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**BOOK OF ABSTRACTS**

- Agronomy
- Chemistry
- Technology
- Physiological effects
- Sustainability, climate changes

## First steps on the resistance profiling of Kawisari coffee hybrid through cytological and gene expression analyses

Diniz Inês<sup>1</sup> (inesdiniz@isa.utl.pt), Figueiredo Andreia<sup>2</sup>, Sebastiana Mónica<sup>3</sup>, Muñoz-Pajares Antonio Jesus<sup>4</sup>, Valverde Javier<sup>5</sup>, Azevedo Herlander<sup>4,6</sup>, Rodrigues Ana Sofia<sup>7</sup>, Prakash Rao Surya<sup>8</sup>, Pereira Ana Paula<sup>1</sup>, Guerra-Guimarães Leonor<sup>1</sup>, Azinheira Helena<sup>1</sup>, Várzea Vítor<sup>1</sup>, Batista Dora<sup>1</sup>, Silva Maria do Céu<sup>1</sup>

<sup>1</sup>CIFC, LEAF, Instituto Superior de Agronomia, Universidade de Lisboa, Oeiras, Portugal ; <sup>2</sup>BioISI, Faculdade de Ciências de Lisboa, Universidade de Lisboa, Lisboa, Portugal ; <sup>3</sup>BioISI, Faculdade de Ciências de Lisboa, Universidade de Lisboa, Lisboa, Portugal ; <sup>4</sup>CIBIO, InBIO, Universidade do Porto, Porto, Portugal ; <sup>5</sup>Estación Biológica de Doñana, Seville, Spain ; <sup>6</sup>Departamento de Biología, Faculdade de Ciências, Universidade do Porto, Porto, Portugal ; <sup>7</sup>cE3c, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal ; <sup>8</sup>Central Coffee Research Institute, Karnataka, India

### RATIONALE

Coffee leaf rust (CLR), caused by *Hemileia vastatrix* (*Hv*) has been a permanent threat to Arabica coffee production. Breeding for CLR resistance has been the most appropriate and sustainable strategy for disease management. The most widely used sources of resistance to CLR were Timor hybrids – HDTs (*C. arabica* x *C. canephora*). The recent breakdown of resistance in some HDT-derived varieties, due to the occurrence of more virulent *Hv* races, as well as the current CLR epidemics in Central America, highlights the importance and obvious need for the discovery and characterization of new sources of resistance. This work aims to start unveiling the cellular and molecular resistance profile of the Kawisari hybrid (*C. arabica* x *C. liberica*) derivative, recently used as donor for resistance in Arabica breeding programs in India.

### METHODS

The Kawisari hybrid was challenged with two distinct *Hv* races in order to establish an incompatible (resistance) and a compatible (susceptibility) interaction for a comparative analysis. Samples were collected during infection time-course, simultaneously for evaluation of fungal growth and plant responses by light microscopy and qPCR gene expression analysis [1]. Whole genome sequencing data previously obtained for Kawisari hybrid was aligned against the *C. arabica* reference genome using BWA and variants were called using bcftools. The resulting variants were used to identify and select polymorphic target genes putatively involved in defense/resistance responses. Expression analysis of selected candidate genes was initiated.

### RESULTS

In the incompatible interaction, *Hv* ceased its growth more frequently after the formation of the first haustorium (post-haustorial resistance) inducing a hypersensitive-like reaction, accumulation of phenolic-like compounds and haustorium encasement with callose. SNPs retrieved from Kawisari's data analysis were mapped back to the annotated genome to identify the variant loci. From these, 50 genes with a functional category assigned were identified, including specifically pathogen defense-related. Assessment of the candidate genes' differential expression profiles throughout the infection process is in progress.

### CONCLUSIONS & PERSPECTIVES

Our study provides the first insights on the characterization of the resistance response of a coffee hybrid with a high potential to be explored as a new source of resistance.

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### References:

- 1- Diniz, I. et al. European Journal of Plant Pathology. 2012. DOI:10.1007/s10658-011-9925-9.