



HAL
open science

Investigating the mechanism of action of mads Tfs in Arabidopsis

Véronique Hugouvieux, Xuelei Lai, Antonin Galien, Catarina da Silva, Arnaud Stigliani, Agnès Jourdain, Jérémy Lucas, François Parcy, Chloé Zubieta

► **To cite this version:**

Véronique Hugouvieux, Xuelei Lai, Antonin Galien, Catarina da Silva, Arnaud Stigliani, et al.. Investigating the mechanism of action of mads Tfs in Arabidopsis. M2 Student Day, Sep 2019, Col de Porte, France. hal-04823902

HAL Id: hal-04823902

<https://hal.science/hal-04823902v1>

Submitted on 6 Dec 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

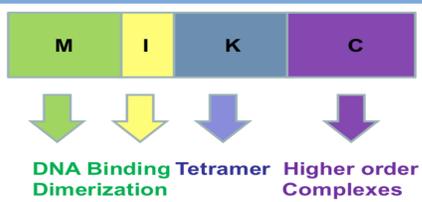
L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

INVESTIGATING THE MECHANISM OF ACTION OF MADS TFs IN ARABIDOPSIS

V. Hugouvieux, X. Lai, A. Galien, C. da Silva, A. Stigliani, J. Lucas, A. Jourdain, F. Parcy and C. Zubieta
LPCV laboratory, STRUCDEV team, contact chloe.zubieta@cea.fr, veronique.hugouvieux@cea.fr

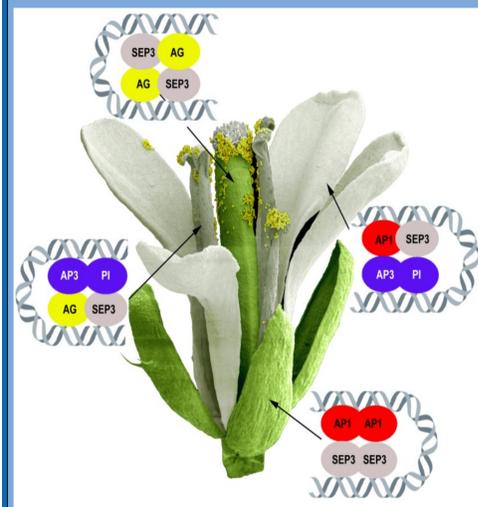
Our team uses a combination of genetics and genome wide *in vivo* and *in vitro* techniques, together with biophysics, to better understand how MADS-domain transcription factor family regulates gene expression and flower morphogenesis (see the poster of X. Lai). Here we described *in vivo* experiments performed in the lab to better understand how MADS trigger specific gene expression and organ development.

MADS-MODULAR DOMAIN STRUCTURE AND TETRAMERS FORMATION

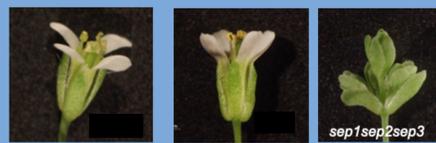


MADS TFs are comprised of four domains- M, I, K and C with different function. The M domain is highly conserved among all eucaryotes and can recognize similar DNA binding domains. Where does the specificity come from?

In the flower, the quartet model explains that MADS (AP1, AP3, PI, AG and SEP3) forms tetramers that bind to two CarG boxes cooperatively and triggers specific gene expression. SEP3 is important for the formation of all the flower organs because it belongs to each tetramers.

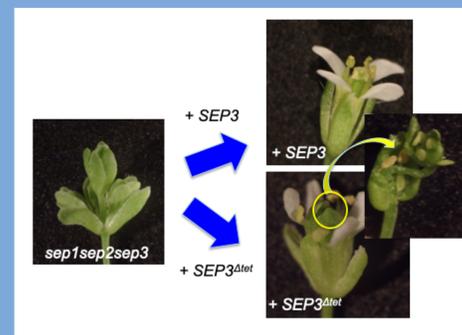


Theissen and Saedler, *Nature*, 2001



In the *sep1sep2sep3* mutant, the 4 whorls are represented by sepals and the flower is indeterminate (Pelaz *et al.*, *Nature*, 2000)

