Abstract

Abrus precatorius is a medicinal plant known for their triterpenoid saponin content, that undergoes structural modification through glycosylation. Glycosyltransferases (GTs) are key enzymes that catalyze this modification, enhancing the solubility, stability and bioactivity of these secondary metabolites. This study builds on previously conducted transcriptomics analysis, and aims to validate the in-silico data using semi-quantitative PCR. The main objective was to identify differentially expressed genes (DEGs) under various stress conditions and uncover potential GT candidates involved in modification of plant defense-related metabolites like abrusoside and glycyrrhizin. PCR amplification and sequencing of a candidate GT gene, LOC113846739 (C1), revealed expression trends consistent with the original transcriptomic dataset. Bioinformatics characterization further supports that C1 encodes a protein with similarities to known plant UDP-glycosyltransferases. These results reinforce the validity of the transcriptomics analysis and support the continuation of this investigation using quantitative PCR for more precise and reliable gene expression profiling.

Keywords: *Abrus precatorius*, glycosyltransferases, semi-quantitative PCR, transcriptomics validation,