Population Structure, Genetic Diversity and Host Specificity of Section *Alternaria* from Diverse Regions and Host Plants

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Christian-Albrechts-University Kiel

Euroblight 2026

Gonne Clasen, 20/05/2026

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Part 1

Section *Alternaria* in Europa on potato and tomato

Distribution and Shared Pathogenicity of Small-Spored *Alternaria* on Solanaceous Crops in Europe

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doi: https://doi.org/10.64898/2025.12.11.693629

Introducing the Genus *Alternaria*

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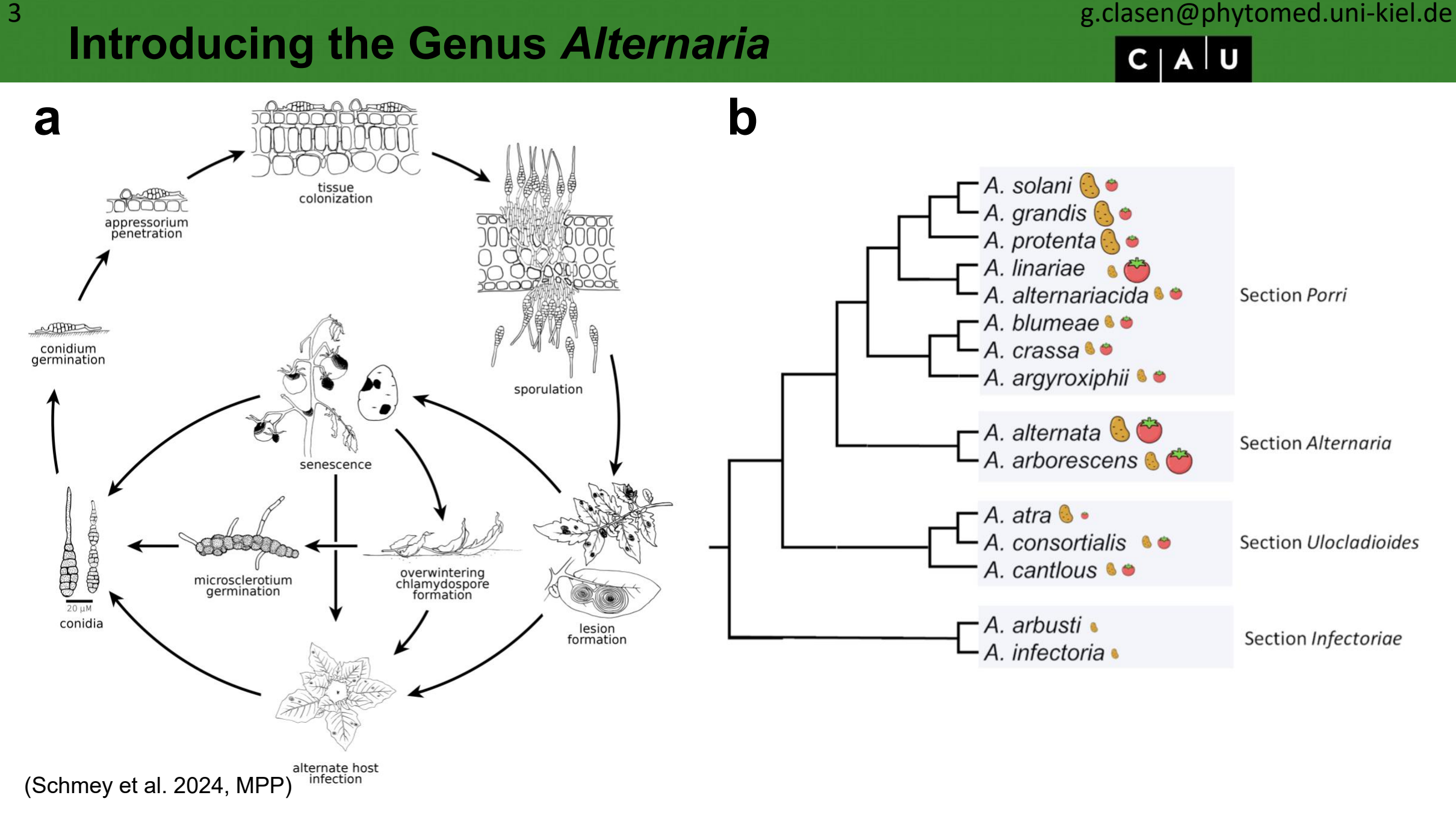

(Schmey et al. 2024, MPP)

Section *Alternaria* in Europa

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1. Can all Section *Alternaria* species cause infection?

Collect from tomato and potato in Germany, Poland and Serbia.

2. Do we see geographical variation between species?

Permutation test on species distribution from Germany, Poland and Serbia.

3. What is the genetic diversity of *A. alternata* and *A. arborecens* within Europe?

Statistical analysis of the distribution of the major haplotypes.

Sampling in Germany, Poland and Serbia

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Sampling in Germany, Poland and Serbia

