Cloning and Expression Analysis of Carboxyltransferase of Acetyl-CoA Carboxylase from *Jatropha curcas*

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A full-length cDNA of the carboxyltransferase (accA) gene of acetyl-coenzym A (acetyl-CoA) carboxylase from *Jatropha curcas* was cloned and sequenced. The gene with an open reading frame (ORF) of 1149 bp encodes a polypeptide of 383 amino acids, with a molecular mass of 41.9 kDa. Utilizing fluorogenic real-time polymerase chain reaction (RT-PCR), the expression levels of the accA gene in leaves and fruits at early, middle and late stages under pH 7.0/8.0 and light/darkness stress were investigated. The expression levels of the accA gene in leaves at early, middle and late stages increased significantly under pH 8.0 stress compared to pH 7.0. Similarly, the expression levels in fruits showed a significant increase under darkness condition compared to the control. Under light stress, the expression levels in the fruits at early, middle and late stages showed the largest fluctuations compared to those of the control. These findings suggested that the expression levels of the accA gene are closely related to the growth conditions and developmental stages in the leaves and fruits of *Jatropha curcas*.

Key words: Carboxyltransferase, Fluorogenic Quantitative Real-Time PCR, Overexpression, Physiological Environment