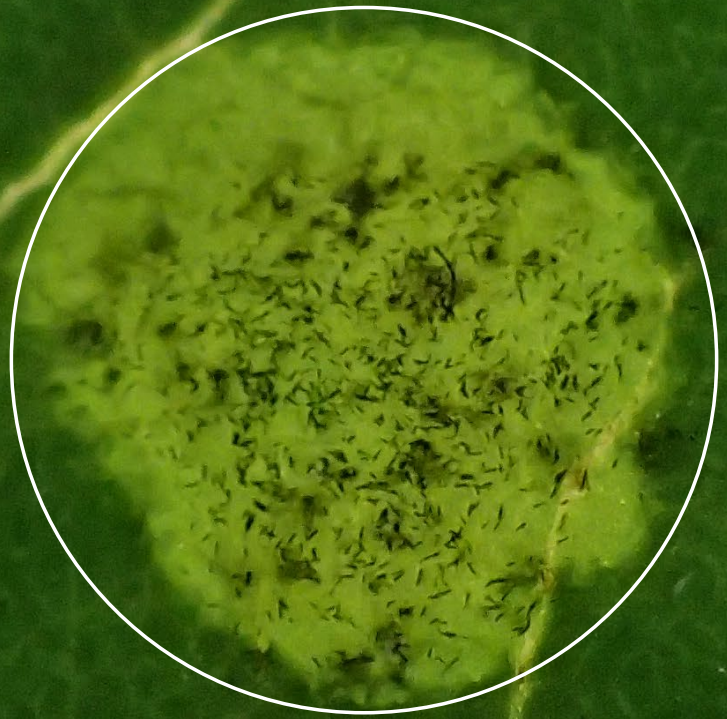


Studying wild relatives of potato to develop early blight-resistant cultivars

21st Euroblight workshop

20/05/2026| Jaap Wolters

LWV20239

Co-funded by the European Union
HORIZON-CL6-2023-BIODIV-01-14

Early blight background

- Foliar disease of potato and tomato
- Caused by *Alternaria solani* (and related large-spored species)
- Necrotrophic fungus
- No (strong) resistance in cultivars

Wild relatives of potato as a source of blight-resistance

WUR/PBR *Solanum* collection consists of wild relatives of potato collected from 14 countries in North/Middle and South America

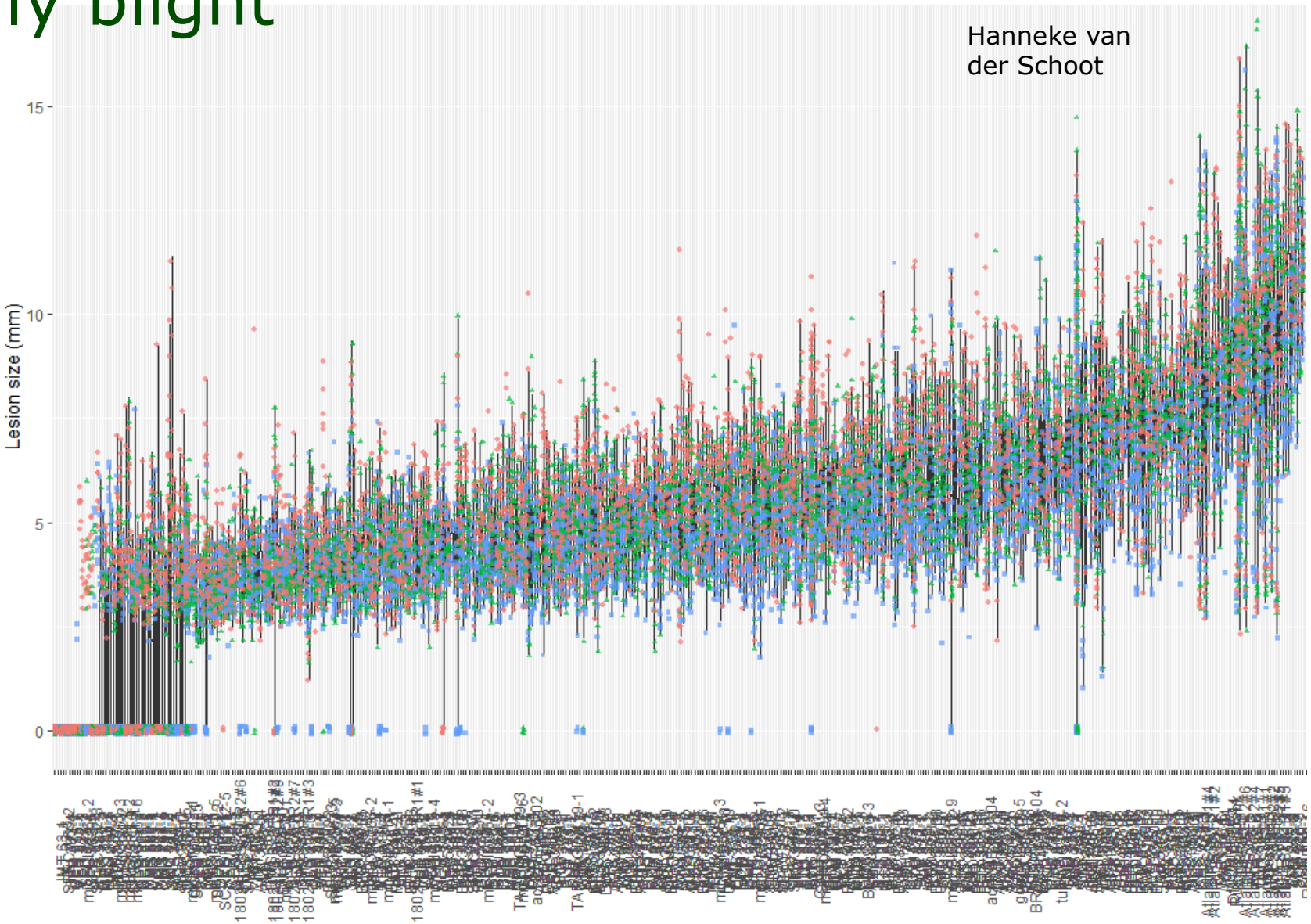
Various *R* genes against *Phytophthora infestans* were identified in the collection

