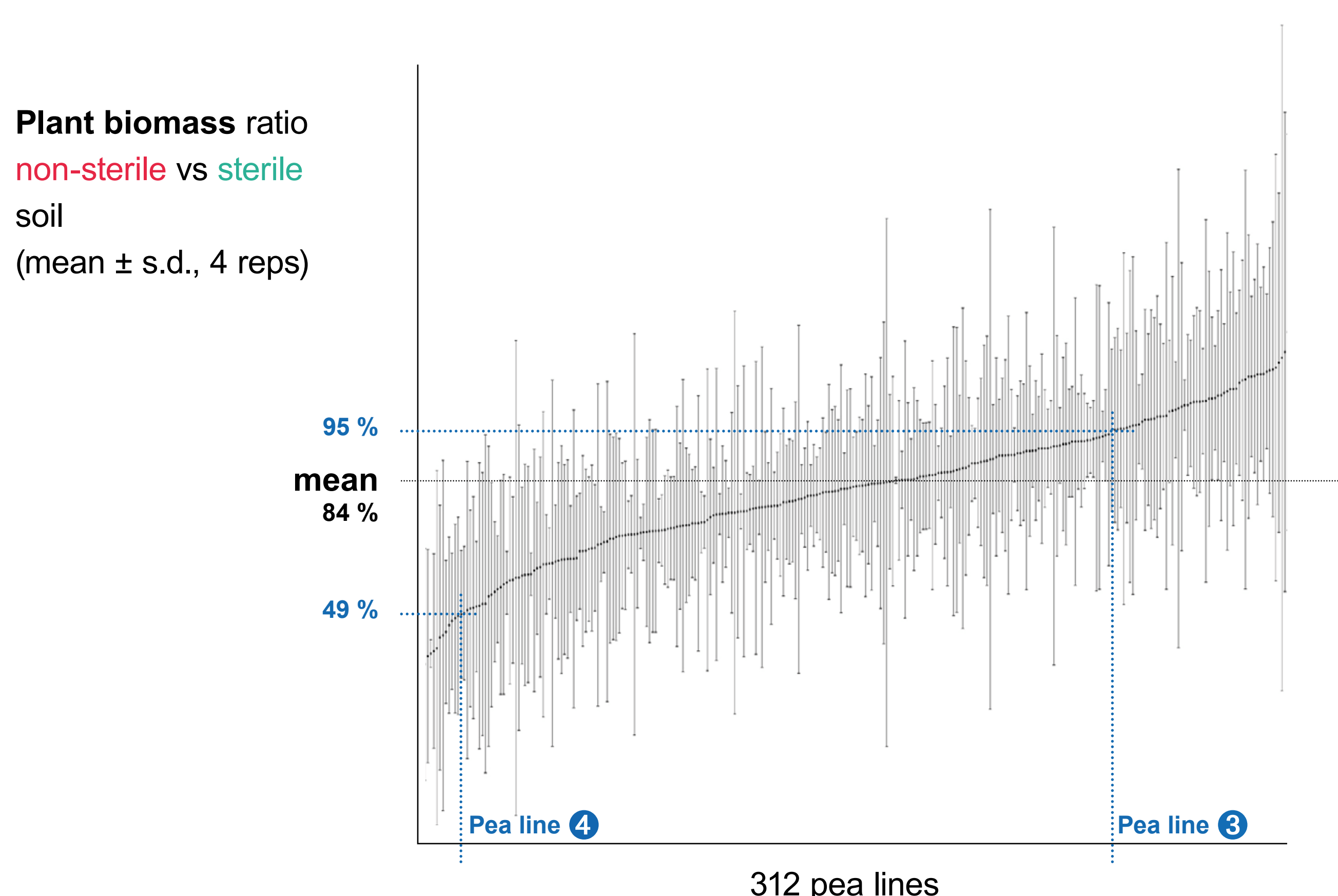
3) Screening of 312 pea lines for resistance

Field soil infested with pea pathogens (=‘sick soil’)

After 21 days of growth under standardized conditions various disease indices, growth parameters and biomass is recorded, and diseased roots are sampled for DNA based microbiome analysis.



