

Ancestral state reconstructions of *Xylella fastidiosa*-host plant relationships

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Xylella Conference 2019





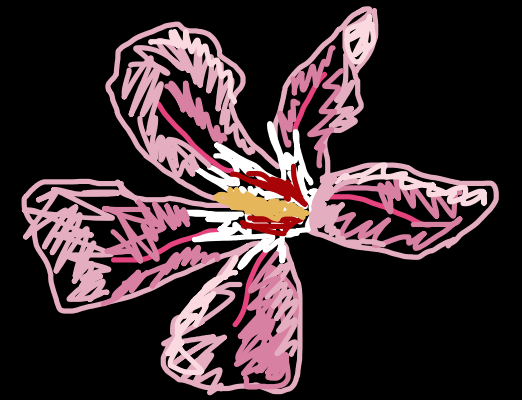
Olea



Coffea



Prunus



Nerium



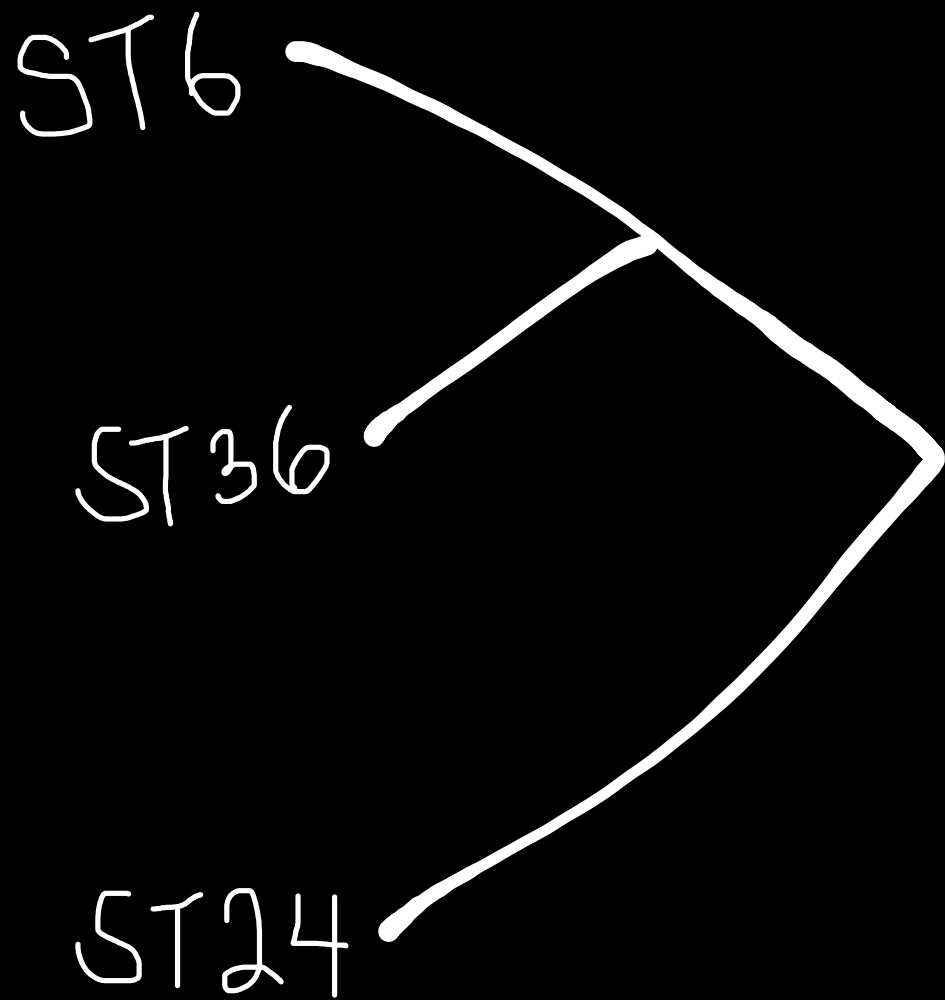
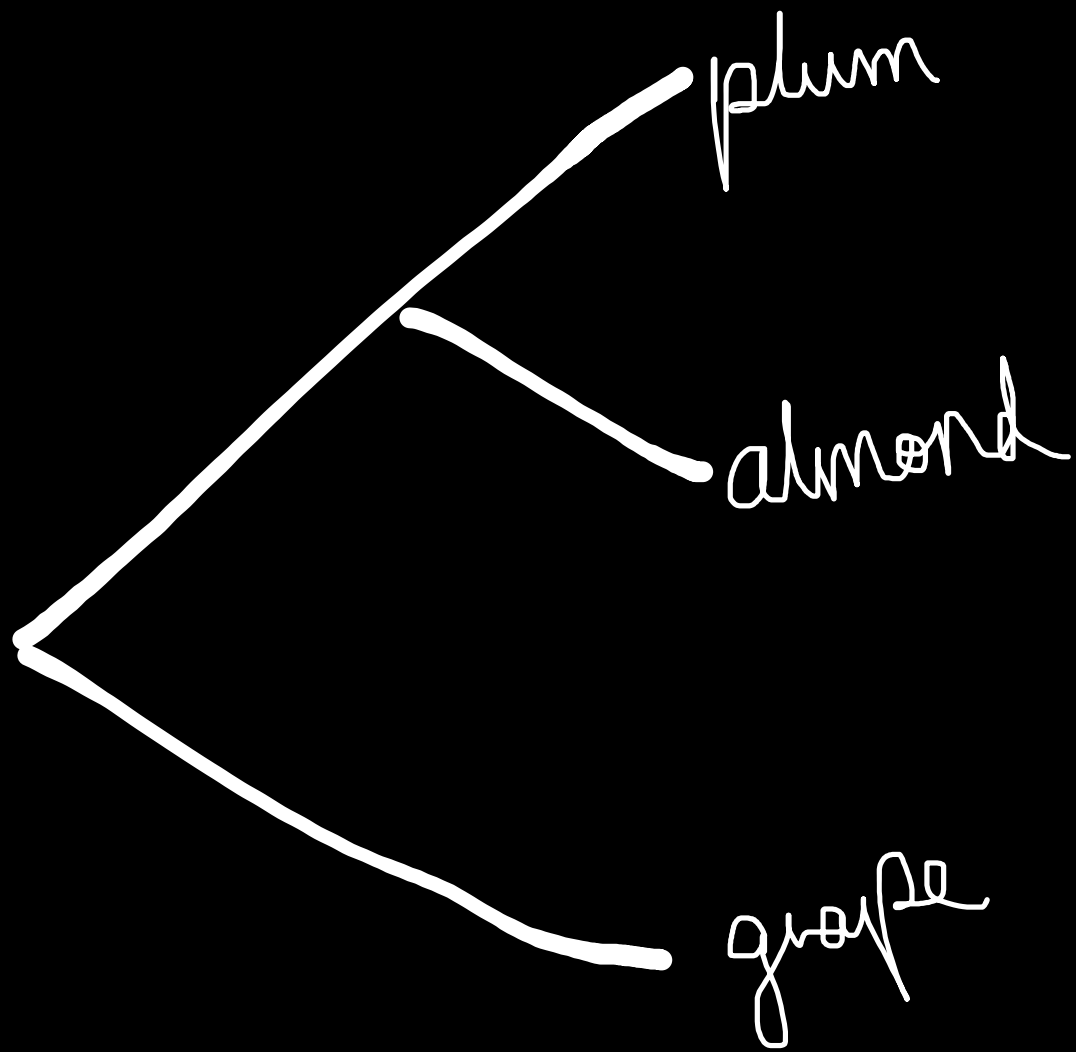
Helianthus

