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Genome-wide analysis of *Corynespora cassiicola* putative effectors involved in the CLF disease of rubber tree

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Corynespora cassiicola is an Ascomycete with a large host range, mostly in the plant kingdom. It was also reported in other fungi, nematodes and in rare cases of human disease. It was mostly described as a necrotroph, but also as an endophyte or a saprobe. The species was previously placed in the Fungal Tree of Life where it formed a distinct clade among the Pleosporales, together with *Corynespora smithii*. Several studies have demonstrated the important genetic diversity among the species.

In rubber tree, it is responsible for the *Corynespora* Leaf fall (CLF) disease which causes massive defoliations on susceptible cultivars, thus impairing rubber production. We have previously purified and characterized a small protein toxin, secreted by the highly virulent rubber tree isolate CCP and playing a role in virulence. However the existence of other effectors, yet uncharacterized, was evidenced.

The objective of the present study was to identify *in silico* all potential effectors involved in CLF. The genome of our reference isolate CCP was sequenced and assembled by DOE-Joint Genome Institute in frame of the 1000 Fungal Genome project, and putative effectors identified. PCA based on the composition in effectors of 45 fungal species was only weakly related to phylogeny. However, *C. cassiicola* was found associated with species sharing common life style features, ie large host range and diverse trophic capacities. Transcripts profiling was conducted to identify functional effectors differentially expressed during the compatible interaction with rubber tree. Finally, intraspecific comparative analysis of 37 newly-assembled *C. cassiicola* genomes was conducted in order to compare their respective sets of putative effectors. These results will be discussed in relation with the genetic diversity and the known physiological specificities of the studied isolates.

Keywords: *Corynespora cassiicola*, *Hevea brasiliensis*, genomics, transcriptomics, effectors, Cassiicolin