

Isolation and characterization of full-length cellulose synthase gene (HsCesA1) from Roselle (*Hibiscus sabdariffa* L. var. UMKL)

ABSTRACT

The *Hibiscus sabdariffa* var. UMKL (Roselle) investigated here may potentially be used as an alternative fibre source. To the best of our knowledge, there was no study focusing on the genetics underlying the cellulose biosynthesis machinery in Roselle thus far. This paper presents the results of the first isolation of the cellulose synthase gene, HsCesA1 from this plant, which is fundamental for working towards understanding the functions of CesA genes in the cellulose biosynthesis of Roselle. A full-length HsCesA1 cDNA of 3528 bp in length (accession no: KJ608192) encoding a polypeptide of 974 amino acid was isolated. The full-length HsCesA1 gene of 5489 bp length (accession no: KJ661223) with 11-introns and a promoter region of 737 bp was further isolated. Important and conserved characteristics of a CesA protein were identified in the HsCesA1 deduced amino acid sequence, which strengthened the prediction that the isolated gene being a cellulose synthase belonging to the processive class of the 2-glycosyltransferase family 2A. Relative gene expression analysis by semi-quantitative reverse transcription polymerase chain reaction (RT-PCR) on young leaf and stem tissues found that HsCesA1 had similar levels of gene expression in both tissues. Phylogenetic and Blast analyses also supported the prediction that the isolated HsCesA1 may play roles in the cell wall depositions in both leaf and stem tissues.

Keyword: Cellulose; Cellulose synthase gene (CesA); Fibre; HsCesA1; Promoter; Semi-quantitative RT-PCR