Vleeshouwers et al. 2011

Screening WUR/PBR Solanum collection for resistance to early blight

~600 genotypes tested

Resistant as well as susceptible genotypes were identified

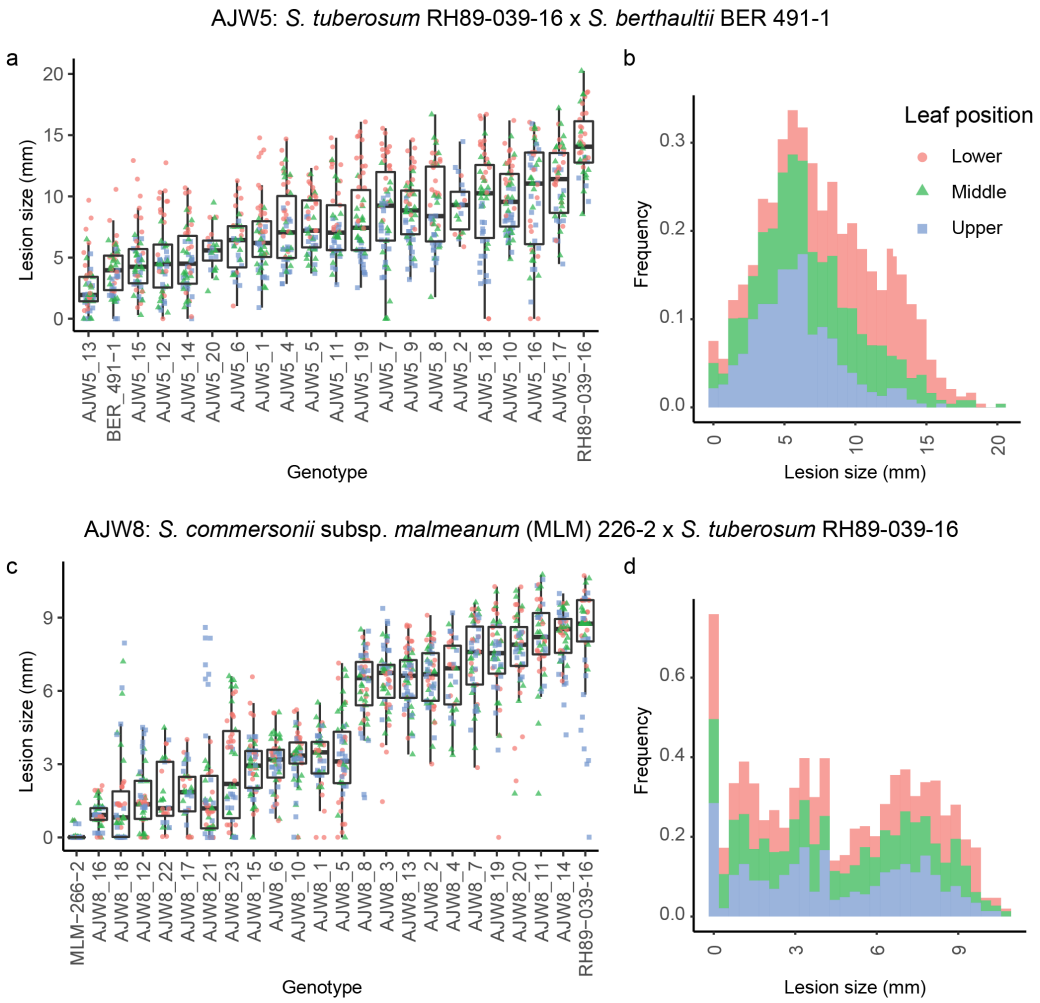


WAGENINGEN
UNIVERSITY & RESEARCH

