



Molecular cloning and characterization of two novel *NAC* genes from *Mikania micrantha* (Asteraceae)

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ABSTRACT. NAC proteins, which are plant-specific transcription factors, have been identified to play important roles in plant response to stresses and in plant development. The full-length cDNAs that encode 2 putative NAC proteins, designated as *MmATAF1* and *MmNAP*, respectively, were cloned from *Mikania micrantha* by rapid amplification of cDNA ends. The full-length cDNAs of *MmATAF1* and *MmNAP* were 1329 and 1072 bp, respectively, and they encoded deduced proteins of 260- and 278-amino acid residues, respectively. The proteins MmATAF1 and MmNAP had a calculated molecular mass of 29.81 and 32.55 kDa and a theoretical isoelectric point of 7.08 and 9.00, respectively. Nucleotide sequence data indicated that both *MmATAF1* and *MmNAP* contained 2 introns and 3 exons and that they shared a conserved genomic organization. Multiple sequence alignments showed that MmATAF1 showed high sequence identity with

ATAF1 of *Arabidopsis thaliana* (61%) and that MmNAP showed high sequence identity with NAP of *A. thaliana* (67%) and CitNAC of *Citrus sinensis* Osbeck (62%). Phylogenetic analysis showed that the predicted MmATAF1 and MmNAP proteins were classified into the ATAF and NAP subgroups, respectively. Transient expression analysis of onion epidermal cells indicated nuclear localization of both MmATAF1-GFP and MmNAP-GFP fusion proteins. Semi-quantitative reverse transcription polymerase chain reaction (RT-PCR) analysis indicated that *MmATAF1* was expressed in all the tissues tested, but in varying abundance, while *MmNAP* was specifically expressed in stems, petioles, shoots, and leaves, but not in roots. The transcript levels of *MmATAF1* and *MmNAP* in shoots and in infected stems were induced and strengthened by wounding, exogenous ZnSO₄, abscisic acid, salicylic acid, and *Cuscuta campestris* infection on the basis of semi-quantitative RT-PCR and real-time PCR analyses, respectively. Collectively, these results indicated that *MmATAF1* and *MmNAP*, besides having roles in *M. micrantha* adaptation to *C. campestris* infection and abiotic stresses, also integrated signals derived from both *C. campestris* infection and abiotic stresses.

Key words: *Mikania micrantha*; NAC genes; Sequence characterization; Transcript expression