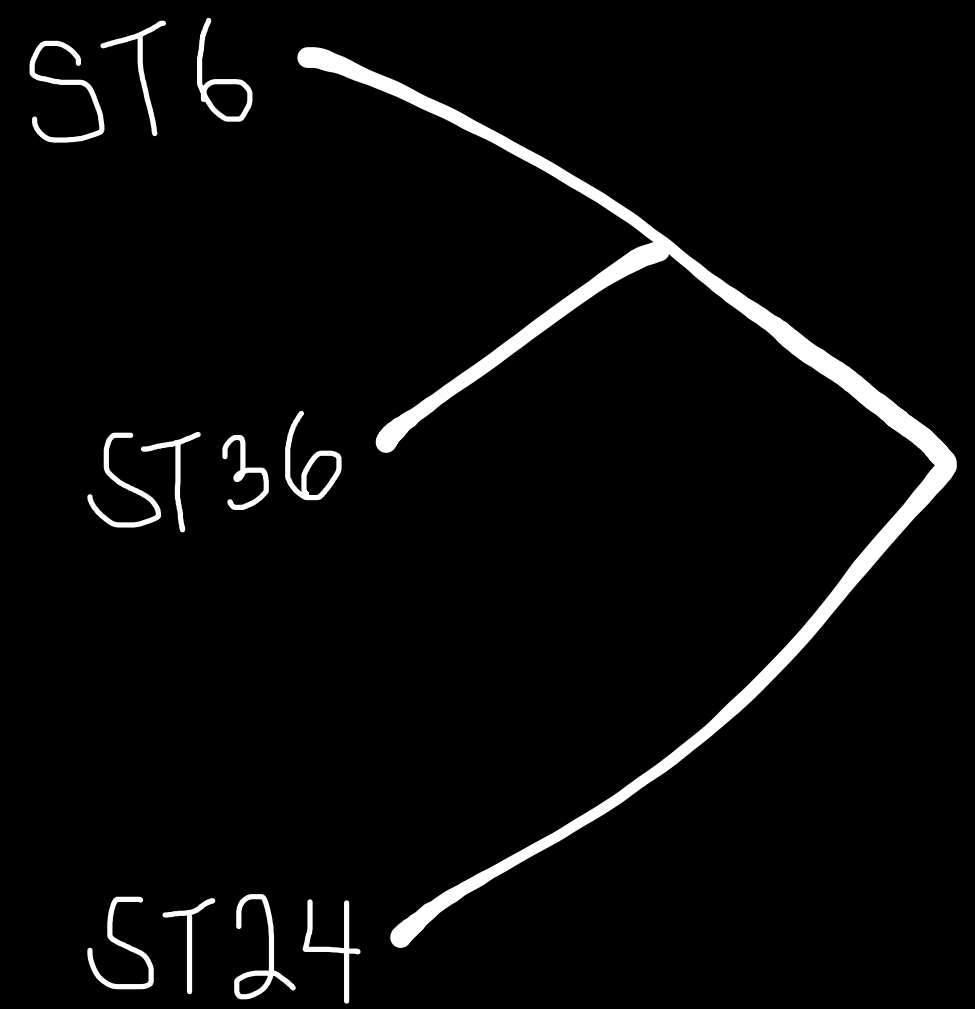
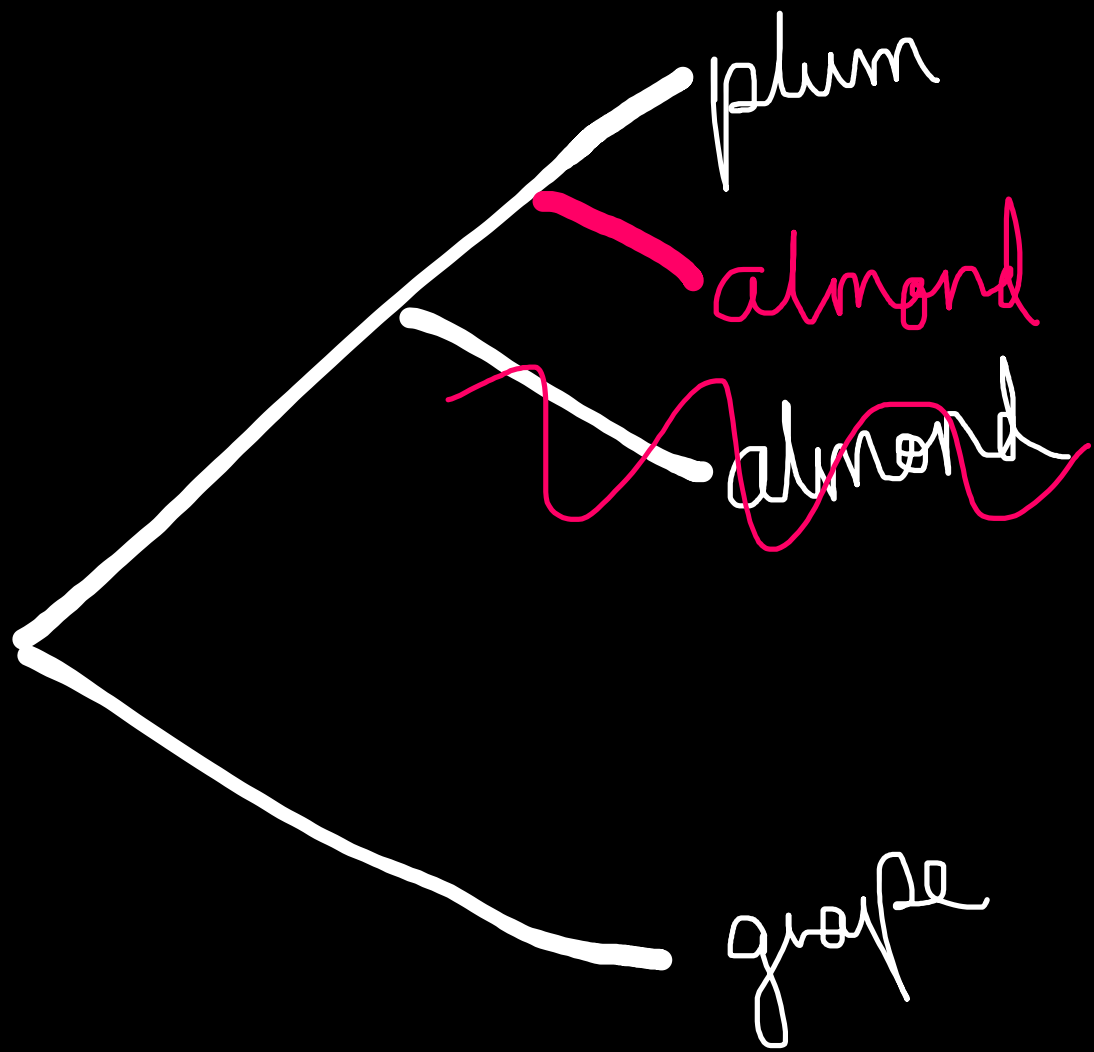


