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Genome-Wide Analysis of *Corynespora cassiicola* Leaf Fall Disease Putative Effectors

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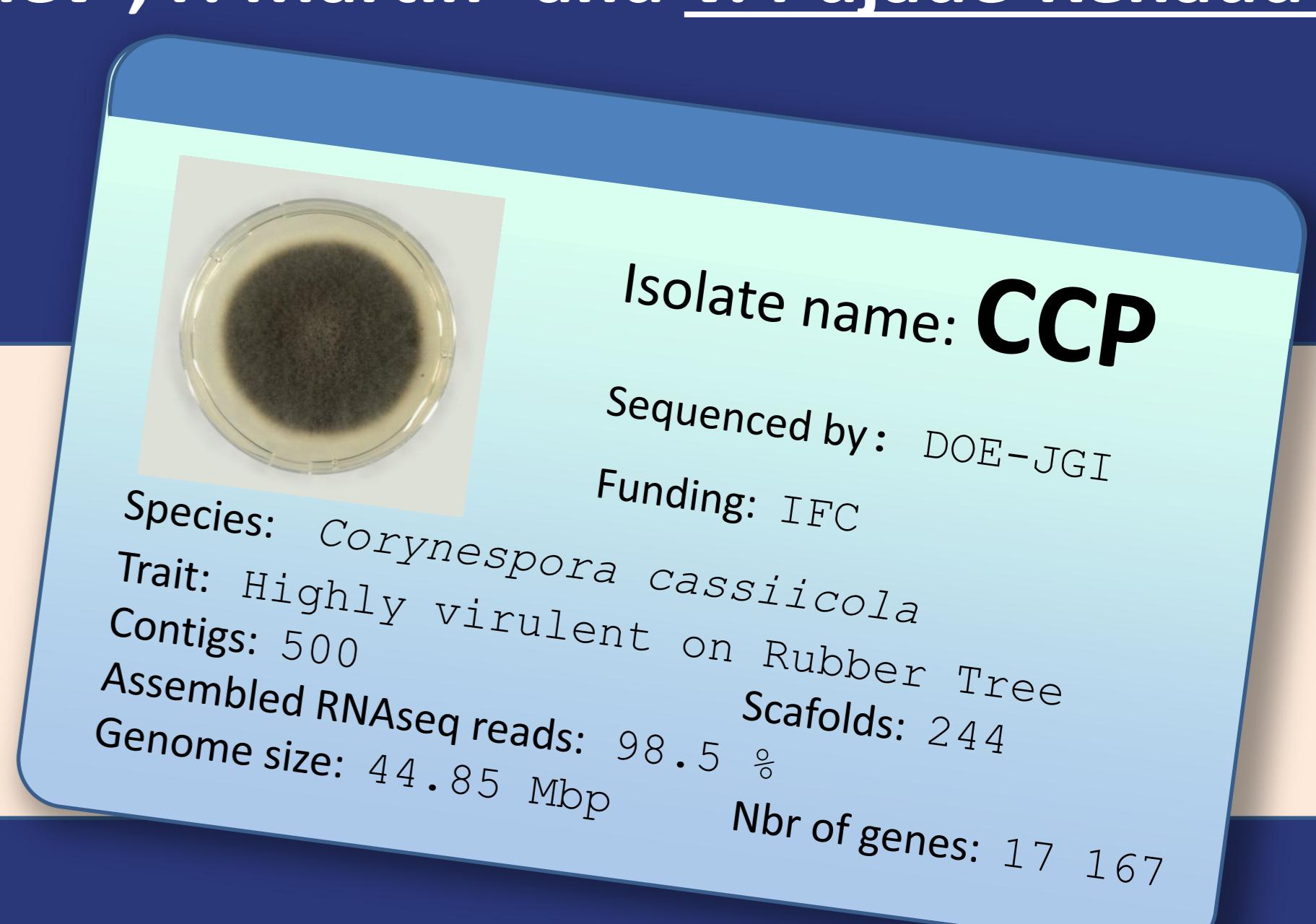
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Background:

Corynespora cassiicola is an Ascomycete fungus (Pleosporale order) with a large host range and diverse life styles¹. In rubber tree, it is responsible for the *Corynespora Leaf Fall* (CLF) disease which causes massive defoliation on susceptible cultivars, thus impairing natural rubber production²⁻⁶. Genomic and transcriptomic analyses were conducted in order to identify all potential effectors involved in CLF.



