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BOOK OF ABSTRACTS

Assessment of carbon metabolism of Coffee Kawisari hybrid challenged by Hemileia vastatrix, the causal agent of Coffee Leaf Rust.

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Plants have evolved sophisticated mechanisms to coordinate carbon metabolism during growth and development both under optimal and stress conditions. In coffee-rust biotrophic interactions, plants try to limit pathogen access to nutrients (e.g., sugars and sugar derivatives) and trigger immune responses, while *Hemileia vastatrix* (Hv) attempts to circumvent plant defences and control the host's primary metabolism for its own benefit. Previous proteomics data highlighted the up-regulation of proteins from photosynthesis, primary metabolism, and redox-related enzymes along the coffee resistance response. Coffee Kawisari hybrid - Hv interactions (resistant and susceptible reactions) were evaluated using a single sample fractionation method for metabolite and protein extraction. The microscopic evaluation of the Hv infection process revealed that coffee resistance was associated with early hypersensitive response and accumulation of phenolic-like compounds in host cell walls. GC-TOF-MS untargeted metabolomics allowed the identification of metabolic components, such as sugars, sugar derivatives, amino acids, phenylpropanoids, chlorogenic acids, alkaloids, and fatty acids (using the Golm Metabolome database). The overrepresentation of several caffeoylquinic acids in the resistance reaction may be linked to the accumulation of the phenolic-like compounds that were cytologically observed at the infection sites. Furthermore, sugar-related features also played a role in distinguishing between resistant and susceptible reactions, such as glucose and galactose. The cellular availability of mono and disaccharides is the result of the activity of several enzymes, e.g., sucrose synthase and invertases, that can be targeted by Hv in its strategy to manipulate plant carbon metabolism. The activity profile of these enzymes along the infection will be discussed. Proteomic analysis of the same samples (using the single sample fractionation method previously mentioned) is foreseen. The ultimate goal is to establish a connection between the metabolite and protein signatures.

Keywords: Resistance and susceptible reactions, cytology, semi-high throughput enzyme activity profiling, GC-TOF-MS untargeted metabolomics.

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