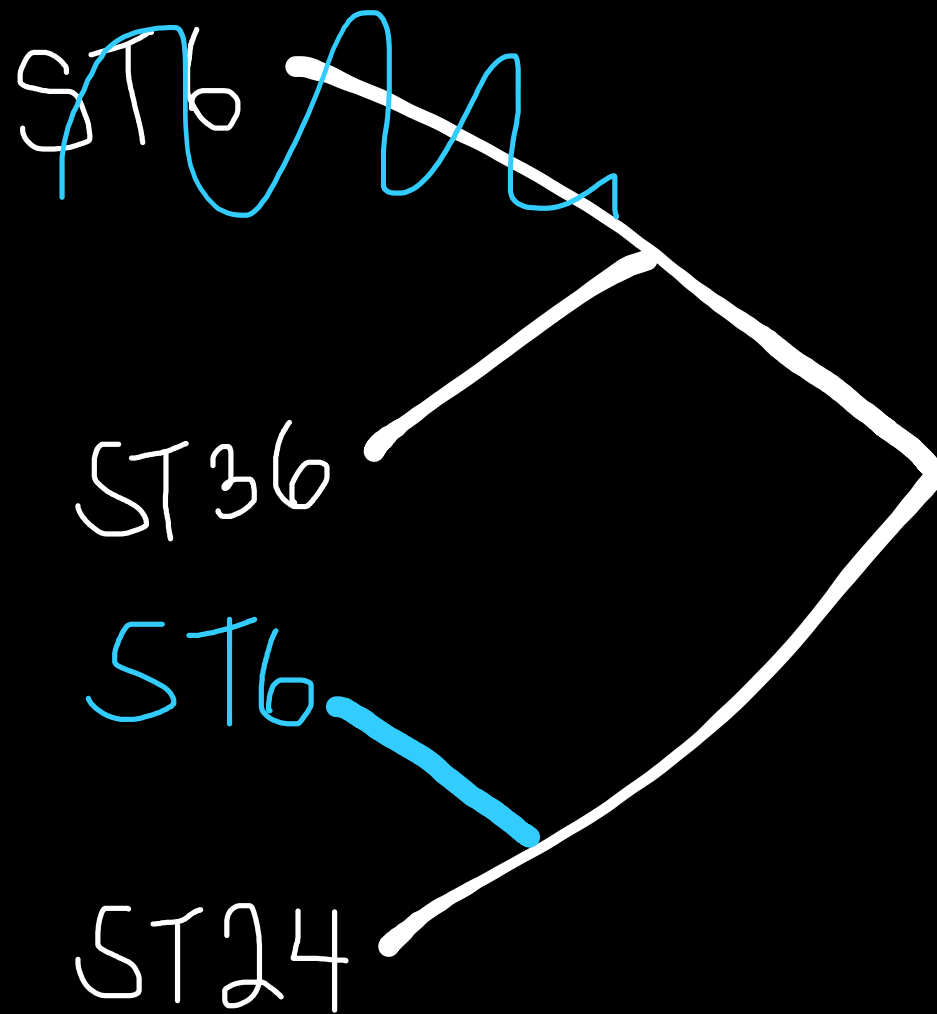
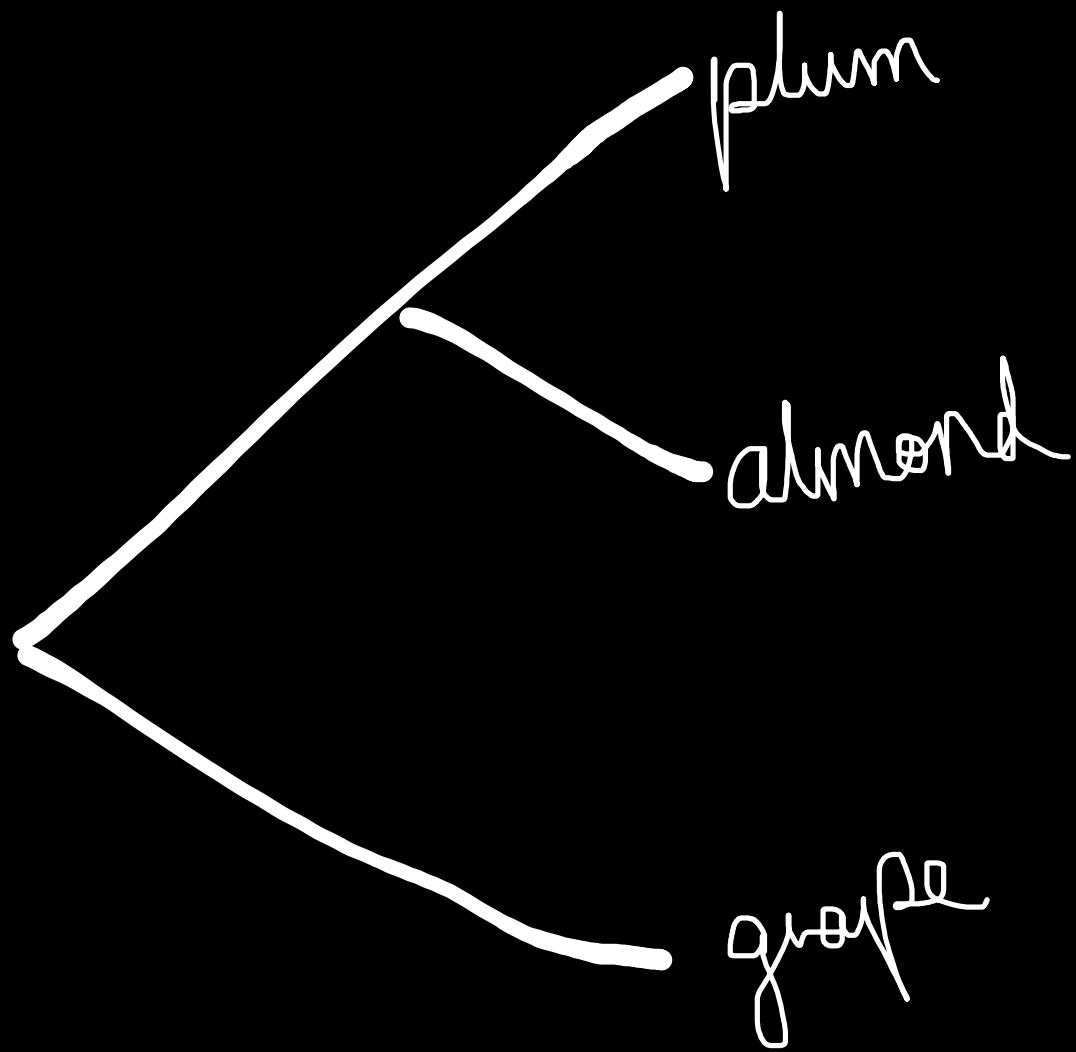
Citrus