Quantitative and qualitative resistance against early blight in potato

Resistance of *S. berthaultii, S. virgultorum, S. sparsipilum* and others

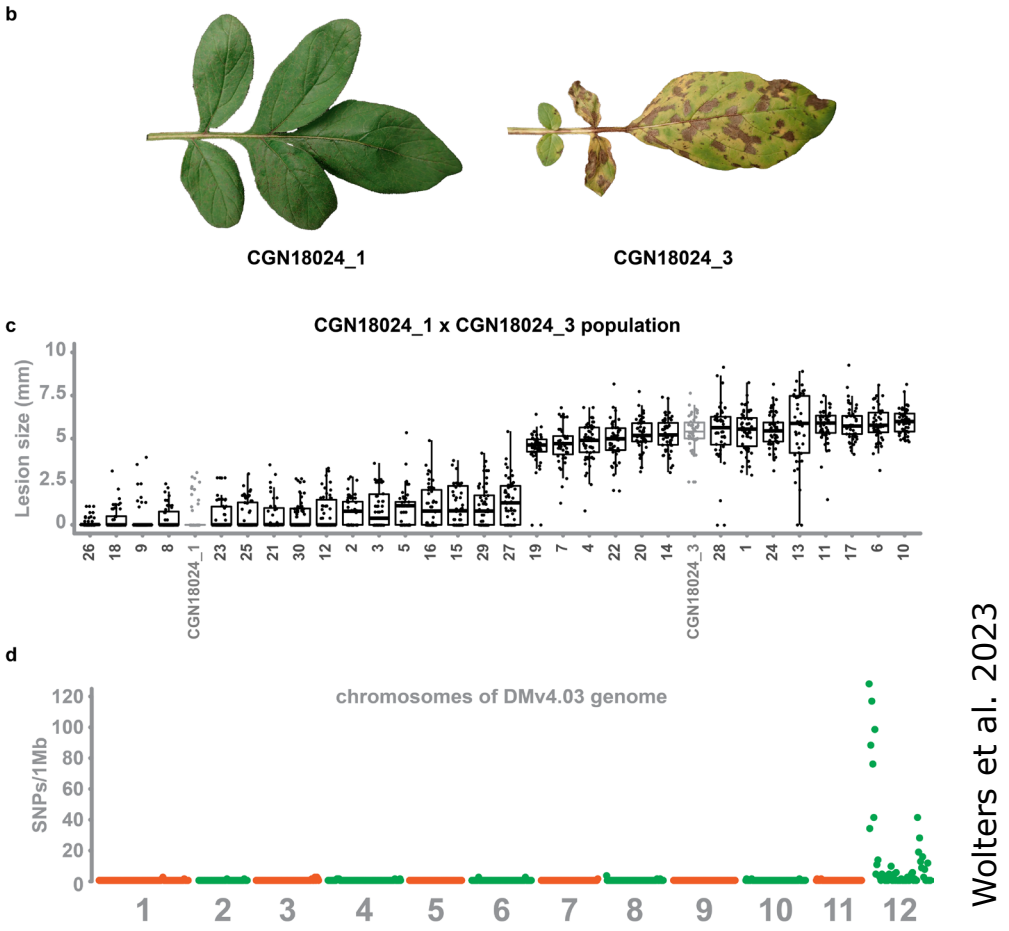
Resistance of *S. commersonii* and *S. raphanifolium* shows qualitative inheritance pattern



