

EVALUATION OF WRKY AND MYB TRANSCRIPTION FACTORS IN SOME DOWNY MILDEW INFECTED SUNFLOWER LINES; MICROARRAY DATA ANALYSIS

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ABSTRACT

Downy mildew, which is caused by *Plasmopara halstedii*, is a major plant disease significantly affecting the sunflower (*Helianthus annuus*) production. Yield losses can reach up to 100% in heavily contaminated fields, even could lead the abandoning of cultivation. When considering the worldwide cultivation of sunflower as oil crop, plant losses have serious impact on the country economy as well as on the global food security. So far, thirty-six *P. halstedii* pathotypes/races were identified all over the world. In this study, expression profiles of *WRKY* and *MYB* transcription factor (TF) genes were analyzed in four downy mildew (race 334 and 710) infected sunflower genotypes such as PSC8 (susceptible), XRQ (resistant), and RIL43 and 88 (cross between XRQ and PSC8). Microarray data, including 60 normal vs disease samples were retrieved from NCBI GEO Data Sets (access. GSE25717). For array analyses, sunflower lines were grown in compost under 70% humidity, 20°C temperature and 16h day/8h night light periods. Germinated seeds (2-3 days) were inoculated with downy mildew or water for control for 3hrs, and then following 6 or 10 days of inoculation, plants were harvested for RNA extraction and array analyses. Data were normalized with GCRMA algorithm in Bioconductor package. Analyses demonstrated the 18 putative *WRKY* and 49 putative *MYB* TFs in downy mildew infected sunflower genotypes. In *WRKY* TFs, *WRKY-b* (Heli023654), *WRKY4* (Heli013712 and Heli000574), *WRKY1* (Heli029273) and *WRKY30* (Heli009222) TFs demonstrated significant downregulation in most downy mildew-sunflower interactions while the rest mainly upregulated in infected lines. Hierarchical clustering with Euclidean distance showed that *WRKY-b* (Heli023654) and *WRKY4* (Heli013712 and Heli000574) TFs in genes, and 10 days PSC8, RIL43 and RIL88 lines infected with race 710 in conditions have similar expression profiles. In addition, without line consideration, 6 or 10 days plants infected with race 334 had similar expression pattern and clustered closely, however, plants infected with 710 race demonstrated divergence in clustering based on plant age (6 or 10 days). In *MYB*, hierarchical clustering of TFs demonstrated three main clusters, including considerably up- and downregulated genes, and the genes with mosaic pattern. In addition, plant age seemed to have determinative effect in gene expression patterns. All these implicate that infection period (plant age) and pathotype (race 334 or 710) play an important role in modulation of expression profiles of *WRKY* and *MYB* TFs. However, further molecular and physiological studies are required to elucidate the relationship between these two TFs as well as with their interactors. Comparative analyses of *WRKY* and *MYB* TFs in susceptible, resistant and cross sunflower lines could significantly provide valuable insights to understand the gene regulatory elements in downy mildew-sunflower interactions as well as could pave the way for their biotechnological manipulation to improve the commercially important sunflower lines.

Key Words : Pathotype, race, array, mildew, inoculation, TF