DROUGHT-INDUCIBLE WRKY GENES IN TOBACCO (NICOTIANA TABACUM L.)

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ABSTRACT

Drought is one of the most important environmental stresses that effects crop production causing crop losses of several billion dollars per year in the US alone. The WRKY family of transcription factors (TFs) is one of the biggest families of TFs in plants. They are key regulators of many stress responses. Recently, there have been several reports linking WRKY TFs with regulating drought responses. Our data from oligo array analyses show that at least 15% of tobacco WRKY genes are strongly induced at the mRNA level during dehydration (at least 8-fold). A total of 12 genes, including eight WRKY genes, were selected for further study. Four of these genes are not available as complete genomic sequences and these are being isolated by thermal asymmetric interlaced-polymerase chain reaction (TAIL-PCR). The promoters from the other genes were cloned in front of the GUS reporter gene and transformed into tobacco plants. Several transgenic lines were generated and maintained in a phytochamber. Transgenic lines (T0) are being tested for gene expression under drought conditions and samples of leaves are being taken for GUS activity measurements. Our results indicate that many WRKY genes respond to multiple stresses such as water stress, wounding and pathogens and that several are also up-regulated by senescence and cell death. WRKY TFs are therefore central nodes in multiple signaling networks that are parts of plant responses to stress.