# Interpreting noise in stem cell regulation in the shoot apical meristem of *Arabidopsis thaliana*



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#### **Declaration**

I hereby declare that except where specific reference is made to the work of others, the contents of this dissertation are original and have not been submitted in whole or in part for consideration for any other degree or qualification in this, or any other university. This dissertation is my own work and contains nothing which is the outcome of work done in collaboration with others, except as specified in the text and Acknowledgements. This dissertation contains fewer than 65,000 words including appendices, bibliography, footnotes, tables and equations and has fewer than 150 figures.

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### **Abstract**

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## List of tables

## Nomenclature

#### **Acronyms / Abbreviations**

CLV3 CLAVATA-3

CZ Central zone

KAN1 KANADI-1

SAM Shoot Apical Meristem

WUS WUSCHEL

## Introduction

#### 1.1 The Shoot Apical Meristem of Arabidopsis thaliana

Plant stem cells are governed by two developing centra – the Shoot Apical Meristem (SAM) and the Root Apical Meristem (RAM). The SAM is the region responsible for development of all aerial organs in the plant, which includes aspects of cell proliferation and specification, as well as an ability of the plant to maintain and regulate the stem cell identity of the cells at the very apex of the shoot. **ADD CITATION**As opposed to the RAM, which has two stem cell pools in the inside of the root, the SAM maintains a single stem cell pool centered at the apex. It also lacks the root's cap, which protects the stem cells on the inside of the root, whereas these in the shoot are directly exposed to the plant's surroundings.

The stem cells at the SAM contribute to the construction of new organs and general tissue by dividing frequently at the top and subsequently being mechanically pushed out of the center in order to differentiate. The steady maintenance of the stem cell niche allows for a constant production and supply of cells that the plant utilises during both growth and repair of damaged tissue. **ADD CITATION** 

In a simple outline of the SAM, it can be said to consist of three core regions: 1. The *central zone* (CZ), which harbors the aerial *stem cell niche* of the plant; 2. The *Rib Meristem*, which is located beneath the CZ and consists of the cells constructing the stem of the plant; 3. The *Peripheral Zone* (PZ), where cells form organs and new tissue through differentiation. In addition to these regions, the SAM is also often separated into the different layers of the dermis, denoted *L1* for the epidermal layer, *L2* for the sub-epidermal one, and *L3* for the inner ground and vascular tissues. For cells in both L1 and L2, proliferation happens orthogonally to the shoot surface, i.e. so that cell lineages are preserved within L1 or L2 correspondingly. In contrast, this is not the case for L3, where cells can divide in all directions. In addition, it has been shown that the epidermis is involved in both promoting and restricting shoot development, adding to the notion of coordination and regulation between the different cell layers in order to accurately direct plant growth.

2 Introduction

#### 1.2 Modelling Biological Systems

Due to the interaction of molecules in various ways, e.g. the activation or repression of transcription by certain proteins, organismal development can be considered in the framework of being a *complex system*. In a *systems biology* setting, molecular and mechanical interactions are treated as abstract entities, each representing some fundamental part of the whole system in question, much like how machinery can be explained by its separate cogs and gears working together. In a molecular setting, the typical descriptive approach is through *Gene Regulatory Networks* (GRNs), where each component represents some molecular aspect of the system that is involved in producing expression levels of mRNA and proteins. **ADD CITATION** 

GRNs are commonly understood both through analytical and computational means, where in the latter computer-generated models provides as a modern tool for better understand the complex nature of many biological systems. Typically, reaction kinetics are modelled using various types of *Ordinary Differential Equations* (ODEs). However, due to the large supplies of computer power available in the modern day, many recent studies also utilise more computationally demanding resources such as *Stochastic Differential Equations* (SDEs), where also the inherently random nature of molecular motions, interactions, and processes are accounted for. The increase in computability has also allowed for the development of spatiotemporal modelling, where models are evaluated not only in a static context, but also in a changing setting. A straightforward example taken directly out of the context of plant development is how the distribution of gene expression varies during plant growth and organ formation, both spatially and over time. Typical modelling aspects at such a problem case involves the formulation of which genes and molecules are imporant for the problem of interest, as well as how the discretisation and representation of spatial elements is done. **ADD CITATION** 

Computer models in general have two separate aims: exploration and verification. In the former case, computer simulations can be the core for designing experimental experiments, where observed theoretical phenomena can be experimentally tested. An example of this is the classic example of the *Repressilator* **ADD CITATION**, where researchers set up a model framework for how oscillations could occur due to cyclic repressive interactions between three genes. This was then verified to occur by synthetically implementing the system in a bacterium, showing how gene expression profiles could oscillate due to the system motif constructed.

In the latter case, which is the more prevalent in modern computational biology, computer models are established in order to verify or support the potential of an hypothesis due to experimental observations. **ADD CITATION** 

#### 1.3 Regulatory Mechanics of Plant Stem Cells

In order for the plant to undergo phyllotaxis in the correct manner, and to know when and where to initiate new organs – primordia – patterning of various types play an important role. In particular genetic and molecular patterning due to hormones, proteins and gene expression are known to be

essential parts in understanding plant development, although also patterns of stress and strain have in recent studies been shown to play a role in determining growth. **ADD CITATION** 

#### 1.3.1 The role of WUSCHEL-CLAVATA interactions

## Methodology

#### 2.1 Describe the data here

The Yellow Fluorescent Protein (YFP) marker for the plasma membrane was amplified using PCR with primers attb1-mYfwd (5'-AGAAAGCTGGGTTTACTTGTACAGCTCGTCCATGCCGAGAGTG) and attb2-YFPrev (5'-AGAAAGCTGGGTTTACTTGTACAGCTCGTCCATGCCGAGAGTG), with the forward primer sequence containing a motif known to acetylate in plant cells CITEHERE. 50 μL solution was amplified in 96 °C for 1 minute, followed by 25 cycles of 96 °C for 30 seconds, and a final elongation for 30 seconds. 5 μL of the result was then used in a second reaction consisting of 40 μL solution in total, with primers B1 adapt (5'-GGGGACAAGTTTGTACAAAAAAGCAGGCT) and B2 adapt (5'-GGGGACCACTTTGTACAAGAAAGCTGGGT) included. Similar to the first solution, the second mixture was amplified by PCR in 95 °C for 2 minutes, followed by 94 °C for 30 seconds, 48 °C for 30 seconds, and 72 °C for 1 minute, 20 cycles of 94 °C for 30 seconds, 55 °C for 30 seconds, and 72 °C for 1 minute. Finally, elongation took place under 72 °C for 1 minute.

6 Methodology

- 2.2 Describe the processing of the data here
- 2.3 Mathematical formulation of molecular interactions
- 2.3.1 Numerically solving stochastic systems
- 2.4 Organism
- 2.5 Models of Gene Regulatory Networks
- 2.6 Epidermal Model
- 2.7 Internal Model

## Results

- 3.1 Derivations?
- 3.2 Simulations and stuff

## **Discussion**

- 4.1 This does that. Why?
- 4.2 Because.

## References

# **Appendix A**

# How to install LATEX

All makt åt Tengil, vår befriare

# **Appendix B**

This is an appendix