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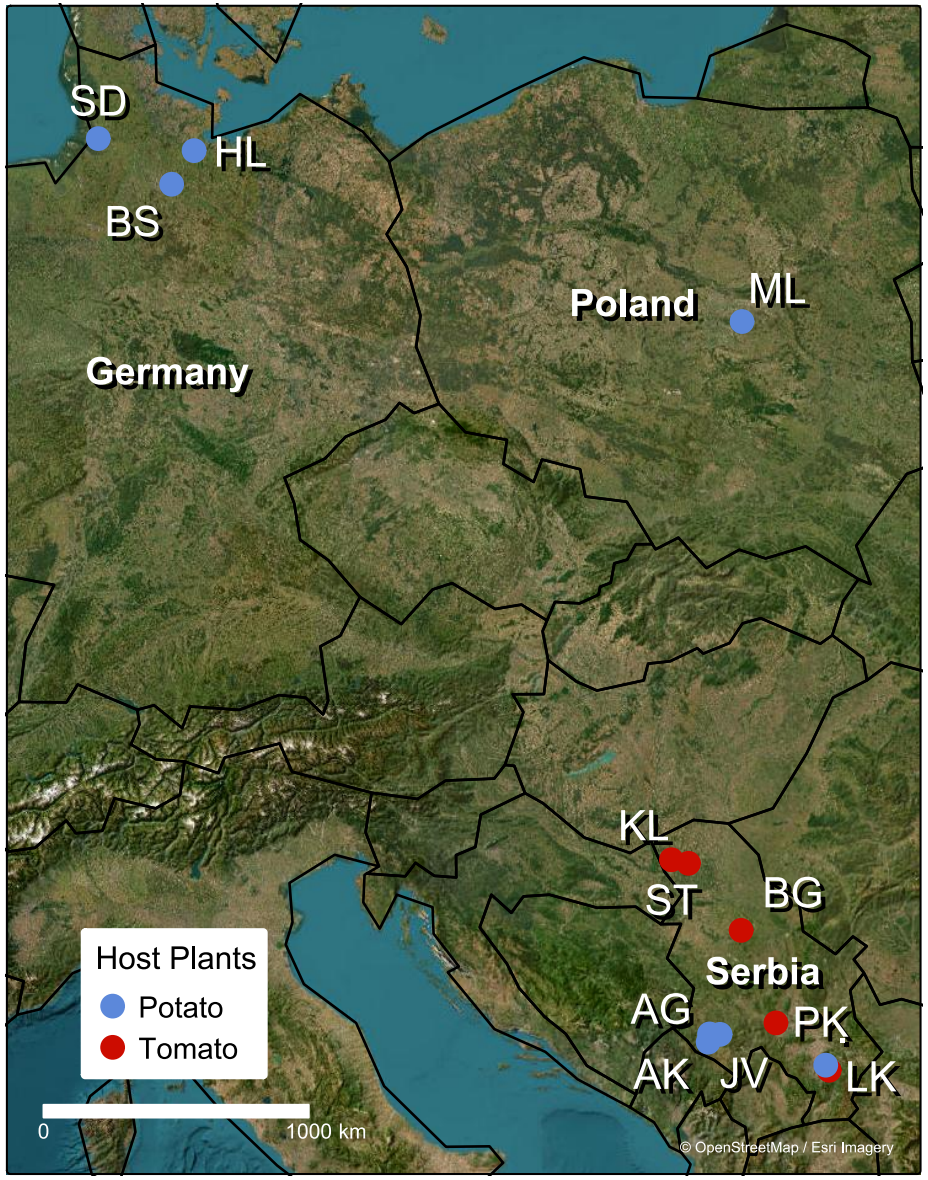

- collection of 10 leaves per field
- 5 from the front, 5 from the rear
- at least 50 m apart

Species Identification via Sanger Sequencing

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C | A | U

AB12PHYLO [nsq]

Welcome to AB12PHYLO! To show or hide this help, press **F1** or **Ctrl+H**.
Please define your dataset of ABI trace files or sequence data in *.fasta* format here. For automatic mapping of reference data from different genes to the same strain, it is recommended to use GenBank *.fasta* records such as AF347033.1. If wellsplates are used in conjunction with sequence data for multiple genes, please make sure the plate layouts are identical.

open test

read data
map
trim data
align
trim MSA
BLAST
infer tree
visualize

Trace / Sequence Files

.ab1 ☑
.seq ☐
.fasta ☐
.fa ☐
.txt ☐

select manually +
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add references +

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Wellsplates (optional)

from folder
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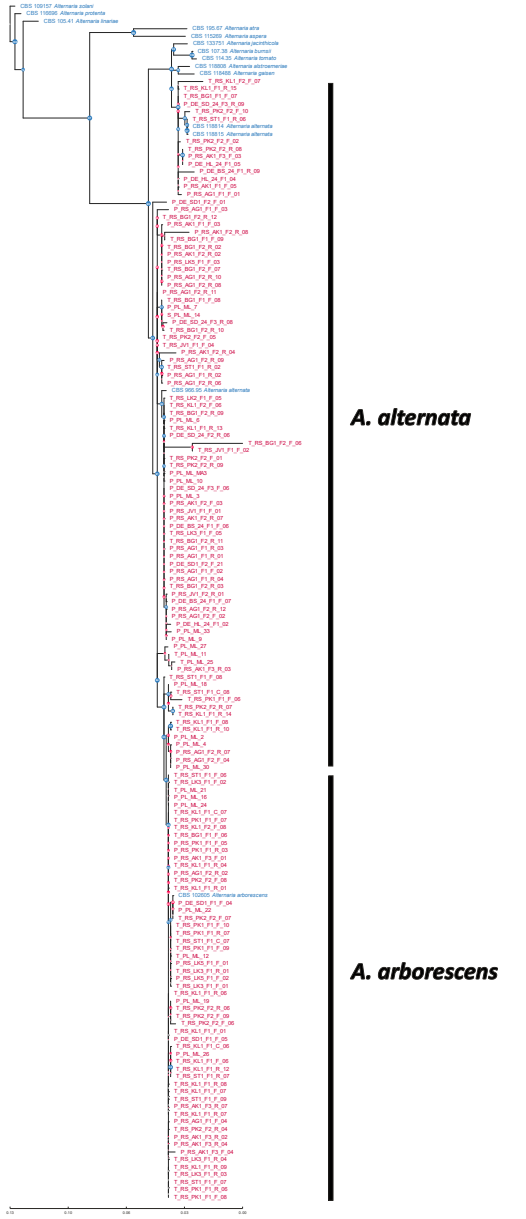

(Kaindl et al. 2022, Phytofrontiers)

