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Genome-wide association studies to detect new resistance alleles for apple scab and fire blight



Paul Galleron¹, Laval Jacquin¹, Caroline Denancé¹, Romane Lapous¹, Charles-Eric Durel¹, Hélène Muranty¹, Julie Ferreira de Carvalho¹

Context

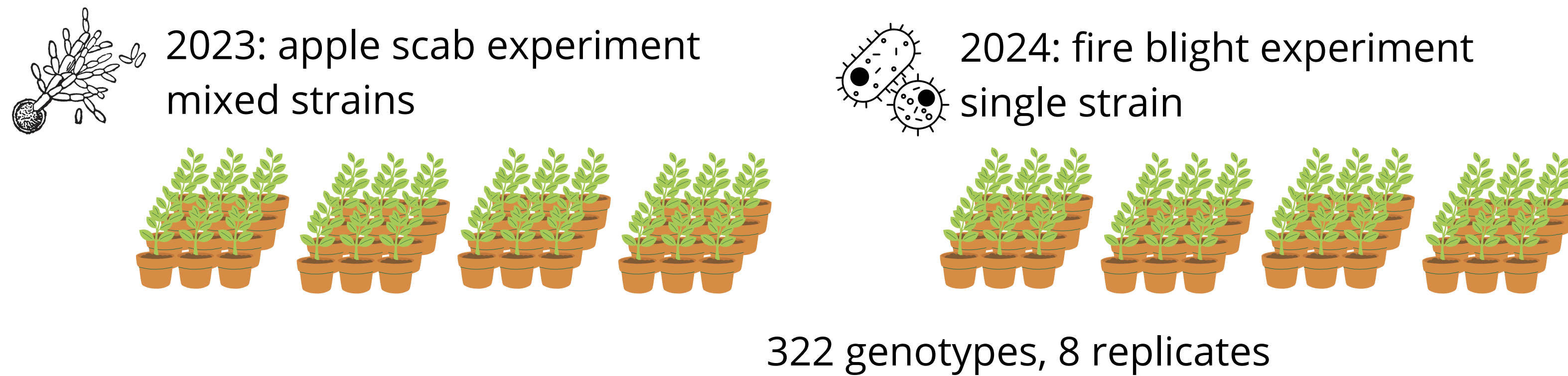
Malus domestica is one of the world's most heavily treated cultivated species. The varieties that dominate world production are susceptible to multiple pathogens, including fungi such as *Venturia inaequalis* and bacteria such as *Erwinia amylovora*. *V. inaequalis* is the agent responsible for apple scab and *E. amylovora* is the agent responsible for fire blight. Both diseases can lead to significant yield losses. To reduce the use of phytosanitary products, it seems necessary to create new varieties resistant to various bioaggressors. The use of association studies should provide solutions.

Research question:

