

# The Phytochrome-Interacting Factor genes in grapevine and their association to the gibberellin signal transduction pathway

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As sessile organisms, the plants have to maximize their ability to sense and interpret the environment in order to adequate growth and development. Members of the PIF (Phytochrome-Interacting Factor) family, a subset of the basic helix-loop-helix (bHLH) group of transcriptional regulators, function as cellular integrators of multiple signals to coordinate the regulation of several gene expression networks controlling plant morphogenesis. Although several plant genome sequences are currently available, the PIF/PIF-Like (PIL) family has only been characterized in *Arabidopsis thaliana* and *Oryza sativa*. In the present work, we describe the identification, structural characterization, chromosomal location and in silico expression profiling of PIF/PIL genes in *Vitis*. In grapevine, the family consists of 12 genes exhibiting the family characteristic bHLH DNA-binding domain and the conserved binding sites for photoactivated phytochrome B (APB) and phytochrome A (APA). The presence of highly conserved APB and APA sites in grapevine PILs may indicate conserved function to *Arabidopsis* and *Oryza* counterparts in regulating light-mediated responses. The number of PIF/PIL sequences in other plant species is variable and does not appear to correlate with the total number of bHLH coding sequences in the genome, as in *Vitis*, where a large subset of the family has been proposed to be involved in anthocyanin biosynthesis regulation. Homologs of the photomorphogenesis regulator LONG HYPOCOTYL IN FAR-RED 1 (HFR1) are absent from *Vitis vinifera* genome. In silico expression analyses have demonstrated an induction of PIF/PIL genes expression in libraries from abiotically stressed organs, including leaves, buds and ripening berries. Moreover, hierarchical clustering of the expression profile of grapevine PIF/PILs demonstrated a significant co-regulation pattern to gibberellic-acid (GA) signaling pathway genes. Thus, comprehensive expression and protein sequence analyses may help to elucidate the role the photoreceptor-interacting transcription factors in several developmentally important GA-controlled processes in family with a distinct growth habit such as Vitaceae, a heliophilous liana. Financial Support: CNPq (307031/2010-1 to VQ) and Embrapa (02.10.10.02.00.00 to CGL, 02.08.07.04.00.00 to PSR and 03.09.12.03.00.00 to VQ).