Integrating two patterning processes in the flower

Simon van Mourik,1,6,* Aalt D.J. van Dijk,1,2,6 Gerco C. Angenent,2,6,4,6 Roeland M.H. Merk3,5,6 and Jaap Molenaar1,6

1Biometris; Plant Sciences Group; Wageningen University and Research Center; Wageningen, The Netherlands; 2Bioscience; Plant Research International; Wageningen University and Research Center; Wageningen, The Netherlands; 3Centrum Wiskunde&Informatica; Amsterdam, The Netherlands; 4Center for BioSystems Genomics; Wageningen, The Netherlands; 5Netherlands Institute for Systems Biology; Amsterdam, The Netherlands; 6Netherlands Consortium for Systems Biology; Amsterdam, The Netherlands

Spatial organ arrangement plays an important role in flower development. The position and the identity of floral organs is influenced by various processes, in particular the expression of MADS-box transcription factors for identity and dynamics of the plant hormone auxin for positioning. We are currently integrating patterning processes of MADS and auxin into our computational models, based on interactions that are known from experiments, in order to get insight in how these define the floral body plan. The resulting computational model will help to explore hypothetical interactions between the MADS and auxin regulation networks in floral organ patterning.

The flower is a complex structure that consists of multiple tissues and organs. During flower development the fate of each cell has to be determined, and its identity has to be maintained. Spatial organ arrangement plays an important role in flower development. The bodyplan of the flower is evolutionarily highly conserved, yet between species there is a great diversity in flower forms. How many organs are formed, and at what positions, is determined via self-organized patterning mechanisms that are still poorly understood.

When plants start flowering, the shoot apical meristem is transformed into an inflorescence meristem, which goes on to produce the floral meristem, which in turn produces the sepals, petals, stamens and carpels that constitute the flower. The position and the identity of floral organs is influenced by various processes, in particular the expression of MADS-box transcription factors for identity (according to the ABC model1), and dynamics of the plant hormone auxin for positioning. Both processes have been studied using experiment-driven, mathematical models. These models can aid experimental design, for example by pointing out which process rates or concentrations should be measured in order to make a verifiable prediction.

We showed with a modeling approach that timing and positioning of initiating organs could be related to auxin accumulation patterns, governed by known auxin transport mechanisms.2 The interacting MADS genes form a gene regulatory network that has been studied previously with the help of mathematical modeling.3-5 Recently, Urbanus et al. have reported that MADS proteins are transported from cell to cell within the meristem epidermal tissue.6 Such intercellular transport suggests a role for the MADS gene network in the spatial patterning mechanisms that shape the floral meristem. To what extent such intercellular protein transport is required for laying down the spatial MADS gene expression patterns is under current investigation.7

Interactions between the MADS factors and auxin are likely to play an important role. The search for interactions between MADS genes and auxin is embedded in an active research field. This, and the ever increasing availability of quantitative experiments, will enable and require quantitative modeling in order to design and test new hypotheses on interactions. It would be particularly interesting to investigate if both patterns are formed...
sequentially or in parallel, in order to distinguish organizational hierarchy.

Modeling studies have hitherto described auxin transport and the MADS gene network independently, despite the myriad known interactions between the two patterning mechanisms. For example, recent evidence suggests interactions between the shoot-apical meristem MADS genes APETALA1 and SEPALLATA3 and the auxin-regulated transcription factors. Apart from MADS genes, examples of downstream targets of auxin that play key roles in floral organ patterning include AINTEGUMENTA and members of the AINTEGUMENTA-LIKE family. In petunia, auxin may be regulated by the FLOOZY protein, which is first expressed in the center of the floral meristem, and later on the flanks of the initiating petal and stamen primordia and at several sites in maturing stamens and carpels. In the Arabidopsis root, the PLETHORA transcription factors, which are essential for quiescent center specification and stem cell activity, are transcribed in response to auxin accumulation.

**Future Research**

We are currently integrating patterning processes of MADS and auxin into our computational models, based on interactions that are known from experiments, in order to get insight in how these define the floral body plan. Figure 1 schematically depicts such an approach in which dynamics of MADS proteins and auxin concentrations are governed by both internal processes and exchange between neighboring cells.

The resulting computational model will help explore hypothetical interactions between the MADS and auxin regulation networks in floral organ patterning. For example, it is still unknown whether MADS proteins function mainly in dimers, or in tetramers, or even higher order complexes. In the new modeling framework these alternative scenarios concerning protein-protein interactions will be studied. Similarly, the fast increasing amount of ChIP-seq data will indicate putative novel regulatory connections between MADS genes as well as between MADS genes and genes related in auxin dynamics. Regarding auxin transport mechanisms, both flux-based and concentration-based transport still form valid hypotheses. New experimental data on auxin transport and MADS gene dynamics will progressively validate and fine-tune this model. Ultimately, unraveling the mechanisms that constitute floral patterning is a fundamental question in developmental biology and evolutionary biology that is key to explaining the staggering diversity of flower patterns and forms in nature.

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**References**


![Figure 1. The concentration dynamics of MADS proteins and auxin concentrations are governed by both internal processes and transport between adjacent cells. The question how identity determination by MADS proteins and organ primordia positioning are coupled at the molecular level, is the topic of recently started research.](image-url)