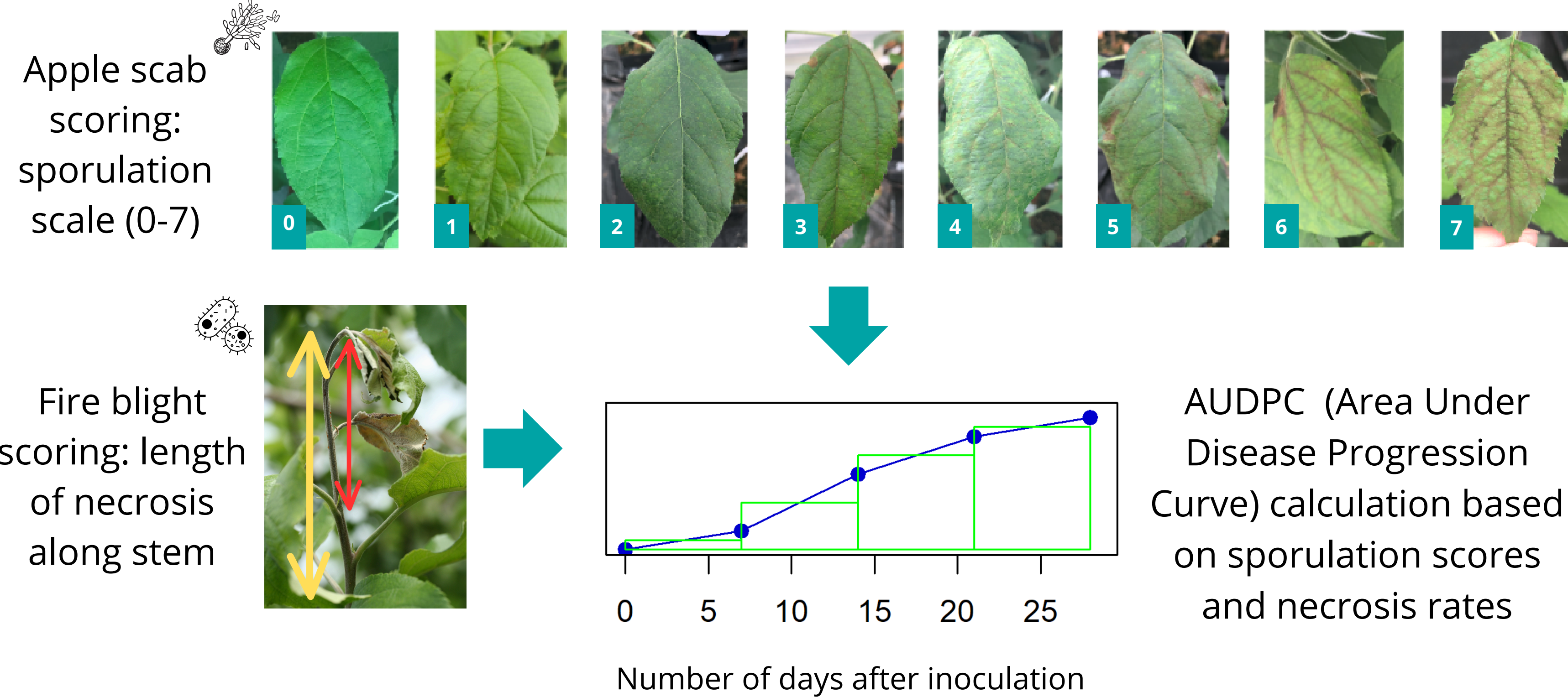
In a pre-breeding approach, how can we implement and exploit association studies to identify new sources of resistance in *Malus domestica* to apple scab and fire blight?