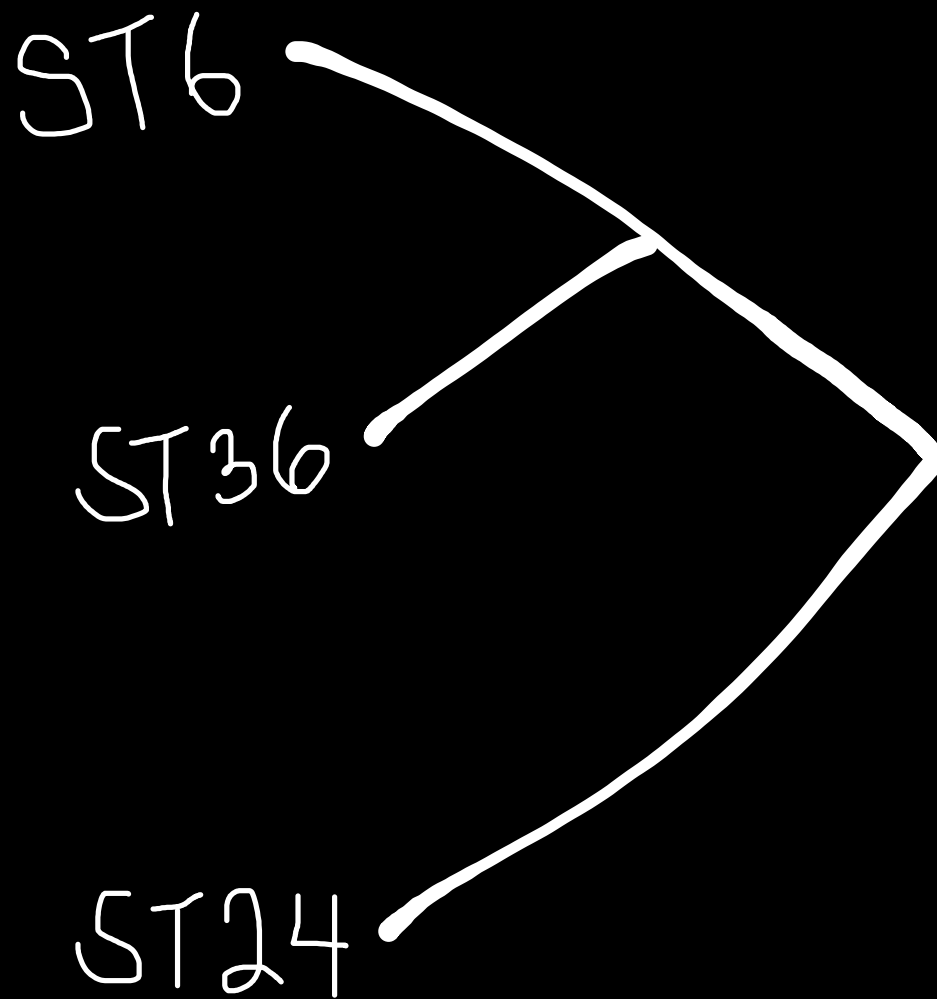
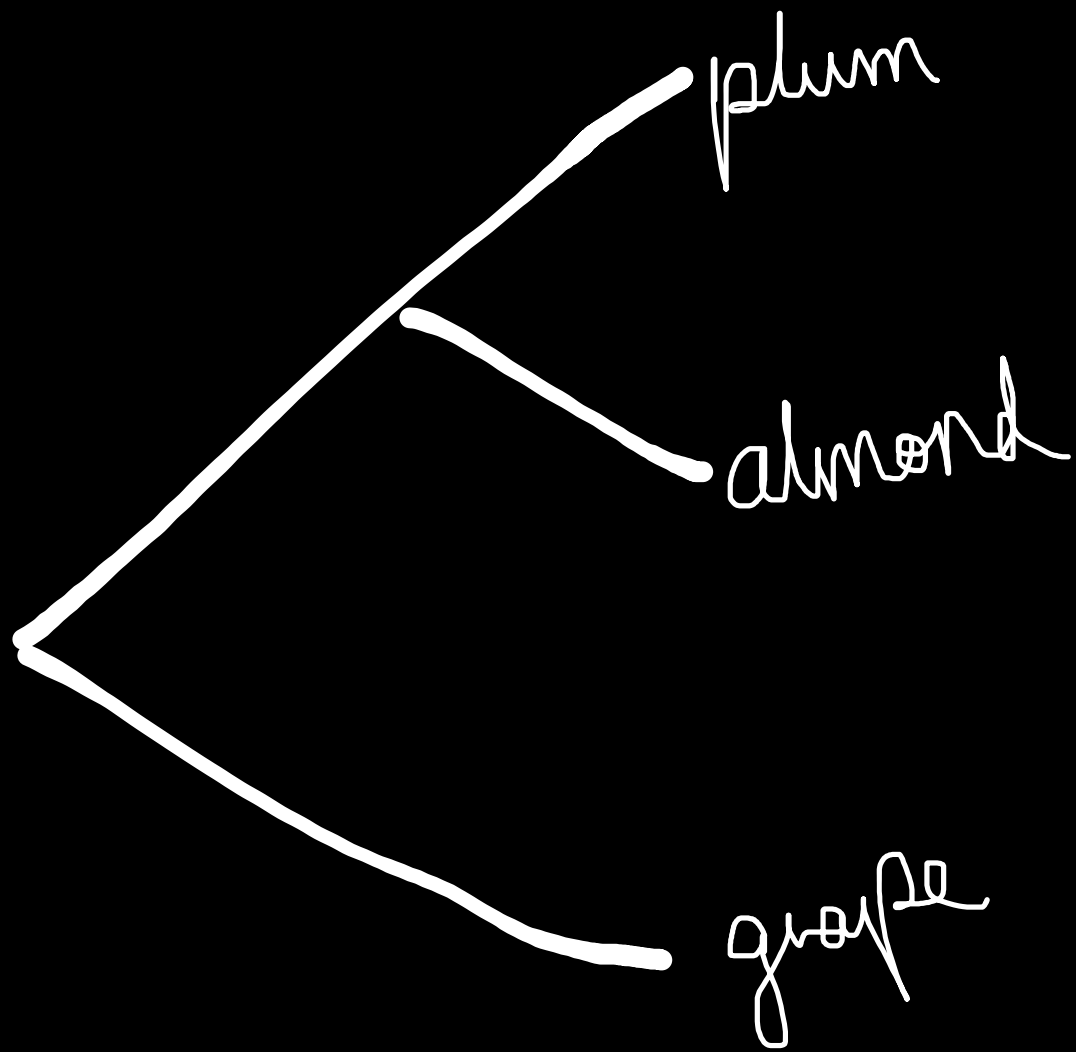