Wolters et al. 2021

Resistance of *S. commersonii* is caused by the production of specific glycoalkaloid variants

- *S. commersonii* is exceptionally resistant
- Resistant *S. commersonii* produces specific glycoalkaloid variants
- Similar glycoalkaloids are detected in other resistant *Solanum* accessions
- Cultivated potato typically produces α-solanine and α-chaconine – breeders try to reduce the levels of these compounds
- Toxicity of tetraose glycoalkaloids is unknown

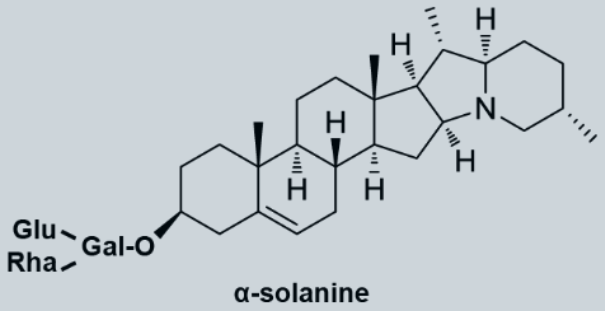


Wolters et al. 2023

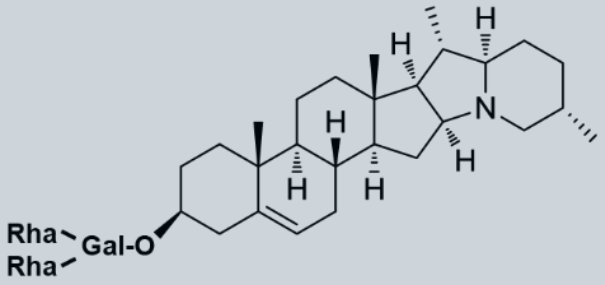
The difference between glycoalkaloids from cultivated potato and *S. commersonii* is in the sugars

S. tuberosum

(triose SGAs)



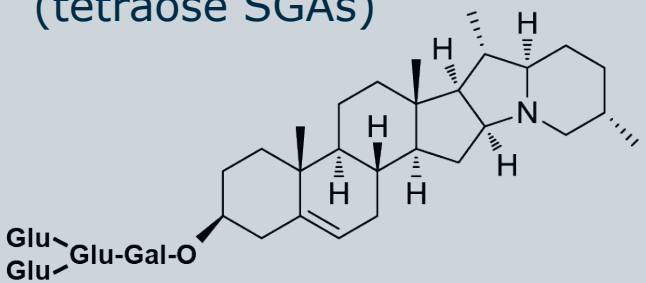
α-solanine



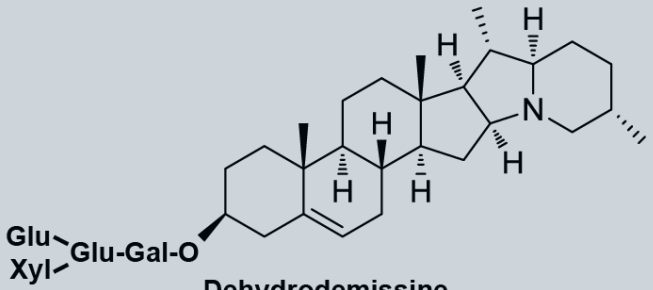
α-chaconine

S. commersonii

(tetraose SGAs)