1. All Section *Alternaria* isolates can infect

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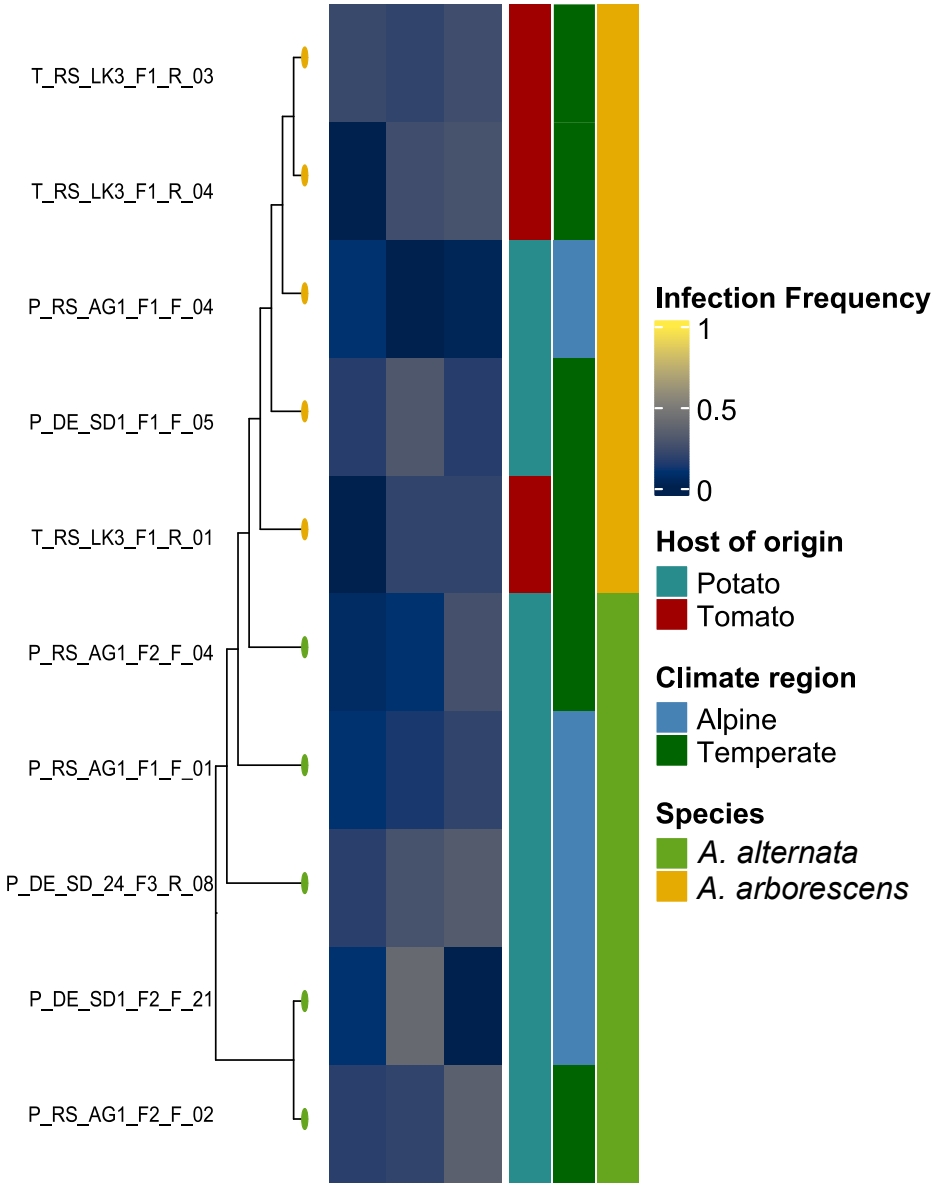
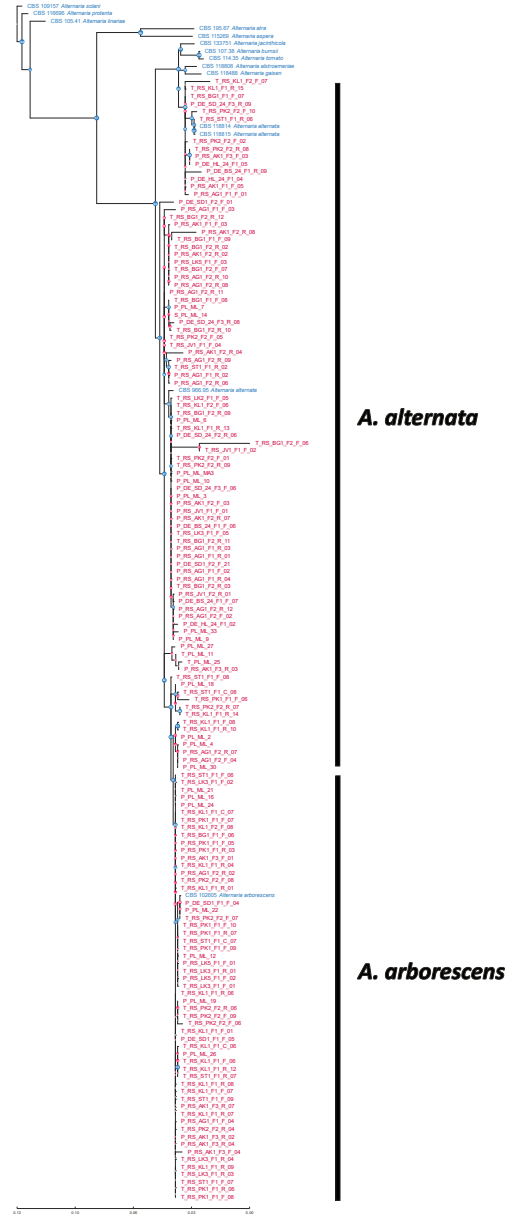
1. Sample Collection