Methodology

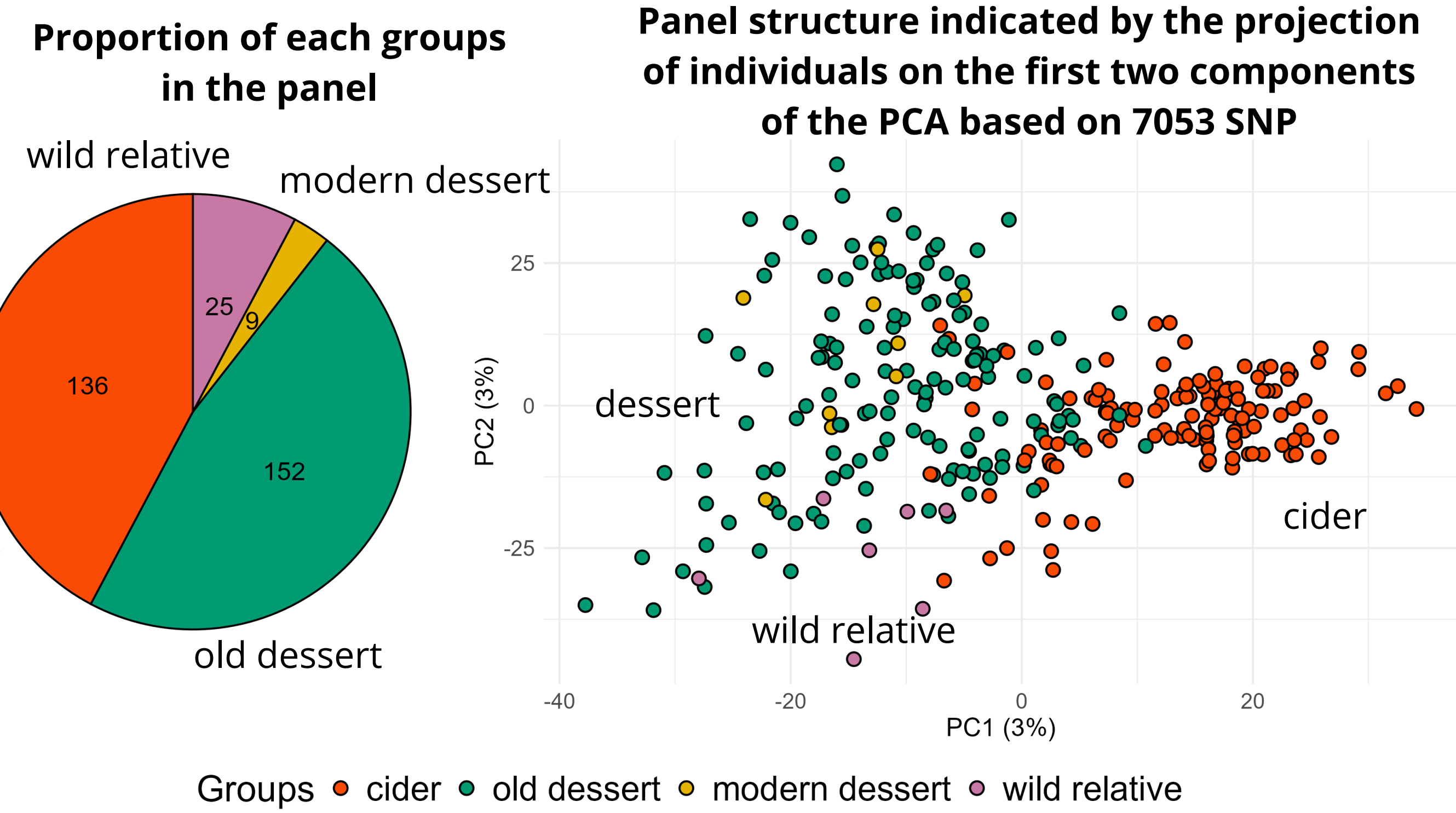
Experimental design, greenhouse inoculation



