



Translational Research in Crops

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Characterization of the transcriptional signatures associated with resistance and susceptibility to *Hemileia vastatrix* in the Kawisari coffee hybrid

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Coffee leaf rust (CLR), a disease caused by the biotrophic fungus *Hemileia vastatrix* (*Hv*), is the main threat to the worldwide production of Arabica coffee. The gradual breakdown of resistance in coffee varieties in the last years has highlighted the need for novel sources of resistance to CLR. This work aimed to unveil the cellular and molecular resistance profile of the Kawisari hybrid (*C. arabica* x *C. liberica*), a genotype used as a resistance donor in Arabica breeding programs in India. This coffee genotype was inoculated with two *Hv* races that triggered either resistance or susceptibility. Progress of infection was monitored using light microscopy. Simultaneously, we conducted a time-course RNA-seq characterization of the transcriptional responses. The microscopic studies showed that the post-haustorial resistance of Kawisari was associated with the hypersensitive response, accumulation of phenolic-like compounds and haustorium encasement with callose. The transcriptomic analysis suggest the downregulation of host primary metabolism genes at the early onset of infection, followed later by activation of genes functionally associated with multiple plant defense responses, including salicylic acid and jasmonate hormonal signaling. Resistance was also accompanied by the differential regulation of genes associated with phenylpropanoid metabolism and lignin biosynthesis. Our results, further validated by qPCR, provide important new insight into the molecular mechanisms underpinning resistance against CLR in this coffee genotype.

Funding: Foundation for Science and Technology (FCT) and FEDER funds through PORNorte under the project CoffeeRES PTDC/ASP-PLA/29779/2017 and by FCT UNIT LEAF (UID/AGR/04129/2020).

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