

Quantitative Analysis of Gene Expression Related to Saponin Production using Real-Time PCR

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Abstract:

Saponins are vital secondary metabolites responsible for many of the pharmacological properties of Aloe vera. This study aimed to analyze the expression patterns of key genes involved in saponin biosynthesis under stress conditions, using quantitative real-time PCR. Ten transcripts of genes implicated in saponin biosynthesis were selected from transcriptome data and analyzed after treatment with methyl jasmonate (MeJa) at 5, 10, and 15-hour intervals. Real-time PCR, with its sensitivity, large dynamic range, and sequence specificity, proved effective for comparing the expression levels of specific genes identified from next-generation sequencing data. Results revealed that genes involved in the saponin biosynthesis pathway were mostly upregulated after 15 hours of MeJa treatment. Notably, maximum expression was observed for mevalonate kinase (MVK) and mevalonate phosphate kinase (MVAPK), key regulatory enzymes in the isoprenoid biosynthetic pathway. However, HMG-CoA reductase (HCR) was downregulated, indicating a potential role in feedback inhibition at a metabolic branch point. These findings suggest that Aloe vera overproduces saponins in response to stress, emphasizing the role of saponins in the plant's defense mechanism.