Scoring and calculation of AUDPC

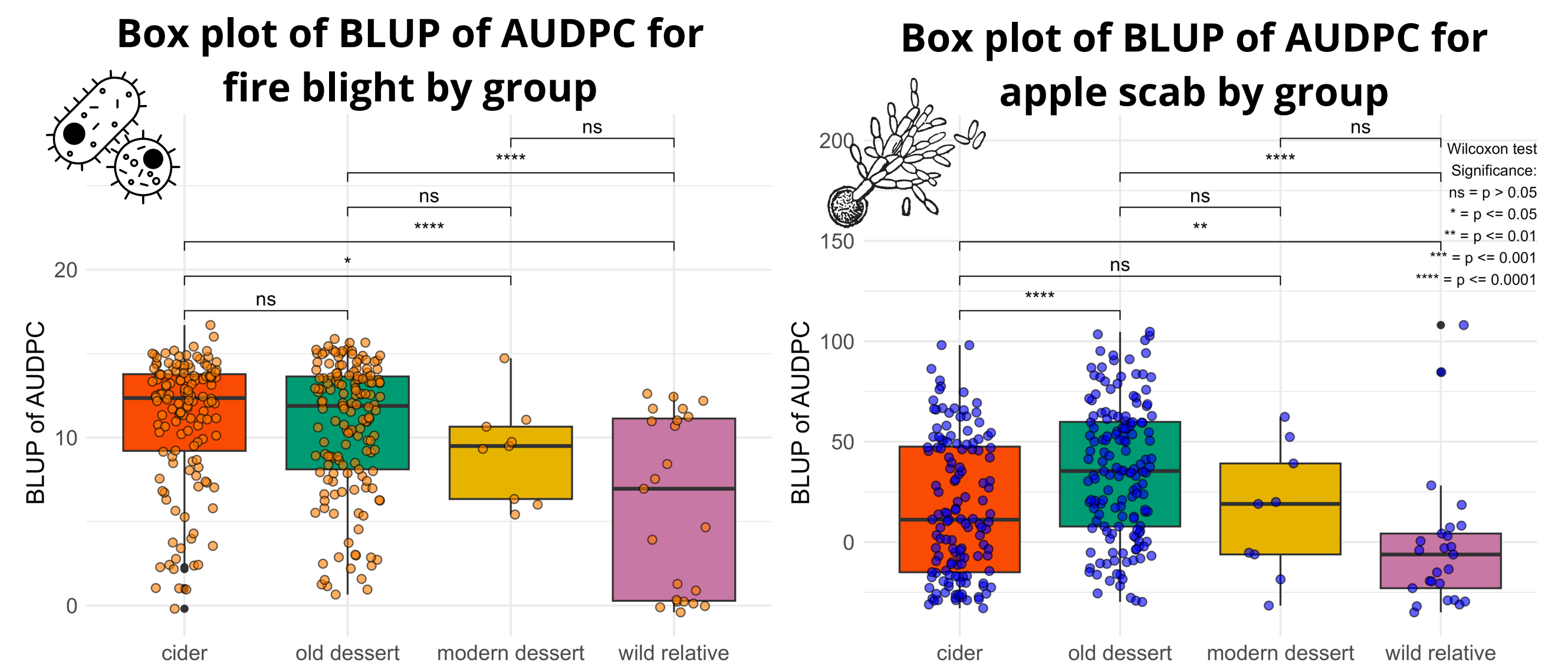


1. Diversity panel: 4 groups



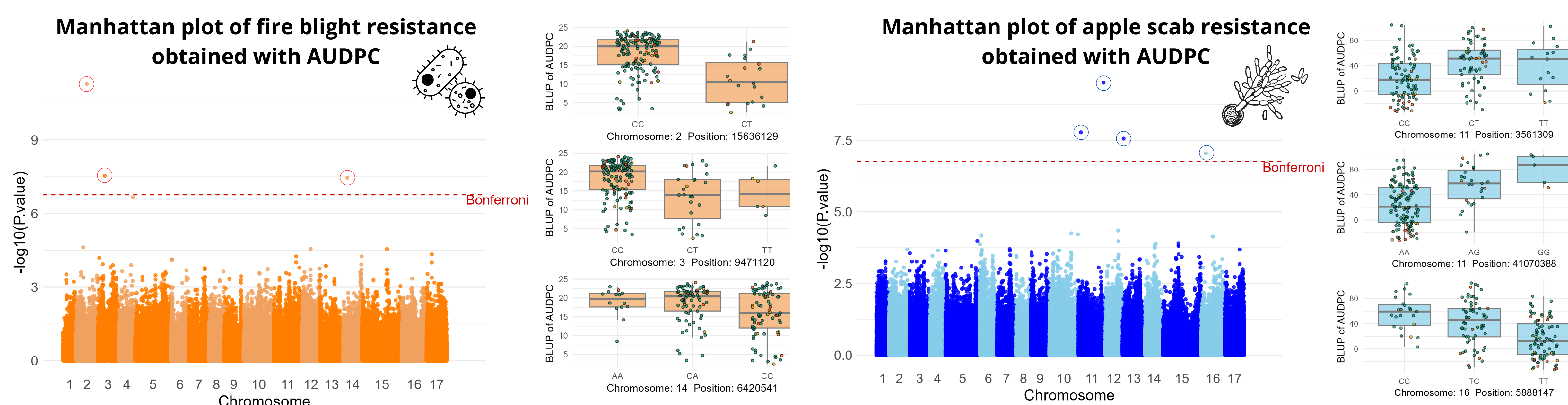
2. Variability of phenotypes

Adjusted phenotypic values correspond to BLUP (Best Linear Unbiased Prediction) Differences between and within groups

