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Interactions and regulatory networking of MADS-domain Transcription factors in model plants (*Arabidopsis thaliana*)

The development of the different organs and segments of multicellular organisms is usually controlled by a few key regulatory transcription factors. In previous years, much has been learned about the genetic function of these regulators. However, the biochemical and biophysical basis of their activity is often only poorly understood. One intriguing example is the specification of organs within flowers. Few key transcriptional regulators govern floral organ identity. However, even though their functions have been dissected with remarkable precision at the genetic level, it is still largely unclear how these “molecular architects of the flower” interact molecularly among each other, with DNA and the basic transcriptional machinery. Recent evidence from in vitro experiments suggests that these proteins bind as tetrameric complexes cooperatively to DNA. It is likely to be of key importance for understanding their developmental role. However, compelling in planta evidence for the importance of this complex formation remains scarce. The goal of this project is to study the various interactions of transcription factors controlling floral organ identity with diverse techniques in planta at the molecular and biochemical level. Proteins defective in complex formation will be generated and characterized using transgenic techniques. The action at specific loci will be studied using in vivo footprinting.

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Start of PhD

April 26, 2010

Doctoral Disputation

February 4, 2014