2. Whole Plant Infections

3. Phylogeny and Characterisation





2. *A. arborescens* more prevalent in dry climates

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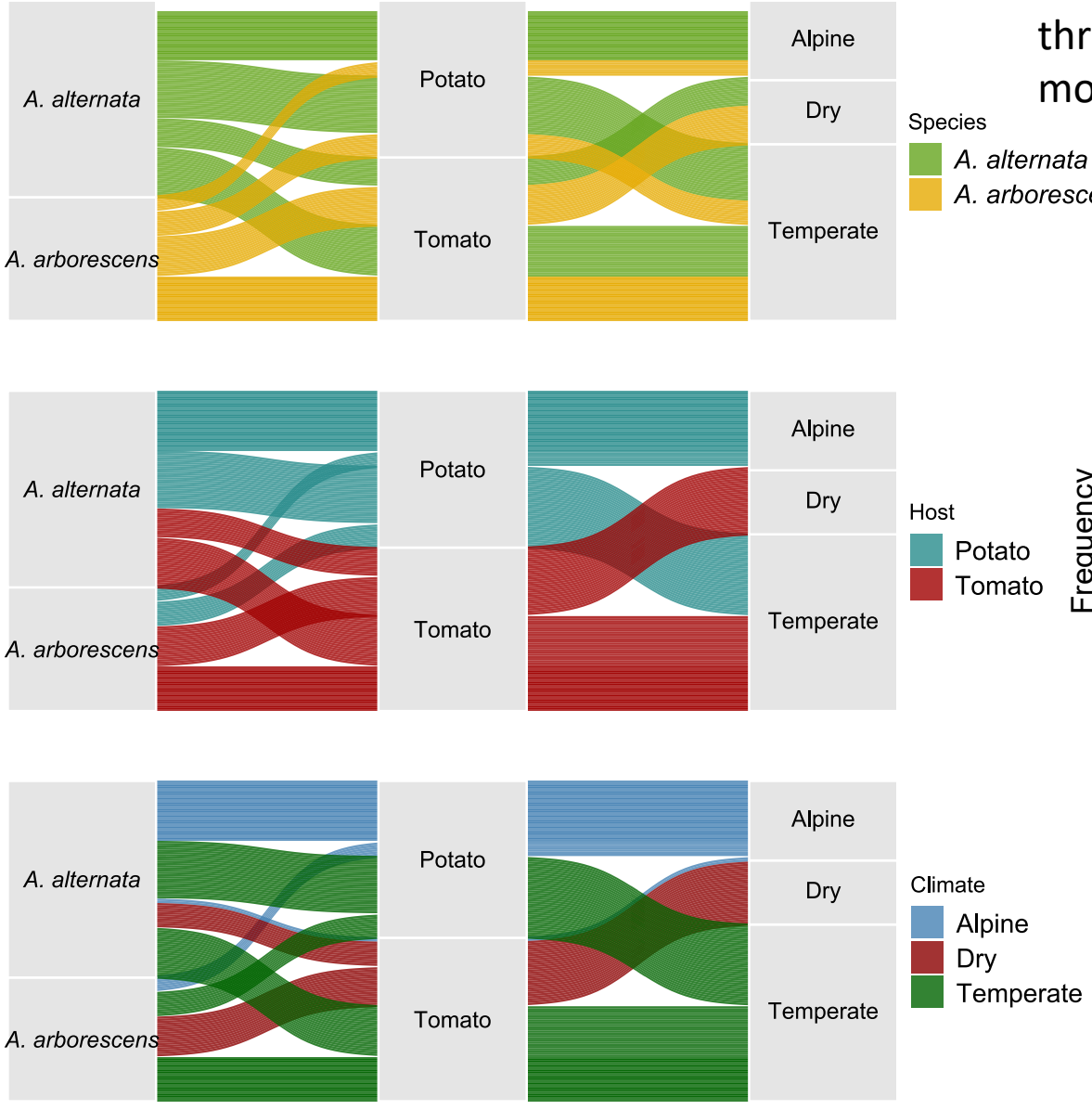
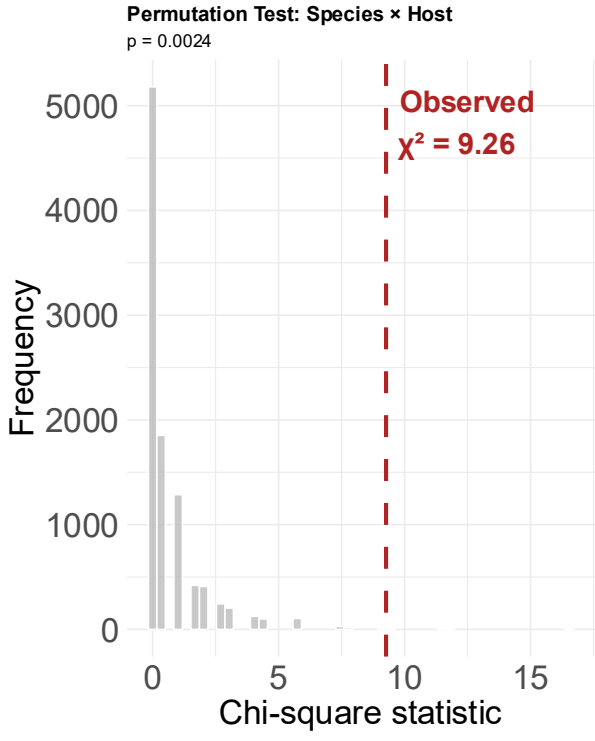
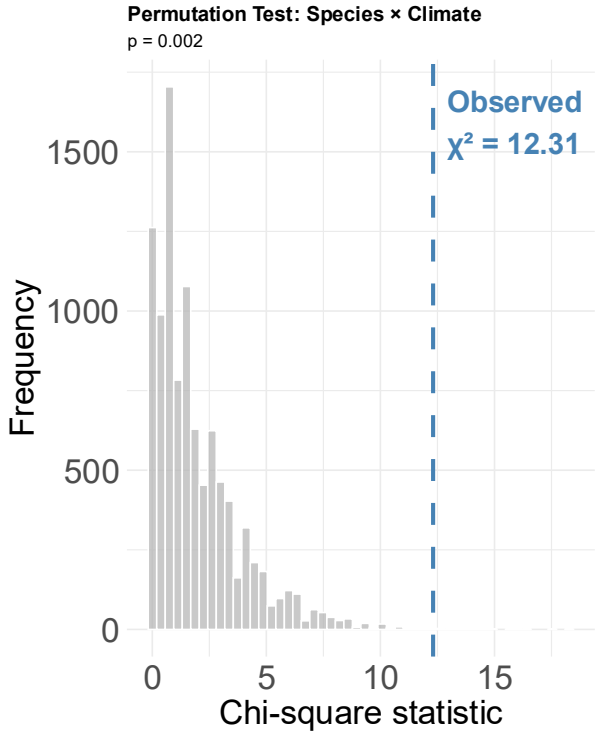
three-way log-linear model (*Species* × *Host* × *Climate*)

model_full <- loglm(~ Species * Host * Climate, data = table3D)







