

Arabidopsis SEPALLATA proteins differ in cooperative DNA-binding during the formation of floral quartet-like complexes.

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Abstract

The SEPALLATA (SEP) genes of *Arabidopsis thaliana* encode MADS-domain transcription factors that specify the identity of all floral organs. The four Arabidopsis SEP genes function in a largely yet not completely redundant manner. Here, we analysed interactions of the SEP proteins with DNA. All of the proteins were capable of forming tetrameric quartet-like complexes on DNA fragments carrying two sequence elements termed CArG-boxes. Distances between the CArG-boxes for strong cooperative DNA-binding were in the range of 4-6 helical turns. However, SEP1 also bound strongly to CArG-box pairs separated by smaller or larger distances, whereas SEP2 preferred large and SEP4 preferred small inter-site distances for binding. Cooperative binding of SEP3 was comparatively weak for most of the inter-site distances tested. All SEP proteins constituted floral quartet-like complexes together with the floral homeotic proteins APETALA3 (AP3) and PISTILLATA (PI) on the target genes AP3 and SEP3. Our results suggest an important part of an explanation for why the different SEP proteins have largely, but not completely redundant functions in determining floral organ identity: they may bind to largely overlapping, but not identical sets of target genes that differ in the arrangement and spacing of the CArG-boxes in their cis-regulatory regions.

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