4) Preliminary results: Biomass of different pea lines

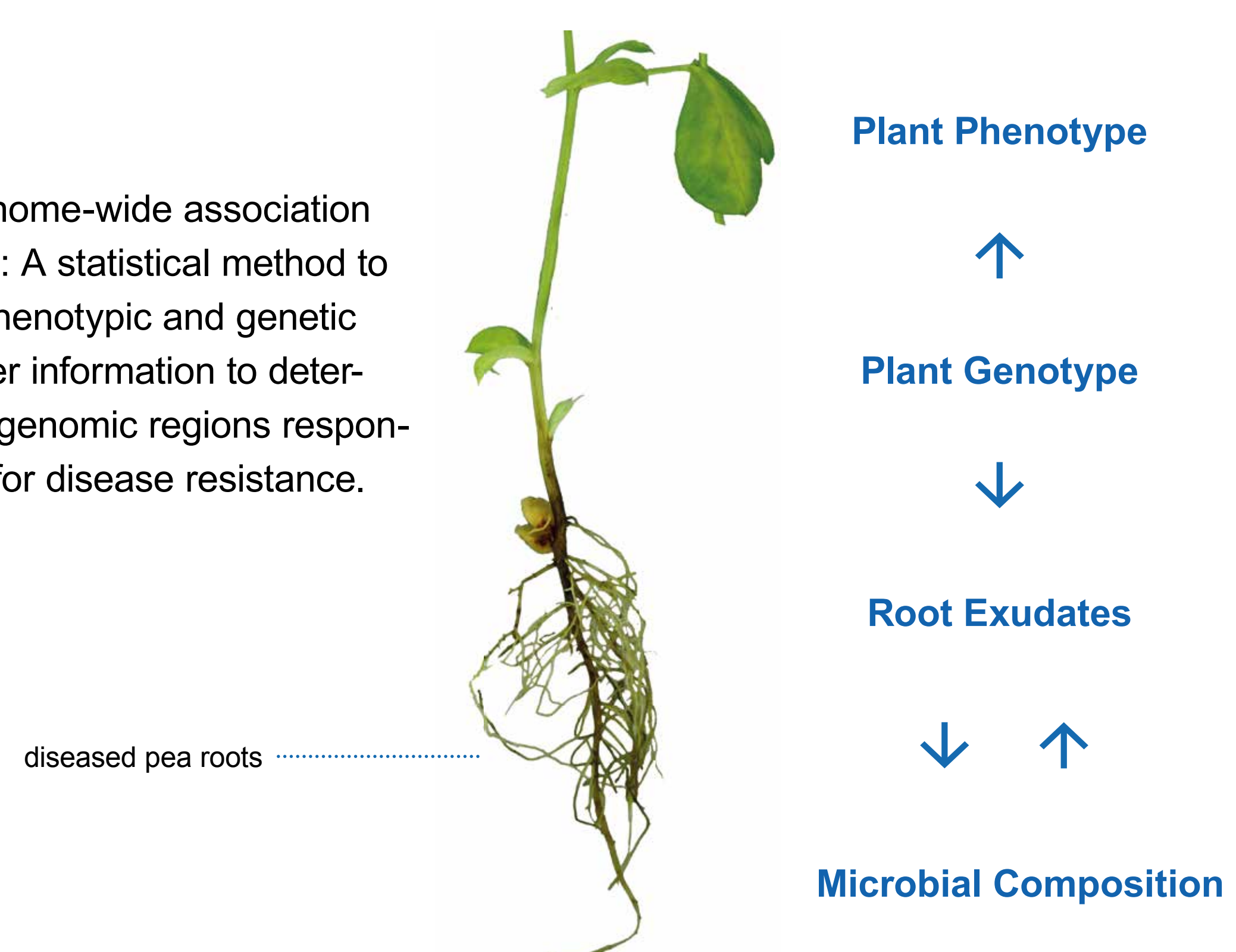


Conclusion:

About 25% of the evaluated pea lines grow as good on the infested field soil as on the sterilised soil - these lines are potentially resistant/tolerant to the pathogen complex present in the soil.

5) Next: GWAS* & plant-microbe interactions

* 'Genome-wide association study': A statistical method to link phenotypic and genetic marker information to determine genomic regions responsible for disease resistance.



Hypothesis:

Susceptible pea lines (eg. line ④) release molecular compounds that favor pathogenic fungi. Roots get infected and destroyed. Resistant pea lines (eg. line ③) release molecular compounds that repel pathogenic fungi directly or that attract non-pathogenic/beneficial fungi.