# A Multicellular Model of a Feedback Network Regulating Spatial Gene Expression Domains in the Shoot Apical Meristem

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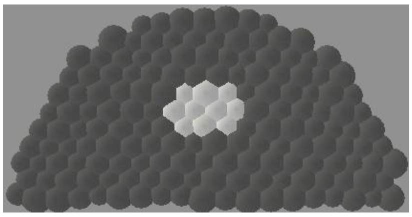
Development and growth of a postembryonic plant is mainly regulated by the *Shoot apical meristem* (SAM). Different gene expression patterns can be used to define subregions within the SAM. Although individual cells move in and out of these subregions, their spatial locations and sizes stay remarkably constant over time. The dynamical regulation of the sub-regions is to a large degree unknown, although a feedback network including the CLAVATA3 and WUSCHEL genes has recently been explored[1]. CLV3 is expressed in a small domain at the very apex, and WUS is expressed in a few cells, immediately beneath the CLV3 region.

We are developing a simulation–experimental setup which will allow us to compare multicellular models with expression patterns in living plants using protein-GFP fusions[2]. The models allow for cell growth and proliferation, gene regulation within cells, and signalling and molecular transportation between cells. In previous work we have presented a model which generates the correct CLV3 expression domain, as long as the WUS region is correctly initiated[3]. In this study, we investigate possible models to generate a dynamically stable WUS domain (see Figure). This also allows us to investigate the dynamics of the feedback network between the CLV3 and WUS regions, which is essential for the regulation of the SAM, and thereby the development of the complete plant.



Result of a simulation generating a dynamically stable WUS expression region. In the vertical section of the SAM, the bright cells represent the generated WUS region. An activator-inhibitor type of model is used, where the activator induces WUS expression. Degradation of the activator by a signal from the epidermis stabilizes the WUS expression to the central region.

## References and Acknowledgements

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