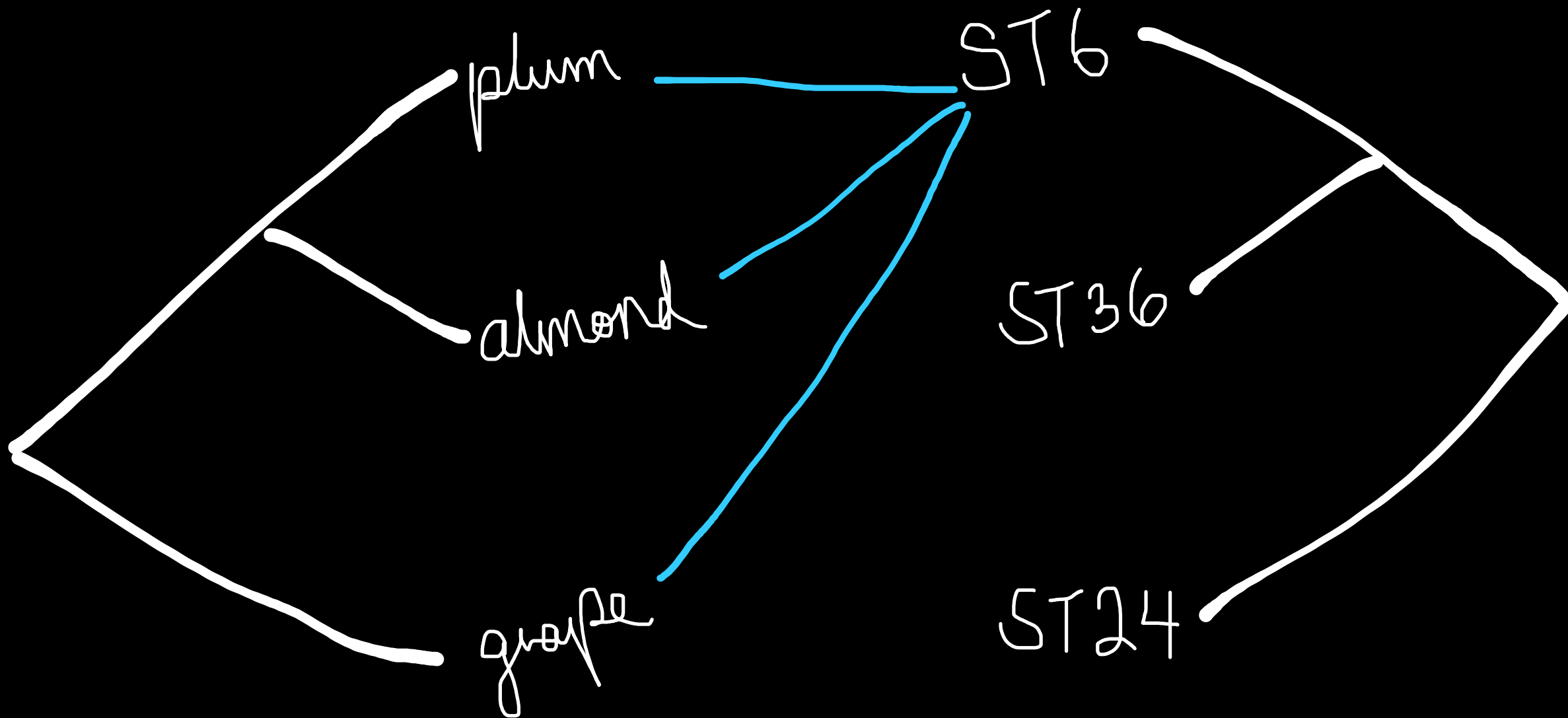
Vitis

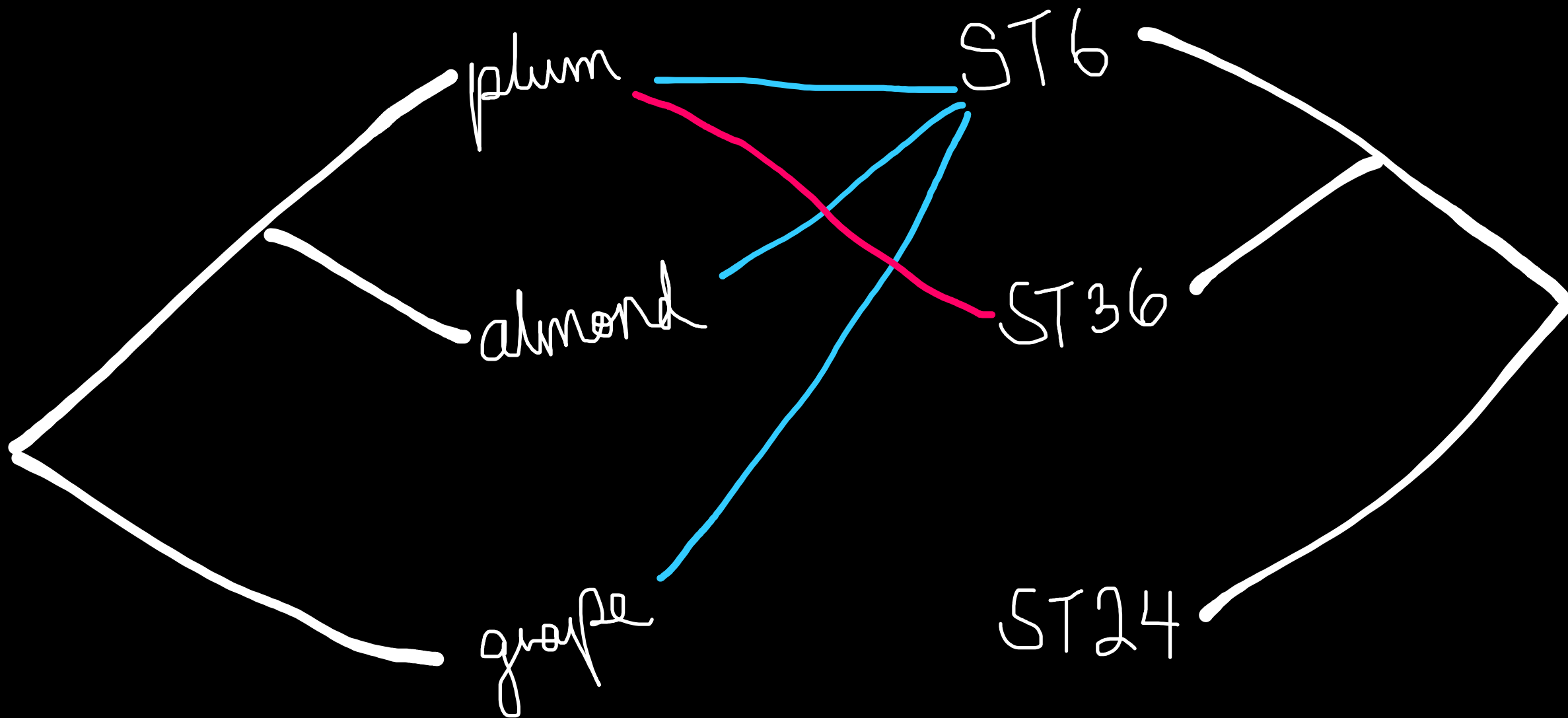


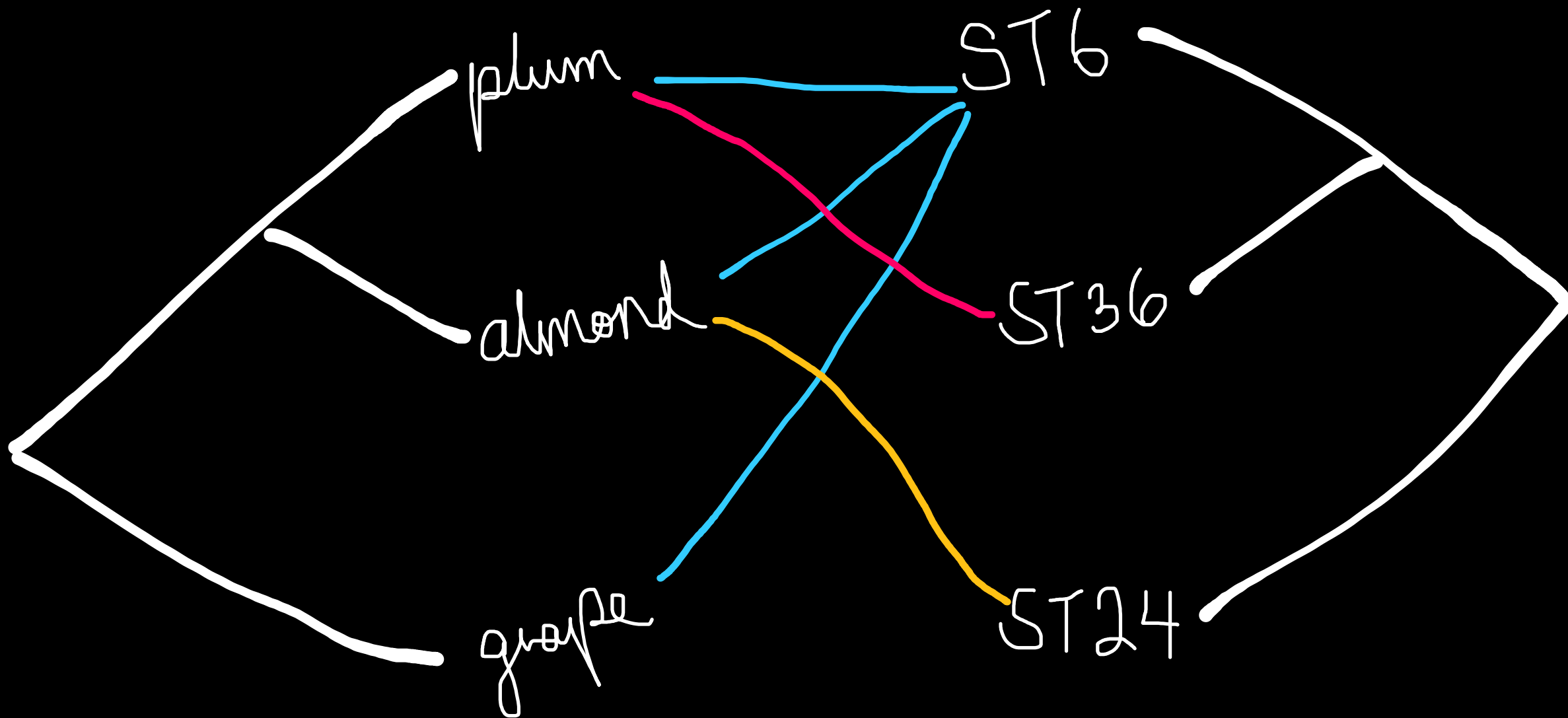












Xylella Dataset

- 349 whole genomes with host information to at least genus level

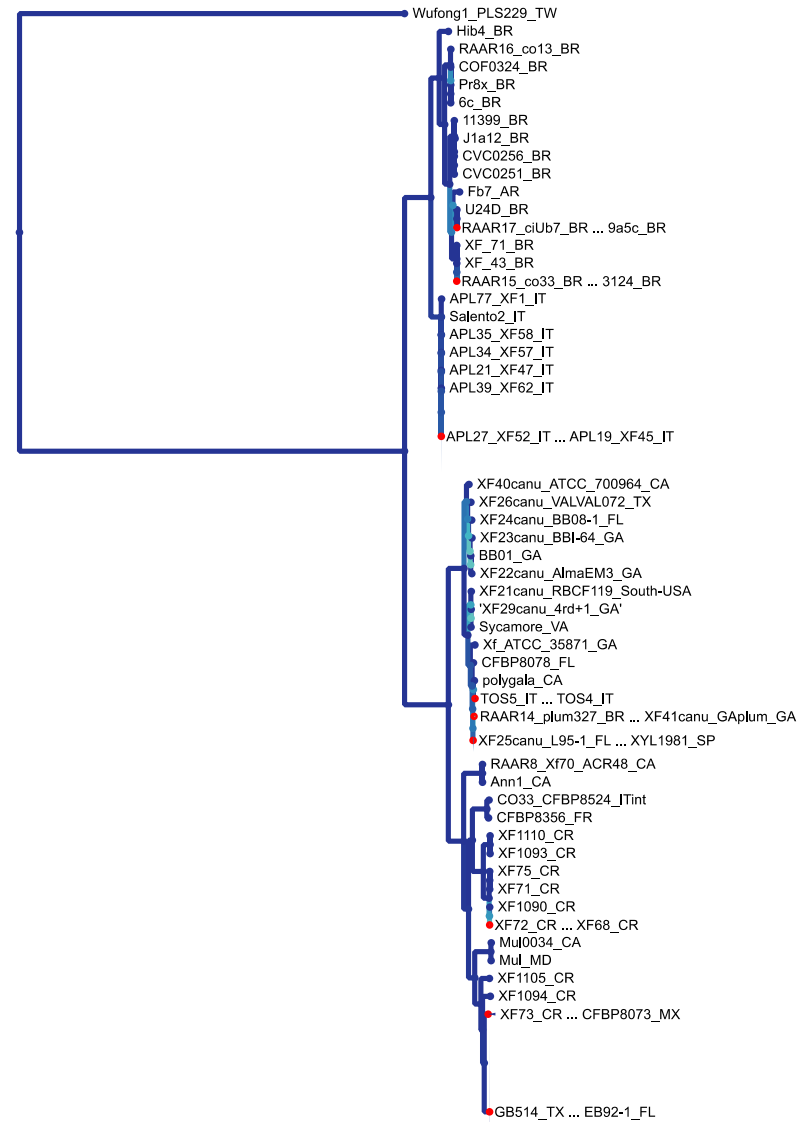
Xylella Dataset

- 349 whole genomes with host information to at least genus level

Phylogenies of unique genetic loci

- **MLST (7 genes)**
- **Core genome (1,061 genes – 566,421 bp)**
