Arun Krishnaraj – ak37738

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Dr Mehdy

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**Abstract**

Abscisic acid (ABA) is a hormone that helps regulate stress tolerance responses and regular developmental processes in plants by regulating gene expression. Transgenic Arabidopsis, which differ in their expression of cell wall protein AGP31, can be used to better understand the effect of ABA on expression of stress response proteins. OLE1 and RD29B are genes thought to be regulated by ABA, and this regulation can be quantified by comparing AGP31 mutant and wild type Arabidopsis expression following ABA exposure; RNA extracted from plant tissue can be used to generate cDNA, upon which qPCR can be run to measure gene expressivity. Following initial RNA purification from other cellular material, spectroscopic analysis was used to determine sample purity and quantity: wild type control and wild type ABA treatment samples were found to have RNA concentrations of 645.1 and 502.9 ng/µL respectively. Using UV spectrum absorption ratios to account for sample purity, both treatments were found to contain acceptable levels of contaminating DNA, residual carbohydrates, salts, and reagents. Gel electrophoresis with ethidium staining revealed highly fluorescent, clear bands of ethidium-bound RNA, indicating high levels of RNA intactness. Following reverse transcription, qPCR primers were designed and standardized, and a threshold level of fluorescence was established; level of expression was quantified using the number of PCR cycles to reach the threshold (CT). Expression of genes of interest were compared to the reference gene Actin 2; both treatment groups had higher CT values for the OLE1 and RD29B cDNA segments compared to Actin 2, and both genes of interest had lower CT values when treated with ABA.