Dehydrocommersonine

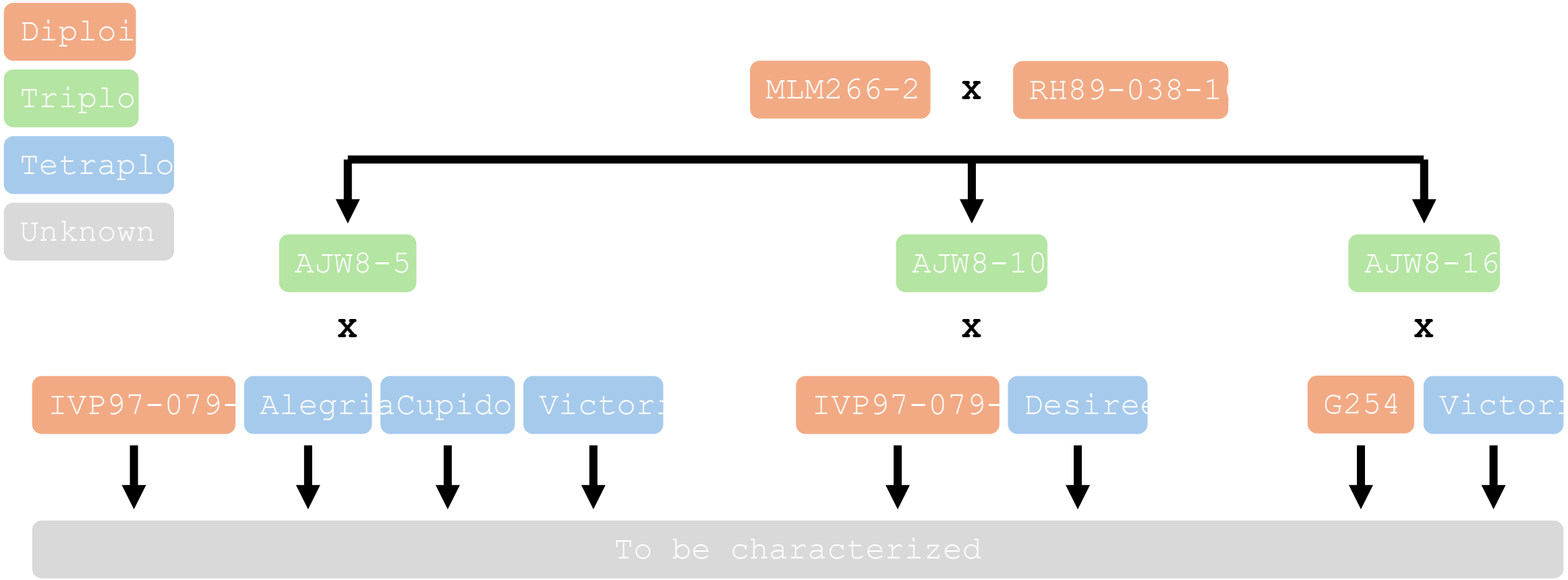


Dehydrodemissine

Resistance in *S. commersonii* is explained by a single sugar addition (triose -> tetraose)

Simple trait in *S. commersonii*, but multiple biosynthetic genes missing in *S. tuberosum*

Introgressing SGA biosynthesis genes to assess their performance in a cultivar background



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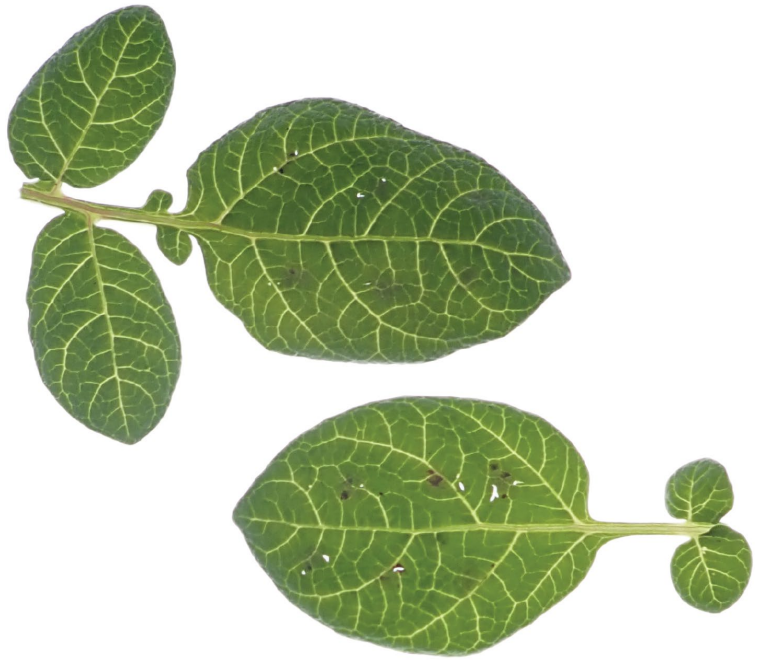
S. raphanifolium as an alternative source of resistance