3. No host-preference of major haplotypes

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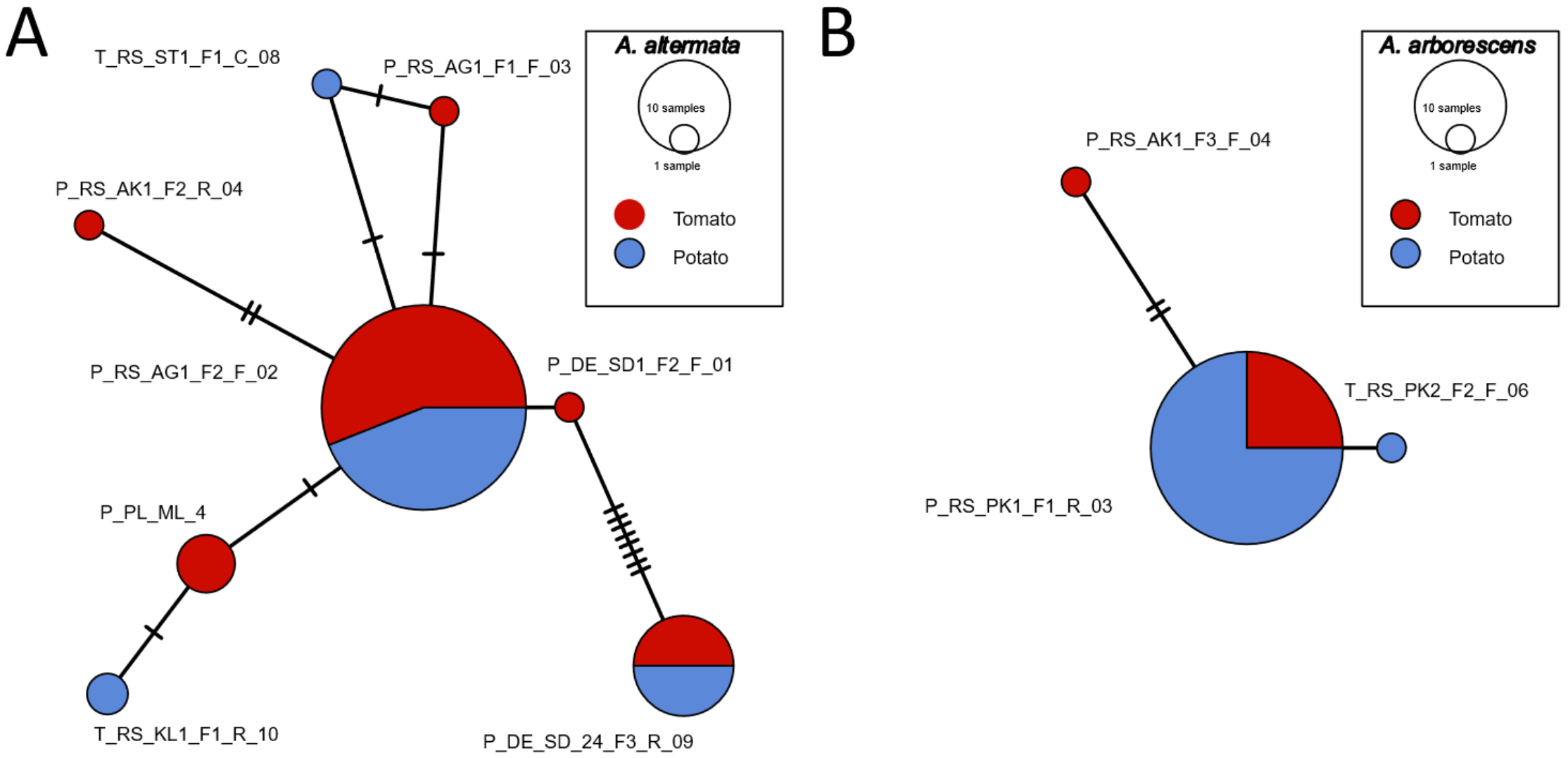