- **Core genome without recombination (236,929 bp)**
- **Accessory genome (25,778 genes)**

Core Genome Tree



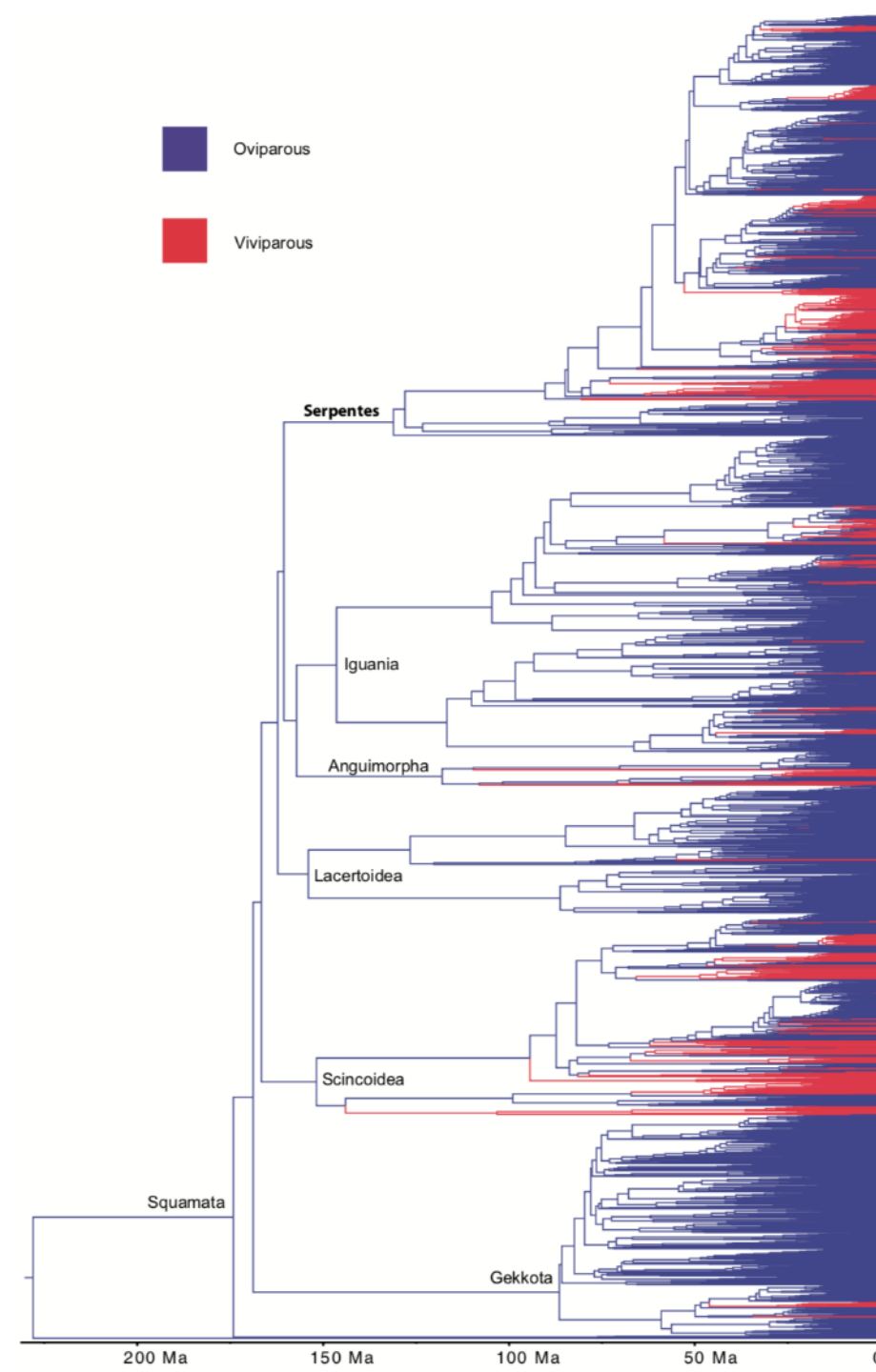
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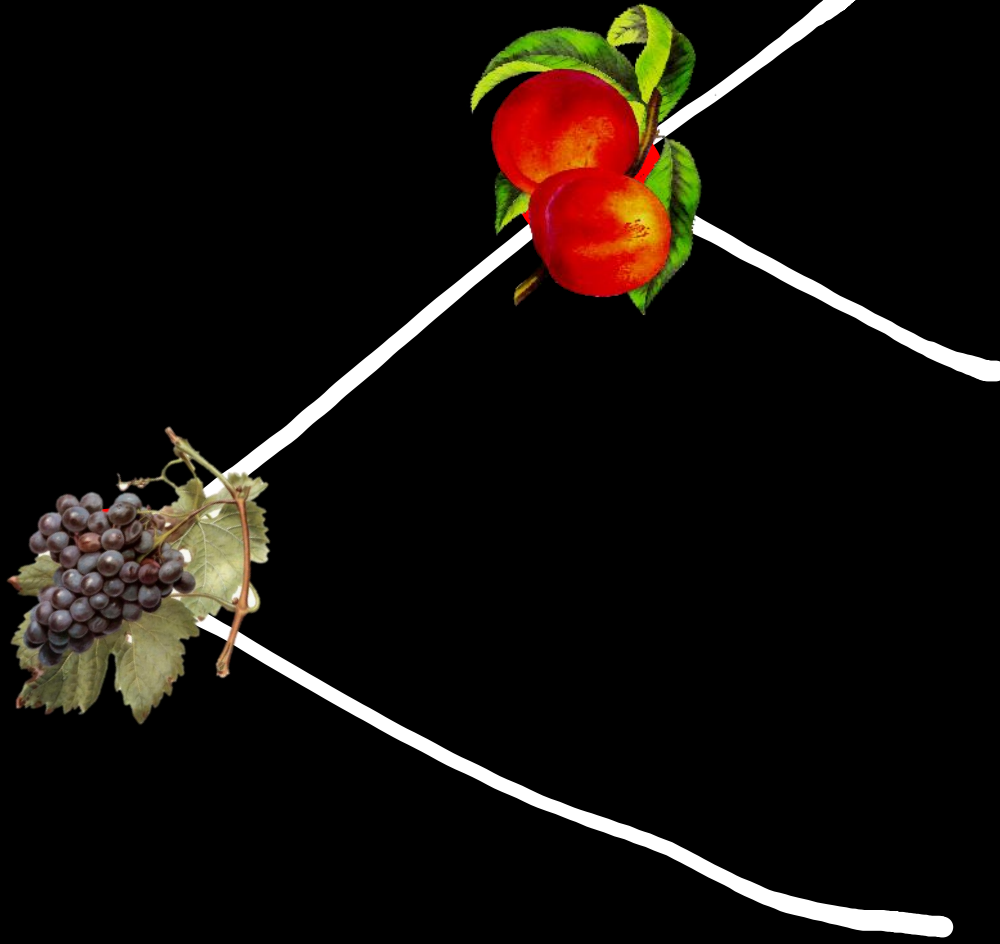
phylo.io





Ancestral state reconstruction


method where we use the modern distribution of a trait to predict the historic variation and patterns. If we can see patterns in the past, maybe we will be able to make better predictions looking forward.





