MOLECULAR CHARACTERIZATION OF PATHOGEN DEFENSE-RELATED GENES IN COFFEE

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Plant resistance to microbial pathogens comprises a multi-component defense response that is being extensively investigated at the molecular level. Important effectors genes, such as *pr1* (pathogenesis-related gene type 1), or regulator genes, like *npr1* (non-expresser of PR genes), were identified in model plants. Based on studies employing different pathosystems, it has become evident that transcriptional activation of specific defense-related genes is a vital and major part of this response. Several transcriptional factors and *cis*-elements in defense-related gene promoters have been identified. The key limiting factors of coffee (*Coffea* sp.) production is the fungal diseases caused by *Hemileia vastatrix* and *Colletotrichum kahawae*. The objective of the present study was to verify whether important components of plant resistance are conserved among model plants and coffee (*Coffea arabica*). This work presents the orthologous *Capr1* and *Canpr1* gene promoter isolation from the coffee genomic DNA. Functional promoter analysis was positively assessed with regard to the *ß-glucuronidase* (GUS) reporter gene, via *Agrobacterium*-mediated transient expression assay in tobacco leaves. We identified regions in the promoter sequences which are a potential binding motif for WRKY, ERF, TGA and MYB transcription factors. Stable transformations also are being conducted in *Arabidopsis.* The mechanisms underlying transcriptional regulation will be investigated by the analysis of the previously identified CaWRKY1 protein as trans-acting factor of the *Capr1* and *Canpr1* promoters. Analyses of a series of 5'-deletions of these promoters will be conducted to identify those *cis*-acting elements that are necessary for the induction of gene expression after exposure to pathogen and abiotic elicitors.

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