3. No country-preference of major haplotypes

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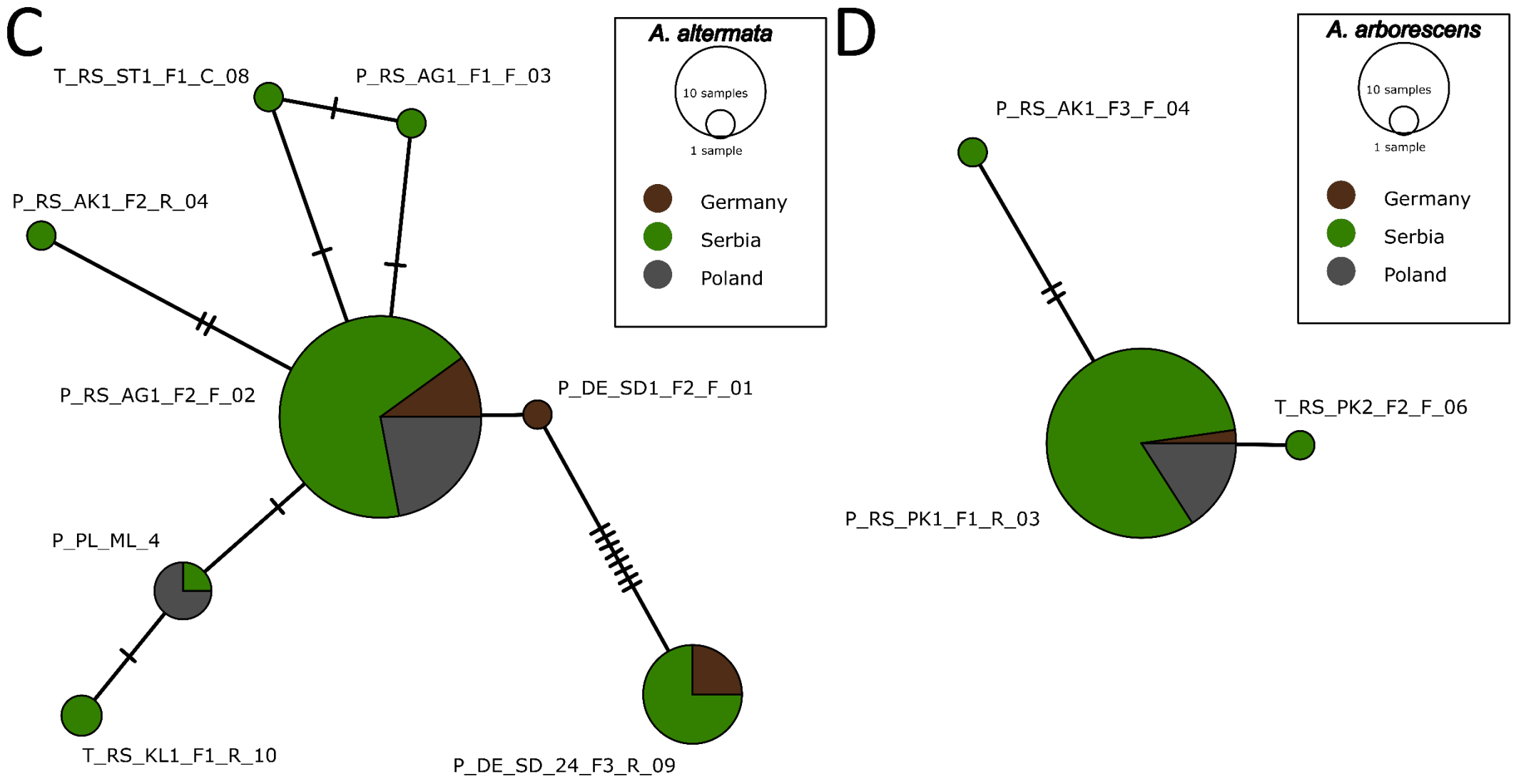

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Farmers treating Section *Alternaria* epidemics are really dealing with two different species

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Part 2

Section *Alternaria* in Europe and northern Africa

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Section *Alternaria* in Europa

1. Do we see geographical or host driven variation between isolates?

Collect from all over Europe and northern Africa.

2. Do we see host adaptation between isolates?

Clustering analysis of isolates from *Solanaceae*, *Brassicaceae* and wild hosts.

3. What is the distribution of fungicide resistance and mating types throughout Europe?

Statistical analysis of the distribution of the two mating types and fungicide resistance within our populations.

1. Geographic clustering only for *A. alternata*

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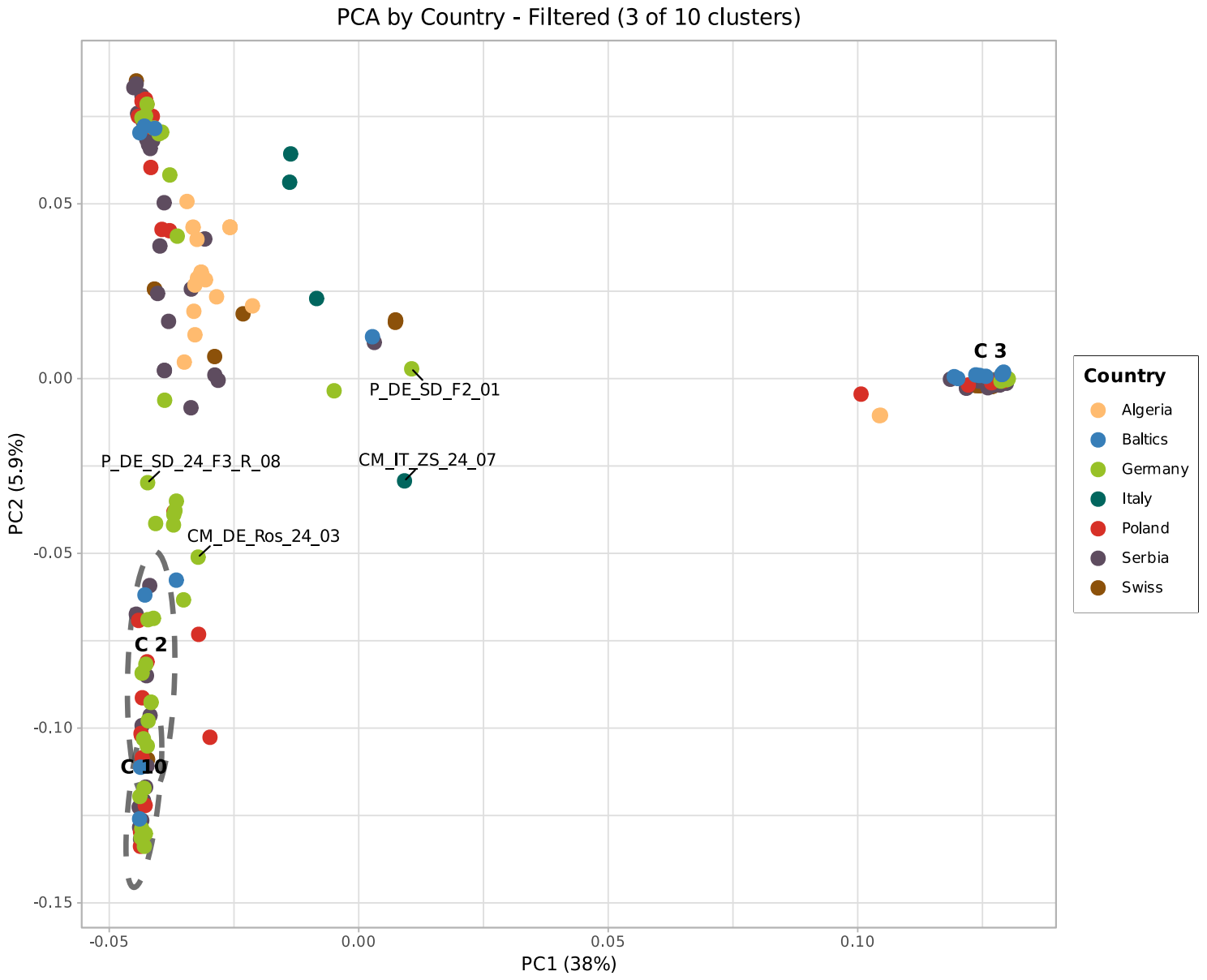

