Combining Transcriptomics, Bioinformatics, Biosynthesis Networks and **Chromatographic Analyses for Cotton Gossypium hirsutum L. Defense Volatiles Study**

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Abstract : Cotton Gossypium hirsutum L. is one of the most important industrial crops, producing the world leading natural textile fiber, but is very prone to arthropod attacks that reduce crop yield and quality. Cotton cultivation, therefore, makes an outstanding use of chemical pesticides. In reaction to herbivorous arthropods, cotton plants nevertheless show natural defense reactions, in particular through volatile organic compounds (VOCs) emissions. These natural defense mechanisms are nowadays underutilized but have a very high potential for cotton cultivation, and elucidating their genetic bases will help to improve their use. Simulating herbivory attacks by mechanical wounding of cotton plants in greenhouse, we studied by gPCR the changes in gene expression for genes of the terpenoids biosynthesis pathway. Differentially expressed genes corresponded to higher levels of the terpenoids biosynthesis pathway and not to enzymes synthesizing particular terpenoids. The genes were mapped on the G. hirsutum L. reference genome; their global relationships inside the general metabolic pathways and the biosynthesis of secondary metabolites were visualized with iPath2. The chromatographic profiles of VOCs emissions indicated first monoterpenes and sesquiterpenes emissions, dominantly four molecules known to be involved in plant reactions to arthropod attacks. As a result, the study permitted to identify potential key genes for the emission of volatile terpenoids by cotton plants in reaction to an arthropod attack, opening possibilities for molecular-assisted cotton breeding in benefit of smallholder cotton growers.

Keywords : biosynthesis pathways, cotton, mechanisms of plant defense, terpenoids, volatile organic compounds **Conference Title :** ICPPF 2018 : International Conference on Plant Protection and Fertilisers

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