

# Molecular and phylogenetic analysis of MADS-box genes of MIKC type and chromosome location of *SEP*-like genes in wheat (*Triticum aestivum* L.)

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**Abstract** Transcription factors encoded by MIKC-type MADS-box genes control many important functions in plants, including flower development and morphogenesis. The cloning and characterization of 45 MIKC-type MADS-box full-length cDNA sequences of common wheat is reported in the present paper. Wheat EST databases were searched by known sequences of MIKC-type genes and primers were designed for cDNA cloning by RT-PCR. Full-length cDNAs were obtained by 5' and 3' RACE extension. Southern analysis showed that three copies of the MIKC sequences, corresponding to the three homoeologous genes, were present. This genome organization was further confirmed by aneuploid analysis of six *SEP*-like genes, each showing three copies located in different homoeologous chromosomes. Phylogenetic analysis included the wheat MIKC cDNAs into 11 of the 13 MIKC subclasses identified in plants and corresponding to most genes controlling the floral homeotic functions. The expression patterns of the cDNAs corresponding to different homeotic classes was analysed in 18 wheat tissues and floral organs by RT-PCR, real time RT-PCR and northern hybridisation.

Potential functions of the genes corresponding to the cloned wheat cDNAs were predicted on the basis of sequence homology and comparable expression pattern with functionally characterized MADS-box genes from *Arabidopsis* and monocot species.

**Keywords** Wheat · MADS-box genes · Phylogenesis · Chromosome location · Expression analysis

## Introduction

Transcription factors encoded by genes of the MADS-box family play key roles in controlling development and signal transduction in eukaryotes (Messenguy and Dubois 2003). Phylogenetic analyses split the MADS-box gene family into two classes or lineages, termed type I (SRF-like) and type II (MEF2-like) genes (Alvarez-Buylla et al. 2000a); both gene types are present in plants, animals and fungi. All MADS-box genes possess a 5' end highly conserved region of about 180 bp, which encodes the MADS-box or MADS domain of 60 amino acids. This domain is responsible for protein nuclear localization, recognition and binding to CArG box motives within the promoter of their target genes and MADS protein dimerization (de Folter and Angenent 2006).

In *Arabidopsis* phylogenetic and structural analyses identified three categories among 98 MADS-box genes: type I, type II and MADS-like (Becker and Theissen 2003; De Bodt et al. 2003; Parenicova et al. 2003). Type II MADS-box proteins of plants are also named MIKC-type because of their conserved modular structure consisting of four functional domains: the highly conserved MADS (M) domain; the less conserved intervening (I) and keratin-like (K) domains, which are responsible for protein dimerization;

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