IN PLANTA EXPRESSION OF PROTEIN WITH ALTERED K DOMAIN

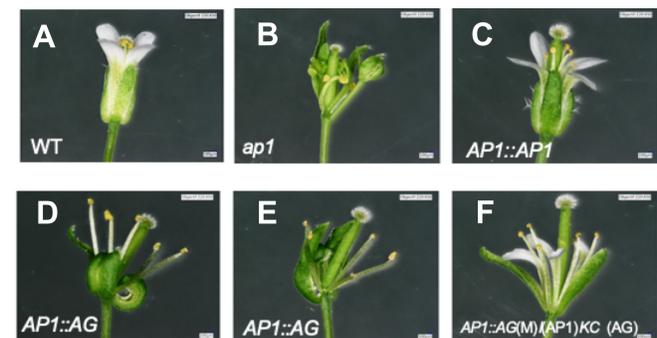


Hugouvieux *et al.*, *NAR*, 2018

K domain is a key domain for tetramer formation. What happens if we abolish tetramer formation *in vivo*? Expression of SEP3^{Δtet}, impaired in the K domain (Puranik *et al.*, *Plant Cell*, 2012), restores petals and stamen formation but not the 4th whorl neither flower determinacy, in *sep1sep2sep3* mutant.

Tetramer formation is required for carpel development and flower determinacy

IN PLANTA EXPRESSION OF CHIMERIC PROTEIN WITH DOMAIN EXCHANGE

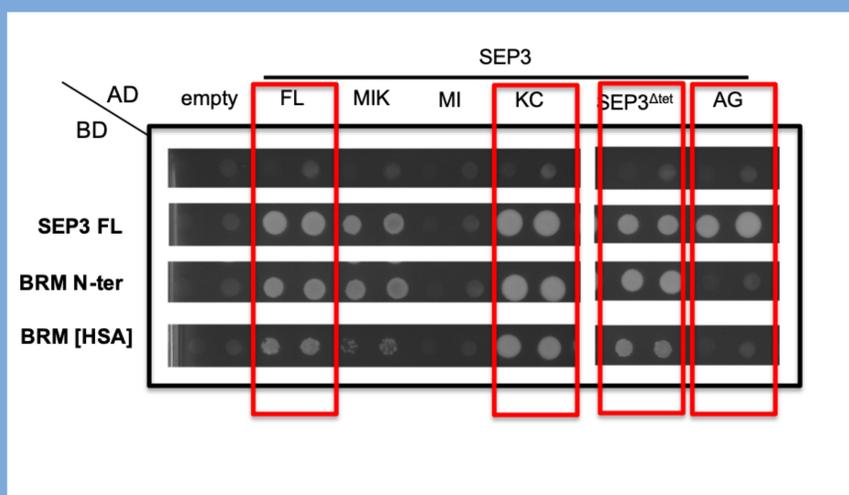


ap1 mutant (B) lacks petals in the second whorl compared to WT (A). It produces seeds because it has stamens and carpels. Expression of AP1 under the expression of its own promoter in the *ap1* mutant restores petals formation (C). AG, naturally expressed in the 3 and 4 whorls, when expressed in the first and second whorls (D-E) in *ap1* triggers unfused carpels in the first whorls and no petale in the second whorl. A chimeric version of AG with only the I domain of AP1 is able to restore petale formation (F) in *ap1*.

AP1 I domain confers AP1 activity and specificity

IDENTIFICATION OF MADS DOMAINS INTERACTING WITH CHROMATIN REMODELERS IN YEAST

SEP3 not only interacts with MADS partners but also with chromatin remodeler to open closed region of chromatin. Using yeast-two hybrids we identified that the KC domain of SEP3 interacts with the HSA domain of BRAHMA (BRM). Experiments are being done to identify with amino acids are involved in the interaction. Genetics analysis will further analyse the impact of such interaction in flower development.



In parallel, DAP-seq experiments (*in vitro*) are performed, to determine the specificity of binding to DNA of WT and mutated complexes (see the poster of X. Lai).

RNA-seq TO IDENTIFY HOW A MUTATED PROTEIN AFFECTS GENE EXPRESSION

