

## Identification of Tissue-Specific Transcription Factors in *C. roseus* with Emphasis to the TIA Biosynthetic Pathway

**Authors :** F. M. El-Domyati, A. Atef, S. Edris, N. O. Gadalla, M. A. Al-Kordy, A. M. Ramadan, Y. M. Saad, H. S. Al-Zahrani, A. Bahieldin

**Abstract :** Transcriptome retrieved from SRA database of different tissues and treatments of *C. roseus* was assembled in order to detect tissue-specific transcription factors (TFs) and TFs possibly related to terpenoid indole alkaloids (TIA) pathway. A number of 290 TF-like transcripts along with 12 transcripts related to TIA biosynthetic pathway were divided in terms of co-expression in the different tissues, treatments and genotypes. Three transcripts encoding peroxidases 1 and 12 were downregulated in hairy root, while upregulated in mature leaf. Eight different transcripts of the TIA pathway co-expressed with TFs either functioning downstream tryptophan biosynthesis, e.g., *tdc*, *str1* and *sgd*, or upstream vindoline biosynthesis, e.g., *t16h*, *omt*, *nmt*, *d4h* and *dat*. The results showed no differential expression of TF transcripts in hairy roots knocked down for *tdc* gene (TDCi) as compared to their wild type controls. There were several evidences of tissue-specific expression of TF transcripts in flower, mature leaf, root/hairy root, stem, seedling, hairy root and immature/mature leaves. Regulation included transcription factor families, e.g., bHLH, MYB and WRKY mostly induced by ABA and/or JA (or MeJA) and regulated during abiotic or biotic stress. The information of tissue-specific regulation and co-expression of TFs and genes in the TIA pathway can be utilized in manipulating alkaloid biosynthesis in *C. roseus*.

**Keywords :** SRA database, bHLH, MYB, WRKY, co-expression

**Conference Title :** ICSRD 2020 : International Conference on Scientific Research and Development

**Conference Location :** Chicago, United States

**Conference Dates :** December 12-13, 2020