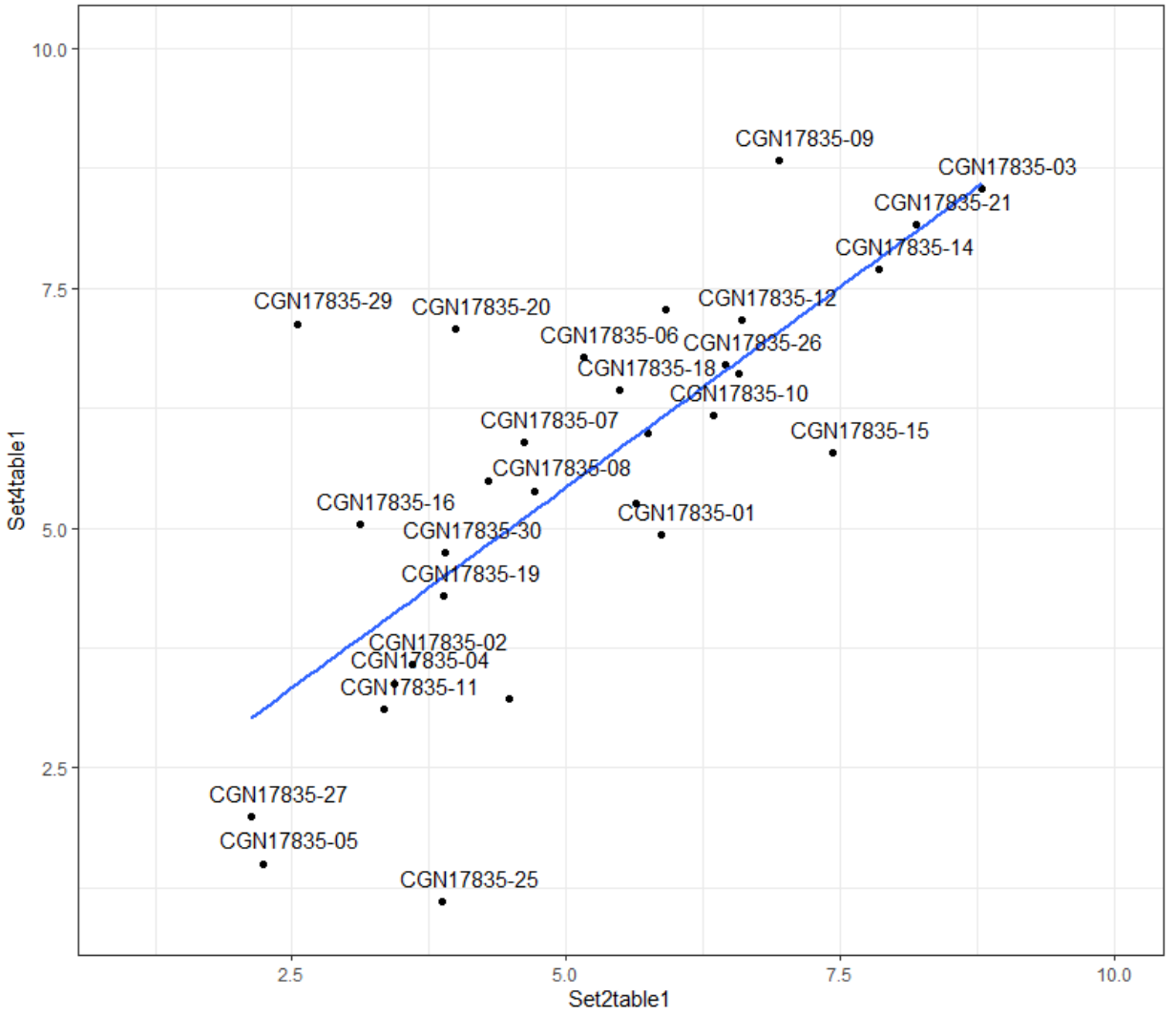
CGN17835#2

CGN17835#3

Testing segregation of early blight resistance in a *S. raphanifolium* accession

Decent correlation between experiments, phenotype is not as black and white as observed for resistance of *S. commersonii*

