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Cloning and expression of an *APETALA1*-like gene from *Nelumbo nucifera*

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ABSTRACT. The objective of this study was to clone the full-length cDNA of the *APETALA1* (*AP1*) gene from lotus and analyze its sequence and expression pattern. The full-length cDNA sequence of the *NnAP1* gene was amplified from the petals of *Nelumbo nucifera* 'Hongxia' using RT-PCR and rapid amplification of cDNA ends. Bioinformatic methods were used to analyze the sequence characteristics of the gene. Quantitative real-time PCR methods were used to investigate the expression pattern of *NnAP1* in various organs and during different developmental stages. The cloned full-length *NnAP1* cDNA (GenBank accession No. KF361315) was 902 bp, containing a 795-bp open reading frame encoding 264 amino acids with a relative molecular mass of 30,288.4 and an isoelectric point of 9.13. *NnAP1* had a MADS-box domain and a K-box domain, which is typical of the *SQUA*/*AP1* gene family. A protein sequence identity search showed that NnAP1 was 75-96% similar to other plant AP1s. Phylogenetic tree analysis indicated that *NnAP1* was very closely related to *AP1* of *Glycine max*, suggesting that they shared the same protein ancestor. Quantitative real-time PCR analysis showed that *NnAP1* was expressed in various organs during different developmental stages; it had the highest expression in blooming

flowers and had trace expression in the young vegetative and flower senescence stages. Our analysis suggests that *NnAP1* plays an important role in controlling floral meristem identity and floral organ formation.

Key words: *Nelumbo nucifera*; *NnAP1*; Gene cloning; Expression analysis

