



Pre-haustorial resistance of coffee HDT832/2 to leaf rust unveiled by transcriptome 454 pyrosequencing

P. Talhinhos¹, H.G. Azinheira¹, I. Diniz¹, D. Santos², A. Loureiro¹, V. Várzea¹, D. Batista¹, O.S. Paulo², A.-S. Petitot³, D. Fernandez³, M.C. Silva¹

¹*Centro de Investigação das Ferrugens do Cafeeiro/IICT, Oeiras, Portugal*

²*Computational Biology and Population Genetics Group, Centro de Biologia Ambiental, Faculdade de Ciências da Universidade de Lisboa, Lisbon, Portugal*

³*Institut de Recherche pour le Développement - UMR 186 IRD-UM2-CIRAD, Montpellier, France*

Abstract

Coffee leaf rust, caused by *Hemileia vastatrix*, is one of the most important diseases of Arabica coffee. The discovery of natural *Coffea arabica* x *canephora* hybrid, named “Híbrido de Timor” (HDT), with most of its genotypes showing resistance to all known rust races, was a major breakthrough in breeding for rust resistance, leading to the release of resistant and productive cultivars. However, after 30-40 years of cultivation, the resistance in some of these cultivars broke down due to the appearance of new rust races. Still, cultivars derived from genotype HDT832/2 retain good levels of disease resistance in the field in different countries, suggesting that HDT832/2 resistance may be more durable. Previous studies showed that HDT832/2 hypersensitive-like response is mostly pre-haustorial, with similarities at the cellular and molecular levels to coffee non-host resistance to *Uromyces vignae*. In this work, 454 pyrosequencing was employed to characterise the transcriptome of HDT832/2 resistance to *H. vastatrix* race II by comparison to a mock-inoculated control and to the non-host resistance response of HDT832/2 to *U. vignae*. A total of 18892 genes could be inferred, 5% of which were expressed only in rust inoculated samples, including proteins involved in the response to biotic and abiotic stresses. About 2400 genes had no predicted function or homologies in public databases, 11% of which were activated (>10 fold) in response to rusts, putatively constituting uncharacterised factors involved in resistance. This study will allow an in depth transcriptomic characterisation of the immunity components shared between host and nonhost resistance, in the quest for explaining the longer durability of HDT832/2 resistance.