X f 1 

X f 2 

X f 3 

Why asterids and rosids?

They don't tend to overlap in susceptibility.

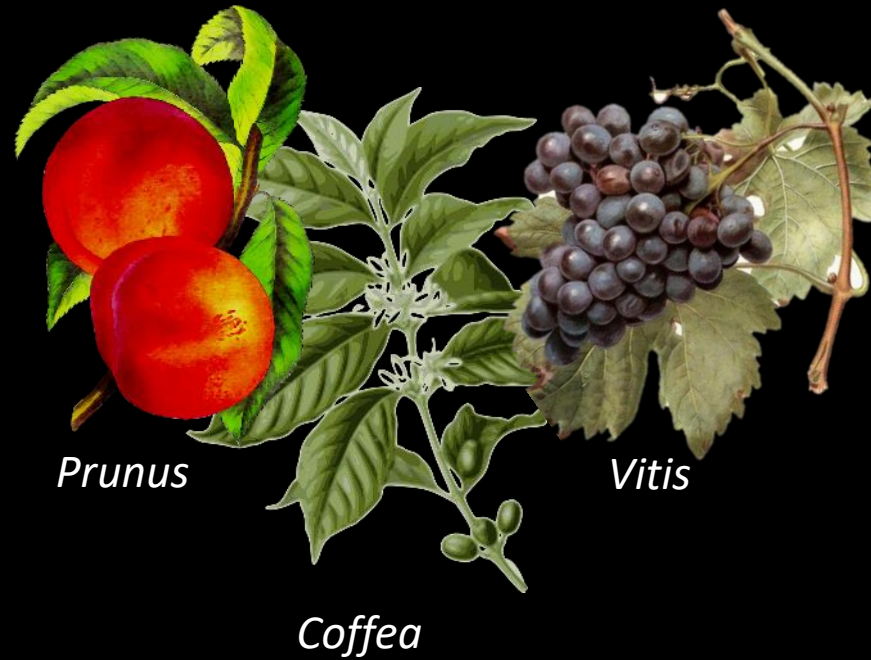
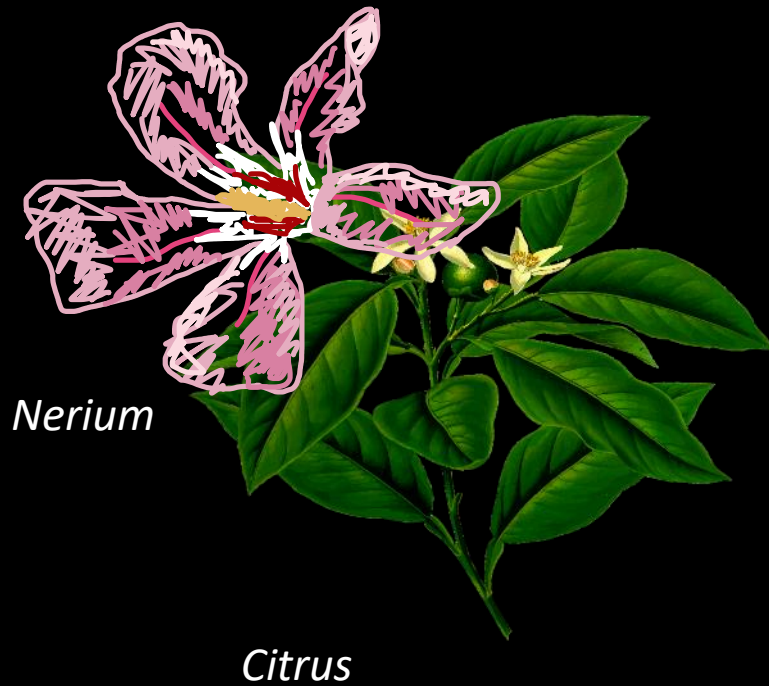