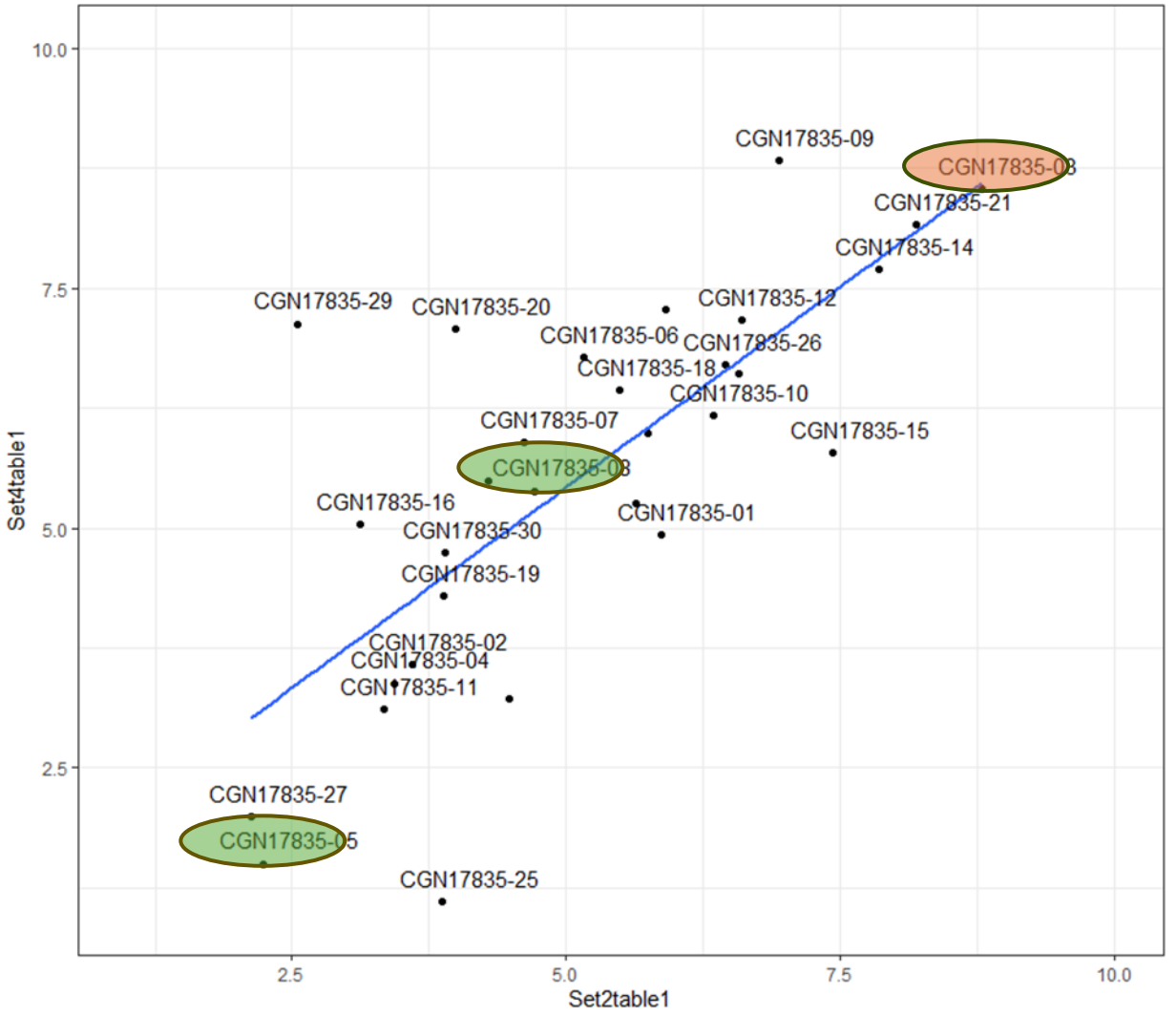
```
> CGNcor_mat
            Set2table1 Set4table1
Set2table1  1.0000000  0.7397108
Set4table1  0.7397108  1.0000000
```



Testing segregation of early blight resistance in a *S. raphanifolium* accession

CGN17835-3 (susceptible) crossed with CGN17835-5 (very resistant) and CGN17835-8 (intermediate resistance)