2. Trends of host-driven clustering do appear!

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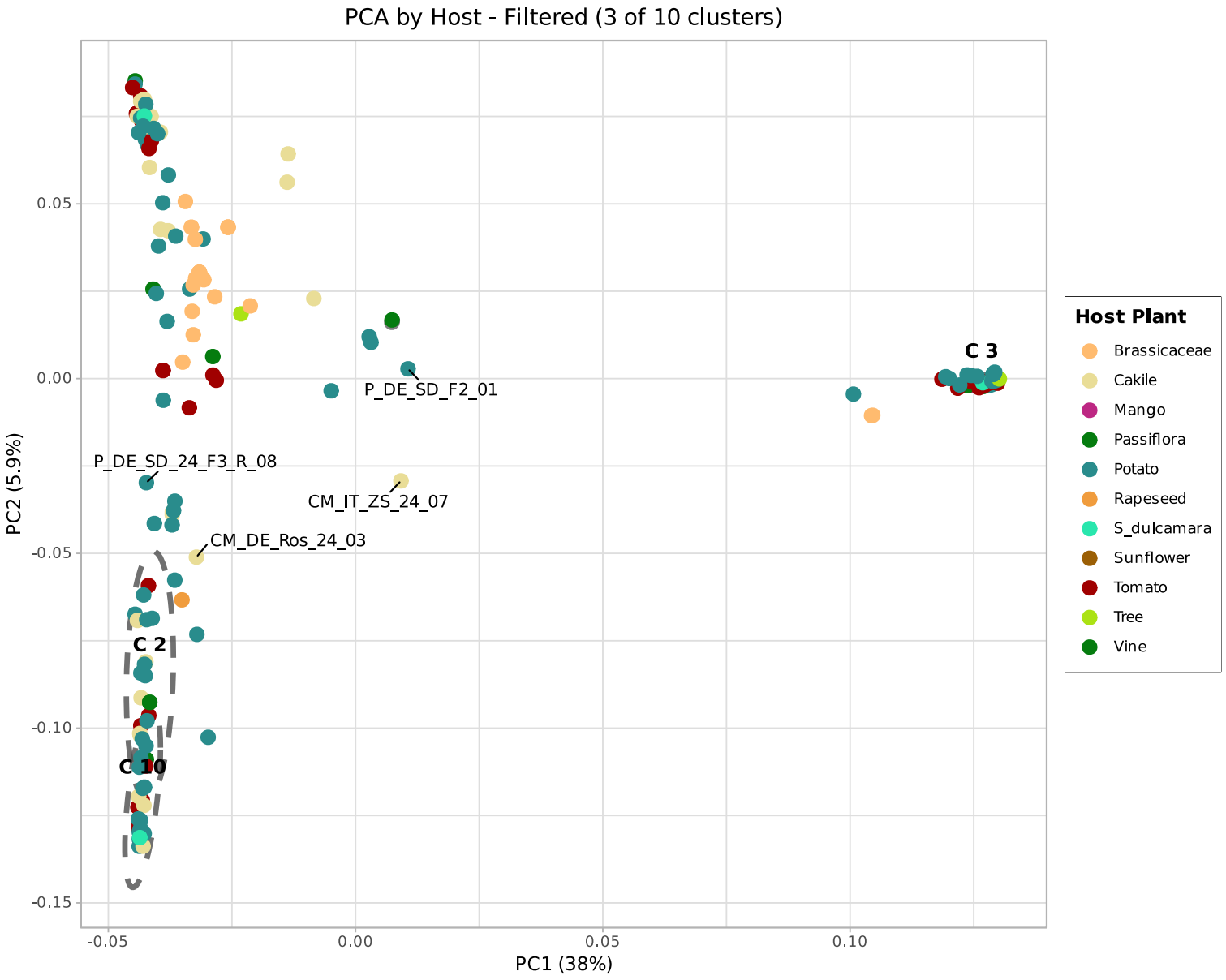

