

WRKY GENES DRIVE DORMANCY IN ONION BULBS (*ALLIUM CEPA* L.)

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Dormancy in bulbous plants is an important physiological state regulated by complex genetic that permit a temporal cessation of vegetative growth during unfavorable seasons. Onion (*Allium cepa* L.) is one of the most widely cultivated bulbous plants; however, limited knowledge into the molecular mechanisms regulating bulb dormancy is available until now. This work aimed to identify key genes and metabolic pathways involved in the dormancy modulation, during the transition between endo-dormancy, eco-dormancy, and internal sprouting, by comparing transcriptomic profiles of uninfected and OYDV-infected bulbs. Indeed, virus infection causes a high number of symptoms like leaf striping, growth reduction and dormancy alteration. A total of 5,390 Differentially Expressed Genes (DEGs) were found among the physiological steps investigated in uninfected samples, while the number of DEGs was significantly reduced (1,322) in OYDV-infected plants at different dormancy stages. The most enriched metabolic pathways were related to cell wall modification, proteolysis and hormone signaling, like ABA, GA, auxins and brassinosteroids, already reported as important dormancy related pathways. In addition, several Transcription Factors (TFs) were found up-regulated only in the uninfected bulbs. Among these, 14 TFs belonging to WRKY family were isolated by comparisons and appeared to be involved in dormancy modulation. More interestingly, through GO enrichment and network analysis, four out of fourteen WRKY genes (AcWRKY2, AcWRKY30, AcWRKY32 and AcWRKY52) seemed to drive the dormancy release, resulting significantly down-regulated in the OYDV-infected samples. These evidences were confirmed by using Arabidopsis WRKY knocked-down transgenic lines. Overall, our work well describes for the first time the key genes and metabolic pathways involved in onion bulb dormancy, providing a deeper understanding of the significant role played by WRKY family in dormancy modulation.