

## Transcriptomics of Resistance Response in *Coffea arabica* L.

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### INTRODUCTION

Coffee is one of the most important agricultural export commodities in the world. It represents the he main export resource for some developing countries. Despite the tremendous economic importance of coffee, our understanding of its biology is still very poor and the genetics of *Coffea* is almost non existing. The reasons for such a low research effort are several and they range from the low economic resources allocated to fundamental genetic research to the complexity of its genome.

*Coffea arabica*, is affected by an array of diseases caused by fungi, bacteria, flagellates and viruses. The two most devastating coffee pest and diseases are the leaf rust or orange rust (*Hemileia vastatrix*) and the coffee berry disease or CBD (*Colletotrichum coffeanum*). Leaf rust ruined the economy of Sri Lanka in the last quarter of the 19<sup>th</sup> century, rendering it bankrupt and changing the social habit of people from coffee drinking to tea. In addition, nematodes are in some areas very damaging to *C. arabica*, especially the so-called root-knot nematodes (*Meloidogyne* spp.) and the root-lesion nematodes (*Pratylenchus* spp.) (Carvalho, 1988). Pesticides provide effective protection but their applicability can be compromised by adverse environmental effects and by the emergence of resistant pathogen strains. For these reasons, much effort has been invested towards understanding the innate resistance mechanisms in plants (McDowell and Woffenden, 2003). To counteract the pathogenic infection, plants activate a variety of defence responses. A local defence include strengthening of cell walls, activation and/or synthesis of antimicrobial compounds, and expression of many defence-associated proteins, including the pathogenesis-related (PR) proteins. A hypersensitive response, characterised by a genetically programmed suicide of infected cells, frequently develops. The local response can, intern, trigger a long lasting systemic response (systemic acquired resistance, SAR) that primes the plant for resistance against a large spectrum of pathogens (Shirano et al., 2002). Plants maintain constant vigilance against pathogens by expressing large arrays of “R genes” (R, resistance). R genes encode putative receptors that respond to the products of “Avr genes” (Avr, avirulence) expressed by the pathogen during infection. Avr signal recognition initiate downstream signalling that make the infection unsuccessful.

Plant-pathogen interactions and downstream signalling are extremely complex and dynamic. The ongoing interactions between the pathogen and the plant are difficult to monitor with more traditional genetic and biochemical methods. With the advent of the large-scale genomic sequencing, EST (expressed sequence tag) projects and development of DNA microarray technologies, it is now possible to monitor the expression of thousands of genes simultaneously irrespective of different defence-related treatments and timing of the analysis.

Furthermore, SAR-inducing chemical compounds provide a unique opportunity to investigate the induced resistance mechanisms in plants in the absence of biological model systems. In particular, the two components, 2,6-dichloroisonicotinic acid (INA) and benzo(1,2,3) thiadiazole-7-carbothionic acid S-methyl ester (BTH) were demonstrated to be the potent inducers, acting independently or downstream of SA in SAR signalling but activating the SAR signal transduction pathway through the same signalling cascade. A biologically induced SAR response in Coffee has not been previously described. Based on the previous studies on SAR responsive system in tobacco, arabidopsis and other dicots, it is likely that the resistance and gene activation in *Coffea arabica* are SAR-like responses induced by BTH. The present study describes SAR response in *Coffea arabica*, induced by BTH, analysing the cDNA microarray expression profile of two different tissue, leaf and root as these tissues are eventually the target of most pathogens.