1. Interspecies analysis of all putative effectors. Genomes sequences by DOE-JGI ("1000 genomes project")

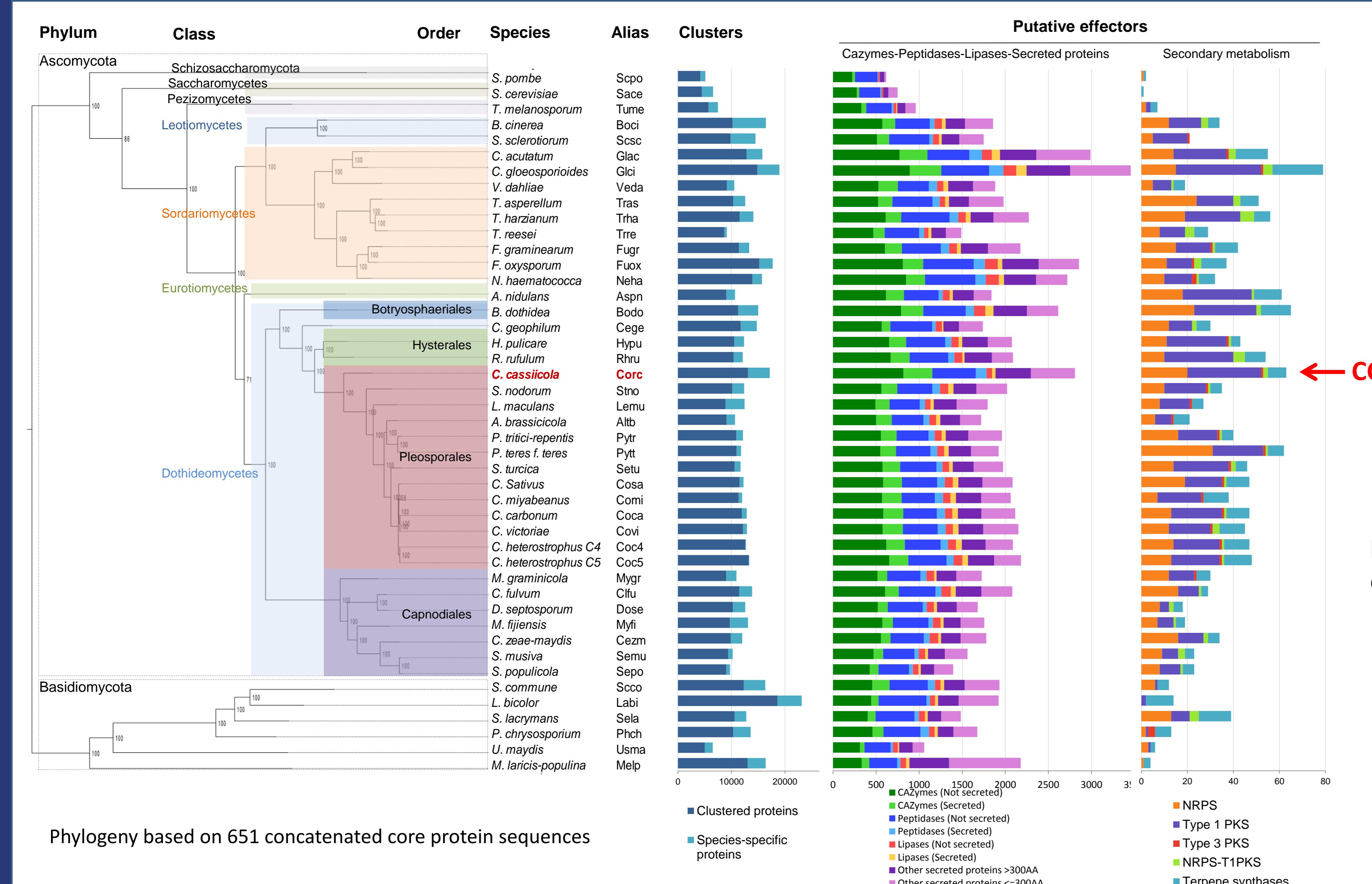


Fig. 1: Interspecific phylogeny , protein clustering and putative effectors of 45 fungal species