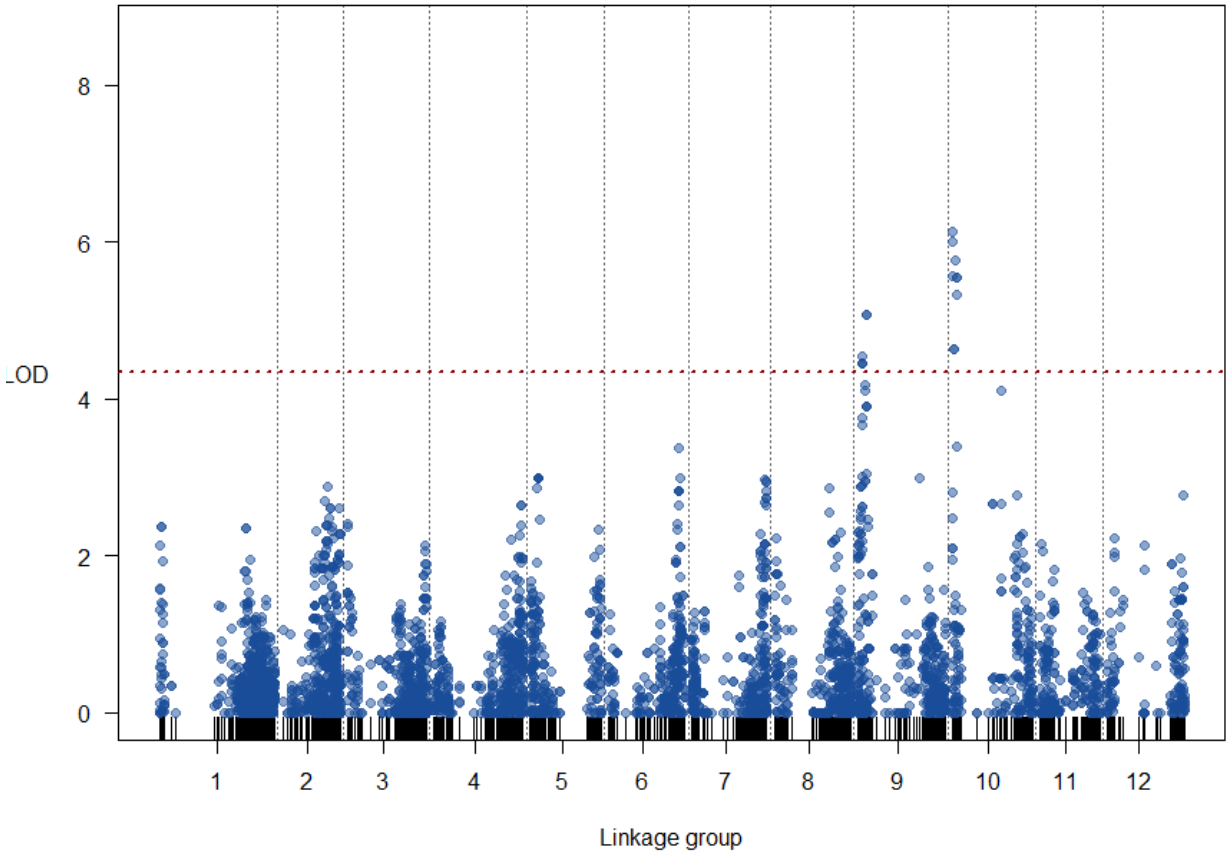
```
> CGNcor_mat
            Set2table1 Set4table1
Set2table1  1.0000000  0.7397108
Set4table1  0.7397108  1.0000000
```



QTL scan reveals peaks on chromosome 9 and 10

Using 30 genotypes from a segregating *S. raphanifolium* accession and including 2 populations derived from crosses within the accession
(90 genotypes in total)

Genotyping on Solseq platform developed by Jack Vossen



Conclusions

- Wild *Solanum* species are a good source of resistance of early blight
- Resistance is often quantitative, but qualitative inheritance is observed in some cases
  - *S. commersonii* and *S. raphanifolium* show clear segregation of resistance
- Early blight resistance in wild *Solanum* can often be explained by the production of specific glycoalkaloid variants
  - Research to evaluate their effect in cultivated potato is in progress
- Alternative resistance mechanisms exist, such as in *S. raphanifolium*
  - QTL scan shows clear peaks on chr09 and chr10, resistance mechanism remains to be characterized

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