

Review Article

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MADS-Box Transcription Factors in *Arabidopsis thaliana*: Molecular Control of Floral Organ Identity and Development

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Abstract MADS-box transcription factors are central regulators of plant development, particularly in reproductive processes. This review integrates molecular, phylogenetic, transcriptomic, and functional analyses of the complete MADS-box gene family in *Arabidopsis thaliana*. These transcription factors regulate gene expression through binding to CArG-box cis-elements, with specificity determined by combinatorial protein interactions and higher-order complex formation. Genome-wide studies reveal diversification of MADS-box genes into distinct lineages with specialized developmental roles. Transcript profiling during silique development demonstrates coordinated expression patterns associated with embryogenesis, seed maturation, and fruit development. Protein interaction mapping supports the quartet model, highlighting the importance of multimeric complexes in floral organ specification. Functional analyses of B-sister genes confirm their conserved roles in ovule and seed development, particularly in endothelium differentiation. Additionally, transcriptional networks controlled by AGAMOUS reveal feedback regulation and direct target gene activation during floral organogenesis. Advances in chromatin immunoprecipitation and protein tagging approaches have enabled in vivo identification of target genes. Overall, MADS-box transcription factors act as key integrators of gene regulatory networks, coordinating plant developmental processes. This review uniquely integrates molecular, genomic, and regulatory network perspectives of MADS-box transcription factors and highlights emerging research gaps and applications in crop improvement.

Keywords MADS-box genes; *Arabidopsis thaliana*; Transcription factors; CArG-box; Gene regulation; Floral development; Protein-protein interactions; Gene regulatory networks; Chromatin immunoprecipitation (ChIP); Plant development

1 Introduction

Transcriptional regulation is a key mechanism governing plant growth and development, mediated by transcription factors that bind specific cis-regulatory elements in target genes. Among these, the MADS-box transcription factor family represents one of the most important regulators of plant developmental processes, particularly in reproductive organ formation (Riechmann and Meyerowitz, 1997; Theissen et al., 2000). In *Arabidopsis thaliana*, MADS-box genes control diverse processes including floral transition, organ identity determination, ovule development, and fruit formation, highlighting their central role in plant developmental biology (Ng and Yanofsky, 2001; Ferrario et al., 2004).

MADS-domain proteins regulate gene expression through binding to conserved CArG-box cis-elements with the consensus sequence CC(A/T)₆ GG. However, DNA-binding specificity is not solely determined by this motif but is influenced by combinatorial interactions among transcription factors, their spatial and temporal expression patterns, and chromatin context (Shore and Sharrocks, 1995; Kaufmann et al., 2005). Despite possessing a conserved DNA-binding domain, different MADS-box proteins regulate distinct target genes, while multiple factors may act on the same regulatory regions, reflecting complex transcriptional control (de Folter and Angenent, 2006). These regulatory mechanisms are summarised in Figure 1. Importantly, these regulatory layers do not function independently. DNA-binding specificity emerges from the coordinated interplay between chromatin accessibility, higher-order MADS-box protein complex formation, cofactor recruitment, and developmental context. This integrative regulatory framework helps explain how closely related transcription factors achieve distinct developmental outputs despite recognizing similar CArG-box motifs. Furthermore, comparative studies increasingly suggest that while core regulatory principles are conserved across angiosperms, species-specific diversification of interaction networks contributes to developmental innovation in crop plants.