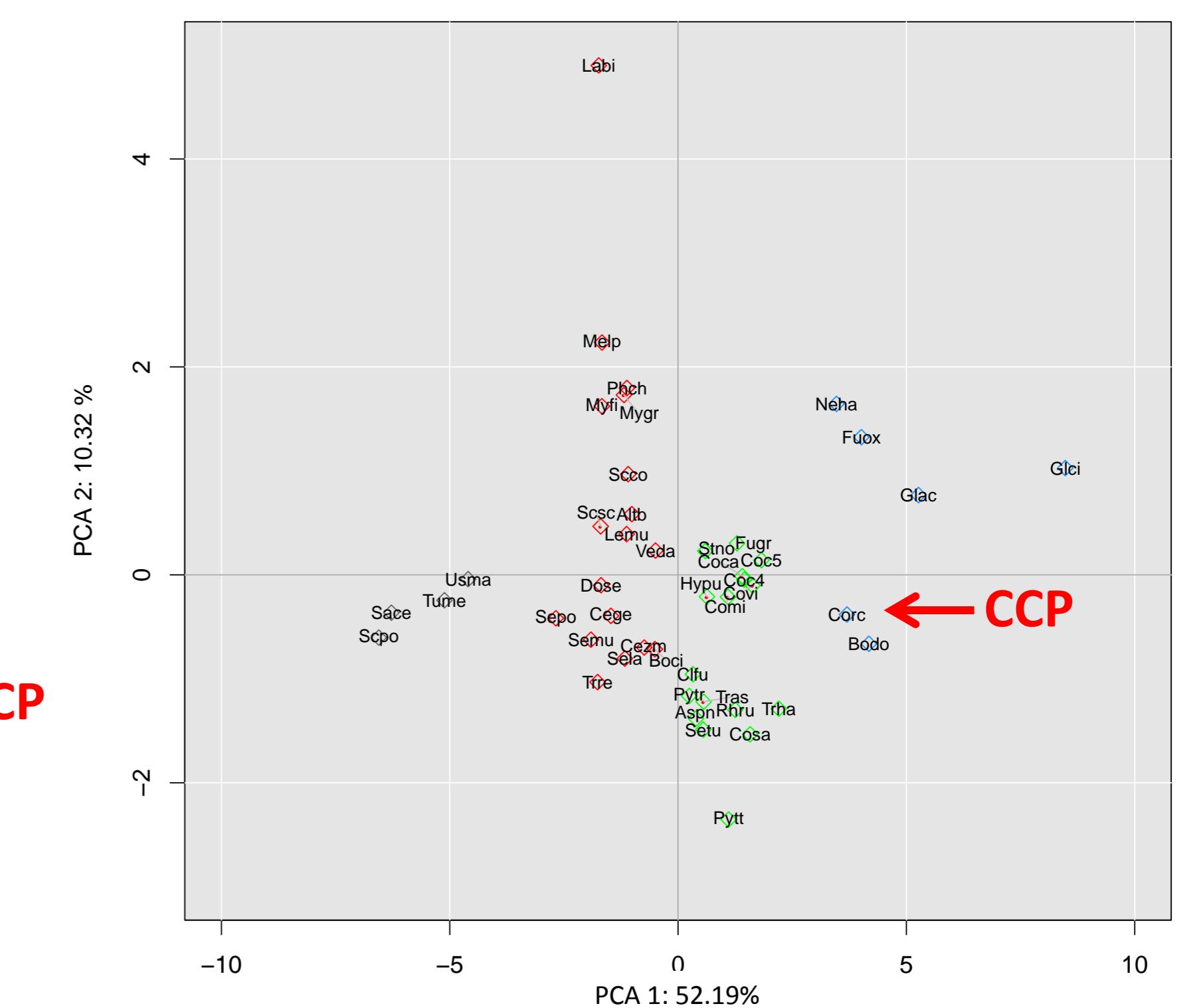


Fig. 2: Principal Component Analysis (PCA) based on the composition in all putative effectors from the 45 fungal species.

Result 1

- CCP genome is expanded in putative effectors
- Effector-based PCA is only weakly related to phylogeny
- CCP was clustered with two *Colletotrichum* sp., *F. oxysporum*, *N. hematococca* and *B. dothidea*, in coherency with life style (large host range and multiple trophic modes).

