

Cloning and comparative protein modelling of two MADS-box genes, HsMADS1 and HsMADS2 isolated from *Hibiscus sabdariffa* L. var. UMKL (roselle)

Abstract

'*Hibiscus sabdariffa*' L. var. UMKL or commonly known as roselle is cultivated in Malaysia mainly for its calyx, which is high in vitamin C and anthocyanin. Unfortunately, the genetic information regarding the flowering pathway of roselle is very scarce. It is essential to understand the genetics underlying roselle's flower developmental process by studying MADS-box transcription factor genes that play crucial roles in controlling the development of calyx in flowering plants. Designated as 'HsMADS1' and 'HsMADS2', two MADS-box genes were isolated from the calyx tissues of roselle from different developmental stages using 3'- RACE PCR and primer walking approaches. The different motifs in the C domain region of 'HsMADS1' and 'HsMADS2' deduced amino acid sequences suggested that both genes probably originated from 'SEP' and 'AGL6' subfamilies of MADS-box gene respectively. The putative functions of the genes based on BLAST searches and phylogenetic analyses suggested that 'HsMADS1' possibly involves in the expression of SEP gene in stem, leaf, bud and flower organs of roselle, whereas 'HsMADS2' may probably involve in the late expression of floral tissue for stem branching. The alpha helix rich structures of SRF-TF identified in the deduced amino acid sequences of HsMADS1 and HsMADS2 supported the involvement of both proteins in DNA binding and dimerisation.

Keyword: Gene isolation; In silico analyses; Molecular modelling; Flower development; Transcriptional Factor