



Hanoi VIETNAM

11-14 Sept. 2023 Melia Hanoi Hotel

BOOK OF ABSTRACTS

  
29<sup>th</sup> Conference  
**Asic** **2023**

Agronomy | Chemistry | Technology | Physiological effects

## Integrative transcriptomic and metabolomic approaches to unravel the resistance profile of Kawisari coffee against *Hemileia vastatrix*

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### Rationale:

Most of coffee commercial varieties are highly susceptible to *Hemileia vastatrix*, the causal agent of coffee leaf rust. The increasing societal expectations for sustainable coffee production demand the replacement of fungicide treatments with alternative strategies of plant protection, such as the use of coffee-resistant varieties without yield and quality losses. This work aims to unveil metabolite and transcriptional key signatures of coffee resistance by integrated omic's data analysis.

### Methods:

Leaves of Kawisari hybrid coffee (*Coffea arabica* × *C. liberica*) were inoculated with urediniospores of *H. vastatrix* race II and race XIII to establish an incompatible (Resistance - R) and compatible (Susceptibility - S) interaction, respectively. Leaves were collected at 1, 4, and 7 days after infection for: cytological evaluation of fungal growth and host responses; transcriptome analysis (RNA-seq); and untargeted metabolic analysis (GC-TOF-MS). Integrative analysis of transcriptomics/metabolomics data at the pathway level was performed using the MetaboAnalyst5.0 platform.

### Results:

The post-haustorial resistance of Kawisari was associated with callose deposition around haustoria, hypersensitive response, and accumulation of phenolic-like compounds in host cells. A significantly higher percentage of infection sites with host responses were observed in resistance than in susceptible. When comparing resistant vs susceptible (R/S) transcriptomes and metabolomes, the expression of 127 genes and the amount of 117 metabolites change significantly in all time points. MetaboAnalyst integrative analysis unveiled 5 pathways that were significantly impacted: Photosynthetic carbon fixation; Pentose phosphate pathway; Glyoxylate and dicarboxylate metabolism; Phenylpropanoid biosynthesis; Glycine, serine, and threonine metabolism. The results highlighted the modulation of carbon and secondary metabolism as a response to *H. vastatrix* infection.

### Conclusions & Perspectives:

Similarly, to our previous proteomic approach, carbon metabolism and stress/defence pathways were associated with coffee resistance. The integration of multi-omics data can provide systems-level insights, opening new perspectives for coffee breeding programs.