2. RNAseq of CCP compatible interaction with rubber tree

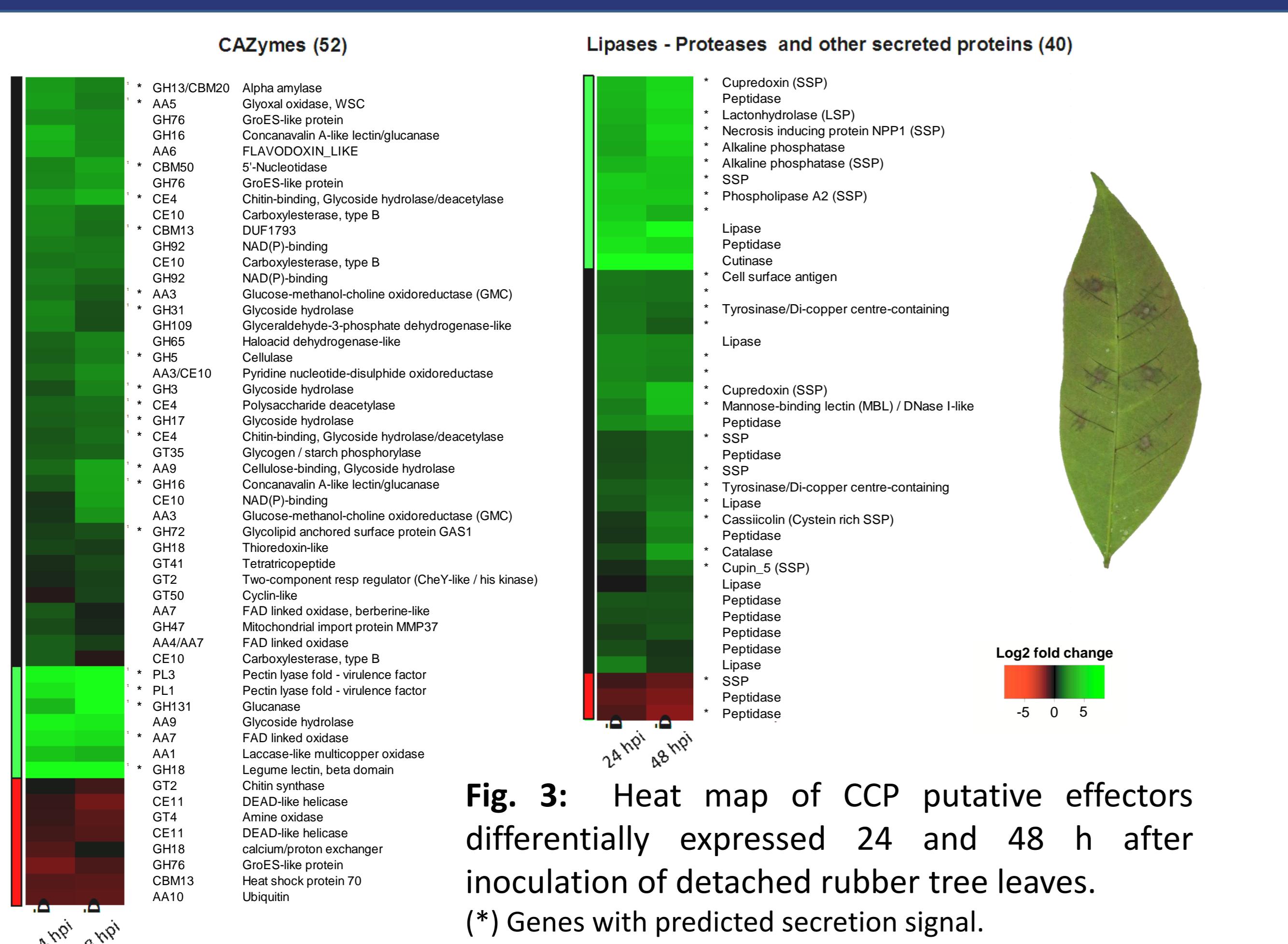


Fig. 3: Heat map of CCP putative effectors differentially expressed 24 and 48 h after inoculation of detached rubber tree leaves.
(*) Genes with predicted secretion signal.

Result 2: 353 genes were differentially expressed among which 92 putative effectors (52 CAZymes; 40 lipases/peptidases/other secreted proteins; 0 secondary metabolism), including 45 potentially secreted.