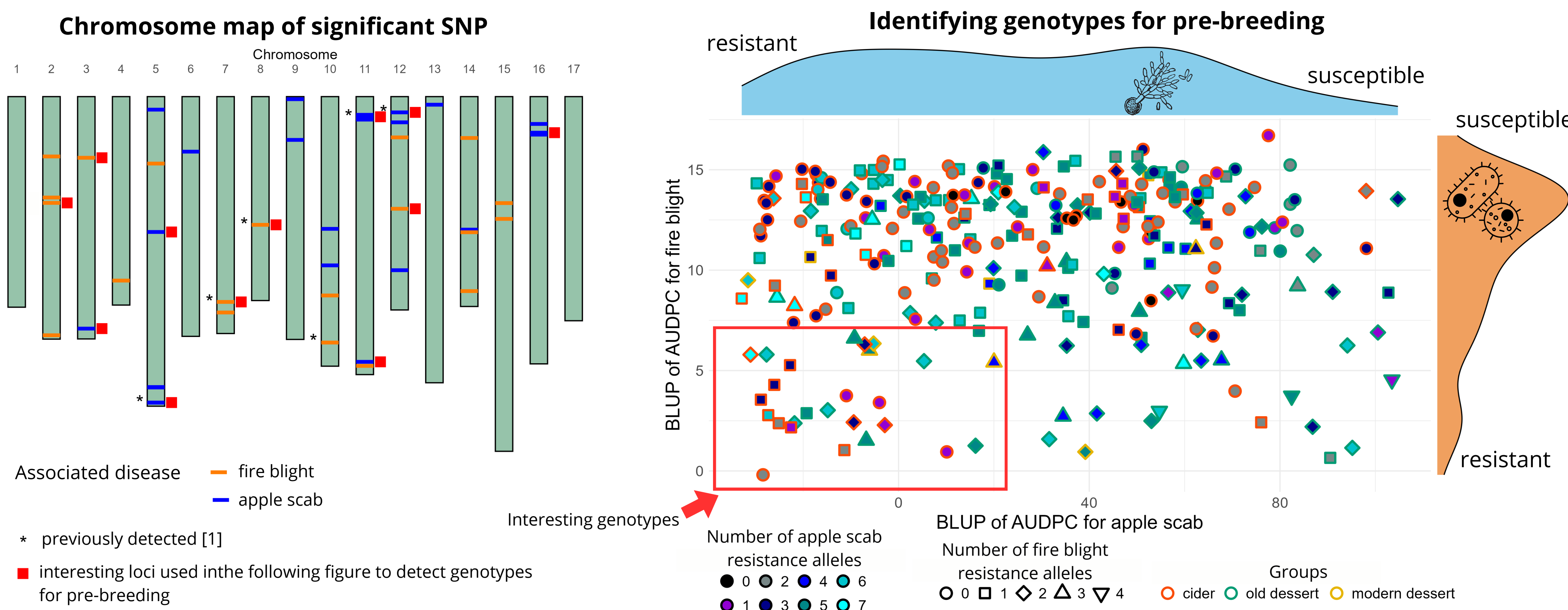


3. Genome-Wide Association Study

Significant SNP associated with phenotypes were detected by studying the BLUP of sporulation scores, necrosis rates and AUDPC with the MLM and BLINK models. Genotypic data from two microarrays with different densities were used (20K and 480K).



4. Identification of new alleles and progenitors carrying resistance alleles



Conclusion and perspectives

- Cider and old dessert apple varieties represent an unexplored genetic pool containing fire blight and apple scab resistance alleles.
- New and previously detected QTL have been identified.
- Interesting genotypes carrying several resistant alleles have been chosen to be used in biparental crosses.
- Major sources of resistance from rare alleles were not detected. Linkage studies will help characterize them.

[1] Benejam, J. (2021). *Résistances du pommier à la tavelure et au feu bactérien : interactions entre les résistances génétiques et induites par les SDP* [PhD thesis, University of Angers].

