

and microRNAs have been implicated in post-transcriptional regulation of MADS-box genes. An important emerging concept is that transcription factor complex formation and chromatin regulation are mechanistically interconnected. MADS-box complexes may preferentially bind accessible chromatin regions, while simultaneously recruiting chromatin modifiers that reinforce transcriptional states. This reciprocal relationship likely contributes to regulatory specificity and developmental robustness. These multilayered regulatory systems ensure precise spatial and temporal gene expression during development. Advances in systems biology have enabled reconstruction of gene regulatory networks governing floral development (Chen et al., 2018). Epigenetic regulation, including chromatin modifications, plays a crucial role in modulating MADS-box gene activity. This gap highlights a broader issue in plant molecular biology: the need to move from static interaction models to dynamic, systems-level understanding. An overview of these regulatory interactions and developmental pathways is presented in Figure 3.

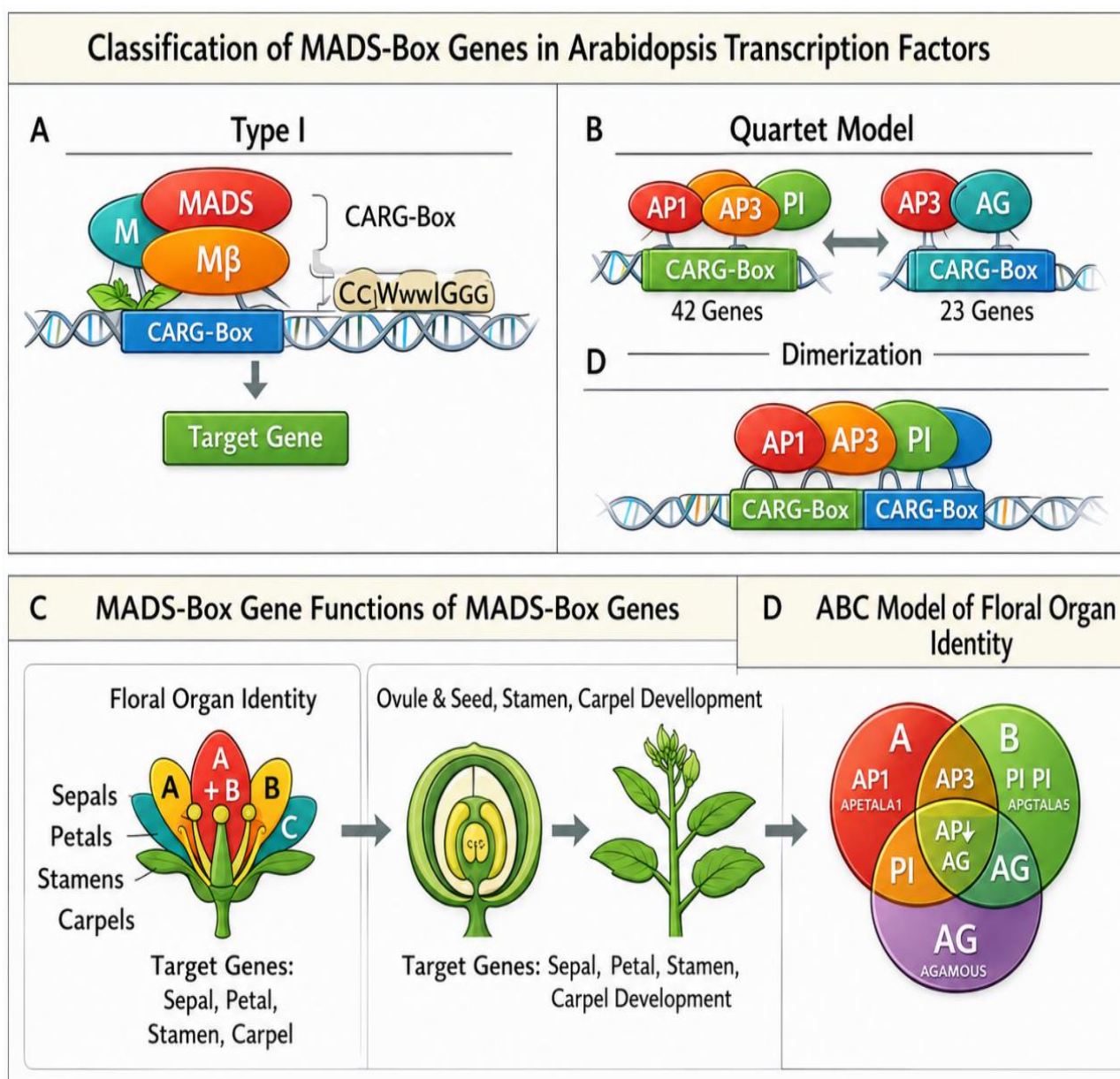


Figure 3 Regulatory roles of MADS-box transcription factors in *Arabidopsis thaliana*. MADS-box proteins bind CARG-box elements, form dimers and higher-order complexes (quartet model), and regulate floral organ identity through the ABC model, controlling key developmental processes

Importantly, these regulatory layers do not function independently but operate as an interconnected system that determines developmental specificity. The formation of distinct MADS-box transcription factor complexes influences DNA-binding selectivity, while chromatin accessibility and epigenetic modifications further determine