3. Intraspecific comparative genomics

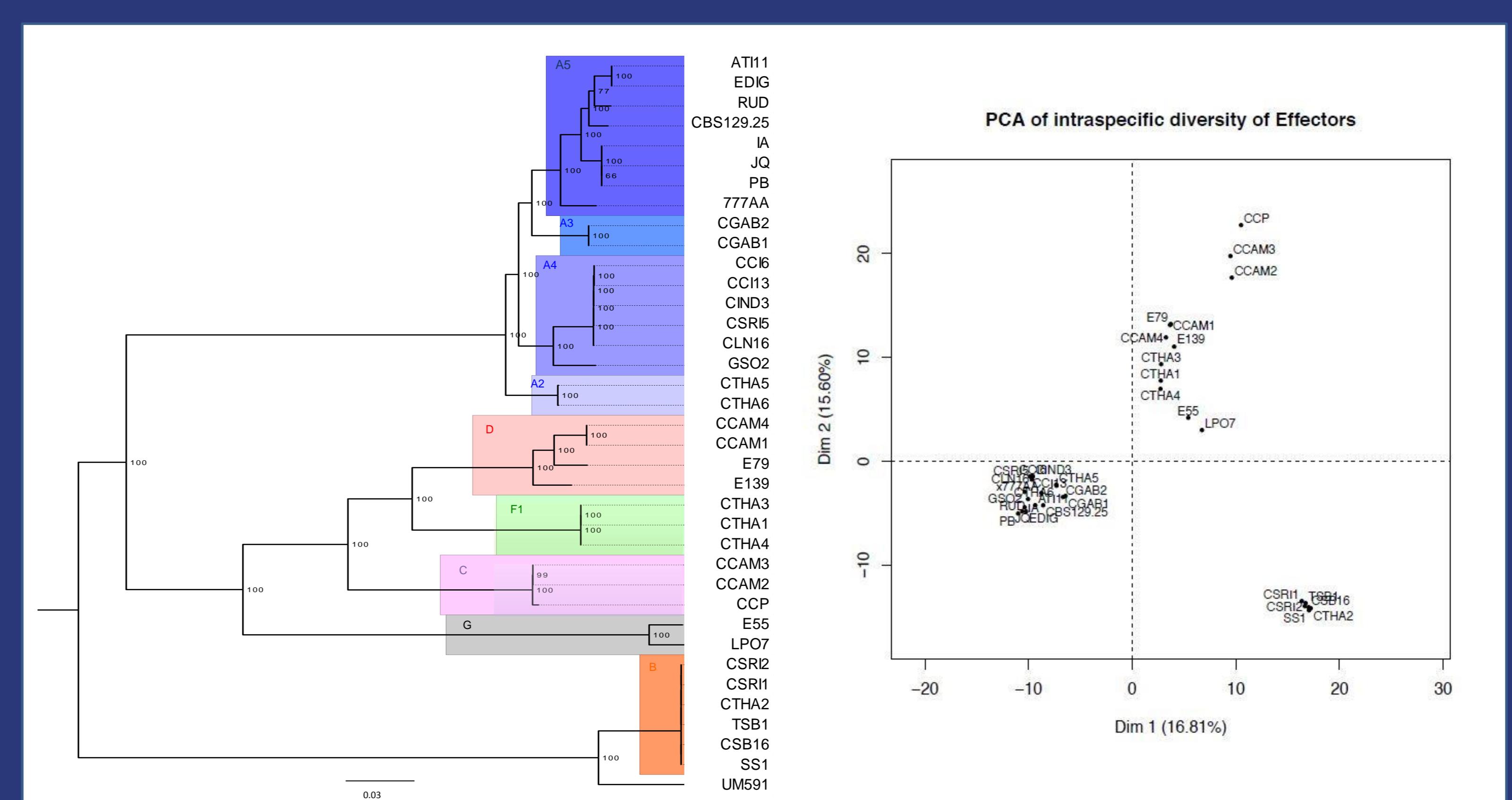


Fig. 4: Intraspecific phylogeny (left) and effector-based PCA (right) of 37 *C. cassiicola* isolates
Phylogeny based on 12 112 concatenated core protein sequences
PCA based on the composition in accessory effectors (612)

Result 3:

Intraspecific effector-PCA based is coherent with the genome-wide phylogeny.

Conclusion:

- We have identified *C. cassiicola* (CCP) putative effectors, and more specifically those modulated during its compatible interaction with rubber tree.
- Our comparison of all effectors in phylogenetically diverse *C. cassiicola* isolates will help understanding virulence mechanisms and may provide tools for effector-based selection of more tolerant cultivars⁷.

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