Citrus

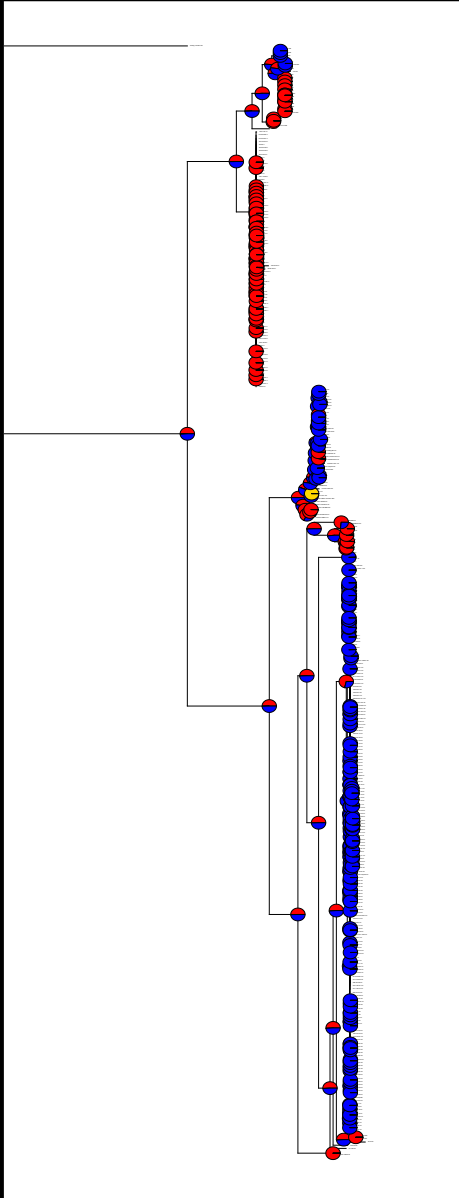


Coffea

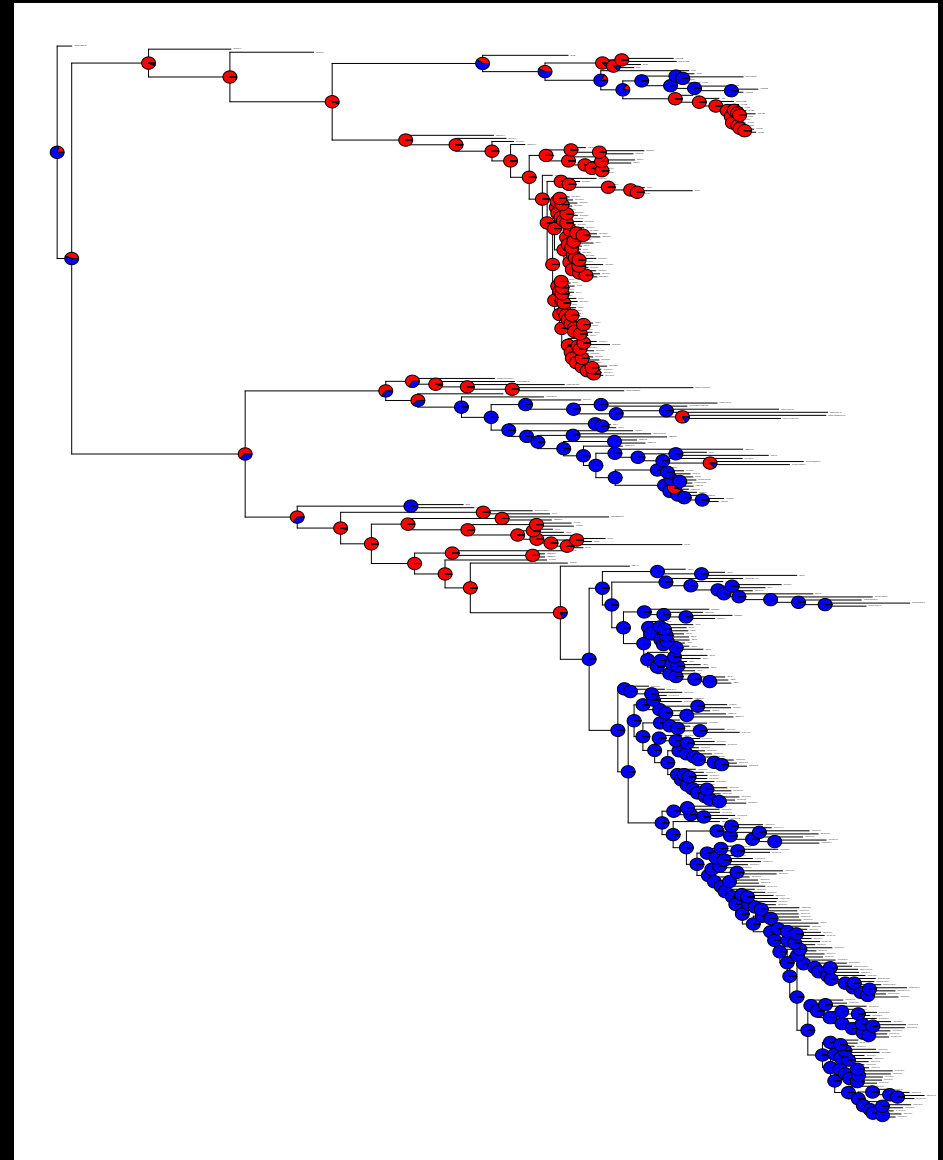
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They don't tend to overlap in susceptibility.



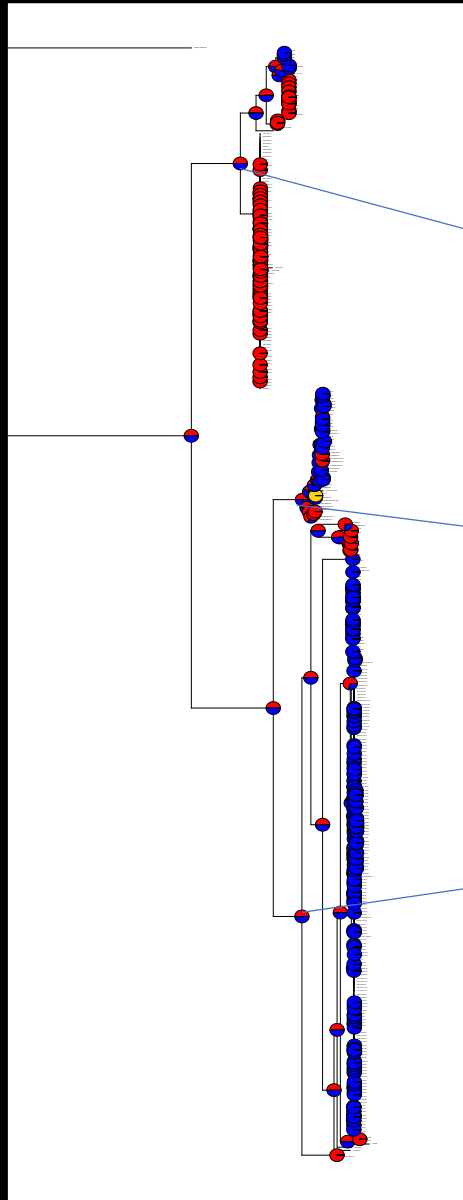
Core



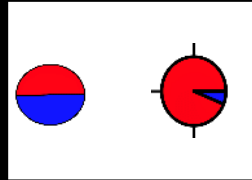
Accessory



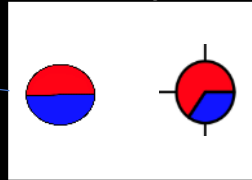
Core



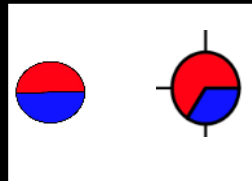
pauca



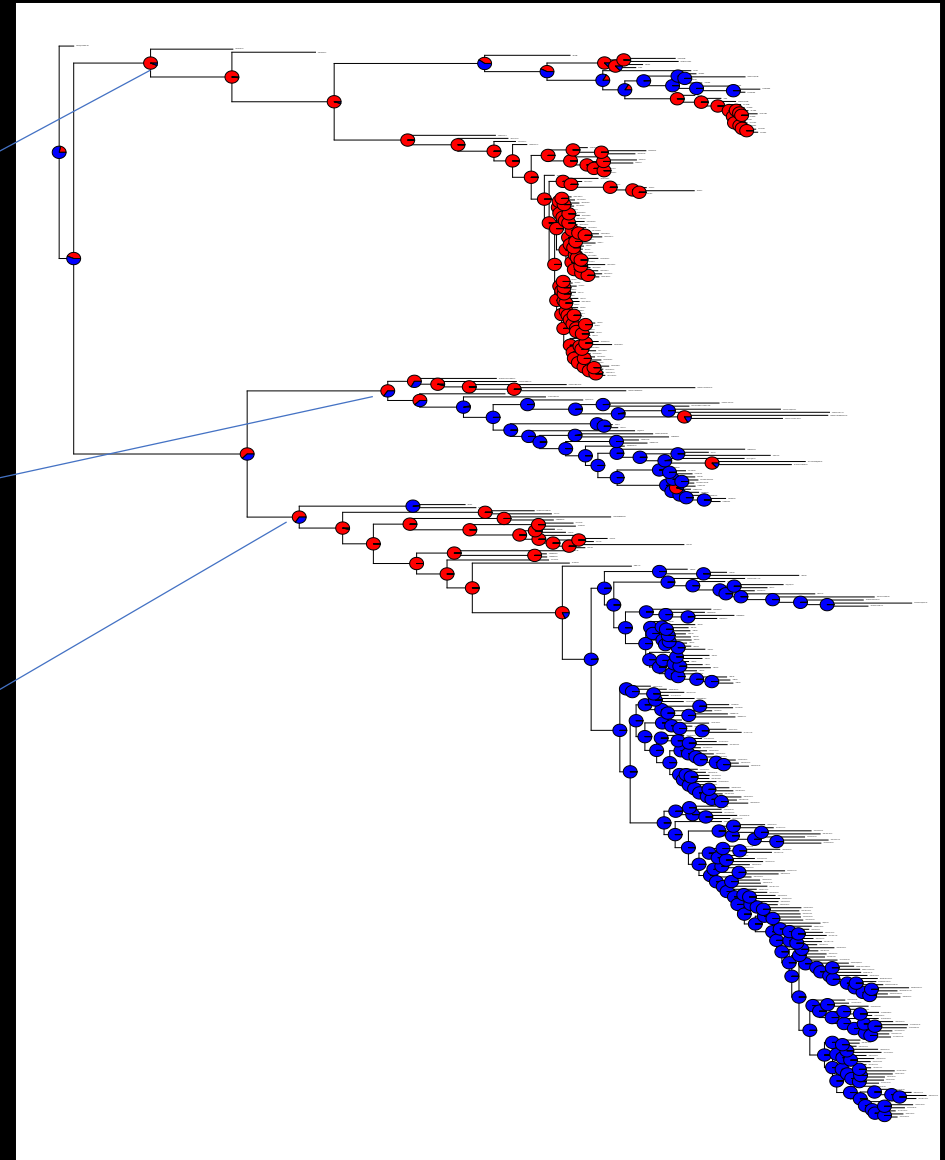
multiplex



fastidiosa



Accessory





Can we use these different loci to try to understand relationships between plant hosts and *X. fastidiosa* strains?

Thank you

-Almeida Lab

-UC Berkeley ESPM

-CDFA