3. Fungicide resistance prevalent in *A. arborescens*

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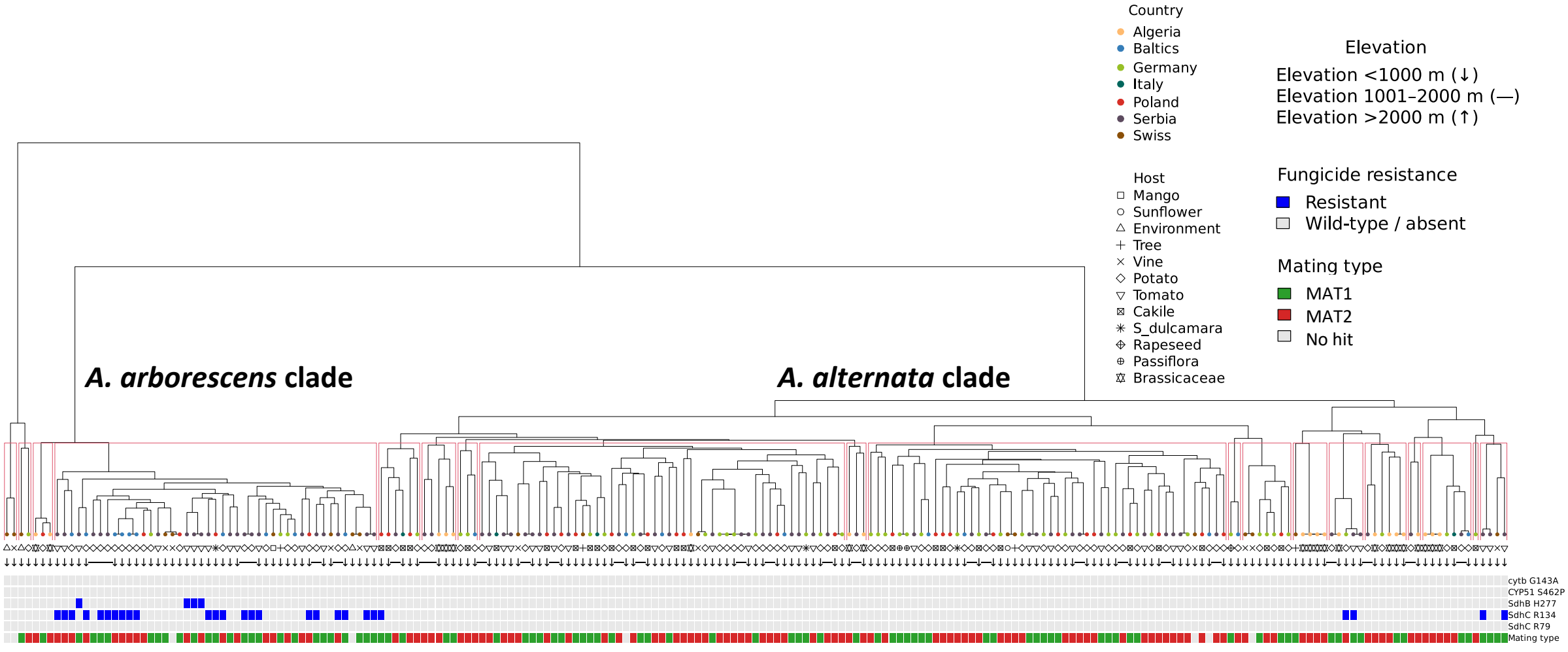

Thanks to our collaborators!

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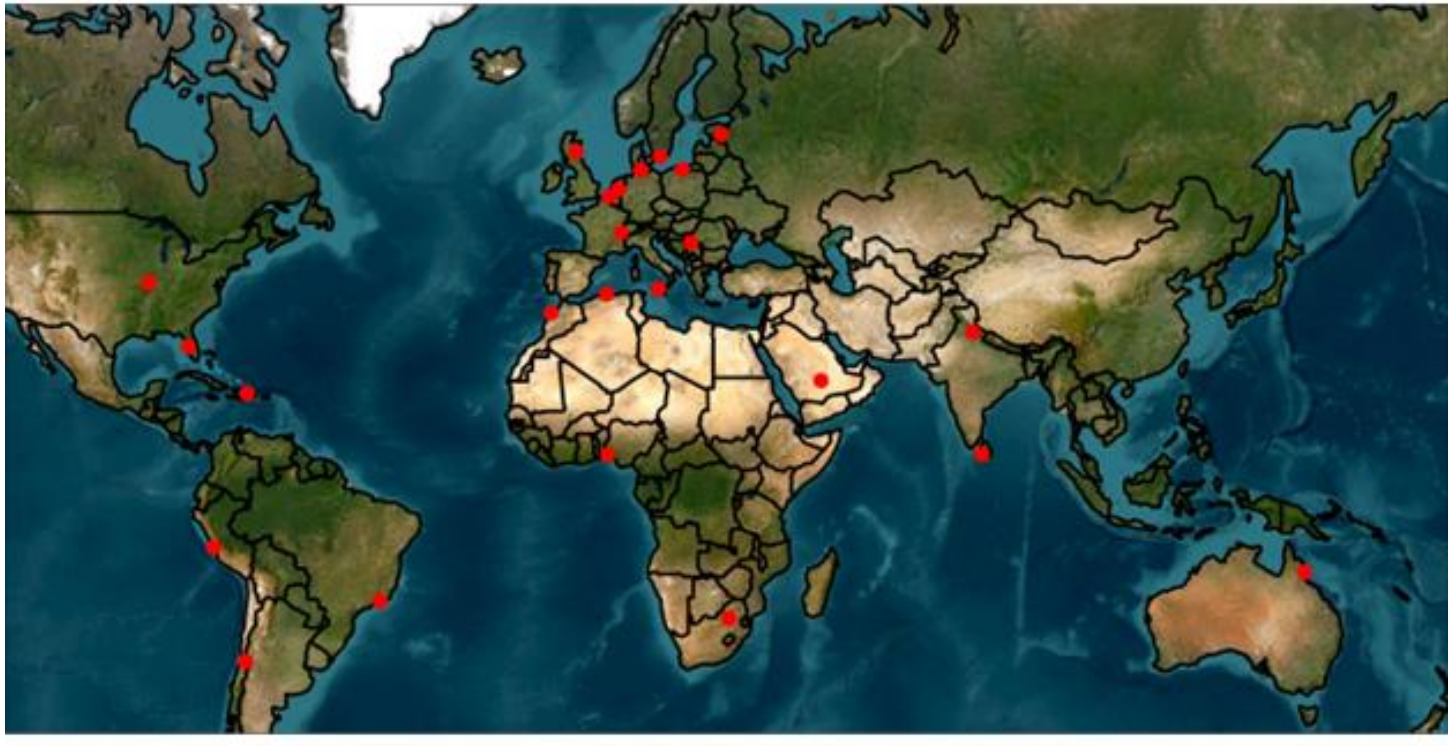

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